

Supplementary information:

S. cerevisiae and *S. kluyveri* proteins were aligned using ClustalW

(<http://www.ebi.ac.uk/clustalw/>) using the default parameters. * indicates amino acid residues that are identical between the *S.kluyveri* protein and at least one of the *S. cerevisiae* proteins.

Orc1 KLIVIAVANTMDLPERQLGNKITSRIGFTRIMFTGYTHEELKNIIDLRLKGLNDSFFYVD 651

 Sk KLIVIAVANTMDLPERQLGNKVSSRIGFTRIMFTGYTHEELKSIINFRLKGLNDSFFYVD 780
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 Sir3 KLSIICVGGHNVITIREQINIMPSLKAHFTEIKLNKVDKNELOQMIITRLKSLKPFHVKV 749

Orc1 TKTGNAILIDAAGNDTTVKQTLPELVKVRRLMSADAIEIASRKVASVSGDARRALKVCK 711
 * * * * *
 Sk IASGSAHIAVDG----ETPNFDIEGTTKVRKISDDAVEIASRKIASVSGDARRALKACK 836
 * * * * *
 Sir3 NDKKEMTIYNNIRE--GONQKIPDNVIVINHKNKIN KITQLIAKNVANVSGSTEFKICE 807

Orc1 RAAEIAEKHYMAKHGYGYDGKTVIEDENEEQIYDDEDKDLIESNKA KDDNDDDDNDGVO 771
 ** * * * * *
 Sk RAVEIAENDYMRKHGYGYDGE-----KITDPNKVDNDGDEFQ 873
 * * * * *
 Sir3 AAVEISKKDFVRKGLQ-----KGKLVVSQ 832

Orc1 TVHITHVMKALNETLNSHVITFMTRLSFTAKLFIYALLNLMKKNGSQEQELGDIVDEIKL 831
 * * * * *
 Sk TVEISHIMKALNETVNSPTTVFITRLSFTGKLFYAML SLIKRNGIQEQPLGDIVDEIRL 933
 * * * * *
 Sir3 EMVPRYFSEAINGFKDETISKKIIGMSLLMRTFLYTLAQETEGTNRHTLALETVLIKMKV 892

Orc1 LIEVNGSNKFMVEIAKTLFOGSDNI-SEOLRIISWDFVLNQLLDAGILFKQTMKNDRIC 890
 ** * * * * *
 Sk LIDVNGKKNKFIVEMNRVLFNONTPLN-EEQLRVVSWEYIINQLVEAGILIKONLKNERSV 992
 * * * * *
 Sir3 MLRDNPGYKASKEIKKVICGAWEPAITIEKCLKQFSWISVVNDLVGEKLVVVVLEEPSASI 952

Orc1 CVKLNISVEEAKRAMNEDETLRNL--- 914

 Sk AIKLNISFEDVLRAVEQDEVLKTL--- 1016
 * * * * *
 Sir3 MVELKLPLEINY-AFSMDEEFKNMDCI 978

Snf12 MSKVMKPSNGKGSRKSSKAATPDTKNFFHAKKKDPVNQDKANNASQITPTVPHSHPSDMV 60
 * * * * *
 Sk MQREMT-----SR--PRNLSTDMQ-----QQQQQQQQQQQQQQQQQTNPIPVTOPTDSY 47
 * * * * *
 Rsc6 -----MVTQTNPVPVPTYPTDAY 17

Snf12 IPDHLE-ELIPELYSFQQLVDSEKRLDHF IHLRNLHMCRMVAQWERSKLSQEFLYPHLNF 119
 ** * * * * *
 Sk IPPFLP-QLIPELNSYEKLC EAERKIDVYLSRKKIDLHQSVSQWNNNSKT-----TSVEI 100
 ** ** * * * * *
 Rsc6 IPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRLDTSINLPTNTKTKD-----HP 68

Snf12 PNVKFLRIFISNVSENQPWQMDTNNEADLMALENATWTMTRIEGRLLDNVQANDPAREKFS 179
 * * * * *
 Sk ASKRYLRVFSVSNIAENQPWQVNDSSNDLES----SWTLRIEGRLLDNQDAQDPARPKFS 156
 * * * * *
 Rsc6 PNKEMLRIYVYNTTESSPRSDSGTPADSGKT----TWTLRIEGKLLHESAN---GKHPFS 121

Snf12 SFIESIVVDFKNKENDNVPSTKFNAAPEENATEGSPDKKLNPLQFSLPNGDNSTTTN 239
 ** * * * * *
 Sk SFLSGIAVDFKKADT-----NGOQGLAE-----LPVVPVAP----- 187
 ** * * * * *
 Rsc6 EFLEGVAVDFKRLKP-----LGMGKKRKRDSLSLPLNLQOPEYNDQDSTM 167

Snf12 TDQNNATMGEETAKKMSSTTPKLESVKWQYDPNNPVDFDGLDIKRVGSENVECTISILR 299
 * * * * *
 Sk -----IPVPQLEPKVVEWHS DPNTPVDFDGLDVKRTGTENVPCTITIQP 231
 * * * * *
 Rsc6 GDNDN---GEDESAEAE SREEI VDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQ 224

Snf12 KSSPEEPFMSYSPOLTAIIGLKSGETSHDAIFSIYKYIHLNELLTND ESAFEENLM-----G 354
 * * * * *
 Sk KGFTG-SLLQFSPQLSTIIGISKGTLHDAVYSLYKYILLNDLLVND S----- 277
 * * * * *
 Rsc6 RGVDG-GKVQYSPNLATLIGMQTGSVND AVYSIYKYILINNL FVTEQTEAQDGSNDAEDS 283

Snf12 NRRNNHNSNTSTSKMLDAASSQVSVIKLDTQLITLLPSSLKESPDMKLTDLLSLINSTH 414
 * * * * *
 Sk TNDATPANTSSS----STNGEKTIIKIDYMLAALFSE-----SRDKMKLAEIPHVVN-AH 327
 * * * * *
 Rsc6 SNENNNKNGAGDDDDGVEGSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVN-KL 342

Snf12 LLPLQPIEIDYTVRVDKASTYGELVLDIEVPDVNALKFNNTQRESQIGAAELNENARELE 474
 * * * * *
 Sk ISPIPPVKIEYTVRVDKASTYGELVDFLEVP--SAVMPQPLNPVAOQGMNLLTEFNQIST 385
 ** ** * * * * *
 Rsc6 VSPLPPIILDYITIDLSKDTTYGATTLDVDVS-----HILHQPQPQPNLQKEE 389

Snf12 QIKPKIALQDKEITSVLSNLHESNKRYRFFKKISED PVKALNECIASTSNALKVLSGDEG 534
 * * * * *
 Sk DSEPQFQALS KKLNILQLQNASANKYQFFSKLADDPVVLQ EYIQSSSNALKVLLGGDEG 445
 * * * * *
 Rsc6 ETDAEDTAKLREITKLALQLNSSAQKYQFFHELHPRETTLTHYLWSSKQNELVLQGDQY 449

Snf12 YNEDMVRANFYKEN--EAMLRENIEVILSNGRM 566
 * * * * *
 Sk FNEDTVRRSSFYEON--EAMLFENLSVLLSNGRI 477
 ** * * * * *
 Rsc6 FNEDAARTSDIYSNNNNDRSLMGNISLLYSQGR 483

Hbs1 -----MAYSDYSDGADDM-----PDFHDEGEFDDYLNDDEYDLMNEVFP
Sk -----MAKYDEDDMDYHSDVPEFQDESEFDDYLNDDEYGLMNDMFP
Ski7 MSLLLEQLARKRIEKSKGLLSADQSHSTSKSASLLERLHKNRETKDNNAETKRKDLKTLA

Hbs1 TLKAQLQDYQGD---NLSLKLALFDNNFDLESTLAEKKTLLKTKKTPKK-----
Sk RAKKEMADYQGN---NLAVKLAIFDQNFDFNQAMIELKRIYRKKQFAQPKQEAACK---
Ski7 KDKVKRSDFTPNQHSVLSLKLKLSALKKSNLDLEKQKSVTLDSKENELPTKRKSPDDKLN

Hbs1 -----
Sk -----
Ski7 LEESWKAIKEMNHYCFLKNDPCINQTDFFAFTNFIIKDKKNSLSTSIPLSSQNSSFLSLK

Hbs1 -----PIAAANGSANVTQKLANISISQORPNDRLPDWLDEEESSEGERNGEEANDE-KTVQ
Sk -----QAINSNFNKPSDDVVLTAQKKAFTDVEKVANEVSKLSVN
Ski7 KHNNELLGIFVPCNLPKTTRKVAIENFNRPSPDDIIQSAQLNAFNEKLENLNKISVPAE

Hbs1 -----RYYKTTVPTKPKKPHDISAFVKSALPHLSFVVL
Sk GGSDDQIDIESEESDDDRKPKAEPVTKTYKKITPTKPRNPVDIQSYVSSRKPFLNFVVL
Ski7 -----KKEPINLQTPPTESIDIHSFIATHPLNLTCLFL

Hbs1 GHVDAGKSTLMGRLLYDLNIVNQSOLRKLQRESETMGK-SSFKFAWIMDOTNEERERGVT
Sk GHVDAGKSTLMGRLLYDVGAVNYKLIRKLLKKESEQAGK-GSFHLAWVMDOTSEERDRGVT
Ski7 GDTNAGKSTLLGHELLYDLNEISMSSMRELQKSSNLDPSSSNSFKVILDNTKTERENGF

Hbs1 VSICTSHFSTHRAN----FTIVDAPGHRDFVPNAIMG---ISQADMAILCVDCSTNAFES
Sk VDICTSDFETDRAT----FTIIDAPGHRDFVPNAITG---ISQADAALVTIDCCVDAFES
Ski7 MFKKVIQVENDLLPPSSTLTLIDTPGSIKYFNKETLNSILTFDPEVYVVLVIDCNYSWEK

Hbs1 GFDLDG--QTKHEMLLASSLG-----IHNLIIAMNKMDNVDWSQORFEEIKSKLLPYLV
Sk GFSLDG--QTKHEMLLASSLG-----ARHIVVAMNKMDHEGWYPTFRFFDIKWELESFFK
Ski7 --SLDGPNNQIYEILKVISYLNKNSACKHLIILLNKADLISWDKHRLEMIQSELNYVLK

Hbs1 D-IGFFEDNINWVPISGFSGEGVYKIEYT-----DEVROWYNGPNLMSTLENA
Sk D-IGIKKEQVSWVTCGLSGEGVYNIKRP-----LGIDWYNDPSLVDCLEDV
Ski7 ENFQWTDAEFQFIPCSGLLGSNLNKTENITKSKYKSEFDSINYVPEWYEGPTFFSOLYLL

Hbs1 AAFKISKENEGINKDDPFLFSVLEIIPSK-KTSNDLALVSGKLE--SGSIQPGESLTIYP
Sk AAKKLNKDESSEAIEANFLFSILDVSPS-KNEV--IVSGKVE--AGSIQPGETITIYP
Ski7 VVEHNMNKIE-TTLEEPFVGTILQSSVLQPIAEIN--YVSLKVLINSGYIQSGQTIEIHT

Hbs1 SEQSCIVDKIQVGSQOQO----STNHEETDVAIKGDFVTLKLRKAYPEDIQNGDLAASVD
Sk SEQSVLVDLSILSGN-----DRASVKIGVAGDFVMLKLREAYYEDIQSGDLATTVG
Ski7 QYEDFHYYGIVSRMKNKQILETNTKNNISVGLNPDILEVLVKIHNTEDFTTKQFHIRKG

Hbs1 YSSIHAQCFVLELTTFDMMRPLLPGTFFILFIGVKEQPARIKRLISFIDKGN--TASKK
Sk N-DIPTAQEFTAQLLTFKLDRLPPLPGTSFMLFRGGCEQPARIKKLVSIKCKDPKILKK
Ski7 D-IIHSRKTNTLSPNLPNTLKLALRLIKLSIQTHALSDPVDLGSSELLYHNLTHNAVK

Hbs1 KIRHLGSKORAFVEIELIEVKRWIPLLTAHENDRLGRVVLKDGRTIAAGKISEITQ----
Sk KVKHLGSDQAAIVEIELIEKRRIPILTIEKSKHLGRIVLRKEGRTVAAGVVESLDF----
Ski7 LVKILGTNDISINPNQSLIVEVEIIEPDFALNVIDSKYITNNIVLTSIDHKVIAVGRIACQ