

Figure S1.1: Sequence alignment and tertiary structure for gene *pdxA*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0052; PDB ID: 1ps6; chain ID: A

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-----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
E_coli_K12 -----MVKTORVVIIPGEPAGIGPDLVVLAQREWPVELVVCADATLLTNRRAAMLGPLTLRPPSPNSPAQPCTAGILTLPLVALRRAAPVTAQOLAV
E_coli_CFT073 -----MVKTORVVIIPGEPAGIGPDLVVLAQREWPVELVVCADATLLTDRRAAMLGPLTLRPPSPNSPAQPCTAGILTLPLVALRESVTVGQLAV
S_enterica_CT18 -----MSSAQRVVIIPGEPAGIGPDLVVLAQRAWPIELVVCADGALLTERAAMLGPLTLRPPSPDVPAAPOGAGILTLPLPVSLRAPAIIPGQLTIV
S_enterica_Ty2 -----MSSAQRVVIIPGEPAGIGPDLVVLAQRAWPIELVVCADGALLTERAAMLGPLTLRPPSPDVPAAPOGAGILTLPLPVSLRAPAIIPGQLTIV
S_boydii -----MVKTQRVVIIPGEPAGIGPDLVVLAQREWPVELVVCADATLLTDRAAMLGPLTLRPPSPNSPAQPCTAGILTLPLVALRESVTAGOLAV
S_dyssenteriae -----MVKTQRVVIIPGEPAGIGPDLVVLAQREWPVELVVCADATLLTDRAAMLGPLTLRPPSPNSPAQPCTAGILTLPLVALRESVTAGOLAV
P_luminescens -----MATMHNNKPLIIINKPVVIIPGEPAGVGPDPLVLAQSQWPMQPLVACADPNLIDRARQNLPLQOEYSAKTPPEAQAGILTLILPVPLHVPAIAGELNQ
Y pestis -----MHNHNNRLVITPGEPAVGVPGLAITLACQGPWPLVLEVVVCADPALLARASQNLNPLQREYQADQFAIAQAGELTLILPVKTAVVNVPGKLDV
A_ferrooxidans -----MITEPRLLLIVGEPAIGIGPDICLQAFHALPSGVLLIGDLHCLRSRALTLGLSLRLEPWLEGNPWPALERGVHLVLDVPLAQPCRGRLDW
L_pneumophila -----MNFLILISGEPAGIGPDLCLALAETDLP--VVILGDSLSEEARASENLNSIKEYESHSQSFEXXAGYLTVWVPCAEPPVISQELNP
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100
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XXXXX-
E_coli_K12 ENGHYVVEILARACDGCLNGEFAALITGPVHKGVINDAGIPPTGHTEFFFEERSQAKKVVVMLATEELRVALAATHLPLRDIAADAIIPALLEHEVIAILHH
E_coli_CFT073 ENGHYVVEILARACDGCLNGEFAALITGPVHKGVINDAGIPPTGHTEFFFEERSQAKKVVVMLATEELRVALAATHLPLRDIAADAIIPALLEHEVIAILHH
S_enterica_CT18 ENGPYVVEILARACDGCLNGEFAALITGPVHKGVINDAGIPPTGHTEFFFEERSQAKKVVVMLATEELRVALAATHLPLRDIAADAIIPALLEHEVIAILHH
S_enterica_Ty2 ENGPYVVEILARACDGCLNGEFAALITGPVHKGVINDAGIPPTGHTEFFFEERSQAKKVVVMLATEELRVALAATHLPLRDIAADAIIPALLEHEVIAILHH
S_boydii ENGHYVVEILARACDGCLNGEFAALITGPVHKGVINDAGIPPTGHTEFFFEERSQAKKVVVMLATEELRVALAATHLPLRDIAADAIIPALLEHEVIAILHH
S_dyssenteriae ENGHYVVEILARACDGCLNGEFAALITGPVHKGVINDAGIPPTGHTEFFFEERSRACKKVVVMLATEELRVALAATHLPLRDIAADAIIPALLEHEVIAILHH
P_luminescens ENGRYVVEILAQACDGCLNGEFSALVTGPVHKGVINDAGIPPTGHTEFFFADRSGCORVVMMLATEELRVALAATHLPLIVDVFKSITFDSLREVITLHNH
Y pestis GNSHYVVEILAKACDGAISGEFAALITGPVQKSIINDAGIPPTGHTEFFFADRSHCORVVMMLATEELRVALAATHLPLLAQVAAVHQEGLEGTRILRHLRA
A_ferrooxidans ANAPAVLATLDDKAMHLLRAGAADALVTPVHKGIDNDAGIPPTGHTEYLAACGSPKVVMMLAGRLRVALAATHLPLAQVAAVHQEGLEGTRILRHLRA
L_pneumophila RRAAYVMEILLGASLCSKGEFSALVTGPVHKANIAAGITFTGHTEFFFADPFEVETVVMMLACSQMKVAPVTTTHLPLRMVPDTISILLIVVKVIQQLHHS
ruler .....110.....120.....130.....140.....150.....160.....170.....180.....190.....200
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E_coli_CFT073 LRTKFGIAEPRILVCGLNPHAGEGGHMGEEDIDTIIPVNLNEQGMKLNGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
S_enterica_CT18 LRTKFGIAEPRILVCGLNPHAGEGGHMGEEDIDTIIPVLDLRAQGMKLNGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
S_enterica_Ty2 LRTKFGIAEPRILVCGLNPHAGEGGHMGEEDIDTIIPVLDLRAQGMILNGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
S_boydii LRTKFGIAEPRILVCGLNPHAGEGGHMGEEDIDTIIPVLDLRAQGMILNGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
S_dyssenteriae LRTKFGIAEPRILVCGLNPHAGEGGHMGEEDIDTIIPVLDLRAQGMILNGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
P_luminescens LRTKFGIAEPRILVCGLNPHAGEGGHMGEEDIDTIIPVLDLRAQGMILNGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
Y pestis LRTKFGITOPQIYVCGLNPHAGEGGHMGEEDIDTIIPALNTLQQQGINLIGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYQGFGRGVNIITLGLPFI
A_ferrooxidans LREDFALSEPRILVAGLNPHAGEGGHMGHEEEIDTIIPALNTLQQQGINLIGPLPADTLEOPKYLDNADAVLAMYHDQGLPVLKYHAFGEAVNIITLGLPIV
L_pneumophila LKHDFGIQSPRINVAGLNPHAGESGYLGREEEIDTIIPALNTLKNQGIDVQGPLPADTMITTNHINHCDAYVAMYHDQGLPVLKYAGFNEAVNIITLGLPII
ruler .....210.....220.....230.....240.....250.....260.....270.....280.....290.....300
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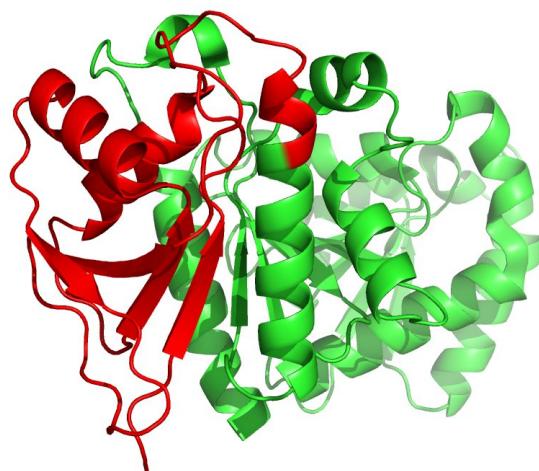


Figure S1.2: Sequence alignment and tertiary structure for gene *acnB*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0118; PDB ID: 1l5j; chain ID: A

<i>E_coli_K12</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>E_coli_CFT073</i>	MLLFCKQINTSSSKSCYSARGTGHLPYKLLSHRSVKRIACRTMTMRARR	VVLLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>S_enterica_CT18</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>S_enterica_Ty2</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>S_boydii</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>S_dyssenteriae</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>P_luminescens</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
<i>Y_pestis</i>	-----	VLEEYRKHVAERAEEGIAAPKPLDANQMAALVELLKNNPPAGEEEEFLDDLL
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100	
 XXXXXXXXX-----		
<i>E_coli_K12</i>	TNRVPPGVDEAAVVKAGFLAIAIAKGEAKSPLLIPEKAIELLCTMOGGYNINHPLIDALDAKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNEYAKQVMQS	
<i>E_coli_CFT073</i>	TNRVPPGVDEAAVVKAGFLAIAVAKGEAKSPLLIPEKAIELLCTMOGGYNINHPLIDALDAKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNEYAKQVMQS	
<i>S_enterica_CT18</i>	INRVPNGVDEAAVVKAGFLAAVAKGDTTSPLVSPKEKAIELLCTMOGGYNINHPLIDALDAKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNEYAKQVMQS	
<i>S_enterica_Ty2</i>	INRVPNGVDEAAVVKAGFLAAVAKGDTTSPLVSPKEKAIELLCTMOGGYNINHPLIDALDAKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNEYAKQVMQS	
<i>S_boydii</i>	INRVPNGVDEAAVVKAGFLAAIAKGEAKSPLLIPEKAIELLCTMOGGYNINHPLIDALDAKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNEYAKQVMQS	
<i>S_dyssenteriae</i>	INRIPPGVDEAAVVKAGFLAAIVKDETISPLITPEKAVELLCITMOGGYNINHPLIDALNEKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNEYAKQIMQS	
<i>P_luminescens</i>	INRIPPGVDEAAVVKAGFLAAIAKGEAKSPLLIPEKAIELLCTMOGGYNINHPLIDALNEKLAPIAAAKALSHILLMMFDNFYDVVEEKAKAGNPQAKQIMQS	
<i>Y_pestis</i>	TNRVPPGVDEAAVVKAGFLAIAIAKGEAKSPLLIPEKAIELLCTMOGGYNINHPLIDALNEKLAPIAAAKALSHILLMMFDNFYDVVEDKAKAGNPYAKQIIQS	
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200	

<i>E_coli_K12</i>	WADAENFLNRPALAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEALQQKGFPPLAYGVVVGTGSSRKSA	
<i>E_coli_CFT073</i>	WADAENFLNRPALAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEALQQKGFPPLAYGVVVGTGSSRKSA	
<i>S_enterica_CT18</i>	WADAENFLSRPPLAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEALQQKGFPPLAYGVVVGTGSSRKSA	
<i>S_enterica_Ty2</i>	WADAENFLSRPPLAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEALQQKGFPPLAYGVVVGTGSSRKSA	
<i>S_boydii</i>	WADAENFLSRPPLAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEALQQKGFPPLAYGVVVGTGSSRKSA	
<i>S_dyssenteriae</i>	WADAENFLNRPALAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEALQQKGFPPLAYGVVVGTGSSRKSA	
<i>P_luminescens</i>	WADAENFLSRPPLAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEPDQPGVVGPPIKQIEELNKKGFPPLAYGVVVGTGSSRKSA	
<i>Y_pestis</i>	WADAENFLSRPPLAELKLTIVVFKVIGETNTDDLSPADWSRPDIPLHALAMLKNAREGIEHPDQPGSVGPPIKQIEELNKKGFPPLAYGVVVGTGSSRKSA	
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300	

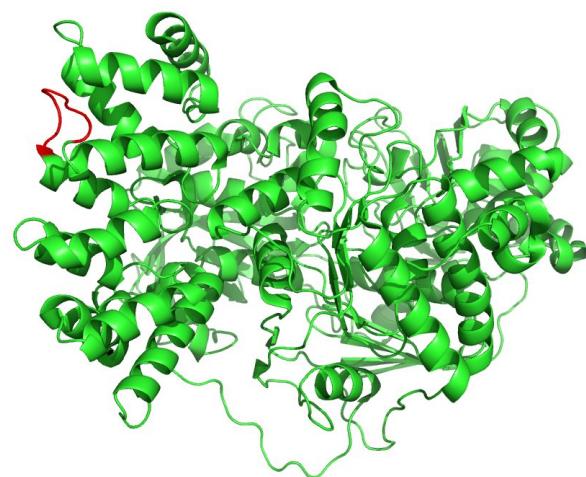


Figure S1.3: Sequence alignment and tertiary structure for gene *btuF*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0158; PDB ID: 1n2z; chain ID: A

<i>E_coli</i> _K12	MAKSLEFRALVALSFLAPLWLNAAP--RVITLSPANTELAFAAGITP--VGVSYSIDYPPQAQKIEQVSTWOGMNLIERIVALKPDLVIAWRGGNAER
<i>E_coli</i> _CFT073	MAKSLEFRALVALSFLAPLWLNAAP--RVITLSPANTELAFAAGITP--VGVSYSIDYPPQAQKIEQVSTWOGMNLIERIVALKPDLVIAWRGGNAER
<i>S_enterica</i> _CT18	MAKQMFRALGALLTLPVWLHYAAP--RVITLSPANTELAFAAEITP--VGVSYSIDYPPQAQKIEQVSTWOGMNLIERIVALKPDLVIAWRGGNAER
<i>S_enterica</i> _Ty2	MAKQMFRALGALLTLPVWLHYAAP--RVITLSPANTELAFAAEITP--VGVSYSIDYPPQAQKIEQVSTWOGMNLIERIVALKPDLVIAWRGGNAER
<i>S_boydii</i>	MAKSLEFRALVALSFLAPLWLNAAP--RVITLSPANTELAFAAGITP--VGVSYSIDYPPQAQKIEQVSTWOGMNLIERIVALKPDLVIAWRGGNAER
<i>S_dyenteriae</i>	MAKSLEFRALVALSFLAPLWLNAAP--RVITLSPANTELAFAAGITP--VGVSYSIDYPPQAQKIEQVSTWOGMNLIERIVALKPDLVIAWRGGNAER
<i>P_luminescens</i>	MKWIKSIGSICLSLLLFLSSFSHSLYAAPLRVISLSPSTTELAYAAGLGDNLIAASAYSIDYPPQARKLEQAVANWOGINLERIITLKPPELLAWRGGNPQR
<i>Y pestis</i>	MMPLGLFLPLPRAAAVLLISLLTLPAQAAE--RVISLSPSTTELAYAAGLGDKLVAVASAYSDYPEAKKLBHVATWOGINVERILALKPDLIARWGGNPQR
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

<i>E_coli</i> _K12	QVDOLASLGIKVMWWDATSIEQIANALRQLAPWSPOPDKAEQAAQSLLDQYAQCLAQYADKPKKRVRVFLQFGINPPFTSGKEIQNQVLEVCGGENIFKD
<i>E_coli</i> _CFT073	QVDOLASLGIKVMWWDATSIEQIANALRQLAPWSPOPDKAEQAAQSLLDQYAQCLAQYADKPKKRVRVFLQFGINPPFTSGKEIQNQVLEVCGGENIFKD
<i>S_enterica</i> _CT18	QVNQLTSLGIKVMWWDAVIEQIAQDALRQLAAWSPQPEKAQAAQSLLDQYAQCLAQYADKPKKRVRVFLQFGINPPFTSGKEIQHQLITTCGGENVFADS
<i>S_enterica</i> _Ty2	QVNQLTSLGIKVMWWDAVIEQIAQDALRQLAAWSPQPEKAQAAQSLLDQYAQCLAQYADKPKKRVRVFLQFGINPPFTSGKEIQHQLITTCGGENVFADS
<i>S_boydii</i>	QVDOLASPGIJKVMWWDATSIEQIANALRQLAPWSPOPDKAEQAAQSLLDQYAQCLAQYADKPKKRVRVFLQFGINPPFTSGKEIQNQVLEVCGGENIFKD
<i>S_dyenteriae</i>	QVDOLASLGIKVMWWDATSIEQIANALRQLAPWSPOPDKAEQAAQSLLDQYAQCLAQYADKPKKRVRVFLQFGINPPFTSGKEIQNQVLEVCGGENIFKD
<i>P_luminescens</i>	PLEQOLAAGFIKIFYSDPTTIEQIAQDLERLAEGSPHPQAKKSATELRQRFANLQQYATTIPKPAFLQFGTYPLFTTSQGQILOSEVLSICGGRNIFADS
<i>Y pestis</i>	PUDOLAALGIPIFYSDPTTHIDQIASDLDKLQAQYSPHPQAHQAEQFRQHVNTRLDYARSQPKRTFLQFGIOPLFSTSGLQLOSEEVSSLCGGENIFADS
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

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<i>E_coli</i> _K12	RVPWPQVSREQVLARSPQAIVITGGPDQIPKIKOYWGEQOLKIPVPIPLTSDFERASPRIILAAQCLCNALSQVD-----
<i>E_coli</i> _CFT073	RVPWPQVSREQVLARSPQAIVITGGPDQIPKIKOYWGEQOLKIPVPIPLTSDFERASPRIILAAQCLCNALSQVD-----
<i>S_enterica</i> _CT18	RVPWPQVSREQVLARHPQAIIVVAGKAGEILKIEQYWGNLLKIPVPIPLNSDWFERASPRIILAAQCLCNALSQVN-----
<i>S_enterica</i> _Ty2	RVPWPQVSREQVLARHPQAIIVVAGKAGEILKIEQYWGNLLKIPVPIPLNSDWFERASPRIILAAQCLCNALSQVN-----
<i>S_boydii</i>	RVPWPQVSREQVLARSPQAIVITGGPDQIPKIKOYWGEQOLKIPVPIPLTSDFDVQAH--VLSSLNNSVMRFIR-----
<i>S_dyenteriae</i>	RVPWPQVSREQVLARSPQAIVITGGPDQIPKIKOYWGEQOLKIPVPIPLTSDFERASPRIILAAQCLCNALSQVD-----
<i>P_luminescens</i>	FVFPWPQVSREQVLIRKPEIIVISGGQEIVKLIEWFHWFOLRAKVITLHEDWFHFRAGPRIILAAQCLCQLNDNGS-----
<i>Y pestis</i>	RVPWPQVSREQVMTRKPOVIVVGTQSIVDNVSAFWLQLVVPVIALNEDWFNRASPRILLAAQCLCQOMASIPTPVAESH-----
ruler210.....220.....230.....240.....250.....260.....270.....280.

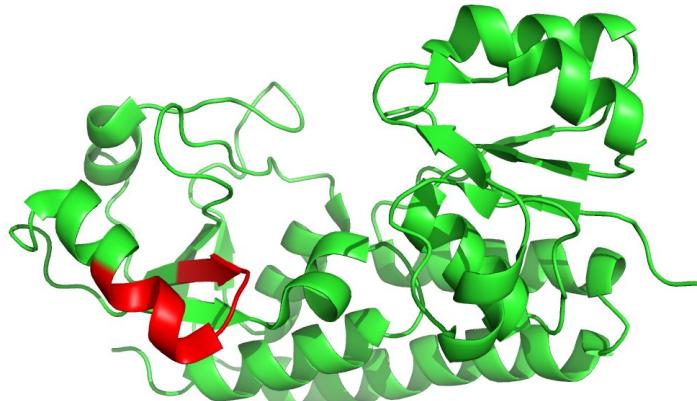


Figure S1.4: Sequence alignment and tertiary structure for gene *map*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0168; PDB ID: 2gg2; chain ID: A

<i>E_coli</i> _K12	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVSTGELDRICNDYIVNEQHAVSACLG _H -----	GYPKSVCISINEVVCHGIPDDAK
<i>E_coli</i> _CFT073	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVSTGELDRICNDYIVNEQHAVSACLG _H -----	GYPKSVCISINEVVCHGIPDDAK
<i>S_enterica</i> _CT18	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVTTGELDRICNDYIVNEQHAISACLG _H -----	GYPKSVCISINEVVCHGIPDDAK
<i>S_enterica</i> _Ty2	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVTTGELDRICNDYIVNEQHAISACLG _H -----	GYPKSVCISINEVVCHGIPDDAK
<i>S_bordetii</i>	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVSTGELDRICNDYIVNEQHAISACLG _H -----	GYPKSVCISINEVVCHGIPDDAK
<i>S_dyenteriae</i>	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVSTGELDRICNDYIVNEQHAVSACLG _H -----	GYPKSVCISINEVVCHGIPDDAK
<i>P_luminescens</i>	-----MAISIKI _N SEDIEKKMRVAGRLAAEVLEMI _E PPVVKPGVTTGELDRICNDYIVNEQHAVSACLG _H -----	GFPKSVCISVNDDVCHGIPSDDK
<i>Y_pestis</i>	-----MAISIKI _N PEDIEEKMRVAGRLAAEVLEMI _E PPVVKPGVTTGELDRICNDYIVNEQHAISACLG _H -----	GFPKSVCISVNVEICHGIPSDEK
<i>B_aphidicola</i>	MTCIFIKNNEINKMRVLVGKLVADVLDMIKEYIVPGITTEELNNICHNYITYKQHAKPACLG _Y -----	GFPKSICTSINDIVCHGIPNKNs
<i>A_ferrooxidans</i>	MLQRSKNSPOGSIKKAEVEEKMRVAGRLAAMVLMKMGHEVKAGVTIDELDRICHDYIVNDLQGIPAPLHYQPSP _E YPPFPKSVCI _S LNVHVICHGIPG _E R	
<i>L_pneumophila</i>	-MGVI _N KIPDEIEKMRVAGRLAAEVLEMI _E PPVVKPGVTTGELNTICHDYIVNVOKAIPALN _N N-----	GFPKSICTSINHVVCHGIPGK-K
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100	

<i>E_coli</i> _K12	LLKDGDIVNIDVTVIKDGPFHGDTSKMFIVGKP _T IMGERLCRITOESLYLALRMVKPGINLREIGAAIDKFVEAEGF-----	VVREYCGHGIGRGFHEEPQVLHY
<i>E_coli</i> _CFT073	LLKDGDIVNIDVTVIKDGPFHGDTSKMFIVGKP _T IMGERLCRITOESLYLALRMVKPGINLREIGAAIDKFVEAEGF-----	VVREYCGHGIGRGFHEEPQVLHY
<i>S_enterica</i> _CT18	LLKDGDIVNIDVTVIKDEFHGDTSKMFIVGKP _T ILGERLCRVTSYLYLGIKMVKPGIRLRTIGAAIDKFVEAEGF-----	VVREYCGHGIGRGFHEEPQVLHY
<i>S_enterica</i> _Ty2	LLKDGDIVNIDVTVIKDEFHGDTSKMFIVGKP _T ILGERLCRVTSYLYLGIKMVKPGIRLRTIGAAIDKFVEAEGF-----	VVREYCGHGIGRGFHEEPQVLHY
<i>S_bordetii</i>	LLKDGDIVNIDVTVIKDGPFHGDTSKMFIVGKP _T IMGERLCRITOESLYLALRMVKPGINLREIGAAIDKFVEAEGF-----	VVREYCGHGIGRGFHEEPQVLHY
<i>S_dyenteriae</i>	LLKDGDIVNIDVTVIKDGPFHGDTSKMFIVGKP _T IMGERLCRITOESLYLALRMVKPGINLREIGAAIDKFVEAEGF-----	VVREYCGHGIGRGFHEEPQVLHY
<i>P_luminescens</i>	LLKDGDIVNIDVTVIKEFGFHGDTSKMFIVGKP _T IQGERLCRITOESLYLALKMVKPGIRLRTLGRAIQDFVEANDF-----	VVREYCGHGIGAGFHEEPQVLHY
<i>Y_pestis</i>	VLKEGDIVNIDVTVIKDGPFHGDTSKMFIVGKP _T ILGERLCRITOESLYLALKMVKPGIRLRTLGRAIQDFVEANDF-----	VVREYCGHGIGAGFHEEPQVLHY
<i>B_aphidicola</i>	VLDGDIVNIDVTVIKDGPFHGDTSKMFIVGKP _T ILGERLCRITOESLYLALKMVKPGIRLRTLGRAIQDFVEANDF-----	VVREYCGHGIGAGFHEEPQVLHY
<i>A_ferrooxidans</i>	VIRDGDMLNIDVTVIKDGPHGDSSKMFIVGEVPLRSRRVMVAHEAMVRGIQQVRPGATLGDIGHAI _S YAEAQHC _S IVREFCGHGIGRKFHDEPQVLHY	
<i>L_pneumophila</i>	LLKDGDIVNIDVTVIKNEYHGDTSKMFIVGTP _S VKAHV _N TAHECLYIGIDMVKPGVQLG _I GHAIQHAEKNRC _S VVRDVCGHGIGRVPHEDPQVLHY	
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200	

<i>E_coli</i> _K12	-X-XXXX-	
<i>E_coli</i> _CFT073	DS-REI _N VVLKPGMIFTIIEPMVNAGKKEIRTMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIL _N LRKDDT-----	IPAIISHDE
<i>S_enterica</i> _CT18	DS-REI _N VVLKPGMIFTIIEPMVNAGKKEIRTMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIL _N LRKDDT-----	IPAIISHDE
<i>S_enterica</i> _Ty2	DA-DDGGVVLQPGMTFTIIEPMLNAGDYIRITMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIL _N LRKDDT-----	IPAIITHDE
<i>S_bordetii</i>	DS-REI _N VVLKPGMIFTIIEPMVNAGKKEIRTMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIL _N LRKDDT-----	IPAIISHDE
<i>S_dyenteriae</i>	DS-REI _N VVLKPGMIFTIIEPMVNAGKKEIRTMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIL _N LRKDDT-----	IPAIISHDE
<i>P_luminescens</i>	DA-DDGGVVLQPGMTFTIIEPMLNAGDYIRITMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIM _N LRKDDT-----	EPALSSVLVNE
<i>Y_pestis</i>	DA-DDGGVVLQAGMAFTIIEPMVNAGDYIRITMKDGWIVKTKDRSLSAQYEHTIVVIDNGCEIM _N LRKDDT-----	IPNII _N THE
<i>B_aphidicola</i>	NY _N KSNTTILQSGMTFTIIEPMVNAGKRYIKA _N LDGWIVVTKDHSASAOWEETILVDDG _N GEIEL _N QLPGD _N P-----	ISRLIKNL _N T
<i>A_ferrooxidans</i>	GN-PGBGIELVPGMTFTIIEPMVNAGKRYIKA _N LDGWIVVTKDHSASAOWEETILVDDG _N GEIEL _N QLPGD _N P-----	
<i>L_pneumophila</i>	GV-PG _N GMRL _N PGMTFTIIEPMVNAGKHH _N RLLPDHWIVVTKDHSASAOWEETLLVDTG _N GEIEL _N QLPGD _N P-----	
ruler210.....220.....230.....240.....250.....260.....270.....280.	

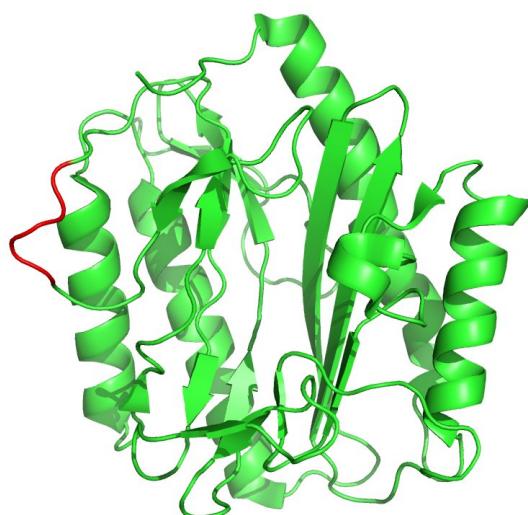


Figure S1.5: Sequence alignment and tertiary structure for gene *ispU*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0174; PDB ID: 1x06; chain ID: A

	VMLSATOPLSKEKLPAPHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>E.coli_K12</i>	VMLSATOPLSKEKLPAPHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>E.coli_CFT073</i>	VMLSATQPVSSENLPAPAHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>S.enterica_Ct18</i>	-MLSATQPVSSENLPAPAHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>S.enterica_Ty2</i>	-MLSATQPVSSENLPAPAHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>S.boydii</i>	-VMLSATQPVSSENLPAPAHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>S.dysenteriae</i>	-VMLSATQPVSSENLPAPAHGCRHVAIIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPAQEVSALMELFVWAI
<i>P.luminescens</i>	-VILSSDHHQNDLSSLLPK--HVAIIIMDGNGRWAKKRGKLRAGIKAVRSASVSFKAKHNIESTLYAFSSENWNRPEEVSLMELFIFAL
<i>Y.pestis</i>	-MSPVKEDRANLSPRSRPR--HVAIIIMDGNGRWAKKNGKLRVFGHKAGAKSVRRAVSFAANNGIEALIYAFSSENWNRPDQEVTALMELFVRAI
<i>B.aphidicola</i>	MSYSKNNMLFKNVLNFKNNIPS--HVAIIIMDGNGKWKARKGKSRRGFSGFYAARRAISFALFHKKILITLYAFSSDNWNRSPREIKVLMELFFYAL
<i>A.ferrooxidans</i>	-MPR--HIAVIMDGNGRWAYRRHLPRVAHGRRGAEVVREMVSACDLGIPYLILFAFSTEWRRAPIEVRLMMNLFRLLL
<i>L.pneumophila</i>	-LNHKLPO--HIAVVMGNGRWAESRGLPVEGHKAGLDVKKIIINCCLEKKISCLSLFAFSSENWSRPTEVNPLMLFLFAL
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAEKVQOGNLOPDQIDEEMLNQHVCMHELAPEVDLVIXXXXXX
<i>E.coli_K12</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAEKVQOGNLOPDQIDEEMLNQHVCMHELAPEVDLVIXXXXXX
<i>E.coli_CFT073</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAEKVQOGNLOPDQIDEEMLNQHVCMHELAPEVDLVIXXXXXX
<i>S.enterica_Ct18</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAELVQAGVLRPDQIDEERLGQICMHELAPEVDLVIXXXXXX
<i>S.enterica_Ty2</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAELVQAGVLRPDQIDEERLGQICMHELAPEVDLVIXXXXXX
<i>S.boydii</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAEKVQOGNLOPDQIDEEMLNQHVCMHELAPEVDLVIXXXXXX
<i>S.dysenteriae</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAEKVQOGNLOPDQIDEEMLNQHVCMHELAPEVDLVIXXXXXX
<i>P.luminescens</i>	DSEIKSLHKHNIIRLSVIIDIGRFSERLQDRIHRSVKLTJANNIGLQLNIAANYGGRWDIVGSVQKIAQIKDNSLEQQDITEELVNNVMNLSQPQVLDVIXXXXXX
<i>Y.pestis</i>	DSEVKSLHRHNVRLLIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVGVROLAEKVQOGNLOPDQIDEEMLNQHVCMHELAPEVDLVIXXXXXX
<i>B.aphidicola</i>	SNETNNILNKVNIRLKVGKKEFNTVLRKIRVVEKEILKNTLNNLIAANYGGRWDIIGVVRHLLAEQVKGELOPTDISERSLNSVICLHEQSQVLDVIXXXXXX
<i>A.ferrooxidans</i>	RREARKLHENGVRLLIIGDRSALDPEICLIDEAEALTRNQRLQLNLAVNYGGRWDIAQARAAMAAVQAGDLALEDFSAAHIAHLCLADIPEPDLLI
<i>L.pneumophila</i>	RKEIDDNLQHGIHLKFTGDRREPLSQVLQMSDAEALTKNNQOLILVVVNYGGRWDIVTAARKLIRTVDLGRILAYDEINEAVFAQPLDKGMPEPDLLI
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDETA-----
<i>E.coli_K12</i>	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDETA-----
<i>E.coli_CFT073</i>	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDETA-----
<i>S.enterica_Ct18</i>	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDDKA-----
<i>S.enterica_Ty2</i>	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDDKA-----
<i>S.boydii</i>	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDETA-----
<i>S.dysenteriae</i>	RIGGEHRISNFLLWQIAYAELYFIDVLNPDFDEQDFEGALNAFAKANRERRFGGT-----EPGDETA-----
<i>P.luminescens</i>	RIGGEHRISNFLLWQIAYAELYFDILNPDFDEENVFEGAINNAFAKANRERRFGGT-----IPDDADVGS-----
<i>Y.pestis</i>	RIGGEHRISNFLLWQIAYAELYFDILNPDFDEENVFEGALNAFAKANRERRFGGT-----TFIDATAS-----
<i>B.aphidicola</i>	RIGGECRISNFLLWQIAYAELYFDILNPDFDEENVFEGALNAFAKANRERRFGR-----VSH-----
<i>A.ferrooxidans</i>	RIGGEERISNFLLWQIAYAELYFDILNPDFDEENVFEGALNAFAKANRERRFGR-----VSH-----
<i>L.pneumophila</i>	RISGELRISNFLLWQIAYAELYFDILNPDFDEENVFEGALNAFAKANRERRFQCI-----QSE-----
ruler210.....220.....230.....240.....250.....260.....

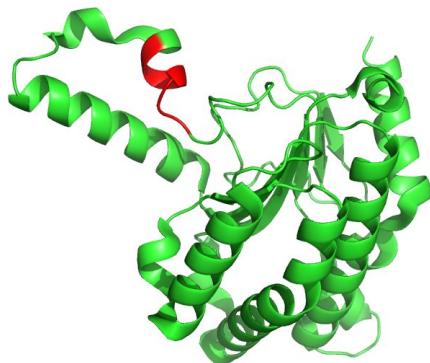


Figure S1.6: Sequence alignment and tertiary structure for gene *codA*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0337; PDB ID: 1ra0; chain ID: A

	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
<i>E_coli</i> _K12	-VSNNALQTIIINARLPGEEGLWQIHLQDGKISAIADASGVMPTTENSLLDAEQLVIPPFVPRPHIHLDTTQTAGQPWNQSGILFEGIERWAE
<i>E_coli</i> _CFT073	-MWRLTVSNNAALQTIIINARLPGKEGLWQIHLHDGKISAIADTQSVMPTTENSLLDAEQLVIPPFVPRPHIHLDTTQTAGQPWNQSGILFEGIERWAE
<i>S_enterica</i> _CT18	-MGNNNI-TIQRTRLQGHEGLWQIINIENGFSRIEPQEATSLPQGEVLDAAEGLLAIPPFVPRPHIHLDTTQTAGEPSWNQSGILFEGIERWAE
<i>S_enterica</i> _Ty2	-MGNNNI-TIQRTRLQGHEGLWQIINIENGFSRIEPQEATSLPQGEVLDAAEGLLAIPPFVPRPHIHLDTTQTAGEPSWNQSGILFEGIERWAE
<i>Y_pestis</i>	VEALMAQSVPNYSLTIVNVRRLGLQI
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100

<i>E_coli</i> _K12	RKALLT FDDVK QRAWQTLKWOIANGIQHVRTHVDVSDATLTALKAMLEVQEVAPWIDLQIVAFPOEGILSVPNGEALLEEALRLGADVVGAIIPHFEFTR
<i>E_coli</i> _CFT073	RKALLT HDDVK QRAWQTLKWOIANGIQHVRTHVDVSDATLTALKAMLEVQEVAPWIDLQIVAFPOEGILSVPNGEALLEEALRLGADVVGAIIPHFEFTR
<i>S_enterica</i> _CT18	RKAML TEDVK KARAMQTLKWMANGIQHVRTHVDVSDPILTALKAMLEVQEVAPWIDLQIVAFPOEGILSVPNGEALLEEAVRLGADVIGAIIPHFEFTR
<i>S_enterica</i> _Ty2	RKAML TEDVK KARAMQTLKWMANGIQHVRTHVDVSDPILTALKAMLEVQEVAPWIDLQIVAFPOEGILSVPNGEALLEEAVRLGADVIGAIIPHFEFTR
<i>Y_pestis</i>	RKARLT REDVK QRAWQTLKWOIANGIQHVRTHVDVSDPHTLALSAMLEVKEEVSPWVDMQIVAFPOEGILSVPDGAALLEEALRLGADVVGAIIPHFEFTR
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

<i>E_coli</i> _K12	EVGVESLHKTFALAOKYDRLLIDVHCDEIDDEQSRFVEITVAALAHHEGMGARVTASHTTAMHSYNGAYTSRLFRLKMGSINFVANPLVNIIHLQGRFDTYP
<i>E_coli</i> _CFT073	EVGVESLHKTFALAOKYDRLLIDVHCDEIDDEQSRFVEITVAALAHREGMGARVTASHTTAMHSYNGAYTSRLFRLKMGSINFVANPLVNIIHLQGRFDTYP
<i>S_enterica</i> _CT18	EVGVESLHKTFALAOKYDRLLIDVHCDEIDDEQSRFVEITVAALAHRDGMGARVTASHTTAMHSYNGAYASRLFRLKMGSINFVANPLVNIIHLQGRFDTYP
<i>S_enterica</i> _Ty2	EVGVESLHKTFALAOKYDRLLIDVHCDEIDDEQSRFVEITVAALAHRDGMGARVTASHTTAMHSYNGAYASRLFRLKMGSINFVANPLVNIIHLQGRFDTYP
<i>Y_pestis</i>	EVGVESLHIAFALAOKYQRLVDVHCDETDDDEQSRFIRTVAAALALRENMGARVTASHTTAMHSYNGAYTSRLFRLKLISGINFVANPLVNIIHLQGRFDTYP
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300

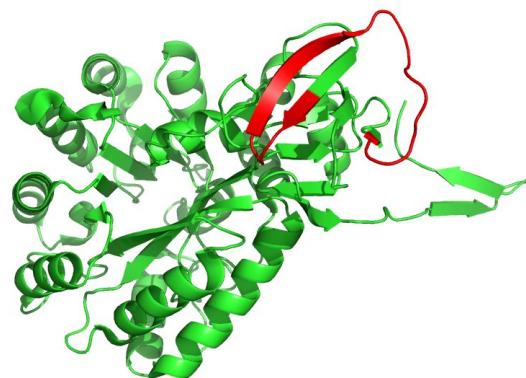


Figure S1.7: Sequence alignment and tertiary structure for gene *maa*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0459; PDB ID: 1ocx; chain ID: A

	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
<i>E_coli_K12</i>	MSTEKEKMIAGELYRSADETLSRDRLRARQLIHRYNHSLAEEHTLRQQILADLFGVTSEAYIEPTFRCDYGYNIFLGNNFFANFDCVMLDVCPPIRIGDNC
<i>E_coli_CFT073</i>	MSTEKEKMIAGELYRSADEALSRDRLRARQLIHRYNHSLAEEHTLRQQILADLFGVTSEAYIEPTFRCDYGYNIFLGNNFFANFDCVMLDVCPPIRIGDNC
<i>S_enterica_CT18</i>	MSDEKQKMIAGALYCTIDEFLCQDRLRARQLIHRYNHSLAEEHTLRQQILADLFGVTSEAYIEPTFRCDYGYNIFLGHSFYANFDCVMLDVCPPIRIGDNC
<i>S_enterica_Ty2</i>	MSDEKQKMIAGALYCTDEFLCQDRLRARQLIHRYNHSLAEEHTLRQQILADLFGVTSEAYIEPTFRCDYGYNIFLGHSFYANFDCVMLDVCPPIRIGDNC
<i>S_boydii</i>	MSTEKEKMIAGELYRSADETLSRDRLRARQLIHRYNHSLAEEHTLRQQILADLFGVTSEAYIEPTFRCDYGYNIFLGNNFFANFDCVMLDVCPPIRIGDNC
<i>S_dyenteriae</i>	MSTEKEKMIAGELYRSADETLSRDRLRARQLIHRYNHSLAEEHTLRQQILADLFGVTSEAYIEPTFRCDYGYNIFLGNNFFANFDCVMLDVCPPIRIGDNC
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	MLAPGVHIIYTATHPIDDPPVARNSGAELGKPVTIGNNVWIGGRAVINPGVTIGDNVVVASGAVVTKDVPDNVVVGGNPARIKKL
<i>E_coli_K12</i>	MLAPGVHIIYTATHPIDDPPVARNSGAELGKPVTIGNNVWIGGRAVINPGVTIGDNVVVASGAVVTKDVPDNVVVGGNPARIKKL
<i>E_coli_CFT073</i>	MLAPGVHIIYTATHPIDDPPVARNSGAELGKPVTIGNNVWIGGRAVINPGVTIGDNVVVASGAVVTKDVPDNVVVGGNPARIKKL
<i>S_enterica_CT18</i>	MLAPGVHIIYTATHPLDAVERNSGRELGKPVTIGNNVWIGGRAVNNPGVTIGDNVVVASGAVVTKNVPPDVVVGGNPARIKKL
<i>S_enterica_Ty2</i>	MLAPGVHIIYTATHPLDAVERNSGRELGKPVTIGNNVWIGGRAVNNPGVTIGDNVVVASGAVVTKNVPPDVVVGGNPARIKKL
<i>S_boydii</i>	MLAPGVHIIYTATHPIDDPPVARNSGAELGKPVTIGNNVWIGGRAVINPGVTIGDNVVVASGAVVTKDVPDNVVVGGNPARIKKL
<i>S_dyenteriae</i>	MLAPGVHIIYTATHPIDDPPVARNSGAELGKPVTIGNNVWIGGRAVINPGVTIGDNVVVASGAVVTKDVPDNVVVGGNPARIKKL
ruler110.....120.....130.....140.....150.....160.....170.....180...

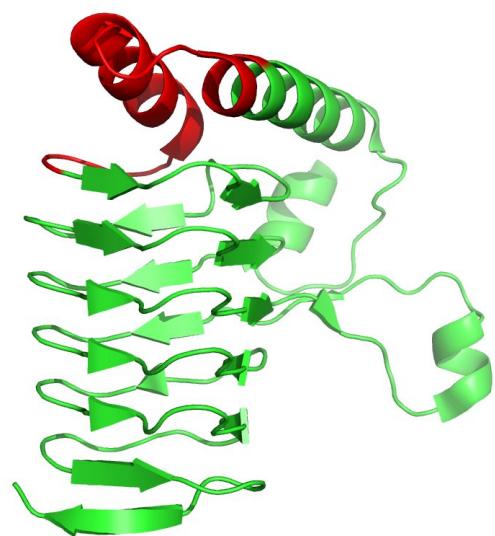


Figure S1.8: Sequence alignment and tertiary structure for gene *1bs0*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0776; PDB ID: 1bs0; chain ID: A

<i>E_coli</i> K12	--MSWQEKINAALDARRAADALRRRYPVAGGAGR--	WLVADDROVLNFSSNDYLGHLHPQIIRRAWOOGABFGIGSGGSCHVSGYSVUHQALEEEELA
<i>E_coli</i> CFT073	--MIWQEKIDAALDARRADALRRRYPVAGGAGR--	WLVADDQCQVLNFSSNDYLGHLHPQIIRRAWOOGADQFGVGSGGSCHVSGYSVUHQALEEEELA
<i>S_enterica</i> CT18	--MSWQQRVDDALTARRATD--	WLVANGRQYVLNFSSNDYLGHLHPQIIRRAWOQAATRFGVGGSGSGHISGYSVUHQALEEEELA
<i>S_enterica</i> Ty2	--MSWQEKINAALDARRAADALRRRYPVAGGAGR--	WLVANGRQYVLNFSSNDYLGHLHPQIIRRAWOQAATRFGVGGSGSGHISGYSVUHQALEEEELA
<i>S_boydii</i>	--MSWQEKINAALDARRAADALRRRYPVAGGAGR--	WLVADDROVLNFSSNDYLGHLHPQIIRRAWOQAOFGVGGSGGSCHVSGYSVUHQALEEEELA
<i>S_dyssenteriae</i>	--MSWQEKINAALDARRAADALRRRYPVAGGAGR--	WLVADDROVLNFSSNDYLGHLHPQIIRRAWOQAOFGVGGSGGSCHVSGYSVUHQALEEEELA
<i>P_luminescens</i>	--MDWSSYLSQLSERSTSLWRNQVNLKSDGR--	FLYAAADGKVNLNFSSNDYLGHLSPANPAIIISAWRGRAEQYGVGSGGSCHINGYTAKAHQLLLEECOLA
<i>Y_pestis</i>	--MSWQDKIAQGLQRRDAAAAYRTQVNNEGANGR--	WLQSGSERQYVLNFSSNDYLGHSNDIVLAANQQARRYGVGSGGSCHVTCYSCOPHARLEECOLA
<i>B_aphidicola</i>	--MNWNKRINHKLNMHIFNKKFRVKKVAVQKNNNNK--	IINVNNGMOWINVFNSNDYLGRLRNNAARIQANKTAAATRYGIGSTGSLSITGYSTITHQSLEEKLA
<i>A_ferrooxidans</i>	MHSERESWSRAELSALRAHDLWRELQVLTQAPERGPPF	AEASALRDAAAEIQOSGVGAGAAPLLGGERPAHAVANALALA
<i>L_pneumophila</i>	--MTLNKINNEVTAQLOEQQLLRTQ--	ILEEDKIDVIRFDSNDYLSLIEDRRKIAEAYQKGYBLYPCCSSGAAMVLCGYHSSHQTLERAFA
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100	
<i>E_coli</i> K12	EWLGYSRALLFISGFAANGQAVIAAMMAKEDRIAADRLSHASILLEAASLSPS	QLRFFAHNDVTHLARLLASPCCPGQQMVTTTEGVFSMDGDSAPLAIEQCVI
<i>E_coli</i> CFT073	EWLGYSRALLFISGFAANGQAVIAAMMAKEDRIVADRLSHASILLEAASLSPS	PLRFFAHNDVTHLARLLASPCCPGQQLVTTTEGVFSMDGDSAPLAIEQCVI
<i>S_enterica</i> CT18	EWLGYPRALLFISGFAANGQAVITALMKNDRIVADRLSHASILLEAANLSP	QPLRFFAHNDVTQHLSRLLQSPCVCQQLVTTTEGVFSMDGDSAPLAIEQCVI
<i>S_enterica</i> Ty2	EWLGYPRALLFISGFAANGQAVITALMKNDRIVADRLSHASILLEAANLSP	QPLRFFAHNDVTQHLSRLLQSPCVCQQLVTTTEGVFSMDGDSAPLAIEQCVI
<i>S_boydii</i>	EWLGYSRALLFISGFAANGQAVIAAMMAKEDRIVADRLSHASILLEAASLSP	QPLRFFAHNDVTQHLSRLLQSPCVCQQLVTTTEGVFSMDGDSAPLAIEQCVI
<i>S_dyssenteriae</i>	EWLGYSRALLFISGFAANGQAVIAAMMAKEDRIVADRLSHASILLEAASLSP	QPLRFFAHNDVTQHLSRLLQSPCVCQQLVTTTEGVFSMDGDSAPLAIEQCVI
<i>P_luminescens</i>	DWLGYPKALLFISGYSANGQVIAALMTEQDRIIADRLSHASILMMEAAMHSP	QPLRFFAHNDVTQHLSRLLQSPCVCQQLVTTTEGVFSMDGDSAPLAIEQCVI
<i>Y_pestis</i>	DWLGYPKALLFISGYSANGQVIAALMTEQDRIIADRLSHASILMMEAAMHSP	QPESELANLIAATPCVGKTLVTTTEGVFSMDGDSAPLAIEQCVI
<i>B_aphidicola</i>	KWLDYPKAILEFISGYVANTALISI	LIQKNDRIPMDKLHSISILEPSYNSNNQCKCYRFIHNPSSLMNKFYSSCKNPILLTEGIFSMGDIAPLS1ISSFS
<i>A_ferrooxidans</i>	RWLGVAAALLFGSYGLANLGVISL	VLRGDRRVYADRLNHSALVDGVRLSGARLHRVRHDMTHIAQWLERGGRGQANIIITDGVSMDGDIAPLPELATLA
<i>L_pneumophila</i>	EMLRVDDCLLSSGYCANLAVTALLGRGLTHCFIDKSVHASYIDGLALSRTVTSYVHNDMNAI	PALL-KSHLGDSVLITEGIFSMSSQIAPLSTISMIC
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200	
<i>E_coli</i> K12	XXXXXXXXXXXXXXXXXXXXXX--XXX-	
<i>E_coli</i> CFT073	QHNGNLMVDDAHGTGVIGEQGRGSC--WLOKVKP-E	LLVVTFGKGFGVSGAAVLCSSIVADYLLQFARHLIYSTSMPAAQALRASLAVIRSDEGDAR
<i>S_enterica</i> CT18	QHNGNLMVDDAHGTGVIGEQGRGSC--WLOKVKP-E	LLVVTFGKGFGVSGAAVLCSEIVADYLLQFARHLIYSTSMPAAQALRASLAVIRSDEGDAR
<i>S_enterica</i> Ty2	QHNGNLMVDDAHGTGVIGEQGRGSC--WLOKVKP-E	LLVVTFGKGFGVSGAAVLCSEIVADYLLQFARHLIYSTSMPAAQALRASLAVIRSDEGDAR
<i>S_boydii</i>	QHNGNLMVDDAHGTGVIGEQGRGSC--WLOKVKP-E	LLVVTFGKGFGVSGAAVLCSSIVADYLLQFARHLIYSTSMPAAQALRASLAVIRSDEGDAR
<i>S_dyssenteriae</i>	QHNGNLMVDDAHGTGVIGEQGRGSC--WLOKVKP-E	LLVVTFGKGFGVSGAAVLCSSIVADYLLQFARHLIYSTSMPAAQALRASLAVIRSDEGDAR
<i>P_luminescens</i>	RISGNWLMVDDAHGTGVIGEQGRGSC--WQOKVKP-E	LLVVTFGKAFGLSGAAVLCSNIAEYLWQFSKHLMFSTAMPIAQAYAIRQALYCIOH--ADKL
<i>Y_pestis</i>	SAAGGNLLVDDAHGTGVIGEQGRGSC--WQOKVKP-E	LLVVTFGKAFGLSGAAVLCSNIAEYLWQFSKHLMFSTAMPIAQAYAIRQALYCIOH--ADKL
<i>B_aphidicola</i>	KKIKGGLMVDDAHGTGVIGEQGRGSC--WQOKVKP-E	LLVVTFGKAFGLSGAAVLCSNIAEYLWQFSKHLMFSTAMPIAQAYAIRQALYCIOH--ADKL
<i>A_ferrooxidans</i>	QYVGAGIILDEAHAFGVLTGEGCTAAHNMDI	HGVDVIMGLKGAFGVYAFVAGSQDVV DLLRNRARSFIVHTALPSALAAAALVALDLRRH--GDAR
<i>L_pneumophila</i>	KENGSELFVDEAHAFGVMGPGMGSVPGEGLTQNVEPLRVIPFGKAFASQAVVVGRKDWHALLOTARSFVYSTAISPALCYCLLKTEITAA--ADSR	
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300	

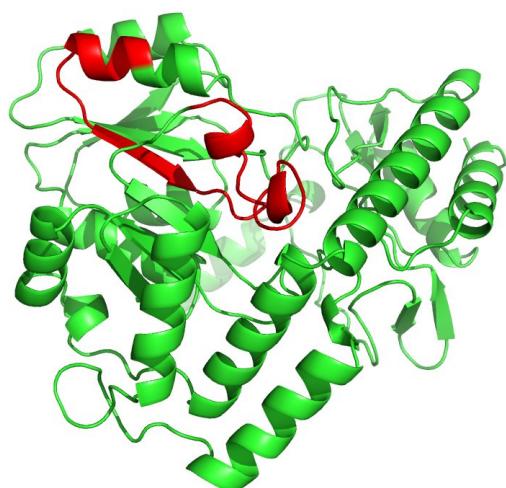


Figure S1.9: Sequence alignment and tertiary structure for gene *pepN*. The mutation cluster is highlighted in red.

E. coli K12 entry: b0932; PDB ID: 2dq6; chain ID: A

<i>E_coli_K12</i>	KV1PLQKGGHPVNSVLNVQTAEQTFVFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>E_coli_CFT073</i>	KV1PLQKGGHPVNSVLNVQTAEQTFVFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>S_enterica_CT18</i>	NV1PLQKGGHPVNAVLNVQTAEQTFITFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>S_enterica_Ty2</i>	NV1PLQKGGHPVNAVLNVQTAEQTFITFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>S_boydii</i>	KVISLQKGGHPVNSVLNVQTAEQTFITFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>S_dyssenteriae</i>	KV1PLQKGGHPVNSVLNVQTAEQTFITFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>P_luminescens</i>	HVVPLRVDGQPVHNVLNVINAQTFVFDNVYFQPVPA	LCEFSAPVKLEYKWSDQQLTFLMRHARNDF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>Y pestis</i>	NV1PLQINGLPVHHNVLNVEAEQTITFDNVAKQPIPSS	LREFSAPVKLDYFTSDQQLTFLMOHARNEF	FRWDAAQSLLATYIKLNVARHQGQPLSLPVH												
<i>A_ferrooxidans</i>	QRVPLEVVGGASETVLLPSEQSQWNFAANLPGVIPSS	LRLREFSAPVRLQDSLDDAAHGFLARHDDPFNRWES	MDLAVKALLAAVA-DSSVAP--LPIN												
<i>L_pneumophila</i>	EM1PIE-----NELLEKEKEQRFIFSGLNKEPKVVS	LLREFSAPVKIYDDLDQDLLLFLRYETDGYAKWDAA	QRLVNLCLNENLKLPASEWQ--VSK												
ruler510.....520.....530.....540.....550.....560.....570.....580.....590.....600														
 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-----															
<i>E_coli_K12</i>	VADAFRAVLLDEKIDP	LAEEILTLPSVNEMAE	LFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>E_coli_CFT073</i>	VADAFRAVLLDEKIDP	LAEEILTLPSVNEMAE	LFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>S_enterica_CT18</i>	VADAFRAVLLDEKIDP	LAEEILTLPSANEIA	ELFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>S_enterica_Ty2</i>	VADAFRAVLLDEKIDP	LAEEILTLPSANEIA	ELFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>S_boydii</i>	VADAFRAVLLDEKIDP	LAEEILTLPSANEIA	ELFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>S_dyssenteriae</i>	VADAFRAVLLDEKIDP	LAEEILTLPSANEIA	ELFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>P_luminescens</i>	VVDAFRAVLLDEKIDP	LAEEILTLPSANEIA	ELFIDIDP	I	IAEVREAL	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>Y pestis</i>	VADAFRAIILDEHLD	FLAALQILTLPSNE	EMAELFTIDIDP	QIASTVHE	LAELFV	TRILATELADELLAIY	NANY-QSEYRVEHE	EDIAKR	ILRNACLRFLA	FGE					
<i>A_ferrooxidans</i>	LRNAVAA	TLLADRODP	PAFCAE	LLPQMP	VVAEAIHRDGM	RAI	GRHFAKEW	LYHD	-AAAYQ	RGLSIGRRRLRNL	ALIAGEG				
<i>L_pneumophila</i>	LVAAPF	EVLLDDSDM	DMLDRAEL	PPGFFEVAA	TMKVW	DVS	SKVES	TDYF	QLG	GLNT	ASDLYKEL	WEVD	HRMHG	QAYGRRK	LRNVCLWLMMKAK
ruler610.....620.....630.....640.....650.....660.....670.....680.....690.....700														
 -----XXXXXXXX-----															
<i>E_coli_K12</i>	--THLADVLVKQFHEANNMTD	ALAALSAV	--AAOLPCR	DALM	OEQYDDKWHQ	ONGLVMDKWFILQ	ATSPAA	VNL	ETVRGL	LOHRSFTMSNP	NRIRSLIGAF				
<i>E_coli_CFT073</i>	--THLADVLVKQFHEANNMTD	ALAALSAV	--AAOLPCR	DALM	OEQYDDKWHQ	DGLVMDKWFILQ	ATSPAA	VNL	ETVRGL	LOHRSFTMSNP	NRIRSLIGAF				
<i>S_enterica_CT18</i>	--TELANTLVSKQYRDANN	MTD	ALAALSAV	--AAOLPCR	DALM	OEQYDDKWHQ	DGLVMDKWFILQ	ATSPAA	VNL	ETVRSL	LKHSRFSMSNP	NRIRSLIGAF			
<i>S_enterica_Ty2</i>	--TELANTLVSKQYRDANN	MTD	ALAALSAV	--AAOLPCR	DALM	OEQYDDKWHQ	DGLVMDKWFILQ	ATSPAA	VNL	ETVRSL	LKHSRFSMSNP	NRIRSLIGAF			
<i>S_boydii</i>	--THLADVLVKQYHEANN	MTD	ALAALSAV	--AAOLPCR	DALM	OEQYDDKWHQ	DGLVMDKWFILQ	ATSPAA	VNL	ETVRGL	LOHRSFTMSNP	NRIRSLIGAF			
<i>S_dyssenteriae</i>	--THLADVLVKQYHEANN	MTD	ALAALSAV	--AAOLPCR	DALM	OEQYDDKWHQ	DGLVMDKWFILQ	ATSPAA	VNL	ETVRGL	LOHRSFTMSNP	NRIRSLIGAF			
<i>P_luminescens</i>	--QEQADKVVSNQYHQ	SDNMTD	ALAALSAV	--AAOLPC	CDQQLMAEF	DGRWHQ	DGLVMDKWFSLQ	QASSP	ADV	VLANVRHLLN	HRFSFMSNP	NRVRLALIGAF			
<i>Y pestis</i>	--EEFANKLVSSQYHQAD	NMTDSL	AALAAAV	--AAOLPCR	DELLA	AFDVR	WNVHDGLVMDKWFALQ	ATSPAA	VNL	QVVRTLLK	HPAF	LSNP	NRTRSLIGAF		
<i>A_ferrooxidans</i>	--NSREGAILHARQOYIC	ADNM	TDRLAAFQ	LLA	-QHRHMDAED	WVLD	FYQRWHEYPLV	IDKWF	AI	AAAPV	PKTLRQ	VEHLLV	HPAF	DWRVP	PRVRAVLGAF
<i>L_pneumophila</i>	--ESDALELCRE	QFKDSRTM	IDQIASC	LLVNC	CSRES	IRNEAIE	GFYKQWSHNE	LVLDKWFAMQ	AA	CELPG	ILGHV	KLTQ	PAF	CIKNPKV	RALVGAF
ruler710.....720.....730.....740.....750.....760.....770.....780.....790.....800														

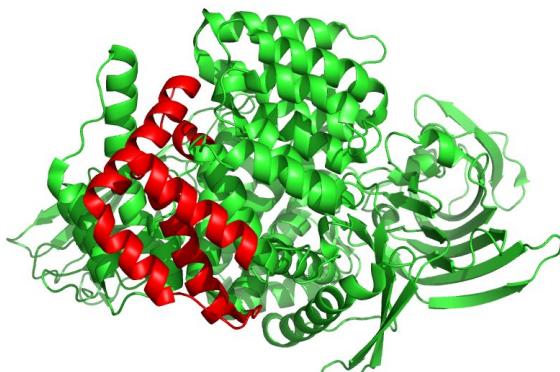


Figure S1.10: Sequence alignment and tertiary structure for gene *pabC*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1096; PDB ID: 1i2k; chain ID: A

	-----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-----	-----XXXXXX-----
<i>E_coli_K12</i>	-----MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWPOLEQEMKIL-----	-----AAEQQNGVLKVIIERGSGGRRGYST-----
<i>E_coli_CFT073</i>	-----MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWPOLEQEMKIL-----	-----AAEQQNGVLKVIIERGSGGRRGYST-----
<i>S_enterica_Ct18</i>	-----MFLINGHAQDQLAVSDRATQFGDGCFTTARVIDGNICHLEAHQRLQVAC ELK LRIAFSHWSTLRQEMTML-----	-----ATGHDSGVLKVIISRGSGGGRRGYFA-----
<i>S_enterica_Ty2</i>	-----MFLINGHAQDQLAVSDRATQFGDGCFTTARVIDGNICHLEAHQRLQVAC ELK LRIAFSHWSTLRQEMTML-----	-----ATGHDSGVLKVIISRGSGGGRRGYFA-----
<i>S_boydii</i>	-----MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGNICHLEAHQRLQVAC ELK LRIAFSHWSTLRQEMTML-----	-----AAEQQNGVLKVIIERGSGGRRGYST-----
<i>S_dyssenteriae</i>	-----MFLINGYHKQESLAVSDRATQFGDGCFTTARVIDGNICHLEAHQRLQVAC ELK LRIAFSHWSTLRQEMTML-----	-----AAEQQNGVLKVIIERGSGGRRGYST-----
<i>P_luminescens</i>	-----MYWINGERCDYL P ANDRSRVQFGDGCFTTAKIEQGQVALLSLHIIQRLQKGVERLYLPOPDWRLESHIROI-----	-----ASTTE Q GVLKVIIISRGSGGGRRGYSA-----
<i>Y pestis</i>	-----MFNINGVRONLISASDRSVQFGDGCFTTARVSDGRVVWLQHVRLRGRATERLLLPVWNWKLTKEVMVEA-----	-----ASHTESGVLKVIIISRGSGGGRRGYSC-----
<i>A_ferrooxidans</i>	-----MDGDP PLVAGACDA IL---DRAHMGDFETIAVIRGVPLFWEELARLERGATINIPAPHPPEVWREDLRL ALDAI PAOPRLLLKLTLGRGP-----CPGYGS-----	-----
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	-----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-----	-----XXXXXX-----
<i>E_coli_K12</i>	LNSGPARI LS VTAVPAHYDR LR NREGI TL ALSPVRLGRNP H LAGIKH N RL Q V L R S H Q TNADEALVLD D EGWV T EECCAA N LFWRKG N V V Y T PRLD C	-----
<i>E_coli_CFT073</i>	LN S GPARI LS VTAVPAHYDR LR NREGI TL ALSPVRLGRNP H LAGIKH N RL Q V L R S H Q TNADEALVLD D EGWV T EECCAA N LFWRKG N V V Y T PRLD C	-----
<i>S_enterica_Ct18</i>	MNCQAATR IL SV A PA Y ISQWRK G I T LT B PI L GRNP V YLAG K HL N RL Q V L R S H Q TNADEALVLD D EGWV T EECCAA N LFWR T RTGDIVFT T PRLD C	-----
<i>S_enterica_Ty2</i>	MNCQAATR IL SV A PA Y ISQWRK G I T LT B PI L GRNP V YLAG K HL N RL Q V L R S H Q TNADEALVLD D EGWV T EECCAA N LFWR T RTGDIVFT T PRLD C	-----
<i>S_boydii</i>	LN S GPARI LS VTAVPAHYDR LR NREGI TL ALSPVRLGRNP H LAGIKH N RL Q V L R S H Q TNADEALVLD D EGWV T EECCAA N LFWRKG N V V Y T PRLD C	-----
<i>S_dyssenteriae</i>	LN S GPARI LS VTAVPAHYDR LR NREGI TL ALSPVRLGRNP H LAGIKH N RL Q V L R S H Q TNADEALVLD D EGWV T EECCAA N LFWRKG N V V Y T PRLD C	-----
<i>P_luminescens</i>	CGFTQPNC IL LS P YEDK W LKQRQK G MLV S PM V AM G IN P YLAG K HL N RL Q V L R S H Q TNADEALVLD D EGL L VECC T ANIFWRKG G V V Y T PDLRG C	-----
<i>Y pestis</i>	TAQCHP PR I IS LS D YPAH Y STWR D RG I LS A SPV L PLAN R PL A GI K HL N RL Q V L R S H Q TNADEAVD V L D EGL L VECC T ANIFWRKG G V V Y T PDLSH C	-----
<i>A_ferrooxidans</i>	ACAGPFR Y WL S SR F ERN H W Y PG I AA A ACE V ALL T GA P YLG V KS L NR N QVM D ALA P EY A -EGVMM D QS G LL R EGIM S NLFW V MT G V H PELEN C	-----
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

	-----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-----	-----XXXXXX-----
<i>E_coli_K12</i>	AGVNGIMR O FC C IR L LA Q SSYQL V Q A SL E ES L Q A DEM V IC N ALMPVMPVCAC-----	-----GDVSFSSA I LYEY L AP C ERP N -----
<i>E_coli_CFT073</i>	AGVNGIMR O FC C IR L LA Q SSYQL V Q A SL E EA L Q A DEM V IC N ALMPVMPVRAC-----	-----GDVSFRQQR M N I -----
<i>S_enterica_Ct18</i>	AGVNGIMR O FC C IR L Q A Q S PF O V L E V Q A RE E EV R Q A DE I I I IC N ALMP I I PI R AY-----	-----HGT S Y S R I L F Q F LA P FC E HPN N -----
<i>S_enterica_Ty2</i>	AGVNGIMR O FC C IR L Q A Q S PF O V L E V Q A RE E EV R Q A DE I I I IC N ALMP I I PI R AY-----	-----HGT S Y S R I L F Q F LA P FC E HPN N -----
<i>S_boydii</i>	AGVNGIMR O FC C IR L LA Q SSYQL V Q A SL E EA L Q A DEM V IC N ALMPVMPVRAC-----	-----GDVSFSSA I LYEY L AP C ERP N -----
<i>S_dyssenteriae</i>	AGVNGIMR O FC C IR L LA Q SSYQL V Q A SL E EA L Q A DEM V IC N ALMPVMPVRAC-----	-----GDVSFSSA I LYEY L AP C ERP N -----
<i>P_luminescens</i>	CGVEGV M ER I LA L SS E D W H F SC V SC V Y P ET L AD A DE V V C N S LM P V I A V KE I -----	-----D A H E N O PR W O Q SR E LYE V LL P E C L K I -----
<i>Y pestis</i>	SCVGDGIMR O RI I LA L SS E D W H F SC V SC V Y P ET L AD A DE V V C N S LM P V I P V N K V -----	-----GK W V I K S R V L F D L L N H C D I -----
<i>A_ferrooxidans</i>	GGIAGVQ R A I IL W LQ A H M P E V I V Q P I N V L A DE D V I V C N S LM P V I P V N K V -----	-----GGHD G P I T S V I L A WT E RM G L G P Q -----
ruler210.....220.....230.....240.....250.....260.....270.....280..

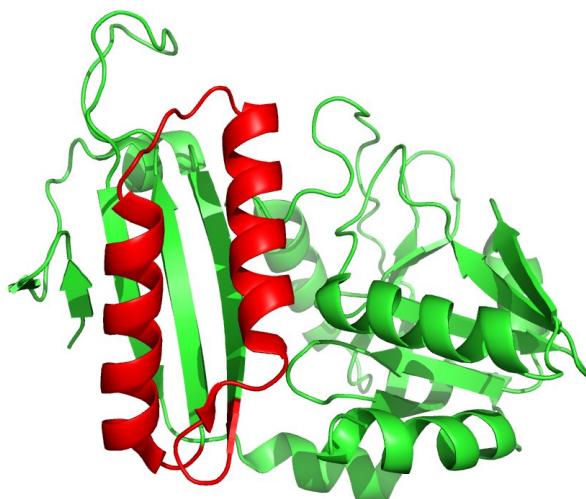


Figure S1.11: Sequence alignment and tertiary structure for gene *ycfH*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1100; PDB ID: 1yix; chain ID: A

<pre> E_coli_K12 -MFLVDSSHCHLDGLDYE<ins>S</ins>LHKDVDVLAKAAAARDVKFCLAVATTTLPGYLMRDLVGERDNVVFSCGVHPLNG-NDPYDVED E_coli_CFT073 <ins>LSITCNRALCYRFLIFKRD</ins>IMFLVDSSHCHLDGLDYE<ins>S</ins>LHKDVDVLAKAAAARDVKFCLAVATTTLPGYLMRDLVGERDNVVFSCGVHPLNG-NDPYDVED S_enterica_Ct18 -MFLVDSSHCHLDGLDYE<ins>S</ins>LHKDVDVLAKAAAARDVKFCLAVATTTLPGYLMRDLVGERDNVVFSCGVHPLNG-DEVVYDVVE S_enterica_Ty2 -MFLVDSSHCHLDGLDYE<ins>S</ins>LHKDVDVLAKAAAARDVKFCLAVATTTLPGYLMRDLVGERDNVVFSCGVHPLNG-DEVVYDVVE S_boydii -MFLVDSSHCHLDGLDYE<ins>S</ins>LHKDVDVLAKAAAARDVKFCLAVATTTLPGYLMRDLVGERDNVVFSCGVHPLNG-DEVVYDVVE S_dyssenteriae -MFLVDSSHCHLDGLDYE<ins>S</ins>LHKDVDVLAKAAAARDVKFCLAVATTTLPGYLMRDLVGERDNVVFSCGVHPLNG-NDPYDVED P_luminescens -MLLVDSSHCHLDCLDYENLHKNVDDVVAKAADREVKFMLAVATTTLPGFQOMKTLGERENIVFSCGTHPLNL-DECYVNDFE Y pestis -MLLVDSSHCHLDCLDYENLHKNVDDVVAKAADREVKFMLAVATTTLPGFQAMTALIGERKNVAFSCGVHPLNL-DGGYDFC B_aphidicola -MFLIDSSHCHLDLLNNYNIHTGIQDVLNKSKKHVNVLIJVTSIENFCYLLFKIKGNRNVLLSCGTHPHYIPENKNEILK A_ferrooxidans -MLVDSSHCHLDLFEDFDA---DRSEILLARARAAGVGEMLIAAAVVEAHWPRVQALAAGHAGVVAAVGVHPNEPAGATPEWER L_pneumophila -VLVDSSHCHLNFDIDLTHFHDLAQVINQARENEVEHFLSVCVELSDYPOLERLAKDYPDISISVGVHPNSMNYPVTAQM ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100 </pre> <pre> XXXXXXXXXXXXXXXXXXXXXX- E_coli_K12 LRRRLAAE<ins>EG</ins>VVALGET<ins>G</ins>LDVYYT-ETIKVRQOESFIIHHIQIGRELNKPVIVHTRDARADTLAILREEKVTDCGGVLHCFTEDRETAGKLLDLGFYISFS E_coli_CFT073 LRRRLAAE<ins>EG</ins>VVALGET<ins>G</ins>LDVYYT-ETIKVRQOESFIIHHIQIGRELNKPVIVHTRDARADTLAILREEKVTDCGGVLHCFTEDRETAGKLLDLGFYISFS S_enterica_Ct18 LRLLAADDVVAMGET<ins>G</ins>LDVYYT-ETIKRQOASFIIHHIQIGRELHKPVIVHTRDARADTLAILREEKVTDCGGVLHCFTEDRETAGKLLDLGFYISFS S_enterica_Ty2 LRLLAADDVVAMGET<ins>G</ins>LDVYYT-ETIKRQOASFIIHHIQIGRELHKPVIVHTRDARADTLAILREEKVTDCGGVLHCFTEDRETAGKLLDLGFYISFS S_boydii LRLLAABEEGVPLCET<ins>G</ins>LDVYYT-ETIKVLRQOESFIIHHIQIGRELHKPVIVHTRDARADTLAILREEKVTDCGGVLHCFTEDRETAGKLLDLGFYISFS S_dyssenteriae LRLLAABEEGVPLCET<ins>G</ins>LDVYYT-ETIKVLRQOESFIIHHIQIGRELHKPVIVHTRDARADTLAILREEKVTDCGGVLHCFTEDRETAGKLLDLGFYISFS P_luminescens LARLASGEVVAGET<ins>G</ins>LDVYYQQ-DNAELRTSFREHIRIGCKLNKPVIVHTRSADDTLRLVRLEEQQARECGGVHCFTEDKDATARELLDLGFYISFS Y pestis LREELAAGTHVVAMGET<ins>G</ins>LDVYYQQ-DNIPLQOASFREHIRIGCKLNKPVIVHTRDARADTLISLRLEEQQARECGGVHCFTEDKDATARELLDLGFYISFS B_aphidicola LKKYSNNEKVVAIGET<ins>G</ins>LDVYYRNN-DNKKLQOILFREHIRISITLKKPLLIHTRNSINDTINLKEENSKQCIGVLHSEDMHSARILLNMGFYISFS A_ferrooxidans LLVALAADKVVAVGET<ins>G</ins>LDVYYRE-GDSLWRERFAQHIAAAKAGKPLIVHTRAAADTLLMLRSEDAAAGVVIHCFTENRDFARTALDMGFYISFS L_pneumophila LCELAQNPACIAIGET<ins>G</ins>LDVYYRNTEEASLSORFREHIKAALISKPLIHTRQAAEDTLLMAKEGASQIGGVMHCFAEDLDIAQRADLNFYISFS ruler 110.....120.....130.....140.....150.....160.....170.....180.....190.....200 </pre> <pre> XXXXXXXXXXXXXXXXXXXXXX- E_coli_K12 GIVTFRNAEQLRDAARYVPLDRLLVETDSPYLAPVPHRGKENPAMVRDVAEYMAVLKGVAEELAQVTTDNFARLFHIDASRLQSIR- E_coli_CFT073 GIVTFRNAEQLRDAARYVPLDRLLVETDSPYLAPVPHRGKENPAMVRDVAEYMAVLKGVAEELAQVTTDNFARLFHIDASRLQSIR- S_enterica_Ct18 GIVTFRNAEQLRDAARYVPLDRLLVETDSPYLAPVPHRGKENPAMVRDVAEYMAVLKGVAEELAQVTTDNFARLFHIDASRLQSIR- S_enterica_Ty2 GIVTFRNAEQLRDAARYVPLDRLLVETDSPYLAPVPHRGKENPAMVRDVAEYMAVLKGVAEELAQVTTDNFARLFHIDASRLQSIR- S_boydii GIVTFRNAEQLRDAARYVPLDRLLVETDSPYLAPVPHRGKENPAMVRDVAEYMAVLKGVAEELAQVTTDNFARLFHIDASRLQSIR- S_dyssenteriae GIVTFRNAEQLRDAARYVPLDRLLVETDSPYLAPVPHRGKENPAMVRDVAEYMAVLKGVAEELAQVTTDNFARLFHIDASRLQSIR- P_luminescens GIVTFRNAEQIREAARYVPLDRLLVETDSPYLAPVPHRGKENPAYVRDVAEYMAVLKGVSIEALAEVTTQNCDFDHFVVDVKI- Y pestis GIVTFRNAEQIREAARYVPLDRLLVETDSPYLAPVPHRGKENPAYVRDVAEYMAVLKGVSIEALAEVTTANFCRLFLHDPSEKRPLP B_aphidicola GIVTFKNSKIVHETAKFVPIDRLLILTETDSPYLAPVPHRGKENPAYLYDTMLYIAQLKNMSPECFAIQTTKNFLKLFNLPSYFTNMS- A_ferrooxidans GIVTFRKSVELQAVAKMPLADRLLVETDSPYLAPVPHRGKENPAYLYDTMLYIAQLKNMSPECFAIQTTKNFLKLFNLPSYFTNMS- L_pneumophila GIVTFKNAVSQLDVARQIPLERLILTETDSPYLAPVPHRGKENPAYLYDTMLYIAQLKNMSPECFAIQTTKNFLKLFNLPSYFTNMS- ruler 210.....220.....230.....240.....250.....260.....270.....280.....290.. </pre>

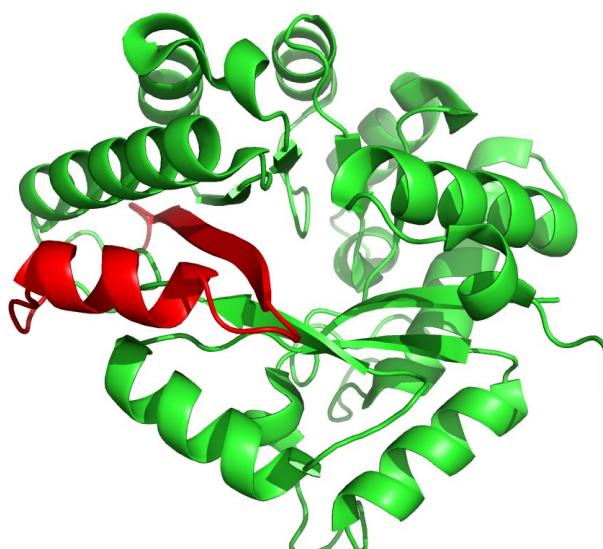


Figure S1.12: Sequence alignment and tertiary structure for gene *narH*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1225; PDB ID: 1q16; chain ID: B

<i>E_coli_K12</i>	MKIRSQVGMVLNLDKCIGCHTC	S	V	C	K	N	V	T	S	R	E	G	V	A	W	F	N	N	V	E	T	K	P	G	G	P	T	D	W	E	N	E	E	K	Y	K	G	G	W	I	R	K	I	G	L	O	P	R	M	G	N	R	A	M	L	L	G	K	I	F	A	N	P	H	L	P	G	I	D	D
<i>E_coli_CFT073</i>	MKIRSQVGMVLNLDKCIGCHTC	S	V	C	K	N	V	T	S	R	E	G	V	A	W	F	N	N	V	E	T	K	P	G	G	P	T	D	W	E	N	E	E	K	Y	K	G	G	W	I	R	K	I	G	L	O	P	R	M	G	N	R	A	M	L	L	G	K	I	F	A	N	P	H	L	P	G	I	D	D
<i>S_enterica_CT18</i>	MKIRSQVGMVLNLDKCIGCHTC	S	V	C	K	N	V	T	S	R	E	G	V	A	W	F	N	N	V	E	T	K	P	G	G	P	T	D	W	E	N	E	E	K	Y	K	G	G	W	I	R	K	I	G	L	O	P	R	M	G	N	R	A	M	L	L	G	K	I	F	A	N	P	H	L	P	G	I	D	D
<i>S_enterica_Ty2</i>	MKIRSQVGMVLNLDKCIGCHTC	S	V	C	K	N	V	T	S	R	E	G	V	A	W	F	N	N	V	E	T	K	P	G	G	P	T	D	W	E	N	E	E	K	Y	K	G	G	W	I	R	K	I	G	L	O	P	R	M	G	N	R	A	M	L	L	G	K	I	F	A	N	P	H	L	P	G	I	D	D
<i>S_boydii</i>	MKIRSQVGMVLNLDKCIGCHTC	S	V	C	K	N	V	T	S	R	E	G	V	A	W	F	N	N	V	E	T	K	P	G	G	P	T	D	W	E	N	E	E	K	Y	K	G	G	W	I	R	K	I	G	L	O	P	R	M	G	N	R	A	M	L	L	G	K	I	F	A	N	P	H	L	P	G	I	D	D
<i>S_dyenteriae</i>	MKIRSQVGMVLNLDKCIGCHTC	S	V	C	K	N	V	T	S	R	E	G	V	A	W	F	N	N	V	E	T	K	P	G	G	P	T	D	W	E	N	E	E	K	Y	K	G	G	W	I	R	K	I	G	L	O	P	R	M	G	N	R	A	M	L	L	G	K	I	F	A	N	P	H	L	P	G	I	D	D
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100																									

<i>E_coli_K12</i>	YEPFD ^D FDYQNLHTAPEGSKS ^Q PIARPRLITGERMAKIEKGP	N	WED	DLG	G	E	F	D	K	L	A	D	K	N	F	D	N	I	C	A	M	Y	S	O	F	E	N	T	F	M	M	Y	L	P	R	L	C	E	H	C	L	N	P	A	C	V	A	C	P	S	G
<i>E_coli_CFT073</i>	YEPFD ^D FDYQNLHTAPEGSKS ^Q PIARPRLITGERMAKIEKGP	N	WED	DLG	G	E	F	D	K	L	A	D	K	N	F	D	N	I	C	A	M	Y	S	O	F	E	N	T	F	M	M	Y	L	P	R	L	C	E	H	C	L	N	P	A	C	V	A	C	P	S	G
<i>S_enterica_CT18</i>	YEPFD ^D FDYQNLHTAPEGSKS ^Q PIARPRLITGERMAKIEKGP	N	WED	DLG	G	E	F	D	K	L	A	D	K	N	F	D	N	I	C	A	M	Y	S	O	F	E	N	T	F	M	M	Y	L	P	R	L	C	E	H	C	L	N	P	A	C	V	A	C	P	S	G
<i>S_enterica_Ty2</i>	YEPFD ^D FDYQNLHTAPEGSKS ^Q PIARPRLITGERMAKIEKGP	N	WED	DLG	G	E	F	D	K	L	A	D	K	N	F	D	N	I	C	A	M	Y	S	O	F	E	N	T	F	M	M	Y	L	P	R	L	C	E	H	C	L	N	P	A	C	V	A	C	P	S	G
<i>S_boydii</i>	YEPFD ^D FDYQNLHTAPEGSKS ^Q PIARPRLITGERMAKIEKGP	N	WED	DLG	G	E	F	D	K	L	A	D	K	N	F	D	N	I	C	A	M	Y	S	O	F	E	N	T	F	M	M	Y	L	P	R	L	C	E	H	C	L	N	P	A	C	V	A	C	P	S	G
<i>S_dyenteriae</i>	YEPFD ^D FDYQNLHTAPEGSKS ^Q PIARPRLITGERMAKIEKGP	N	WED	DLG	G	E	F	D	K	L	A	D	K	N	F	D	N	I	C	A	M	Y	S	O	F	E	N	T	F	M	M	Y	L	P	R	L	C	E	H	C	L	N	P	A	C	V	A	C	P	S	G
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200											

<i>E_coli_K12</i>	IYKREEDGIVLIDQDKCRGWRM	C	I	T	GCP	V	K	K	I	F	N	W	K	S	G	E	K	C	I	F	C	P	R	I	E	A	G	Q	P	T	V	C	S	E	T	C	V	G	R	I	R	L	G	V	L	L	D	A	D	A	I	E	R	A	A	S	T	E	N	E	K	D	L	Y	Q	R	D	V
<i>E_coli_CFT073</i>	IYKREEDGIVLIDQDKCRGWRM	C	I	T	GCP	V	K	K	I	F	N	W	K	S	G	E	K	C	I	F	C	P	R	I	E	A	G	Q	P	T	V	C	S	E	T	C	V	G	R	I	R	L	G	V	L	L	D	A	D	A	I	E	R	A	A	S	T	E	N	E	K	D	L	Y	Q	R	D	V
<i>S_enterica_CT18</i>	IYKREEDGIVLIDQDKCRGWRM	C	I	T	GCP	V	K	K	I	F	N	W	K	S	G	E	K	C	I	F	C	P	R	I	E	A	G	Q	P	T	V	C	S	E	T	C	V	G	R	I	R	L	G	V	L	L	D	A	D	A	I	E	R	A	A	S	T	E	N	E	K	D	L	Y	Q	R	D	V
<i>S_enterica_Ty2</i>	IYKREEDGIVLIDQDKCRGWRM	C	I	T	GCP	V	K	K	I	F	N	W	K	S	G	E	K	C	I	F	C	P	R	I	E	A	G	Q	P	T	V	C	S	E	T	C	V	G	R	I	R	L	G	V	L	L	D	A	D	A	I	E	R	A	A	S	T	E	N	E	K	D	L	Y	Q	R	D	V
<i>S_boydii</i>	IYKREEDGIVLIDQDKCRGWRM	C	I	T	GCP	V	K	K	I	F	N	W	K	S	G	E	K	C	I	F	C	P	R	I	E	A	G	Q	P	T	V	C	S	E	T	C	V	G	R	I	R	L	G	V	L	L	D	A	D	A	I	E	R	A	A	S	T	E	N	E	K	D	L	Y	Q	R	D	V
<i>S_dyenteriae</i>	IYKREEDGIVLIDQDKCRGWRM	C	I	T	GCP	V	K	K	I	F	N	W	K	S	G	E	K	C	I	F	C	P	R	I	E	A	G	Q	P	T	V	C	S	E	T	C	V	G	R	I	R	L	G	V	L	L	D	A	D	A	I	E	R	A	A	S	T	E	N	E	K	D	L	Y	Q	R	D	V
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300																												

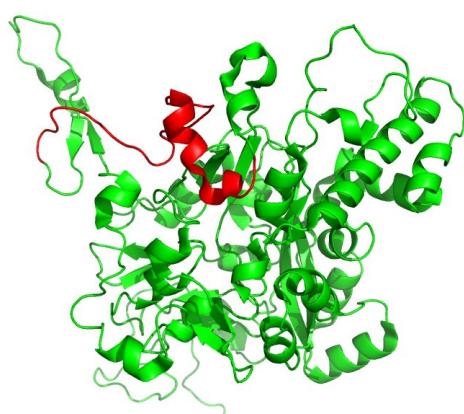


Figure S1.13: Sequence alignment and tertiary structure for gene *trpE*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1264; PDB ID: 1i1q; chain ID: A

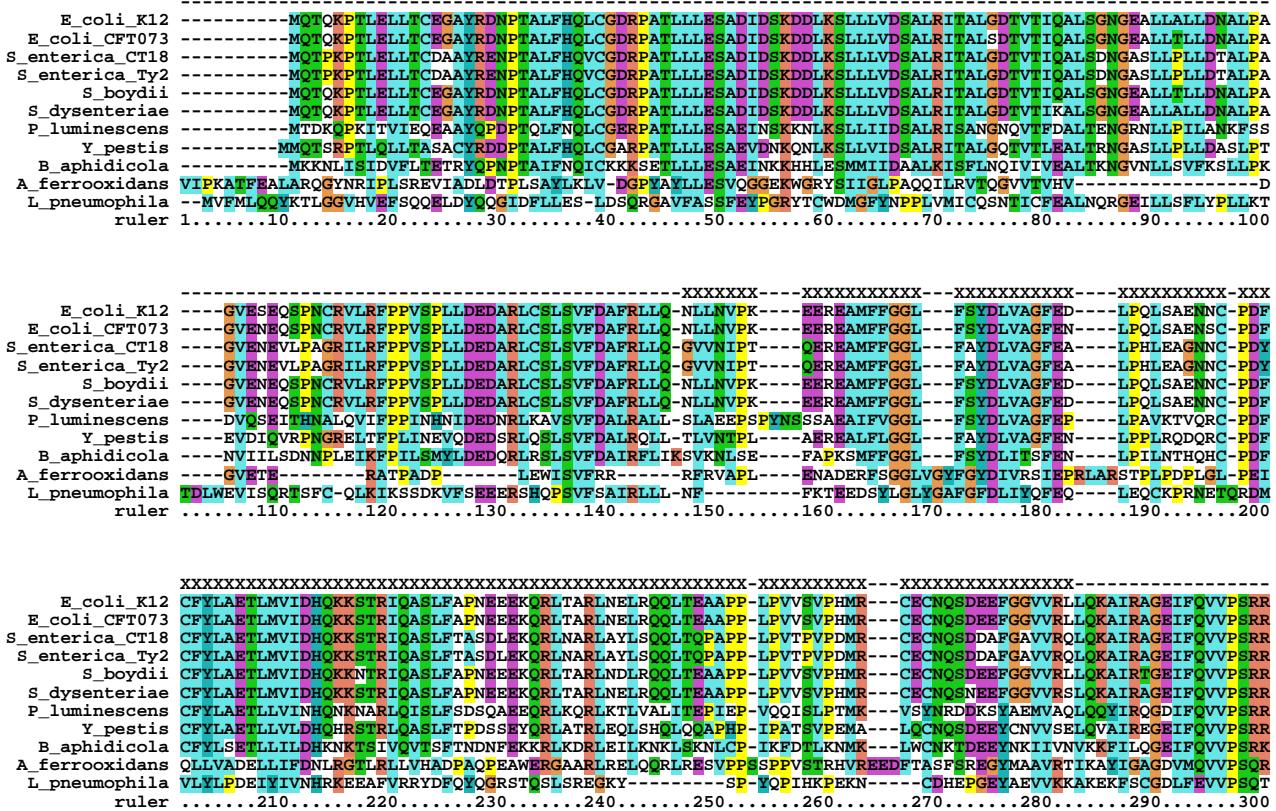


Figure S1.14: Sequence alignment and tertiary structure for gene *kate*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1732; PDB ID: 1qf7; chain ID: A

<i>E_coli_K12</i>	KLIPEELVPVQRVGKMLVLNRNPDNFFAENEQAAFHPGHIVPGGLDFNDPLLQGRLFPSYIDTQI	<i>S_enterica_CFT073</i>	KLIPEELVPVQRVGKMLVLNRNPDNFFAENEQAAFHPGHIVPGGLDFNDPLLQGRLFPSYIDTQI	<i>S_enterica_CT18</i>	KLIPEELVPVQRVGKMLVLNRNPDNFFAENEQAAFHPGHIVPGIDFNDPLLQGRLFPSYIDTQI	<i>S_enterica_Ty2</i>	KLIPEELVPVQRVGKMLVLNRNPDNFFAENEQAAFHPGHIVPGIDFNDPLLQGRLFPSYIDTQI	<i>P_luminescens</i>	KVWPWHDYPMIDVGYFELNRNPDNFFSDEVEQAAFPHGIVPGIDFNDPLLQGRLFPSYIDTQI	<i>Y_pestis</i>	KVWPWHDYPMIDVGYFELNRNPDNFFSDEVEQAAFPHGIVPGIDFNDPLLQGRLFPSYGAQRYRLG-VNHHQIPVNTPRCPPHNHYHRDGAMRVDGNSGN
ruler	360.....370.....380.....390.....400.....410.....420.....430.....440.....450.....										
<i>E_coli_K12</i>	PANYEPNS--INDNWPREPPGPKRGGFESYQERVEGNKVRERSPFGEYSSHPRLFWL	<i>E_coli_CFT073</i>	PANYEPNS--INDNWPREPPGPKRGGFESYQERVEGNKVRERSPFGEYSSHPRLFWL	<i>S_enterica_CT18</i>	PANYEPNS--INDNWPREPPAPKRGGFESYQERVGNEIRERSPFGEYSSHPRLFWL	<i>S_enterica_Ty2</i>	PANYEPNS--INDNWPREPPAPKRGGFESYQERVGNEIRERSPFGEYSSHPRLFWL	<i>P_luminescens</i>	TVTYEPNNAGLFQEQPEFKHPSLSLEGDAADHWNHRQDE-----DVFSPQRPKLFLMILNSKEHORMFDRIASELSQAHEED	<i>Y_pestis</i>	GATYEPNNAGLFQEQPEFKHPSLSLEGDAADHWNHRQDE-----DVFSPQRPKLFLMILNSKEHORMFDRIASELSQAHEED
ruler	460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....										
<i>E_coli_K12</i>	LAQAVAKNLGIELIDDDQLNITPPPDVNGLKKDPSSLVIAIPDGDVKGRVVAILLNDE	<i>E_coli_CFT073</i>	LAQAVAKNLGIELIDDDQLNITPPPDVNGLKKDPSSLVIAIPDGDVKGRVVAILLNDE	<i>S_enterica_CT18</i>	LAQAVAHNLGFALTHEOTQIAPPDVNGLKKDPALSILAVPDGDVKGRVVAILLNDKVNAEELLTIFQALKAKGVHVKLLYSRMGEVTADDGSTLTIAAT	<i>S_enterica_Ty2</i>	LAQGVAVHNLGFALTHEOTQIAPPDVNGLKKDPALSILAVPDGDVKGRVVAILLNDKVNAEELLTIFQALKAKGVHVKLLYSRMGEVTADDGSTLTIAAT	<i>P_luminescens</i>	YGAGVENAL-----	<i>Y_pestis</i>	YGAGVKKKALGIN-----
ruler	560.....570.....580.....590.....600.....610.....620.....630.....640.....650.....										
<i>E_coli_K12</i>	FAGAPSLLTVDAVIVPCGNIAIDIADNGDANYYLMEEAYKHLKPTIALAGDARKFKATIKIAIDGEECIVEADSADGSFMDELLTLMAAHRRWWSRIPKIDKIP	<i>E_coli_CFT073</i>	FAGAPSLLTVDAVIVPCGNIAIDIADNGDANYYLMEEAYKHLKPTIALAGDARKFKATIKIAIDGEECIVEADSADGSFMDELLTLMAAHRRWWSRIPKIDKIP	<i>S_enterica_CT18</i>	FAGAPSLLTVDAVIVPCGNIAIDIADNGDANYYLMEEAYKHLKPTIALAGDARKFKATIKIAIDGEECIVEADSADGSFMDELLTLMAAHRRWWSRIPKIDKIP	<i>S_enterica_Ty2</i>	FAGAPSLLTVDAVIVPCGNIAIDESCGDARYYLLEAYKHLKPTIALAGDARRFKALLNIDS	<i>P_luminescens</i>	-----KKIKG	<i>Y_pestis</i>	-----KKIKG
ruler	660.....670.....680.....690.....700.....710.....720.....730.....740.....750.....										

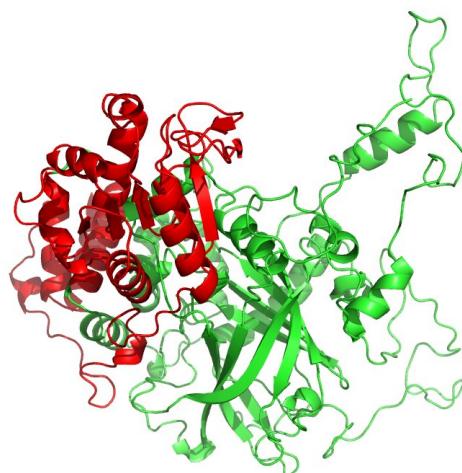


Figure S1.15: Sequence alignment and tertiary structure for gene *rnd*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1804; PDB ID: 1yt3; chain ID: A

<i>E_coli</i> _K12	RDP <i>SIT</i> TKFLHAGS <i>ED</i> LEVFLNVFGELP <i>OPLIDT</i> QILAAFCGRPM <i>S</i> NGFA <i>S</i> MVEEYSGV <i>V</i> LDK <i>SE</i> SRTDWLARPLTER <i>OCE</i> YAAADVYLL <i>P</i> ITAKLMVET
<i>E_coli</i> _CFT073	RDP <i>SIT</i> TKFLHAGS <i>ED</i> LEVFLNVFGELP <i>OPLIDT</i> QILAAFCGRPM <i>S</i> NGFA <i>S</i> MVEEYSGV <i>V</i> LDK <i>SE</i> SRTDWLARPLTER <i>OCE</i> YAAADVYLL <i>P</i> ITAKLMVET
<i>S_enterica</i> _CT18	RDTG <i>I</i> TKFLHAGS <i>ED</i> LEVFLNAF <i>GELP</i> <i>BPLIDT</i> QILAAFCGRPL <i>S</i> WGF <i>A</i> SMVEEYSGV <i>V</i> VALDK <i>SE</i> SRTDWLARPLSER <i>OCE</i> YAAADVYLL <i>P</i> IAKKLMIEET
<i>S_enterica</i> _Ty2	RDTG <i>I</i> TKFLHAGS <i>ED</i> LEVFLNAF <i>GELP</i> <i>BPLIDT</i> QILAAFCGRPL <i>S</i> WGF <i>A</i> SMVEEYSGV <i>V</i> VALDK <i>SE</i> SRTDWLARPLSER <i>OCE</i> YAAADVYLL <i>P</i> IAKKLMIEET
<i>S_boydii</i>	RDP <i>SIT</i> TKFLHAGS <i>ED</i> LEVFLNVFGELP <i>OPLIDT</i> QILAAFCGRPL <i>S</i> WGF <i>A</i> SMVEEYSGV <i>V</i> VALDK <i>SE</i> SRTDWLARPLSER <i>OCE</i> YAAADVYLL <i>P</i> IAKKLMIEET
<i>S_dy</i> sentieriae	RDP <i>SIT</i> TKFLHAGS <i>ED</i> LEVFLNVFGELP <i>OPLIDT</i> QILAAFCGRPM <i>S</i> NGFA <i>S</i> MVEEYSGV <i>V</i> LDK <i>SE</i> SRTDWLARPLTER <i>OCE</i> YAAADVYLL <i>P</i> IAKKLMIEET
<i>P_luminescens</i>	THP <i>QI</i> KL <i>LL</i> HAGS <i>ED</i> LEVFLNAF <i>OCLPBPMDT</i> QVLAAFIGHPL <i>S</i> CGFA <i>ALVAEV</i> IHV <i>ELDKSE</i> SRTDWLARPLSE <i>KOCE</i> YAAADVYLL <i>P</i> LA <i>DILM</i> T
<i>Y</i> pestis	YDLNVV <i>Y</i> KLHAGS <i>ED</i> LEVFLNAF <i>DMP</i> T <i>PMDT</i> QVLAAF <i>GRSL</i> <i>SCCFAM</i> LA <i>EF</i> GV <i>ELD</i> K <i>SE</i> SRTDWLARPL <i>SEKOC</i> DYAAADVFYLL <i>P</i> LA <i>AKL</i> VEAT
ruler80.....90.....100.....110.....120.....130.....140.....150.....160.....170

<i>E_coli</i> _K12	EASGWL <i>PA</i> ALDECRL <i>M</i> MR <i>R</i> QE <i>VV</i> AP <i>ED</i> AWR <i>DIT</i> NAW <i>QLR</i> <i>T</i> ROL <i>A</i> COL <i>L</i> LA <i>D</i> W <i>RLR</i> K <i>AR</i> <i>E</i> RD <i>LA</i> V <i>NF</i> V <i>V</i> REE <i>HL</i> WS <i>V</i> ARY <i>M</i> PG <i>S</i> LG <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
<i>E_coli</i> _CFT073	EASGWL <i>PA</i> ALDECRL <i>M</i> MR <i>R</i> QE <i>VV</i> AP <i>ED</i> AWR <i>DIT</i> NAW <i>QLR</i> <i>T</i> ROL <i>A</i> COL <i>L</i> LA <i>D</i> W <i>RLR</i> K <i>AR</i> <i>E</i> RD <i>LA</i> V <i>NF</i> V <i>V</i> REE <i>HL</i> WS <i>V</i> ARY <i>M</i> PG <i>S</i> LG <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
<i>S_enterica</i> _CT18	EAAGWL <i>PA</i> ALDECRL <i>M</i> QR <i>R</i> QE <i>I</i> Q <i>AP</i> EE <i>AWR</i> <i>DIT</i> NAW <i>QLR</i> <i>T</i> ROL <i>A</i> COL <i>L</i> LA <i>D</i> W <i>RLR</i> K <i>AR</i> <i>E</i> RD <i>MA</i> V <i>NF</i> V <i>V</i> REE <i>ENL</i> WA <i>V</i> ARY <i>M</i> PG <i>S</i> LG <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
<i>S_enterica</i> _Ty2	EAAGWL <i>PA</i> ALDECRL <i>M</i> QR <i>R</i> QE <i>I</i> Q <i>AP</i> EE <i>AWR</i> <i>DIT</i> NAW <i>QLR</i> <i>T</i> ROL <i>A</i> COL <i>L</i> LA <i>D</i> W <i>RLR</i> K <i>AR</i> <i>E</i> RD <i>MA</i> V <i>NF</i> V <i>V</i> REE <i>ENL</i> WA <i>V</i> ARY <i>M</i> PG <i>S</i> LG <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
<i>S_boydii</i>	EASGWL <i>PA</i> ALDECRL <i>M</i> MR <i>R</i> QE <i>VV</i> AP <i>ED</i> AWR <i>DIT</i> NAW <i>QLR</i> <i>T</i> ROL <i>A</i> COL <i>L</i> LA <i>D</i> W <i>RLR</i> K <i>AR</i> <i>E</i> RD <i>LA</i> V <i>NF</i> V <i>V</i> REE <i>HL</i> WS <i>V</i> ARY <i>M</i> PG <i>S</i> LG <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
<i>S_dy</i> sentieriae	EASGWL <i>PA</i> ALDECRL <i>M</i> MR <i>R</i> QE <i>VV</i> AP <i>ED</i> AWR <i>DIT</i> NAW <i>QLR</i> <i>T</i> ROL <i>A</i> COL <i>L</i> LA <i>D</i> W <i>RLR</i> K <i>AR</i> <i>E</i> RD <i>MA</i> V <i>NF</i> V <i>V</i> REE <i>ENL</i> WA <i>V</i> ARY <i>M</i> PG <i>S</i> LG <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
<i>P_luminescens</i>	AQAGYMEAA <i>T</i> GE <i>C</i> R <i>L</i> <i>I</i> <i>S</i> RR <i>R</i> <i>K</i> ILE <i>P</i> ES <i>SAY</i> K <i>Q</i> IGN <i>I</i> COL <i>R</i> <i>P</i> OL <i>A</i> CL <i>K</i> LA <i>AW</i> R <i>L</i> <i>S</i> <i>Q</i> AR <i>E</i> RD <i>LA</i> V <i>NF</i> V <i>I</i> RE <i>ENL</i> W <i>Q</i> V <i>A</i> RY <i>M</i> PT <i>S</i> <i>L</i> <i>A</i> <i>E</i> <i>D</i> <i>L</i> <i>A</i> <i>G</i> <i>L</i> <i>S</i> <i>Q</i> <i>E</i> <i>I</i> <i>R</i> <i>C</i>
<i>Y</i> pestis	EAAGRMD <i>AA</i> K <i>DE</i> <i>C</i> <i>L</i> <i>L</i> <i>C</i> <i>R</i> <i>R</i> <i>S</i> <i>E</i> <i>T</i> <i>D</i> <i>P</i> <i>E</i> <i>L</i> <i>A</i> <i>Y</i> <i>R</i> <i>E</i> <i>T</i> <i>NA</i> W <i>QLR</i> <i>G</i> <i>H</i> <i>O</i> <i>L</i> <i>A</i> <i>C</i> <i>L</i> <i>K</i> <i>A</i> <i>E</i> <i>W</i> <i>R</i> <i>L</i> <i>R</i> <i>Q</i> <i>A</i> <i>R</i> <i>E</i> RD <i>LA</i> V <i>NF</i> V <i>V</i> REE <i>HL</i> W <i>Q</i> V <i>A</i> RY <i>Q</i> <i>P</i> <i>T</i> <i>S</i> <i>L</i> <i>G</i> <i>E</i> LD <i>S</i> IG <i>L</i> SG <i>S</i> SE <i>E</i> IR <i>E</i>
ruler180.....190.....200.....210.....220.....230.....240.....250.....260.....270

<i>E_coli</i> _K12	-----XXXXXXXXXXXXXX-----
<i>E_coli</i> _CFT073	HGKT <i>LL</i> AL <i>V</i> EK <i>A</i> QT <i>L</i> <i>P</i> <i>E</i> <i>D</i> <i>AL</i> <i>P</i> <i>Q</i> <i>P</i> <i>M</i> <i>L</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> MP <i>G</i> Y <i>R</i> <i>K</i> <i>A</i> <i>F</i> <i>K</i> <i>A</i> <i>I</i> <i>S</i> <i>L</i> <i>I</i> <i>T</i> <i>D</i> <i>V</i> <i>S</i> <i>E</i> <i>T</i> <i>H</i> <i>K</i> <i>I</i> <i>S</i> <i>A</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>N</i> <i>W</i> <i>W</i> <i>W</i> <i>L</i> <i>K</i> <i>P</i> <i>Q</i> <i>N</i> <i>N</i> <i>L</i> <i>P</i> <i>E</i> <i>L</i> <i>I</i> <i>S</i> <i>G</i> <i>W</i> <i>R</i> <i>G</i> <i>E</i> <i>L</i> <i>M</i> <i>A</i> <i>E</i> <i>A</i> <i>L</i> <i>H</i> <i>N</i> <i>L</i>
<i>S_enterica</i> _CT18	HGKT <i>LL</i> AL <i>V</i> EK <i>A</i> QT <i>L</i> <i>P</i> <i>E</i> <i>D</i> <i>AL</i> <i>P</i> <i>Q</i> <i>P</i> <i>M</i> <i>L</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> MP <i>G</i> Y <i>R</i> <i>K</i> <i>A</i> <i>F</i> <i>K</i> <i>A</i> <i>I</i> <i>S</i> <i>L</i> <i>I</i> <i>T</i> <i>D</i> <i>V</i> <i>S</i> <i>E</i> <i>T</i> <i>H</i> <i>K</i> <i>I</i> <i>S</i> <i>A</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>N</i> <i>W</i> <i>W</i> <i>W</i> <i>L</i> <i>K</i> <i>P</i> <i>Q</i> <i>N</i> <i>N</i> <i>L</i> <i>P</i> <i>E</i> <i>L</i> <i>I</i> <i>S</i> <i>G</i> <i>W</i> <i>R</i> <i>G</i> <i>E</i> <i>L</i> <i>M</i> <i>A</i> <i>E</i> <i>A</i> <i>L</i> <i>H</i> <i>N</i> <i>L</i>
<i>S_enterica</i> _Ty2	HGKT <i>LL</i> IS <i>L</i> V <i>A</i> K <i>A</i> Q <i>A</i> <i>L</i> <i>P</i> <i>E</i> <i>A</i> <i>P</i> <i>L</i> <i>P</i> <i>E</i> <i>P</i> <i>L</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> MP <i>G</i> Y <i>R</i> <i>K</i> <i>A</i> <i>F</i> <i>K</i> <i>A</i> <i>I</i> <i>S</i> <i>L</i> <i>I</i> <i>T</i> <i>D</i> <i>V</i> <i>S</i> <i>E</i> <i>T</i> <i>H</i> <i>K</i> <i>I</i> <i>S</i> <i>A</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>N</i> <i>W</i> <i>W</i> <i>W</i> <i>L</i> <i>K</i> <i>P</i> <i>Q</i> <i>N</i> <i>N</i> <i>L</i> <i>P</i> <i>E</i> <i>L</i> <i>I</i> <i>S</i> <i>G</i> <i>W</i> <i>R</i> <i>A</i> <i>E</i> <i>L</i> <i>M</i> <i>K</i> <i>L</i> <i>L</i> <i>L</i>
<i>S_boydii</i>	HGKT <i>LL</i> IL <i>V</i> EK <i>A</i> QT <i>L</i> <i>P</i> <i>E</i> <i>D</i> <i>AL</i> <i>P</i> <i>Q</i> <i>P</i> <i>M</i> <i>L</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> MP <i>G</i> Y <i>R</i> <i>K</i> <i>A</i> <i>F</i> <i>K</i> <i>A</i> <i>I</i> <i>S</i> <i>L</i> <i>I</i> <i>T</i> <i>D</i> <i>V</i> <i>S</i> <i>E</i> <i>T</i> <i>H</i> <i>K</i> <i>I</i> <i>S</i> <i>A</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>N</i> <i>W</i> <i>W</i> <i>W</i> <i>L</i> <i>K</i> <i>P</i> <i>Q</i> <i>N</i> <i>N</i> <i>L</i> <i>P</i> <i>E</i> <i>L</i> <i>I</i> <i>S</i> <i>G</i> <i>W</i> <i>R</i> <i>G</i> <i>E</i> <i>L</i> <i>M</i> <i>A</i> <i>E</i> <i>A</i> <i>L</i> <i>H</i> <i>N</i> <i>L</i>
<i>S_dy</i> sentieriae	HGKT <i>LL</i> IL <i>V</i> EK <i>A</i> QT <i>L</i> <i>P</i> <i>E</i> <i>D</i> <i>AL</i> <i>P</i> <i>Q</i> <i>P</i> <i>M</i> <i>L</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> MP <i>G</i> Y <i>R</i> <i>K</i> <i>A</i> <i>F</i> <i>K</i> <i>A</i> <i>I</i> <i>S</i> <i>L</i> <i>I</i> <i>T</i> <i>D</i> <i>V</i> <i>S</i> <i>E</i> <i>T</i> <i>H</i> <i>K</i> <i>I</i> <i>S</i> <i>A</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>N</i> <i>W</i> <i>W</i> <i>W</i> <i>L</i> <i>K</i> <i>P</i> <i>Q</i> <i>N</i> <i>N</i> <i>L</i> <i>P</i> <i>E</i> <i>L</i> <i>I</i> <i>S</i> <i>G</i> <i>W</i> <i>R</i> <i>G</i> <i>E</i> <i>L</i> <i>M</i> <i>A</i> <i>E</i> <i>A</i> <i>L</i> <i>H</i> <i>N</i> <i>L</i>
<i>P_luminescens</i>	HGRR <i>LL</i> AM <i>V</i> A <i>E</i> <i>S</i> <i>G</i> <i>N</i> <i>I</i> <i>P</i> <i>E</i> <i>S</i> <i>C</i> <i>P</i> <i>P</i> <i>M</i> <i>T</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> QP <i>G</i> Y <i>R</i> <i>K</i> <i>A</i> <i>F</i> <i>K</i> <i>D</i> <i>I</i> <i>K</i> <i>L</i> <i>H</i> <i>Q</i> <i>V</i> <i>S</i> <i>E</i> <i>Q</i> <i>R</i> <i>F</i> <i>N</i> <i>S</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>S</i> <i>V</i> <i>W</i> <i>N</i> <i>L</i> <i>K</i> <i>Q</i> <i>L</i> <i>D</i> <i>K</i> <i>P</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>G</i> <i>W</i> <i>R</i> <i>E</i> <i>L</i> <i>A</i> <i>E</i> <i>P</i> <i>V</i> <i>E</i> <i>I</i> <i>L</i>
<i>Y</i> pestis	HGRT <i>LL</i> AL <i>V</i> A <i>E</i> <i>G</i> <i>N</i> <i>A</i> <i>V</i> <i>P</i> <i>E</i> <i>D</i> <i>O</i> <i>L</i> <i>P</i> <i>P</i> <i>P</i> <i>I</i> <i>A</i> <i>N</i> <i>L</i> <i>D</i> <i>D</i> QP <i>G</i> Y <i>K</i> <i>V</i> <i>F</i> <i>K</i> <i>D</i> <i>I</i> <i>K</i> <i>L</i> <i>Q</i> <i>S</i> <i>V</i> <i>E</i> <i>R</i> <i>S</i> <i>G</i> <i>L</i> <i>S</i> <i>E</i> <i>L</i> <i>L</i> <i>S</i> <i>R</i> <i>R</i> <i>O</i> <i>I</i> <i>Q</i> <i>L</i> <i>W</i> <i>W</i> <i>W</i> <i>L</i> <i>K</i> <i>L</i> <i>S</i> <i>D</i> <i>A</i> <i>Q</i> <i>P</i> <i>E</i> <i>L</i> <i>L</i> <i>T</i> <i>G</i> <i>W</i> <i>R</i> <i>G</i> <i>D</i> <i>L</i> <i>S</i> <i>S</i> <i>E</i> <i>L</i> <i>I</i> <i>L</i>
ruler280.....290.....300.....310.....320.....330.....340.....350.....360.....370

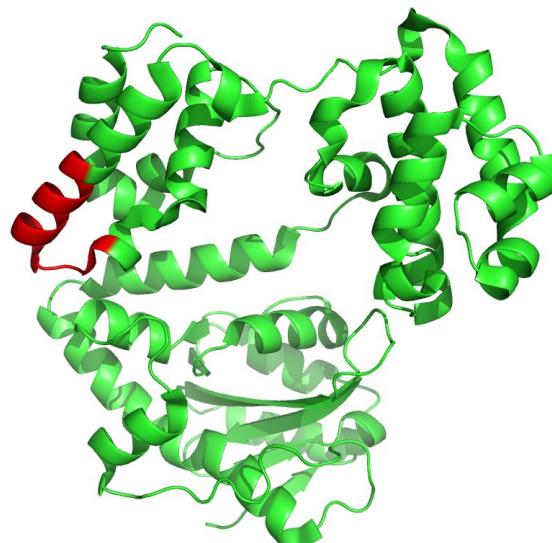


Figure S1.16: Sequence alignment and tertiary structure for gene *vsr*. The mutation cluster is highlighted in red.

E. coli K12 entry: b1960; PDB ID: 1cw0; chain ID: A

	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
<i>E_coli_K12</i>	MADVHDKATRSKNMRAIAATRDTAIEKRLASLLIGQGLAFRVDASLPGRPDFVVDEYRCVIFTGCFWHHHH-CYLFKVPAPTRTEFWLEKIGKNVERDRR
<i>E_coli_CFT073</i>	MVDVHDKATRSKNMRAIAATRDTAIEKRLASLLIGQGLAFRVDASLPGRPDFVVDEYRCVIFTGCFWHHHH-CYLFKVPAPTRTEFWLEKIGKNVERDRR
<i>S_enterica_CT18</i>	MADVHDKATRSKNMRAIAATRDTAIEKRLAGLLSAOGITFFHTQDTTILPGKPDFVVNDYDCVIFTGCFWHHHH-CYLFKVPAPTRTEFWLEKIGKNVERDRR
<i>S_enterica_Ty2</i>	MADVHDKATRSKNMRAIAATRDTAIEKRLAGLLSAOGITFFHTQDTTILPGKPDFVVNDYDCVIFTGCFWHHHH-CYLFKVPAPTRTEFWLEKIGKNVERDRR
<i>S_boydii</i>	MADVHDKATRSKNMRAIAATRDTAIEKRLASLLIGQGLAFRVDASLPGRPDFVVDEYLCVIFTGCFWHHHH-CYLFKVPAPTRTEFWLEKIGKNVERDRR
<i>S_dyenteriae</i>	MADVHDKATRSKNMRAIAATRDTAIEKRLASLLIGQGLAFRVDASLPGRPDFVVDEYLCVIFTGCFWHHHH-CYLFKVPAPTRTEFWLEKIGKNVERDRR
<i>P_luminescens</i>	MADVHNPS TRSKNMRAIRNC TAIEKKLVKILHDLGVITYRVQVRELPGKPDFV IDEYQAVLFVHGCFW GHN-CHLFKTPA TRTEFWLDKIEKNIRR DQF
<i>L_pneumophila</i>	M DKITPE HRSRNMAAIKNNTRP LEVRSYLF KNGFRYRLHRKDLP GKPDLT LTKYK TIFINGCFW RHTGCKLAYTPK NFEFWEOQ KFRKNVANDL W
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
<i>E_coli_K12</i>	DISRLQELGWRVLIIVWECALRGRE-KLIDEALTERLEEWI CCEGA SAQID TQGIR -LLA
<i>E_coli_CFT073</i>	DINRLQALGWRVLIIVWECALRGRE-KLIDEALTERLEEWI CCEGA SAQID TQGIR -LLA
<i>S_enterica_CT18</i>	DIQRQLALGWRVLIIVWECALRGRA-KLDAALAERLEEWI CGGGA SAQID TQGIR -LLA
<i>S_enterica_Ty2</i>	DIQRQLALGWRVLIIVWECALRGRA-KLDAALAERLEEWI CGGGA SAQID TQGIR -LLA
<i>S_boydii</i>	DISRLQELGWRVLIIVWECALRGRE-KLIDEALTERLEEWI CCEGA SAQID TQGIR -LLA
<i>S_dyenteriae</i>	DISRLQELGWRVLIIVWECALRGRE-KLIDEALTERLEEWI CCEGA SAQID TQGIR -LLA
<i>P_luminescens</i>	VMSLSDNSWKILVIWEC TLRGRL -KLIDNELSERIEEWLCASETHAEID VGTH ILL
<i>L_pneumophila</i>	KLKOLKMLGWKVIIIVWECEIKDKN WHDNEIK NGLDK DNK Y
ruler110.....120.....130.....140.....150.....

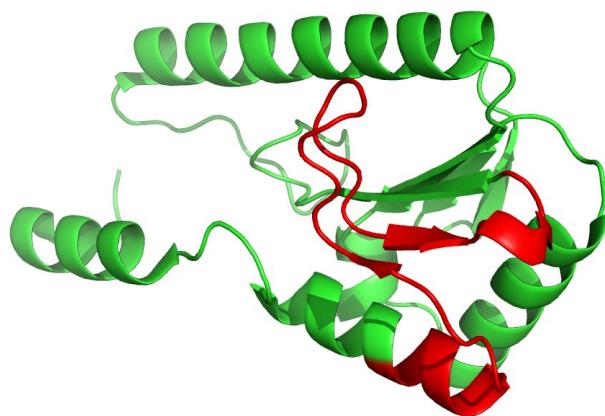


Figure S1.17: Sequence alignment and tertiary structure for gene *alkA*. The mutation cluster is highlighted in red.

E. coli K12 entry: b2068; PDB ID: 1mpg; chain ID: A

	XXXXXXXXXXXXXXXXXXXXXX
<i>E_coli_K12</i>	MYTLLNWQPPYDWSWMLGFLAARAVSVETVADSYYARESLAVGEYRGVTTAIPDIARHTLHINLSAGLEPVAECLAKMSRLFEDLOCNPQIVNGALGRLGA
<i>E_coli_CFT073</i>	MYTLLNWQPPYDWSWMLGFLAARAVSVETVADSYYARESLAVGEYRGVTTAIPDIARHTLHINLSAGLEPVAECLAKMSRLFEDLOCNPQIVNGALGKLGA
<i>S_enterica_CT18</i>	MYTLLSWQPPYDWSWMLGFLAARAVDGVEITVGEFYARSLSVVGEEHRLGLVSVRPHLTHTVQSVSAGLLEVAPACLAKVSRLEFDLDCQPEQVAAVLGPLGE
<i>S_enterica_Ty2</i>	MYTLLSWQPPYDWSWMLGFLAARAVDGVEITVGEFYARSLSVVGEEHRLGLVSVRPHLTHTVQSVSAGLLEVAPACLAKVSRLEFDLDCQPEQVAAVLGPLGE
<i>S_boydii</i>	MYTLLNWQPPYDWSWMLGFLAARAVSGVETVADDYYARESLAVCEYRGVTTAIPDIARHTLHINLSAGLEPVAECLAKMSRLFEDLOCNPQIVNGALGKLGA
<i>S_dyenteriae</i>	MYTLLNWQPPYDWSWMLGFLAARAVNGVEIVADDYYARESLAVGEYRGVTTAIPDIARHTLHINLSAGLEPVAECLAKMSRLFEDLOCNPQIVNGALGKLGV
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	XXXXXXXXXXXXXXXXXXXXXX
<i>E_coli_K12</i>	ARPGLRLPGCVDAFEQGVRAILGQLVSVAMAALKLTARVAOLYGERLDDFPEYICFFTPDRLAAADPQALKALGMPKRAEALIHLANAALEGTLPMTIPG
<i>E_coli_CFT073</i>	ARPGLRLPGCVDAFEQGVRAILGQLVSVAMAALKLSRVAOLYGERLDDFPEYICFFTPDRLAAADPQALKALGMPKRAEALIHLANAALEGTLPMTIPG
<i>S_enterica_CT18</i>	DRPGLRLPGSVDTFEGVRAILGQLVSVAMAARLTAKVARRGEALPDADPVCFPGPGETLALADPALKALGMPKRAEALIHLAQTALIAGKLALSAPP
<i>S_enterica_Ty2</i>	DRPGLRLPGSVDTFEGVRAILGQLVSVAMAARLTAKVARRGEALPDADPVCFPGPGETLALADPALKALGMPKRAEALIHLAQTALIAGKLALSAPP
<i>S_boydii</i>	ARPGLRLPGCIDAFCQGVRAILGQLVSVAMAALKLTAKVVLQLYGERLDDFPEYICFFTPDRLAAADPQALKALGMPKRAEALIHLANAALEGSLPMTIPG
<i>S_dyenteriae</i>	ARPGLRLPGSVDAFEQGVRAILGQLVSVAMAALKLTAKVAOLYGERLDDFPEYICFFTPDRLAAADPQALKALGMPKRAEALIHLANAALEGTLPMTIPG
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

	XXXXXXXXXXXXXXXXXXXXXX
<i>E_coli_K12</i>	DVEQAMKTLQTFPGIGRWIANYFALRGWQAKDVFLPDYDYLICKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDDEA-----
<i>E_coli_CFT073</i>	DVEQAMKTLQTFPGIGRWIANYFALRGWQAKDVFLPDYDYLICKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDDEA-----
<i>S_enterica_CT18</i>	DIEGSVKNLQTFPGIGRWIANYFALRGWQAKDIFLPDYYLIKICKRFAGMTAAQIRRYAERWKPWRSYALLHIWYTHGWQPSMDSEIAIGIO-----
<i>S_enterica_Ty2</i>	DIEGSVKNLQTFPGIGRWIANYFALRGWQAKDIFLPDYYLIKICKRFAGMTAAQIRRYAERWKPWRSYALLHIWYTHGWQPSMDSEIAIGIO-----
<i>S_boydii</i>	DVEQAMKTLQTFPGIGRWIANYFALRGWQAKDVFLPDYDYLICKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDGTDEL-----
<i>S_dyenteriae</i>	DVEQAMKTLQTFPGIGRWIANYFALRGWQAKDVFLPDYDYLICKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDDEA-----
ruler210.....220.....230.....240.....250.....260.....270.....280.....

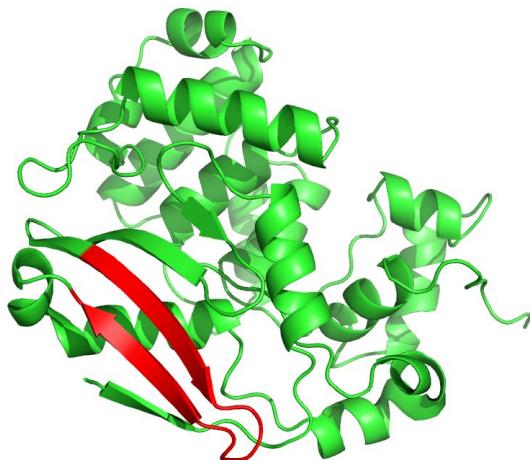


Figure S1.18: Sequence alignment and tertiary structure for gene *purN*. The mutation cluster is highlighted in red.

E. coli K12 entry: b2500; PDB ID: 1jkx; chain ID: A

	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
<i>E_coli</i> _K12	--MNIIVVLI <ins>CNGNSNLQAIIDACK</ins> [NKI]-KGTVRAVE <ins>SNKADAFGLERAR</ins> QAGIA <ins>THTLI</ins> IASAFDSREAYDREL <ins>IHEIDMYAPDV</ins> VVLAGFMRILSPAFV
<i>E_coli</i> _CFT073	--MNIIVVLI <ins>CNGNSNLQAIIDACK</ins> [NKI]-KGTVRAVE <ins>SNKADAFGLERAR</ins> QAGIA <ins>THTLI</ins> IASAFDSREAYDREL <ins>IHEIDMYAPDV</ins> VVLAGFMRILSPAFV
<i>S_enterica</i> _CT18	--MNIIVVLI <ins>CNGNSNLQAIIDACEAKK</ins> I-KGTVRAVE <ins>SNKADAFGLERAR</ins> QAGIA <ins>THTLI</ins> IASAFDSREAYDREL <ins>IHEIDMYAPDV</ins> VVLAGFMRILSPPMF
<i>S_enterica</i> _Ty2	--MNIIVVLI <ins>CNGNSNLQAIIDACEAKK</ins> I-KGTVRAVE <ins>SNKADAFGLERAR</ins> QAGIA <ins>THTLI</ins> IASAFDSREAYDREL <ins>IHEIDMYAPDV</ins> VVLAGFMRILSPPMF
<i>S_boydii</i>	--MNIIVVLI <ins>CNGNSNLQAIIDACK</ins> [NKI]-KGTVRAVE <ins>SNKADAFGLERAR</ins> QAGIA <ins>THTLI</ins> IASAFDSREAYDREL <ins>IHEIDMYAPDV</ins> VVLAGFMRILSPAFV
<i>S_dyssenteriae</i>	--MNIIVVLI <ins>CNGNSNLQAIIDACK</ins> [NKI]-KGTVRAVE <ins>SNKADAFGLERAR</ins> QAGIA <ins>THTLI</ins> IASAFDSREAYDREL <ins>IHEIDMYAPDV</ins> VVLAGFMRILSPAFV
<i>P_luminescens</i>	-MKNIVVLI <ins>GGGSNSNLQAOAVIDACQCNRI</ins> -NGQVCAVLNTANAY <ins>GLLRAK</ins> ADIP <ins>THVISPKN</ins> ADRQYDEALRK <ins>IDQYQPDLLV</ins> LAGYMRILTPDFV
<i>Y pestis</i>	-MKKIVVLI <ins>GGGSNSNLQAOALIDAQQGRI</ins> -SGKISAVFSEN <ins>NPAAYGLERAESAGI</ins> PHALDAKPTDRVSFDLALAQAIDQYQPDLLVLAGYMRILSPPEFV
<i>A_ferrooxidans</i>	<ins>L</ins> KRLVILV <ins>GRGSNLQSLAA</ins> CK <ins>GQI</ins> PTDQVVAVISNRPAAGALELAVLAGI <ins>PALTVDHRD</ins> Y <ins>GARVDFDAA</ins> LQRRI <ins>DYAPDV</ins> VVALAGFMRQLTPAFV
<i>L_pneumophila</i>	<ins>M</ins> RNL <ins>G</ins> TRGTNMLAL <ins>DAINEG</ins> IL-KAKIELVINS <ins>NSKSDAII</ins> LERAK <ins>SLG</ins> LNQAFVN <ins>PEG</ins> -NRIDFDKKV <ins>SDII</ins> LNH <ins>QIDLIVLIGY</ins> MRILSADFV
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
<i>E_coli</i> _K12	SHYAGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDSEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>E_coli</i> _CFT073	SHYAGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>S_enterica</i> _CT18	AHYYGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDSEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>S_enterica</i> _Ty2	AHYYGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>S_boydii</i>	SHYAGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>S_dyssenteriae</i>	SHYAGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>P_luminescens</i>	QHYLGRLLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>Y pestis</i>	KHYAGRMLN <ins>IHPSPLLPKYPG</ins> --LHTH <ins>RALENGDEEHGT</ins> VHFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>A_ferrooxidans</i>	QHYEGRMLN <ins>VEPSPLLPAFP</ins> --LHTH <ins>RALEQGV</ins> VLNEGA <ins>S</ins> HVFV <ins>I</ins> DEL <ins>DGGPV</ins> VILQAKV <ins>PVFAGDTEDDIT</ins> TARVQT <ins>QEHA</ins> IYPLVI <ins>SWFADGR</ins> LKMHEN
<i>L_pneumophila</i>	NKWNN <ins>W</ins> VIN <ins>VPSLPAFA</ins> CKMDVH <ins>I</ins> AVLD <ins>SGLKETGCT</ins> THFV <ins>I</ins> EEV <ins>DAGPV</ins> VILQKK <ins>CPVLEGDT</ins> ACTL <ins>KARV</ins> QLEG <ins>MALVAA</ins> INL <ins>IA</ins> SKG <ins>I</ins> --
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

<i>E_coli</i> _K12	AA-WLDG <ins>CORLPPQGYAADE</ins>
<i>E_coli</i> _CFT073	AA-WLDG <ins>CORLPPQGYAADE</ins>
<i>S_enterica</i> _CT18	AA-WLDG <ins>RRLPPQGYASDE</ins>
<i>S_enterica</i> _Ty2	AA-WLDG <ins>CORLPPQGYASDE</ins>
<i>S_boydii</i>	AA-WLDG <ins>CORLPPQGYAADE</ins>
<i>S_dyssenteriae</i>	AA-WLDG <ins>CORLPPQGYAADE</ins>
<i>P_luminescens</i>	KA-YLDG <ins>KILPPPEGYAAE</ins>
<i>Y pestis</i>	AA-WLDGV <ins>RVLPLQGYAAE</ins>
<i>A_ferrooxidans</i>	RAQWRD <ins>---</ins> PPETAMREA <ins>IAP</ins> SLEM
<i>L_pneumophila</i>	
ruler210.....220.....



Figure S1.19: Sequence alignment and tertiary structure for gene *glyA*. The mutation cluster is highlighted in red.

E. coli K12 entry: b2551; PDB ID: 1eqb; chain ID: B

<i>E_coli</i> _K12	--MLKREMNIAODYDAELWQAMEQEKVREEEHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDIVEGLAIDRAKELFGADYANVCPHSG
<i>E_coli</i> _CFT073	MRMLKREMNIAODYDAELWQAMEQEKVREEEHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDIVEGLAIDRAKELFGADYANVCPHSG
<i>S_enterica</i> _CT18	--MLKREMNIAODYDAELWQAMEQEKVREEEHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDVVEGLAIDRAKELFGADYANVCPHSG
<i>S_enterica</i> _Ty2	--MLKREMNIAODYDAELWQAMEQEKVREEEHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDIVEGLAIDRAKELFGADYANVCPHSG
<i>S_bordetiae</i>	--MLKREMNIAODYDAELWQAMEQEKVREEEHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDIVEGLAIDRAKELFGADYANVCPHSG
<i>S_dyenteriae</i>	--MLKREMNIAODYDAELWQAMEQEKVREEEHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDIVEGLAIDRAKELFGADYANVCPHSG
<i>P_luminescens</i>	--MLKREMNIAASYDPFLWQAMEQEVVRQEEHHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDVVEGLAIDRAKELFGADYANVCPHSG
<i>Y pestis</i>	--MLKREMNIAASYDPFLWQAMEQEVVRQEEHHIELIASENYTSPRVMCAOGSOLNTNKYAEGYPGKRYYGCCEYVDVVEGLAIDRAKELFGADYANVCPHSG
<i>B_aphidicola</i>	--MF1KNTIISNYDADAVYRMMKQYQRQBNHIELIASENYTSCVMBAOGSOLNTNKYAEGYPGKRYYGCCEYVDIAE E KIAIKRAKLLFNANYANVCPHSG
<i>A_ferrooxidans</i>	--MFSKLTIIADFD P LWDAMRKEARROEDHVVELIASENYAPMVMAOGSVLTNKYAEGYPGKRYYGCCEYVDIAE E LMANDRALELFGAEBHANVCAHSG
<i>L_pneumophila</i>	--MFDES T TKNFDDVLKAISDEKRRQEEHHIELIASENYTSPRLEAOGSVLTNKYAEGYPGKRYYGCCEFVDVAEELAISRALKLFGAHVNVPHSG
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100
 XXXXXXXXXXXXXX	
<i>E_coli</i> _K12	SQANFAVVTALLEPGDTIVLGMNLAHGGLLTHGS PVNFSGKLYNIVPVGID -ATGHIDYADELEKQAEHKPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>E_coli</i> _CFT073	SQANFAVVTALLEPGDTIVLGMNLAHGGLLTHGS PVNFSGKLYNIVPVGID -ATGHIDYADELEKQAEHKPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>S_enterica</i> _CT18	SQANFAVVTALLQPGDTIVLGMNLAQGGHLTHGS PVNFSGKLYNIVPVGID -ESCKIDYDEMAKLAKHEHPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>S_enterica</i> _Ty2	SQANFAVVTALLQPGDTIVLGMNLAQGGHLTHGS PVNFSGKLYNIVPVGID -ESCKIDYDEMAKLAKHEHPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>S_bordetiae</i>	SQANFAVVTALLEPGDTIVLGMNLAHGGLLTHGS PVNFSGKLYNIVPVGID -ATGHIDYADELEKQAEHKPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>S_dyenteriae</i>	SQANFTVVTALLEPGDTIVLGMNLAHGGLLTHGS PVNFSGKLYNIVPVGID -ESCKIDYDEMAKLAKHEHPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>P_luminescens</i>	SQANAAVVMALLQPGDTIVLGMNLAHGGLLTHGS PVNFSGKLYNIVPVGID -ESCKIDYDDIAAQAEHKPKMIIIGGF SAYSGVVWDWAKMREIAD IGAYL
<i>Y pestis</i>	SQANAVVSALLKPKDITVLMGMSLAHGGLLTHGS PVNFSGKLYNIVPVGID -ESQGIDYEDLARQAEHKPKMIIIGGF SAYSGIVWDWAKMREIAD IDAWF
<i>B_aphidicola</i>	SQANAVAVSALLKPKDITVLMGMSLAHGGLLTHGS PVNFSGKLYNIVPVGID -ESQGIDYEDLARQAEHKPKMIIIGGF SAYSGIVWDWAKMREIAD IDAWF
<i>A_ferrooxidans</i>	SQANQAVYLSVLQPGDKIMGMSLAHGGLLTHGAKVNVS GKLFQVAAGVRAEDGRIDYD AMAE AAERERPKMIVAGASAYSRVIDFARIGEIAR IGAIL
<i>L_pneumophila</i>	SQANAAVVMALLSPGD TFMGMALP FGGLLTHGS KVNFSGKLYHSVE GVVD N TLGLIDYDALEK LAQ HPK L IIAGF SAYSRILDWARFREIAD KGAYL
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200
 XXXXXXXXXXXXXX	
<i>E_coli</i> _K12	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPGG GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>E_coli</i> _CFT073	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPGG GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>S_enterica</i> _CT18	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPSA GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>S_enterica</i> _Ty2	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPSA GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>S_bordetiae</i>	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPSA GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>S_dyenteriae</i>	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPGG GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>P_luminescens</i>	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPGG GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>Y pestis</i>	FVDMAHVAGLVAAAGVPPNPVP PHAHVTTTTHK LAGPRGG LILAKGGSSEELYKKLN SAVFPGG GGPLMHVIA AGKAVALKEAMEPEEFKTYQQQVAKNAKA
<i>B_aphidicola</i>	FVDMAHISGLVAAAGLYPNPLKYAHVTTTTHK TL LSGP RGG LILAKG D QNV SLFKLNNS V PGC GGPLMHVIA AAKATAAFKEAMEPEEFKDY Y YQV1KNAQE
<i>A_ferrooxidans</i>	LVDMAHIAGLVAT GLE PS P V H AD V TTT THK LRGPRGG LILCR --EQYAKKVNSL I PG GGPLMHVIA AAKAVAFREAL O PEFKSYQQQV1HNAQE
<i>L_pneumophila</i>	MADIAHVG L VAVG Y PS P V P YAD V TTT THK LRGPRGG LILCR -ENEEIEKKLN S AV PPGM GGPLMHVIAAKAVAFEAELLPEFKTYQQQV1HNAQE
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300



Figure S1.20: Sequence alignment and tertiary structure for gene *truD*. The mutation cluster is highlighted in red.

E. coli K12 entry: b2745; PDB ID: 1si7; chain ID: A

<i>E_coli</i> K12	MIEFDNLITYLHGKPQGTGLLLKAN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>E_coli</i> CFT073	MIEFDNLITYLHGKPQGTGLLLKAN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>S_enterica</i> CT18	MIEFDNLITYLHGKPQGTGLLLKAN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>S_enterica</i> Ty2	MIEFDNLITYLHGKPQGTGLLLKAN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>S_boydii</i>	MIEFDNLITYLHGKPQGTGLLLKAN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>S_dyssenteriae</i>	MIEFDNLITYLHGKPQGTGLLLKAN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>P_luminescens</i>	-MVLAEILNWLYGQP-----PAGILKLN-----PEDIFFFFVEDLGFEPPDGEGERHILVMVIRKTGCNTQFVADSLAREFAGIPRSRSVSYAGLKDRHAVTEWFLCLHLPGK
<i>Y pestis</i>	-MDMENLTWLHGKPPTASGLKLN-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>A_ferrooxidans</i>	-MSESLNPRIY-----PAESGLLGAEMRQS-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
<i>L_pneumophila</i>	-MYSL-----WPRAXGIPNSTATPKLC-----PEDIFFFFVEDLGFEPPDGEGERHILVRILKNGCNTRFVADALAKEPLKIHAREVSFAGQDKKHAVTIEWLCLARVPGK
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

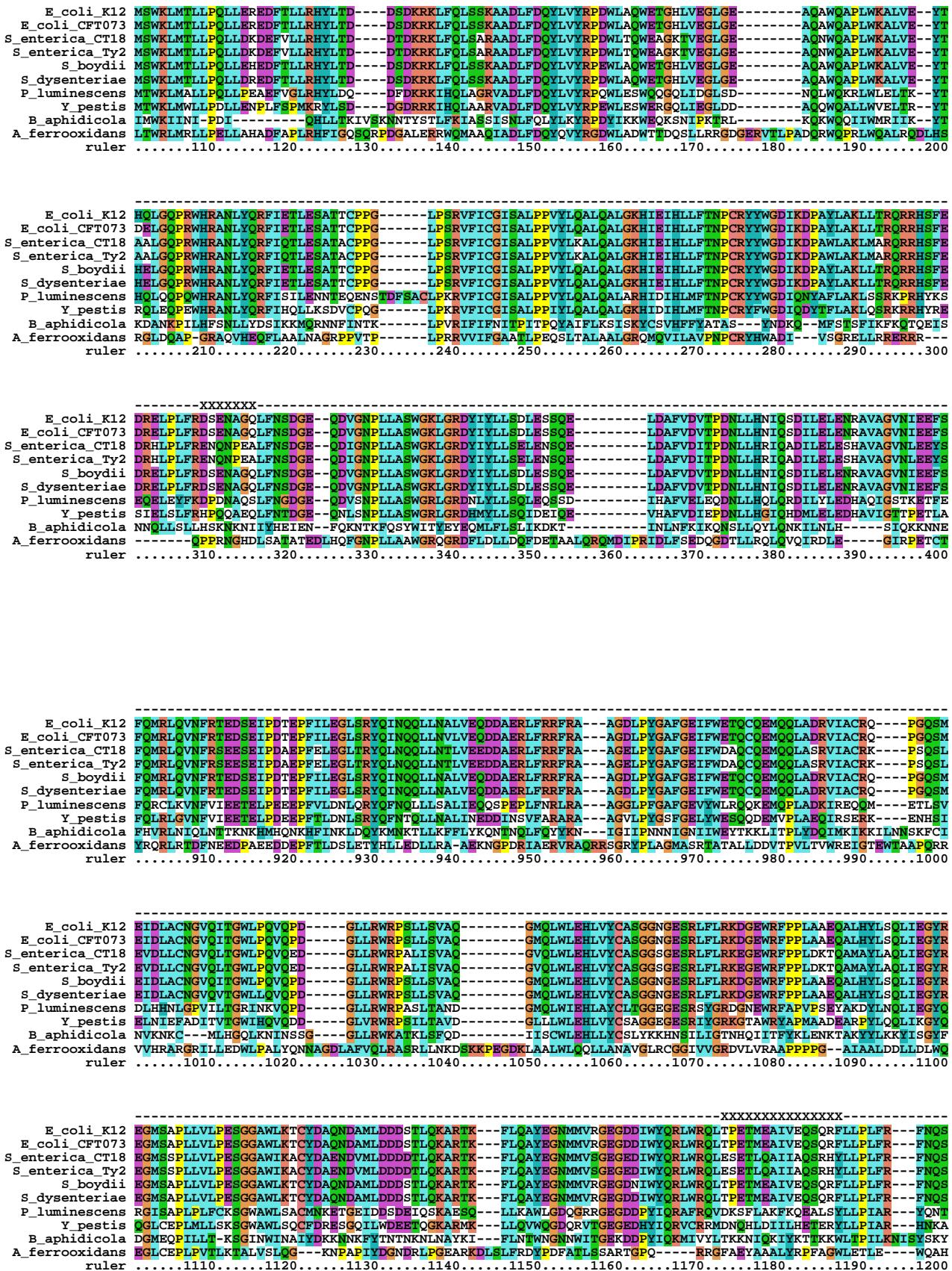
<i>E_coli</i> K12	-----XXXXXXXX-----XXXXXXXXXXXXX-----
<i>E_coli</i> CFT073	EMPDLSAFQLEGCVLVEYARHKRKRLRGALKGNAFTLVLREVSNRDDV-----EQRLLIDICVKGVVPNYFGAORFGIGGSNLOGAQWQINTPVDRDRNKRFSFWL
<i>S_enterica</i> CT18	EMPDLSAFQLEGCVLVEYARHKRKRLRGALKGNAFTLVLREVSNRDDV-----EQRLLIDICVKGVVPNYFGAORFGIGGSNLOGAQWQINTPVDRDRNKRFSFWL
<i>S_enterica</i> Ty2	EMPDLSAFQLEGCKVLEYARHKRKRLRGALKGNAFTLVLREISDRRDV-----EQLRQAIRDGGVPNYFGAORFGIGGSNLOGAQWQSNAPVDRDRNKRFSFWL
<i>S_boydii</i>	EMPDLSAFQLEGCVLVEYARHKRKRLRGALKGNAFTLVLREISDRRDV-----EQLRQAIRDGGVPNYFGAORFGIGGSNLOGAQWQSNAPVDRDRNKRFSFWL
<i>S_dyssenteriae</i>	EMPDLSAFQLEGCVLVEYARHKRKRLRGALKGNAFTLVLREISDRRDV-----EQLRQAIRDGGVPNYFGAORFGIGGSNLOGAQWQSNAPVDRDRNKRFSFWL
<i>P_luminescens</i>	EPDFASAFQLEGCEILTARQKRKRLRGALKGNSFTLILREISHHHOLV-----ENRLRLIQQGGVPNYFGEORFFGRDGQNLQIAQWRANNEIRVKERSKRSFYI
<i>Y pestis</i>	EAPDLA-----FELEGCEVLEAVRHKRKLRIGSLKGNAFTLVLRHITDQDV-----EQRLLQIAAQGPVNPFYFGSDFRGEGNNLIVQARLWANNEIRVKERSKRSFYI
<i>A_ferrooxidans</i>	SNPDWSLSEDDSLHLL-----OGRHEDRKLRLRRGVLRGNNHFQQLLRAFTGAHSLWDARLQILRKRFNPFYFGAORFFGH-----RNLDCAARLLSGOPMRVDRHRRGLHW
<i>L_pneumophila</i>	VIEGIE-----LEAPGWKILECTRHNKKLRLPGFLSGNHTFLRNVDSPESDL-IHRIEQIKFKGVPNYFGEORFFGRDGQNLKIAEEILVQGRKVKDRFLKGMYF
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

<i>E_coli</i> K12	SAARSALFNCIVAERLKKADVNQVVDGDAOLAGRGSWFVATTEELAEL-----RRVNDKELMITAALPGSGEWGTREALAFEQAAVAEETE-----L
<i>E_coli</i> CFT073	SAARSALFNCIVAERLKKADVNQVVDGDAOLAGRGSWFVATTEELAEL-----RRVNDKELMITAALPGSGEWGTREALAFEQAAVAEETE-----L
<i>S_enterica</i> CT18	SAARSALFNCIVHQRLKKPDPNQVVDGDAOLAGRGSWFVATTEELAEL-----RRVNDKELMITAALPGSGEWGTREALAFEQAAVAEETE-----L
<i>S_enterica</i> Ty2	SAARSALFNCIVHQRLKKPDPNQVVDGDAOLAGRGSWFVATTEELAEL-----RRVNDKELMITAALPGSGEWGTREALAFEQAAVAEETE-----L
<i>S_boydii</i>	SAARSALFNCIVHQRLKKPDPNQVVDGDAOLAGRGSWFVATTEELAEL-----RRVNDKELMITAALPGSGEWGTREALAFEQAAVAEETE-----L
<i>S_dyssenteriae</i>	SAARSALFNCIVHQRLKKPDPNQVVDGDAOLAGRGSWFVATTEELAEL-----RRVNDKELMITAALPGSGEWGTREALAFEQAAVAEETE-----L
<i>P_luminescens</i>	SASRSAMFNAVASARIALKQQQVIKGDALQLIQRGSWFVADTELPLLQQRVIDGEQITTAAPLPGDGELGTQHQADFERQYLOPYES-----L
<i>Y pestis</i>	SASRSAMFNLISSYRLAQQLSTTVLEGDALQLSGRGSWFVAQADEELAALQORVTAGELNITAPLPGDSLGTHGEALAFEQACLAEOTE-----L
<i>A_ferrooxidans</i>	SAARSALFNLVLAERVRCAWTBILPGEVVVLQLAGSHBIFLAEDDDLADLQARATWDLHPTGPLPGRGGLAPTLVAAALETSALGAGPVIAGTTDDGLHW
<i>L_pneumophila</i>	SAARSNLNLILSRVKESSWNLPLLGDIQLVGSNLFVNDKSLDEQILQIGEKDVSFASPLPGRSKNLVKGTALQIINEVYAWSA-----W
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300



Figure S1.21: Sequence alignment and tertiary structure for gene *recC*. The mutation cluster is highlighted in red.

E. coli K12 entry: b2822; PDB ID: 1w36; chain ID: C



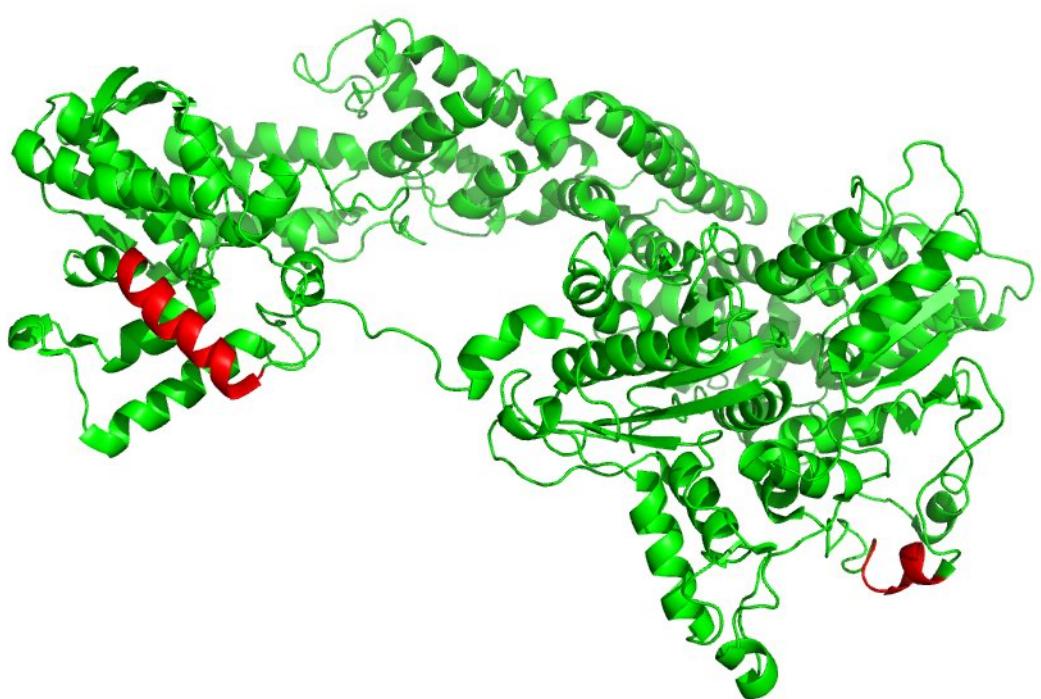


Figure S1.22: Sequence alignment and tertiary structure for gene *lysA*. The mutation cluster is highlighted in red.

E. coli K12 entry: b2838; PDB ID: 1knw; chain ID: A

	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
<i>E. coli</i> K12	-MPHSLSFSTDIDLTAAEN--LLRLPAEFGCPVWVYDAIIIRRCI	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>E. coli</i> CFT073	-MPHSLSFSTDIDLTAAEN--LLRLPAEFGCPVWVYDAIIIRRCI	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>S. enterica</i> CT18	-MSLPHYHAETDLNAEN--LLRLPAEFGCPVWVYDAIIIRRCI	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>S. enterica</i> Ty2	-MSLPHYHAETDLNAEN--LLRLPAEFGCPVWVYDAIIIRRCI	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>S. boydii</i>	-MPHSLSFSTDIDLTAAEN--LLRLPAEFGCPVWVYDAIIIRRCI	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>S. dysenteriae</i>	-MPHSLSFSTDIDLTAAEN--LLRLPAEFGCPVWVYDAIIIRRCI	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>P. luminescens</i>	VRETLMSSTTPNCFNLIPES--LGRLPETYGPLWVYDSEIIKI --NLLQFDVVRFAQKACSNITHILRLMREYGVKVDASLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL	-AALKQFDVVRFAQKACSNIHILRLMRQGVKVDVSLSLGEIERAL
<i>Y. pestis</i>	-MPRALNDRSALTAQN--LIALPERFGCPVWAYDGDIIAERKI	-NQLRHFDVVRFAQKACSNITHILRLMRQGVKVDVSLSLGEIERAL	-NQLRHFDVVRFAQKACSNITHILRLMRQGVKVDVSLSLGEIERAL
<i>B. aphidicola</i>	-VSGLLKKQRFSNCND--ILKIVSKYGPPLWVYDSNIIVKCI	-KELSQFDVIRFAQKSCSNIHILNLFYKYNVKIDAVSLGEIERAL	-KELSQFDVIRFAQKSCSNIHILNLFYKYNVKIDAVSLGEIERAL
<i>A. ferrooxidans</i>	-MNTFHYRDHALYGEDLPLQEEIAAHYGPVCVVYSEALREYHSP	-SAALQDNTRVCYAVKANBNGILRIFAEEMGAGFDIVSGGEELERV	-SAALQDNTRVCYAVKANBNGILRIFAEEMGAGFDIVSGGEELERV
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
<i>E. coli</i> K12	AAGYNPQTHPDDIVFTADVIDQAIL-ERVSELQIPVNAGSVDM L-DLGQVSPGHRVWLVRNPVPGFQGHGSQKTNTGGENSKHGI-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH
<i>E. coli</i> CFT073	AAGYNPQTHPDDIVFTADVIDQAIL-ERVSELQIPVNAGSVDM L-DLGQVSPGHRVWLVRNPVPGFQGHGSQKTNTGGENSKHGI-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH
<i>S. enterica</i> CT18	AAGYDPQTCPDDIVFTADVIDAATL-ARVSELHIPVNAGSVDM L-DLGQVSPGHRVWLVRNPVPGFQGHGSQKTNTGGENSKHGI-WHSDLPAALAVMOKYR	-WHSDLPAALAVMOKYR	-WHSDLPAALAVMOKYR
<i>S. enterica</i> Ty2	AAGYDPQTCPDDIVFTADVIDAATL-ARVSELHIPVNAGSVDM L-DLGQVSPGHRVWLVRNPVPGFQGHGSQKTNTGGENSKHGI-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH
<i>S. boydii</i>	AAGYNPQTHPDDIVFTADVIDQAIL-ERVSELQIPVNAGSVDM L-DLGQVSPGHRVWLVRNPVPGFQGHGSQKTNTGGENSKHGI-WHSDLPAALAVMOKYR	-WHSDLPAALAVMOKYR	-WHSDLPAALAVMOKYR
<i>S. dysenteriae</i>	AAGYNPQTHPDDIVFTADVIDQAIL-ERVSELQIPVNAGSVDM L-DLGQVSPGHRVWLVRNPVPGFQGHGSQKTNTGGENSKHGI-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH	-WYTDLPAALDVIQRH
<i>P. luminescens</i>	RAGFCPCQEVSDIIFTADLIDVSIL-QRVTEILDIPVNAGSIDMLEIIGQYKKGHPWLRLNPVPGFQGHGSQKTNTGGENSKHGI-WYQNLPOQAIKEKIRHYG	-WYQNLPOQAIKEKIRHYG	-WYQNLPOQAIKEKIRHYG
<i>Y. pestis</i>	HAGYQPQEPEAEIVFTADLIDQAIL-LRVIEELNIPVNAGSIDMLEDOLGQQAPGHPVWLRLNPVPGFQGHGSQKTNTGGENSKHGI-WHEELPRALKKIEHIG	-WHEELPRALKKIEHIG	-WHEELPRALKKIEHIG
<i>B. aphidicola</i>	ISKYRF-TMDQDVVFITSDIILEREL-NKVVQYKIPINIGSIDMLEVQGKISPGHNIWLRINPKFQGHGSKKTNTGGENSKHGI-WDINL--AFPYITKIN	-WDINL--AFPYITKIN	-WDINL--AFPYITKIN
<i>A. ferrooxidans</i>	RAGGDAGTIVPSGVFKSSVIRAAALGAGIFCFLNVESEAELWRADIADMGKRAPVALRVNPDPDVGTHRHYIAVGLKESKFGIPMDQARHLYLQAQHPA	-MDQARHLYLQAQHPA	-MDQARHLYLQAQHPA
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200110.....120.....130.....140.....150.....160.....170.....180.....190.....200110.....120.....130.....140.....150.....160.....170.....180.....190.....200

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<i>E. coli</i> K12	LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI SAGGLSVPYQCGEAVDTEHYYGLWNAAREQIARHLGHPVKLEIEPGRFLVAQSG	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI
<i>E. coli</i> CFT073	LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI SAGGLSIPYQCGEAVDTEHYYGLWNAAREQIARHLGHPVKLEIEPGRFLVAQSG	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI
<i>S. enterica</i> CT18	LKLVGIMMHIGSGV-DYGHLEQVCG--AMVROVIEFGODLQAI SAGGLSIPYHEGEEAVDTEHYYGLWNAAREQIARHLGHAVKLEIEPGRFLVAQSG	-LKLVGIMMHIGSGV-DYGHLEQVCG--AMVROVIEFGODLQAI	-LKLVGIMMHIGSGV-DYGHLEQVCG--AMVROVIEFGODLQAI
<i>S. enterica</i> Ty2	LKLVGIMMHIGSGV-DYGHLEQVCG--AMVROVIEFGODLQAI SAGGLSIPYHEGEEAVDTEHYYGLWNAAREQIARHLGHAVKLEIEPGRFLVAQSG	-LKLVGIMMHIGSGV-DYGHLEQVCG--AMVROVIEFGODLQAI	-LKLVGIMMHIGSGV-DYGHLEQVCG--AMVROVIEFGODLQAI
<i>S. boydii</i>	LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI SAGGLSIPYHEGEEAVDTEHYYGLWNAAREQIARHLGHAVKLEIEPGRFLVAQSG	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI
<i>S. dysenteriae</i>	LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI SAGGLSIPYHEGEEAVDTEHYYGLWNAAREQIARHLGHAVKLEIEPGRFLVAQSG	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI	-LQLVGIMMHIGSGV-DYAHLEQVCG--AMVROVIEFGODLQAI
<i>P. luminescens</i>	LKLLGLMHMHIGSGV-DYHHIASVCN--AMVEQVILCGEDIAI	-SAGGLSIPYQCGEAVDTEHYYGLWNAAROQIARHLGHPVKLEIEPGRFLVAQSG	-SAGGLSIPYQCGEAVDTEHYYGLWNAAROQIARHLGHPVKLEIEPGRFLVAQSG
<i>Y. pestis</i>	LTLVGIMMHIGSGV-DYQHLEQVCD--AMVQQVITLGHDI	-SAISAGGLSIPYQDFGDVDTTEHYYGLNSARERIAAHLGHPVSLEIEPGRFLVAESG	-SAISAGGLSIPYQDFGDVDTTEHYYGLNSARERIAAHLGHPVSLEIEPGRFLVAESG
<i>B. aphidicola</i>	FKLIGLMMHIGSGV-DYCHLKRVCK--AMIDQVLCKFKIHVI	-SAGGLSIPVPHCNDEPVNVKNYFFLWNKARKIIISNYLNRPPIRLEIEPGRFLVAESG	-SAGGLSIPVPHCNDEPVNVKNYFFLWNKARKIIISNYLNRPPIRLEIEPGRFLVAESG
<i>A. ferrooxidans</i>	LELKGIACHIGSQLDLTPGEAAGRVRALYDELAANGIALQHLDIGGGVGIRHDEIPPSAD VAWTIDQALC-----CVAVRVRVELGRALAGNAG	-VAWTIDQALC-----CVAVRVRVELGRALAGNAG	-VAWTIDQALC-----CVAVRVRVELGRALAGNAG
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300210.....220.....230.....240.....250.....260.....270.....280.....290.....300210.....220.....230.....240.....250.....260.....270.....280.....290.....300

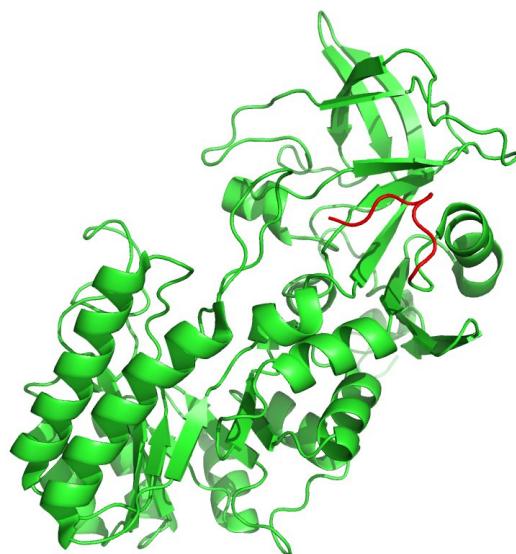


Figure S1.23: Sequence alignment and tertiary structure for gene *malP*. The mutation cluster is highlighted in red.

E. coli K12 entry: b3417; PDB ID: 1ahp; chain ID: A

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<i>E_coli_K12</i>	MSQPIFNDK	FQEALIROWQRVGLNSAAEMTPROWL	AVSEALAEMLRAOPFAKPVANQREHVNYISMEFLIGRLTGNNLLNLG
<i>E_coli_CFT073</i>	MSQPIFNDK	FQEALIROWQRVGLNSAAEMTPROWL	AVSEALAEMLRAOPFAKPVANQREHVNYISMEFLIGRLTGNNLLNLG
<i>S_enterica_Ct18</i>	MSQPIFNDK	FQAALIROWRFGLLSASDMTPROWQ	AVSGALAEELLASAOPVAQPTKGOREHVNYISMEFLIGRLTGNNLLNLG
<i>S_enterica_Ty2</i>	MSQPIFNDK	FQAALIROWRFGLLSASDMTPROWQ	AVSGALAEELLASAOPVAQPTKGOREHVNYISMEFLIGRLTGNNLLNLG
<i>S_bordetii</i>	MSQPIFNDK	FQEALIROWQRVGLNSAAEMTPROWL	AVSEALAEMLRAOPFAKPVANQREHVNYISMEFLIGRLTGNNLLNLG
<i>S_dyenteriae</i>	MSQPIFNDK	FQEALIROWQRVGLNSAAEMTPROWL	AVSEALAEMLRAOPFAKPVANQREHVNYISMEFLIGRLTGNNLLNLG
<i>P_luminescens</i>	MQSRLDKA	FQIAALIROWRFGLLSASDMTPROWQ	AVSAALSELVPACPVINHSEQQRHNVYISMEFLIGRLTGNNLLNLG
<i>Y pestis</i>	-MTSPFSYTS	-PVVSVD-LKHSIAYKLMF-I-GKDPTIATQHDWLNLATLF	FAVDRMRVERLRSNRNQLSQDVRQVYVLSMEFLLGRLSALLSMG
<i>A_ferrooxidans</i>	VSQPLSKTACPLPPLGMDALSRLMD	TCYLLRT-LGAETTAEPANSVYTALAMSLRDLRVERWKNTQKKVAABESGRRTF	YLSLEFLLGRAMGNALLNLG
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100		

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<i>E_coli_K12</i>	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRNSYPWFRRHEALDVGVCIG	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>E_coli_CFT073</i>	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>S_enterica_Ct18</i>	WYQDVSDVLKAHDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	WYQDVSDVLKAHDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>S_enterica_Ty2</i>	WYQDVSDVLKAHDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	WYQDVSDVLKAHDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>S_bordetii</i>	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>S_dyenteriae</i>	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	WYQDVQDSLKAYDINLTDLLEEEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>P_luminescens</i>	WYEDVQAYLAEEENIIILSDLEEQEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	WYEDVQAYLAEEENIIILSDLEEQEIDPAIGNGGLGRLAACFLDSMAIVGOSATGYGLFRQSFDGKQVEAPDDWHRGSYPWFRRHEALDVGVCIG	
<i>Y pestis</i>	INDEIEQALDEMGLSLSELLKEENDPGIGNGGLGRLAACFLDSLATLALPGRGYCIRYEGMFSSKIVNGQOMESPDNWLEYGNAWEFPFRHNTRKVRF	INDEIEQALDEMGLSLSELLKEENDPGIGNGGLGRLAACFLDSLATLALPGRGYCIRYEGMFSSKIVNGQOMESPDNWLEYGNAWEFPFRHNTRKVRF	
<i>A_ferrooxidans</i>	LEDAARAEALTREHRELVDIMELEPDAGLGNGLGRLAACFLDSCLGLPVIGYIRYSGMFRQEIRGGEVEEPDHWRNGCPNELKPERVRRVHF	LEDAARAEALTREHRELVDIMELEPDAGLGNGLGRLAACFLDSCLGLPVIGYIRYSGMFRQEIRGGEVEEPDHWRNGCPNELKPERVRRVHF	
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200		

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<i>E_coli_K12</i>	GK-VTKDG	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM
<i>E_coli_CFT073</i>	GK-VTKDG	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM
<i>S_enterica_Ct18</i>	GK-VTKEG	RWKPGFVIITCOSWDLPVLCYRNGVAOPLRLWQATHAHPFDLTKFDNGAFLRAEQQGIDAELKTKVLYPNDNHTAGKKLRM	RWKPGFVIITCOSWDLPVLCYRNGVAOPLRLWQATHAHPFDLTKFDNGAFLRAEQQGIDAELKTKVLYPNDNHTAGKKLRM
<i>S_enterica_Ty2</i>	GK-VTKEG	RWKPGFVIITCOSWDLPVLCYRNGVAOPLRLWQATHAHPFDLTKFDNGAFLRAEQQGIDAELKTKVLYPNDNHTAGKKLRM	RWKPGFVIITCOSWDLPVLCYRNGVAOPLRLWQATHAHPFDLTKFDNGAFLRAEQQGIDAELKTKVLYPNDNHTAGKKLRM
<i>S_bordetii</i>	GK-VTKDG	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM
<i>S_dyenteriae</i>	GK-VTKDG	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM	RWEPEFTIITCQAWDLPVVGYRNGVAOPLRLWQATHAHPFDLTKFDNGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRM
<i>P_luminescens</i>	GKVVIIDDGHE	TWQPEFTLIGEAWDLPVIGYRNGVTOPRLRWQATHASPFDLDKFNAGQFLITAEOQGVRAEAKLTTKVLYPNDNHTAGKKLRM	TWQPEFTLIGEAWDLPVIGYRNGVTOPRLRWQATHASPFDLDKFNAGQFLITAEOQGVRAEAKLTTKVLYPNDNHTAGKKLRM
<i>Y pestis</i>	GR-IQEGSK	IRWLETEELLLACAYDQIIIPGFDTDATNTLRLWSAQASNEINLGKFNQGDYFAAVEEDKNHSENVSRVLYFDDS-TYSGRELRLR	IRWLETEELLLACAYDQIIIPGFDTDATNTLRLWSAQASNEINLGKFNQGDYFAAVEEDKNHSENVSRVLYFDDS-TYSGRELRLR
<i>A_ferrooxidans</i>	GR---SDGTHDAQGRFHQRWVDTEDVLAVPYDIPIPGYRNEVVNTLRLWRATAIDIFDQLEFNAAGAEAVAAKNAEHIIMVLYPNDSSENGKELRIR	GR---SDGTHDAQGRFHQRWVDTEDVLAVPYDIPIPGYRNEVVNTLRLWRATAIDIFDQLEFNAAGAEAVAAKNAEHIIMVLYPNDSSENGKELRIR	
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300		



Figure S1.24: Sequence alignment and tertiary structure for gene *coaD*. The mutation cluster is highlighted in red.

E. coli K12 entry: b3634; PDB ID: 1qjc; chain ID: A

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<i>E_coli_K12</i>	MOKRAIYPGTFDPITNGHIDIVTRATQMFDEVILAIAAASP SKKKPMFTL LEERVALAQQATAHLGNVEVVGFS DL MANFARNQHATVLI R GLRAV
<i>E_coli_CFT073</i>	MOKRAIYPGTFDPITNGHIDIVTRATQMFDEVILAIAAASP GKPKPMFTL NERVALAQQATAHLGNVEVVGFS DL MANFARNQHATVLI R GLRAV
<i>S_enterica_Ct18</i>	MOKRAIYPGTFDPITNGHLDIVTRATQMFDEVILAIAAASP GKPKPMFTL NERVALAQQATAHLGNVEVVGFS DL MANFARNQHATVLI R GLRAV
<i>S_enterica_Ty2</i>	MOKRAIYPGTFDPITNGHIDIVTRATQMFDEVILAIAAASP GKPKPMFTL NERVALAQQATAHLGNVEVVGFS DL MANFARDQANIL R GLRAV
<i>S_boydii</i>	MOKRAIYPGTFDPITNGHLDIVTRATQMFDEVILAIAAASP GKPKPMFTL LEERVALAQQATAHLGNVEVVGFS DL MANFARNQHATVLI R GLRAV
<i>S_dyssenteriae</i>	MOKRAIYPGTFDPITNGHIDIVTRATQMFDEVILAIAAASP GKPKPMFTL NERVALAQQATAHLGNVEVVGFS DL MANFARNQHATVLI R GLRAV
<i>P_luminescens</i>	LMKTKAIYPGTFDPITNGHIDIVTRATQMFDEVILAIAAASP GKPKPMFTL LEERVALAQQATAHLGNVEVVGFS DL MANFARNQHATVLI R GLRAV
<i>Y pestis</i>	MITKAIYPGTFDPITNGHIDIVTRATQMFDEVILAIADSS KKPMFTL DERVALAKKVTAPE L KNVEVLGFS EL MAEFAKKHANILV R GLRSV
<i>A_ferrooxidans</i>	MTK P TERRVAYPGTFDPITNGHEDLVRRAAALFDEVVVA AA TAKTTIFPLAERVALAA A LGAI P GVRVPPGFLLI H LGEERAHLIL R GLRAI
<i>L_pneumophila</i>	MDMVINEMK M KRAIYPGTFDPITNGHIDIVTRA T IFP E LLIVAVAS N KNKR Y LS W ESRIS L LEESVG H LTGV R V V GF D NLL I DFV L E Q AG T ILE R GLRAV
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

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<i>E_coli_K12</i>	ADFEYE M LAHMNRHLMPE S VF L MP S KEWSFI SS SLV K EVARH Q GD V THFLP E NVHO Q ALMAKLA-----
<i>E_coli_CFT073</i>	ADFEYE M LAHMNRHLMPE S VF L MP S KEWSFI SS SLV K EVARH Q GD V THFLP E NVHO Q ALMAKLA-----
<i>S_enterica_Ct18</i>	ADFEYE M LAHMNRHLMPE S VF L MP S KEWSFI SS SLV K EVARH Q GD V THFLP E NVHO Q ALMDKLK-----
<i>S_enterica_Ty2</i>	ADFEYE M LAHMNRHLMPE S VF L MP S KEWSFI SS SLV K EVARH Q GD V THFLP E NVHO Q ALMAKLA-----
<i>S_boydii</i>	ADFEYE M LAHMNRHLMPE S VF L MP S KEWSFI SS SLV K EVARH Q GD V THFLP E NVHO Q ALMAKLA-----
<i>S_dyssenteriae</i>	ADFEYE M LAHMNRHLMPE S VF L MP S KEWSFI SS SLV K EVARH Q GD V THFLP E NVHO Q ALMAKLA-----
<i>P_luminescens</i>	SDFEYE W Q L ANMMNRHMP K LESV F LLPSQNLS F LI K D V AL H CGDI S FLP E PIA Q MLKKLK-----
<i>Y pestis</i>	SDFEYE W Q L ANMMNRHMP K LESV F LLPSQNLS F LI K D V AL H CGDI S FLP E PIA Q MLKKLK-----
<i>A_ferrooxidans</i>	SDFEHE F OLASINRRMDARIETLF L MTD Q H H TF L SS S LV R EISRL I R L GG D V A F V QP V AA A ALK R HFC C I G DPGAET-----
<i>L_pneumophila</i>	SDFEYE F OLAGMN R KL S KK V EL F LP A E H LM I IS S TV V REIA A LN D I E Q V PP N V R E L KK R QNE E -----
ruler110.....120.....130.....140.....150.....160.....170.....

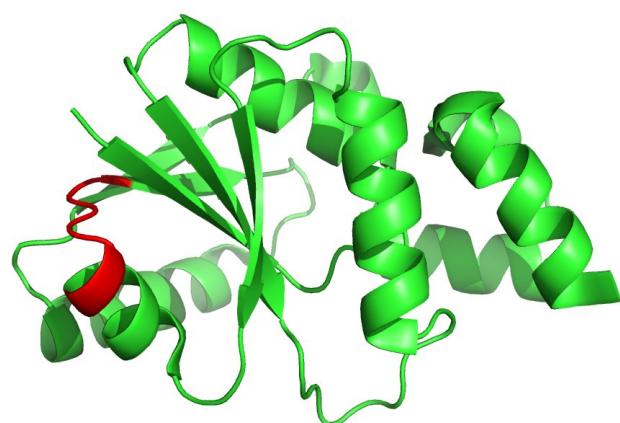


Figure S1.25: Sequence alignment and tertiary structure for gene *yicI*. The mutation cluster is highlighted in red.

E. coli K12 entry: b3656; PDB ID: 2f2h; chain ID: A

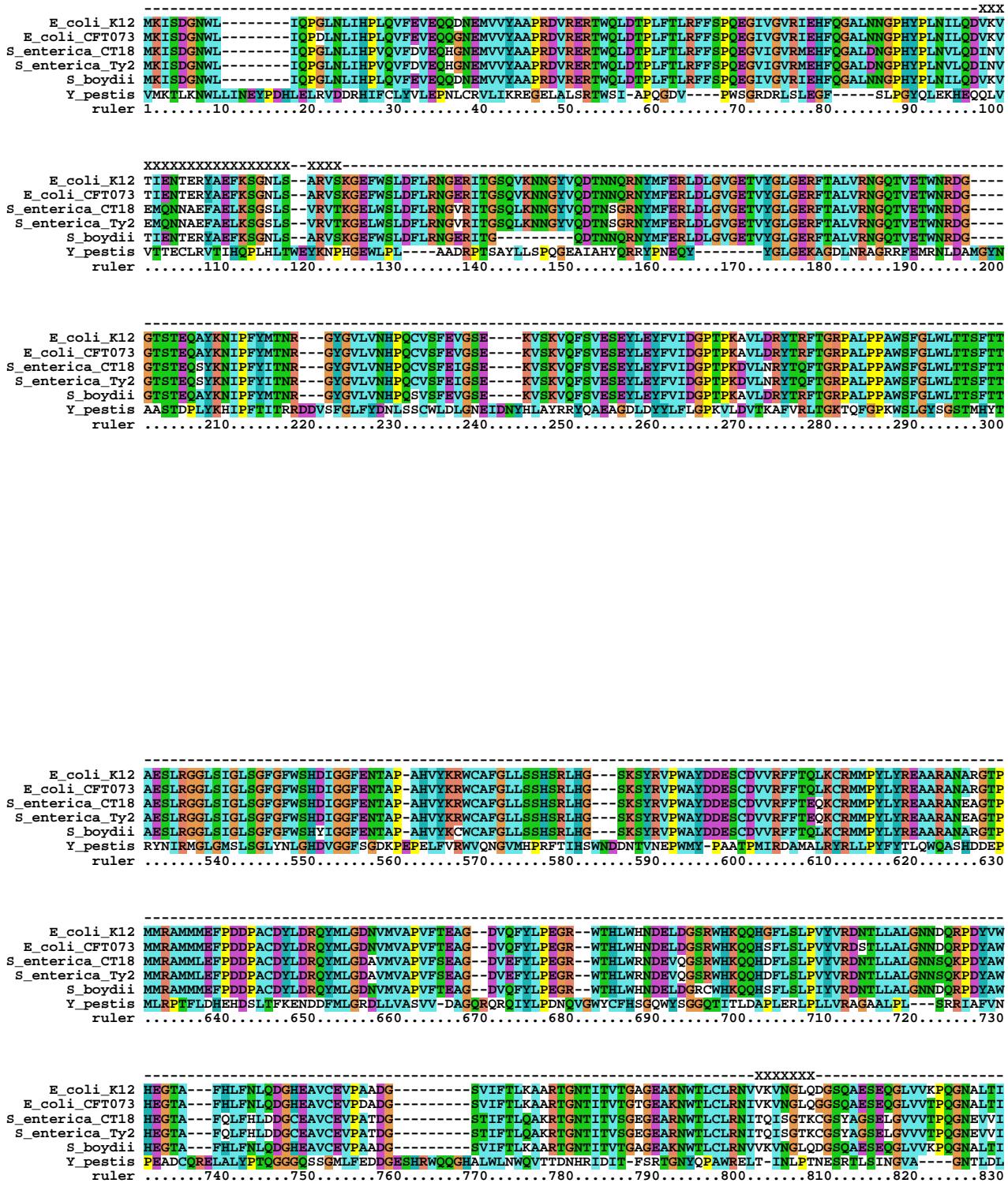




Figure S1.26: Sequence alignment and tertiary structure for gene *ubiC*. The mutation cluster is highlighted in red.

E. coli K12 entry: b4039; PDB ID: 1tt8; chain ID: A

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<i>E_coli</i> _K12	MRLLRFCCVL <ins>DHLICFTSPVNTFLRYNAFTLCNGEFGM</ins> SHPA <ins>L</ins> TQLR <ins>A</ins> LYCKE <ins>I</ins> -PAIDPO <ins>L</ins> LDW <ins>L</ins> LED <ins>S</ins> M <ins>K</ins> R <ins>F</ins> EQGKTV <ins>V</ins> SV <ins>V</ins> MI <ins>R</ins> GF <ins>V</ins> E <ins>N</ins> E <ins>I</ins> P
<i>E_coli</i> _CFT073	-----MSHPALTQ <ins>L</ins> R <ins>A</ins> LYCF <ins>T</ins> DAI-PALEP <ins>H</ins> L <ins>D</ins> W <ins>L</ins> LED <ins>S</ins> V <ins>I</ins> K <ins>R</ins> FEQ <ins>Q</ins> GKTV <ins>V</ins> SV <ins>V</ins> MI <ins>R</ins> GF <ins>V</ins> E <ins>N</ins> E <ins>I</ins> P
<i>S_enterica</i> _CT18	-----MSHPALTQ <ins>L</ins> R <ins>A</ins> LYCF <ins>T</ins> DAI-PALEP <ins>H</ins> L <ins>D</ins> W <ins>L</ins> LED <ins>S</ins> V <ins>I</ins> K <ins>R</ins> FEQ <ins>Q</ins> GKRV <ins>V</ins> SV <ins>V</ins> LI <ins>R</ins> EA <ins>F</ins> V <ins>G</ins> SE <ins>V</ins> E
<i>S_enterica</i> _Ty2	-----MSHPALTQ <ins>L</ins> R <ins>A</ins> LYCF <ins>T</ins> DAI-PALEP <ins>H</ins> L <ins>D</ins> W <ins>L</ins> LED <ins>S</ins> V <ins>I</ins> K <ins>R</ins> FEQ <ins>Q</ins> GKRV <ins>V</ins> SV <ins>V</ins> LI <ins>R</ins> EA <ins>F</ins> V <ins>G</ins> SE <ins>V</ins> E
<i>S_boydii</i>	<i>M</i> RLLRFCC <ins>C</ins> ALD <ins>D</ins> H <ins>L</ins> ICFTSPVNTFLRYNAFTLCNGEFGM <ins>SHPA</ins> <ins>L</ins> TQLR <ins>A</ins> LYCF <ins>I</ins> -PAIDPO <ins>L</ins> LDW <ins>L</ins> LED <ins>S</ins> M <ins>K</ins> R <ins>F</ins> EQGKTV <ins>V</ins> SV <ins>V</ins> MI <ins>R</ins> GF <ins>V</ins> E <ins>N</ins> E <ins>I</ins> P
<i>S_dy_senteriae</i>	<i>M</i> RLLRFCC <ins>C</ins> ALD <ins>D</ins> H <ins>L</ins> ICFTSPVNTFLRYNAFTLCNGEFGM <ins>SHPA</ins> <ins>L</ins> TQLR <ins>A</ins> LYCF <ins>I</ins> -PALEP <ins>P</ins> O <ins>L</ins> LDW <ins>L</ins> LED <ins>S</ins> M <ins>K</ins> R <ins>F</ins> EQGKTV <ins>V</ins> SV <ins>V</ins> MI <ins>R</ins> GF <ins>V</ins> E <ins>N</ins> E <ins>I</ins> P
<i>P_luminescens</i>	-----MEKRM <ins>S</ins> TDS <ins>I</ins> LTTVP <ins>I</ins> QWL <ins>S</ins> V <ins>D</ins> SPV <ins>L</ins> P <ins>D</ins> E <ins>V</ins> L <ins>D</ins> W <ins>L</ins> M <ins>E</ins> L <ins>G</ins> S <ins>M</ins> T <ins>R</ins> R <ins>F</ins> EO <ins>Y</ins> C <ins>N</ins> S <ins>V</ins> R <ins>I</ins> I <ins>P</ins> F <ins>R</ins> E <ins>C</ins> F <ins>I</ins> TE <ins>E</ins> Q <ins>S</ins>
<i>Y_pestis</i>	-----MF <ins>I</ins> G <ins>D</ins> A <ins>S</ins> I <ins>L</ins> K <ins>P</ins> I <ins>Q</ins> W <ins>C</ins> A <ins>T</ins> E <ins>H</ins> PE <ins>L</ins> F <ins>A</ins> I <ins>D</ins> W <ins>L</ins> M <ins>E</ins> L <ins>G</ins> S <ins>M</ins> T <ins>R</ins> R <ins>F</ins> EO <ins>H</ins> C <ins>R</ins> V <ins>H</ins> V <ins>E</ins> P <ins>O</ins> R <ins>C</ins> F <ins>I</ins> TR <ins>D</ins> AL <ins>G</ins>
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	XXXX
<i>E_coli</i> _K12	EELPL <ins>L</ins> KE <ins>S</ins> RYWL <ins>R</ins> RE <ins>I</ins> LLCADGE <ins>P</ins> W <ins>L</ins> A <ins>G</ins> RT <ins>V</ins> V <ins>P</ins> V <ins>S</ins> T <ins>L</ins> SG <ins>P</ins> E <ins>L</ins> AL <ins>O</ins> KL <ins>G</ins> K <ins>P</ins> PLGR <ins>Y</ins> L <ins>F</ins> T <ins>S</ins> ST <ins>L</ins> TR <ins>D</ins> FI <ins>E</ins> I <ins>G</ins> R <ins>D</ins> A <ins>G</ins> L <ins>W</ins> GR <ins>R</ins> S <ins>R</ins> R <ins>L</ins> R <ins>L</ins> S <ins>G</ins> K <ins>P</ins> L <ins>L</ins> LT <ins>E</ins> LF <ins>L</ins> PA <ins>S</ins>
<i>E_coli</i> _CFT073	EELPL <ins>L</ins> KE <ins>S</ins> RYWL <ins>R</ins> RE <ins>I</ins> LLCADGE <ins>P</ins> W <ins>L</ins> A <ins>G</ins> RT <ins>V</ins> V <ins>P</ins> V <ins>S</ins> T <ins>L</ins> SG <ins>P</ins> E <ins>L</ins> AL <ins>O</ins> KL <ins>G</ins> K <ins>P</ins> PLGR <ins>Y</ins> L <ins>F</ins> T <ins>S</ins> ST <ins>L</ins> TR <ins>D</ins> FI <ins>E</ins> I <ins>G</ins> R <ins>D</ins> A <ins>G</ins> L <ins>W</ins> GR <ins>R</ins> S <ins>R</ins> R <ins>L</ins> R <ins>L</ins> S <ins>G</ins> K <ins>P</ins> L <ins>L</ins> LT <ins>E</ins> LF <ins>L</ins> PA <ins>S</ins>
<i>S_enterica</i> _CT18	EASGLL <ins>P</ins> SE <ins>S</ins> RYWL <ins>R</ins> RE <ins>I</ins> LLCADGE <ins>P</ins> W <ins>L</ins> A <ins>G</ins> RT <ins>V</ins> V <ins>P</ins> V <ins>S</ins> T <ins>L</ins> SG <ins>P</ins> E <ins>L</ins> AL <ins>O</ins> KL <ins>G</ins> K <ins>P</ins> PLGR <ins>Y</ins> L <ins>F</ins> T <ins>S</ins> ST <ins>L</ins> TR <ins>D</ins> FI <ins>E</ins> I <ins>G</ins> R <ins>D</ins> A <ins>G</ins> L <ins>W</ins> GR <ins>R</ins> S <ins>R</ins> R <ins>L</ins> R <ins>L</ins> S <ins>G</ins> K <ins>P</ins> L <ins>L</ins> LT <ins>E</ins> LF <ins>L</ins> PA <ins>S</ins>
<i>S_enterica</i> _Ty2	EASGLL <ins>P</ins> SE <ins>S</ins> RYWL <ins>R</ins> RE <ins>I</ins> LLCADGE <ins>P</ins> W <ins>L</ins> A <ins>G</ins> RT <ins>V</ins> V <ins>P</ins> V <ins>S</ins> T <ins>L</ins> SG <ins>P</ins> E <ins>L</ins> AL <ins>O</ins> KL <ins>G</ins> K <ins>P</ins> PLGR <ins>Y</ins> L <ins>F</ins> T <ins>S</ins> ST <ins>L</ins> TR <ins>D</ins> FI <ins>E</ins> I <ins>G</ins> R <ins>D</ins> A <ins>G</ins> L <ins>W</ins> GR <ins>R</ins> S <ins>R</ins> R <ins>L</ins> R <ins>L</ins> S <ins>G</ins> K <ins>P</ins> L <ins>L</ins> LT <ins>E</ins> LF <ins>L</ins> PA <ins>S</ins>
<i>S_boydii</i>	EELPL <ins>L</ins> KE <ins>S</ins> RYWL <ins>R</ins> RE <ins>I</ins> LLCADGE <ins>P</ins> W <ins>L</ins> A <ins>G</ins> RT <ins>V</ins> V <ins>P</ins> V <ins>S</ins> T <ins>L</ins> SG <ins>P</ins> E <ins>L</ins> AL <ins>O</ins> KL <ins>G</ins> K <ins>P</ins> PLGR <ins>Y</ins> L <ins>F</ins> T <ins>S</ins> ST <ins>L</ins> TR <ins>D</ins> FI <ins>E</ins> I <ins>G</ins> R <ins>D</ins> A <ins>G</ins> L <ins>W</ins> GR <ins>R</ins> S <ins>R</ins> R <ins>L</ins> R <ins>L</ins> S <ins>G</ins> K <ins>P</ins> L <ins>L</ins> LT <ins>E</ins> LF <ins>L</ins> PA <ins>S</ins>
<i>S_dy_senteriae</i>	EELPL <ins>L</ins> KE <ins>S</ins> RYWL <ins>R</ins> RE <ins>I</ins> LLCADGE <ins>P</ins> W <ins>L</ins> A <ins>G</ins> RT <ins>V</ins> V <ins>P</ins> V <ins>S</ins> T <ins>L</ins> SG <ins>P</ins> E <ins>L</ins> AL <ins>O</ins> KL <ins>G</ins> K <ins>P</ins> PLGR <ins>Y</ins> L <ins>F</ins> T <ins>S</ins> ST <ins>L</ins> TR <ins>D</ins> FI <ins>E</ins> I <ins>G</ins> R <ins>D</ins> A <ins>G</ins> L <ins>W</ins> GR <ins>R</ins> S <ins>R</ins> R <ins>L</ins> R <ins>L</ins> S <ins>G</ins> K <ins>P</ins> L <ins>L</ins> LT <ins>E</ins> LF <ins>L</ins> PA <ins>S</ins>
<i>P_luminescens</i>	DENERLLT <ins>G</ins> Q <ins>R</ins> YWL <ins>R</ins> RE <ins>I</ins> VL <ins>C</ins> GD <ins>N</ins> IP <ins>W</ins> L <ins>G</ins> R <ins>T</ins> L <ins>P</ins> E <ins>T</ins> LL <ins>I</ins> GP <ins>D</ins> E <ins>S</ins> V <ins>D</ins> L <ins>G</ins> T <ins>V</ins> PLGR <ins>Y</ins> L <ins>F</ins> S <ins>G</ins> N <ins>K</ins> L <ins>P</ins> RD <ins>Y</ins> I <ins>H</ins> V <ins>G</ins> Q <ins>G</ins> NR <ins>W</ins> ARR <ins>S</ins> LL <ins>R</ins> L <ins>S</ins> G <ins>K</ins> P <ins>L</ins> LT <ins>E</ins> V <ins>F</ins> L <ins>P</ins> E <ins>S</ins>
<i>Y_pestis</i>	EEAEH <ins>H</ins> LEVS <ins>Q</ins> RYWL <ins>R</ins> RE <ins>I</ins> VL <ins>F</ins> GD <ins>N</ins> V <ins>P</ins> W <ins>L</ins> G <ins>R</ins> T <ins>V</ins> PE <ins>E</ins> IL <ins>S</ins> SG <ins>P</ins> D <ins>R</ins> A <ins>L</ins> V <ins>D</ins> L <ins>G</ins> T <ins>L</ins> PLGR <ins>Y</ins> L <ins>F</ins> S <ins>G</ins> D <ins>A</ins> L <ins>P</ins> RD <ins>Y</ins> I <ins>H</ins> V <ins>G</ins> R <ins>Q</ins> D <ins>N</ins> L <ins>W</ins> ARR <ins>S</ins> LL <ins>R</ins> L <ins>S</ins> G <ins>N</ins> P <ins>L</ins> LT <ins>E</ins> V <ins>F</ins> L <ins>P</ins> E <ins>S</ins>
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

<i>E_coli</i> _K12	PLY-----
<i>E_coli</i> _CFT073	PLY-----
<i>S_enterica</i> _CT18	PLY-----
<i>S_enterica</i> _Ty2	PLY-----
<i>S_boydii</i>	PLY-----
<i>S_dy_senteriae</i>	PLY-----
<i>P_luminescens</i>	PVVKR-----
<i>Y_pestis</i>	PLYTH <ins>C</ins> S <ins>I</ins> PK-----
ruler210.



Figure S1.27: Sequence alignment and tertiary structure for gene *frdA*. The mutation cluster is highlighted in red.

E. coli K12 entry: b4154; PDB ID: 1kf6; chain ID: A

<i>E. coli</i> K12	ELGPRDKVSQAFWHEWRKGNTI	STPRGDVVYLDLRHLGEKKLHERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ETRIKG
<i>E. coli</i> _CFT073	ELGPRDKVSQAFWHEWRKGNTI	STPRGDVVYLDLRHLGEKKLHERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ETRIKG
<i>S. enterica</i> _CT18	ELGPRDKVSQAFWHEWRKGNTI	STPRGDVVYLDLRHLGEKKLHERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ESRVKG
<i>S. enterica</i> _Ty2	ELGPRDKVSQAFWHEWRKGNTI	STPRGDVVYLDLRHLGEKKLHERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ESRVKG
<i>S. boydii</i>	ELGPRDKVSQAFWHEWRKGNTI	STPRGDVVYLDLRHLGEKKLHERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ETRIKG
<i>S. dysenteriae</i>	ELGPRDKVSQAFWHEWRKGNTI	STPRGDVVYLDLRHLGEKKLHERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ETRIKG
<i>P. luminescens</i>	ELGPRDKVSQAFWHEWRAGRIT	STPRGNVVYLDLRHLGEKKLLERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQKC	ETRIKG
<i>Y. pestis</i>	ELGPRDKVSQAFWHEWRAGRITVA	STPRGDVVYLDLRHLGEKKLLERLIPFICELAKAYGVDPVKEPIPVRPTAHYTMGGIEIDQNC	ETRIKG
<i>A. ferrooxidans</i>	ELAPRDIVARAIDLEMK	-----HOLDIVTLDISAQFATLVRRHFAIAFHCRAGIDLTRESIPVPPAHHYSCGGVVDEAG	-RTTIPG
<i>L. pneumophila</i>	DLASRDVVARAMALEIRAGKGFDPKGVDHVVKLKLHDGLMSRLPGIRELSMKFAGWDPIVEPIPVPVTCHYSMGGIP	TNMHGQVITRKDGDKEHVVEG	
ruler310.....320.....330.....340.....350.....360.....370.....380.....390.....400		

<i>E. coli</i> K12	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-	
<i>E. coli</i> _CFT073	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM		
<i>S. enterica</i> _CT18	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM		
<i>S. enterica</i> _Ty2	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM		
<i>S. boydii</i>	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM		
<i>S. dysenteriae</i>	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM		
<i>P. luminescens</i>	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQATERAAITAG-NGNEAAIEAQAAVGVEORLKDVLVNQDGGENWAKIRDDEMGLAMEEGCGIYRTPPELM		
<i>Y. pestis</i>	LFAVGECSSVGLHGANRLGSNSLAELLVFGRLAGEQALERAAITAG-PANGSALDAQTRDVETRLSNLMLQEGENWSKIRDDEMGLAMEEGCGIYRTPPELM		
<i>A. ferrooxidans</i>	LVAAGEVSTIGLHGANRLASNLLECVV-----AAAIIVADLEQARLPPRQTPGRSPGCOPTTAARRDINAA-----LRQNLOQNMWQAAIGIVRNRDEGL		
<i>L. pneumophila</i>	LVAAGEVACAVSVHGANRLASNLLECVV-----AAAIIVADLEQARLPPRQTPGRSPGCOPTTAARRDINAA-----LRQNLOQNMWQAAIGIVRNRDEGL		
ruler410.....420.....430.....440.....450.....460.....470.....480.....490.....500		

<i>E. coli</i> K12	QKTIDKLAELQERFKRVRIDTSSVFNTIDLLYTIELGGGLNVAECMAHSAMARKESRGAHORLDEGCTERDDVNFLKHTLAFRDAADGTTRELEYSDVK	--	
<i>E. coli</i> _CFT073	QKTIDKLAELQERFKRVRIDTSSVFNTIDLLYTIELGGGLNVAECMAHSAMARKESRGAHORLDEGCTERDDVNFLKHTLAFRDAADGTTRELEYSDVK	--	
<i>S. enterica</i> _CT18	QKTVDKLAELQERFKRVRIDTSSVFNTIDLLYTIELGGGLNVAECMAHSAMARKESRGAHORLDEGCTERDDVNFLKHTLAFRDAADGTTRELEYSDVK	--	
<i>S. enterica</i> _Ty2	QKTVDKLAELQERFKRVRIDTSSVFNTIDLLYTIELGGGLNVAECMAHSAMARKESRGAHORLDEGCTERDDVNFLKHTLAFRDAADGTTRELEYSDVK	--	
<i>S. boydii</i>	QKTIDKLAELQERFKRVRIDTSSVFNTIDLLYTIELGGGLNVAECMAHSAMARKESRGAHORLDEGCTERDDVNFLKHTLAFRDAADGTTRELEYSDVK	--	
<i>S. dysenteriae</i>	QKTIDKLAELQERFKRVRIDTSSVFNTIDLLYTIELGGGLNVAECMAHSAMARKESRGAHORLDEGCTERDDVNFLKHTLAFRDAADGTTRELEYSDVK	--	
<i>P. luminescens</i>	LKTIDKLAELKDRFKRVRIDTENVNFNTIDLLYTIELGSLDVAECMHSAIRKESRGAHORLDEGCTERDDDEKCLKHTLAFYDPESPVHLEYSDVK	--	
<i>Y. pestis</i>	QKTVDKLAELKERFKRVRIDHSSVFNTIDLLYTIELGYLDVAECMAHSALNRKESGRAHORLDEGCTERDDVNFLKHTLAFHPTPGGAPRIEYSDVK	--	
<i>A. ferrooxidans</i>	RAACAYWDE-RGTHISDSLCPQPYO-ELRNLCOCAKILTCACALLREESRGCHFN--SDHPQRRAV--AADSIQRDQQ--SPF--	--	
<i>L. pneumophila</i>	ASGLKRLQALRDRLAHAKLDDKQIFNTERVEAMLDNLMAAYAALSAIARTESRGAHSR-----EDYPRDDANWIKHTLYFEEGE--VIDYRPFVNTSE	--	
ruler510.....520.....530.....540.....550.....560.....570.....580.....590.....600		

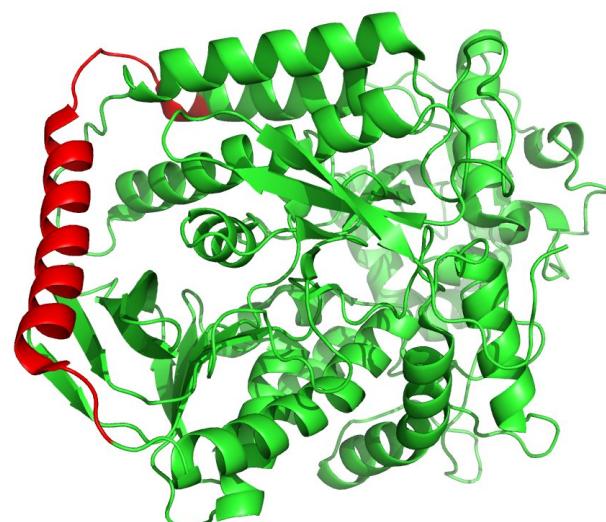


Figure S1.28: Sequence alignment and tertiary structure for gene *treC*. The mutation cluster is highlighted in red.

E. coli K12 entry: b4239; PDB ID: 1uok; chain ID: -

<i>E_coli</i> _K12	SSTSLEHCQRYAALTGSELSMTFNFHHLKVDYPGGEKWTLAKPDFVALKILFRHWNQGMHNVAWNALFWCNHDOPRIVSRFGDEGEYRVPAAKMLAMVLH
<i>E_coli</i> _CFT073	SSTSLEHCQRYAALTGSELSMTFNFHHLKVDYPGGEKWTLAKPDFVALKILFRHWNQGMHNVAWNALFWCNHDOPRIVSRFGDEGEYRVPAAKMLAMVLH
<i>S_enterica</i> _CT18	SSTTLENCQRYAALSGDELSMTFNFHHLKVDYPNGEKWTLAKPDFVALKALFRQNQGMHNVAWNALFWCNHDOPRIVSRFGDEGEYRVPAAKMLAMALH
<i>S_enterica</i> _Ty2	SSTTLENCQRYAALSGDELSMTFNFHHLKVDYPNGEKWTLAKPDFVALKALFRQNQGMHNVAWNALFWCNHDOPRIVSRFGDEGEYRVPAAKMLAMALH
<i>S_boydii</i>	SSTSLEHCQRYAALTGSELSMTFNFHHLKVDYPGGEKWTLAKPDFVALKILFRHWNQGMHNVAWNALFWCNHDOPRIVSRFGDEGEYRVPAAKMLAMVLH
<i>S_dyssenteriae</i>	SSTSLEHCQRYAALTGSELSMTFNFHHLKVDYPGGEKWTLAKPDFVALKILFRHWNQGMHNVAWNALFWCNHDOPRIVSRFGDEGEYRVPAAKMLAMVLH
<i>P_luminescens</i>	SSTSLEHCQRYSSLDGEELSMVFAFHHLKVDYPNGEKWVAAAPPDFIELKKIFAKWQGMYERAWNALFWCNHDOPRIVSRFGGEGVWRVPSAKMLAMVLH
<i>Y_pestis</i>	SSTRLEHCQRYAALGDELSTMFTNFHHLKVDYLNQGEKWSLMPPNRVELKHIFNQWQGMHNRAWNALFWCNHDOPRIVSRFGHEGALRLPAAKMLAMVLH
ruler270.....280.....290.....300.....310.....320.....330.....340.....350.....360

<i>E_coli</i> _K12	GMCGTPVIYQGEETGMTPHFTTRITDYDRDVESELNMFAE-LRNDGRDADELLAILAASKSRDNSRPFMOWSNGDNAGFTAGEPWIIGLGDNYQGINVEAALAD
<i>E_coli</i> _CFT073	GMCGTPVIYQGEETGMTPHFTTRITDYDRDVESELNMFAE-LRNDGRDADELLAILAASKSRDNSRPFMOWTNGDNAGFTAGEPWIIGLGDNYQGINVEAALAD
<i>S_enterica</i> _CT18	GMCGTPVIYQGEETGMTPHFTTRITDYDRDVESELNMFAA-LRAAGRPDELLAILAASKSRDNSRPFMOWDNGKNAAGFTQGEPWISLCNDNTTEVNVAALRD
<i>S_enterica</i> _Ty2	GMCGTPVIYQGEETGMTPHFTTRITDYDRDVESELNMFAA-LRAAGRPDELLAILAASKSRDNSRPFMOWDNGKNAAGFTQGEPWISLCNDNTTEVNVAALRD
<i>S_boydii</i>	GMCGTPVIYQGEETGMTPHFTTRITDYDRDVESELNMFAE-LRNDGRDADELLAILAASKSRDNSRPFMOWSNGDNAGFTAGEPWIIGLGDNYQGINVEAALAD
<i>S_dyssenteriae</i>	GMCGTPVIYQGEETGMTPHFTTRITDYDRDVESELNMFAE-LRNDGRDADELLAILAASKSRDNSRPFMOWSNGDNAGFTAGEPWIIGLGDNYQGINVEAALAD
<i>P_luminescens</i>	GMCGTPVIYQGEETGMTPHFSHIEEYRDIESLNLYQE-KIEQGNDQOILSVLAKKSRDNGRTPMQWDTTANAGFTQGEPWIALNSDYQDVNAENAMQD
<i>Y_pestis</i>	GMCGTPVIYQGEETGMTPNPTEDTQYDRDVESELNMFAE-LSVAGRPDELLAILAAKSRSRDPFMOWDSSDAGFSQGTPWIAPCSNYHEINVNAALAD
ruler370.....380.....390.....400.....410.....420.....430.....440.....450.....460

<i>E_coli</i> _K12	XX--XXXXXXXXXXXXXXXXXXXX
<i>E_coli</i> _CFT073	ESSVFYTQKLIALRKQEAVLTWGNYQDLPNPSPVLCYRREWKQQLLLVIANLREICDPWQACQMR--GNWOLVMHNYYEEASPOPCAMNLRPFEAVWWL
<i>S_enterica</i> _CT18	ESSVFYTQKLIALRKQEAVLTWGNYQDLPNPSPVLCYRREWKQQLLLVIANLREICDPWQACQMR--GNWOLVMHNYYEEASPOPCAMNLRPFEAVWWL
<i>S_enterica</i> _Ty2	ESSVFYTQKLIALRKQEAVLTWGNYQDLPNPSPVLCYRREWKQQLLLVIANLREICDPWQACQMR--GNWOLVMHNYYEEASPOPCAMNLRPFEAVWWL
<i>S_boydii</i>	ESSVFYTQKLIALRKQEAVLTWGNYQDLPNPSPVLCYRREWKQQLLLVIANLREICDPWQACQMR--GNWOLVMHNYYEEASPOPCAMNLRPFEAVWWL
<i>S_dyssenteriae</i>	ESSVFYTQKLIALRKQEAVLTWGNYQDLPNPSPVLCYRREWKQQLLLVIANLREICDPWQACQMR--GNWOLVMHNYYEEASPOPCAMNLRPFEAVWWL
<i>P_luminescens</i>	DDSVFHCYARLIKLRKEYPVLTIGSYEDLLPSHPSLWCYVRRWENQTLVIANLSEVEVKWSLDASLDCSNVKLMGNYPENHVPAKDMQLQPYEAVYWL
<i>Y_pestis</i>	ADSVFAYQYLIALRKQYDIFTGQYDLCPOHQPDWLCYLRSWQKQLLVANLSEEPQRWQPEGLTLDGNWLLMSSYDQAFQDMILRGYEGIYVW
ruler470.....480.....490.....500.....510.....520.....530.....540.....550.....560

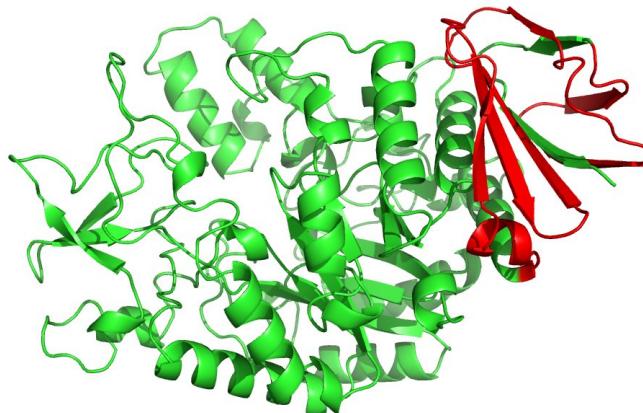


Figure S1.29: Sequence alignment and tertiary structure for gene *yjjV*. The mutation cluster is highlighted in red.

E. coli K12 entry: b4378; PDB ID: 1zzm; chain ID: A

	10.....	20.....	30.....	40.....	50.....	60.....	70.....	80.....	90.....	100.....
<i>E. coli</i> K12											
<i>E. coli</i> CFT073	LICRFIDTHCHFDF	PPFGSGDEEASLQRAAQAGVGKIIIVPATEAENFARVQALAEK	VLALAENQPLYAALGLPGMLEKHSVDVSLEQLQQALERPAKVVAVGE								
<i>S. enterica</i> CT18	VSWRFIDTHCHFDF	PPFTGDERASIQRACEAGVEKIIIVPATEAAHFPRVLALAARFFSLQYAAALGLPIVIERHADD	PDKLQQALAAQQQN-VVAVGE								
<i>S. enterica</i> Ty2	VSWRFIDTHCHFDF	PPFTGDERASIQRACEAGVEKIIIVPATEAAHFPRVLALAARFFSLQYAAALGLPIVIERHADD	PDKLQQALAAQQQN-VVAVGE								
<i>S. boydii</i>	LICRFIDTHCHFDF	LPFGSGDEEASLQRAAQAGVGKIIIVPATEAENFARVQALAEK	QPLYAALGLPGMLEKHSVDVSLEQLQQALERPAKVVAVGE								
<i>S. dysenteriae</i>	LICRFIDTHCHFDF	LPFGSGDEEASLQRAAQAGVGKIIIVPATEAENFARVQALAEK	QPLYAALGLPGMLEKHSVDVSLEQLQQALERPAKVVAVGE								
<i>P. luminescens</i>	-MFIDTHCHFDF	-PPFRDDEQSLQRAAQAGVGKIIIVPATEAENFARVQALAEK	-FLKQKHEKLVAVGE								
<i>Y. pestis</i>	MYPIDTHCHFDF	-PPFTGDEAASLACAAEVRLIVPSVKAAYFSRILALADRPLPFAALGLPLYIAEHEDLAALASHLADKPKLVAIGE									
<i>A. ferrooxidans</i>	MHGIDSHCHLDD	-AAPDDDRDAVLCRAGMAGVRKMVLPAYTPKYWGRLLRETCCRWPGLMPAYGVPLYILEDRDQWEATLASFLAD---	AVALGE								
<i>L. pneumophila</i>	--VLDPSHCHLNFD	--LTHPHHDLAQVNIQARNEVEFLSVCCVELSDYPSLERLAKDIPDISISVGVVPN--SEMNYPVIAQMLCELAQNPACIAIGE									
ruler	10.....	20.....	30.....	40.....	50.....	60.....	70.....	80.....	90.....	100.....

	10.....	20.....	30.....	40.....	50.....	60.....	70.....	80.....	90.....	100.....
<i>E. coli</i> K12	IGLDLFGDDPQFER	-QWLDEQLKAKRYDLPLVILHSRRTHDKLAMHLKRHDLP	-IGVHGFSGSLQQAERFVOLGYKIGVGGTTITVPRASKTRDV								
<i>E. coli</i> CFT073	IGLDLFGDDPQFER	-QWLDEQLKAKRYDLPLVILHSRRTHDKLAMHLKRHDLP	-IGVHGFSGSLQQAERFVOLGYKIGVGGTTITVPRASKTRDV								
<i>S. enterica</i> CT18	IGLDLYRDDPQFER	-QERFLDAQLQLAKAKRYDLPLVILHSRRTHDKLAMRLKRQSILP	-IGVHGFSGSLQQAERFVOLGYKIGVGGTTITVPRASKTRDV								
<i>S. enterica</i> Ty2	IGLDLYRDDPQFER	-QERFLDAQLQLAKAKRYDLPLVILHSRRTHDKLAMRLKRQSILP	-IGVHGFSGSLQQAERFVOLGYKIGVGGTTITVPRASKTRDV								
<i>S. boydii</i>	IGLDLFGDDPQFER	-QWLDEQLKAKRYDLPLVILHSRRTHDKLAMHLKRHDLSR	-IGVHGFSGSLQQAERFVOLGYKIGVGGTTITVPRASKTRDV								
<i>S. dysenteriae</i>	IGLDLYRDDPQFER	-QWLDEQLKAKRYDLPLVILHSRRTHDKLAMHLKRHDLSR	-IGVHGFSGSLQQAERFVOLGYKIGVGGTTITVPRASKTRDV								
<i>P. luminescens</i>	IGLDLYMTEPQFEK	-OKALLCDPLRLAKQYELPVLILHSRRSHDQALAIIRRLNLR	-IGVHGFAGSISQAFAFIGLGYYLGVGGTTITVERAQKTRRV								
<i>Y. pestis</i>	IGLDLYMDEPQFPH	-OLVILNMOLELAKQHDLPLVILHSRRSHDPLAAALRKAALPR	-AGVINGFAGSISQAFAIFRLGYYIGVGGTTITVRAQKTRRV								
<i>A. ferrooxidans</i>	IGLDASAGTPDAAC	-ORAGFTTQLAMAQQLGLPVILHSRRSHDPLAAALRKAALPR	-FPLRGLVHSFGSFVQARLLIDMGFLLGGLGALTTRARRRLRAIA								
<i>L. pneumophila</i>	IGLDYFRNPTBEA	QS1QLQRDRFREHIIKALAITSKPLIITRAAED	LLMMAKEGAGSISQGGVMHCAEIDDIAARAIDLNFYISFSGIVTFKNAVSLQDVA								
ruler	110.....	120.....	130.....	140.....	150.....	160.....	170.....	180.....	190.....	200.....

	10.....	20.....	30.....	40.....	50.....	60.....	70.....	80.....	90.....	100.....
<i>E. coli</i> K12	AKLPLASLILLETDAPDPMPLNGFOCOPNRPQAAARVFAVLCELREP	ADAEIAQALLNNNTYTLFNVP									
<i>E. coli</i> CFT073	AKLPLASLILLETDAPDPMPLNGFOCOPNRPQAAARVFAVLCELREP	ADAEIAEVLLNNNTYTLFNVP									
<i>S. enterica</i> CT18	ARLPLDALLLLETDAAPDPMPLKGFCQCPNRPQAAARVFDALCELREP	PEPAEVIAIDLRLRNTVFLFRL									
<i>S. enterica</i> Ty2	ARLPLDALLLLETDAAPDPMPLKGFCQCPNRPQAAARVFDALCELREP	PEPAEVIAIDLRLRNTVFLFRL									
<i>S. boydii</i>	AKLPLASLILLETDAPDPMPLKGFCQCPNRPQAAARVFDALCELREP	PEPAEVIAIDLRLRNTVFLFRL									
<i>S. dysenteriae</i>	AKLPLASLILLETDAPDPMPLKGFCQCPNRPQAAARVFDALCELREP	PEPAEVIAIDLRLRNTVFLFRL									
<i>P. luminescens</i>	AELPLTSVLLETDAAPDPMPLFGFCQEPNRPKEKIAGVFAFLCELREP	ADAEIAEVLLNNNTYALFSVSG									
<i>Y. pestis</i>	ASLPLSILLLETDAAPDMPLASFOCQANRPERAANVFALCELREP	ADAEIAELMCNSQRLFSLPPPLR									
<i>A. ferrooxidans</i>	ATLPAEFLLAETDAPWQPPPHAPGARNEPAYLREIIIADIAQRLHTSVQEIRARIATAQNALSLFLHQDVS-										
<i>L. pneumophila</i>	RQIPLERLILETDSPYLAPVPHRGQNMHPALVKHVAEAIAQURGMDFQEIAEITINNFINCNFNIKROG										
ruler	210.....	220.....	230.....	240.....	250.....	260.....				

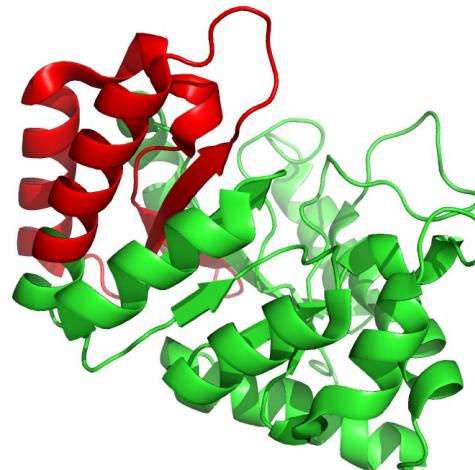


Figure S1.30: Sequence alignment and tertiary structure for gene *wbl*. The mutation cluster is highlighted in red.

D. melanogaster FlyBase ID: FBgn0004003; PDB ID: 1ovn; chain ID: B

<i>D_melanogaster</i>	MMHILVVL--LLVAI	HSIPTTW-AVCTGCVVLDDELSPFETKTVVERPPYSVVKFDIAVPYGEKEHEAFTAFSKSAHKATKDLLIATVGVKDYGEBLENKALG
<i>D_simulans</i>	MMHILVVL--LLVAC	HSIPTTW-AVCTGCVVLDDELSPQTKTVERPPYSIVKFDIAVPYGEKEHEAFTAFSKSAHKATKDLLIATVGVKDYGEBLENKALG
<i>D_yakuba</i>	MMHILVVL--LLVAF	HAIPISTW-AVCTGCVVLDDELSPQQTVERPPYSIVKFDIAVPYGEKEHEAFTAFSKSAHKATKDLLIATVGVKDYGEBLENKALG
<i>D_erecta</i>	MMHILVVL--LLVAF	HAIPISTW-AVCTGCVVLDDELSPQQTVERPPYSIVKFDIAVPYGEKEHEAFTAFSKSAHKATKDLLIATVGVKDYGEBLENKALG
<i>D_ananassae</i>	MMRILVVL--LLVAF	HAIPISTW-AIISCGGCVLDDELINFQTKTVERPPYSIVKFDIAVPYGEKEHEAFTAFSKSAHKATKDLLIATVGVKDYGEBLENKALG
<i>D_persimilis</i>	MMRILVVL--LLAAL	HAIPISTW-AIISAGCCVLDDELINFQTKTVERPPYSIVKFDIAFPYGEKEHEAFAFSKAHKVTKDLLVATVGIKDYGEBLENKALG
<i>D_pseudoobscura</i>	MMRILVVL--LLAAI	HGRHATW-AIISAGCCVLDDELINFQTKTVERPPYSIVKFDIAFPYGEKEHEAFAFSKAHKVTKDLLVATVGIKDYGEBLENKALG
<i>D_willistoni</i>	MIRRLLELF--LLTGLNHLGYHATL	AICPGCVVLDDELINFQTKTIERFPNTYIICKFDIAFPYGDKEHEAFAFSRAAHKVINDLLIATVGIKDYGEMENKELG
<i>D_mojavensis</i>	MLKLLLTM--LLAAL	MLKLLLTM--LLAAL--AIAACGGCVVLDDELINFQTKTIVVERPPYSIVKFDIAFPYGEKEHEAFAFSKAHKVTAELLVATVGIKDYGEBLENKALG
<i>D_virilis</i>	MTKLLLTM--LLAAL	MLRHTR--AISCGGCVLDDELINFQTKTIVVERPPYSIVLKLIDIAFPYGEKEHEAFAFSKAHKVTDELLVATVGIKDYGEBLENKALG
<i>D_grimshawi</i>	MIKLMILPPLLAL	LAQSPPLSDAISAGCCVLDDELINFQTKTIAFPYPALIKFDIAFPYGEKEHEAFAFSMAAHKTAELLVATVGIKDYGEBLENKALG
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100	

<i>D_melanogaster</i>	DRYKVDDKNFPSIIFLFGKNADEYVOLPSHVDTVLDNLKAFVSANTPLYIIGRDGCIKEFNEVLKNYANIPDAEQLKLIKELOAKQEQLTD	P-EQQQNARAY
<i>D_sechellia</i>	DRYKVDDKNFPSIIFLFGKNADEYVOLPSHVDTVLDNLKAFVSANTPLYIIGRDGCIKEFNEVLKNYANIPDAEQLKLIKELOAKQEQLTD	P-EQQQNARAY
<i>D_simulans</i>	DRYKVDDKNFPSIIFLFGKNADEYVOLPSHVDTVLDNLKAFVSANTPLYIIGRDGCIKEFNEVLKNYANIPDAEQLKLIKELOAKQEQLTD	P-EQQQNARAY
<i>D_yakuba</i>	DRYKVDDKNFPSIIFLFGKNADEYVOLPSHVDTVLDNLKAFVSANTPLYIIGRDGCIKEFNEVLKNYANIPDAEQLKLIKELOAKQEQLTD	P-EQQQNARAY
<i>D_erecta</i>	DRYKVDDKNFPSIIFLFGKNADEYVOLPSHVDTVLDNLKAFVSANTPLYIIGRDGCIKEFNEVLKNYANIPDAEQLKLIKELOAKQEQLTD	P-EQQQNARAY
<i>D_ananassae</i>	ERYEVDDKNFFAIIILFKGKNADEFVRFPYSHLDVTLNDNLKAFVSNTPLYIIGRDGCIKEFNDALKNYANLKEDEAQKLKIQFEAKQEFNT	P-EQQQNAKAY
<i>D_persimilis</i>	ERFEIDDKKFPAIILFKGSVEQYIIRFPYSHLDVTLNDNLKAFVSNTPLYIIGREGCLIKEFDAIKNYANLDEAQKLKIQFEAKQEFNT	P-EQQQNAKAY
<i>D_pseudoobscura</i>	ERFEIDDKKFPAIILFKGSVEQYIIRFPYSHLDVTLNDNLKAFVSNTPLYIIGREGCLIKEFDAIKNYANLDEAQKLKIQFEAKQEFNT	P-EKKLSGKYY
<i>D_willistoni</i>	DRFGVBDQKKPPAIHLFKGNMDEFVFKPFDHLDITLDNLKAFVSSNTELYIIGRDGCLQFNDALRNKYANKEDEQKLKIP-DEQANAKVY	
<i>D_mojavensis</i>	ERFKLNPKQFPGIFLFKGKVNDFVFKPAHLDVTLNDNLKTFVSSNTPLYIIGCDGCLIKEFDAIKNYANRHDQKLKIP-DEQANAKVY	
<i>D_virilis</i>	ERYKVDEKKFPFGIFLFKGSLLDYIOPFPADLVDLNDNLKSFVSSNTALYIIGRDGCLQFNDALKNYANKDADAEQLALTQEMOPQIOOLSLKP-DDQOQHAKVY	
<i>D_grimshawi</i>	ERFKLDEKQLPGIFLFTGSSNYLQFPADLVDLNDNLKSFVSSNTPLYIIGRDGCLIKEFDAIRNYANKEPDNEQLAVIDSEMQLKAAELSLP	-DEQQNAKVY
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200	

<i>D_melanogaster</i>	XX-----LIYMRKIHEVGYDFLEEEITKRLLRLKAGKVTEAKKEELLRKLNILEVFRVHKVTKTAPE-----KEEL	
<i>D_sechellia</i>	XX-----LIYMRKIHEVGYDFLEEEITKRLLRLKAGKVTEAKKEELLRKLNILEVFRVHKVTKTAPE-----KEEL	
<i>D_simulans</i>	XX-----LIYMRKIHEVGYDFLEEEITKRLLRLKAGKVTEAKKEELLRKLNILEVFRVHKVTKTAPE-----KEEL	
<i>D_yakuba</i>	XX-----LIYMRKIHEVGYDFLEEEITKRLLRLKAGKVTEAKKEELLRKLNILEVFRVHKVTKTAPE-----KEEL	
<i>D_erecta</i>	XX-----LIYMRKIHEVGYDFLEEEITKRLLRLKAGKVTEAKKEELLRKLNILEVFRVHKVTKTAPE-----KEEL	
<i>D_ananassae</i>	XX-----LVFMRKIQDQGYGFVEEEITKRLLRLKAGKVTEAKKEELLRKLNILEVFRVHKVTKTAPE-----KEEL	
<i>D_persimilis</i>	XX-----LVYMRKIINENGYDFLEEEITKRLLRLKAGKVTAACKLELQQQLNILEAFRVHNLTKAAPKKESSKEDL	
<i>D_pseudoobscura</i>	XX-----VLYMRKIINENGYDFLEEEITKRLLRLKAGKVTAACKLELQQQLNILEAFRVHNLTKAAPKKESSKEDL	
<i>D_willistoni</i>	XX-----LVMKKLNLNELGYEFLEEEITKRLLRLKAGVTAACKLELQQQLNILEAFRVHKLTKAKSDKPEPKKEL	
<i>D_mojavensis</i>	XX-----LVVMOKINELGYSFVEEEITKRQLQRLKAGKVTAACKLELQQQLNILEAFRVHKLTKAAPEKA--KAEL	
<i>D_virilis</i>	XX-----LLYMQKINEHGYSFVEEEITKRLLRLKAGVTAKKVLEQHKLNILEAFRVHKLTKTRPEKA--KAEL	
<i>D_grimshawi</i>	XX-----LVVMRRNIEHGYNFVEQETKRLLRLRAGKVTAAKKLELQQQLNILEAFRVHKLTKSP-----KVEL	
ruler210.....220.....230.....240.....250.....260.....	

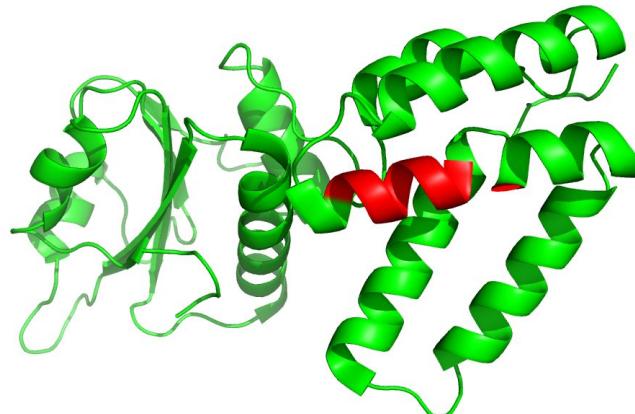


Figure S1.31: Sequence alignment and tertiary structure for gene *l(2)05070*. The mutation cluster is highlighted in red.

D. melanogaster FlyBase ID: FBgn0010590; PDB ID: 1iru; chain ID: H

	MOPDFDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNKDALVFEAASEFRN
<i>D_melanogaster</i>	MOPDFDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNKDALVFEAASEFRN
<i>D_simulans</i>	MOPDFDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNKDALVFEAASEFRN
<i>D_yakuba</i>	MOPDFDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNKDALVFEAASEFRN
<i>D_erecta</i>	MOPDFDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNKDALVFEAASEFRN
<i>D_ananassae</i>	MDSGLDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNKDALVFEAASEFRN
<i>D_persimilis</i>	MVYEMDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGPYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTSKDALVFEAASEFRN
<i>D_pseudoobscura</i>	MVYEMDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGPYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTSKDALVFEAASEFRN
<i>D_willistoni</i>	-MDDFNVIDKPVSTGTTIMAVEFIDGGVVVGADSRRTSSGAYVANRVTDKLTTRITDKVYCCRS...SAADTQAIADIVAYSLNYHENQTNRDAEVWEAASEFRN
<i>D_mojavensis</i>	MGPDFDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTQISDKVYCCRS...SAADTQAIADIVAYSLNYHRNOTNKEPLVWEAASEFRN
<i>D_virilis</i>	MGPDIIDFTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTQISENIYCCRS...SAADTQAIADIVAYSLNYHRNOTNKEPLVCEEAASEFRN
<i>D_grimshawi</i>	MGPGFDFDTDIPVSTGTTIMAVEFIDGGVVIGADSRRTSSGAYVANRVTDKLTQISDKVYCCRS...SAADTQAIADIVAYSLNYHRNOTSKEPLVWEAASEFRN
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

	XXXXXXXXXXXXXXXXXX-
<i>D_melanogaster</i>	YCYSYRES SLLAGIIVAGWDEORGGVYVSIPLGGMLTRESC
<i>D_sechelliae</i>	YCYSYRES SLLAGIIVAGWDEORGGVYVSIPLGGMLTREACT
<i>D_simulans</i>	YCYSYRES SLLAGIIVAGWDEORGGVYVSIPLGGMLTREACT
<i>D_yakuba</i>	YCYSYRES SLLAGIIVAGWDORGGVYVSIPLGGMLTRESC
<i>D_erecta</i>	YCYSYRES SLLAGIIVAGWDORGGVYVSIPLGGMLTRESC
<i>D_ananassae</i>	FCYNYRD SLLAGIIVAGYDEERGGVYVSIPLGGMLTREACT
<i>D_persimilis</i>	FCYNYRD SLLAGIIVAGWDEORGGVFIPLGGMLTREPC
<i>D_pseudoobscura</i>	FCYNYRD SLLAGIIVAGWDEORGGVFIPLGGMLTREPC
<i>D_willistoni</i>	FCYNYRD SLMAGIIVAGWDORGGVYVSIPLGGMLTREACT
<i>D_mojavensis</i>	FCYNYRD SLMAGIIVAGWDEERGGVYVSIPLGGMLTRESC
<i>D_virilis</i>	FCYNYRD SLLAGIIVAGWDEERGGVYVSIPLGGMLTREGC
<i>D_grimshawi</i>	FCYNYRD SLLAGIIVAGWDEERGGVYVSIPLGGMLTRESC
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

	RRIFYNTESGASAVSST--PSFISSE-----
<i>D_melanogaster</i>	RRIFYNTESGASAVSST--PSFISSE-----
<i>D_sechelliae</i>	RRIFYNTESGSSTVSVST--PSFISSE-----
<i>D_simulans</i>	RRIFYNTESGASAVSST--PSFISSE-----
<i>D_yakuba</i>	RRIFYNTESGASAVSST--PSFVSAT-----
<i>D_erecta</i>	RRIFYNTESGASAVSST--PSFISSE-----
<i>D_ananassae</i>	RRLFYNTESGDPQVAGT--ASFIAAEQKMEA
<i>D_persimilis</i>	RRLFYNTESGESEIIGTGGSAILAQ-----
<i>D_pseudoobscura</i>	RRLFYNTESGESEIIGTGGSAILAQ-----
<i>D_willistoni</i>	RRLFFNTETGLPEVSESESSFIVAA-----
<i>D_mojavensis</i>	RRLFFNTESGQSEIEGS--KSFLV-----
<i>D_virilis</i>	RRLFNTVTGESTIESQS--QSFIN-----
<i>D_grimshawi</i>	RRLFYNTESGESEKIAGS--QSFIN-----
ruler210.....220.....230.

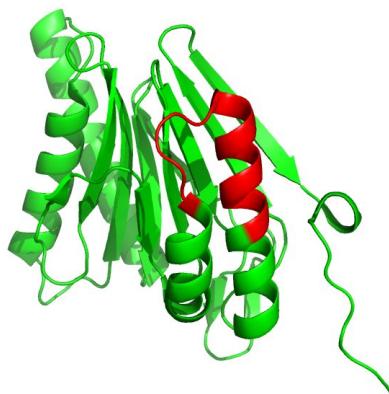


Figure S1.32: Sequence alignment and tertiary structure for gene α -Man-II. The mutation cluster is highlighted in red.

D. melanogaster FlyBase ID: FBgn0011740; PDB ID: 1qx1; chain ID: A

	-----XXXXXX-----	-----XXXXXX-----
<i>D_melanogaster</i>	LSAWHSWDGMAR--IEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMCQEALKACQVMQOSVYRLLTKPSIYSPDFESFYFTLDDSRWPMSGVEDSR	
<i>D_sechelliae</i>	LSAWHSWDGMAR--IEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMCQEALKACQVMQOSVYRLLTKPSIYSPDFESFYFTLDDSRWPMSGVEDSR	
<i>D_simulans</i>	LSAWHSWDGMAR--IEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMCQEALKACQVMQOSVYRLLTKPSIYSPDFESFYFTLDDSRWPMSGVEDSR	
<i>D_yakuba</i>	LSAWHSWDGMAR--IEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMCQEALKACQVMQOSVYRLLTKPSIYSPDFESFYFTLDDSRWPMSGVEDSR	
<i>D_erecta</i>	LSAWHSWDGMAR--IEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMCQEALKACQVMQOSVYRLLTKPSIYSPDFESFYFTLDDSRWPMSGVEDSR	
<i>D_ananassae</i>	LSAWHSWDGMAR--IEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMCQEALKACQVMQOSVYRLLTKPSIYSPDFESFYFTLDDSRWPMSGVEDSR	
<i>D_persimilis</i>	LSAWHNWPNSTD--FERQLSNARQRLSLFQHHDGITGTAKNHVVLQDEKRMVKALKGCSVMOQSIVRLLTKPSIYSPDFINFVYFMLDDSRLPMSGVEDSR	
<i>D_pseudoobscura</i>	LSAWHNWPNSTD--FERQLSNARQRLSLFQHHDGITGTAKNHVVLQDEKRMVKALKGCSVMOQSIVRLLTKPSIYSPDFINFVYFMLDDSRLPMSGVEDSR	
<i>D_willistoni</i>	LHSWHLHWDEIASGVFDKLQGARRDLISLFQHHDGITGTAKSHVVVIDYEQRQLEALRGCFVMQAVYRLLTKPSIYSPDFINFAIFSIDDSSRPMSGVEDSR	
<i>D_mojavensis</i>	LHAWHNWDSAAQ--FDRKLEMARREMSLQHHDGITGTAKTHVMQDVEKRMVKALKGCSVMOQSIVRLLTKPSIYSPDFINFAIFSIDDSSRPMSGVEDSR	
<i>D_virilis</i>	LHAWHNWDSAAQ--FSQKLELARRELSLFQHHDGITGTAKTHVMQDVEKRMVKALKGCSVMOQSIVRLLTKPSIYSPDFINFAIFSIDDSSRPMSGVEDSR	
<i>D_grimshawi</i>	LHAWQFWDSMAG--FNAKLEQARRELSLFQHHDGITGTAKTHVVQDVEKRLVEALKNSCQFVMQAVYRLLTKPSIYSPDFNFHYFTLDDSRWPVGVEESSR	
ruler520.....530.....540.....550.....560.....570.....580.....590.....600.....610..	
	-----XXXXXX-----	-----XXXXXX-----
<i>D_melanogaster</i>	TIILEDILPSKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKYRIIFKARVPPMGLATYVLTISDSKPEH	
<i>D_sechelliae</i>	TIILEDILPSKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKYRIIFKARVPPMGLATYVLTISDSKPEH	
<i>D_simulans</i>	TIILEDILPSKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKYRIIFKARVPPMGLATYVLTISDSKPEH	
<i>D_yakuba</i>	TIILEDILPSKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKYRIIFKARVPPMGLATYVLTISDSKPEH	
<i>D_erecta</i>	TIILEDILPSKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKYRIIFKARVPPMGLATYVLTISDSKPEH	
<i>D_ananassae</i>	TIILEDILPTKHVVLHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKFRLIFKARVPPMGLSTYLTIBSKPAH	
<i>D_persimilis</i>	TIILEDILPTKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKFRLIFKARVPPMGLSTYLTIBSKPAH	
<i>D_pseudoobscura</i>	TIILEDILPTKHVVMHNTLPHWRQLVDFVSSPFVSVIDLANNPVEAQSPVWSWHDTLTKTIPOGSTTCKFRLIFKARVPPMGLSTYLTIBSKPAH	
<i>D_willistoni</i>	TIILEDILPTKHVVIHNTLPRWREOMDFVVSSEVSDLSGNIEAQSPVWSWHDTLTKTIPOGSTTCKYRIFLIFQARVPPMGLSTYLTIBSKPAH	
<i>D_mojavensis</i>	TIILEDILPTKHVVLHNTVPHWRQLVDFVSSPFVSVDSLAGNSVEAQSPVWSWHDTIISKTVNPQGSTTCKYRILFKARVPPMGLITYLTTIBSKPAH	
<i>D_virilis</i>	TIILEDILPTKHVVLHNTVPHWRQLVDFVSSPFVSVDSLGNAVEAQSPVWSWHDTIISKTVNPQGSTTCKYRILFKARVPPMGLITYLTTIBSKPAH	
<i>D_grimshawi</i>	TIILEDILPTKHVVLHNTVPHWRQLVDFVSSPFVSVDSLGNAVEAQSPVWSWHDTIISKTVNPQGSTTCKYRILFKARVPPMGLITYLTTIBSKPAH	
ruler620.....630.....640.....650.....660.....670.....680.....690.....700.....710....	
	-----XXXXXX-----	-----XXXXXX-----
<i>D_melanogaster</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_sechelliae</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_simulans</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_yakuba</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_erecta</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_ananassae</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_persimilis</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_pseudoobscura</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_willistoni</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_mojavensis</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_virilis</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
<i>D_grimshawi</i>	TSYASNLRLRKNPTSLPLIGQYPEDVKFGDPREISLRVGN-GPFLAFLSEQGLLKSICLTLQDSPHPVVFHKFLKYGVRSHGDRSGAYLFLPNPGASPVELGQPV	
ruler	...720.....730.....740.....750.....760.....770.....780.....790.....800.....810.....	

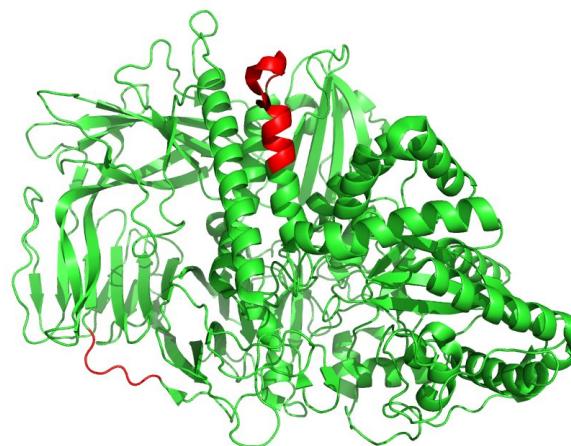


Figure S1.33: Sequence alignment and tertiary structure for gene *Proso7*. The mutation cluster is highlighted in red.

D. melanogaster FlyBase ID: FBgn0023175; PDB ID: 1iru; chain ID: G

<i>D_melanogaster</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDAVVLAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLVADGNFVADIARQEAAANYR
<i>D_simulans</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDAVVLAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLVADGNVVAIDIARQEAAANYR
<i>D_yakuba</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDAVVLAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLVADGNVVAIDIARQEAAANYR
<i>D_erecta</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDAVVLAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLVADGNVVAIDIARQEAAANYR
<i>D_ananassae</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVILAVEKIIISSKLHEEDAAGRIFTIEKNIGMAIAGLVADGNVVAIDIARQEAAANFR
<i>D_persimilis</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVILAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLVADGNVVAIDIARQEAAANYR
<i>D_pseudoobscura</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVILAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLVADGNVVAIDIARQEAAANYR
<i>D_willistoni</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVILAVEKIIITSKLVEPDAGGRIFTIEKNIGMAVAGLMADANYIADIARQEAAANYR
<i>D_mojavensis</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVVLAVEEKIVADOLYEPDAASRIFTIEKNIGMAIAGLMADGNFVVAIDIARQEAAANFR
<i>D_virilis</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVVLAVEEKIVADOLYEPDAASRIFTIEKNIGMAIAGLMADGNFVVAIDIARQEAAANFR
<i>D_grimshawi</i>	MSTIGIGYDLSASQFSPDGRVFQIDYAKAVEREKGTVIGIRGKDCVVLAVEEKIVADOLYEPDAASRIFTIEKNIGMAIAGLMADGNVVAIDIARQEAAANFR
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

<i>D_melanogaster</i>	QQFEQAIPLKHLCHRVA _G VHAYTLYSAVRPFGLSIIILASWDEVEGPOLWKIEP _G SSPGYFACASGKAKQLAKTEMEKLKM-DMR _I DELVESAGEIIINK
<i>D_sechelliae</i>	QQFEQAIPLKHLCDRVAGV _H HAYTLYSAVRPFGLSIIILASWDEVEGPOLWKIEP _G SSPGYFACASGKAKQLAKTEMEKLKM-DMR _I DELVESAGEIIINK
<i>D_simulans</i>	QQFEQAIPLKHLCDRVAGV _H HAYTLYSAVRPFGLSIIILASWDEVEGPOLWKIEP _G SSPGYFACASGKAKQLAKTEMEKLKM-DMR _I DELVESAGEIIINK
<i>D_yakuba</i>	QQFEHAIPLKHLCDRVAGV _H HAYTLYSAVRPFGLSIIILASWDEVEGPOLWKIEP _G SSPGYFACASGKAKQLAKTEMEKLKM-DMK1DDLVKSAGEIIINK
<i>D_erecta</i>	QQFEHAIPLKHLCDRVAGV _H HAYTLYSAVRPFGLSIIILASWDEVEGPOLWKIEP _G SSPGYFACASGKAKQLAKTEMEKLKM-DMK1DDLVKSAGEIIINK
<i>D_ananassae</i>	QQFEHAIPLKHLCEVRAGV _H HAYTLYSAVRPFGLSIIIFASWDEVEGPOLWKIEP _G SSPGYFACASGKAKQQAKTEM _E KLKF-NME _I ELVVK _S AGEIIINK
<i>D_persimilis</i>	QQFEQVIPLKHLCDRVSA _V VHAYTLYSAVRPFGLSIIILASWDENDGPOLWKIEP _G SSPGYFACASGKAKQQAKTEM _E KSRFVDLN _I EELVVK _K AGEIIINK
<i>D_pseudoobscura</i>	QQFEQVIPLKHLCDRVSA _V VHAYTLYSAVRPFGLSIIILASWDENDGPOLWKIEP _G SSPGYFACASGKAKQQAKTEM _E KSRFVDLN _I EELVVK _K AGEIIINK
<i>D_willistoni</i>	QQFEKP _I PLKHLCDRVSGY _H HAYTLYSAVRPFGLSIVSLLASWDETDGPOLWKIEP _G SSPGYFACASGKAKQQAKTEM _E KFKFAEMD _I EELVVKRAGEIIYR
<i>D_mojavensis</i>	QQFER _I PLKHLCDRVSGY _H HAYTLYSAVRPFGLSIVSLLASWDEVDPOLWKIEP _G SSPGYFACASGKAKQQAKTEM _E KFKESDMT _I EELVVKSGGGKIIYQ
<i>D_virilis</i>	QQFER _I PLKHLCDRVAGV _H HAYTLYSAVRPFGLSIVSLLASWDETDPOLWKIEP _G SSPGYFACASGKAKQQAKTEM _E KYKFADMS _I DELVOSGGKIIYQ
<i>D_grimshawi</i>	QQFER _I PLKHLCDRVSGY _H HAYTLYSAVRPFGLSIVSLLASWDEADQOLYKIEP _G SSPGYFACASGKAKQQAKTEM _E KFKFADMN _I DELVRSGGKIIYQ
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

<i>D_melanogaster</i>	XX-
<i>D_sechelliae</i>	VHDELKD _R FEMGLVGRV _T GGGLHLINPSELTEKARKAGDAANKP _E DSDNETH--
<i>D_simulans</i>	VHDELKD _R FEMGLVGRV _T GGGLHLINPSELTEKARKAGDAANKEEDDSDNETH--
<i>D_yakuba</i>	VHDDLKDADFRFEMGLVGRV _T EGGLHLINPPELT _E KARNAGDAANKEEDDSDNETH--
<i>D_erecta</i>	VHDDLKD _R FEMGLVGRV _T EGGLHLINPPELT _E KARNAGDAANKEEDDSDNETH--
<i>D_ananassae</i>	VHDDLKD _R FEMGLVGRD _T INGLHLINPAEYT _E IARNAGDAARKDDDSDNETH--
<i>D_persimilis</i>	VHDELKDKEFRFEMGIVGVSETQGIVQINPAVLT _E LARKAGENANKEDDSGDEAN--
<i>D_pseudoobscura</i>	VHDELKD _R FEMGIVGVSETQGIVQINPAVLT _E LARKAGENANKEDDSGDEAN--
<i>D_willistoni</i>	VHDELKDKNFRFEMGLVA _P TQGTHCINHELYT _E L _S ARNAGESAKDDDDGS _N E _G P _O
<i>D_mojavensis</i>	VHDELKD _R FEMGIVGVGETQGIVQINPAVLT _E LARKAGENANKEDDSGDEAN--
<i>D_virilis</i>	VNDEVNNKD _R FEMGIVGVGETQGIVQINPAVLT _E LARKAGENANKEDDSGDEAN--
<i>D_grimshawi</i>	VHDELKD _R FEMGIVGVGETQGIVQINPAVLT _E LARKAGENANKEDDSGDEAN--
ruler210.....220.....230.....240.....250.....



Figure S1.34: Sequence alignment and tertiary structure for gene *CkIIβ2*. The mutation cluster is highlighted in red.

D. melanogaster FlyBase ID: FBgn0026136; PDB ID: 1jwh; chain ID: D

	XXXXXXXXXX
<i>D_melanogaster</i>	MTDSDDES SWIHWFCCKQRGNNEFFCEVDEEVYIQDKFNLNPLDSNVKNYKCALEVILDLNPGSASEDPAEPLEASAEKLVGLI HARFILTNRGIELMLDKYN
<i>D_sechelliae</i>	MTDSDES SWIHWFCCKQRGNNEFFCEVDEEVYIQDKFNLNPLDSNVKNYKCALEVILDLNPGSASEDPAEPLEASAEKLVGLI HARFILTNRGIELMLDKYN
<i>D_simulans</i>	MTDSDES SWIHWFCCKQRGNNEFFCEVDEEVYIQDKFNLNPLDSNVKNYKCALEVILDLNPGSASEDPAEPLEASAEKLVGLI HARFILTNRGIELMLDKYN
<i>D_yakuba</i>	MTDSDES SWIHWFCCKQRGNNEFFCEVDEEVYIQDKFNLNPLDSNVNTNYRCALEVILDLNPGSASDAPEPELEASAEKLVGLI HARFILTNRGIELMLDKYN
<i>D_erecta</i>	MTDSDES SWIHWFCCKQRGNNEFFCEVDEEVYIQDKFNLNPLDSNVNTNYRCALEVILDLNPGSASDAPEPELEASAEKLVGLI HARFILTNRGIELMLDKYN
<i>D_ananassae</i>	MTDSDD IAWIHWFCCKQRGNNEFFCEVEEDYIHDKFNLNPLDSNVNTNYRCALEVILDLNPGSASDQPEPELEASAEKLVGLI HARFILTNRGIELMLDKYN
<i>D_persimilis</i>	MTDSDETA IAWIHWFCCKQRGNNEFFFAMVEDYIHDKFNLNPLDIDVNYYRCALEVILDLNNGSGSDNVTADVEASAEKLVGLI HARFILTNRGIDLMLLEKFO
<i>D_pseudoobscura</i>	MTDSDETA IAWIHWFCCKQRGNNEFFFAMVEDYIHDKFNLNPLDIDVNYYRCALEVILDLNNGSGSDNVTADVEASAEKLVGLI HARFILTNRGIDLMLLEKFO
<i>D_willistoni</i>	MTDSERGA WIHWFCCKQRGNNEFFFAMVEDYIHDKFNLNPLDIDVNYYRCALEVILDLNNGSGSDNVTADVEASAEKLVGLI HARFILTNRGIDLMLLEKFO
<i>D_mojavensis</i>	MSDSEEGAWI IPWFCKQRGNNEFFCEVDEDYIHDKFNLNPLDSNVSNYRRSLEVILDFLEPEGS GDPPPEAELQCAOKLYGLI
<i>D_virilis</i>	MTDSDEGAW IIPWFCKQRGNNEFFCAIDEDYIHDKFNLNPLDSNVSNYRRALEVILDDTGSGSDAPPEI ELEQCAEKLVGLI
<i>D_grimshawi</i>	MTDSEQTA IAWIHWYCKQRGNHEFFCEVDEDYIQDKFNLNSLDSNITNYRRALEVILDDTGSGSDAPPEAELQCAEKLVGLI HARFILTNRGIDMMLEKYO
ruler10.....20.....30.....40.....50.....60.....70.....80.....90.....100
<i>D_melanogaster</i>	KGEFG ICPRAFCHSOPVLPPIGLSDNPGEEDMVRIVCPKCNDVYIPKASRHSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLYGFKIHPPTAYRTAAE
<i>D_sechelliae</i>	KGEFG ICPRAFCHSOPVLPPIGLSDNPGEEMVAIYCPKCNDVYIPKASRHSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHTAYRTAAE
<i>D_simulans</i>	KGEFG ICPRAFCHSOPVLPPIGLSDNPGEEMVAIYCPKCNDVYIPKASRHSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHTAYRTAAE
<i>D_yakuba</i>	KGEFG ICPRAFCHSOPVLPPIGLSDNPGEEDMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQMAVRTLAE
<i>D_erecta</i>	KGEFG ICPRAFCHSOPVLPPIGLSDNPGEEMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQNAVRTTAE
<i>D_ananassae</i>	KGAGF ICPRAFCHSOPVLPPIGLSDNPGEEMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQMAXRSQQD
<i>D_persimilis</i>	KGVFG ICPRAFCHSOPVLPPIGLSDNPGEEMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQALAVRSES
<i>D_pseudoobscura</i>	KGVFG ICPRAFCHSOPVLPPIGLSDNPGEEMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQALAVRSES
<i>D_willistoni</i>	KGVFG ICPRAFCHSOPVLPPIGLSDNPGEEMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQALAVRSES
<i>D_mojavensis</i>	KSAFGIC CPRAFCHSOPVLPPIGLSDNPGEEDMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQMALRSLS
<i>D_virilis</i>	KSAFGIC CPRAFCHSOPVLPPIGLSDNPGEEDMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQMAXRSVA
<i>D_grimshawi</i>	KSVFGIC CPRAFCHSOPVLPPIGLSDNPGEEDMVRIVCPKCNDVYIPKAARHNSNLDGAGFGTGFPHMFMEKP DARPKRAKQKFVPRLFGFKIHQPMAYKPLLE
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200
<i>D_melanogaster</i>	IQKD V-TMTPVGEIDPSH I
<i>D_sechelliae</i>	NQKDA -TVSPVGEIDPSH I
<i>D_simulans</i>	NQKDV -TTSPVGEIDPSH I
<i>D_yakuba</i>	IQK---DMTP VGEIDPSH I
<i>D_erecta</i>	IQKDI -MMAPVGEIDPT PHN
<i>D_ananassae</i>	PFS ---EQPQNREVEPT VG
<i>D_persimilis</i>	GNS ----KDLQEVEPT ---
<i>D_pseudoobscura</i>	GNO ----KDLQEVEPT ---
<i>D_willistoni</i>	GTI ----FKEQOODSH ---
<i>D_mojavensis</i>	NIAVS-KDQ OPGEGDSN ---
<i>D_virilis</i>	NIK ----MPOGDVDSN ---
<i>D_grimshawi</i>	PYSAS KDQOHDADAE SN---
ruler210.....220

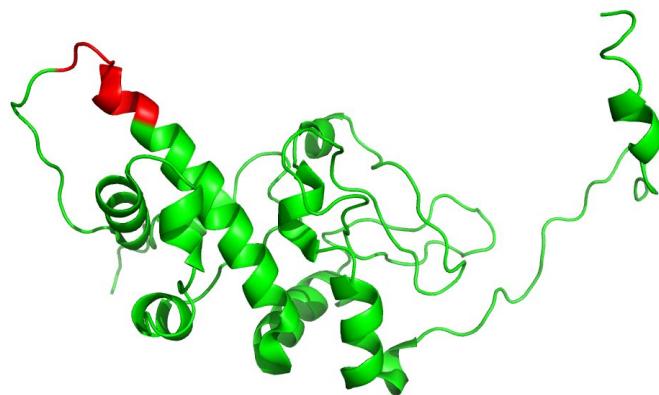


Figure S1.35: Sequence alignment and tertiary structure for gene *GPI*. The mutation cluster is highlighted in red.

Human Ensembl Gene ID: ENSG00000105220; PDB ID: 2cxn; chain ID: A

	-----XXXXXXXXXXXXXXXXXXXXXX-----
Human	MAALTTRDPQFQKLQDWYREHRSQELNLLRRLFDANKDRFNHFSLTLLNTNHGHILVLDYSKLNLVIEDVMRMLVDLAKSRGV EAARERMFNGEKINYTEGRAVLH
Chimp	MAALTTRDPQFQKLQDWYREHGSQNLRLRRLF DANKDRFNHFSLTLLNTNHGHILVLDYSKLNLVIEDVMRMLVDLAKSRGV EAARERMFNGEKINYTEGRAVLH
Macaque	MAALTTRDPQFQKLQDWYREHRSQELNLLRRLFDADKDRFNHFSLTLLNTNHGHILVLDYSKLNLVIEDVMRMLVDLAKSRGV EAARERMFNGEKINYTEGRAVLH
Mouse	MAALTTRNPQFQKLLEWHRANSANLKLRLFEADPERFNNFSLNLNTNHGHILVLDYSKLNVNKEVMQMLVELAKSRGV EAARDNMFSGLKINSTIEDRAVLH
Rat	MAALTTRNPFQKLQDWYREHGSQNLRLRLEFADPERFNNFSLNLNTNHGHILVLDYSKLNVEVLHMLVDLAKSRGV EAARDNMFSGLKINSTIEDRAVLH
Cow	MAALTQNPOFKKLKTWYEQHQGSDLNLLRRLFEGDRDRFNRFSLNLNTNHGHILVLDYSKLNLVIEDVMQMLVDVAKSRGV EAARERMFNGEKINYTEGRAVLH
Cat	MAALTQNPOFLKLQDWYREHGSQNLRLRLEF-GDKERFTHF-----AKSRGV EAARERMFNGEKINYTEGRAVLH
Chick	-MPLSADPHFKKLLEWTKANASKLVLRLQLEFADKDRFHKKFSLTLLTDHGDI LLDYSKLNVIEEVKMLIELAKSRGV ESARERMFNGEKINYTEGRAVLH
Zebrafish	-MGLTSIDPFPNQNLKWKVKSNAANLNRQMFEEDKTRFQKFSLTLKDGDGI LLDYSKLNLINEEVVKMLVELAKSRGV EAARDKMFSGEKINYTEGRAVLH
x_tropicalis	-MALSCDPVYOKLSDWYEAHHAGLNMRQMFSEADKGFRFSKFLTVLDHGDI LLDYSKLNLINEEVVKMLIELAKSRGV ESAROKMFSAEKINYTEGRAVLH
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

Human	VALRNRNSNTPIILVDGKDVMPEPVNKVLVLDKMKSFQCVRSGDWKGTYGKTIIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Chimp	VALRNRNSNTPIILVDGKDVMPEPVNKVLVLDKMKSFQCVRSGDWKGTYGKTIIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Macaque	VALRNRNSNTPIILVDGKDVMPEPVNKVLVLDKMKSFQCVRSGDWKGTYGKTIIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Mouse	VALRNRNSNTPIKVDGKDVMPEPVNRVILVLDKMKSFQCVRSGDWKGTYGKTIIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Rat	VALRNRNSNAPISIMMDGKDVMPEPVNKVLVLDKMKSFQCVRSGDWKGTYGKAIIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Cow	VALRNRNSNAPILLDVGKDVMPEPVNRVILEKMKSFQCVRSGDWKGTYGKAIIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Cat	VALRNRNSNTPIILVDGKDVMPEPVNRVILEKMKSFQCVRSGDWKGYSCKPVIDVINIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Chick	IALRNRNSNTPILLDVGKDVMPEPVNKVLVLDKMKHFCQKVRSGEWKGTYGKAIIDDVVNIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
Zebrafish	VALRNRNSNTPILLDVGKDVMPEPVNKVLVLDKMKGFCHKVRSGEWKGFGNGKSIDDVVNIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
x_tropicalis	IALRNRNSNTPTLLEGKDVMPEPVNAVLEKMKAFQCQKVRSGDWKGTYGKAITDVVNIGIGGSDLGPMVTEALKPYSSGGPRVWYVSNI DGTHIAKTLAELN
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

Human	PESSLFIIASKTFTTQETITNAETAKEWFQAAKDP SAVAKHFVALSTNTTKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHVGFDNFECOLLSGA
Chimp	PESSLFIIASKTFTTQETITNAETAKEWFQAAKDP SAVAKHFVALSTNTTKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHVGFDNFECOLLSGA
Macaque	PESSLFIIASKTFTTQETITNAETAKEWFQAAKDP SAVAKHFVALSTNTTKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHVGFDNFECOLLSGA
Mouse	PETSLFIIASKTFTTQETITNAETAKEWFQAAKDP SAVAKHFVALSTNTAKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHVGFDNFECOLLSGA
Rat	PESSLFIIASKTFTTQETITNAETAKEWFQAAKDP SAVAKHFVALSTNTDKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHVGFDNFECOLLSGA
Cow	PESSLFIIASKTFTTQETITNAETAKEWFLLSAKDP SAVAKHFVALSTNTAKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHVGFDNFECOLLSGA
Cat	PESSLFIIASKTFTTQETITNAETAKEWFLLSAKDP SAVAKHFVALSTNTAKVKEFGIDPQNMF FFWDVVGGRYSLWSAIGL SIALHIGFDNFESLLAGG
Chick	PETTLFIIASKTFTTQETITNAETAKEWFLLSAKDP SAVAKHFVALSTNTNGPKVKDFGIDPENMF FFWDVVGGRYSLWSAIGL SIALHIGYENFEKLLAGA
Zebrafish	AETTLFIIASKTFTTQETITNAESAKEWFQAAKDA SAVAKHFVALSTNTNGPKVKDFGIDTANMF FFWDVVGGRYSLWSAIGL SIALHIGYENFEKLLAGA
x_tropicalis	PETSLFIIASKTFTTQETITNAETAKEWFLLSAKDA SAVAKHFVALSTNTNGPKVKDFGIDTANMF FFWDVVGGRYSLWSAIGL SIALHIGYDNFEKLLAGA
ruler210.....220.....230.....240.....250.....260.....270.....280.....290.....300

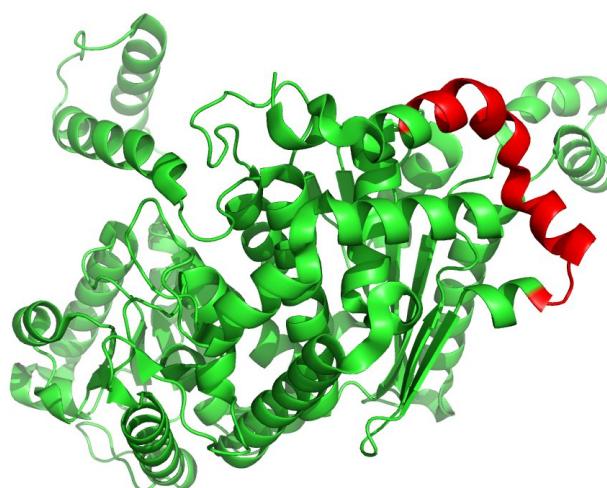


Figure S1.36: Sequence alignment and tertiary structure for gene *NEDD8*. The mutation cluster is highlighted in red.

Human Ensembl Gene ID: ENSG00000129559; PDB ID: 1bt0; chain ID: A

	-XXXX-	
Human	MLIKVKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKILGGSVLHLVLIALRGGGGLRQ	
Chimp	MLIKVKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKILGGSVLHLVLIALRGGGGLRQ	
Macaque	MLIKVKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKILGGSVLHLVLIALRGGGGLRQ	
Mouse	MVLEQKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKILGGSVLHLVLIALRGGGGLRQ	
Rat	MVLEQKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKILGGSVLHLVLIALRGGGGLRQ	
Cow	MLIKVKTILTTRKEIEIDIEPDKVEREKERVEEKEGIPPEQQRLTVSGROINVKKISTDYRLISGSVHLVLIALRGGGGLRQ	
Cat	MLIKVKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKILGGSVLHLVLIALRGGGGLRQ	
Zebra_fish	MLIKVKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKIQGGSVLHLVLIALRGGGQIHOKPDRLLLNM	
x_tropicalis	MLIKVKTILTGKEIEIDIEPDKVERIKERVEEKEGIPPOQQRLIYSGKQMNDDEKTAADYKIQGGSVLHLVLIALRGGC	
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....	

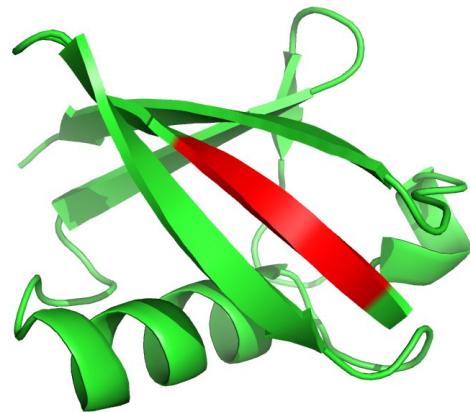


Figure S1.37: Sequence alignment and tertiary structure for gene *CBR3*. The mutation cluster is highlighted in red.

Human Ensembl Gene ID: ENSG00000159231; PDB ID: 2hrb; chain ID: A

Human	MSSCSRVALVTGANRGIGLAIARELCROFSGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Chimp	MSSCSRVALVTGANRGIGLAIARELCROFSGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Macaque	MSSCSRVALVTGANRGIGLAIARELCROFSGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Mouse	MSSCSRVALVTGANKGIGFAITRDLCKFSGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Rat	MSSCSRVALVTGANKGIGFAITRDLCKFSGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Cow	MSSYTRVALVTGANKGIGFAIARDLCKREFPGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Cat	MSSCSRVALVTGANKGIGFAIARDLCKREFPGDVVLITARDVARGAAVQQLQA-EGLSPRFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAAVAFKSDD
Chick	IMSNVPVAVVIGSNKGIGLAIVRDLCKQFKGDVYLITARDPARGEAVAKLQE-EGLHPLFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAVIAFPDD
Zebrafish	-MSQCKVALVIGSNKGIGFAIVRALCKEYTIDDVYLISRDVGRGTAAVDSLKK-EGLHPLFHQLDIDDLQSIRALRDFLRKEYGGLNVLVNNAVIAFKVSD
<i>x_tropicalis</i>	-MASAKVAVVTTGGNKGIGLAIVRALCKQFKGDVYLITARDPKLGEEAVRALEKEQEGLSPPHFHQLDINDLQSIRALGGFLKEYGGIDVVLINNAGIAFKVAD
ruler1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100

Human	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSLOCLRAFEN-CSEDLQERFHSETLTTEGDLVDLMKKF-VEDTKNEVHEREGWPNSPYGV
Chimp	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSLOCLRAFEN-CSEDLQERFHSETLTTEGDLVDLMKKF-VEDTKNEVHEREGWPNSPYGV
Macaque	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSLOCLRAFEN-CSEDLQERFHSETLTTEGDLVDLMKKF-VEDTKNEVHEREGWPNSPYGV
Mouse	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSLOGLKALEN-CREDLQEKFRCDILTEGDLVDLMKKF-VEDTKNEVHEREGWPNSPYGV
Rat	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSLOGLKALEN-CSEDLOEKFRCDILTEGDLVDLMKKF-VEDTKNEVHEREGWPNSPYGV
Cow	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSSOGLKALEN-CSEDLOEKFRCEILTEGDLVDLMKKF-VEDTKNEVHEREGWPNSPYGV
Cat	PMPFDIKAEMILKTNFFATRNCNELLPIMKPHGRVVNISSLEGSKALEN-CSPDLOKKFRCEILTEGDLVDLMKKF-VEDANNEVHEREGWPNSPYGV
Chick	RIPFGTQAEVILKTNFFATRNCNELLPIKPYGRVVNVSSMVSISALGG-CSQELQFRFRSDITTEEDLVMKTF-VEDTKKSVHEKEGWPNTAYGV
Zebrafish	TPPFGTQAEVILKTNFFATRNCNVLPIKPGGRLVNVSSGMGSMALGR-CSPLEOARFRSDDITTEELNLGLMERF-VREADEGVHSERGPSTAYGIS
<i>x_tropicalis</i>	TPPFGTQAEVILKTNFFATRNCNVLPIKPGGRLVNVSSMASIMALGRCCSPELQKVFRSDITTEELVTLMEKF-VEDAACKGAHQKEGWPNTAYGV
ruler110.....120.....130.....140.....150.....160.....170.....180.....190.....200

Human	-----XXXXXX-----
Chimp	KLGTVLTSRILARRLDEKRKADRILVNAACCPGPVKIDMDGKDSIRIVVEGAETPVVLALLPPDATEPQQLVLHDKVVQN
Macaque	KLGTVLTSRILARRLDEKRKADRILVNAACCPGPVKIDMDGKDSIRIVVEGAETPVVLALLPPDATEPQQLVLHDKVVQN
Mouse	KLGTVLTSRILARRLDEKRKADRILLLNACCPGPWKIDMDGKYSIRIVVEGAETPVVLALLPPDATEPQQLVLHDKVVQN
Rat	KLGTVLTSRILARRLDEKRKADRILLLNACCPGPWKIDMDQGSRTIVVEGAETPVVLALLPPDATEPQQLVLHDKVVQN
Cow	KLGTVLTSRILARRLDEKRKADRILLLNACCPGWVKIDLGGAHASRIVVEGAETPVVLALLPPDATEPQQLVLHDKVVQN
Cat	KLGTVLTSRILARRLDEKRKADRILLLNACCPGWVKIDLGPCGPRIVVEGAETPVVLALLPPDATEPQQLVLHDKVVQN
Chick	KIGTVLTSRILARRLDEKRKADRILLLNACCPGWVRIDMAGPKAPKSPPEGAETPVVLALLPSADGPHGGFVSEKTVRTW
Zebrafish	KIGLTTLIRIQAARNLTKERPDGGDILCNACCPGWVRIDMAGPNATKSPDEGAITPVVLALLPAGAKEPHGFQFVSEMKVPPW
<i>x_tropicalis</i>	KVGTVLTSRILARRLDEKRKDDGILLNACCPGWVRIDMAGPKAPKSPDEGAETPVVLALLPNNAHSPHGEVLVSEKKVVPPW
ruler210.....220.....230.....240.....250.....260.....270.....280

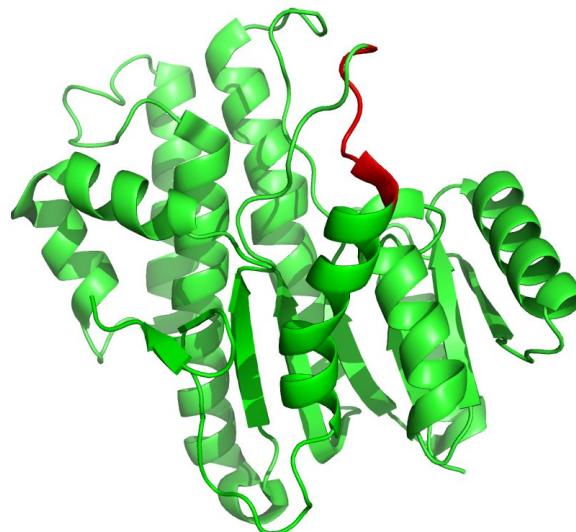


Figure S1.38: Sequence alignment and tertiary structure for gene *LPO*. The mutation cluster is highlighted in red.

Human Ensembl Gene ID: ENSG00000167419; PDB ID: 2gjm; chain ID: A

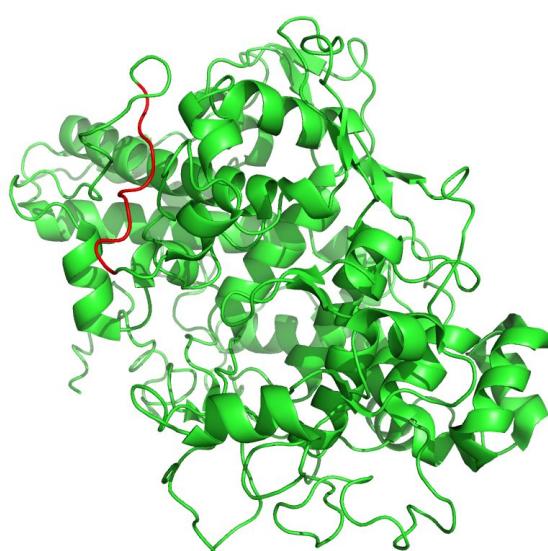
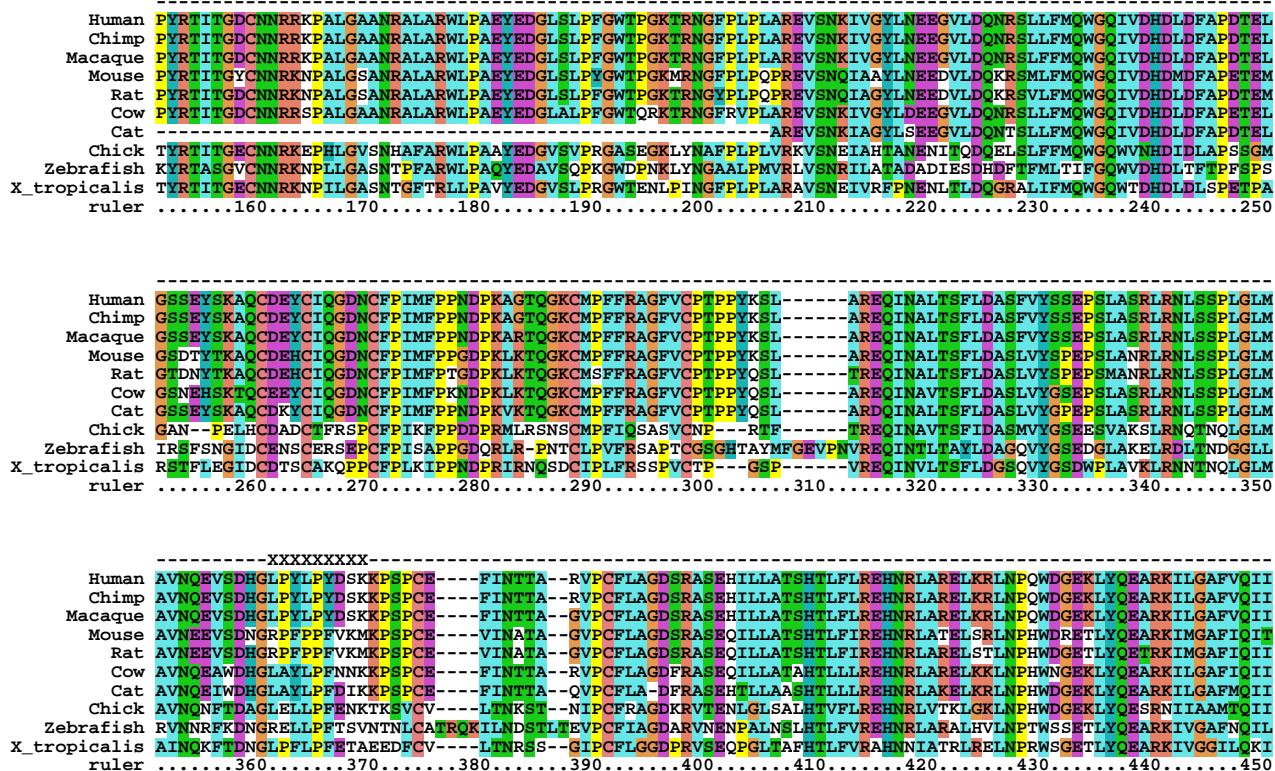


Figure S1.39: Sequence alignment and tertiary structure for gene *NAGA*. The mutation cluster is highlighted in red.

Human Ensembl Gene ID: ENSG00000198951; PDB ID: 1ktb; chain ID: A

	Human	Chimp	Macaque	Mouse	Rat	Cow	Cat	Chick	Zebrafish	x_tropicalis	ruler
	FPHGIPFLADYVHSLGLKLGIYADMGNFTCMGYPGTTLDKVVOQDAQTF	FPHGIPFLADYVHSLGLKLGIYADMGNFTCMGYPGTTLDKVVOQDAQTF	FPHGIPFLADYVHSLGLKLGIYADMGNFTCMGYPGTTLDKVVOQDAQTF	FPHGIAFLADYAHSLGLKLGIYEDMGKMTCMGYPGTTLDKVVOQDAQTF	FPHGIAFLADYAHSLGLKLGIYEDMGKMTCMGYPGTTLDKVVOQDAQTF	FPHGIAFLADYAHSLGLKLGIYEDMGKMTCMGYPGTTLDKVVOQDAQTF	FPHGIAFLADYAHSLGLKLGIYEDMGKMTCMGYPGTTLDKVVOQDAQTF	FPRGIKALADYVHAKGLKLGIYSDMGNFTCGGYPGTTLDTIKI	FPRGIKALADYVHAKGLKLGIYSDMGNFTCGGYPGTTLDTIKI	FPSGMKALADYVHAKGLKLGIYSDMGNFTCGGYPGTTLDTIKI110.....120.....130.....140.....150.....160.....170.....180.....190.....200
	FAEWKVDMKLKDGCFSPEERAGYPKMAAAALNATGRPIAFCSWPAYEGGLP	FAEWKVDMKLKDGCFSPEERAMGYPKMAAAALNATGRPIAFCSWPAYEGGLP	FAEWKVDMKLKDGCFSPEERAMGYPKMAAAALNATGRPIAFCSWPAYEGGLP110.....120.....130.....140.....150.....160.....170.....180.....190.....200							

	Human	Chimp	Macaque	Mouse	Rat	Cow	Cat	Chick	Zebrafish	x_tropicalis	ruler
	PRVNYSLLADICNLWRNYDDIQDSWWSVLSILNWVFEHQDILQPVAGPGHWNDPDMLLICNFGLSLEQSRQMALWTVLAAPLLMSTDLRTI	PRVNYSLLADICNLWRNYDDIQDSWWSVLSILNWVFEHQDILQPVAGPGHWNDPDMLLICNFGLSLEQSRQMALWTVLAAPLLMSTDLRTI	PRVNYSLLADICNLWRNYDDIQDSWWSVLSILNWVFEHQDILQPVAGPGHWNDPDMLLICNFGLSLEQSRQMALWTVLAAPLLMSTDLRTI	PKVNYTEVSRVCNLWRNYKDIQDSWKSVLSILDDWFVRHQDVLOPVAQPGHWNDPDMLLICNFGLSFDESRQMALWTVLAAPLLMSTDLRTI	PKVNYTEVAGCICNLWRNYKDIQDSWKSVLSILDDWFVRHQDVLOPVAQPGHWNDPDMLLICNFGLSFDESRQMALWTVLAAPLLMSTDLRTI	PKVNYTEVAGCICNLWRNYKDIQDSWKSVLSILDDWFVRHQDVLOPVAQPGHWNDPDMLLICNFGLSFDESRQMALWTVLAAPLLMSTDLRTI	PKVNYTEVAGCICNLWRNYKDIQDSWKSVLSILDDWFVRHQDVLOPVAQPGHWNDPDMLLICNFGLSFDESRQMALWTVLAAPLLMSTDLRTI	PKVNYTLLGEICNLWRNYDDIQDSWSDSVLSILDDWFVDHQDILQPVAGPGHWNDPDMLLICNFGLSFECARQMALWTVLAAPLFMSTDLRTI	PKVNYTLLGEICNLWRNYDDIQDSWSDSVLSILDDWFVDHQDILQPVAGPGHWNDPDMLLICNFGLSFECARQMALWTVLAAPLFMSTDLRTI	PKVNYTLLGEICNLWRNYDDIQDSWSDSVLSIVDWFEDNODALQPAAPGQWNPDPMLLICGDFSLSLDQSRQMALWSIMAAPLFMSNDLRTI210.....220.....230.....240.....250.....260.....270.....280.....290.....300
	SAQNMIDIL	SAQNMIDIL	SAQNMIDIL	SPQNMDIL	SPQNIDIL	SAQNMIDIL	SAQNMIDIL	SPAKKIL	SAQNMIDIL	SAQNMIDIL210.....220.....230.....240.....250.....260.....270.....280.....290.....300

	Human	Chimp	Macaque	Mouse	Rat	Cow	Cat	Chick	Zebrafish	x_tropicalis	ruler
	QNPPLMIKINQDPLGIQGRRIIKEKSLIEVYMRPLSNKASALVFFFICRTD-MPYRYHSSLQQLNFTGSV-IYEADDVYSGDIISGLRDETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSLIEVYMRPLSNKASALVFFFICRTD-MPYRYHSSLQQLNFTGSV-IYEADDVYSGDIISGLRDETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSLIEVYMRPLSNKASALVFFFICRTD-MPYRYHSSLQQLNFTGSV-IYEADDVYSGDIISGLRDETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGR-VYEGCNVFTGDIIFSGLOTEVNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGR-VYEGCNVFTGDIISGLHPETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGS-VYEGCNVFTGDIISGLHPETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGS-VYEGCNVFTGDIISGLHPETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGS-VYEGCNVFTGDIISGLHPETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGS-VYEGCNVFTGDIISGLHPETNFTVIIINPSGV	QNPPLMIKINQDPLGIQGRRIIKEKSHIEVKRYLSNQASALVFFFICRTD-MPFRFHCSLIELNVPKGS-VYEGCNVFTGDIISGLHPETNFTVIIINPSGV310.....320.....330.....340.....350.....360.....370.....380.....390.....400
	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV	QNLKINFTVIIINPSGV310.....320.....330.....340.....350.....360.....370.....380.....390.....400

