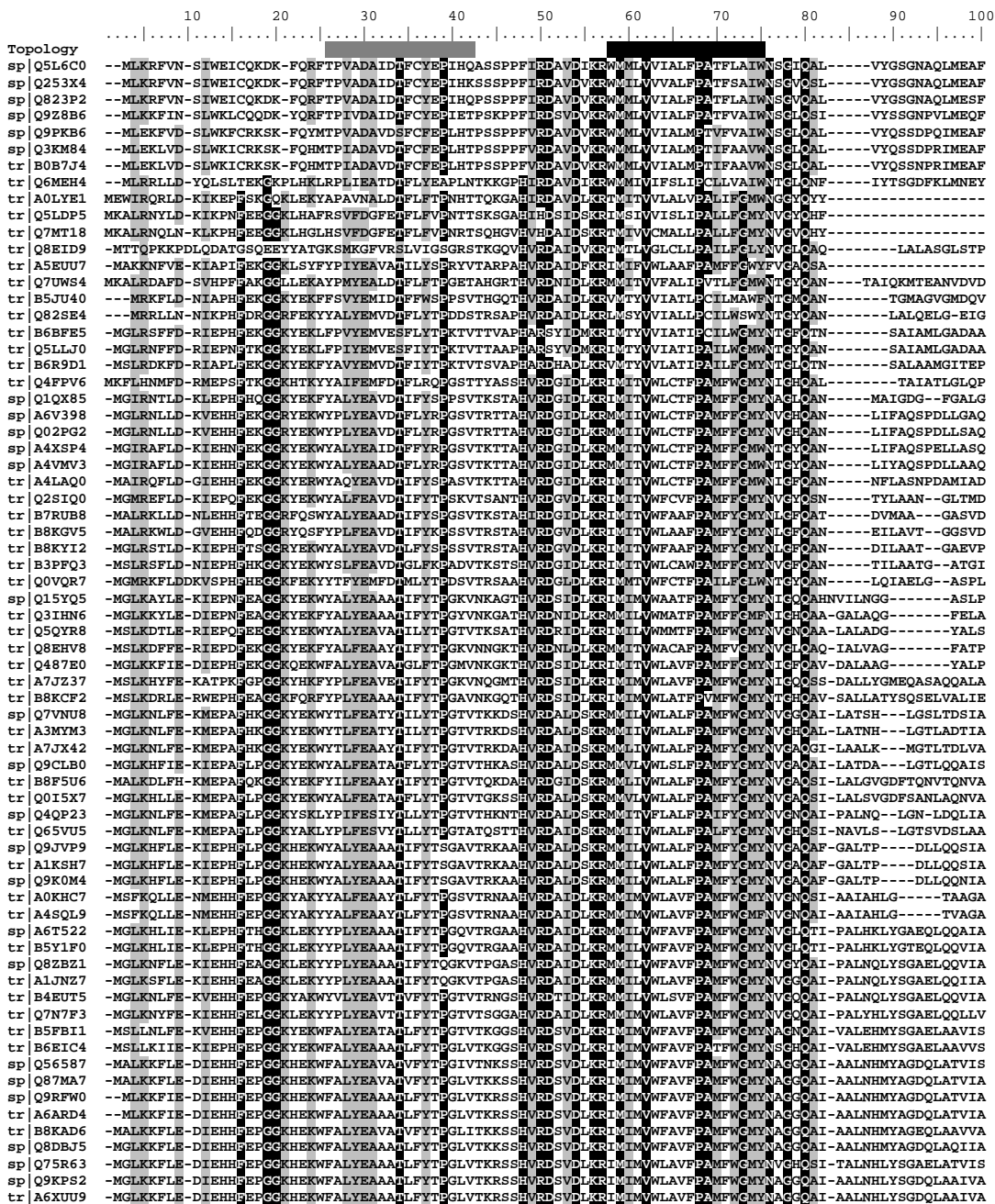


**LOCALIZATION AND FUNCTION OF THE MEMBRANE-BOUND RIBOFLAVIN IN THE Na<sup>+</sup> TRANSLOCATING NADH:QUINONE OXIDOREDUCTASE (Na<sup>+</sup>-NQR) FROM *VIBRIO CHOLERAE* \***

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**Fig. S1.** Sequence alignment of non-redundant NqrB homologues. NqrB-related proteins from 69 organisms were retrieved from the UniProt knowledge base. Multiple sequence alignment was performed using the ClustalW algorithm (1) implemented in the BioEdit Sequence Alignment Editor (Version 7.0.9.0, (2)) with default settings. Identical residues and similar residues (BLOSUM62 scoring matrix) are underlaid with black and grey bars, respectively, and were identified with the BioEdit program using an identity and similarity threshold of 85% and the BLOSUM62 scoring matrix (3). Black bars indicate transmembrane helices, grey bars indicate hydrophobic stretches, as predicted from a consensus model based on 11 different topology prediction algorithms (see Materials and Methods and supplementary Table Fig. S2).



110 120 130 140 150 160 170 180 190 200  
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
Topology  
sp|Q5L6C0 LHISG-FRYSLSFIFN---DIGMFSVLWTCCKHFLPDLIISYVGGACVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q253X4 LHISG-FRYSLSFIFN---DVGVFSLVWACVYKFLPDLIISYVGGACVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q823P2 LHISG-FRYSLSFIFN---DIGVFSILMTYCKIIFLPIISYVGGVGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q9Z8B6 LHISG-FGSYLSFYVYK---EIHVPLILWGLKIFDPLTIISYVGGTCVFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q9PKB6 LHISG-FTSYFSFYVSK---EIGIASVLFACCKIFLPLIFISYAVGGTCVFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q3KM84 LHISG-FKSYFSFYVYQ---EIGIASVLFACCKIFLPLIFISYAVGGTCVFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B07J74 LHISG-FKSYFSFYVYQ---EIGIASVLFACCKIFLPLIFISYAVGGTCVFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q6MEH4 LSGSNLSQQYIDFAFK---DMRPLTIKIKLITLPLIISYAVGGCLCFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A0LYE1 -----TQLGEAFT-----FWEAIGHCKALKIENIAVSYGVLGIFFAFATFRCHEVNEGELVGTIPMINEIDIEPLMVGLVFAVWVWAKEDF  
tr|Q5LDP5 -----LTHGAQGG-----FIEMFYFGLALDLKLIIVSVVGGVGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q7MT18 -----MAIDAPVV-----FWPAFLFGLLAVLKLIVSYAVGLGIFFAVVAQYRKRKBTQEGELVSGGLIPMIVEVDTPLMILATATARAIFAKEDF  
tr|Q8EID9 DTWKLALFNALSGGLT---AETSIVGLFLYLCLSFYFLPYLITALLTCLFVWVFAKVHQCDEHGEFVTSALLLPLVSVLPLWLVVGLISFVWVWAKEDF  
tr|A5EUU7 -----HAA---GIERGFANLACACVHLPTYLVTFAVGGTCVFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q7UW54 FDWHTTHTAVGFGHD---PANHVDNFVCAITFHLPIYVTCMVEFGCHIFLPIYVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B5JU40 NNWRFALIGALAGQAA---AEGNLANVHFPCFLVPLPYLTTLVVGGIWFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q82SE4 QNRNRNLLTLNMG---F-DPQSVLSTIHLCLYELPYLITLLVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B6BFE5 TGWRVAVLQALGIS---L-DASNPLANIAHFVLYFLPIYVTVLVACGFVEVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q5LLJ0 TGWRIALLQALGIS---L-DASNPLANVAFGLYFLPYLITLLVGGIWFVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B6R9D1 AGWRAAILSLGGIG---F-NPDNFIFANMAHGALYFLPIYVTVLVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q4FPV6 EGWRTIITSMAGYNPD---SIWASFVYACMCFELPYLVTFGVGLLCEIFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q1X85 G-WREAVFTMALAGSHD---GAGLWNDFVYMAYFHPITYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|A6V398 DGWRFALIGALAG-FD---PNSLWDCLVQCAAAYFLPYLVTFFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q02PQ2 GWRFRALIGALAG-FD---PNSLWDCLVQCAAAYFLPYLVTFFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|A4XSP4 EGWRFALIGSAG-FD---PNSLWDFNFIQCAAAYFLPYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|A4VMV3 EGWRFALIGAFAG-FD---PNSLWDFNFIQCAAAYFLPYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A4LAQ0 GGLREAFITLALVGD---L-ESYGLMFLYCACFVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q2S1Q0 MDWGVILIAMLAGNDA---AS-IWDFNYGAVYFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B7RUB8 G-WHGWLIELLGG-YD---ASNLIWHCFWYACVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B8KGV5 G-WRGSLLIAGLGG-ND---SGNIWNHMFYCALVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B8Y12 G-WRGTIIAGLGG-YD---SGNIWDCMVFYCALVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
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tr|Q0VQR7 AGWRSDVLAALTG-FD---PASIWANVHLCAVYFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q15YQ5 DMWQALFTLALVGD---L-ESYGLMFLYCACFVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q3IHN6 NITWQVDFLQGLGQLT---ADA-GWGAKMFLYCACFVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
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tr|A7J327 SSWQ---LSVWVGSQDA---VSGQWASQMLKCAVYFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B8KCF2 QSWR---LSVWVGSQDA---MVDSHWAMQMLKCAVYFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
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tr|A3MYM3 NNWHYGFADALGATLT---ADAGWGSKMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A7JX42 NNWHYSLADLSGLS---V---ADAGWTKMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q9CLB0 GHWQYALSHALGADLT---LSAGWASKMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
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sp|Q4QP23 NDWHYALASLLGLDLT---ANATGWSKMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|Q65VU5 NDWHYALASLLGLDLT---AAAGWGSKMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q9JVP9 NDWHYALANALGINMS---SEAGVLGKMLFGAIVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A1KSH7 NDWHYTLADALGINMS---SEAGVLGKMLFGAIVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q9KOM4 NDWHYAFANALGINMS---SEAGVSDKMLFGAIVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A0KHC7 DTWQYTIATLLGASLD---PAVAGISKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A4SQL9 DTWQYTIATLLGASLD---PAVAGISKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|A6T522 NNWHYSVAQWLGVFSFS---ADAGWLSMMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
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tr|B6ETC4 GNWHYWLTEMLGGTIS---ADAGWSSMMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
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sp|Q9RFW0 GNWHYWLTEMLGGTIS---ADAGWGSKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A6ARD4 GNWHYWLTEMLGGTIS---ADAGWGSKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|B8KAD6 GNWHYWLTEMLGGTIS---ADAGWGSKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q8DBJ5 GNWHYWLTEMLGGTIS---ADAGWGSKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q75R63 GNWHYWLTEMLGGTIS---TQAGWASMMLLCATVFLPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
sp|Q9K9S2 GNWHYWLTEMLGGTIS---SDAGWGSKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF  
tr|A6XUU9 GNWHYWLTEMLGGTIS---SDAGWGSKMLLCAAFELPIYAVTFVGGVFAVTRRKHRIAEGLLVGMLYPLTPPTTFYMAALGIFAGVWSKEDF

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                210           220           230           240           250           260           270           280           290           300
          .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....
Topology
sp|Q5L6C0|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPHTHKDSLTTMNATAGKSIIDGFSQSTCQOTLNSTPPSVKRIHVDAIASNILHMTHTVPTQNVIE
sp|Q253X4|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPMKIKESLLAMNSTAGKSIIDGFSQSTCQOTLNSTPPSVKRVHVDIAIASNILHMTHTVPTQNVIQ
sp|Q823P2|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPTKIKESLLAMNSTAGKSIIDGFSQSTCQOTLNSTAPAVKRVHVDIAIASNILQMPHVPTESVVIH
sp|Q9Z8B6|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPGVTKDSLMMKNSSTGKVLIDGFSQSTCQOTLNSTPPSVKRLHVDIAIASNMLHHPHVPTQDVVIH
sp|Q9PKB6|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPSKIKESLAMNSLAERSNFDGFSQSTCQOTLNSTPPSVKRVHVDIAIASNILKLEHVPSQDVLIH
sp|Q3KM84|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPSRIKESLATMSSLAEKSHFDGFSQSTCQOTLNSTPPSVKRVHVDIAIASNILNLEHVPTQDVLIH
tr|B0B7J4|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGSNPSRIKESLATMSSLAEKSHFDGFSQSTCQOTLNSTPPSVKRVHVDIAIASNILNLEHVPTQDVLIH
tr|Q6MEH4|GGTGMMNINPALSGRAFLFFTEPAKMSGD-VVVGNTPTLVRESLTKMNHDAHTGSLDGYSCQTHAFRNFTPEIKRIHVDAIASNDLGNQVHSPFPIIE
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tr|Q5LDP5|GGTGMMNINVALVTRAFLEFAYPTKMSGDVVVQAQDSI-----FGLGN--TVDGLTATSTSGVA
tr|Q7MT18|GGTGRNFINPALVTRAFLEFAYPAAMSGDQVFRVTDAT-----FGLGAGTVA--VDGFSGATPISGQI
tr|Q8EID9|GGMGYNFINPALAGRAFLFFAYPSEVTIVKQLVA-----VDGFSGATPISQA
tr|A5EUU7|GGTGRNFINPALAGRAFLFFAYPTQMSGD-VVIVASVKG-----HA-----WIDGFSGATPISATI
tr|Q7UWS4|GGTGRNFINPALVTRAFLEFAYAGQISGDVWVTA-----VDGFSGATPISGM
tr|B5JU40|GGTCKNFINPALVTRAFLEFAYPAHLISGDSVWVTA-----VDGVTGATPISGLA
tr|Q82SE4|GGTCKNFINPALVTRAFLEFAYPADISGDLVVVA-----VDGYTATPISGLG
tr|B6BFE5|GGTCKNFINPALVTRAFLEFAYPAMISGDSVWVTP-----VDGFSGATPISGVT
tr|Q5LLJ0|GGTCKNFINPALVTRAFLEFAYPAMISGDSVWVTP-----VDGFSGATPISAVS
tr|B6R9D1|GGTCKNFINPALVTRAFLEFAYPAAMSGDQVFRVTDAT-----VDGFSGATPISGVA
tr|Q4FPV6|GGTCKNFINPALSGRAFLFFAYPAYMSGDVWVTA-----VDGFSGATPISGLA
sp|Q1QX85|GGTCKNFINPALVTRAFLEFAYPAQISGDVWVVA-----ADGYTATPISSTA
sp|A6V398|GGTCKNFINPALVTRAFLEFAYPAQMSGDVAVTIS-----VDGFAGATPISSLA
sp|Q02PG2|GGTCKNFINPALVTRAFLEFAYPAQMSGDVAVTIS-----VDGFAGATPISSLA
sp|A4XSP4|GGTCKNFINPALVTRAFLEFAYPAQMSGDVAVTIS-----VDGFAGATPISSLA
sp|A4VMV3|GGTCKNFINPALVTRAFLEFAYPAQMSGDVAVTIS-----VDGYAGATPISLG
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tr|Q2SIQ0|GGTCKNFINPALVTRAFLEFAYPAQISGDVAVTIS-----VDGFSGATPISVA
tr|B7RUB8|GGTCKNFINPALVTRAFLEFAYPAQISGDVWVVA-----VDGYTATPISLV
tr|B8KGV5|GGTCKNFINPALVTRAFLEFAYPAQISGDVAVTIS-----VDGYSGATPISGLV
tr|B8KYI2|GGTCKNFINPALVTRAFLEFAYPADISGDLVVTA-----VDGYSGATPISGLV
tr|B3PFQ3|GGTCKNFINPALVTRAFLEFAYPAEISGDLVVTA-----VDGYTATPISVA
tr|Q0VQR7|GGTCKNFINPALVTRAFLEFAYPAQMSGDVAVTIS-----VDNFSGATPISLA
sp|Q15YQ5|GGTGRNFINPALSGRAFLFFAYPAQISGDVAVTIS-----ADGFSGATPISQA
tr|Q3IHN6|GGTGRNFINPALAGRAFLFFAYPAQISGDVWVTA-----VDGFSGATPISQA
tr|Q5QYR8|GGTGRNFINPALVTRAFLEFAYPASMSGDSVWVTA-----VDGFSGATPISGA
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tr|A7JZ37|GGTGRNFINPALAGRAFLFFAYPAMISGCAVVVA-----ADGYSGATPISQW
tr|B8KCF2|GGTGRNFINPALAGRAFLFFAYPAMISGCAVVVA-----ADGYTATPISQW
sp|Q7VNU8|GGVCKNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
tr|A3MYM3|GGVCKNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
tr|A7JX42|GGVCKNFINPALAGRAFLFFAYPGQISGDVWVVA-----ADGFSGATPISQW
sp|Q9CLB0|GGVCKNFINPALAGRAFLFFAYPAQISGDLVVVA-----ADGFSGATPISQW
tr|B8F5U6|GGVCKNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
tr|Q0I5X7|GGVCKNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
sp|Q4QP23|GGVCKNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
tr|Q65VU5|GGVCKNFINPALAGRAFLFFAYPGQISGDLVVTA-----TDGFSGATPISQW
sp|Q9JVP9|GGTCKNFINPALAGRAFLFFAYPAMISGDLVVTA-----VDGYSGATPISQW
tr|A1KSH7|GGTCKNFINPALAGRAFLFFAYPAMISGDLVVTA-----VDGYSGATPISQW
sp|Q9KOM4|GGTCKNFINPALAGRAFLFFAYPAMISGDLVVTA-----VDGYSGATPISQW
tr|A0KHC7|GGTCKNFINPALAGRAFLFFAYPGQISGDVWVVA-----VDGYSGATPISQW
tr|A4SQI9|GGTCKNFINPALAGRAFLFFAYPGQISGDVWVVA-----VDGYSGATPISQW
sp|A6T522|GGTGRNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
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sp|Q9RFW0|GGTGRNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
tr|A6ARD4|GGTGRNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
tr|B8KAD6|GGTGRNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGFSGATPISQW
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sp|Q9KPS2|GGTGRNFINPALAGRAFLFFAYPAQISGDLVVTA-----ADGYSGATPISQW
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Topology

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sp|Q5L6C0|SQFSIWTES-HPGLLLDKLTLEQLQSFVTSPLSEGGGLLLPTQFDSAYAITDVIYIGIKFSSGNLFWGNLIGSLGETSTFACLLCAVFLVITGLASWRITM
sp|Q253X4|SQFSIWTES-HPGLMLDKLTLEQLQSFVTSPLSEGGGLLLPTQFDSAYAITDVIYIGIKFSSGNLFWGNLIGSLGETSTFACLLCAIFLLVITGLASWRITM
sp|Q823P2|SQFSIWAES-HPGLMLDKLTLEQLQNFVTSPLSEGGGLLLPTQFDSAYSITDVIYIGIKFSSGNLFWGNLIGSLGETSTFACLLCAIFLLVITGLASWRITM
sp|Q9Z8B6|SQFSLWTET-HPGWVLDNLTLTQLQTFVAPVAEGGLGLLPTQFDSAYAITDVIYIGIKFSSAGNLFWGNLIGSLGETSTFACLLCAIFLLVITGLASWRITM
sp|Q9PKB6|SQFSTWAES-FPGLTVDQLSLDQLQNFVTSPTAEGGLGLLPAHFDAAYSILTDAIYIGIKFSTGNLFFGNLIGSLGETSTVACLLCAGLLLLTGLASWRITM
sp|Q3KM84|TQFATWAES-YPGLTVDQLSLDQLQNFVTSPTIEGGGLLLPAHFDSACSLTEAVYIGIKFSTGNLFFGNLIGSLGETSTVACLLCAGLLLLTGLASWRITM
tr|B0B7J4|TQFATWAES-YPGLTVDQLSLDQLQNFVTSPTIEGGGLLLPAHFDSACSLTEAVYIGIKFSTGNLFFGNLIGSLGETSTVACLLCAGLLLLTGLASWRITM
tr|Q6MEH4|KQFNQMKVEVGHQATLTQLSDQLRQFVTSPLQDGGGLGLSAGNYEDAYHFASLNYGLGHNSDWHCFCLCDLKLQGETSVFACLLCAILLIWTGVGQSWRITM
tr|A0LYE1|-----ASG-----SEVSY-----SAMNMFSEVTFGSHAEFVICILACALILLVTKVGSWRITM
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tr|Q7UWS4|-----ANASEDAVGLSVAQYVWG-----AEE-PITWMSAFIETIQCCVGETSALLCLVCAILLIATGHSWRITM
tr|B5JU40|-----ATGGIQAVERAEG-----FTLQQSFGLMIFGSLGETSTLACLCAAFLLFTKTIASWRITM
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Topology

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tr|Q7MT18|LSGLVCSAMALVFNALIC-----TT-----AAMQITP-LMHLVYGGFAGCFVFMATDPVTSARNEKGRWVYGLFICFGLTILIRVNDPAMPPEGVMLAAILLGN
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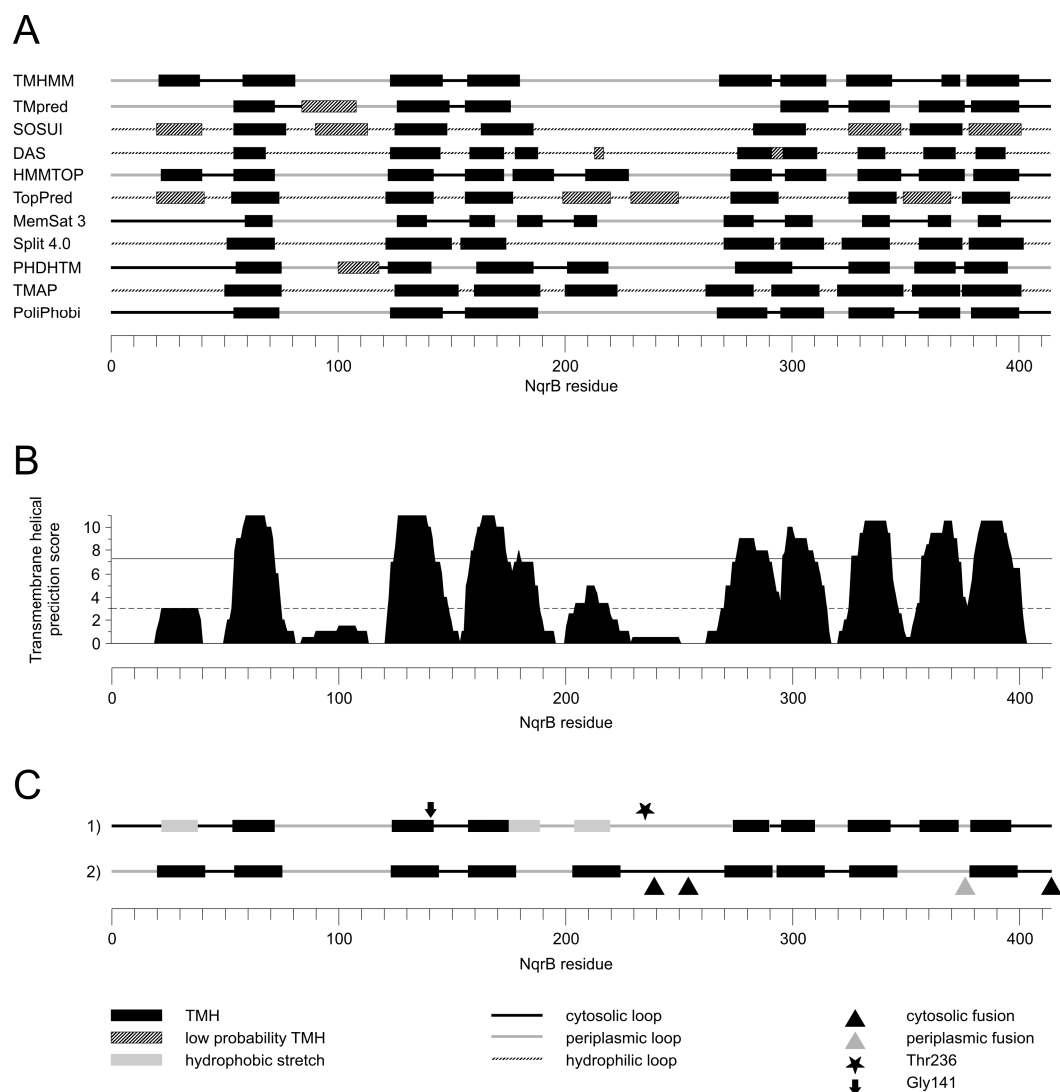
Topology

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sp|Q02PG2|LFAPLIDHFFVQANIKRRLRANG-----
sp|A4XSP4|LFAPLIDHFFVQANIKRRLRANV-----
sp|A4VMV3|LCAPLIDHFFVQANIKRRLRANV-----
tr|A4LAQ0|LFAPLIDHYVVOQANIKRRLRARG-----
tr|Q2SIQ0|VFAPLIDHILVVOQANIKRRLRARG-----
tr|B7RUB8|LFAPLIDNFVVOQANIKRRLRARG-----
tr|B8KGV5|VFAPLIDHFAVQANIKRRLRARG-----
tr|B8KYI2|LFAPLIDHFAVQANIKRRLRARG-----
tr|B3PFQ3|VFAPLIDHFAVQANIKRRLRARG-----
tr|Q0VQR7|LCAPLIDHFFVQANIKRRLRRRGGEV-----
sp|Q15YQ5|LWAPLIDYFVVOQANIKRRLRARG-----
tr|Q3IHN6|LFAPLIDHFFVQANIKRRLRARG-----
tr|Q5QYR8|VFAPLIDHFAVQANIKRRLRARG-----
tr|Q8EHV8|VFAPLIDHFAVQANIKRRLRARG-----
tr|Q487E0|LFAPLIDHFFVQANIKRRLRANV-----
tr|A7JZ37|LFAPLIDYLVKESNIRKREMKRARPS-----
tr|B8KCF2|LFAPLIDHILVKECNIRKRRNRKIKRQA-----
sp|Q7VNU8|LFAPLIDYLVVQSNIKRRLKAKAA-----
tr|A3MYM3|LFAPLIDYLVVQGNIKRRLKAKAA-----
tr|A7JX42|LFAPLIDYLVVQGNIKRRLRANVANG-----
sp|Q9CLB0|LFAPLIDYLVVQANIKRRLRANV-----
tr|B8F5U6|LFAPLIDYLVVQANIKRRLRANG-----
tr|Q0I5X7|LFAPLIDYLVVQANIKRRLRANG-----
sp|Q4QP23|LFAPLIDYLVVQANIKRRLRANG-----
tr|Q65VU5|LFAPLIDYLVVQANIKRRLRANG-----
sp|Q9JVP9|LFAPLIDYLVVQANIKRRLRANG-----
tr|A1KSH7|LFAPLIDYLVVQANIKRRLRANG-----
sp|Q9K0M4|LFAPLIDYLVVQANIKRRLRANG-----
tr|A0KHC7|LFAPLIDHFAVQANIKRRLRANG-----
tr|A4SQL9|LFAPLIDHFAVQANIKRRLRANG-----
sp|A6T522|LFAPLIDYLVVQANIKRRLRANG-----
tr|B5Y1F0|LFAPLIDYLVVQANIKRRLRANG-----
sp|Q8ZBZ1|LFAPLIDYLVVQANIKRRLRANG-----
tr|A1JNZ7|LFAPLIDYLVVQANIKRRLRANG-----
tr|B4EUT5|LFAPLIDYLVVQANIKRRLRANG-----
tr|Q7N7F3|LFAPLIDYLVVQANIKRRLRANG-----
tr|B5FB11|LFAPLIDHILVVECNIRKRLKRYGK-----
tr|B6EIC4|LFAPLIDHILVVECNIRKRLKRYGK-----
sp|Q56587|LFAPLIDHVVIEKNIRKRLRANG-----
sp|Q87MA7|LFAPLIDHVVIEKNIRKRLRANG-----
sp|Q9RFW0|LFAPLIDHVVIEKNIRKRLRANG-----
tr|A6ARD4|LFAPLIDHVVIEKNIRKRLRANG-----
tr|B8KAD6|LFAPLIDHVVIEKNIRKRLRANG-----
sp|Q8DBJ5|LFAPLIDHILVVECNIRKRLRANG-----
sp|Q75R63|LFAPLIDHILVIEKNIRKRLRANG-----
sp|Q9KPS2|LFAPLIDHVVIEKNIRKRLRANG-----
tr|A6XUU9|LFAPLIDHVVIEKNIRKRLRANG-----

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**Fig. S2.** Consensus membrane topology prediction of NqrB. **(A)** Graphical representation of results from individual topology prediction algorithms (see Material and Methods). Regions classified as transmembrane helices (TMH) are indicated as black bars, regions classified as low probability TMHs or aliphatic helices are indicated as striped bars. Hydrophilic loops are represented by dashed lines or, if the prediction algorithm distinguishes between cytosolic and periplasmic loops with solid black and grey lines, respectively. **(B)** A histogram from the individual prediction results from (A) was constructed by scoring an NqrB residue from a predicted TMH region by a value of 1 and a residue from a low probability TMH or an aliphatic helix by a value of 0.5. The solid line at a score of 7.33, which is  $2/3$  of the maximal score, represents the cut-off for defining a TMH in the consensus topology prediction. Three larger regions of the histogram show intermediate scores (between 3 and 7) and were considered as hydrophobic stretches. **(C)** Comparison of 1) the consensus topology prediction derived from (B) with 2) the topology model proposed by Duffy *et al.* (4). TMHs and hydrophobic stretches are indicated by black and grey bars, respectively. Results from PhoA fusion analyses reported in (4) are indicated by black and grey triangles for cytosolic and periplasmic PhoA localization, respectively. The asterisk indicates Thr236 with its covalently attached FMN. The arrow indicates Gly141, which was proposed to interact with the inhibitor korormicin (5).



**Tab. S1.**  $\pi$ -stacking interaction of aromatic amino acid residues in riboflavin-containing proteins to riboflavin

Protein	Source	$\pi$ -stacking interaction	PDB code	REF
<b>redox enzyme:</b>				
flavodoxin	<i>Desulfovibrio vulgaris</i>	Y97	1BU5	(6)
<b>riboflavin pathway:</b>				
6,7-Dimethyl-8-ribityllumazine synthase	<i>Schizosaccharomyces pombe</i>	H94	2A58	(7)
FAD synthetase	<i>Thermotoga maritima</i>	no stacking	1T6Z	(8)
riboflavin kinase	<i>Homo sapiens</i>	no stacking	1NB9	(9)
riboflavin synthase	<i>Escherichia coli</i>	no stacking	1HZE	(10)
<b>riboflavin storage/homeostasis:</b>				
riboflavin binding protein	chicken	Y57, W156	---	(11)
dodecin	<i>Halobacterium salinarum</i>	W35, riboflavin <sup>b</sup>	1MOG	(12)
original yellow antibody	<i>H. sapiens</i>	Y33, F59, Y105	2FL5	(13)
<b>other function:</b>				
liver glycogen phosphorylase <sup>c</sup>	<i>H. sapiens</i>	Y614, F286	1L5R	(14)
lumazine protein	<i>Photobacterium leiognathi</i>	no stacking	3DDY	(15)

<sup>a</sup> Native cofactor for flavodoxin is FMN (16).

<sup>b</sup> Dodecin is a small dodecameric flavoprotein that contains two flavins stacked between two tryptophan residues to form an aromatic tetrad.

<sup>c</sup> Riboflavin is an inhibitor of the liver glycogen phosphorylase a.

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