

Figure Legends for Supplementary Figures

Supplementary Figure S1: *N-terminal NLS is important in full length Rif1*

A. Western blot showing Rif1 (anti-FLAG antibody) and Pgk1 (anti-Pgk1 antibody, control) protein levels of indicated strains. B. Southern blot hybridized with a Y' probe to visualize "bulk" XhoI restriction fragments of indicated strains (See Materials and Methods).

Supplementary Figure S2: *Structure-based sequence alignment*

A. Workflow of structure-based sequence alignment (see Materials and Methods). B. Phylogenetic tree of the Multiple Sequence Alignment (MSA) generated using ConSurf. C. Conservation graph generated using GraphPad Prism of sequence alignment with position in Rif1 protein on the X-axis. The height of the bar indicates ConSurf Grade, with a higher bar having higher conservation. Purple indicates high conservation, and green indicates low conservation. Rif1 domain map is depicted to scale above the bar graph, with the newly defined NLS added, and Rif1 aa 177-196 are depicted with a blue dotted line (RBM: Rap1 binding motif; CTD: Carboxyl-terminal domain; Dbf4 binding overlaps CTD). D. MSA mapped onto the Rif1 crystal structure (PDB: 5NW5, showing one Rif1 monomer and DNA) visualized using PyMOL. Purple indicates high conservation, and green indicates low conservation.

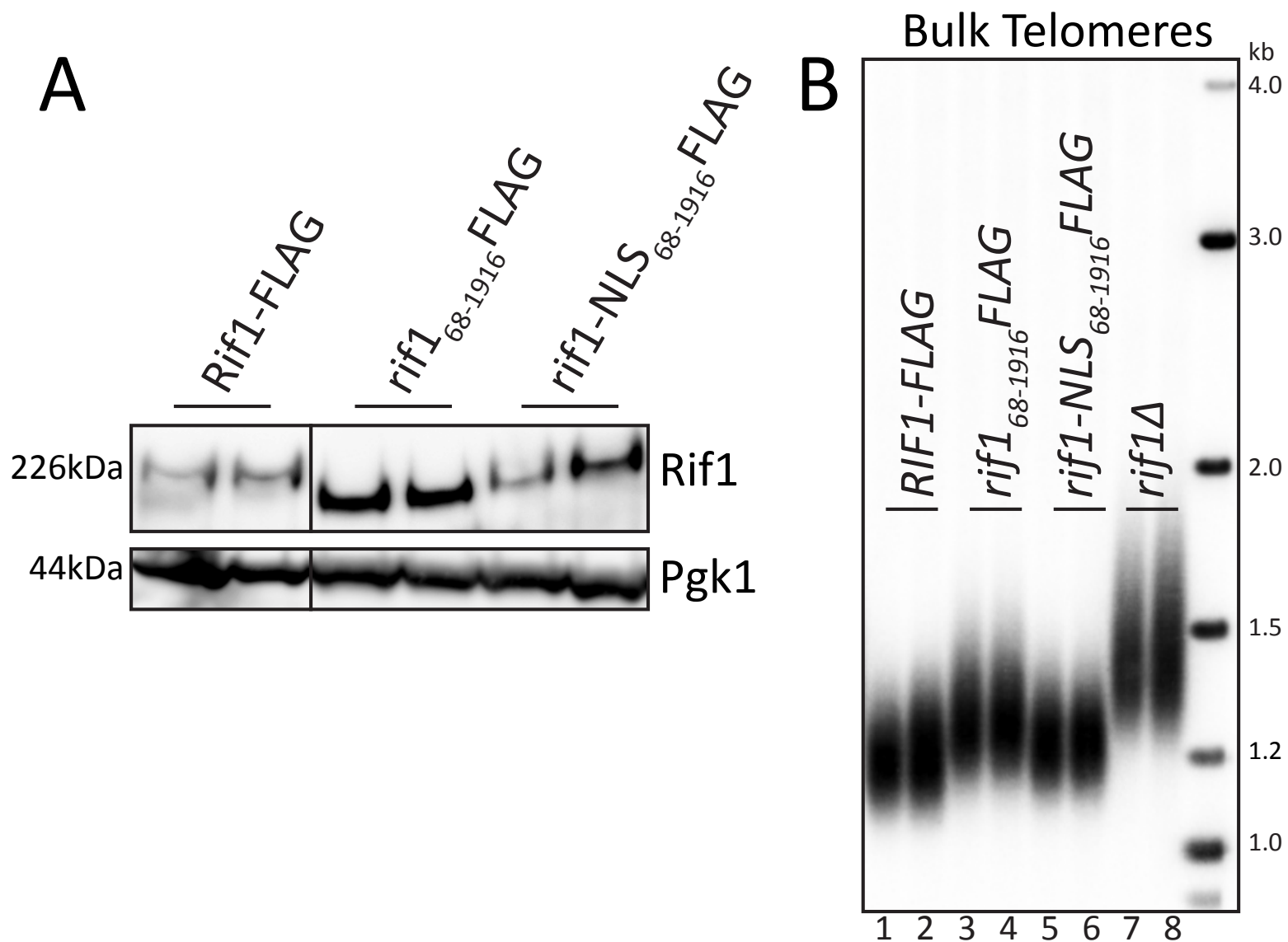
Supplementary Figure S3: *Protein levels for strains mutated in conserved HEAT repeats*

A. Western blot showing Rif1 (anti-FLAG antibody) and Pgk1 (anti-Pgk1 antibody, control) protein levels of indicated strains, related to Figure 6A,B. B. Western blot showing Rif1 (anti-FLAG antibody) and Pgk1 (anti-Pgk1 antibody, control) protein levels of indicated strains, related to Figure 6F,G. C. Conserved residues with corresponding distance from lysine cluster and 1L telomere length, related to Figure 6A. D. Western blot showing Rif1 (anti-FLAG antibody) and Pgk1 (anti-Pgk1 antibody, control) protein levels of indicated strains.

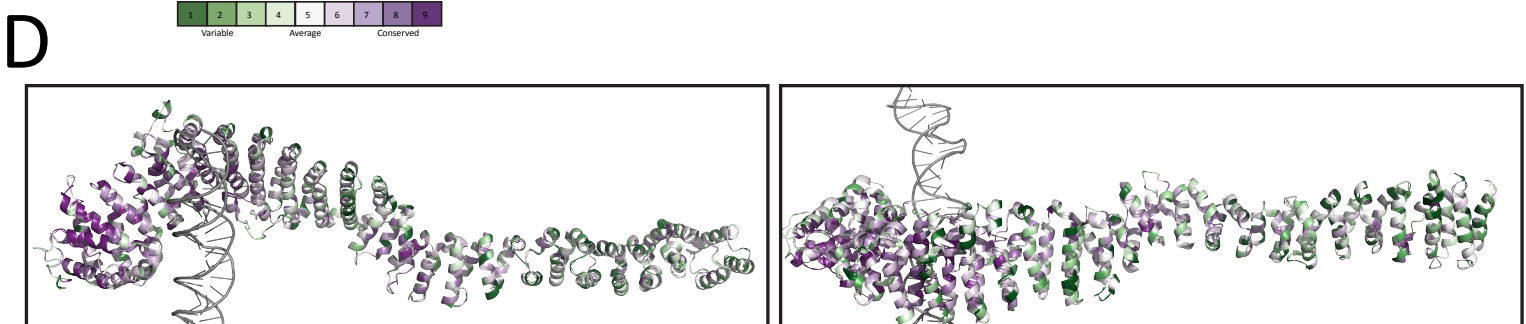
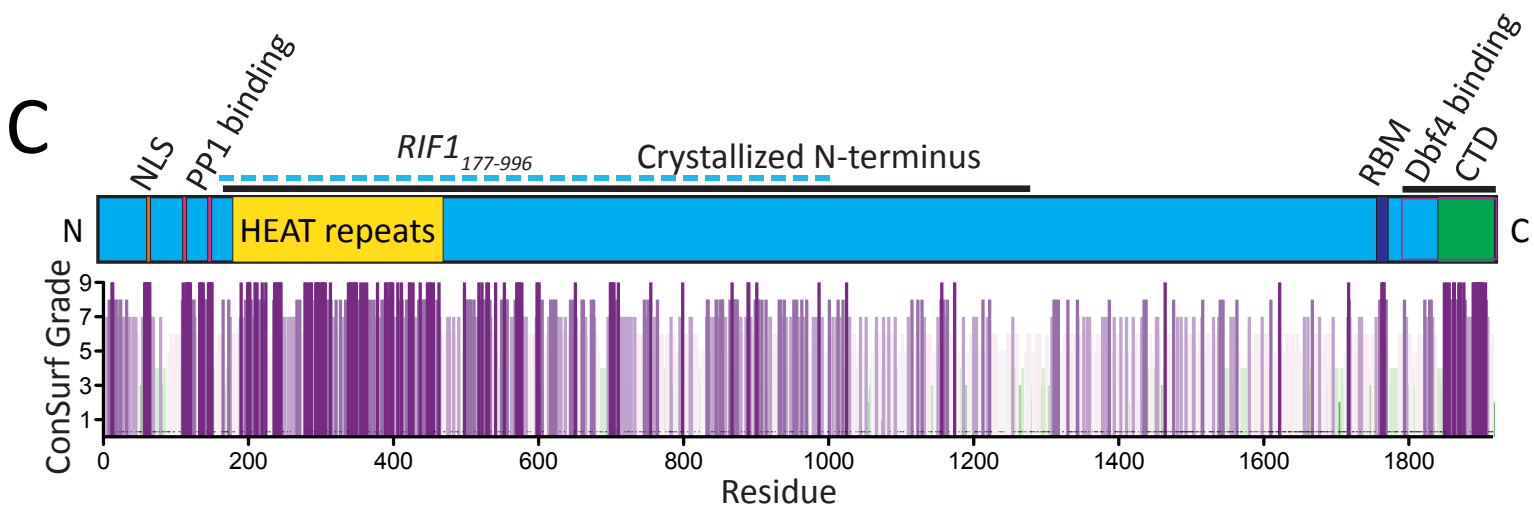
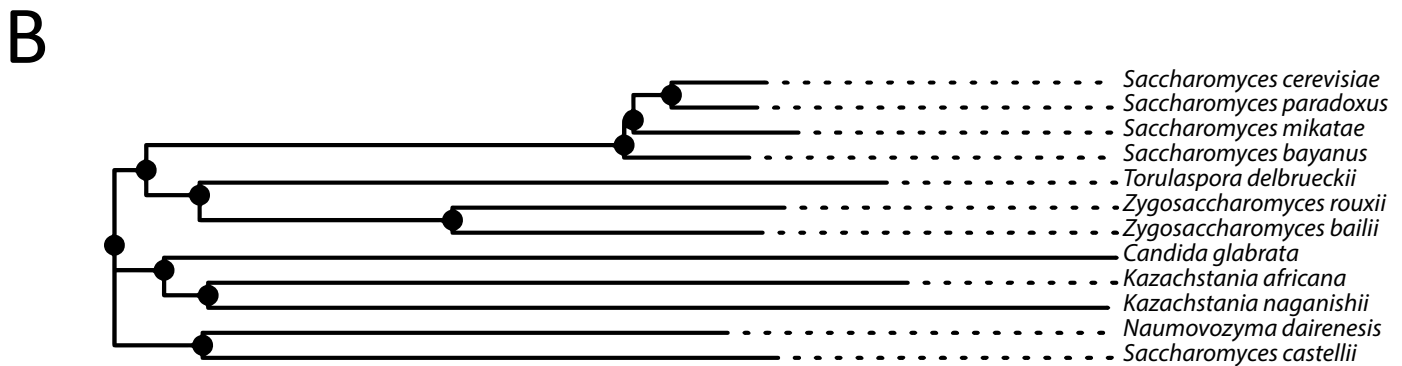
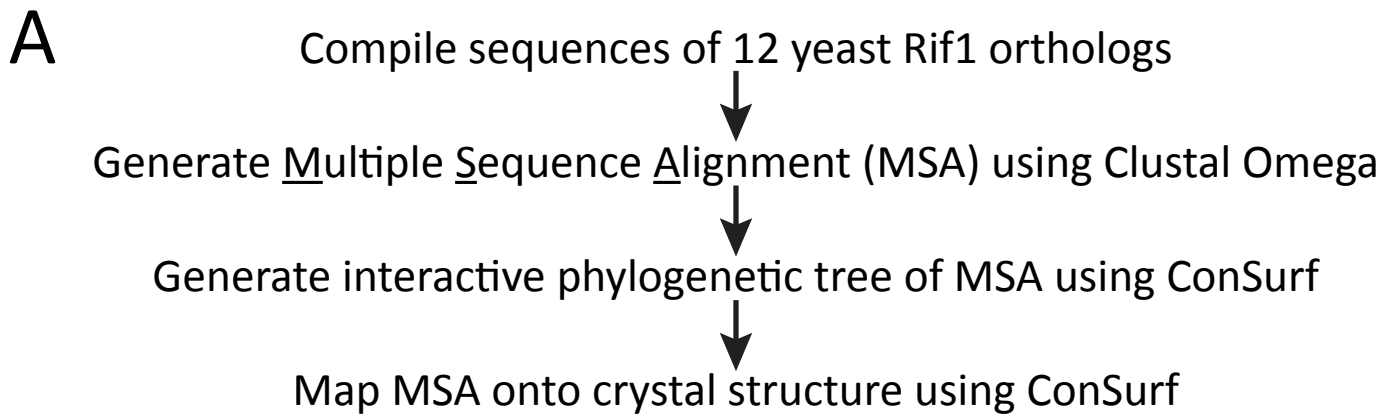
Supplementary Figure S4: *Mutation of Rif1 palmitoylation sites does not affect telomere length*

A. Western blot showing Rif1 (anti-FLAG antibody) and Pgc1 (anti-Pgc1 antibody, control) protein levels of indicated strains. B. Southern blot hybridized with a Y' probe to show bulk telomeres for the indicated strains (See Materials and Methods).

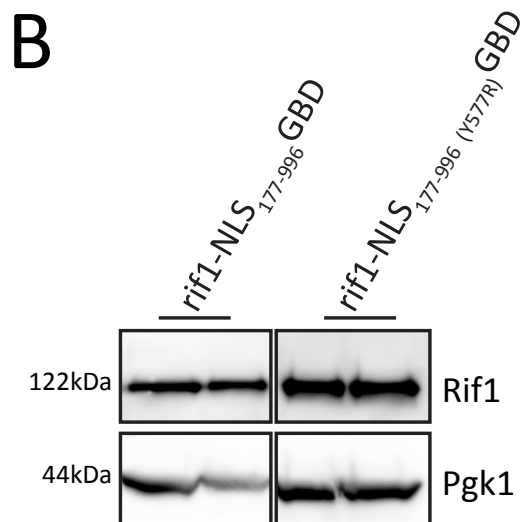
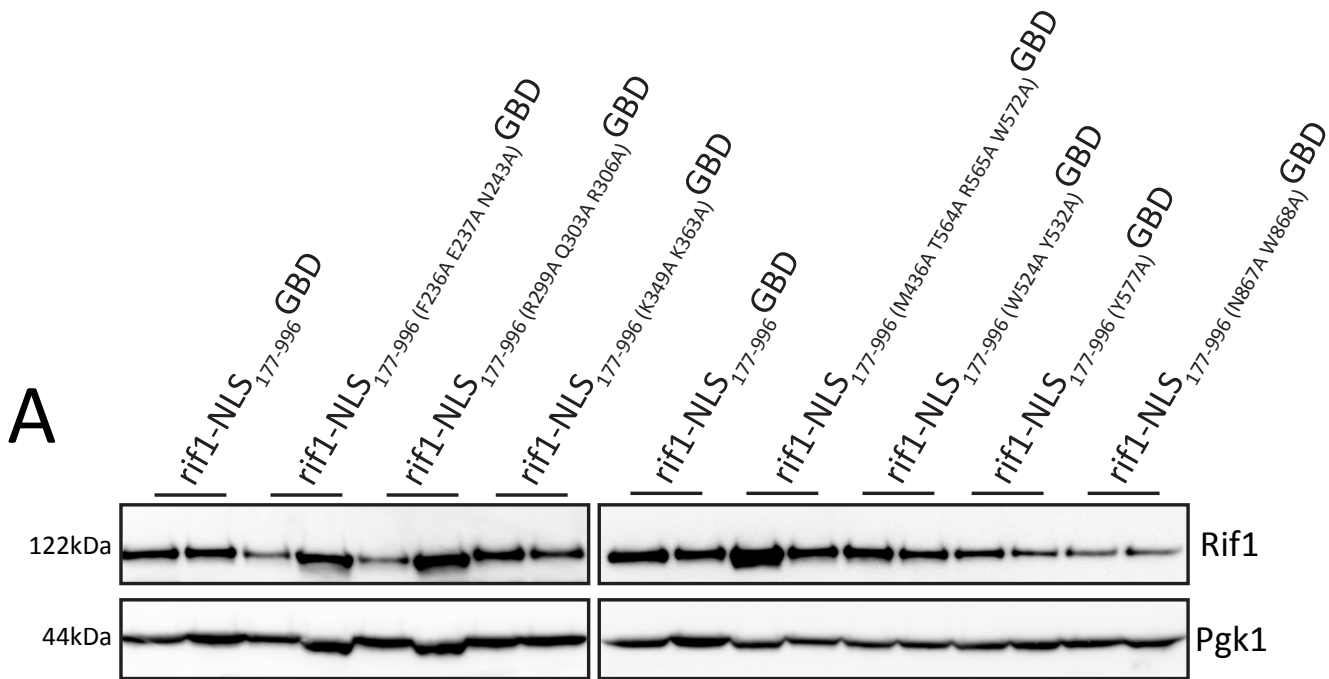
Supplementary Figure S1



Supplementary Figure S2

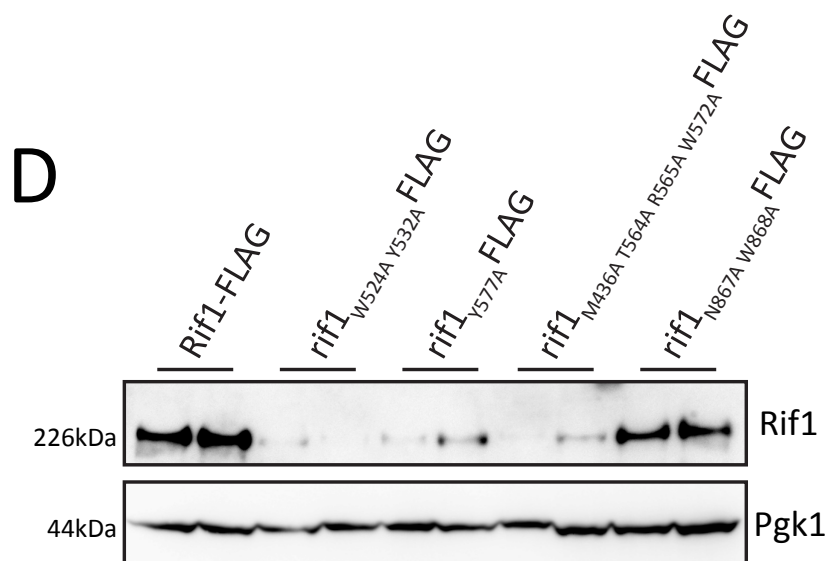


Supplementary Figure S3



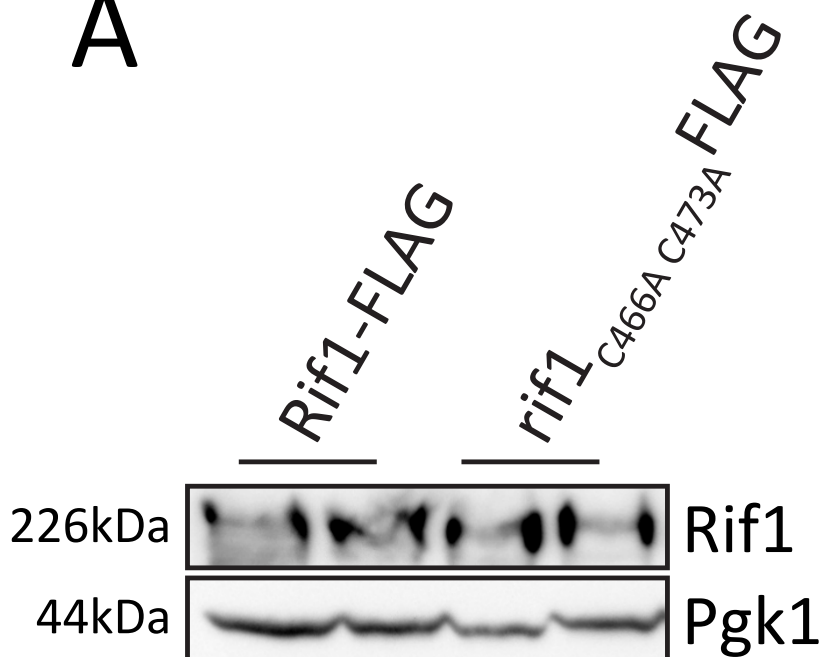
C

Residues Interrogated	Distance from Lysine cluster	1L Telomere length
F236A E237A N243A	194	Wild type
R299A Q303A R306A	131	Wild type
K349A K363A	74	Wild type
M436A T564A R565A W572A	0	Long
K437A K563A K570A	0	Long
W524A Y532A	0	Long
Y577A	7	Long
N867A W868A	297	Wild type



Supplementary Figure S4

A



B

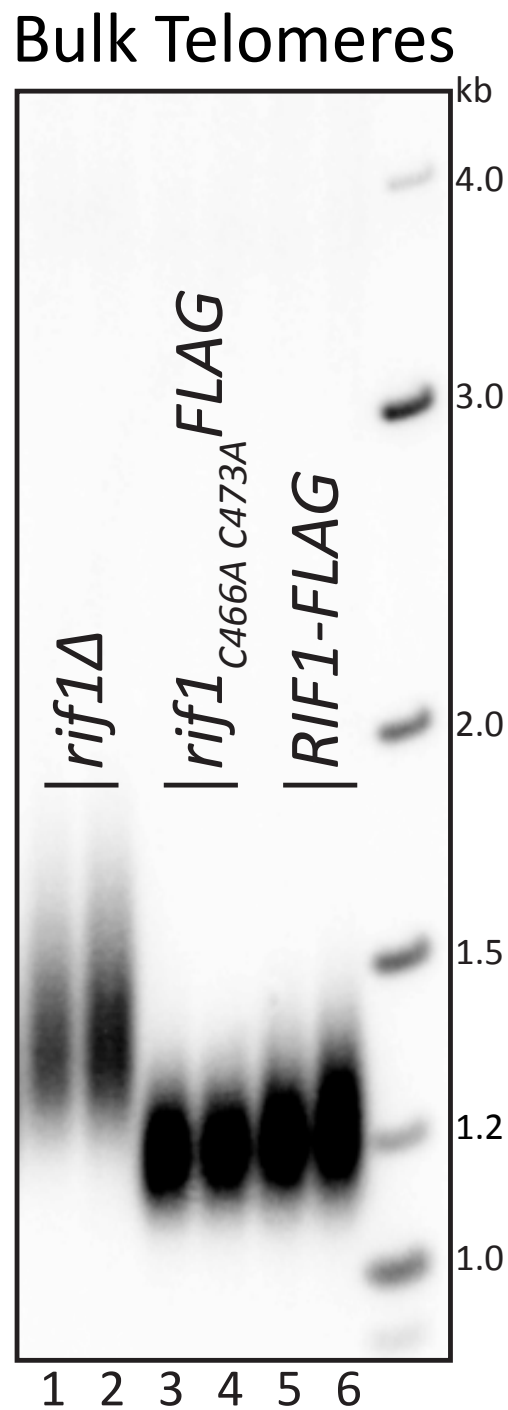


Figure Legend for Supplementary Table

Supplementary Table 1: *Strain list, plasmid list, and cloning specifics and reagents*

Supplementary Table 1

Strain ID	Genotype	Source	Construct for cloning	Primer 1	Primer 2	Additional information
SSy161	MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 bar1::hisG	N/A				
CVy61	SSy161 + TRP1::BrdU- <i>inc</i>	https://doi.org/10.1002/yea.1406				
CALy11	CVy61 + rif1Δ::kanmx	https://doi.org/10.7554/eLife.58066				
CALy320	CALy117 + rif11-1322-6xFLAG-KANMX	This study	pAS35	AS101	CS201	Extend homology by PCR with CS315, AS100
JHUy783	tel1Δ::HYGR	Greider Lab				
CALy117, 118	CVy61 + 1L 5XUAS landing pad	This study	pCS33	CS155	CS218	Digest PCR product I-Sce1 DpnI
CALy202, 203	CALy117 + rif1Δ::KANMX	This study	gDNA (CALy11)	OCC23	OCC84	
CALy286, 287	CALy117 + rif11-1322GBD-6xFLAG-KANMX	This study	pCS172	RW432	OCC84	
CALy290, 291	CALy117 + rif11-1322(K437E K563E K570E) GBD-6xFLAG-KANMX	This study	pCS171	RW428	OCC84	
CALy328, 329	CALy117 + rif11-1322-6xFLAG-KANMX	This study	gDNA (CALy320)	RW431	CS323	
CALy375, 376	CALy117 + rif1177-1322GBD-6xFLAG-KANMX	This study	pCS184	OCC23	OCC84	
CALy408, 409	CALy117 + rif1-cmycNLS177-1322GBD-6xFLAG-KANMX	This study	pCS189	OCC23	OCC84	
CALy428, 429	CALy117 + rif1-996GBD-6xFLAG-KANMX	This study	pCS193	RW430	CS323	
CALy432, 439	CALy117 + rif1-cmycNLS177-996GBD-6xFLAG-KANMX	This study	pCS193	OCC23	CS323	
CALy442, 443	CALy117 + RIF1-6xFLAG-KANMX	This study	pCS177	AS100	CS383	
CALy454, 455	CALy117 + rif1-cmycNLS177-996 (K437E K563E K570E)GBD-6xFLAG-KANMX	This study	pCS195	OCC23	OCC84	
CALy460, 461	CALy117 + rif1-cmycNLS177-996 (M436A T564A R565A W572A)GBD-6xFLAG-KANMX	This study	pCS198	OCC23	OCC84	
CALy462, 463	CALy117 + rif1-cmycNLS177-996 (K437R K563R K570R)GBD-6xFLAG-KANMX	This study	pCS196	OCC23	OCC84	
CALy465, 465	CALy117 + rif1-cmycNLS177-996 (T504E S584E T775E S824E)GBD-6xFLAG-KANMX	This study	pCS210	OCC23	OCC84	
CALy472, 473	CALy117 + tel1Δ::HYGR	This study	gDNA (JHUy783)	OCC25	OCC80	
CALy478, 479	CALy117 + rif1-cmycNLS177-996 (T504A S584A T775A S824A)GBD-6xFLAG-KANMX	This study	pCS209	OCC23	OCC84	
CALy480, 481	CALy117 + rif1-cmycNLS177-996 (K349A K363A)GBD-6xFLAG-KANMX	This study	pCS207	OCC23	OCC84	
CALy486, 487	CALy472 + rif1-cmycNLS177-996GBD-6xFLAG-KANMX	This study	pCS193	OCC23	CS323	
CALy488, 489	CALy472 + rif1-cmycNLS177-996 (T504A S584A T775A S824A)GBD-6xFLAG-KANMX	This study	pCS209	OCC23	OCC84	
CALy490, 491	CALy472 + rif1-cmycNLS177-996 (T504E S584E T775E S824E)GBD-6xFLAG-KANMX	This study	pCS210	OCC23	OCC84	
CALy498, 499	CALy117 + rif1-cmycNLS177-996 (N867A W868A)GBD-6xFLAG-KANMX	This study	pCS211	OCC23	OCC84	
CALy503, 539	CALy117 + rif1-cmycNLS177-996 (F236A E237A N243A)GBD-6xFLAG-KANMX	This study	pCS214	OCC23	OCC84	
CALy505, 546	CALy117 + rif1-cmycNLS177-996 (R299A Q303A R306A)GBD-6xFLAG-KANMX	This study	pCS215	OCC23	OCC84	
CALy506, 507	CALy117 + rif1-cmycNLS177-996 (W524A Y532A)GBD-6xFLAG-KANMX	This study	pCS216	OCC23	OCC84	
CALy508, 509	CALy117 + rif1-cmycNLS177-996 (Y577A)GBD-6xFLAG-KANMX	This study	pCS217	OCC23	OCC84	
CALy520, 521	CALy117 + rif1-cmycNLS177-996 (K437A K563A K570A) GBD-6xFLAG-KANMX	This study	pCS222	OCC23	OCC84	
CALy530, 531	CALy117 + rif1-cmycNLS177-996 (Y577R)GBD-6xFLAG-KANMX	This study	pCS230	OCC23	OCC84	
CALy532,533	CALy117 + rif1-68-1916-6xFLAG-KANMX	This study	pCS227	Kpn1	NotI	Digested plasmid, gel extracted top band for transformation
CALy534,535	CALy117 + rif1-cmyc-68-1916-6xFLAG-KANMX	This study	pCS226	Kpn1	NotI	Digested plasmid, gel extracted top band for transformation
CALy547,548	CALy117 + rif1-W524A Y532A-6xFLAG-KANMX	This study	pCS234	RW428	CS323	
CALy549,550	CALy117 + rif1-Y577A-6xFLAG-KANMX	This study	pCS233	RW428 or CS509	CS323	
CALy551,552	CALy117 + rif1-M436A T564A R565A W572A-6xFLAG-KANMX	This study	pCS235	RW428	CS323	
CALy553,554	CALy117 + rif1-C466A C473A-6xFLAG-KANMX	This study	pCS237	RW428	CS323	
CALy557,558	CALy117 + rif1-N867A W868A-6xFLAG-KANMX	This study	pCS239	RW429	CS323	

Figure 1

CALy117, 118
CALy202, 203
CALy328, 329
CALy286, 287
CALy442, 443

Figure 2

CALy117, 118
CALy202, 203
CALy328, 329
CALy286, 287
CALy375, 376
CALy408, 409

Figure 3

CALy117, 118
CALy328, 329
CALy286, 287
CALy408, 409
CALy428, 429
CALy432, 439
CALy202, 203

Figure 4

CALy117, 118
CALy328, 329
CALy202, 203
CALy472, 473
CALy432, 439
CALy486, 487
CALy478, 479
CALy488, 489
CALy465, 465
CALy490, 491

Figure 5

CALy117, 118
CALy328, 329
CALy286, 287
CALy290, 291
CALy432, 439
CALy454, 455
CALy462, 463
CALy520, 521

Figure 6

CALy117, 118
CALy503, 539
CALy505, 546
CALy480, 481
CALy460, 461
CALy506, 507
CALy508, 509
CALy498, 499
CALy432, 439
CALy530, 531

Supplementary Figure S1

CALy442, 443
CALy532,533
CALy534,535
CALy202, 203

Supplementary Figure S3

CALy117, 118
CALy503, 539
CALy505, 546
CALy480, 481
CALy460, 461
CALy506, 507
CALy508, 509
CALy498, 499
CALy432, 439
CALy530, 531
CALy442,443
CALy547,548
CALy549,550
CALy551,552
CALy557,558

Supplementary Figure S4

CALy442, 443
CALy553,554
CALy202, 203

1L TELOMERE PROBE FOR SOUTHERN- PCR from pCS206

CS414	ATCACCAGCAACATGTTTGG	This study
CS432	GCAAATTAAAGCCTTCGAGCG	This study

Y' PROBE FOR SOUTHERN- PCR from gDNA

YPrimeFWD	CGCGAATTGCCCCTACAGCACTTCTACATAGC	doi.org/10.1534/genetics.115.177899
YPrimeREV	CGAGAATTCCAGCGTTTGCGTTCCATGACG	doi.org/10.1534/genetics.115.177899

YEAST MEDIA SUPPLEMENTS

NAM (Nicotinamide)	5mM final to plates	Sigma: 72340-100G
G418 (Geneticin)	200µg/ml final to plates	Life Tech: 11811031
Hygromycin	200µg/ml final to plates	Corning: 30-240-CR

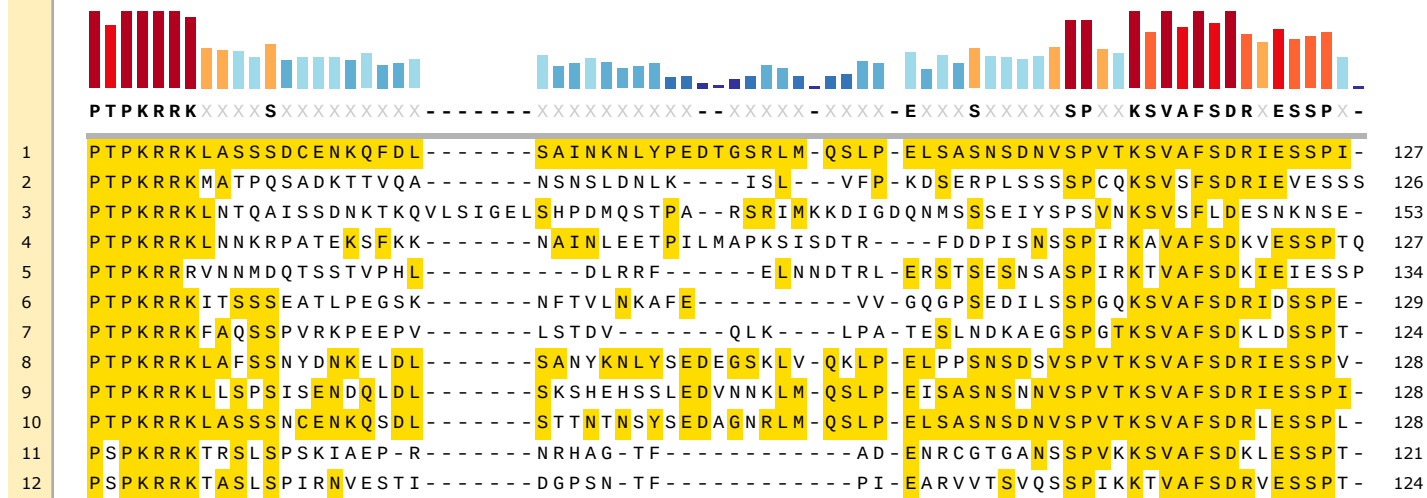
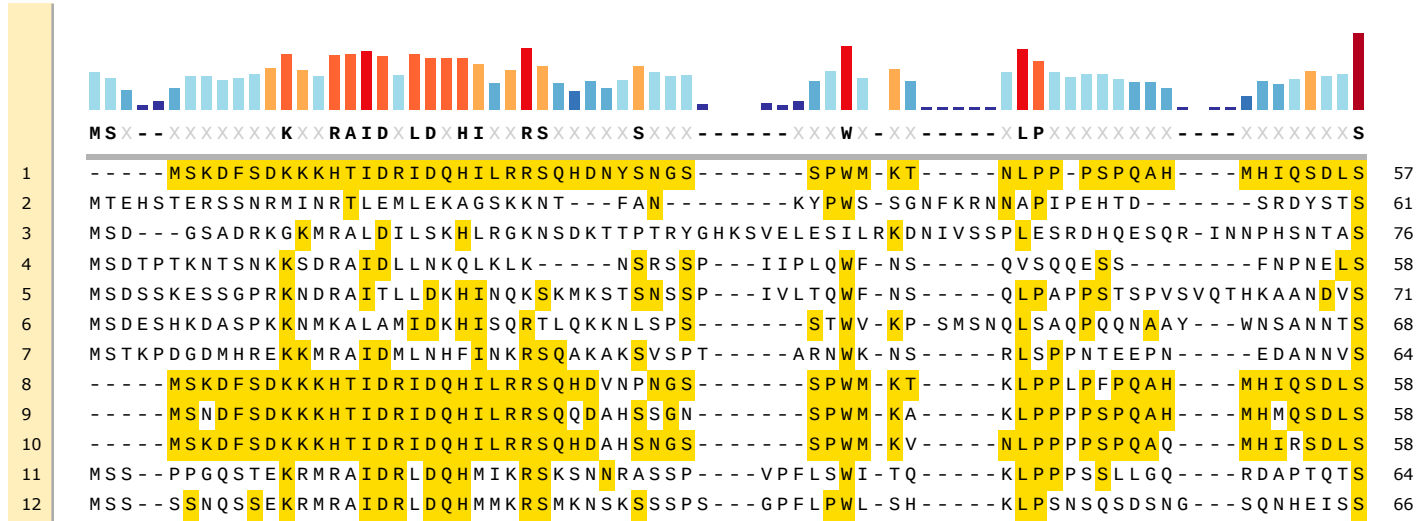
Figure Legend for Supplementary File

Supplementary File 1: *Multiple Sequence Alignment (MSA) of Rif1*

MSA of Rif1 generated as described in Materials and Methods and visualized using SnapGene software.

Consensus

- 1. Saccharomyces_cerevisiae
- 2. Kazachstania_naganishii
- 3. Candida_glabrata
- 4. Saccharomyces_castellii
- 5. Naumovozyma_dairenensis
- 6. Kazachstania_africana
- 7. Torulaspora_delbrueckii
- 8. Saccharomyces_mikatae
- 9. Saccharomyces_bayanus
- 0. Saccharomyces_paradoxus
- 1. Zygoaccharomyces_bailii
- 2. Zygosaccharomyces_rouxii





1	-YRIPGSSPK--PSPSSK-PGKSILRNRLPSVR-TVSD-----LSYNKLQYTQHKLHNGNIFT-SPYKET-RVNPRAL	193
2	AQTNSAASPR--PSSTSKLRSPKILKLNRYSLQKGDIV-----TE-----Q-----RL--TFSARTTFSLNPMEL	182
3	-STSSNSSPR--HSPTS-KPKSILRNSSSPEHNKQRM-----NDKYGKPIAANV-----HL-SRSENHSKNQYSPDNL	217
4	QSPMPDSSPRRPSSATKPPGKSILRNPDFITNRTKSD-----LSSNKDK--LVDSMSPLQLDPGNI	187
5	TQTLPESSPRHPPSSDRKPPSKSILRNSTPSSPVKYNTIKASSDVTYSKTVS--NNLAASNA--GVATNDFLHADPRKV	210
6	-RITAKSSPT--PSSTSKPPVKSILRNPGATQD-TDEE-----LNHEKSQR-----DSI--VPIDNDSSETNPNNI	189
7	-QRTMNSSPR--QTPASA-PSKSILRNPIEFQK-NVSL-----MADP-AGKPKSKLA-GR-G-GQVNDTSDDDIDPTSL	188
8	-HHVPGSSPK--PSPSSR-PGKSILRNKMSSAR-TVSD-----LSYNKLQHPEHRLHNGNILT-SPYKETIVINPRTL	195
9	-HHVPGSSPK--PSPSSK-PGKSILRNRMPPMR-TVSD-----LSYNKLQHSQQLHNGNIFT-SPYKESTGVDPRTL	195
10	-HHVPGSSPK--PSPSSK-PGKSILRNRMPSVR-TVSD-----LSYNKLQYTQHKLHNGNIFT-SPYKETIGLNPHSL	195
11	-QKSPRSSPR--PTSVSK-PSKSILRNADTFRKSTGD-----LTAKRSEMLT----SHIGSARLENNTSPTDPHSL	186
12	-QQTPRSSPR--PSSLQK-PVKSILRNT-DALRKCVD-----ISFKRPPFLNQ-----NIDR-NKTDRTAGIDPHRL	186



1	EYWVSGEIHGLVDNESVSEFKEIEGGLGILRQES-EDYVARRFEVYATFNNIIPILTT-KNVNEVD-QKFNILIVNIES	270
2	AYWRSGEIHNMTDIKNINELKNIFEGGLSLLAVSE-PEHVSKRFEIYATFNAILERQFGDNTPTGMEDKVCVSLCAHME	261
3	QFWNGEIHSLSSNNSVAEFKFLGALKILMQSKNPEYGAKKFEVHATINNIMPSFSS-TTNSQFIEKAAHIVKDNLKI	296
4	EYWVSGEIHSLFNNENVKEFEFEGIIIGGIHILQLENVENSSNRRFEIYATFNNIIPILPTDKDIDPITENKVKVIVNLP	267
5	EYWADGEIHSLLYPNNIKEFRDIEGGISFLNM-----GLKKFEIFATFNNIIPINPFGMATDVIDKKIGIIVENLDN	284
6	SYWTGGEIHSKLDHNNLAEFKQVIEGGLYVLLSSNS-DPHNSRRFEIYATFNNLCRGLSASDHVSETNEKKINILFQKLET	268
7	AFWEFGEVHKMLDSSNFKEFKQIEGGLEILANNE-RSHVARRFEVYASFNNIIPPNNL-KYHSELIEKKFDILIHNLKK	266
8	NYWVSGEIHGLIDNESISEFKEIEGGLNILRKES-EYVAKRFEVYATFNNIIPILTT-KNVNEVD-QKFNVLIVNIEA	272
9	DYWVSGEIHSLIDNESVSEFKDIEGGLGILRQES-EYVARRFEVYATFNNIIPILTT-KNVNEVD-QKFNVLIVNVET	272
10	NYWVSGEIHSLIDNESVSEFKEIEGGLGILRQES-EYVARKFEVYATFNNIIPILTT-KNVNEVD-QKFNVLIVNIES	272
11	DYWVSGEVHSMLEFNNVHEFKNIEGGLKILSQTD-AVSITKRFEIYATFNNIMPVISG-KGSSEIAERKINVLIDHMDI	264
12	DFWVGGEVHSMLEDPYNVHEFFNIIDGGLRILSEKT-DECVVKRFEIYATFNNIMPSSST-KGLNDINERKVNVLIDQMEF	264



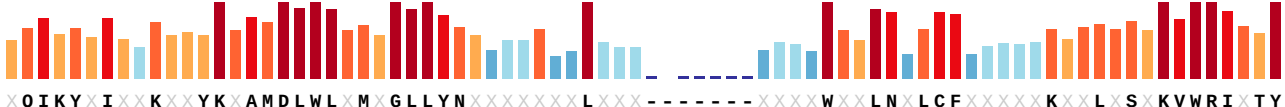
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2	IVNVCPHLKLEQSSLEENVSVKNPFSTRLYIQIVRFFTHLLSNFKVICALSSKRNIQTSMKQVFESSYEALSSPHCNKQ	341
3	IANISIEHLRDEQMSLLQDKKKNPFISIRLYIQIVRFFTNLFGSFIINKFLISSKALCERMKQVYELSLEALKNENSXKM	376
4	LKIVATLNLQEEQTELLKSHNKNPFITRLYVQIVRFFGSILSNFMIIKRISTDPELQKELRIIYKISVEALSNEYVNKM	347
5	LKILISNLKDEQKELLEGNEKKNPFTSRQYVQIIRLLGIMLSNFKIICWLDKRKPLQVMLKEIYKLSEALVNENSXKV	364
6	ITDVCLPHLDWEQKLLGTTTKKDPFSSRIYIQIVRFFTILLSNQILVRRLSKRKTLIAKLSSTFYEYSIDTILSNNSXKV	348
7	IIEVCLPHLRTEQKLLGAGNKNPFSGSRIYIQIVRFLFGSLLAHYRVMRALTKLPSLKEQLGEVLELSKEALVHPNANKV	346
8	IIEICPHLQMTAQEKLLSSNEKNPFIRLYVQIVRFFATIMSSFIVKWLKRPDLVNKLKVIYRWTTGALRNENSXKI	352
9	IIEICPHLQMTAQEKLLSSNEKNPFIRLYVQIVRFFATIMSSFIVKWLKRPDLVNKLKVIYRWTTGALRNENSXKI	352
10	IIEVCLPHLQMTAQEKLLSSNEKNPFIRLYVQIVRFFATIMSSFIVKWLKRPDLVNKLKVIYRWTTGALRNENSXKI	352
11	VVDTCLSHLEEEQEKLLSTNSKDPFVSRLYVQIVRFLNSILSNFKIWKWLTKRPDLVNKLKVIYRWTTGALRNENSXKI	344
12	IVNVCLPHLKEEQKLLSTGKKNPFSTRLYVQIVRFFNFILSNFKLLKWLKRPDLVNKLKVIYRWTTGALRNENSXKI	344



1 IITAQVSFLRDEKFGTFFLSNEEIKPIISTFTEIMEINSHNLIYEKLLLRGFLSKYPKLM IETVTSWLPGEVLPRIIIG 430
 2 MITAQMIFLRQEKFGTSYLTENERNKLVNIITEVNEIDSYNLKYEKLLLIKALFGKYLKQMLQDVPKWLCGEVLARILVE 421
 3 MLICQMTFLRDEKLSYISFTEDEGKHMIIQINQIRDIPSTNAICEKLMLIKQFLIKFPGPMISTIPEWLPTQVISKIVFS 456
 4 MIISQLTFLRDEKFSRRYLPMSEITKMINVITQVKDMASTNLICEKLYLVKCFLDKFPVLMIDEIKVWLPGEVLPRIILLM 427
 5 IISQLTFLKDEKFSYYLNKNEILRIIDTFTKIKDLKSTNLMNEKLLLMRCYINKFPKLMIPKISDWLPGELLISKIVLD 444
 6 MIISHISFLKEEKFGSYLPSHTIDNLTISIVPNIKEVDSVNLSTEKLMLLRRFLEKYPDMMFNKASWLPGEVLLRILLD 428
 7 IIGAQYTLLAYEKYGAYFLQKEDVMSIIRSVIRTKDIQSTNLICEKLLMRKFLSKYTSVMLEIPEWLPSEVLAQILSD 426
 8 IITAQVSFLRDEKFGTFFLSDEEIKPIISTFTEIIEINSHNLIYEKLLLRGFLSKYPKLM IETVTSWLPGEVLPRIIIG 432
 9 IITAQVSFLRDEKFGTFFLSDEEIKPIIDTFTTEIIEINSNLI>CEKLLLRGFLSKYPKLM IETVTSWLPGEVLPRIIIG 432
 10 IITAQVSFLRDEKFGTFFLSNEEIKPIISTFTKIMEINSHNLIYEKLLLRGFLSKYPKLM IETVTSWLPGEVLPRIIIG 432
 11 IVAAQVAVLGDVKFGTFFLNDDEELTSIIHTIPTIKETQSTNLICEKLLIKNLLAKYPRLM IENVSIWLCGEVLPRIILID 424
 12 MVAQVAVLGDVSKFGSFFLNDDEITSLIRIIPSIKETQSTNLINEKLLIRSLIAKYPRLMIDQVSIWFCGEVLPRIILIE 424



1 DE--IYSMKILITSIVVLELLKKCLDFVD-EHERIYQCIMLSPVCETIPEKFLSKLPLNS--YDS-ANLDKVTIGHLLT 504
 2 TQ--TYANKLAVVALEILLDLLKQLLGGKDSVTASIIYESMEEKPAKDVLSPSMKMMLQSVL--PDT-YDFETITIGSMLR 496
 3 ED--VYSTKTGFTAISVLELLKRCIDHSI-GHEYVFQCLHIDSTALYFGDSKDKKLQWSNNTLEQTYDINETHLAAAILR 533
 4 EEENNHSAKIIVTAISIIILLDLLKKCLDVEK-GHKDIYQCVEIDKVKDVI>PRKFLSRIELSL---KEIEN>VGEKTLGTLIR 503
 5 ED--MYAIKITHTSIAVLLDLLKKCLDVEE-GHQEIFKYVEVKT>LN>ESV>EGTLEKFNSTAVLNDLEIDINSMTLGQLLR 521
 6 DG--SNGWKCI>AAISVLLDFLRLCLDHDN-TQINIYQ>SI>EVDKLNDVVP>Q>KFLPKMQQYL--KDK-SL>LESMTLGQVIR 502
 7 EE--VH>SLSIL>QAGIAVLLDLLK>SLD>SSA-I>H>QTINRCIR>N>LAKDVM>PEGAQNR>SVHG-----H>SEW>SG>ST>LEEM>L>Q 498
 8 DE--VYSMKILITSIVVLELLKKCLDFVE-EHERIYQCIM>V>SPITETIPEKFLSKLP>V>SS--HDT-AS>L>G>K>V>T>I>G>H>L>L>T 506
 9 DE--VYSMKILITSIVVLELLKKCLDFVE-EHERIYQCV>V>SPV>TETIN>K>K>F>L>S>R>L>PL>NS--N>DA-G>D>L>N>K>I>T>I>G>H>L>L>T 506
 10 DE--VYSMKILITSIVVLELLKKCLDFVD-EHERIYQCV>V>L>SPITETIPEKFLSKLPLNS--S>E>T>A>D>L>S>K>V>T>I>G>H>L>L>T 506
 11 SE--I>NC>S>K>I>V>L>T>AV>ST>I>L>D>L>L>K>K>C>L>D>V>S>K-G>H>E>D>I>Y>N>S>V>Q>I>C>T>V>R>E>V>V>P>A>K>L>L>P>K>L>L>P>S>Q--N>D>P-E>S>I>S>Q>T>L>G>Q>L>L>R 498
 12 NE--L>N>S>T>K>I>V>A>T>AV>ST>T>L>D>L>L>K>K>C>L>D>F>S>K-G>H>E>E>I>Y>R>C>V>E>V>L>F>V>K>D>V>V>P>K>K>L>L>T>K>L>T>P>S>Q--D>D>N>L>D>S>I>A>Q>T>T>L>G>Q>L>L>R 499



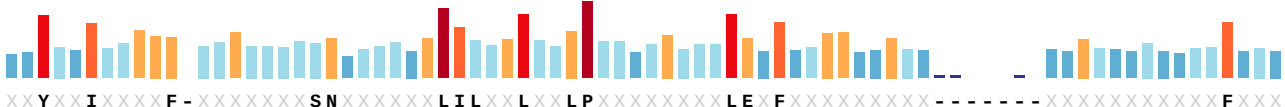
1 QQIKNYIVVKNDNKIAMDLWLSMTGLLYDSGKRYYDLTSE-----SNKVWFDLNNLCFINNHPKTRLM>SI>K>V>R>I>I>T>Y 577
 2 DHLRNQITEQKAYIGIDLWLALV>G>IL>F>N>S>P>R>N>I>T>K>L>L>P>T-----D>D>R>G>D>S>W>L>S>L>N>E>L>A>F>K>T>N>D>E>K>A>M>L>L>A>L>K>S>W>R>V>V>I>Y 571
 3 DHIDYLVNSKREYK>L>A>M>D>L>W>L>S>F>M>G>L>L>F>N>S>K>G>R>L>A>F>L>A>S>K-----E>G>E>K>W>V>D>I>N>L>N>C>L>S>V>N>D>P>K>C>R>I>L>S>L>K>V>R>I>L>I>Y 606
 4 NQIKYLIL>V>K>K>E>Y>K>L>A>M>D>L>W>I>G>M>V>G>L>L>F>N>N>A>N>S>L>E>M>L>T>K>E>N>A>E>T>D>A>N>R>S>D>T>W>I>D>L>N>K>L>C>Y>N>K>G>T>G>K>V>K>Y>F>S>S>K>V>R>I>L>F>Y 583
 5 NKIKYLVL>V>Q>D>Y>K>V>G>I>D>L>W>L>A>M>V>G>L>L>F>N>N>K>K>N>I>I>H>L>L>D>K>D-K>T>H>D>K>S>S>A>D>W>L>N>L>V>Q>L>C>F>K>N>S>D>G>K>T>K>L>L>S>L>K>V>R>I>L>T>Y 600
 6 DHINYFLLANKHYKIAADLWLAM>V>G>L>L>Y>R>K>A>D>K>I>E>E>L>S>A>G>T-----Y>E>N>N>W>L>S>L>N>S>S>C>F>E>I>P>E>E>H>I>K>L>M>S>L>K>V>R>I>L>F>Y 576
 7 KEITFLI>IS>K>K>E>I>K>F>A>M>D>L>W>L>A>M>G>L>L>Y>N>T>T>E>A>L>L>E>L>S>D>T-----D>E>R>G>W>L>R>L>N>H>I>C>F>L>S>G>N>S>S>A>K>F>I>A>L>K>A>W>R>I>I>T>Y 571
 8 QQV>K>Y>I>V>H>K>H>D>N>K>I>A>M>D>L>W>L>S>I>T>G>L>L>Y>D>N>E>K>R>V>Y>D>L>T>L>E-----S>N>E>V>W>F>D>L>N>L>C>F>I>N>D>H>P>K>T>R>L>M>S>I>K>V>R>I>I>T>Y 579
 9 EQIKYYIVVKNDNKIAMDLWLSMTGLLYDNGKTVYDLISE-----S>S>K>T>W>F>D>L>N>L>C>F>M>N>E>Q>P>K>T>R>L>M>S>I>K>V>R>I>I>T>Y 579
 10 KQIKNYIVVKNDNKIAMDLWLSMTGLLYDNGKRYYDLTSD-----S>N>K>G>W>F>S>L>N>N>L>C>F>I>N>N>Q>P>K>T>R>L>M>S>I>K>V>R>I>I>T>Y 579
 11 KQLKYLIL>V>K>Q>E>Y>K>L>A>M>D>L>W>L>A>M>T>G>L>L>Y>N>S>T>D>R>L>Q>Q>L>T>S>A-----T>D>R>E>W>L>D>L>N>F>L>C>F>Q>A>D>D>P>Q>A>K>L>L>A>I>K>V>R>I>L>T>Y 571
 12 KQIRYLIVAKQEYK>L>A>M>D>L>W>L>A>L>T>G>L>L>Y>N>N>I>D>R>D>L>Y>L>S>T>H-----I>D>N>E>W>L>S>L>N>L>L>C>F>H>A>S>S>A>Q>A>K>L>L>S>I>K>V>R>V>L>T>Y 572



1 CICTKISQK-NQEGNKSLLSLLRTPFQMTLPYVNDPSAREGIYHLLGVVYTAFTS-NKNLSTDMFELFWDHLLITPIYED 655
 2 LVSVNITSLESDEVQLQLLQLLLTPFDQLPNVLEKDCVREGLLYCLNGVVFCSVSMINSLGTQNAISLFWDNLLQPLFHK 651
 3 CVTNNIDFL-GEKEAKKISQVLLNPVNVTVNKLEDNSTFMGVKYLNDFFFSTCGI-TNKCKPTTNIVLWGNFIIPMLAT 684
 4 CVSKHLDEF-NETSKPMVLDLLKTPFDMSRPYINDSDVSKALLYCLRGLVYANLCGP-AQSSKESLSLFIISNLLKPIILIG 661
 5 CICTHVTEL-DSAYQIPLLNILKIPLEISKTEHGNDNVRDGIYIYVTVGIIYTAFLLLQKNLSYETFQFFFDNLVKPIYEN 679
 6 GVCSEISGK-FDEKDLLMLNLLRRPFELSEGQHTMPAVRDGLLYCLNGLTFTIVSTVNVNDAKRFGFFWDNLLKPLFIS 655
 7 YSWAHVQGK-SLHHDHALIRLLKMPFEFSSTSHLEPDVCEGLIYYLTGMVVFVTCGN-SKAQEQTFRFFWENLISPIYHD 649
 8 CICTKISLK-NQEGNKRLFSLLQTPFQMTLSHVNDPSAREGIYHLLGVVYTAFTS-NRNLSTDIFEHFWDHLLIAPIYEN 657
 9 CICTKISLK-NEERNESLLSLLQTPFQMTLSHVNDPSAREGIYHFLGIVYTAFTS-NKNLSMDMFLFWDYLIAPIYEK 657
 10 CICTKISLK-NQEGNKMLLSLLQTPFQMTLPYVNDPSTREGIYHLLGVVYTAFTS-NKNLSADMFLFWDHLLIAPIYED 657
 11 SICSHLETFS-TENLRRIKLLQRPFTFSREDQYDFNIMEGLLFHLTGIIYTAFA-SATNLLSTAKFDLFWEHLVRPIYVE 648
 12 SICTHLEHE-T-VKNIRIVNLLQRPFEFTQQEQYEFNVMGLIFHLTGIIYTAFA-SG-HSTISGEKFSLLWEHVVKPVYMR 649



1 YVFKYDSIHLQNVLFVTLVHLLIGGKNADVAL-----ERKYKHHIHPMSVIASEGVKLDISSLPPQIIK 719
 2 WNSAASSNELQTRTMDIFIKILRGKFPKTSTQRSNS-----PNTKQQQHFRPVRVIAARGIVISDIPNLSNNFIH 722
 3 LLNYSANEDVKFELDTIYIGKLLTKAIQN-----QKNVDKTKSLHPKVIASEGVSVDDISALQLSPL 747
 4 IILVNQH--LHHEVVSVLLRLLGKPLPETSPEK-----G-----NRNGLRPAPIKVIASGTGIATNDISKMTNHLIK 726
 5 FIFNSP SFHVQTRLLGILLQLL GAPLFNLVSTSKHITSNAGKSKNIRNDK KVSPPNPKVIASVGISRDHIVPLPHTLSH 759
 6 FLKTSPPNQLRARVIHLLALMMGGHGF DVVKKRRRPGDQEP-YTTKKQKVIRAYADPVRVVAATGISLDDITSLHPNVLN 734
 7 FLFTSDSIKLSAAIKLLAVLDGKSETGTS-----KTSSFPKVIASVGVMTKEIEPVPADTV 710
 8 YVFLYDSIQLQNILFTILHLLIGGKNDFAT-----ERRNKKHHIHPMSVIASEGVKVDISSIPSQIIK 721
 9 FVFNYNSIQLQNVPLTVLHLLIGGKNSDVV-----ERKNKKHHISMSVIASEGVKIKDISSLPPSIIK 721
 10 YVFKYDSIHLQNVLLTVLHLLIGGKNADVAL-----ERKNKKHHISMSVIASEGVKLDISSLPSQIIK 721
 11 RILISQSIQLKARANALLRLLGGKITPEPQH-----KQVCKKIVHSIKIIASAGVTARDIQPLPLNVIK 712
 12 KIFPSTSIQLRNRAIVLLRLLGSKVMEQQANQQHQEKQQ-P-HTHRNIKNGAHPIRVIASAGVSARDIQPLSANVIG 727



1 REYDKIMKVVV-QAVEVAISNVNLAHDLILTSLKHLPEDRKDQTHLESFSSILIKVTQ-----NPKDTPIFRDFFGAV 791
 2 IWYMQMAKSAS-DLLRTRSFEDHAKSLFLSLIDTVPESSLNDEVFDYFLLVLKHYLEP-----TYDYTFNQLSVLTLF 795
 3 YLLETLSGVILLYVLNKSQNHSTQTRMLILEYLEEQIPNNQITLSTLCRCISMFYEYYN-----SIDFIANSRSLISD 820
 4 QLYYPLSDLIF-SILRKHILKPPSSELLISLLNNTPLELKTVSYLEEVNQVMIDILKT-----SDDHTEISLLFQTY 798
 5 PGYTLISRLFL-NSLPINAKFLT VKTEIILDLIAQIPDELKTEEVFQEYRNIVVSLTKLYKTSYTTKNKNDVLFECFSRC 838
 6 ENYLSIMGLCM-DNTGAHPLS-YLTDKLLYLLSKLPEHLRNTEVLEAFSDVLSFVFNRS---V-RISSKANTVRIFSTH 808
 7 DAYELVLTLS-NALSIDSSEWATRFELFDSMLRLLPAEFIDDTHTLITFLDLVSRLFS-----QASLPKDPSTVLCPL 782
 8 YAYDKIMKVVV-KAVEVAMSNVNLAHDLILTSLKQLPEDKQDQNHLEAFRTILKVA-----NNKDKPIFRDFFVT 793
 9 SAYDKIMKVVV-QGVKTAMSNVNLAHDLILTSLKHLPEDRKDQSHLEAFSSILIEVAE-----NNKDKPIFRDFFGAV 793
 10 SAYDKIMKVVV-QAVEAAISNVNLAHDLILTSLKHLPEDKQDQIHLEAFSSILIKVAQ-----NNKDKPIFRDFYGA 793
 11 SSYEAIKDLVF-QAIESDSSNLCQNFDLITALLKVLPNKFIDKEHLREFTNAIFGVAI-----QRKEDQNLADVFIQI 784
 12 TNFETIKDLIF-EAIRSNSSNLSQNSELITALLKQMPKSFVNENSLEDFAEIIREISI-----QRKDDKNVGSHFVQL 799



1 TSSFVYTFDLDFLRKNDSSLVNFNFIQISKVGISQGNMMLDQLLDKDVIRK-ARNETSEFLIIEKFLE-LDDKKTEVYAQNWW 869
 2 ATQLVTKFEKLLLEPSNSGLSSVIALYDSKTFINYDFPLKLMISMLDS-NDCDASLFAIFSKFMD-MKNKNYPDYVTNWL 873
 3 MSRVCIKFKDIIFDDNYNVFRNFILSFLMLFQEEHHVDNLLQELIQNALQANISELKLIEGILS-LKKTDCDLFAINWV 899
 4 THVVVTIFPNLLLNKETNYLEDYLKLFEPFVGWGVKEMLLDVLKDFLRE-KKLAGWEFYMMGIFLK-TKDTLSHLYVENWI 876
 5 TCLLGKTFPNIILNPKRDIFSKYLASFNDLFTDNADMLIKLLKDIKY-TRPQISELTVIELFLTNTNDKNSRDYIQNWV 917
 6 SSKLAITFKDILFDKNSKAFTNYIAKFNMLSDREGTCLLTFLLKQLLNN-SKGIIPELFFVVENFLL-IGNKEVDSYLSNWV 886
 7 VLSLTGPFANFVFESSK-NFQKLLKGVDFHYGQDSEIRLTLMKFEFSKK-LRRQISEFTIIEERFLE-VGDLSCQRYASNWI 859
 8 SSSFVYAFLELFLKHKHSSSLVFEFSIQLSKVGIPQGNMMLDQLLDKDVIRK-ARNETSEFVIEKFLE-LNDKKTEVYAQNWW 871
 9 GSSFVYAFLELFLKHKHSSSLVFEFSIQLSKVGIPQGNMMLDQLLDKDVIRK-ARNETSEFVIEKFLE-LNDKKTEVYAQNWW 871
 10 IPSPVYAFDLDFLRKHSSSLVFEFSIQLSKVGIPQGNMMLDQLLDKDVIRK-ARNETSEFLIIEKFLE-LDDKKTEVYAQNWW 871
 11 TCCLATQFATLFSDERK-IFEEYLGKFSFILLANGETKIKLLKELIVG-LRGKMSSEFFIEAFLQ-QGDLSTKEYVSNWI 861
 12 TCCLMSQFATLFSDERK-IFEEYLGKFSFILLANGETKIKLLKELIVG-LRGKMSSEFFIEAFLQ-QGDLSTKEYVSNWI 876



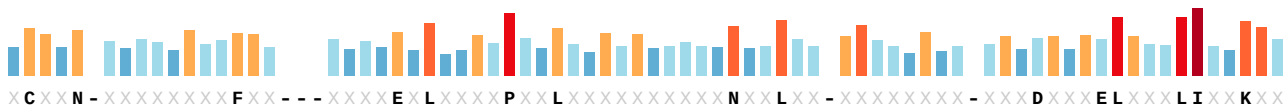
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 2 SVAVLPSNMNRHDMKFLMNIISKNPVLSIENLLTVIADIDREFYGMICTSALTWDDHALLYFIKGVFTSNAPNSCNYL- 952
 3 GKKLLSPSVQEGDFILYSRIVAKISEKQTIIVNFDLADKLGFEVNPTEILRISFWKPSGLVIFLEEYIAKHHVDFADIVS 979
 4 GSTLLSPTMSYTSFLDLANIINQITTDQVMENFLDLCCKMSLSINYPQLLNKQYNDKNSLFFIKTYLSKNSNALDNMS 956
 5 GSTLLSPMLTYPEFQSLTNIVNMIPSSQIVENYLDLCVKTSLAQNPCTTLNIRNWKDKQLIFFIKTYISKCSNRLDDDIL 997
 6 GSTLFPPSLSKDEIIALAHCVSTIHTEKAIENFIDYSKKIE-QLDVVTLHLGAWDESDFCFFVKAYLAKRKNVSVTHLI 965
 7 GSVLLPNTLTTSELHFSFASIVKLLSPQATGALLNFCILNSKDKPDICELLNIDDWGDEKVAILVKAVVSLSSNKLVPSLA 939
 8 GSTLLPPNISFKEFQSLANIVDKVPNENSIENFLDLCCLKLSFPVNFFTLLHVSKWSNNNFYFIQRFFSKNDEKLNADLI 951
 9 GSTLLAPNISFKEFQSLAGIVDQVPNEHSIENFLDLCCLKLTFFPVNLFALIHVSKWSNDFYFIQSYVSKNENKLDLTDLV 951
 10 GSTLLPPNISFREFQSLANIVDKVPNENSIENFLDLCCLKLSFPVNLFTLLHVSKWSNNNFYFIQSYVSKNENRLNADLI 951
 11 GSMLLSPMPHEHFSTLVNIVTLIPTTEVLENFLNLSKSVNYDVLFSLLNIQNWFEFGIIFIKNSILKNHNTIKPELN 941
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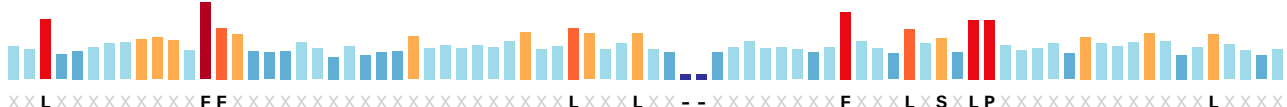
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 2 ---SGCLPTRISKSLFLFKAILNSPELFEKENGIVLRSVLKNPSLIQNLNVAEVT----KLRDLSHDHAPTDFEMKYIN--- 1022
 3 SIIDADRLNNV----ELFSYVLKHLPENQKSAFIKQHYTKCPLIWNQGVLIIDDY----DLIDITLDCEICTFIAHHFSFL 1051
 4 QFLIEILSENRTS--SVPRILLPLLIDIKRYDIKTSIEQRPLILSIVSDPILL----HLKDILPTSKMSYLIINIIGLF- 1029
 5 VLLHDVLPDNI----DVFDSMVPLLIQINRTDLIRHCIEKKPSYLNTPAIMNYH----DLSEILPDDRKYLLNLLKDF- 1068
 6 ALLQKLLPSRP----ETFTELLPTLLEYGHKELVSDCVKKNPIILIESLLPKYPD----NLSDFFSADEILAFVPMKNF- 1036
 7 VKLQMLPSRV----SLFNELFTTLQTLKYEELIRHVIIANPEAANGIILLNGTQAPAVLPKGLPRDTLSYFVQSPLNF- 1014
 8 TLLKTSLPGNP----ELFFGLVPLRLLNKFIDILKYCICSNPALLNSITDLNSD----FLMQLLPLSRASYFAANIQLF- 1022
 9 TLLKTSLPGNT----ELFVGLLPFLKEKKFMSILEYCIQSNPTLLSYISDLNSD----LLELLPRSRTSYFVTNIQSF- 1022
 10 TLLKTSLPGNP----ELFFGLLPFLRNNNFIDILEYCIQSNPTLLNSIPDLNSD----FLIKLLPRSRASYFAANMKLF- 1022
 11 LFLQSVLPNST----PIFSEMLPFLCGAKHYNIYRYTLTKSPKFLNLTTSVDK----SFDEILPLEILPFLQSIQSDY- 1012
 12 SFLENILRENE----QLFSTLLPFLCQLGHYEVLRVLVLRTPFLSHTLGVDEE----SFDQILPLEKLSFFLKNLLNY- 1027



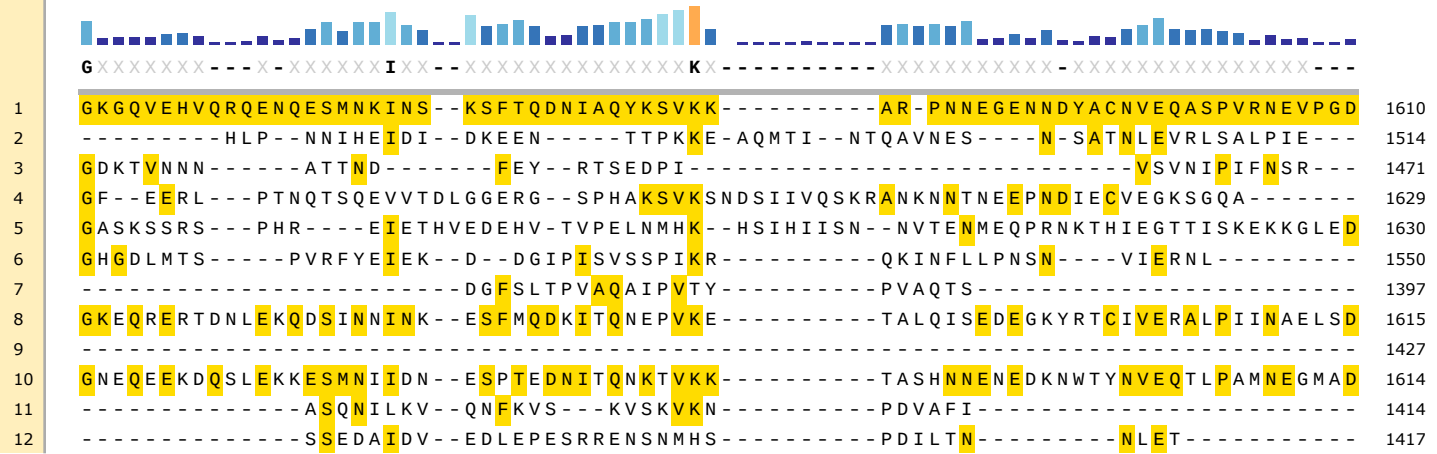
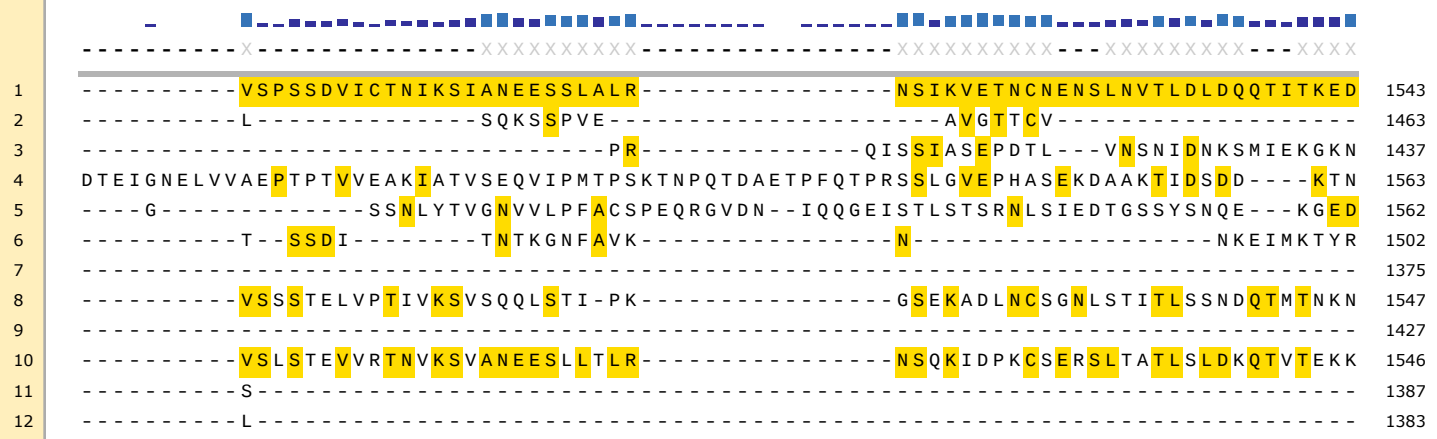
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 2 -----VVYKQIAGTMNNKLSQSGTSTDKSNSECFNEPQLDNQGGTGEDTSVVVLEKLEHCCSNKGDALTEILS 1092
 3 STSSKAKLLIIFIEKDMYDLLVQFRY-----NLIQEFLLPTLTIIYKGD---DIITTVQQHLINYCFAKNSFVLLDCIEP 1121
 4 PQLIQYGIQWVLEKDETALLSNYA-----TIEITILFVD-KPTDTSVNEERKKLIQHILHYLFENRRWVLLSNLID 1100
 5 SAIVQYKIMWVAKTDEFTLFKKNYV-----KIESCLFLD-EPCSENILD-KKAFIKELFTIFYEKQAWQLVAIILVV 1138
 6 SSETQVILLKEAWKSGLSTVVKNF-----SVASCLFEQ-ALDG-SISNVRKILTDSILSSIKDERWDLNFFV 1106
 7 DENAQLGMIKWILDMNEADLLFADRG-----EWKDCVFLR-IGKDGFEFSNEFKILTADAISQLYEKQSWKNLSKCIL 1085
 8 MNSEQLTIIRWLLKGGQLLEEINQNFSEFKSSLQNA-SG---HE-LEKSEIIRELLLLTAKNPIEPLLGGLLE 1089
 9 NHAELTIICWLLLEGEELDQINQNFPEVKNILLHT-PA---DE-LEKSKIIGELFRLATKNPIEPLFSELLN 1089
 10 KSSEQLTLIRWLLKGGQLDQLNQNFSEIESVLQNA-PD---SE-LEKSEIIGELLCLTTRNPIEPLFSGLLY 1089
 11 QDTIQLRILQWCIEHNNINMLFGHYE-----TLEHYLFKK-EYGTES-SRRNQLLLDLLSSLLVGGKWLKYSKIIQ 1082
 12 ETFFQLRTIRWALKHNNINILFENSS-----VLQKCLFQQ-CTSS EDT-MKKEKLLLDLLSVTVLGEKWHYLSLLVI 1097



1 FCIKN-NMADHLDEFCEG---NMTSEVLFKISPELLLKLTYKEKPNGLLA-AVIEKIEN-GDDDYILELLEKIIIQKEI 1161
 2 NLLSQ-DQTTIISNFFCSYAAQNIIEVIKLISPKLLRHLCKFYDPHLHALILPAINYLFQVQKISTLTSLAILLIEKDKDI 1171
 3 STLTSTRLEDVIKLE---KSYEDNITFVPAKYIIFIDNLPMDTKINTTE-ILRVYLVTDGVTQCLFFLTSLINDKMM 1195
 4 SCLSN-SQTDYIISLFS---GGNATELQNILPQTLANMINRCGSLNPSLID-TLKQNYSL-QKADYIITLISELVECGKT 1174
 5 SCINH-GYESNATEFLA---NIDSNTLNSFPPKAIATIVNRCGSMNPKLL-ILHQFFSN-KEKFFLELVSELSLKKI 1212
 6 TAYLNGRDTGLDNFFFT---KVDSESLHFQPNFLVAICDRLGY-SERRKN-VLKKCFV-KEKEYVISLIEALIKSKKF 1180
 7 YCMTC-GQVPCVEQVYV---RMRDKRRENNSPK--SPKADECKSLNSILSE-SIKEIYQG-DAIDTAFEVTTSLIELKVV 1157
 8 ICVEN-SIIDCLNEFCE---AITDELILLKINAELMIRLLTYRDNPNALLT-AVTERIRN-ADSDYTFEFIGKIVARKEI 1163
 9 FCIDN-SMTNNLDEFCE---TINDEILSKINPELLMRLTYRDKPNVTLT-VLAGNIGN-ADSDYKFELLERIARKEL 1163
 10 FCLKN-SMTDHLDEFCE---KVTDEVLLKINPELLLKLTYNDKPNGLLT-AVTEKIGN-ADNDYILELLEKIIAQKEI 1163
 11 SCMKNGQASPVTKTFS---KNDPESLFWLTPVTLASMINKCGLLNPSLIE-VLKKCFSR-KPADFNIELTKELINRNES 1156
 12 WGMEN-NEIGHLTTTCFS---KENLTPLIHLSPQALALMINKCGSLNPTLIE-AVKRSFFT-NDTQFNIGLIEELIVHNKF 1171



1 QILEKLKEPLLFFLNPVSS-NMQKHKKSTNMLRELVLVLLYLTKPLSRSAAKKFFSMLISILPPNPNYQTIDMVNLLIDLI 1240
 2 NGLDRIIDPFSIFLFGKPKKSSDIKHKIAGLFLKMFLLKE--ERGVHLSIVLHRIVRSLPRRRPEYLKKNVINTISTQK 1249
 3 VPLTRCRNEVDFDFIALDSSNDLSIKAKAVTTFESLINVIFL--LRKKVDIGFLSQYIARLPERPSRYLVLDSEKLIINLK 1273
 4 QALILSKQDMLLFIIDSENAALRPVDQRRILELMPRFIQSLQN--KSEKTFIDFLKMLFNLLPEHSNQYLLNLVQLFKESL 1252
 5 DALLSVSSELINFFIDDQHFTEDEQGSIGILEKFLAQLQK--YNERTSFNFTKDLMSLPSKSKTKYLSKLASCVGSQAQ 1290
 6 DVLNDLRSEFIFLLVHVKDPSLTFEKQYVDGINNFILLKE--QSEDVVVDFMVYLSIPMQKQMSINDKTVLKYMISDE 1258
 7 QNFSSCREEFLLNFIRASNFVSVEQAIALELFERFIAVLM--CFDEIILSFVESILSSILKVLTDHSLQVFGLLNHHL 1235
 8 LLEKLKEPLLVLVSPVRS-SEQKYEESANMLRELVLVLLYLTKPLTRSAAKKFFSMLVLSILPSNPNHQITDMVYLLIDLI 1242
 9 LVLEKLKESFFIFLLDPVSRNKENHDNGTKIFCELILLYLTKPLSRGAAKKFFSMLVSTLPERPDRQSIDLVHLLIDII 1243
 10 QLEKLKEPLLFFLNPVRS-NKQKHEKSANMLRELVLVLLYLTKPLSRSAAKKFFSMLISILPPNPNRQTIDMVALLIDLI 1242
 11 QVFFLCGKEVVAFFTVRSKMFTLSEQDAISALFEMMTSLMC--QKDSLILDFVQELYANIPQECDSHLLKILIIAVKKL 1234
 12 QLFILCGKEIVTFFLDNSSLSGVEQDGVLSIFEKLLVSLMG--QKKSLLVDFVEEISEKLEAPDAYLLKIITILVEQL 1249





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2	---TGTQMIDNSNKY---KG---SEMVTGSDLRAEGKVS---	1544
3	---VSGLD---	1477
4	---T---G---QSFKANPSKSSAD---SDKPTNLDTK	1654
5	MTENS SI---G---EAKLALPMATIVDDPQRSSTNV DTE	1663
6	--KATQETEISNNGNATDIVPIEVNGDHMDNDGAVSLAGNAT-GGGKNN---NVVIEAVTPNSES DR---GRHV---	1615
7	---VEE-ITTNKHKD---A---QDPG---	1413
8	GLQNSSGI-MLVNLGLKQ-KEGSKVDTLNHGEDEKVTFAEEDP-QMISVNSSEENAQSIDSVPMQNAVKG---SVEA---	1685
9	---	1427
10	GIHTSSSEA-IFLNNSKQ-TEKSKADALHYNDEDEHGMATGENR-QSDEINSVQNAKKIDSIQIQSVEEE---SRKA---	1684
11	SSTSCPKT-PFTTGS SK-NV-TEINDAV---LE---STRSLERGDD---	1451
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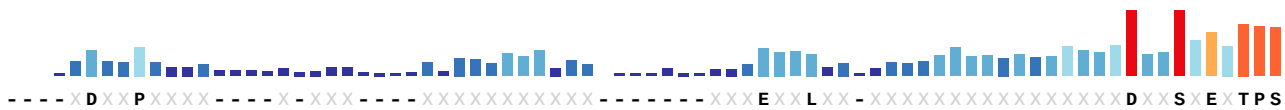
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2	---KTDRSGSII---TRNSNVNH---RPGPE---NSSGLLTLAIYKSTASR---	1583
3	---LNNQKISDEYVSSHDL ELARNGLQNQAQLH---DMHEGYKKKSANLLTQ---	1524
4	EMEE DNLSRNE LR TALDEKETKSRTYIEGEEKGEDDFAPVNT---A---QQDPFLE---AMEKEVSQTEVIL---	1719
5	ERENSTTSKSSH LIGAL---EEQATQDDFVLVEE---P---PKDTLLD---ELDKEISQDMTET---	1716
6	RISSDSITNKV---SRNDDFVPESTRNSSDNDDFVPIEA---A---IEEDNFIE---EMEKEAIRN---	1670
7	---QKKGANIDKKKEATVESNDDFAPAET---D---QDDEFLL---AMEQKLETTSNKLAPIIG	1465
8	ITTEETLTVHLR DSETFNKMMERQQRKGGKINTDDFAPVDE---N-DRNEGFL E---AMEQVASRE---	1747
9	---	1427
10	VTIEESLSERLEGC GTLEPIKNLEGGQ LKEDK KANINDDFVPVEE---D-GRDEGFLK---AMEQVASKE---	1746
11	---F---APVNVAP---KDDFLE---EME EKIK---IKNQKSSSEQ---	1481
12	---VFSRI---LGATEFR TFP---KDEARETKE---VREEKTDNLE---ERPQTVKDD---	1498



XXXXXXXXXEXXSXXXXIRIPIFNSKXXXXXXXXXXXXXXXXXXXXXXXXXX

1	---TG-LEEQPEVADISVLP EIRIPIFNSLKMGGSKSQIKEK LKRLQ---RNELMP---	1792
2	---EAPNTQFAPEVHF---GPKKVEPVTSVVKMIK---RDQGSMGDIV---Q---E---	1623
3	---HNMRPPFE DVAIP THKELKIPIFNSLILKSTNQPPMIPNSQRKV---	1574
4	---KSSPIAKNKRPTSSMHEINIPIFNTLKLTDPSWKERSRTQQESTTRMGQQKIDSSQVTST---RS---D---	1783
5	---NASTAHKD VVLDSPMPAIRIPIFNTLKI GSGRIEKKKHTKIDKA---LNKRLNLDSSAILH---QQE DAPCDV	1784
6	---LERPAKHHP S IRIPLFN VSRPSGRENTKQQKDNHTGT---AISTFSDVGVKINEGNFN TIED---	1730
7	QNPPEQNKLQSVSLDDVDAPASSKIRFPIFNSSKFQGRSVKVLNNTTNLTQ---NA---K---	1519
8	---TSLLKEQTE LADTSVLP EIRIPIFNSLKIQESNGQIKQKLMRLQ---	1798
9	---	1427
10	---TSLLKEQPEVADISVLP EIRIPIFNSLKIQESK SQIKEK LKRLQ---RNELMP---	1797
11	---IEGIEANHNDVSQMSQIRIPIFNSSKLQNKLDLEGPRCDKGE---	1523
12	---DAMASVENKDES QV LGIRIPIFNSSKLQNKPKSKDSVHENDLS---ER---KRKRVDG---	1550



---XDXXPXXXX---X-XXX---XXXXXXXXXXXXX---XXXEXLXX-XXXXXXXXXXXXXXXXXXXXDXSXETPS

1	PDSPPRMTENTNINAQNGLDTVPKTIGGKE-KH-----HEIQLGQAHTADGEP LLGGDGNEDATSREATPS	1858
2	EKD VNTAFEP---FQQDAAIKV-----ALKDDEMSCEIQ-----VSENE NCADD TSSKEGTPS	1674
3	-----R-KR-----PLGNPSTQGGY-----TDIENERVRDYD DSQSLEDSAD	1610
4	KQDVIP-----SHLEVDLHS--SFPYGTPTGNGIDDMDINSRETTPS	1823
5	PIITKDHLPEEIDTVT-KQAPAFGNIPVNNMAEE-----VPLENDLQS--SFVIDG---KEDGGT SRDTTPS	1846
6	---KKNP SFNESTEVL--AG---KTNSKGM EARKDEFKDDIEDDEIE---SSSEDRMQDDEEYRDEASSASTQS	1795
7	-----NADEKEPDN-----NARSNGQTL EESRCSEDAVSRDATPS	1554
8	PDSPPRVASNANTMNVLN---DSTSVGKEGKY---DEIQLAQSHIEKDGDP LLVGE GNE DATSREATPS	1861
9	-----	1427
10	PDSPPRLAANTNIIGRNGLGTAPKAIGGKEEKH-----GEIQLAQAHTADADPSLVGDGNEDATSREATPS	1864
11	---ESPREPR-----D-SSVGKACDK---DAKNSQAIDLES-SQEDNESNILDNMSKEDY-SKEPTPI	1577
12	---NDEEGNDYD-----E-HEVETAREV---DPISTQPEDLAS-S-PDNESTFLQDSRRSDWASQNSAPS	1606



LRXHFPSKKX RKLVRRLXFLXXXDLXXXSXEERNLRIELLD FMMKLEYXXXXXXXXX---

1	LKVHFFS KKSRRLLVARLRGFTPGDLNGISVEERRNLRIELLD FMMRLEYYSNRDNDMN---	1916
2	LHIHFPS K KARKIVNRLRDFKPDQLAALSAAERRNLRVELLD FMMKMEYFEAEE-----	1728
3	IRLHFPNKRARRIVSKLRGFSEYDMGQLS AEEKRNLRIELLD FLMKIEYHTITD-----	1664
4	LRMFFPSRKTRRLVSR LRNFDPSELSTLPTEERRNLRIELLD FLMKLEY YTGDDADKREI	1883
5	LRMHFPCRKSRKLVNRLRRTFNPD ELASLPVEERRNLRIELLD FMMKLEY YTGDKNN---	1902
6	LRDHFPSQ NARKLVRYINELGHEELLQFLPEEKRNLRIELLD FLMKLEHYS DK-----	1848
7	LRMHFPSK KARKLVNRRVRAFTAEDLSHLPPEEKRNLRIELLD FLM SLEHEHGFYQ-----	1609
8	LKIHFSSKKS RKLVSRLRGFTPGDLNGISVEERRNLRIELLD FMMRLEYYSNRDDDMV--	1919
9	-----	1427
10	LKAHFSSKKSRRLLVGR LRGFTPGDLNGISVEERRNLRIELLD FMMRLEYYSNRDNDMG--	1922
11	LRLHFPSK KARKLVSR LRGFTVEDVSDISPEEKRNLRIELLD FMMKLEHESLNGEF----	1633
12	LRLHFPT RKS RKLVS KLRGFSLDDISRISLEEKRNLRIELLD FMMKLEHESLAEEL----	1662

Consensus Threshold: >50%

Compare to: *Saccharomyces_cerevisiae*

Amino acids that match the reference are marked with orange highlighting.

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