Figure S1. NOS alignments. The alignment was done by ClustalX software. Protein sequences are colored by residue as follows: orange – GPST, red – HKR, blue – FWY, green – ILMV. Identical residues denoted by asterics and similar by dots.

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: E:clustalx1.83SequensesNOSfor aln1.ps **Date: Fri Aug 10 15:53:07 2007**

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```
        S.erythraea ------------------------------------------------------------------------------------------------------------------------------------
       S.avermitilis ------------------------------------------------------------------------------------------------------------------------------------
          S.scabiei ------------------------------------------------------------------------------------------------------------------------------------
    S.turgidiscabies ------------------------------------------------------------------------------------------------------------------------------------
       D.radiodurans ------------------------------------------------------------------------------------------------------------------------------------
      D.geothermalis ------------------------------------------------------------------------------------------------------------------------------------
         Rhodococcus ------------------------------------------------------------------------------------------------------------------------------------
         S.arenicola ------------------------------------------------------------------------------------------------------------------------------------
           B.clausii ------------------------------------------------------------------------------------------------------------------------------------
         N.pharaonis ------------------------------------------------------------------------------------------------------------------------------------
       S.epidermidis ------------------------------------------------------------------------------------------------------------------------------------
            S.aureus ------------------------------------------------------------------------------------------------------------------------------------
      S.haemolyticus ------------------------------------------------------------------------------------------------------------------------------------
      G.kaustophilus ------------------------------------------------------------------------------------------------------------------------------------
G.stearothermophilus ------------------------------------------------------------------------------------------------------------------------------------
          B.subtilis ------------------------------------------------------------------------------------------------------------------------------------
 B.amyloliquefaciens ------------------------------------------------------------------------------------------------------------------------------------
     B.licheniformis ------------------------------------------------------------------------------------------------------------------------------------
        B.halodurans ------------------------------------------------------------------------------------------------------------------------------------
            B.cereus ------------------------------------------------------------------------------------------------------------------------------------
B.weihenstephanensis ------------------------------------------------------------------------------------------------------------------------------------
         B.anthracis ------------------------------------------------------------------------------------------------------------------------------------
     B.thuringiensis ------------------------------------------------------------------------------------------------------------------------------------
         O.iheyensis ------------------------------------------------------------------------------------------------------------------------------------
         E.sibiricum ------------------------------------------------------------------------------------------------------------------------------------
      S.officinalis ------------------------------------------------------------------------------------------------------------------------------------
      A.californica -----------MPRAQTYDSGVGCPDSARSVDSGRSVCSPHQKKAIEIVQDDDEITVVVKGDVSVRTTGDGCEPGTPRKFIISTSKNNCSHFFGSSGKGKVVAGTEQTSGINGAANADGDHSQYVDHNDGTYNNNNNNNHYSSKKRKSSK  139
            D.rerio ------------------------------------------------------------------------------------------------------------------------MGNQVTHKSE------  10
          C.auratus ------------------------------------------------------------------------------------------------------------------------MGNQATKASKNVILHQ  16
           G.gallus ------------------------------------------------------------------------------------------------------MLCPWQFAFKPHAVKNQSSEEKDINNNVE  29
      C.familiaris MESQVFSVQQIQPNVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNGQPLVDLNYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTRPLGPPTTAVDLSHQSSASKEHTP--D  148
          B.taurus MESHMFSVQQIQPNVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNGQPLVDLSYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQPLGPPTAAVDLSHQASAGREQTLVVD  150
           S.scrofa ------------------------------------------------------------------------------------------------------------------------MGNLKSVAQEPGP---  13
         H.sapiens ------------------------------------------------------------------------------------------------------------------------MGNLKSVAQEPGP---  13
        M.musculus ------------------------------------------------------------------------------------------------------------------------MGNLKSVGQEPGP---  13
      R.norvegicus ------------------------------------------------------------------------------------------------------------------------MGNLKSVGQEPGP---  13
    D.melanogaster ---MSQHFTSIFENLRFVTIKRSTNAQQQQQQQQQQLQQQQQQLQQQKAQTQQQNSRKIKTQATPTLNGNGLLSGNPNGGGGDSSPSHEVDHPGGAQGAQAAGGLPSSSGTPLRHHKRASISTASPPIRERRGTNTSIVVELDGSGSGSG  147
        A.mellifera ------------------------------------------------------------------------------------------------------------------------------------
            B.mori ------------------------------------------------------------------------------------------------------MSNFFKICCVKDPGGSAKENLRKMD-------  25
     P.polycephalum ------------------------------------------------------------------------------------------------------------------------------------
           O.tauri ------------------------------------------------------------------------------------------------------------------------------------
             ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

Figure S1-1

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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```
        S.erythraea ------------------------------------------------------------------------------------------------------------------------------------
      S.avermitilis ------------------------------------------------------------------------------------------------------------------------MADPSGVGRGRGVWTADGS   19
          S.scabiei ------------------------------------------------------------------------------------------------------------------------------------
   S.turgidiscabies ------------------------------------------------------------------------------------------------------------------------------------
      D.radiodurans ------------------------------------------------------------------------------------------------------------------------------------
     D.geothermalis ------------------------------------------------------------------------------------------------------------------------------------
        Rhodococcus ------------------------------------------------------------------------------------------------------------------------------------
        S.arenicola ------------------------------------------------------------------------------------------------------------------------------------
          B.clausii ------------------------------------------------------------------------------------------------------------------------------------
        N.pharaonis ------------------------------------------------------------------------------------------------------------------------------------
      S.epidermidis ------------------------------------------------------------------------------------------------------------------------------------
          S.aureus ------------------------------------------------------------------------------------------------------------------------------------
     S.haemolyticus ------------------------------------------------------------------------------------------------------------------------------------
     G.kaustophilus ------------------------------------------------------------------------------------------------------------------------------------
G.stearothermophilus ------------------------------------------------------------------------------------------------------------------------------------
          B.subtilis ------------------------------------------------------------------------------------------------------------------------------------
 B.amyloliquefaciens ------------------------------------------------------------------------------------------------------------------------------------
     B.licheniformis ------------------------------------------------------------------------------------------------------------------------------------
        B.halodurans ------------------------------------------------------------------------------------------------------------------------------------
          B.cereus ------------------------------------------------------------------------------------------------------------------------------------
B.weihenstephanensis ------------------------------------------------------------------------------------------------------------------------------------
          B.anthracis ------------------------------------------------------------------------------------------------------------------------------------
     B.thuringiensis ------------------------------------------------------------------------------------------------------------------------------------
        O.iheyensis ------------------------------------------------------------------------------------------------------------------------------------
        E.sibiricum ------------------------------------------------------------------------------------------------------------------------------------
      S.officinalis ------------------------------------------------------------------------------------------------------------------------------------
      A.californica RSSGRASGRS-------------------------------------------------SPNSAQRSSPTRNSRSPVTSPTR-------------------------RAGDSDEDNAARGRSLEKKRLSSPTLGRRRSTDRRGSMNAVMA  215
           D.rerio ------------------------------------------------------------------------------------------------------------------LLQQMKPDMQWEN---------------KVK   26
         C.auratus TKPNTQWE-------------------------------------------------------NNNVILQQIKPNTQWENNNV-------------------------------------ILQQMKPNTQWENKNVKPQQITKNTQWVNKVN   76
          G.gallus ------------------------------------------------------------KDVKVHSFVKDDAKLHSLSK-------------------------------------KQMKMSPIITSAEKHPQ-----NGIKASNQIS   76
      C.familiaris GATGPGNGPQHIQDSGQQASSLLNTNSLAPRPPSQDSTKKSTGVALQDS-QNNELLKEIEPVLSLLTSGNKGINGVGPSKAETKDAEVQVDRGMDSKSHKPLPLGVENDRVFSDLWGKGHVPVVLNNPYSEKEQPPASGKQSPTKNGSPS  297
          B.taurus GATGPGNGPQHAPDPGQEASSLAHAKGLAARPPGQDPAKKSTGVALQGSRENNKLLKEIEPVLNLLTSGGKAINGGGPAKTETKDVEIQVDRDLDGKSHKPLPLGVENDRVFSDLWGKGSMPVVLNNPYSEKEQPPASGKQSPTKNGSPS  300
          S.scrofa -PCGLGLG-------------------------------------------------------LGLGLCGKQGPASPAPEASQ-------------------------------------APAPAPAPAPDHSPAPNSPPLTRPPEG---   67
         H.sapiens -PCGLGLG-------------------------------------------------------LGLGLCGKQGPATPAPEPSR-------------------------------------APASLLPPAPEHSPP--SSPLTQPPEG---   65
        M.musculus -PCGLGLG-------------------------------------------------------LGLGLCGKQGPASPAPEPSQ-------------------------------------APAP---PSPTRPAPDHSPPLTRPPDG---   64
      R.norvegicus -PCGLGLG-------------------------------------------------------LGLGLCGKQGPASPAPEPSQ-------------------------------------APVP---PSPTRPAPDHSPPLTRPPDG---   64
    D.melanogaster SGGGGVGVG-------------------------------------------------------QGAGCPPSGSCTASGKSS-----------------------------RELSPSPKNQQQPRKMSQDYRSRAGSFMHLDDEGRSL  211
       A.mellifera ------------------------------------------------------------------------------------------------------------------------------MKEHEATGT    9
            B.mori ------------------------------------------------------------------QVNGHFVSATCPFSGES-------------------------------------------VELKVDSNQKQVKPNLRI   60
    P.polycephalum ------------------------------------------------------------------------------------------------------------------------------------
          O.tauri ------------------------------------------------------------------------------------------------------------------------MASVGSGATDDDGVDV   16
            ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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Figure S1-2

Figure S1-3

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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       S.erythraea ------------MSGEAPESFFSGAG--------------------RAAAPTRR-------------------------------------LRVASRRP-------AGAPPVD--------------------------------VAEA    41
      S.avermitilis GTGSITGLQGRLLADAPPESAASRPGGDA---------------RDRHGAPSRARGWSTETWCAPHGRKDTAGESEHRPPGPTLPGARGWGAARTRGDRPDGHPDHPTGSPTTDGPARPARPDRREEGDGHDGHEGQDGHDGH-DLLCAA   153
          S.scabiei -MTSEVALGPSLPAPSPTACPALGPD--------------------SSLGPVPS-------------------------------------AEPATPQS-------CGVADPN--------------------------------EA    50
    S.turgidiscabies -MTFEVALGPSLPAPSPTACPALAHD-------------------SPLSPVPS-------------------------------------AEPATSQD-------CGVADPD--------------------------------EA    50
       D.radiodurans ------------MS-------------------------------------CPAA-------------------------------------AVLTP-------------------------------------------DM    13
      D.geothermalis ------------MTPTP-----------------------------------CSPSAR-----------------------------------TAYRRA-------------------------------------------EA    19
          Rhodococcus ------------MSSTG-----------------------------TMSYSLD-------------------------------------VTSRS-----------------------------------------------AAQ    20
          S.arenicola ----------MTVSNTRDCSEQVRYPAR-----------------HINPPSVD-------------------------------------PTEDP-----------------------------------------------STEA    35
            B.clausii ------------------------------------------------------------------------------------------MANR-------------------------------------------------LEDEA     9
           N.pharaonis ------------------------------------------------------------------------------------------MHEPPQEYSREE-----------------------------------------RFAEA    17
        S.epidermidis ------------------------------------------------------------------------------------------M----------------------------------------------------LIDKA     6
             S.aureus ------------------------------------------------------------------------------------------M----------------------------------------------------LFKEA     6
        S.haemolyticus ------------------------------------------------------------------------------------------------------------------------------------------------MEEA     4
       G.kaustophilus --MAGKRGENHVDPSTAWFCAHFFGDFDVYRANVVDRGNLFLDWNWNDCEESNRSKVEEKEAY-------------------MVNIESDMNQTRVRQHDVQ-------------------------------------------LMKKA    85
G.stearothermophilus ------------------------------------------------------------------------------------MVTIESDK----LRQHDEQ-------------------------------------------LMTKA    20
            B.subtilis ------------------------------------------------------------------------------------------GSHMEI-------------------------------------------LWNEA    11
 B.amyloliquefaciens ------------------------------------------------------------------------------------------MKHTEI-------------------------------------------LWDEA    11
      B.licheniformis ------------------------------------------------------------------------------------------MESHEE-------------------------------------------LWREA    11
         B.halodurans ------------------------------------------------------------------------------------------MEEKER-------------------------------------------LQLEA    11
             B.cereus ------------------------------------------------------------------------------------------MSKTKQ-------------------------------------------LIEEA    11
   B.weihenstephanensis ------------------------------------------------------------------------------------------MSKTKQ-------------------------------------------LIEEA    11
            B.anthracis ------------------------------------------------------------------------------------------MSKTKQ-------------------------------------------LIEEA    11
       B.thuringiensis ------------------------------------------------------------------------------------------MSKTKQ-------------------------------------------LIEEA    11
           O.iheyensis ------------------------------------------------------------------------------------------MTIEK--------------------------------------------VSQEA    10
           E.sibiricum ------------------------------------------------------------------------------------------MST----------------------------------------------LLTEA     8
        S.officinalis ------------------MLHLKNSEP-------------VACSPNGCKGSVIYS-----------------------RLK--KPRAESRPKEE-----------------------------------------------VLIQA    43
        A.californica SPKRFAKVKNWVDEKTYVDTLHQKAISN-------------VPCNSDRCMGSLMSM-----------------------QAH--RPPGAPRTTDE-----------------------------------------------LLIHA   277
             D.rerio QCPFSKQLKNYQDSSCHQDVLHHRAVKS-------------HICSSKICEGSIMTP-----------------------KSLTRCPMTTLHCSDD-----------------------------------------------ILVQA    90
            C.auratus QCPFSKKVKNFQDGSCHQDTLHHGAAKS-------------QICMSNVCEGSIMTP-----------------------KAMTCCPSSTLPSSDD-----------------------------------------------ILMQA   140
             G.gallus RCPRHVKVRNMENGSSLLDTLHLTAKEV-------------INCRTRACQGALMTP-----------------------KGLVRSTRDGPVPPAE-----------------------------------------------LLPQA   140
         C.familiaris KCPRFLKVKNWETDVVLTDTLHLKSTLE-------------TGCTEHICMGSIMLP-----------------------SQQIRRP-EDVRTKEQ-----------------------------------------------LFPLA   360
            B.taurus KCPRFLKVKNWETDVVLSDTLHLKSTLG-------------TGCTEHICMGSIMLP-----------------------SQQIRKP-EDVRTKEQ-----------------------------------------------LFPLA   363
             S.scrofa --PKFPRVKNWEVGSITYDTLCAQSQQD-------------GPCTPRRCLGSLVFP-----------------------RKLQSRPSQGPPPTEQ-----------------------------------------------LLSQA   129
            H.sapiens --PKFPRVKNWEVGSITYDTLSAQAQQD-------------GPCTPRRCLGSLVFP-----------------------RKLQGRPSPGPPAPEQ-----------------------------------------------LLSQA   127
           M.musculus --PRFPRVKNWEVGSITYDTLSAQAQQD-------------GPCTSRRCLGSLVFP-----------------------RKLQSRPTQGPSPTEQ-----------------------------------------------LLGQA   126
          R.norvegicus --PKFPRVKNWEVGSITYDTLSAQAQQD-------------GPCTPRRCLGSLVFP-----------------------RKLQSRPTQGPSPTEQ-----------------------------------------------LLGQA   126
        D.melanogaster LMRKPMRLKNIEGRPEVYDTLHCKGREI-------------LSCSKATCTSSIMNI-----------------------GNA----AVEARKSDL-----------------------------------------------ILEHA   271
           A.mellifera CQKKPTKLRNLIYKTEAFDSLHAGNAEK-------------TLCSGQVCLGSVMQL-----------------------PIH----GTEPRSKEE-----------------------------------------------ILLHA    69
              B.mori KVPQPIRLKNHVAHDENFDTLHSRINEVTHF---------MTKCSEKVCQTSIMDI-----------------------PGR----GDTPRTAEE-----------------------------------------------VFKDA   124
      P.polycephalum ---MLTNNQKYTIPETVAQRAHSQETQVAT-----------TDCRERFCTAARMD-----------------------------------MDYVITDITNP-----------------------------------------EIVLREA    59
             O.tauri PVSRCPFAHGTVTVDPYPGYVHGKNPRVCP---------------RGCVPRPP-----------------------------------------SKPTESAES-----------------------------------------ALRREA    69
               ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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                 .         *         :  .  :     *:  ..: ***:  :*:.*  *  : : * *     .         *:  .  .  :   :::              : . ::: *.          .*.   ..
S.erythraea      EDFLRLFHAENRD--SGSLQYRIDRMRYEVETVGTYRHTEAELAFGARVAWRNSARCIGRLYWKSLKVRDLRDVHTVADIAGHCVQHLRQATNGGKIRPVISIFPPDTPSR-PAPRIWNEQLIRYAGYERRDGSVLGDPRYRGFTAAVRS   188
S.avermitilis    TAFLTLHHTEER---LGDPARRIAAAHAEIAETGTYRHTTEELVFGARVAWRNANRCIGRLYWHSLCVRDRRDVRDAKDVAEASADHLREATRDGRIRALITVFAPDAPGR-PGPRIWNEQLIRYAGYARPGGAVTGDPRNAGLTALARR   299
S.scabiei        EEFLRQFHAEQSDQ-PVPLARRLEQVRAAIDATGTYRHTTAELVFGARVAWRNSSRCIGRLYWNSLRVLDRRDATAPDEIHRHLCTHLRQATNGGRIRPVISVFAPDSPGR-PGPQVWNEQLIRYAGYRRDDGTVLGDPRTADLTEAILR   198
S.turgidiscabies EEFLRQFHAEQSDQ-AVPLTRRLDQVRAAIDATGTYRHTTAELVFGARVAWRNSSRCIGRLYWNSLRVLDRRDTTAPEVIHRHLCTHLRQATNGGRIRPVISVFAPDAPSR-PGPRVWNEQLVRYAGHRRDDGTVLGDPRSADLTEAIRG   198
D.radiodurans    RAFLRRFHEEMG---EPGLPARLR----AVEEAGLWWPTSAELTWGAKVAWRNSTRCVGRLYWEALSVRDLRELNTAQAVYEALLQHLDDAFCGGHIRPVISVFG-------PGVRLHNPQLIRYA----------DDPINADFVDKLRR   139
D.geothermalis   EQFLTLYHEESG---LPGLTARLVEVWDEVGRTGSYTLTSSELTYGARVAWRNSTRCVGRLPWRSLEVRDLRHVTRPDDVFTHLLTHLRAALNGGRIRPIISIFG-------PDVRIHNDQLLRYAGYRQPGGGVVGDPQNVPLTEHLRR   159
Rhodococcus      MRECAEFFSEPEL--AHLPTARLADALESIAETGRYEHTVEELEVGSQLAWRNHARCVGRKHWRTLKLIDARHVTTADEIAEACWEHLRVATNGGALRSVITVGPLPLADG-REYKIVSPQLIRYAGYRNADGTVTGDPAQVGITEAVTK   167
S.arenicola      IEFISAYYKERK---LSDVANRIAGVLDEIATTGTYWQTSAELAYGARAAWRQSARCIGRARWSGLQVRDRRAVTTINGIDSELAEHLRVADNGGRIRSVITVFAPDHPQTGPRARIWNDQLIRYCG-WQLDDEVLGDPAQQGMTEAALQ   181
B.clausii        VEFLSLFYEERCL---DGKEARVRDVCEAIRTGGTYEHTAEELAFGARLAWRNSNRCIGRLFWERLTVIDEREARTEEAVAQALFRHIEYATNGGKVIPTITVFKQG-----ASIRIWNAQLVRYAG-YRGDGRIIGDPASLELTDICKQ   150
N.pharaonis      KSFIEQCYTELGR--ESEIDDRLAEIEAEIERRNHYEHTPEELEHGAKMAWRNSNRCIGRLFWQQLNVADERDCETAEAVHEACCRHLEKARNGGDIKPLITVFKPMVDGD-RQVRIWNYELLRYAG-YRTDDGIVGDPDEIELTDYCQS   163
S.epidermidis    RSFIQTMYSELKYN-TNEIENRMKEIEQEINLTGSYTHTYEELSYGAKMAWRNSNRCIGRLFWNSLNVKDARDVCDEKEFIKFIHTHIKEATNGGKIKPVITIFSPEDTPK-----IYNNQLIRYAG-YEN----VGDPSEKKVTRLAEH   145
S.aureus         QAFIENMYKECHYE-TQIINKRLHDIELEIKETGTYTHTEEELIYGAKMAWRNSNRCIGRLFWDSLNVIDARDVTDEASFLSSITYHITQATNEGKLKPVITIYAPKDGPK-----IFNNQLIRYAG-YDN----CGDPAEKEVTRLANH   145
S.haemolyticus   RSFIEMMYRELNYN-PSIFDKRIKEIEKEIEHTGTYTHTLEELSYGAKLAWRNSNRCIGRLFWDSLNVEDARNVDNERDFIDTINHHLEHATNNGKIKPVITIFSPNQAPR-----IYNNQLIRYAG-YEH----AGDPSERKITQLAEH   143
G.kaustophilus   EQFITISYRELGKS-EQEMKRRLNEIRWEVEQTGTYSHTYEELSYGAKMAWRHSNRCIGRLFWQSLYVIDAREAVTVDEVFSYLFHHIEFATNGGKIRPTITIFRP--NGE---VRIWNHQLIRYAG-YETEEGIIGDSSSLTFTRACEQ   228
G.stearothermophilus EQFIIASYRELGKS-EQEIKRRVNEIRWEVEQTGTYRHTYEELSYGAKMAWRHSNRCIGRLFWQSLHVIDAREAVTEEEVFSYLFHHIEVATNGGKIRPTITIFRP--NGE---VRIWNHQLIRYAG-YETEEGIIGDSSSLTFTRACEQ   163
B.subtilis       KAFIAECYQELGK--EEEVKDRLDSIKSEIDRTGSYVHTKEELEHGAKMAWRNSNRCIGRLFWNSLNVIDRRDVRTKEDVRDALFHHIETATNNGKIRPSITIFPPEEKGE-KQVEIWNHQLIRYAG-YESDGERIGDPASRSLTAACEQ   157
B.amyloliquefaciens KDFIDVCYQELGM--ESQINARLHAIKDEIDRTGSYVHTAEELEHGAKMAWRNSNRCIGRLFWQSLNVIDRRGVNTKEEVRDALFEHIEIATNGGKIKPTITIFPEKNGE-KQVEIWNHQLIRYAG-YETEKGRVGDPASYELTAVCEK   157
B.licheniformis  KAFIELCYGELSKS-EEETRMRLHKIDKEIRETGSYTHTLEEIEHGARMAWRNSSRCIGRLFWHSLTVIDQRGVQTEAEVRDALFHHIQLATNGGKIRPFITVFPPEQNGQ-KKVSIWNHQLIRYAG-YETFQGVIGDPASLELTKACEA   158
B.halodurans     ESFLTKCYEELGS--TGELSKRLEEVRKEIDKTGTYVHTTKELAHGARMAWRNSNRCIGRLFWESLHVLDCRHLQTEEEMAEALVDHITYATNDGKILPTISVFRPRHPNK-GDVRIWNQQLIRYAG-YEEGDQVIGDPISTKFTQACER   157
B.cereus         SHFITICYKELNK--EQFIEERMKEIRVEIEKTGTYEHTFEELVHGSRMAWRNSNRCIGRLFWSKMHILDAREVNDEEGVYNALIHHIKYATNDGKVKPTITIFKQYQGEE-NNIRIYNHQLIRYAG-YKTEMGVIGDSHSAVFTDFCQE   157
B.weihenstephanensis SHFITVCYKELNK--EQFIEERIKEIQIEIEKTGTYEHTFEELVHGSRMAWRNSNRCIGRLFWSKMHILDAREVNDEEGVYNALIHHIKYATNDGKVKPTITIFKQYQGEE-NNIRIYNHQLIRYAG-YKTEMGVIGDSHSTAFTDFCQE   157
B.anthracis      SHFITICYKELSK--EHFIEERMKEIQAEIEKTGTYEHTFEELVHGSRMAWRNSNRCIGRLFWSKMHILDAREVNDEEGVYHALIHHIKYATNDGKVKPTITIFKQYQGEE-NNIRIYNHQLIRYAG-YKTEMGVTGDSHSTAFTDFCQE   157
B.thuringiensis  SHFITICYKELSK--EHFIEERMKEIQAEIEKTGTYEHTFEELVHGSRMAWRNSNRCIGRLFWSKMHILDAREVNDEEGVYHALIHHIKYATNDGKVKPTITIFKQYEGEE-NNIRIYNHQLIRYAG-YKTEMGVIGDSHSAAFTDFCQE   157
O.iheyensis      KLFLTQYFNETDKP-YEYLTQRIAQVNSEIDQKGYTQTYDEIVYGAKLAWRNSNRCIGRLFWERIEVADARKADTYEEVFDYLLSHIQLSFNHGRIKPYITIFRPQQEKK-NIIKIWNHQLLRYAG-YQTEEGIIGDSDSIQFTKICEG   157
E.sibiricum      ERFFHDYIEQ-----YPQEAHRLHEVREEILRTGTYTQTLQELTYGAKLAWRNSNRCIGRLFWEQLHVIDARDALTVESIRDTLFHHMEYATNDGRIRSTITIFDP-DRVR-----ILNHQLIRYAG-YDTPDGIIGDSASIAFTQLCES   146
S.officinalis    KAFMDEYYTSIKRLNTPSYHKRWQEVMQSIEKTGLYELNKSELTFGAKTAWRNAPRCIGRIQWSKLQVFDARHIKTARGMFEAICNHIKYGTNKGNLRSAITIFPQRTDGK-HDFRIWNAQIIRYAGYKNPDGSITGDPVSLEFTEICQK   192
A.californica    KDFIDQYFTSIKRNNTPAHHKRWTEIQSSLEAQGNYELTTPELTYGAKLAWRNAPRCIGRIQWSKLQVFDARHILTARGMYEALCNHIKYGSNKGNLRSAITIFPQRKEGR-GDFRVWNAQLIRYAGYKMEDGSIVGDPANVEFTEQCVK   426
D.rerio          VDFINQYYKSVKNSKIEEHLSRVEEVAMEIDATGSYQLTTKELEFGAKQAWRNAPRCIGRIQWANLQLFDARKCQTAEDMFQMLCDHIQFATNGGNLRSAITVFPQRADGQ-HDFRVWNSQLIRYAGYKMIDGTLLGDPASVDFTEICIQ   239
C.auratus        IDFINQYYKSFKNPKVEEHLSRLEEVAKEIEATGSYQLTTKEVEFGAKQAWRNAPRCIGRIQWANLQLFDARKCRTAEDMFQMLCDHIQFATNGGNLRSAITVFPQRTDGQ-HDFRVWNSQLVRYAGYKMTDGTIIGDPASVDFTEICIQ   289
G.gallus         VDFVKQYYSSFKELKIEEHLARLETVTKEIETTGTYHLTKDELIPAAKQAWRNAPRCIGRIQWSNLQVFDARDCKTAKEMFEYICRHIQYATNNGNLRSAITIFPQRTDGK-HDFRVWNSQLIRYAGYQMPDGSVIGDPASVEFTKLCIE   289
C.familiaris     KEFIDQYYSSIKRSGSKAHTERLEEVNKEIETTGTYQLKDTELIYGAKHAWRNASRCVGRIQWSKLQVFDARDCTTAHGMFNYICNHIKYATNKGNLRSAITIFPQRTDGK-HDFRVWNSQLIRYAGYKQPDGSILGDPANVEFTEICTQ   509
B.taurus         KEFIDQYYSSIKRFGSKAHMERLEEVNKEIETTSTYQLKDTELIYGAKHAWRNASRCVGRIQWSKLQVFDARDCTTAHGMFNYICNHIKYATNKGNLRSAITIFPQRTDGK-HDFRVWNSQLIRYAGYKQPDGSILGDPANVEFTEICIQ   512
S.scrofa         RDFINQYYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRENELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCSSAQEMFTYICNHIKYATNRGNLRSAITVFPQRTPGR-GDFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQ   278
H.sapiens        RDFINQYYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCRSAQEMFTYICNHIKYATNRGNLRSAITVFPQRCPGR-GDFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQ   276
M.musculus       RDFINQYYNSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCRTAQEMFTYICNHIKYATNRGNLRSAITVFPQRCPGR-GDFRIWNSQLIRYAGYRQQDGSVRGDPANVEITELCIQ   275
R.norvegicus     RDFINQYYNSIKRSGSQAHEQRLQEVEAEVVATGTYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCRTAQEMFTYICNHIKYATNRGNLRSAITVFPQRYAGR-GDFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQ   275
D.melanogaster   KDFLEQYFTSIKRTSSTAHETRWKQVRQSIETTGHYQLTETELIYGAKLAWRNSSRCIGRIQWSKLQVFDCRYVTTTSGMFEAICNHIKYATNKGNLRSAISIFPQRTDAK-HDYRIWNNQLISYAGYKQADGKIIGDPMNVEFTEVCTK   420
A.mellifera      KDFLEQYFSSIRRLNSEAHRIRWESVQKEVTVTGTYQLTETELVFGAKLAWRNATRCIGRIQWSKLQVFDCRYVTTTSGMFEALCNHIKYSTNKGNIRSAITIFPQRTDGK-HDYRVWNHQLISYAGYKNPDGTIIGDPANIEFTELCMK   218
B.mori           QAFLTQYYASIKRENSEAHKARLDEVKRELKERGTYQLKTSELVFGAKLAWRNATRCIGRIQWKKLQIFDCREVTTASGMFEALCNHIKYATNKGNIRSAITIFPQRTDGK-HDYRIWNPQLINYAGYQEPDGSITGDPARVEFTEICMK   273
P.polycephalum   NEWLAQFYKEKKLP-EEKLAIRMKEVYDEVKKTGTYFQTYEELSYSCKVAWRNAPRCINRIQWSRMEVIDCRKVTTAEEVFEKCLEHLKFATNGGNIITTITVFAQQKAGE-PAPRLWNSQLLRYAGYRQPDGSIIGDPSNVEMTEAAQK   207
O.tauri          EEYIRLFGKEHGWD-DERVEMRVNEVLTSIRETGTYAHTLDEIRHGARVAWRNAPKCINRKYWSTLDVIDARGATTNEDMFEAIKEHLHRGVEADHVPVLMTVFRPQTPGTNDGPRIWNSQLMRYAGHRDASGGVVGDPAEVDFTDVLKK   218
ruler            .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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                 **        :: :*          *      : : *          .*. .* :: : :  **:      *.* ::  *:. *:  *  * :    .  : .      : ::..   . ::  *:    : : :
          S.erythraea -FGWHPPREPG-AFDVLPLVVETAEE-GAHMFALPRDAISEVPLRHPDLRWFGALGLRWHAVPVISNMRLSIGGVSYPAAPFNGWYMGTEIGARNLADPGRYDLLPVVAERLGLDTS-RPDALWKDRALVELTRAVQHSFHEAGVTITDH  334
         S.avermitilis -LGW--PGGPGSPFDVLPLIVQSAGD-RPRWFTLPEDAVLEVALTHPEYPWWRSLGLRWHAVPALAGMCLESGGICYPAAPFNGWYMGTEIGARNLADADRYDLLPHLADRLGLDTR-SDRSLWKDRALVELNRSVLHSFDRAGVTVTDH  444
               S.scabiei -LGWQ--GCPQGPFDVLPLVIDTPDD-KPRFFELPRELVLEVPITHPDVPRLAELGLRWHAVPVISNMRLRIGGMDYPLAPFNGWYMGTEIGARNLVDEDRYNMLPAVAACLQLDTT-SESTLWRDRALVELNVAVLHSFEAAGVRISDH  343
      S.turgidiscabies -LGWQ--GGRQGPFDVLPLVIDAHDD-KPRFFELPREVVLEVPITHPDVPRLAELCLRWHAVPVISNMRLRIGGVDYPLAPFNGWYMGTEIGVRNLVDEARYNLLPAVAACLQLDTT-SESTLWRDRALVELNVAVLHSFAAAGVRISDH  343
         D.radiodurans -FGW--QPR-GERFEVLPLLIEVNG--RAELFSLPPQAVQEVAITHPVCLGIGELGLRWHALPVISDMHLDIGGLHLPCA-FSGWYVQTEIAARDLADVGRYDQLPAVARALGLDTS-RERTLWRDRALVELNVAVLHSFDAAGVKLADH  281
        D.geothermalis -LGW--TGGPGTPWDVLPLAVEGRG--RVRLFSLPEDATCQVPITHPEVPALGGLGLRWFALPVLSRMTLEVGGLSFPAAPFNGWYVQTEIAARNLADEERYNMLPAVARALGLDMR-RDRTLWRDRALVELNVAVLHSFDRAGVRIADH  303
            Rhodococcus -MGWR---GAGTPFDVLPLLISTPDE-PLRWYDVPPDLVLEVEIEHPDYAWFADLGLKWHAVPAVSNMSFSVGGLTYPLAPFSGWYVSTEVGARNLSDQDRYDMLPAIAERLCLDTT-SERTLWRDRALVELNRAVIHSYRQAGVHMVDH  311
            S.arenicola -LGWK-PPDVASRFDLLPWVIETATE-DPTVIDVPRHLVREVALAHPDHAWFADLGLQWHAVPVIANMRLRIGGVNYSCAPFNGHYLADEIGTRNMCDAGRYNQLRTVAAGLGLNTE-NEASLWREHAALLINQAVLHSFRDAGVRISEP  327
              B.clausii -LGWV---GAGGDFDVLPLVISVGA-RPPQLFPIPEHLIKEVALVHPDNEAFARLNLKWYAVPFISNMRLEIGGISYYTAPFNGWYMGTEIGARNLADDFRYNRLPEVAAVLGISME-REASLWRDQALVELNRAVLYSYQEQGVSIVDH  294
            N.pharaonis -RGWE---GDGTDFDILPHVIQMGD-DEPAIFEVPDSAVGEVPLRHPDYEWFEDLGLRWYDVPVVSNMRLELGGIHYTAAPFSGWYVSTEIGARNLADEDRYDMLPTVAERLGLDTD-DNRSLWKDEALVELNRAVLHSYEEAGVTIVDH  307
           S.epidermidis -LGWK---GKGSNFDILPLIYQLPN-DTIKIHELPNDIVKEVSIHHEHYPKLSKLGLKWYAVPIISNMDLKIGGITYPTAPFNGWYMVTEIAVRNFTDTYRYNLLEKVAEAFEFDTL-KNNSFNKDRALVELNHAVYHSFKADGVSIVDH  289
                  S.aureus -LGWK---GKGTNFDVLPLIYQLPN-ESVKFYEYPTSLIKEVPIEHNHYPKLRKLNLKWYAVPIISNMDLKIGGIVYPTAPFNGWYMVTEIGVRNFIDDYRYNLLEKVADAFEFDTL-KNNSFNKDRALVELNYAVYHSFKKEGVSIVDH  289
            S.haemolyticus -LGWK---GKGTDFDVLPLIYQLPN-DSIKWYELPNELIKEVEIEHEHYPKLKDLNLKWYGVPIISNMDLKIGGITYPTAPFNGWYMVTEIAVRNFTDSYRYNLLESIAEAFEFGTL-KNNSFNKDRTLVELNYAVYHSFKSQGVSIVDH  287
           G.kaustophilus -LGWK---GEKTPFDVLPLVIQVGS-QKPVWTPIPKELVLEVPIEHPEFPWFRDLQLKWYAVPIISDMCLEIGGIRYMAAPFNGWYMGTEIGARNFADDYRYNMLPKVASCMGLDTN-SNASLWKDKALVELNIAVLYSYKKAGVSIVDH  372
     G.stearothermophilus -LGWK---GEKTPFDVLPLVIQVGG-QKPVWTPIPKELVLEVPIEHPEFPWFRDLQLKWYAVPIISDMCLEIGGIRYMAAPFNGWYMGTEIGARNFADDYRYNMLPKVASCMGLDTN-SNASLWKDKALVELNIAVLYSYKKAGVSIVDH  307
                B.subtilis -LGWR---GERTDFDLLPLIFRMRGDEQPVWYELPRSLVIEVPITHPDIEAFSDLELKWYGVPIISDMKLEVGGIHYNAAPFNGWYMGTEIGARNLADEKRYDKLKKVASVIGISTN-YNTDLWKDQALVELNKAVLYSYKKQGVSIVDH  302
      B.amyloliquefaciens -LGWR---GKRTDFDILPLLFRMKGDGQPVWYDLPQTLVKEVPITHPDIEEFADLNLRWYGVPIIADMRLEIGGLSYNAAPFNGWYMGTEIGARNLADEKRYDMLKKAAAVMGISAS-LNTDLWKDQVLVELNKAVLYSYKKHGVSIVDH  302
          B.licheniformis -LGWK---GEGTPFDVLPLVFQIDG-RPPVWYELPREIVKEVRIEHPEIEGFKSLGLKWYAVPIIADMKLEVGGIHYNAAPFNGWYMGTEIGARNLADADRYNALEKVAAIMGLDTE-RNTSLWKDKALVELNTAVLHSYKKAGVSIVDH  302
             B.halodurans -LGWS---GERTPFDVLPLVIQDGS-KPPKWFAVPNESVKEVPLRHPEYEWFAGFQLKWYAVPIVSNMRLEIGGIHYPAAPFNGWYMGTEIGARNLADEDRYNILPKMAEYMGLSTG-KDSTLWKDKALVELNVAILYSYKQEGVSIVDH  301
                  B.cereus -LGWQ---GEGTNFDVLPLVFSIDG-KAPIYKEIPKEEVKEVPIEHPEYP-ISSLGAKWYGVPMISDMRLEIGGISYTAAPFNGWYMGTEIGARNLADHDRYNLLPAVAEMMDLDTS-RNGTLWKDKALVELNVAVLHSFKKQGVSIVDH  300
         B.weihenstephanensis -LGWQ---GEGTNFDVLPLVFSING-KAPIYKEIPREEVKEVPIEHPEYP-ISSLGAKWYGVPMISDMRLEIGGISYTAAPFNGWYMGTEIGARNLADHDRYNLLPAVAEMMKLDTS-RNGTLWKDKALIELNVAVLHSFKKQGVSIVDH  300
                B.anthracis -LGWQ---GEGTNFDVLPLVFSIDG-KAPIYKEIPKEEVKEVPIEHPEYP-ISSLGAKWYGVPMISDMRLEIGGISYTAAPFNGWYMGTEIGARNLADHDRYNLLPAVAEMMDLDTS-RNGTLWKDKALIELNVAVLHSFKKQGVSIVDH  300
            B.thuringiensis -LGWQ---GEGTNFDVLPLVFSVDG-KEPVYKEIPKNEVKEVPIEHPEYP-ISSLGVKWYGVPMISDMRLEIGGISYTAAPFNGWYMGTEIGARNLADHDRYNLLPAVAEMMKLDTS-RNGTLWKDKALIELNVAVLHSFKKQGVSIVDH  300
                  O.iheyensis -LGWK---GARTNFDILPLVVQIGD-NHPQWMEIPDDIIPEIPIEHPDYPEIASLNLKWYAIPIISDMRLEIGGLDYIAAPFNGWYMGTEIGARNFADEYRYNMLPKVAEKMNINTK-HESNLWRDRALVELNAAVLYSFKKQGIIITDH  301
                  E.sibiricum -FGWS---GSKTDFDILPLLIELDG--QVSLHPIPDELVLEVTIQHPEQNLFGDRTIKWYAVPMISDMRLEVGGISYPCAPFNGWYMGTEIGARNLADTDRYDLLPLVAKQLGLNTS-RERSLWKDRALVELNYAVLDSFERSGVTIVDH  289
             S.officinalis -LGWK---GKGGMFDVLPLVLQADG-QDPEWFEIPKDLVMEVPIKHPNYPWFEELGLKWFAFPGVSSLLFDCGGLEFTAAPFNGWYMGTEIGARNLCDEFRYNLAKTFGKRMGLDTN-RDSSLWKDRVVVEVNVAILYSFQSMHVTISDH  336
            A.californica -LGWK---PKYGMFDVLPLVLSAAG-SDPEWFEIPPELVLEVNMKHPKHPWFADLGLKWYALPAVSGMLFDCGGLEFPACPFNGWYMGTEIGARDFCDANRYNMMETVATKMGLDTR-KSASLWKDRVLVEVNVAVLYSFQTSGVTIITDH  570
                  D.rerio -LGWT---PKYGLFDVLPLVLQANG-EDPQLFEIPKDLILEVPMEHPQYEWFKDLNLRWYALPAVSNMLLEIGGLEFPACPFNGWYMGTEIGVRNFCDTQRYNVLEHVGRQMSLETQ-NLSSLWKDQALVAINVAVMHSYQKNKVTITDH  383
               C.auratus -LGWT---PNYGQFDVLPLVLQANG-EDPQFFEIPQHLILEVPMEHPQYKWFKDLNLRWYALPAVANMLLEIGGLEFPACPFNGWYLGTEIGVRDFCDTQRYNVLERVGRHMGLETQ-KLSSLWKDQALVAINVAVMHSFQKNKVTITDH  433
                  G.gallus -LGWK---PKYGRFDVVPLILQANG-QDPEIFEYPPEIILEVPMEHPKYEWFKELDLKWYALPAVANMLLEVGGLEFTACPFNGWYMGTEIGVRDFCDVQRYNILKEVGRRMGLESN-KLASLWKDRAVVEINVAVLHSFQKQNVTIMDH  433
             C.familiaris -QGWK---PPRGRFDVLPLLLQANG-NDPELFQIPPELVLEVPIRHPKFEWFKDLGLKWYGLPAVSNMLLEIGGLEFSACPFSGWYMGTEIGVRDYCDNSRYNILEEVAKKMNLDMR-KTSSLWKDQALVEINIAVLYSFQSDKVTIVDH  653
                 B.taurus -QGWK---PPRSRFDVLPLLLQANG-NDPELFQIPPELVLEVPIRHPKFEWFKDLGLKWYGLPAVSNMLLEIGGLEFSACPFSGWYMGTEIGVRDYCDSSRYNILEDVAKKMNLDMR-KTSSLWKDQALVEINIAVLYSFQSDKVTIVDH  656
                 S.scrofa -HGWT---PGNGRFDVLPLLLQAPD-EPPELFALPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTR-TTSSLWKDKAAVEINLAVLHSYQLAKVTIVDH  422
                H.sapiens -HGWT---PGNGRFDVLPLLLQAPD-EPPELFLLPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTR-TTSSLWKDKAAVEINVAVLHSYQLAKVTIVDH  420
              M.musculus -HGWT---PGNGRFDVLPLLLQAPD-EPPELFTLPPEMVLEVPLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSSEIGMRDLCDPHRYNILEDVAVCMDLDTR-TTSSLWKDKAAVEINVAVLYSYQLAKVTIVDH  419
             R.norvegicus -HGWT---PGNGRFDVLPLLLQAPD-EPPELFTLPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSSEIGMRDLCDPHRYNILEDVAVCMDLDTR-TTSSLWKDKAAVEINVAVLYSYQLAKVTIVDH  419
            D.melanogaster -LGWK---SKGSEWDILPLVVSANG-HDPDYFDYPPELILEVPLTHPKFEWFSDLGLRWYALPAVSSMLFDVGGIQFTATTFSGWYMSTEIGSRNLCDTNRRNMLETVALKMQLDTR-TPTSLWKDKAVVEMNIAVLHSYQSRNVTIVDH  564
               A.mellifera -LGWK---SARTRFDILPLILSANG-HDPDYFDIPNELVLEVPLSHPTYDWFEKLELKWFAVPAVSGMVFDCGGLEFTAAPFNGWYMSTEIGSRDLCDVQRYNLLETIATHMGLDTR-TSTSLWKDKAMIEANVAVLHSFQMKNVTIVDH  362
                     B.mori -LGWK---APRTPWDILPLVLSADG-KDPEFFELPKEIVMEVQFEHPEYDWFKDMGWKWYALPAVSNMRLACGGLEFTANSFNGWYMGTEIGCRNLCDESRLNIVEAVAKKMGLDTN-SFVSLWKDKALVEVNIAVLHSFHRDNVSIVDH  417
            P.polycephalum -LGWV---GQGTRFDVLPIVVQMPN-EEPKLFPIPKEYVLTVQFSHPKYPWFEEMKLEWFAVPFVSNIGLTSGGVQYTCTPFNGWFMGTELS-RNIGDPQRYNLLPDIATKLGVDPAGPPSSMWQEKANLELNAAILHSFQKSRVSIVDH  351
                   O.tauri HFGWA--PEKTGMFDALPIVVQINPETPPAMFTLPDQCFLEVPIRHPTIRGISQLGLKWYGIPAVSNITMDLGGLHYTAAPFNGWYMVTEIATRNFGDESRYNLLPQIAEAMGLDTS-THDTLWRDHALAAINYAVFDSFKRDRVSIADH  365
                   ruler .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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Figure S1-5

Figure S1-6

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: E:clustalx1.83SequensesNOSfor aln1.ps **Date: Fri Aug 10 15:53:07 2007**

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                 :  .      *         *:  . .          .
S.erythraea      HTESERFLTHVRREEAAGRKCPADWSWIVPPMS-GGQTPVFHRYYDT---EPQLPDPFT-DE----------------------------------------DATRRALHGGPPHFS----------------------------  406
S.avermitilis    HTESLRFLTHLDREERKGRRVGADWSWIVPPIS-GSATPVFHRTYET---VERHPAYVH-HP----------------------------------------EALARARGEIDEILV----------------------------  516
S.scabiei        HEESRRFLAHLAKEERQGRTVSADWSWIVPPLS-GGITPVFHRYYDN---VDQRPNFYP-HQ--------------------------------------------------------------------------------  400
S.turgidiscabies HEESRRFLAHLTKEERQGRTVPADWSWIVPPLS-SGITPVFHRYYDN---ADQRPNFYP-HQ--------------------------------------------------------------------------------  400
D.radiodurans    HTVTAHHVRFEEREARAGREVRGKWSWLVPPLS-PATTPLWSRRYRA---REESPRFVR-AR------------------------------------CPFHTPTVHASTGHAPTG----------------------------  356
D.geothermalis   HAVTRQFVRFEEAEARAGRAVRGRWSWLIPPLS-PATTPVWHRSYVD---GDESPRFVP-QP------------------------------------------PAWEERQAGRCPLHG----------------------------  375
Rhodococcus      HTVAKQFISHVEREESLGRKCPTDWSWINPPMS-AALTPTFHRLYDAPE-MDIRPNFLP-AA------------------------------------------------TASGCPIGGGSL----------------------------  382
S.arenicola      HRESELFMRFCAHEEQAGRPVYGDWSWLNGSVGWAALHAVHHRYYDT---RMPNPNFWPRAR------------------------------------TPLSEPTLREQNAAALQGG----------------------------  405
B.clausii        HTAAKQFQRFIGNETEAGRDVTGDWTWLIPPMS-PAQTDIFHQSFDN---RIVSPNYFHE------------------------------------------KPPYCRKGIKEEY----------------------------  363
N.pharaonis      HTVTDQFEQFEQNEAEADREVTGDRSWLLPPMS-SATTHVFSNDYDD---RIEKPNFFYQ------------------------------------------AAPEPLSERRESLGR----------------------------  378
S.epidermidis    LTAAKQFEMFERNEHQQNRNVTGKWSWLAPPLS-PTLTSNYHHGYDN---TMHHTNFFYK------------------------------------------KEEP--MKCPFH----------------------------  355
S.aureus         LTAAKQFELFERNEAQQGRQVTGKWSWLAPPLS-PTLTSNYHHGYDN---TVKDPNFFYK------------------------------------------KKESNANQCPFHH----------------------------  358
S.haemolyticus   LTASKQFQLFEEKELANNRDVTGKWSWLAPPLS-PTLTSNYHHGYNN---EIKDPNFHYK------------------------------------------KKQS--MKCPFH----------------------------  353
G.kaustophilus   HTAARQFQLFEQQEKAAGRHVTGDWTWLIPPLS-PATTHIFHRTYDN---TTMLPNFFYQ------------------------------------------DRPYEQQRGEEQ----------------------------  440
G.stearothermophilus HTAARQFQLFEQQEKAAGRHVTGDWTWLIPPLS-PATTHIFHRSYDN---TMMLPNFFYQ------------------------------------------DRPYEPQRGEEQ----------------------------  375
B.subtilis       HTAASQFKRFEEQEEEAGRKLTGDWTWLIPPIS-PAATHIFHRSYDN---SIVKPNYFYQ------------------------------------------DKPYE-----------------------------------  363
B.amyloliquefaciens HTAANQFKRFEEQEQDAGRKLTGDWTWLIPPIS-PASTHIFHKSYDN---TIVKPNYYYQ------------------------------------------DKPYQ-----------------------------------  363
B.licheniformis  HTAASQFKRFEEQEAEAGRELAASWTWLIPPLS-PAATHIFHSYYEN---KTLKPNYFYQ------------------------------------------EKPYLNK---------------------------------  365
B.halodurans     HTAAKQFARFEQAEQAANRKVTGRWSWLIPPVS-PATTHIFHHEYED---ETVLPNYFYQ------------------------------------------PAPYESDTF---------------------------------  366
B.cereus         HTAAQQFQQFEKQEAACGRVVTGNWVWLIPPLS-PATTHIYHKPYPN---EILKPNFFHK--------------------------------------------------------------------------------  356
B.weihenstephanensis HTAAQQFQQFEKQEAACGRVVTGNWVWLIPPLS-PATTHIYHKPYPN---EILKPNFFHK--------------------------------------------------------------------------------  356
B.anthracis      HTAAQQFQQFEKQEAACGRVVTGNWVWLIPPLS-PATTHIYHKPYPN---EILKPNFFHK--------------------------------------------------------------------------------  356
B.thuringiensis  HTAAQQFQQFEKQEAACGRVVTGNWVWLIPPLS-PATTHIYHKPYPN---EILKPNFFHK--------------------------------------------------------------------------------  356
O.iheyensis      HTAAKQFEVFEKHEAAKGRDVTGKWTWLIPPVS-PATTHIWHKPYTN---DILTPNFFYQ------------------------------------------DKSYQPLSCPFH-----------------------------  369
E.sibiricum      HTATKQFARFEKNEAACERDVTGEWSWLVPPMS-GAATHVFHKDFDP---TVKRPNFFARSA----------------------------------PAEEPSVPSGCPFHQEVER-----------------------  366
S.officinalis    HTAAESFMKHFENEQRVRGGCPADWVWIVPPIS-GSLTPVYHQEMLN---YFLKPSYEYQVEPWKTHTWKKDREKSKQLGDRPKRKFGFRDIARAVKFSAKLMGKALARRVKCTILLYGTETGKSERYARTLC----EIFRHAFDAKVMCM  478
A.californica    HAASESFIKHMENEHKLRGGCPGDWVWVVPPMS-GSILEVFHQEMLL---YKLKPSYEYQDEAWRTHVWKKDRDKPKSGADKPKRKFGFKELARAVKFSAKLMGKALARRVKCTILFATETGKSERLANTLC----EIFKHAFGAKVMCM  712
D.rerio          HSASESFMQHMEMEVRLRGGCPADWVWLVPPMS-GSLTPVFHQEMLN---YILSPFFYYQPEAWLTHKWKDMKRKA------RRCTISFKGLIRVVLFSQALIKLAMAKRVCCTVLYATETGKSQTFAKKLN----GIMNCCFSSRVVCM  519
C.auratus        HSASESFMQHMEMEVRLRGGCPADWVWLVPPMS-GSLTPVFHQEMLN---YILSPFFYYQPDPWLTHKWKDKKRME------RRHAISFKGLIRVVLFSQTLIKSALAKRVRCTVLYATETGKSQTFAKKLN----TMMNCAFSSRVICM  569
G.gallus         HSAAESFMKYMQNEYRVRGGCPADWVWIVPPMS-GSITPVFHQEMLN---YVLTPFFYYQVDAWKTHIWHDETRRP------KKREIKLSILAKAVLLASLLLQKTMAARPKVTVIYATETGKSETLANSLC----SLFSCAFNTKILCM  569
C.familiaris     HSATESFIKHMENEYRCRGGCPADWVWIVPPMS-GSITPVFHQEMLN---YRLTPSFEYQPEPWNTHVWKGTNGTPT-----KRRAIGFKKLAEAVKFSAKLMGQAMAKRVKATILYATETGKSQAYAKTLC----EIFKHAFDAKVMSM  790
B.taurus         HSATESFIKHMENEYRCRGGCPADWVWIVPPMS-GSITPVFHQEMLN---YRLTPSFEYQPDPWNTHVWKGTNGTPT-----KRRAIGFKKLAEAVKFSAKLMGQAMAKRVKATILYATETGKSQAYAKTLC----EIFKHAFDAKVMSM  793
S.scrofa         HAATASFMKHLENEQKARGGCPADWAWIVPPIS-GSLTPVFHQEMVN---YVLSPAFRYQPDPWKGSAAKGTG---------IARKKTFKEVANAVKISASLMGTVMAKRVKATILYASETGRAQSYAQQLG----RLFRKAFDPRVLCM  555
H.sapiens        HAATASFMKHLENEQKARGGCPADWAWIVPPIS-GSLTPVFHQEMVN---YFLSPAFRYQPDPWKGSAAKGTG---------ITRKKTFKEVANAVKISASLMGTVMAKRVKATILYGSETGRAQSYAQQLG----RLFRKAFDPRVLCM  553
M.musculus       HAATASFMKHLENEQKARGGCPADWAWIVPPIS-GSLTPVFHQEMVN---YFLSPAFRYQPDPWKGSAAKGAG---------ITRKKTFKEVANAVKVSASLMGTVMAKRVKATILYGSEAGRAQSYAQQLG----RLFRKAFDPRVLCM  552
R.norvegicus     HAATASFMKHLENEQKARGGCPADWAWIVPPIS-GSLTPVFHQEMVN---YFLSPAFRYQPDPWKGSAAKGTG---------ITRKKTFKEVANAVKISASLMGTVMAKRVKATILYGSETGRAQSYAQQLG----RLFRKAFDPRVLCM  552
D.melanogaster   HTASESFMKHFENESKLRNGCPADWIWIVPPLS-GSITPVFHQEMAL---YYLKPSFEYQDPAWRTHVWKKGRGE--SKGKKPRRKFNFKQIARAVKFTSKLFGRALSKRIKATVLYATETGKSEQYAKQLC----ELLGHAFNAQIYCM  704
A.mellifera      HTASESFMKHYENEMRLRNGCPADWLWIVPPIS-GSATPVFHQEMAL---YYLKPSYDAQEPAWKTHVWKKGRDKK-STSKKPRRKFHFKQIARAVKFTSKLFGRALSRRIKATVLFATETGTSQMYAEKLS----ELLGHAFHSQVLSM  503
B.mori           HSASEQFQKHLENENKSRGGCPADWIWIVPPMS-SSLTTVFHQEMAL---YYIRPSYDYQEPPWKTHQWTKSDGT-----KTVHRKFHFKQIARAVKFTSKLFGRALSKRIKATILYATETGKSEHYAKELG----TIFGHAFNAQVHCM  554
P.polycephalum   HTAAAGFMNFWDAEHAAGRAVPGDWVWLVPPCA-GSASPLFHLEMAN---WLQKPAYFPMDFPGRNYKFPKQKRRS--------NVSVKGLARAVLILRKYMTAAYNKRHRVCVLYATETGNSERYAQRLG----KFLSAFAAVTVSNM  484
O.tauri          HTCAEAFADWYVEELKTRGYAPGNWKWIVPPTAS-STSSIYLGLNKMT-EYTLKPALVGGMGLRSLLRRAKDAGF--------LTSDAFSTVSIRVAIAAAKFRRNKLKVKGGIVLYASDGGRSQSRATWLWSFLFQRLPMVRPVNVANP  505
ruler            .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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Figure S1-7

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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         S.erythraea ------------------------------------------------------------------------------------------------------------------------------------ 406
        S.avermitilis ------------------------------------------------------------------------------------------------------------------------------------ 516
            S.scabiei ------------------------------------------------------------------------------------------------------------------------------------ 400
     S.turgidiscabies ------------------------------------------------------------------------------------------------------------------------------------ 400
       D.radiodurans ------------------------------------------------------------------------------------------------------------------------------------ 356
      D.geothermalis ------------------------------------------------------------------------------------------------------------------------------------ 375
         Rhodococcus ------------------------------------------------------------------------------------------------------------------------------------ 382
         S.arenicola ------------------------------------------------------------------------------------------------------------------------------------ 405
           B.clausii ------------------------------------------------------------------------------------------------------------------------------------ 363
         N.pharaonis ------------------------------------------------------------------------------------------------------------------------------------ 378
        S.epidermidis ------------------------------------------------------------------------------------------------------------------------------------ 355
            S.aureus ------------------------------------------------------------------------------------------------------------------------------------ 358
       S.haemolyticus ------------------------------------------------------------------------------------------------------------------------------------ 353
       G.kaustophilus ------------------------------------------------------------------------------------------------------------------------------------ 440
  G.stearothermophilus ------------------------------------------------------------------------------------------------------------------------------------ 375
           B.subtilis ------------------------------------------------------------------------------------------------------------------------------------ 363
   B.amyloliquefaciens ------------------------------------------------------------------------------------------------------------------------------------ 363
      B.licheniformis ------------------------------------------------------------------------------------------------------------------------------------ 365
         B.halodurans ------------------------------------------------------------------------------------------------------------------------------------ 366
             B.cereus ------------------------------------------------------------------------------------------------------------------------------------ 356
   B.weihenstephanensis ------------------------------------------------------------------------------------------------------------------------------------ 356
          B.anthracis ------------------------------------------------------------------------------------------------------------------------------------ 356
      B.thuringiensis ------------------------------------------------------------------------------------------------------------------------------------ 356
          O.iheyensis ------------------------------------------------------------------------------------------------------------------------------------ 369
          E.sibiricum ------------------------------------------------------------------------------------------------------------------------------------ 366
        S.officinalis EDYDIIDLEHEALVLMVTSTFGNGDPPENGWAFADALYEMRHPNGVS---EPEIQKTSYIRMSVSSE----------------TDIT-IKEDIK--EEQTLQMESGPLGNVRYSVFGLGSRAYPNFCAFGHFLDKVCSELGAERISPMVE 606
        A.californica EDYDVISLEHESLVLVVSSTFGNGDPPENGEAFAKSLYEMKPAEEVNGEVSGTTSHSSYVRMSISSE----------------KDGPGGQEDASSINPDELAMVTGPLGNVRFSVFALGSKAYPHYAAFGHYVDKMMGELGAERIFPLGD 846
             D.rerio EDYNVSELEKESLLIVVTSTFGNGDCPGNGESFKKQLLSLKTLRT-------------------------------------------------------------KVRYCVFGLGSRMYPHFCAFAHALDAMFASLGAIRVSSTGE 605
           C.auratus EDYNFSELEKESLLIVVTSTFGNGDCPGNGESFKKQLLSLKNLSN-------------------------------------------------------------KVRYCVFGLGSRMYPQFCAFAHAVDARFAALGAIRVSATGE 655
            G.gallus DEYNISDLEKETLLLVVTSTFGNGDSPNNGKTLKNSLLTLKLLRK-------------------------------------------------------------NIRYAVFGLGSTMYPEFCAFAHAIDQKLSQLGALQLTPVGE 655
       C.familiaris EEYDIVHLEHETLVLVVTSTFGNGDPPENGEKFGCALMEMRHPNS------VHEERKSYKVRFNSVS----------------SYSDSHKSSGDGP-DLRDNFESAGFLANVRFSVFGLGSRAYPHFCAFGHAVDTLLEELGGERILKMRE 918
            B.taurus EEYDIVHLEHETLVLVVTSTFGNGDPPENGEKFGCALMEMRNPNS------VHEERKSYKVRFNSVS----------------SYSDSRKSSGDGP-DLRDNFESTGPLANVRFSVFGLGSRAYPHFCAFGHAVDTLLEELGGERILKMRE 921
            S.scrofa DEYDVVSLEHETLVLVVTSTFGNGDPPENGESFAAALMEMSGPYNGS---PRPEQHRSYKIRFNSVS----------------CSDPLVSSWRRKRKESSNTDSAGALGTLRFCVFGLGSRAYPHFCAFARAVDTRLEELGGERLLQLGQ 686
           H.sapiens DEYDVVSLEHETLVLVVTSTFGNGDPPENGESFAAALMEMSGPYNSS---PRPEQHKSYKIRFNSIS----------------CSDPLVSSWRRKRKESSNTDSAGALGTLRFCVFGLGSRAYPHFCAFARAVDTRLEELGGERLLQLGQ 684
         M.musculus DEYDVVSLEHEALVLVVTSTFGNGDPPENGESFAAALMEMSGPYNSS---PRPEQHKSYKIRFNSVS----------------CSDPLVSSWRRKRKESSNTDSAGALGTLRFCVFGLGSRAYPHFCAFARAVDTRLEELGGERLLQLGQ 683
        R.norvegicus DEYDVVSLEHEALVLVVTSTFGNGDPPENGESFAAALMEMSGPYNSS---PRPEQHKSYKIRFNSVS----------------CSDPLVSSWRRKRKESSNTDSAGALGTLRFCVFGLGSRAYPHFCAFARAVDTRLEELGGERLLQLGQ 683
      D.melanogaster SDYDISSIEHEALLIVVASTFGNGDPPENGELFSQELYAMRVQEESEHGLQDSSIGSSKSFMKASSR-----QEFMKLPLQQVKRIDRWDSLRGSTSDTFTEETFGPLSNVRFAVFALGSSAYPNFCAFGQYVDNILGELGGERLLRVAY 849
         A.mellifera SDYDISNIEHEALLLVITSTFGNGDPPENGEAFAQNLYAMKMNETYINSGNKISLATSKSFIKANSQ-----TEVSNS-----KKLDRLDSLRGSTTDSQTEDNFGPLSNVRFAVFALGSSAYPNFCAFGRYVDNLLGELGGERLLKLAQ 643
             B.mori SEYDMFSIEHETLVLIVASTFGNGEPPANGVDFAEHLFQMLYNETNNNRGDGTSDLGSGTFKTPTPKSLMRSNSMMTPEFEYKRQLTRLESNKSSVAGASSIEQIGPLSNVCFAVFGLGSSAYPKFCHFGKTVDKILGDLGGERILELAC 704
     P.polycephalum ETYDAQKLEKEEVVICVASTFGDGDSPSCASSFKSKLEE-------------------------------------------------------------GNLNLKNVQFSVFGLGSTLYDDFAAFGKFLDSRLAELGAERVNPLAK 570
            O.tauri DVPLTDLLSNVEFILFLASTTGSGQVPTGSDSFIEWTKTEHGR-------------------------------------------------------------TALRGKYFAVCAFGSRAYPKFCAGGEQFAAALAAAGAVAMFPITR 593
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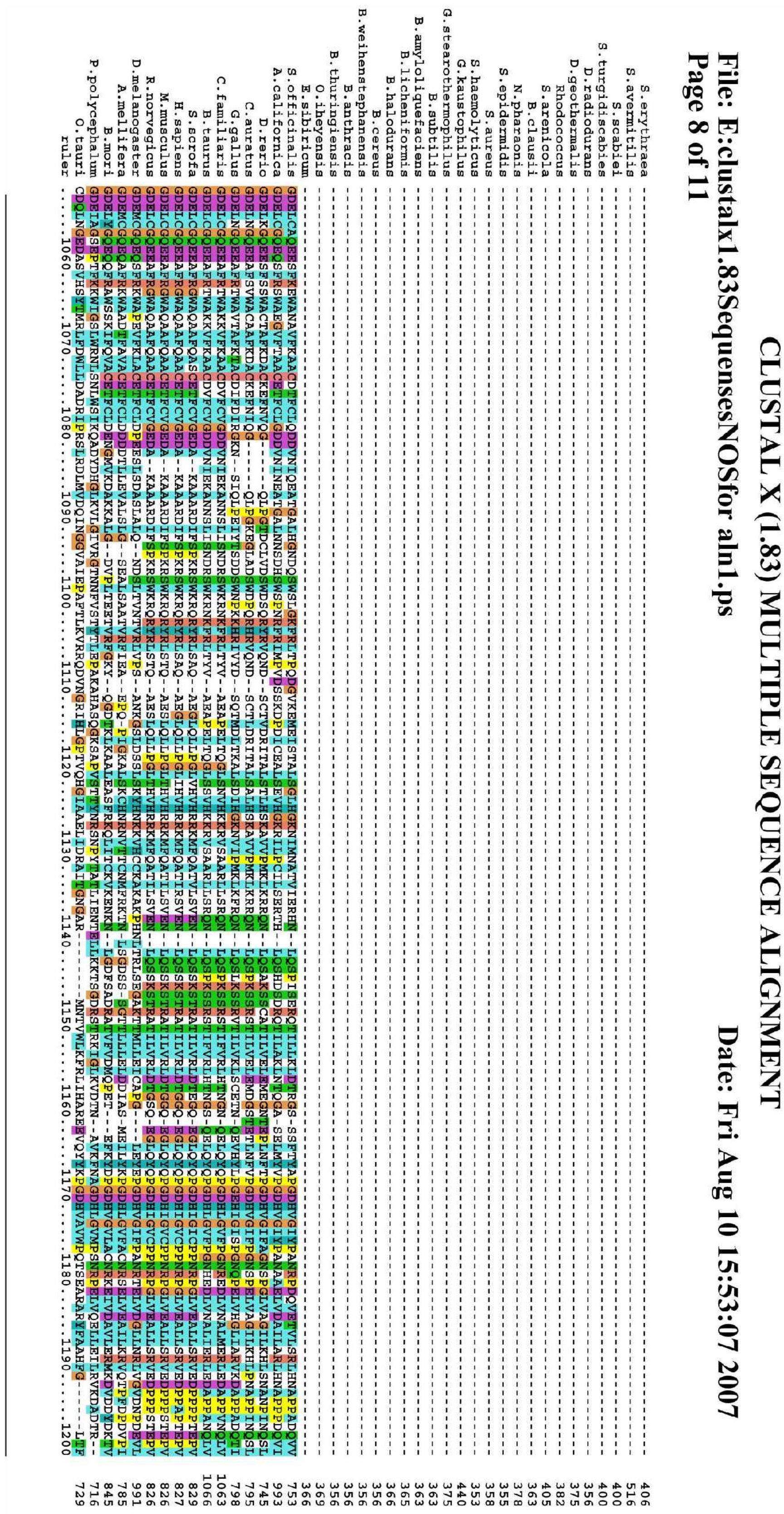
CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT
File: E:clustalx1.83SequensesNOSfor aln1.ps
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Figure S1-8

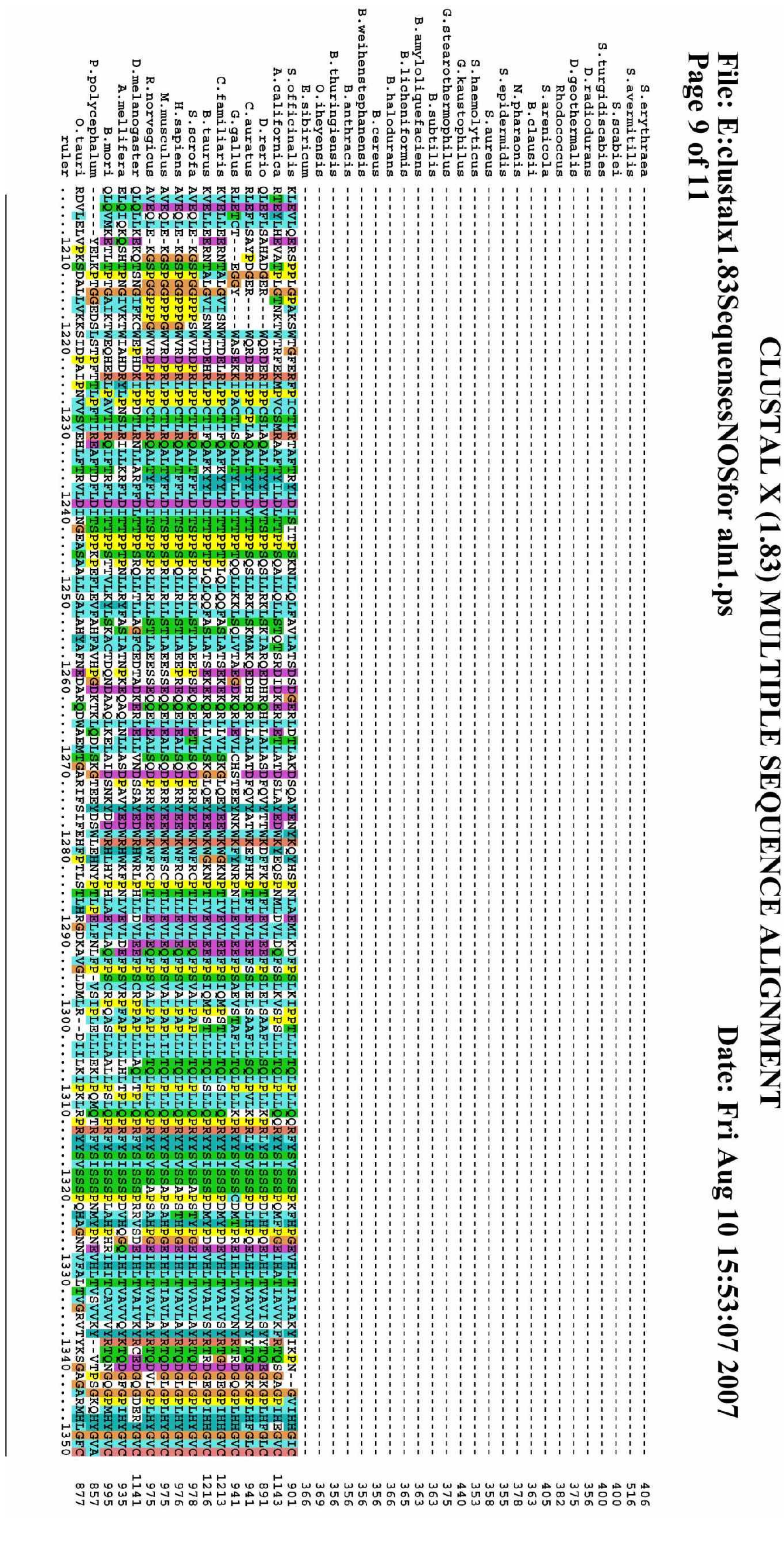
CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT
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Figure S1-9

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: E:clustalx1.83SequensesNOSfor aln1.ps **Date: Fri Aug 10 15:53:07 2007**
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      S.avermitilis ----------------------------------------------------------------------------------------------------------------------------------  516
          S.scabiei ----------------------------------------------------------------------------------------------------------------------------------  400
   S.turgidiscabies ----------------------------------------------------------------------------------------------------------------------------------  400
     D.radiodurans ----------------------------------------------------------------------------------------------------------------------------------  356
    D.geothermalis ----------------------------------------------------------------------------------------------------------------------------------  375
       Rhodococcus ----------------------------------------------------------------------------------------------------------------------------------  382
       S.arenicola ----------------------------------------------------------------------------------------------------------------------------------  405
         B.clausii ----------------------------------------------------------------------------------------------------------------------------------  363
       N.pharaonis ----------------------------------------------------------------------------------------------------------------------------------  378
      S.epidermidis ----------------------------------------------------------------------------------------------------------------------------------  355
          S.aureus ----------------------------------------------------------------------------------------------------------------------------------  358
     S.haemolyticus ----------------------------------------------------------------------------------------------------------------------------------  353
     G.kaustophilus ----------------------------------------------------------------------------------------------------------------------------------  440
G.stearothermophilus ----------------------------------------------------------------------------------------------------------------------------------  375
         B.subtilis ----------------------------------------------------------------------------------------------------------------------------------  363
 B.amyloliquefaciens ----------------------------------------------------------------------------------------------------------------------------------  363
     B.licheniformis ----------------------------------------------------------------------------------------------------------------------------------  365
       B.halodurans ----------------------------------------------------------------------------------------------------------------------------------  366
          B.cereus ----------------------------------------------------------------------------------------------------------------------------------  356
B.weihenstephanensis ----------------------------------------------------------------------------------------------------------------------------------  356
         B.anthracis ----------------------------------------------------------------------------------------------------------------------------------  356
     B.thuringiensis ----------------------------------------------------------------------------------------------------------------------------------  356
        O.iheyensis ----------------------------------------------------------------------------------------------------------------------------------  369
        E.sibiricum ----------------------------------------------------------------------------------------------------------------------------------  366
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CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: E:clustalx1.83SequensesNOSfor aln1.ps **Date: Fri Aug 10 15:53:07 2007**

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          S.scabiei ------------------------------------------------------------------------------------------------  400
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     D.geothermalis ------------------------------------------------------------------------------------------------  375
        Rhodococcus ------------------------------------------------------------------------------------------------  382
        S.arenicola ------------------------------------------------------------------------------------------------  405
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G.stearothermophilus ------------------------------------------------------------------------------------------------  375
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 B.amyloliquefaciens ------------------------------------------------------------------------------------------------  363
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       B.halodurans ------------------------------------------------------------------------------------------------  366
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B.weihenstephanensis ------------------------------------------------------------------------------------------------  356
        B.anthracis ------------------------------------------------------------------------------------------------  356
     B.thuringiensis ------------------------------------------------------------------------------------------------  356
        O.iheyensis ------------------------------------------------------------------------------------------------  369
        E.sibiricum ------------------------------------------------------------------------------------------------  366
      S.officinalis CGDVQMASDVSDTVEMILKEDAPMSSEEAKNYVLKLR-DANRFHEDIFGVTVKRSTPSSVDTSDK-----VHLRSKGRFWKENKILECDEELLKK------ 1139
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           D.rerio CGGVNMACDVAATVKEILVNQMGITVAQAEEYLSRLK-NEKRYHEDIFGY-------------------------------------------------- 1077
         C.auratus CGGMNMAHDVAATIKEILVSRLGITLTQAEEYLSRLK-NEKRYHEDIFGS-------------------------------------------------- 1127
          G.gallus CGDVRMARDVAQTLKRMLVKKLNHTEQQAEEYFFQLK-SQKRYHEDIFGAVFPHEVKRI---------------------------------------- 1136
      C.familiaris CGDVTMAADVLKAIQRIMTQQGKLSVEDAGVFISRLR-DDNRYHEDIFGVTLRTYEVTNRLRSESIAFIEESKK---------DTDEVFSS---------- 1431
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          S.scrofa CGDVTMATSVLQTVQRILATEGNMELDEAGDVIGVLR-DQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERHLRGAVPWAFDPPGPDTPGP---------- 1205
         H.sapiens CGDVTMATNVLQTVQRILATEGDMELDEAGDVIGVLRQDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERQLRGAVPWAFDPPGSDTNSP---------- 1204
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      R.norvegicus CGDVTMATSVLQTVQRILATEGSMELDEAGDVIGVLR-DQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERQLRGAVPWSFDPPTQETPGS---------- 1202
     D.melanogaster CGDVTMAEHVYQTIRKCIAGKEQKSEAEVETFLLTLR-DESRYHEDIFGITLRTAEIHTKSRATAR-IRMASQP-------------------------- 1349
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            B.mori CGDCKMAEEVQQKLKEIMKKHAKMTEQEYEEFILNLM-DENRYHEDIFGITLRTAEVQSASREFAKRTRQESQKSQT------------------------- 1209
     P.polycephalum CGDATMATGVKDAFKQIVQTKMGLSAEASAKYMDELT-KSKRYLTDVFGAALPSKKADAPVPNTISFEVLC---------------------------- 1055
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             ruler ......1510......1520......1530......1540......1550......1560......1570......1580......1590......1600.
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Figure S1-11

Table S1. NO-synthases in bacteria.

Microorganism	position on the chromosome	gene name	orientation	function
Bacillus subtilis	833720..835021	citM	+	secondary transporter of divalent metal ions/citrate complexes
	835077..835871	yflN	+	hypothetical protein
	836071..837081	**yflM**	+	**NO-synthase**
	837072..837347	yflL	-	hypothetical protein
	837414..838079	yflK	+	hypothetical protein
Bacillus licheniformis	794745..795542	-	+	Beta-lactamase-like
	795751..797394	-	+	Hypothetical Peptidase
	797523..798620	**nos**	+	**NO-synthase**
	798708..799346	yvaZ	-	hypothetical protein
	799343..799636	yvbA	-	Winged helix DNA-binding
Geobacillus kaustophilus	1700575..1701009		+	hypothetical protein
	1701097..1703214		+	phage infection protein
	1703349..1704671		+	**NO-synthase**
	1704668..1705450		+	ABC transporter (ATP-binding protein)
	1705486..1706736		-	cytoplasmic trehalase
Bacillus halodurans	892117..892824		-	hypothetical protein
	892979..894298		+	hypothetical protein
	894457..895557		+	**NO-synthase**
	895604..896998		+	glutamate dehydrogenase
	897073..897606		+	hypothetical protein
Bacillus clausii	1386638..1387351	treR	+	GntR family transcriptional repressor of trehalose operon
	1387466..1387951	bsaA	+	glutathione peroxidase
	1388004..1389095		+	**NO-synthase**
	1389108..1390991		+	ABC transporter ATP-binding protein
	1391149..1391913	fruR	+	transcriptional regulator, DeoR family

Bacillus cereus	5161947..5163245		+	major facilitator family transporter
	5163354..5164922		-	osmoprotectant transporter, BCCT family
	5165287..5166357		-	**NO-synthase**
	5166573..5167199	sodA-2	+	superoxide dismutase, Mn
	5167288..5168169		-	hypothetical protein
Bacillus anthracis	5181441..5182742		+	major facilitator family transporter
	5182839..5184407		-	osmoprotectant transporter, BCCT family
	5184770..5185840		-	**NO-synthase**
	5186057..5186683	sodA-2	+	superoxide dismutase, Mn
	5186772..5187650		-	hypothetical protein
Bacillus thuringiensis	5190150..5191448		+	major facilitator family transporter
	5191565..5193133		-	osmoprotectant transporter, BCCT family
	5193496..5194566		-	**NO-synthase**
	5194783..5195409	sodA-2	+	superoxide dismutase, Mn
	5195498..5196379		-	hypothetical protein
Oceanobacillus iheyensis	2759443..2760072		+	hypothetical protein
	2760107..2761528	alsT	+	sodium:alanine symporter
	2762112..2763221		+	**NO-synthase**
	2763272..2764696		+	membrane dipeptidase
	2764965..2765867		-	formyltetrahydrofolate deformylase
Exiguobacterium sp.	2631446..2632303		-	Predicted membrane protein
	2632412..2633587		+	**NO-synthase**
	2633584..2634054		+	NTP pyrophosphohydrolases including oxidative damage repair enzymes (mutT)
	2635041..2635826		-	Histone acetyltransferase HPA2 and related acetyltransferases

Staphylococcus aureus	2096457..2097278		-	putative NAD synthetase
	2097271..2098740		-	hypothetical protein
	2098924..2100000		+	**NO-synthase**
	2100020..2100814		+	putative prephenate dehydratase
	2101004..2102566		-	putative sodium:sulfate symporter
Staphylococcus epidermidis	1651080..1651907		-	NAD synthetase
	1651900..1653369		-	nicotinate phosphoribosyltransferase-like
	1653561..1654628		+	**NO-synthase**
	1654647..1655450		+	chorismate mutase
	1655903..1657000		-	hypothetical protein
Streptomyces avermitilis	1871275..1872198		+	hypothetical protein
	1872321..1873361		-	putative secreted protein
	1873463..1875280		-	**NO-synthase**
	1875451..1877058		-	putative membrane protein
	1877224..1877448		+	hypothetical protein
Deinococcus radiodurans	2601909..2602919		-	oxidoreductase, short-chain dehydrogenase/reductase family
	2602976..2603917		-	hypothetical, metalloprotease, membrane
	2603979..2605049		-	**NO-synthase**
	2605096..2605551		-	hypothetical protein
	2605719..2607164		+	hypothetical protein

Table S1. NO-synthases in bacteria. Protein sequence of *B. subtilis nos* (*yflM*) gene was aligned with all bacterial genomes using the NCBI BLAST program. Bacteria that have proteins with greater than 60% homology to *B. subtilis* NOS are presented in the table. Also shown are two adjacent genes upstream and downstream of each *nos* homolog.