

Supporting Information for

Catalytic Mechanism of SHCHC Synthase in the Menaquinone Biosynthesis of *Escherichia coli*: Identification and Mutational Analysis of the Active Site Residues

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Table S1. Proteins used to construct menaquinone biosynthetic enzyme family trees

Abbreviation	Species	gi number			
		MenB	MenC	MenD	MenH
Arath	<i>Arabidopsis thaliana</i>	30696431	145337303	145337303	145337303
Bacan	<i>Bacillus anthracis</i> A2012	30264918	30264916	30264920	30264919
Bacli	<i>Bacillus licheniformis</i> ATCC 14580	52081566	52081564	52081568	52081561
Bacsu	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	16080132	16080130	16080134	16080124
Geoka	<i>Geobacillus kaustophilus</i> HTA426	56421408	56419461	56421410	56421409
Oceih	<i>Oceanobacillus iheyensis</i> HTE831	23099778	23100168	23099780	23099779
Chlau	<i>Chloroflexus aurantiacus</i>	53794813	53797046	163849183	163845686
Entfa	<i>Enterococcus faecalis</i> V583	29375076	29375081	29375079	29375080
Lisin	<i>Listeria innocua</i> Clip11262	16800849	16801725	16800851	16800850
Lismo	<i>Listeria monocytogenes</i> EGD-e	16803713	16804558	16803715	16803714
Exi	<i>Exiguobacterium</i> sp. 255-15	45532470	45532472	45532468	45532469
Leume	<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> ATCC 8293	23024048	53689596	116617863	116617864
Desha	<i>Desulfotobacterium hafniense</i>	23112824	23112826	23112822	23112823
Staau	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2	21282658	21204904	21282656	21282657
Staep	<i>Staphylococcus epidermidis</i> ATCC 12228	27467664	27468381	27467662	27467663
Vibvu	<i>Vibrio vulnificus</i> YJ016	37679302	37679303	37679300	37679301
Vibpa	<i>Vibrio parahaemolyticus</i> RIMD 2210633	28897705	28897706	28897703	28897704
Vibch	<i>Vibrio cholerae</i> O1 biovar <i>el</i> tor str. N16961	15641975	17369119	15641977	15641976
Phopr	<i>Photobacterium profundum</i>	46916004	46914221	54309785	54309784
Vibfi	<i>Vibrio fischeri</i> ES114	59478708	59712274	59712278	59712277
Salen	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18	16761233	20138545	29136695	29141070
Escco	<i>Escherichia coli</i> K12	16130197	16130196	16130199	16130198
Yerpe	<i>Yersinia pestis</i> CO92	16122744	20138547	16122746	16122745

Erwca	<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043	50120152	50120153	50120150	50120151
Pholu	<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	37526959	37526958	37526961	37526960
Actpl	<i>Actinobacillus pleuropneumoniae</i> serovar 1 str. 4074	46143479	46143800	32035279	32035280
Haeso	<i>Haemophilus somnus</i> 129PT	23467877	23467878	113460762	113460761
Mansu	<i>Mannheimia succiniciproducens</i> MBEL55E	52425847	52425846	52425849	52425848
Pasmu	<i>Pasteurella multocida</i> subsp. <i>multocida</i> str. Pm70	15602961	17368773	15601919	15601920
Haein	<i>Haemophilus influenzae</i> Rd KW20	16272905	17380438	16272239	16272238
Haedu	<i>Haemophilus ducreyi</i> 35000HP	33152905	33152187	33152852	33152853
Sheon	<i>Shewanella oneidensis</i> MR-1	24376211	24376048	24376046	24376047
Chlte	<i>Chlorobium tepidum</i> TLS	21674659	21674660	21674653	21674658
Rubxy	<i>Rubrobacter xylanophilus</i> DSM 9941	46106024	68562469	108805682	108805680
Nospu	<i>Nostoc punctiforme</i> PCC 73102	23126174	23124230	186684098	186680636
Trier	<i>Trichodesmium erythraeum</i> IMS101	48893776	48893757	113477498	113477492
Bdeba	<i>Bdellovibrio bacteriovorus</i> HD100	42524845	42522147	42524837	42524836
Par	<i>Parachlamydia</i> sp. UWE25	46446698	46447297	46446702	46446701
Shifl	<i>Shigella flexneri</i> 2a str. 301	24113638	24113637	56480081	24113639
Klepn	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> MGH 78578	152971198	152971197	152971200	152971199
Ent	<i>Enterobacter</i> sp. 638	146312454	146312453	146312456	146312455
Serpr	<i>Serratia proteamaculans</i> 568	157371518	157371517	157371520	157371519
Aerhy	<i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> ATCC 7966	117620309	117618896	117620190	117619877
Mor	<i>Moritella</i> sp. PE36	149911655	149911656	149911653	149911654
Chlth	<i>Chloroherpeton thalassium</i> ATCC 35110	193215689	193215688	193215691	193215690
Provi	<i>Prosthecochloris vibrioformis</i> DSM 265	145219209	145219208	145219212	145219210
Chlpa	<i>Chlorobaculum parvum</i> NCIB 8327	193212028	193212027	193212035	193212029
Halha	<i>Halorhodospira halophila</i> SL1	121997920	121997921	121997918	121997919

Figure S1. Multiple sequence alignment of MenH proteins

MenH_Escco	-----MILHAQAKHKPGL-----PWLVLHGFSGDCHWQEVGEAFAD-----YSRLYVDLPGHGG--SAAISVDG--FDDVIDLLRKTLVS--YNILDFWL	82
MenH_Shifl	-----MILHAQAKHKPGL-----PWLVLHGFSGDCHWQEVGEAFAD-----YSRLYVDLPGHGG--SAAISVDG--FDDVIDLLRKTLVS--YNILDFWL	82
MenH_Salen	-----MMLHAQHMPGQPGT-----PSLVLHGFSGDCHWQEVGEQFHG-----CSRLYIDLPGHGG--SAAIPVGG--FADVIRLLRATLIS--YNILKFWL	82
MenH_Klepn	-----MILSAAVDNDQPGY-----PWLVLHGFSGDCHWQEVGEAFAD-----WPRLYIDLPGHGG--SADIADVQ--FAGVNTLLQSTLNS--YNIHKYWL	82
MenH_Ent	-----MILNGKTRAGKPGF-----PWLVLHGFSGDCHWQEVGEAFAD-----YPQLHLDLPGHGD--SANIIVAG--FDEVSQLLADTLVS--YNILKFWL	82
MenH_Erwca	-----MTHGAVAPIQP-----MLVCLHGLFGSGEDWSPVLPFFRD-----WPMLLVDLPGHGA--SRAITAD--FAEVSRQLTATLLE--QGIERYWL	78
MenH_Yerpe	-----MTTLACRKLAPHEPSPRHQHAGPWLVLHGLLGGSDQDLVPAQLCGD-----YPSLLIDLPGHGG--SVSLSADG--FADISRQLSQTLLQ--NGIREYWL	90
MenH_Pholu	-----MSLVCRKFNQYNDR-----PWLVLHGLLGGSDQDLVPAQLCGD-----HPSLVIDLPGHGD--STDVRVMD--LLEMSCLLSETLAE--QRISQYWL	82
MenH_Serpr	-----MLATKVLQQGEADR-----PWLVLHGLLGGSDQDLVPAQLCGD-----WPSLAIDLPGHGD--SVAUVCTS--FDDISAQISATLQM--HGIERYWL	82
MenH_Aerhy	-----MAASADQ-----PTLVLLHGLLGGSDQDLVPAQLCGD-----LPSLALDLPGHGS--NRAVRVAG--FEQAHRLWCDELAA--RDIDRYQL	75
MenH_Mansu	-----MINTILVFLHGLLGTSDWAKIIEIEN-----LPHFH--CVSLDLPFHGE--HKFTANN--FEQCADFISHQIKS--AVGNQPYFL	72
MenH_Haein	-----MINIIFLHGLLGTNDWQKVIEN-----LPHFH--CIALDLPFHGG--AKDLEVTN--FEDSAEYLAQIKS--AVGNQPYFL	70
MenH_Haeso	-----MPILVFLHGLLGTNDWQYIIEELKK--NLPHFS--SQSYLCCLDLPFHGE--QTNHYHED--FEQSAQYLSRQITA--KIADKPYIL	77
MenH_Pasmu	-----MPVVFVFLHGLLGSKHQWQKVIEN-----LPHFH--CLALDLPFHDD--AKTVCTVD--FEQTCAYVEQQLQ--QLGDQPYIL	69
MenH_Actpl	-----MLHATWNR-----ETGMPVFLHGLLGGSDQDLVPAQLCGD-----LQNFQCPRLTIDLPHGA--SEHIPCVC--FSHTRELHQTVLH--YIGNQPYFL	83
MenH_Haedu	-----MLACQSHNTNTHNQITTPILFLHGLLGGSDQDLVPAQLCGD-----LQKNPQCPRLTIDLPHAGN--SNKIISDD--FITARQLIDQTIKQ--RLSHRPYIL	88
MenH_Vibch	-----MLSNQLHFAKPT-ART-----PLVVVLHGLLGGSDQDLVPAQLCGD-----QCAALTIDLPHGT--NPERHCDN--FAEAVEMIEQTVQAHVISEVPVIL	87
MenH_Vibvu	-----MSVLSEFNTYQQNGD-DRS-----PVLVFLHGLLGGSDQDLVPAQLCGD-----AYPTLTIDLPHGG--SVGIAPSC--AAKSAEQVATVIEQQLA--QRPICIL	86
MenH_Vibpa	-----MLHSERLSPTEK-HQSGALPTLVFLHGLLGGSDQDLVPAQLCGD-----QFERVVIDLPSSHGR--SQFTKEND--LDDCCKLINSTLSLLFPQOPLIL	88
MenH_Vibfi	-----MPLYSNQLETMTNT-TQP-----CVVFLHGLLGSFKDWSIARAKVAK-----THPVLLIDLPHGHN--SQSTLLDHNEG--FEQSQQLIVEQLE--KSPYQTIL	88
MenH_Phopr	-----MGRSKMRLYSETFGSLNN-----ESQPTLVFLHGLLGGSDQDLVPAQLCGD-----GYPCITIDLPHGK--SQMVQAD--FAHVNQLILQILLH--RNIEQYVL	90
MenH_Mor	MPNLSNIIVITPTLLPLYSELFPAPVNNPVKGVTAAPSLVFLHGLLGGSDQDLVPAQLCGD-----DYQCICIDLPHGAG--SQAVTVND--FQHQQQLIATLAQ--YELEHIVF	104
MenH_Halha	-----MADPVPTTIRT-----VDLVFLHGLLGGSDQDLVPAQLCGD-----TLRCWAPPLPGHGD--ALP-PATT--FEALVDTLWALRV--ELPPRFAL	78
MenH_Sheon	-----MSTLARYGEVVSQ-----PWLVLHGLLGGSDQDLVPAQLCGD-----HFHCICIDLPHGHD--NQPEIASMLTNGFDFCVQDIINRLDR--LGIEAFYL	85
MenH_Lismo	-----MLVNG-QHYHLTAASISGEKPAALLMLHGFGTGSETFQDSISGLKKR-----FNIAPDLLHGN--TASPEEISSYTMENICEDLAGILHQLNVSRFCV	90
MenH_Lisin	-----MLVNG-QHYHLINDISGEKPAALLMLHGFGTGSETFQDSISGLKKR-----FSIAPDLLHGN--TSCPKVARYSIENICDDLASILHQLKIDSCFV	90
MenH_Bacli	MAVLKLTLDGVSYKIEDNGLSEKTAFLVFLHGLLGGSDQDLVPAQLCGD-----MRLIKLNLHGGG--TDSPSDSRRYTTEQAADLIEFDRNLVQAYL	95
MenH_Bacsu	-----MGTVNITVSDGVRYAVADEGNASEAVVCLHGFSGDCHWQEVGEAFAD-----SRLIKIDCLHGE--TDAPLNGKRYSTTRQVSDLAIEFDQLKHLKVKL	95
MenH_Geoka	-----MTMMVNG-VCYHAEQYG--EGEPLLLHGFSGDCHWQEVGEAFAD-----FRVMVNDLLHGR--TEAPKADARRYRIEHAADLAALLDEWGVQVNV	89
MenH_Bacan	-----MNVTLQGS-VSYEYEVVG--SGEPLLLHGFSGDCHWQEVGEAFAD-----FQVILVDIVGHGK--TESPEDVTHYDIRNAALQMKELLDYLHIEKAHI	90
MenH_Oceih	-----MSLDD-KALHFEVVG--DGEPIVLLHGFSGDCHWQEVGEAFAD-----YQLILFDLPGHG--SSKGYTLTMTQACCNQLRKQLTMMNIYKPHL	84
MenH_Desha	-----MTIEG-CRYAAEVKG--SGPTLVCFHGFAGNSGTWEALQ--LQD-----QMVVLDDLHGR--SAKPSLEPYELPVLGLHLEIMAEGLGCTGYSL	85
MenH_Chlaui	MRDRHRAEDTTVKITIND-ITLHIEITG--SGPALLAINGFTGSGQTWQPLVPTLAQD-----HTLVLDLHGHGA--SAAPPDPHRYTIEQCVDLLTLLDYLHIEHTDL	101
MenH_Exi	-----MKLRH-QEYHVEISG--SGPPLLLHGFSGDCHWQEVGEAFAD-----YTVYRIDLHGR--TAS-ASYQRMALTEQVQDLKSLLATR--EEDNSV	86
MenH_Entfa	-----MQYHYQWLIPFDAKR-----TTVVCVHGFSGDCHWQEVGEAFAD-----YNVLGIDLPHGHA--TASLVAPERITYMKQVCHDIAELTESLNLPCFCL	86
MenH_Staep	-----MLHYNFYESKQSKQLLVMLHGFISDATTYHSHIERLVEH-----TNVLTIDLPHGHL--DTSSMDEV-WDFPFITRQLDEVLIQYQTYDVEL	85
MenH_Staau	-----MAHYNYFYANVEINQVLVLLHGFISDSTYYNHIDKYTDI-----CHVITIDLPHGHE--DQSSMDEV-WNFDYITLLDRILDKYKDKSITL	85
MenH_Leume	-----MIIDVNNYPYQAYLTNNNDENQWLLHGFSGDCHWQEVGEAFAD-----QVLTLDLLGFGG--HTTSVEVTRFEMAHQIQDLAIILNQLHWNINL	91
MenH_Rubxy	-----MLFLHGFSGDCHWQEVGEAFAD-----FRTLAADLPCHG--ASVGLPPERYTMEGAAGAVLLGLDGLGVGRCL	69
MenH_Arath	-----RVHDVGENAEGSVLFLHGFSGDCHWQEVGEAFAD-----ARCSISVDIPGHGSRVQSHASETQTSPTFSMEMIAEALYKLEIQTIPGKVTI	89
MenH_Chlte	-----MTTISLHLITVGDPLPKIVFLHGFSGDCHWQEVGEAFAD-----FCISLVDLPGHGEAGIIPA-DGDPE--LFFMQTVEALKSNIRRLRAEPCVL	89
MenH_Chlap	-----MPNIPHLITVGNPSPLPKIVFLHGFSGDCHWQEVGEAFAD-----FCISLVDLPGHGETGIPA-DGDPE--LFFMQTVEALAGEIRQLSAGPCVL	89
MenH_Provi	-----MHPVNPPVPLRFTIEGDAGLPAIVFLHGFSGDCHWQEVGEAFAD-----YRCILVDLPGHGEAAFPPE-TLTPKNASEGYFTRLDALAAELQRLRAPCFL	98
MenH_Chltb	-----MILDVGAIRFYQSLGTVQQAAILFLHGFSGDCHWQEVGEAFAD-----FHCLAILDLPHGHTQVSG-DDEFF--QMKETANGISDFNLQGLITKSNL	92
MenH_Trier	-----MFNGKNYKFNYSLSQNNKTIILLHGFSGDCHWQEVGEAFAD-----FCCLTVDLPGHGKTRVFD-SEKHY--NMHNTATLIGLLDNLNIEKCYL	91
MenH_Nospu	-----MILKKYKFNFLNGNTNKKIIFLHGFSGDCHWQEVGEAFAD-----FCYLTIDLPHGKTEVLG-GDEYY--QMESIAQAIINLLDELRLDKCHL	90
MenH_Par	-----MCNLPYILWAIPLGFLGLPSDDWLFKFTQIK-----KIDVNSFSC--TDLSSWAEHFNAPVKKQPPHFFIL	63
MenH_Bdeba	-----MNLFFLHGFSGDCHWQEVGEAFAD-----EGLRIPTPDYFK-----ELSLGTPHSFETWAEFNFWVVEIHGGGSAARNVL	72

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MenH_Escco VGYSLGGRVAMMAACQG-----LAGLOGVIVEGGHPGLQNA-----EQRAERQPSDRQWVQRFLET-----LTAVFADWYQQPVFASLNDQRRRELVALRSN--- 170
MenH_Shifl VGYSLGGRVAMMAACQG-----LAGLOGVIVEGGHPGLQNA-----EQRAERQPSDRQWVQRFLET-----LTAVFADWYQQPVFASLNDQRRRELVALRSN--- 170
MenH_Salen VGYSLGGRVAMMAACQG-----IPGLOGLVVEGGHPGLQNE-----QARAERRLSDGRWAERFRREP-----LIEVFHDWYQQPVFASLTAQQRQALTALRSQ--- 170
MenH_Klepn IGYSLGGRVAMNFASQF-----RAGMGLIVEGGHPGLQDA-----EARQARRSNDASAWAERFRREP-----LEQVFADWYQQPVFASLNAQRRSELVALRSR--- 170
MenH_Ent VGYSLGGRIAMFHACQH-----PAGLIGLIVEGGHPGLHDE-----PTRKARAESDAQWAERFRREP-----LENVFSAMWQQPVFAALQETERDALVALRSQ--- 170
MenH_Erwca LGYSLGGRIAMYHACEGH-----HDGMLGLLVEGGHPGLATP-----EQTERIHHDARWAQRFQDQF-----LPEALQDWYQQAVFADIDSQVQREQLIARRSA--- 167
MenH_Yerpe AGYSLGGRIAIYHACYGR-----HHGLQGLLVEGGNGLLENA-----ELRQARLQDDQWQWQRFQDQF-----LPQVLDDWYQQAVFADLDPQQRQLVLLRAD--- 179
MenH_Pholu IGYSLGGRIAMHHACYGD-----IRGLQGLLIEGGNPGLFSDQ-----QERNNRLHEDRNWAGFRFRSQ-----IEQVLSDWYQQPVFSDLLPEQRQQLIKVRRH--- 171
MenH_Serpr VGYSLGGRIAMYHACHGE-----PRGLQGVIIIEGGNPGLLADA-----AQRELRLAHDITAWAERFRREP-----LAQVLADWYQQPVFANLSAVHRDALIDARSD--- 171
MenH_Aerhy VGYSLGGRIALYHASQS-----LVGLQALLLENCHPGLP-P-----AERPARLAHDEGWARRFEQEP-----LAAVLADWYRQGVFADLGEDARARQIARRLG--- 162
MenH_Mansu VGYSLGGRIALYYALQ-----SQCE-KGNLQGLLIEGANLGLTCD-----EARKVWKNDEFWAQRFTES-----AESVLNDWYQQPVFAHLNAQQRADLIERKVT--- 163
MenH_Haein VGYSLGGRIALYYALQ-----AQLE-RSNLQGVILEGANLGLTCD-----EEKQARFQDDFAMAQRFMQES-----PEKVLNDWYQQPVFASHLTTEERLQVLEKRRKS--- 161
MenH_Haeso VGYSLGGRIALNYALQ-----SKYP-QSKLVALLIEGANLGLLENE-----QORLERWQNDLAWAKRFSQET-----MSKVLNDWYQQPVFAHLSARERKQLISQRRH--- 168
MenH_Pasmu VGYSLGGRIALYYAFA-----YLSKTAKHHHLGLLIEGANLGLQHD-----EERKIRWQDDAWATFRREP-----MASVLDDWYQQPVFASHLTPQVRQDLIQKRAI--- 163
MenH_Actpl VGYSLGGRIALDYALN-----ANNP-QLQHTLIEGANLGLTCD-----EERQARWQNDHQWAKRFRNEP-----IVKVLNDWYQQAVFANLDQHKNRNLEKRRQN--- 172
MenH_Haedu VGYSLGGRIALDYALN-----GNNP-DLQHTLIEGTHLGLSLA-----NERQARWQTDQWQWAKRFRNEP-----IKQVLQAWYQQPVFADLSAEKRSFLLKRRQH--- 177
MenH_Vibch VGYSLGGRIALMHGLA-----QGAF-SRLNLGALIEGGHPGLQEN-----EKKARWQDDQWQWAKRFSQF-----IEHVLSDWYQQAVFSSLNHQRQTLIAKRSR--- 178
MenH_Vibvu IGYSMGGRIVMQGLV-----EHAF-AALNLGALIEGGHPGLVSE-----QEKQQRWISDSHWAKRFRREP-----IEQVLADWYQQGVFSSLNHAKQTLIAKRSR--- 177
MenH_Vibpa IGYSMGGRIAMHGLA-----GECF-SDINIVGAIVEGGNPGFQTE-----SEIQSRLHNDQKWLAFSEEP-----LERVLSDWYQQAVFSSLNHQRQTLIAKRSR--- 179
MenH_Vibfi VGYSLGGRIALMYLHA-----MYSLPSSLEVGLGALIEGGHPGLVSE-----EKKLLRLLENDIQWAKRFEELP-----IVDVLNDWYQQAVFSSLNHQRQVVLTKRSD--- 180
MenH_Phopr IGYSMGARLAMYHAASHPNAVPHSGVKSACKKTQMLMGVIVEGGHPGLPR-----TECATRFANDQWQWQRFETYP-----LSVLPLDWYQQAVFSSLNHQRQSLVLKRSR--- 193
MenH_Mor IGYSLGARIAMTIAD-----EPAVNWPYITIDGMILEGGNPGLNSS-----AEQQLRGLHDLGWVTRFSESP-----LSQVLPLDWYQQGVFASLTNTKRTALIDTRSQIA--- 199
MenH_Halha VGYSLGGRIALALADRY-----PHRLSALILEGAHPGLQDA-----TARERRRHDAWAQRFETGP-----WQESLDWYRQPVFADLSDPRRQALIQRRAR--- 166
MenH_Sheon VGYSLGGRIALHLAKAYP-----NRVLSLWLESCHPGLTNT-----EQQARSNDQLWAKRLHSL-----SRDFLQWYQQAVFADMSDNVNTLIAKRAAQLD--- 176
MenH_Lismo LGYSMGGRVATAFAATFP-----KRVGLLIVSSSPGLEQE-----DIRASRVADNRLADWIEEG-----LVFFVDYWNELALFASQKVLSPENKRRIRSER--- 179
MenH_Lisin LGYSMGGRVATAFAAKYK-----ELVRGLVLVSSSPGLRDE-----KARASRISADNRLADTLADG-----IEFFVAYWENLALFASQKVLSPENKRRIRLER--- 179
MenH_Bacli IGYSMGGRIALSLAMIHP-----ERVSGLVLVSSSPGLDSP-----EERKARREQDSRLSRILEEG-----IKSFVDYWEGIPLFASQKVLSPENKRRIRSER--- 184
MenH_Bacsu IGYSMGGRIALSLAMITYP-----ERVSALVLESTTPGLKTL-----GERPERIMRDKLADFILRDE-----LEAFVAYWENIPLFSSQQLAEDIRYIRSGR--- 184
MenH_Geoka LGYSMGGRIALAFVAVWHP-----RRVRRLVLESSSPGLETE-----EERPARREADEALARKIETEG-----VRAFVDWKEIPLFATQQTLPDPVRAAIRRR--- 178
MenH_Bacan LGYSMGGRIALITMACLYP-----EYVRSLLENCTAGLERE-----DERKERCEKDERLADKIEREG-----IESFVTWENIPLFETQKSLAQNVQEAVERER--- 179
MenH_Oceih VGYSMGGRIALHAFANFP-----DMVSLILESSSPGLESE-----LEQQRQQRQNDKDLANYILQNG-----IEDFVDYWENIPLFSLQKELSEEKRRQIRNER--- 173
MenH_Desha LGYSLGGRIALAYGAAYP-----DEVQGLILESSAYGIGDE-----EQBALRPEQDVRLAQEILDRG-----IEWFAEHWSLPLFASQTRLPPETIRAKIRARR--- 174
MenH_Chiau LGYSMGGRIALLLTAHAP-----TRIRRRQILIGASPGLDAP-----AERTARLASDEALARLIEEG-----LEWFDYWAQPIFASQQLPFAVLAQAQRAQR--- 190
MenH_Exi LGYSMGGRIALLLAATS-----KQVQQTIAVSTTPGLRSA-----HERRLRRQADRRLADRLLDG-----LADFDIDYWESLPLFASQKHLFVQVESIRGR--- 174
MenH_Entfa LGYSMGGRIALGFFKVS-----QKVQHLLLESGLPGLATA-----AERQARICQDHLAERLLEEP-----LVDFDIDFWQELPLFQTKALSVAQQHAIQER--- 175
MenH_Staep LGYSMGGRIALVYAIHGN-----ETLSGLLLESTSGIQNE-----TDKVERAQVDAARAKVLEIAG-----LDIFVNDWEKLPFASQYNLAPEIRQSIRNRR--- 174
MenH_Staau FGYSMGGRIALVYAIHGN-----IPISNLILESTSPGIEKE-----ANQLERPLVDARAKVLDIAG-----IELFVNDWEKLPFASQQLFVPEIQHQRIRQR--- 174
MenH_Leume LGYSMGGRIALGFTKVS-----ELVRLYLESTTAGLTA-----QERHERVSDYKKAQKIQN-----FETFTDWEQMLFATQGHVSPQKTFMHQQR--- 179
MenH_Rubxy CGYSMGGRIALYLALRSP-----GRFSALLLESASPGLEDP-----AERARRRADEEPARELEGD-----LEGFVGRWYRRPLFASLARRG-ELAGELARRR--- 157
MenH_Arath VGYSMGARIALYMLRFS-----NKIEGAVVVSGLPKDP-----VARKIRSATDDSKARMVNDG-----LYIFIENWYNGGLMKSLRNHP-HFSKIAASRL--- 177
MenH_Chlte VGYSMGGRIALALALLP-----ELFSKALIVSSSPGLQTD-----EKRASRRKSDEGIAR-KIERN-----FEGFIFGWYDQPLFSTLKSLS-LFREVEAQR--- 175
MenH_Chlap VGYSMGGRIALALTLRP-----ELFSKAVIVSSSPGLRTE-----ELHARRRKSDEGIAR-KIERN-----FEGFIFGWYDQPLFSTLKSLS-LFREVEAQR--- 175
MenH_Provi AGYSMGGRIALGVALRHP-----GLFKKALIVSSSPGLRTE-----EQALRRKSDEGIAR-KIERN-----FDSFIEFWYDQPLFSTLKSLS-LFREVEAQR--- 184
MenH_ChltH VGYSMGGRIALGLSLTYP-----NLFKKSLIESSSPGLKTA-----EERARRLRDEKLALDMVQTD-----FSLFLTKWYELPLFETLKQHP-KFSEVFNRR--- 179
MenH_Trier FGYSMGGRIALYLGINFP-----TRFKKILLESASPGLSK-----AERSLRQCSDFQLAN-KLENS-----NFKFELINWYNGPLFESLRQHN-NFEKLIERR--- 178
MenH_Nospu IGYSMGGRIALYLTLHFP-----ORFKIIRRDQAQIAR-KLSRSILQIDFAAFLSNWNQPIFYGIKNHP-QYDRMIERN--- 181
MenH_Par LGYSMGGRIALHALCQDP-----DLWGGGLISTHPGLSQE-----NEKERRLDQCKWAGLFETEE-----WESLILQWNAQDIFAKDLIFYRSNHDYQRSN--- 151
MenH_Bdeba VGYSLGGRIALHALEKFP-----ALFYKVMVLVSTNPGFNDMDSFDPTSEERRQRWMDNSYWAEEFLKAP-----WDMVLARNNAQPVFGGAERPEPSRSEKEYSRET--- 169

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MenH_Escco	-----NNGATLAAMLEATS LAVQPDRLANLSAR-TFAFFYYLOGERDSKFFRALAAELAADCHVIPR-----	AGHNAHRENPAAGVIASLAQILRF-----	252
MenH_Shif1	-----NNGATLAAMLEATS LAVQPDRLANLSAR-TFAFFYYLOGERDSKFFRALAAELAADCHVIPR-----	AGHNAHRENPAAGVIASLAQILRF-----	252
MenH_Salen	-----NNGETLAAMLEATS LAVQPDRLREVLNAL-AFFPFFYYLOGERDSKFFRALAQEVAATCHVIRN-----	AGHNAHRENPAAGVVDLSLAQILRI-----	252
MenH_Klepn	-----NNGATLAAMLQATS LAAQADLRASLQAR-DFFPFFYYLOGERDAKFRAIAQTLLAADLHLIHH-----	AGHNAHRENPAAVIACLAQILAS-----	252
MenH_Ent	-----NNGAALGAMLQATS LAQQPDRLAALRAH-DYFFPFFYYVGEHDDKFGAIAITELTAQHVIPIV-----	AGHNAHRENPAAVAACLAQILRLRIKDIP-----	258
MenH_Erwca	-----NHGASVAAMLEATS LGQPFLAARLQHL-SIPFTYLOGASDVKFTQLAAQYGLPLLSVAL-----	AGHNAHQANPAAYAERVRTFLSH-----PVKD-----	253
MenH_Yerpe	-----NHGPAVAEMLEATS LGHQPWLLPALQAL-NVPYTYLOGERDHHKFLQLAQQYRLPLHTLAR-----	AGHNAHRANPGAFAAQVLAFLSQSSCLPPSSLSR-----	272
MenH_Pholu	-----NNGDGVANMLEATS LGHQPWLVLPVQLQ-LTPFVYLOGENDKKFQHLAKRCALPQTIPR-----	VGHNAHRANAVAFAAVNVHFLSLFNKEYEYDLPERRRTLFFN-----	272
MenH_Serpr	-----NAGAAVAAMLEATS LGTQPCPLAPQLQQL-AVPLVVLGCGDDHKKFQQLTRDAGLPLRIVPQ-----	AGHNSHLANPQAFAAELRNFLVNPQ-----	255
MenH_Aerhy	-----NDGEAVAAMLRATS LGQQPNLGPWLAQGG-ALPVTWVSGKRDHKKFQHLACIMASQHRKINHLE-----	LD-GGHNLAHQPETFARLLAEWVNQQEKKRHD-----	256
MenH_Mansu	-----NCGHNIGKMLEATS LKQPYLGDKVRES-TLPVYVLOGEKDKKFKQMAVQEKLNQLLIAN-----	AGHNAHLENPVEFSQKLTALLRNHKIKKTDNL-----	254
MenH_Haein	-----NCGHNIGKMLLATS LSKQPDFSEKVRSL-SLPFFYFGEERDHHKQVLAKENQIDLVTIPC-----	AGHNSHLENSKYFSKKIENCIL--KIVRP-----	247
MenH_Haeso	-----QSGQNIAMMLIATS LKQPSFHKQVRSF-SLPYIYFGEKDEKFKKMAQENQLNLFIER-----	AGHNAHLENPIAFANKIVEIIN--RT-----	251
MenH_Pasmu	-----HCGEHIAMMLLATS LKQPDFRPYLIAS-TFFPIYFGEKDKKFKQMAEQTKLPLVVIPE-----	AGHNAHVEQPIVFANNIKTHFP--FDV-----	247
MenH_Actp1	-----NNGSAVAAMLEATS LKQPYFLPQLSEA-RQITFLIGEYDRKFKRIVSDNKLHHQLIPN-----	AGHNAHYENPESFTDALLALIKK-----	254
MenH_Haedu	-----NNGHAIAMLEATS LKQPNYLSTVKTQ-IHRETFLIGERDHHKFRQLATQQQLNVQLIRH-----	AGHNSHQENPSDFVETLLQKITCIT-----	261
MenH_Vibch	-----NLGSSVAHMLLATS LKQPYLLPALQAL-KLPIHYVCGEQDSKFFQQLAESGLSYSQVAQ-----	AGHNVHHEQPAFAKIVQAMHISIID-----	263
MenH_Vibvu	-----NLGVPVAEMMLLATS LKQPNLLPQLQSN-SVPLHYVCGEKDKKFKRLVEDTQLQVQVIAS-----	AGHNVHVEQPNAFADIVRAFIHSVYQR-----	263
MenH_Vibpa	-----NLGSAIAMMLMATS LKQAYLLPALQQQ-RIPIYVCGAKDKKFSQLAQTSGLAYRQIEG-----	AGHNVHVEQPKQFAMHIKQIHSHFQ-----	264
MenH_Vibfi	-----NLGPAIGMLRSTS LKQPYLLDALHRS-TIPILYLOGEADKKFQHLAESQSLTYQIIAQ-----	AGHNAHVEQPERFTHVNLFLQQWT-----	264
MenH_Phoqr	-----NLGSGVARMMLLATS LKQPQLLQIMRAL-VLPITIVCGERDHHKFKRLVEDTQLQVQVIAS-----	AGHNVHVEQPYAFSMAINNFFVKQIGINH-----	261
MenH_Mor	NNGFNAGVQISKMLAATS LSKQGFLLPKLQHA-EFPVVMVCGELDPKFFLQLTQASQLNRAVAN-----	AGHNVHADRPVIVFIELVSDFVSEIVTNKALRKHAA-----	258
MenH_Halha	-----HRPEHLAATLRAAS LSGQPDRLPALRRL-SAPCAYIAGKRDHKKFSAIADSLAAQTPGLTVAK-----	LDGVGNHCHAEAPEAAVAVIQSICTGEHP-----	256
MenH_Sheon	-----QHPKHALMHIFLATS LKQASLWDLPANL-ACESHFFAGSQDAKFTAIKAEQWAPQPIILHR-----	IEQAGHNIHQANPAGLLACIRSFVVRPL-----	266
MenH_Lismo	-----LSQNSHGLAMSLRGMGTGKQPSYWNCLANF-TFPVLLITGALDEKFKKIAQEMHQLLPNSTHVS-----	IEQAGHAVYLEQPNFSFSSQLNWLIEDILKEEEK-----	275
MenH_Lisin	-----LAQNPHGLAKSLRGMGTGKQPSYWNCLADF-TFPVLLITGNLDEKFKKIAEMKQLLPNSTHVT-----	VQAGHAVYLEQPNIFSSQLIYNWLEIGILKEEEK-----	275
MenH_Bac1i	-----LNNNPIGLRLGSLIGMTGSGQPSWNNKLSGI-NYPVLLIAGSLDQKFVAINESSMAKRIAPARLEI-----	VEHTGHAVHVEEPDFFGRIVSEFILK-----	273
MenH_Bacsu	-----LRNNKIGLANSLTGMGTGSGQPSLWSRVEEI-DVPVLLICGEWDEKFCIAINQEVHKLPLSSRIEI-----	VPGAGHTVHVVEQPRFLGKIVSEFLTISI-----	274
MenH_Geoka	-----LRHTATGLANSLRGMGTGQPSFWERLGEEL-AMPVLLVCGERDEKFCRIAAQMHRLPNSELIC-----	VKGAGHAIHVEQPGIFAKIVSEFMTKGEV-----	270
MenH_Bacan	-----LANNNSGLANSLRGMGTGAQPSWNNELQNL-KMSVLLMNGEYDEKFFRIILKNIEKCVSDAKFVK-----	IDGAGHAIHVEQPEKFDITIVKGLKIMQ-----	270
MenH_Oceih	-----LSHQPEGLAHS LQSMGTGAQPSFWNDLQF-YMKVLLVTEGKDLKFLVNINKNMREKFPNAALIV-----	CKNVGHAVHVENPQIFGKIVSEFLINPITT-----	267
MenH_Desha	-----LGNAPHALANTLLSGGQGVFPCLREQIPTL-SMPILYIHGEQDEKYKEIGQELMDLNPQIKREM-----	IPGAGHNAHLENPVTFAEIVGNFLQELAKP-----	267
MenH_Ch1au	-----LAGSAQGYANALRGMSVGRQPSLWATLPTI-TPTLLITGALDSKFCIAIAAQMTALMPHARHEI-----	VPDAGHAVHLEQPDVATLVSAPLA-----	278
MenH_Exi	-----LAQSPGELAAS LIAQGTGNMAPVHLLDTS-SID--WIVGNDDDKFKKIAIEAA--PSEKIH-----	IEGASHAPHIDQPEKFTVIVEKLLINQMSELK-----	265
MenH_Entfa	-----LSQSAGLVSSSLWYMGTAQESYWERLAELQPIPTDLLVGGEDQKFFIGIAKKMQARQPLRLTI-----	FPEAGHCIIHQPTIFYEKVTALLEGAI-----	267
MenH_Staep	-----LNQDANKLAKALRDYGTGHMPNLWPHLSLI-RIPTLLIVGEKDKKFFVQIGQQLENHLQDSHKVQ-----	ISNVGHTIIVVEDSTEFDTIILGFLKEEQND-----	267
MenH_Staau	-----LSQSPHMAKALRDYGTGQMPNLWPHLKEI-KVPTLLIAGEYDEKFFVQIAKKMANLIPNSCKKL-----	ISATGHTIIVVEDSTEFDTMILGFLKEEQND-----	267
MenH_Leume	-----INQNIPINVANSLRYMGSGVQPNYWPCLQSL-HTPTQVIVGEQDIKFNILAEEMINLLPNAKISI-----	VPNAGHNAHFEQPAAFIEVLDSN-----	266
MenH_Rubxy	-----LRNDPGEIARSLRGMGTGRQPPILWALPAL-AMPALAVAGELDPKFAALARRMEREAPPLRAAV-----	VPGAGHNVHLERPGAFGRLLREFLE-----ERGLE-----	250
MenH_Arath	-----LHGDPVSVAKLLS DLSSGRQPSLWEELEDC-DTNISLVFGEKDVYKQIATRMVREMSKSKSVNNIIIEIVE-----	IPGAGHAVHLESPLRVILALRKFLTRVHNSSTETELSQMLLLALK-----	293
MenH_Ch1te	-----KQGTQPNLARALRLGTGNQPSFWDKLPGN-RLPMLFCVGEKDAKYVDIAKQVFLCPSSSLEL-----	FEHCQHTLHIEEPERFLASVERFIETHPHNSISHDDL-----	275
MenH_Ch1pa	-----KQGSFENLACALRLGTGNQPSFWDELPGN-LLPMLFCVGEKDAKYVEIGKQMVCLCPQSSLEL-----	FEHCQHTLHIEEPERFLASVSGLSKSKTEISLTKEFVP-----	276
MenH_Provi	-----KQGSFENLACALRLGTGNQPSFWDELPGN-LLPMLFCVGEKDAKYVEIGKQMVCLCPQSSLEL-----	FPQCGHTLHIEEPERFLASVSGLSKSKTEISLTKEFVP-----	278
MenH_Ch1th	-----KQGSFENLACALRLGTGNQPSFWDELPGN-LLPMLFCVGEKDAKYVEIGKQMVCLCPQSSLEL-----	FPQCGHTLHIEEPERFLASVSGLSKSKTEISLTKEFVP-----	278
MenH_Trier	-----KQGSFENLACALRLGTGNQPSFWDELPGN-LLPMLFCVGEKDAKYVEIGKQMVCLCPQSSLEL-----	FPQCGHTLHIEEPERFLASVSGLSKSKTEISLTKEFVP-----	278
MenH_Nospu	-----LQNNPQELDKSLRFMTGTGQPSLWEEKLEN-KIHIILLTTEYDDEKFFISINTEIAQICEFAQLKI-----	IKNAGHNIHFNENTLAFVENIKDFLSTAN-----	272
MenH_Par	-----LAMHLNFS LKQEDLKEKIGLL-QPIILMTTEYDDEKFFISINTEIAQICEFAQLKI-----	IKNAGHNIHFNENTLAFVENIKDFLSTAN-----	272
MenH_Dbeba	-----LSLALTQWSLAQQKNMRGLLEKQ-TQKLIWMVGERDEKFFELMSRRLTEZVPGFHFET-----	VPSSSHRVLFDSPKELGERIRQLLQKLL-----	253

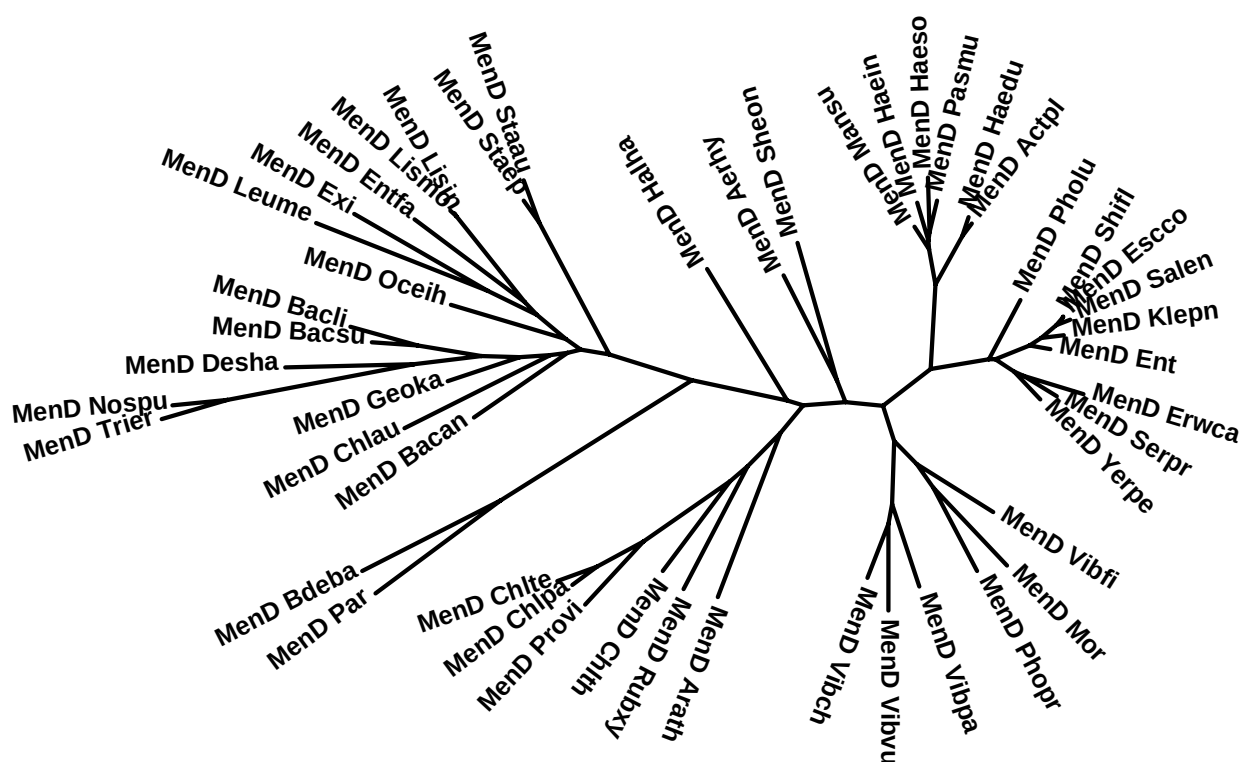


Figure S2. MenD phylogenetic tree.



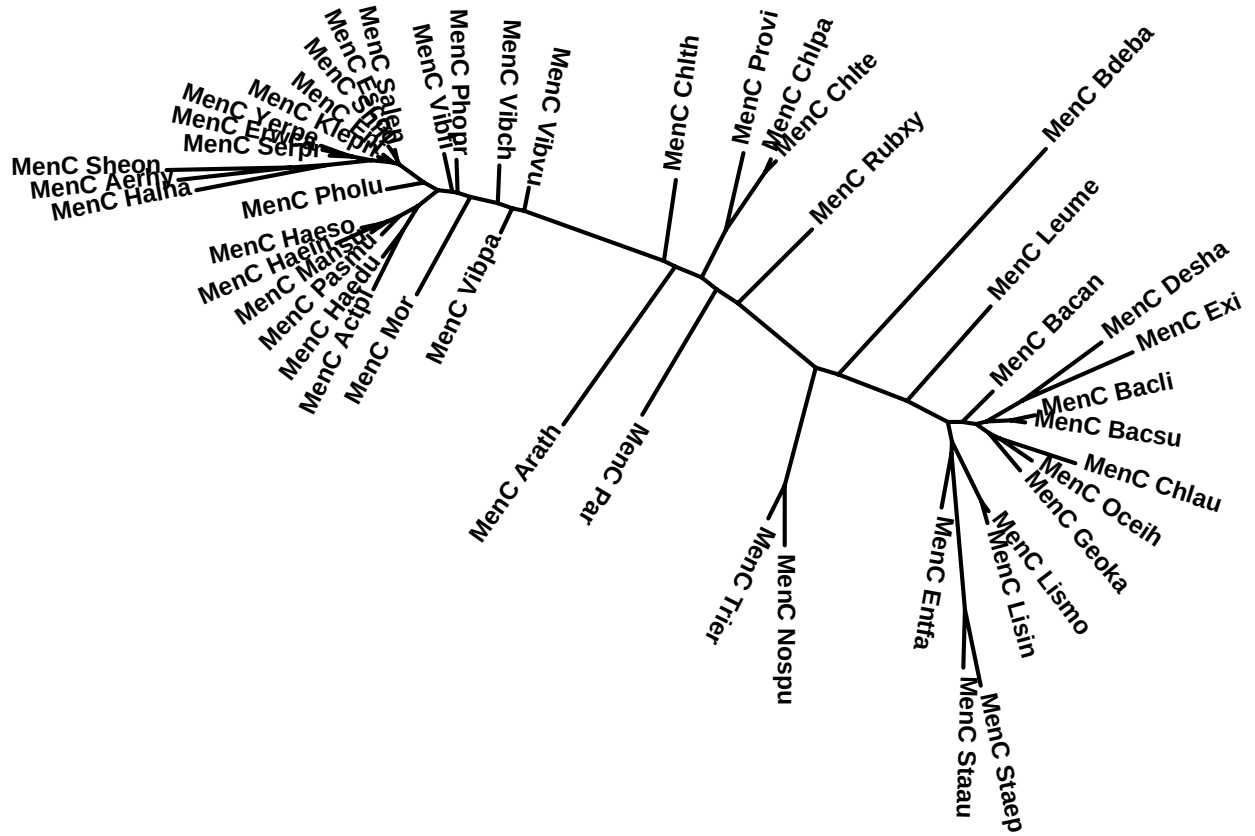


Figure S5. MenC (OSBS/NAAAR) phylogenetic tree.