Supplemental data

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                  20                 30        40                               50                    60
                  |                  |         |                                |                     |
NP_288269.1      MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002403065.1   MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002397981.1   MNK---------AEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002412850.1   MNK---------IEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_001880631.1   MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002391608.1   MNK---------AEFYADLNRDFNALMVGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_001730808.1   MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------INWA
ZP_03003290.1    MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_001743413.1   MNK---------AEFYADFNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002407226.1   MNK---------AEFYSDFNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002329476.1   MNK---------AGFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_002382399.1   MNK---------TEFYADLNRDFRALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
ZP_03445135.1    MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_688895.1      MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
YP_669680.1      MNK---------AEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------VNWA
NP_416346.4      MNK---------TEFYADLNRDFNALMAGETS-----------------------FLATLANTSALLYERLTD------------INWA
ZP_02903917.1    MNK---------TEFYADLNRDFNALMTGETS-----------------------FLATLANTSALLYERLAD------------VNWA
ZP_03282954.1    MNK---------SEFYADLNRDFQALMAGETS-----------------------FLATLANTSALLFERLSG------------VNWA
YP_001452718.1   MSK---------TELYADLNRDFQAVMAGETS-----------------------FLATLANTSALLFERLSG------------VNWA
YP_001570142.1   MSE---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
NP_460803.1      MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_150310.1      MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002141797.1   MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002243298.1   MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
NP_456352.1      MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
NP_804849.1      MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_001587603.1   MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02666379.2    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02832604.2    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_001177122.1   MNK---------TEFYADLNRDFQALMTGETS-----------------------FLATLANTSALLFERLSD------------VNWA
YP_002226291.1   MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
NP_754135.1      --------------------------MAGETS-----------------------FLXTLANTSALLYERLTD------------VNWA
ZP_02347214.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02574893.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02659310.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02663512.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02681881.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_02696584.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002041101.1   MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002045892.1   MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
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Supplemental data

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ZP_03075263.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002114879.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002146178.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03165709.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002215294.1    MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03221812.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03342093.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03347154.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03352578.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03357060.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03371453.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03379701.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03383790.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03412299.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
ZP_03217260.1     MSK---------TELYAALNRDFQSLMAGETS-----------------------FLATLANTSALLFERLTE------------VNWA
YP_002237781.1    MSK---------TEFYADLNRDFQALMAGETS-----------------------FLAMIANTSALLFERLSE------------VNWA
YP_001336004.1    MSK---------TEFYADLNRDFQALMAGETS-----------------------FLAMIANTSALLFERLSE------------VNWA
YP_001437512.1    MNK---------TQFYAELNRDFHSLMAGETS-----------------------FLATLANTSALLFERLEG------------VNWA
ZP_03403067.1     --------------------------------------------------------MATLANTSALLFERLTE------------VNWA
YP_001907453.1    MTK---------AEFYTDLNRDMNALLSGETS-----------------------FLAVMSNCSALLYKRLDG------------VNWA
YP_001006127.1    MKK---------AEFYAELKRDLSALIAGETN-----------------------FIATLANASALIYERLDG------------LNWA
NP_669181.1       MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
NP_993079.1       MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_070893.1       MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_651729.1       MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_647856.1       MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_001163103.1    MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_01888376.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_001400647.1    MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_001607069.1    MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02221459.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02227087.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02229339.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02237158.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02307206.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02314388.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
ZP_02318544.1     MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_001720525.1    MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_001872871.1    MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_002346706.1    MKK---------TEFYAELKRDLCALVAGETN-----------------------FIATLANASALLYERLDG------------LNWA
YP_001478346.1    MTK---------EQFYAELKRDLCALLDGETN-----------------------FIAALSNASALINERLDD------------VNWV
YP_454994.1       MKK---------QQFYAELLQDMSALLDEETH-----------------------FIAALANASALLYERLEG------------VNWA
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Supplemental data

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YP_001217052.1    EVFIFQMEVIMNLEQYQRLTKQAVALLEGETN-----------------------LIANLANLSALLNMELTE------------LNWV
YP_002150764.1    MPQ---------LNFYQELTDNLSALLSGEND-----------------------FIASLANTSALIYEKLDK------------INWV
YP_856816.1       IEK---------QAFYRTLNQQAQALLEGEPD-----------------------LIANLANLSALLNQELAD------------INWV
YP_001093925.1    MST----------PCYTTLTRQVEALFSGEDN-----------------------LVTAMANFSALLNEHLDD------------INWV
YP_269525.1       MSN--------QAEFYHELLGQTKALINDESD-----------------------IIANMANISALLFERLAD------------VNWV
NP_718189.1       MKP----------QFYESLNRQVLALLEGEDD-----------------------LVAAMANFSALLNDNLTE------------LNWV
YP_001366642.1    MKS----------KFYESLNRQALALLEGEDD-----------------------LVAAMANFSALLNDNLTE------------LNWV
YP_001554990.1    MKS----------KFYESLNRQALALLEGEDD-----------------------LVAAMANFSALLNDNLTE------------LNWV
YP_737796.1       MKP----------QFYESLNRQALALLEGEDD-----------------------LVAAMANFSALLNDNLTE------------LNWV
YP_869415.1       MKP----------QFYESLNRQALALLEGEDD-----------------------LVAAMANFSALLNDNLTE------------LNWV
NP_797987.1       ----------MNIEQYQRLTKQAVALIESEPD-----------------------FIANLANLSSLLFMELED------------LNWA
YP_001501790.1    MVN----------AFYDTLNRQVLALLDGEDD-----------------------TIAALANFSALLNDNLTD------------LNWV
YP_927460.1       MKH----------AFYDTLNRQAEALLSGEDD-----------------------LVAAMANFSALLNEHMDD------------LNWV
YP_001474222.1    MIT----------EFYSSLDRQAKALLDGEDD-----------------------LIAAMANFSALINDALDD------------LNWV
YP_963195.1       MKS----------QFYESLNRQALALLEGEDD-----------------------VVAAMANFSALLNDNLTD------------LNWV
YP_001183724.1    MKS----------QFYESLNRQALALLEGEDD-----------------------VVAAMANFSALLNDNLTD------------LNWV
YP_733804.1       MKP----------QFYESLNRQALALLEGEDD-----------------------LVAAMANFSAFLNDNLTE------------LNWV
YP_001050811.1    MKS----------KFYESLNRQALALLEGEDD-----------------------LVAAMANFSTLLNDNLTE------------LNWV
YP_750914.1       MKT----------EFYQTLNRQAQALLEGEDD-----------------------LIAAMANFSALLNDSLED------------LNWA
YP_002126297.1    MK----------EPQYSQLINQAKSLVSGEHD-----------------------LIANMANISALLFNHLEE------------VNWA
YP_130129.1       ----------------------------DEPD-----------------------LIANISNISALLNMELED------------INWV
YP_001445537.1    ----------MNIEQYQRLTKQAVALIESEKD-----------------------YIANLSNISALLFMELEN------------LNWA
YP_661562.1       MTLS-------KTDLYQEVAQQAQALMAGEKD-----------------------LIANLANLSALMYMRLPE------------LNWA
YP_001674584.1    MVD----------AFYDTLNRQVQALFADEDD-----------------------TIAALANFSALINDSLDD------------LNWV
YP_002417027.1    ----------MKIEHYQRLTKQAVALIESEPD-----------------------LTANLANISSLLFMELDE------------LNWA
NP_934438.1       ----------MTIEHYQTLTKQAVALIESERD-----------------------LIANLSNISALLNMGMSD------------LNWV
NP_761466.1       ----------MTIEHYQTLTKQAVALIESERD-----------------------LIANLSNISALLNMGMSD------------LNWV
YP_001760510.1    MDL----------ECYDSLNRQAQALLSGEDD-----------------------LVAAMANFSALINDAVEQ------------LNWV
YP_002312133.1    MTA----------SFYDTLNRQVIALLSGEDD-----------------------QIAALANFSALLNDNLTD------------LNWV
YP_562727.1       MKA----------DFYDTLDRQASALLAGEDD-----------------------VIAAMANFSALLNESLED------------LNWV
NP_693123.1       MFEQKNYSG-EKAKDYELLIKQLDALSEGENN-----------------------KIALLSNASALLNQFLTE------------VNWV
YP_001699747.1    MFTQINYEG-SIADQYLTLSKQLDALLTGEKD-----------------------QIANLSNASALLHQFLTN------------INWV
YP_001343242.1    TIETHS--TGSSEEFYQELNIQLAALLSGERD-----------------------FICNAAQFSAFVMQTVTD------------LNWS
YP_001141806.1    IEK---------QAFYRGLNQQAQALLEGEPD-----------------------LIANLANLSALLALELTD------------INWV
YP_204661.1       ----------MELKHYARLTQQALGLIEGETD-----------------------YIANLANISALLNMELDD------------INWV
YP_301135.1       MTEVK-------ETNYNLLEKQVSSLIEDESN-----------------------LIAILSNVSALLNDSIDQ------------INWV
YP_002156075.1    ----------MELKHYARLTQQALGLIEGETD-----------------------YIANLANISALLNMELDD------------INWV
NP_244074.1       MFQPESYQG-TLEEKYSLVTKQLAALLEGESD-----------------------AIANLANASALLYHFLEE------------VNWV
YP_001559126.1    MDQIDSMYPENKVEMYELLLVQLKAMLEGEQD-----------------------VIANLSNVSALLNQALKD------------INWV
YP_080250.1       VEKTEG----SKEKKYELLLKQIDALTEGEPD-----------------------MIANTANASALLYQSLED------------VNWA
YP_253122.1       MPLIK-------ETNYNLLTKQLQSLIEDEQN-----------------------LIAILSNTSAILNDNLDQ------------INWV
YP_261333.1       MIDLQS--AGQGLDGYGLLCAQLESLLADERD-----------------------FIANAAQFSAFLYSQLED------------LNWA
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Supplemental data

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YP_001187407.1    MIDLSQ--TGAGMDGYPLLAAQLEALLAGERD-----------------------FIANAAQFSAFLFHELAD------------LNWA
YP_001422246.1    VEKQSG----DKEKSYQLLLKQLEAMTEDETD-----------------------AIANYANASALLYHSLHE------------VNWA
YP_001748360.1    MIDLNA--SGAGLDGYDLLAAQVQALFADERD-----------------------FIANAAQFSAFLYNQVDD------------LNWA
YP_155660.1       ----------MSSQLYSDLLAQSRALTEGEPD-----------------------LIANLANISALLYEHIED------------INWL
NP_744032.1       MIDLNA--SGAGLDGYNLLAAQVQALFADERD-----------------------FIANAAQFSAFLYNQVDD------------LNWA
YP_001269146.1    MIDLNA--SGAGLDGYNLLAAQVQALFADERD-----------------------FIANAAQFSAFLYNQVDD------------LNWA
YP_236680.1       MIDLQN--TGAGLDGYGLLAAQLEALLADERD-----------------------FIANAAQFSAFLYTQLDD------------LNWA
YP_001667695.1    MIDINA--SGAGLDGYNLLAAQVQALFADERD-----------------------FIANAAQFSAFLFNQVDD------------LNWA
YP_188854.1       MTKNI-------PTNYKLISKQLASLIEDEKN-----------------------LIAILSNTSALLNDTIDQ------------INWV
YP_002275225.1    ----MTTLPADHRVTLEDLLSTVESVLTG-------ERD----------------LIANMANISALLFEALPD------------INWA
YP_804779.1       MSE----------PINSIIVEQIDALLFNETN-----------------------LIANLSNASALLYSETKD------------VNWC
NP_470973.1       MIEIQKMTG-TKEENYALALKQVQAMIAGEPN-----------------------LIANLSNVSSILNQALSD------------INWV
YP_607257.1       MIDLNA--SGQGLDGYDLLAAQVQALFADERD-----------------------FIANAAQFSAFLYNQVDD------------LNWA
YP_001860169.1    MFEATINTALPKAEFYRELTSQARSLLEGESN-----------------------QIANAANLSALIFHSLPQ------------VNWA
NP_465120.1       MIEIKKMTG-TKEENYALALKQVQAMIHGEPN-----------------------LIANLSNVSSIINQALSD------------INWV
NP_372242.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLNQ------------INWV
NP_374828.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLNQ------------INWV
YP_001247140.1    MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLNQ------------INWV
YP_001316940.1    MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLNQ------------INWV
YP_001442294.1    MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLNQ------------INWV
YP_002314836.1    MFHTQTYTG-TREENYTLVIEQLKALISDEKS-----------------------VVANLANASALLNYFLHD------------INWV
YP_001814701.1    MFETTTYDG-DRTKQYEMLNKQLDALLTGETN-----------------------QIANLSNASALLGQFLDR------------TNWV
NP_646478.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_043764.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_186602.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_494359.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_500333.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_001332646.1    MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_001575592.1    MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
ZP_02759966.1     MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_001487827.1    VEKQAG----DPSKDYQLLVKQVEAITDGEPD-----------------------LIANLANAAALLYHSLPE------------VNWA
YP_417047.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSAILNDNLDQ------------VNWV
YP_041183.1       MTTIN-------PTNYTLLKKQAASLIEDEHH-----------------------MIAILSNMSALLNDNLDQ------------INWV
YP_176251.1       MFSKLDYPT-EQEAAYRLLEQQAVALLEDEPD-----------------------ALANYANLCALLGQFLDD------------INWV
YP_002349929.1    MIEIQKMTG-SKEENYGLALKQVQAMIHCEPN-----------------------LIANLSNVSSILNQALSD------------INWV
YP_001376537.1    MFTKESYVG-SREKQYETVIKQLDALLTGESN-----------------------TVANLANASALLNQFLER------------INWV
YP_784647.1       MFQASTLSTDFKPQFYQELAAQARALLDGEHD-----------------------RIANAANFAALIWQSVPD------------INWS
YP_557760.1       MFEVSTASHLPKAAHYEELVAQARSLLAGETD-----------------------WIANAANFSAFVFHSLSD------------LNWA
YP_275769.1       MIDLQN--TGAGLNGYGLLAAQLEALLADERD-----------------------SIANAAQFSAFLYTQIDD------------LNWA
YP_001118914.1    MFTLSTDPHASKAELYATLAEQARSLVESEPD-----------------------LIANAANFSALVYHSLDR------------LNWA
YP_001782545.1    MFALEDFKGLTEEQKYENMLLFLKGQLLGEKD-----------------------VIANLSNASAIIMALIDN------------LNWA
NP_882192.1       MFDATPISTVSKPVFYAELAAQARALLAGEHD-----------------------RIANAANFSALVYQALPD------------INWA
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YP_001894915.1    MFEVSSASHLPKAAHYEELVAQARSLLAGETD-----------------------WIANAANFSAFVFHSLSD------------LNWA
YP_001647268.1    MFTKESYAG-SREEQYKTVIKQLDALLTGEPN-----------------------VVANLSNASALLNQFLDR------------VNWV
NP_882465.1       MFDATPISTVSKPVFYAELAAQARALLAGEHD-----------------------RIANAANFSALVYQALPD------------INWA
YP_002448219.1    MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
NP_834359.1       MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_002369448.1    MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_191278.1       ----MS--APIHRLSVDELVPMVRSVLQT-------ETD----------------MIANMANIAALLFETLPQ------------INWA
NP_886654.1       MFDATPISTVSKPVFYAELAAQARALLAGEHD-----------------------RIANAANFSALVYQALPD------------INWA
NP_847103.1       MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------IVANLSNASALLNQFLDR------------VNWV
YP_030799.1       MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------IVANLSNASALLNQFLDR------------VNWV
NP_981083.1       MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_038702.1       MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_002340711.1    MFTKESYTG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_085975.1       MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_002453717.1    MFTKESYAG-SRVQQYETVIKQLDALLTGESN-----------------------VVANLSNASALLNQFLDR------------VNWV
YP_772921.1       MFTLSNDPHASKAELYATLVEQARALVESERD-----------------------LIANAANFSALVYHSLDR------------LNWA
YP_001843726.1    KMMSK-------QADYQLLYQQALALFEGETD-----------------------WIANASNLAALLYNGLAD------------VNFA
YP_942902.1       ----------MTFKDYKLLSQQAVALIADETD-----------------------LTANLANLSALLNMNLDN------------INWV
YP_121651.1       SFTVAE-PTGDRVEDYRRLVAQAAALIEGEPD-----------------------RVANAANLSALIYHSLPE------------VNWA
YP_001633478.1    MFTATDLPTDDKPRFYAELAAQARALLDGETD-----------------------RIANAANFAALAYQALPR------------INWA
YP_001392189.1    MFALEDFKGLTEEQKYENMLLFLKGQLLGEKD-----------------------VIANLSNASAIIMALIDN------------LNWA
YP_795394.1       MSE----------SLNPIITKQLDALLYGETN-----------------------LVANLSNAAALLNQTLSD------------INWA
YP_002284153.1    MYATKNIEQGDKRSFYRELADQLQGLLQDERD-----------------------AVANAANLSALVFELVAD------------LNWA
YP_001255404.1    MFALEDFKELTEEQKYENMLLFLKGQLLGEKD-----------------------VIANLSNASAIIMALIDN------------LNWA
YP_001385170.1    MFALEDFKELTEEQKYENMLLFLKGQLLGEKD-----------------------VIANLSNASAIIMALIDN------------LNWA
YP_001388639.1    MFALEDFKELTEEQKYENMLLFLKGQLLGEKD-----------------------VIANLSNASAIIMALIDN------------LNWA
YP_001347703.1    MIDLQQ--TGAGLDGYALLAAQAEALFADERD-----------------------FIANAAQFCAFLFHELDD------------LNWA
NP_103622.1       MFAAKAIDTSDKAAFYSDLAAQLKALLDGESD-----------------------SIANAANTAALIFQMVPD------------LNWA
YP_001807739.1    MFTLSNDPHASKAELYATLVEQARALVESERD-----------------------LTANAANFSALVYHSLDR------------LNWA
YP_001580337.1    MFTLSHDPDASKADQYATLVEQARALVESERD-----------------------LIANAANFSALVYHSLDR------------LNWA
YP_002230176.1    MFTLSNDPTASKADQYATLVEQARALVESERD-----------------------LTANAANFSALVYHSLDR------------LNWA
NP_251512.1       MIDLQQ--SGAGLAGYALLAAQAEALFADERD-----------------------FIANAAQFSAFLFHELGD------------LNWA
YP_459505.1       MFDFAPDETLPAEERYRQLVDAADALTAGEGD-----------------------GVANMANLAALMWEFIPD------------LNWA
YP_790351.1       MIDLQQ--SGAGLAGYALLAAQAEALFADERD-----------------------FIANAAQFSAFLFHELGD------------LNWA
YP_002439846.1    MIDLQQ--SGAGLAGYALLAAQAEALFADERD-----------------------FIANAAQFSAFLFHELGD------------LNWA
YP_001970489.1    MFANAS-LTGSKPEQYAQLLEQARGLVYAESD-----------------------RIANAANLSALVYHALPD------------LNWV
YP_617023.1       MSYTLSFTATEAAERWAEAGEAAAALVAGEHD-----------------------GIANMANVAALIWQAIPD------------LNWA
YP_620554.1       MFTLSNDPTASKADQYATLVEQARALVESERD-----------------------LTANAANFSALVYHSLDR------------LNWA
YP_834795.1       MFTLSNDPTASKADQYATLVEQARALVESERD-----------------------LTANAANFSALVYHSLDR------------LNWA
YP_148653.1       MFRPMAYNG-TREENYALVIEQLKSLISGEPN-----------------------FIANLANAAALLNQFFTD------------INWV
YP_442277.1       MFALSEALPSSKPALYETLAAQARALVETETD-----------------------IVANAANFASLVYHSLDG------------LNWA
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Supplemental data

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YP_001764423.1   MFTLSNDPTASKADQYATLVEQARSLVESERD-----------------------LTANAANFSALVYHSLDR------------LNWA
NP_970249.1      SINYS-----DKTKFYKELHSEAEGLAEK--EWFVN-----------------------LANFSALLKQHLPEIN------------WV
YP_001059788.1   MFALSEALPSSKPALYETLAAQARALVETETD-----------------------IVANAANFASLVYHSLDG------------LNWA
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YP_278248.1      ------------------MLVQQYKSLIADEVK----------------------IYSILANTSAFIYQNFKN------------LNWA
YP_001309672.1   MFDIKIFEGMSTENKLDNMLIMLEGLIQGDEDS----------------------SITKLCNASALINSLIDR------------INWC
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YP_810624.1      YMETK-------QTRYSLLNDQAQSLLDGEHD-----------------------LIANMSNLVSLIFNSDQN------------INGT
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XP_645637.1      AEDLEISKG-SKEEQYENLLPQIEGLLTGENN-----------------------QIANLANVTAALKEQFN-------------FFWV
XP_456263.1      YSSFQT---TDRKKALEQLLISYEALAEGQDNWVCN-----------------------LANAASLIWHCYISLN---VD-----VNWA
YP_001300883.1   ETSFKQTTS-NKVERYRLFLPQFELLISDEKE-----------------------EISVLANTAAALREAFG-------------FFWV
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YP_816246.1      MLKSE------KQSRYQMLNEELSFLLEGETN-----------------------VLANLSNASALIKSRFPN------------TVFA
YP_001694316.1   MLKSE------KQSRYQMLNEELSFLLEGETN-----------------------VLANLSNASALIKSRFPN------------TVFA
YP_001835526.1   MLKSE------KQSRYQMLNEELSFLLEGETN-----------------------VLANLSNASALIKSRFPN------------TVFA
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Supplemental data

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YP_759928.1      ---------MDKAEAYRQLKEEIDSVVAGETS-----------------------DTARYASAACLLAQAFKPR-----------FFWT
YP_002123053.1   MNKTT------KIEHYQLLLAQAKALFSNESN-----------------------ALANLSNASALLKMTLPH------------SVFA
YP_002131343.1   EAFNEIVLPASKAERYAAVAEEIASVLDGEPN-----------------------LVARMATVASMLANSFEH------------YFWT
XP_001683506.1   ---TPAPTFSSKKELYDWLVKQVEALVHDMSKRFTPQAN----------------LVIGLSNTAALCFYELNRFCNPEAALEKLRVNWF
NP_012854.1      HVNYSSN--LNKEEILEQLLLSYEGLSDGQVNWVCN-----------------------LSNASSLIWHAYKSLA---VD-----INWA
XP_460154.1      YTSYSN--DGGKEEILQSVVDSYEALSYDTRNWVAN-----------------------LANCSSLLWHAYHSMK---IN-----VNWS
XP_001801028.1   ASAFA--EGLSKKEVYAQVLEQARILFDGQRNWVCN-----------------------FSNTSSLLWHALHSLPSPSHS-----VNWA
YP_001201197.1   MTKQE------KISNYQLLLAQLEALLDGETN-----------------------ALANLSNASALLNQALPN------------SVFT
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YP_974447.1      MHALHFSAS-DKAALYREVLPQIESVVADETD-----------------------WVANLANTAAVLKEAFG-------------WFWV
XP_001465858.1   ---TPAPTFSSKKELYDWLVKQVEALVHDMSKRFTPQAN----------------LVIGLSNVAALCFYELNRFCNPEAALEKLKVNWF
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YP_596891.1      MNKSK------KIEQYQLMIEQAKELFANESN-----------------------ALANLSNASALLNMTLPN------------SVFA
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Supplemental data

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XP_680937.1      SSYFG---SGSKAEIYAQVIQQAKGLVTGQRNWVRI----------------LISIVSNFSNVASLLWHAYAALPAPSSS-----VNWA
XP_001265696.1   SSYFSTSQEPTKAEVYAQVLEQAKGLVTGQRNWATQ--------------------PSNFSNIASLLWHAYAALPPPSSS-----VNWA
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YP_612063.1      -----------MRVNYEDLSKVVAALTEGETD-----------------------EVALMATVVCELHHADDR------------FDWT
YP_444835.1      -PASSTATASDKAERYADTRRRIDALLDGPTD-----------------------WVSAMATVACELHHSFDH------------YDWT
NP_943356.1      -----------------------------------------------------------------MCWRRIS-----------------
YP_631535.1      AEVTLDLRGMPKAEAYAELKQHVRAVLEGIDD-----------------------DITGMATMSCLLHHAFG-------------HLWT
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NP_390842.2      VEKQSG----DKEKDYQLLLKQLEAMTEDETD-----------------------QIANYANASALLYHSLPE------------VNWA
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XP_719233.1      YSNLKSG-DFSKEETLQHVLDSYKALETD--NWVAN-----------------------LSNCSSLLWHAYKSLN---IN-----VNWT
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XP_001216799.1   SSYFG--GSGSKAEIYTQVLEQAKGLVTGQRNWVTHTNA--------PRHPSELTINSNFSNVASLLWHAYAALPSPSSS-----VNWA
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XP_001390389.1   SSYFGA-GNGSKSEVYTQVLEQARGLVYDQRNWLTN-------------HFSHRQQVSNFSNVASLLWHAYAALPAPSSS-----VNWA
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YP_916587.1      ------------MPDYDDLAARIQALTHDETD-----------------------EVALMATLACEIHHSDER------------FDWT
XP_961529.1      ASNFA--ANVTKEEAYQQVLDQAEGLFYEQRNWVCN-----------------------LSNCAALLWHAFKSLPAPSNQ-----VNWA
YP_351544.1      -------------MDYDQLDQTIEALCHGEQD-----------------------TVALMATVACEIHHAHPL------------SDWT
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XP_001537789.1   -------------------------------------------------------MVSNLANVSSLLWHAYAALPAPSSA-----VNWA
YP_001198994.1   MTKQE------KISNYQLLLAQLEALLDGETN-----------------------ALANLSNASALLNPALPN------------SVFT
NP_390842.1      VEKQSG----DKEKDYQLLLKQLEAMTEDETD-----------------------QIANYANASALLYHSLPE------------VNWA
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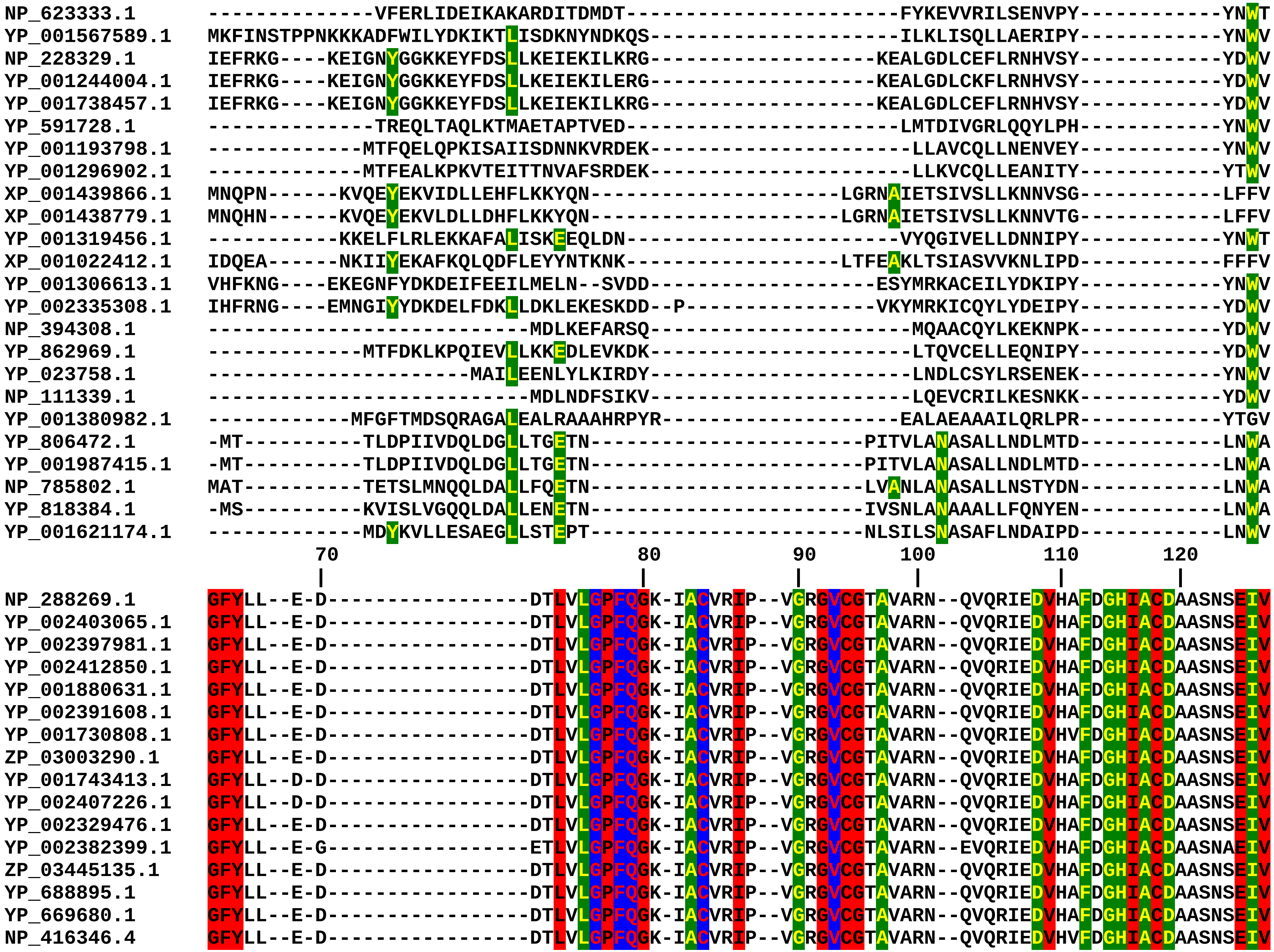
Supplemental data



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YP_001244004.1   IEFRKG----KEIGNYGGKKEYFDSLLKEIEKILERG-------------------KEALGDLCKFLRNHVSY------------YDWV
YP_001738457.1   IEFRKG----KEIGNYGGKKEYFDSLLKEIEKILKRG-------------------KEALGDLCEFLRNHVSY------------YDWV
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XP_001438779.1   MNQHN------KVQEYEKVLDLLDHFLKKYQN---------------------LGRNAIETSIVSLLKNNVTG------------LFFV
YP_001319456.1   -----------KKELFLRLEKKAFALISKEEQLDN-----------------------VYQGIVELLDNNIPY------------YNWT
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YP_862969.1      -------------MTFDKLKPQIEVLLKKEDLEVKDK----------------------LTQVCELLEQNIPY------------YDWV
YP_023758.1      ----------------------MAILEENLYLKIRDY----------------------LNDLCSYLRSENEK------------YNWV
NP_111339.1      ---------------------------MDLNDFSIKV----------------------LQEVCRILKESNKK------------YDWV
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YP_001987415.1   -MT----------TLDPIIVDQLDGLLTGETN-----------------------PITVLANASALLNDLMTD------------LNWA
NP_785802.1      MAT----------TETSLMNQQLDALLFQETN-----------------------LVANLANASALLNSTYDN------------LNWA
YP_818384.1      -MS----------KVISLVGQQLDALLENETN-----------------------IVSNLANAAALLFQNYEN------------LNWA
YP_001621174.1   -------------MDYKVLLESAEGLLSTEPT-----------------------NLSILSNASAFLNDAIPD------------LNWV
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YP_002397981.1   GFYLL--E-D-----------------DTLVLGPFQGK-IACVRIP--VGRGVCGTAVARN--QVQRIEDVHAFDGHIACDAASNSEIV
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Supplemental data

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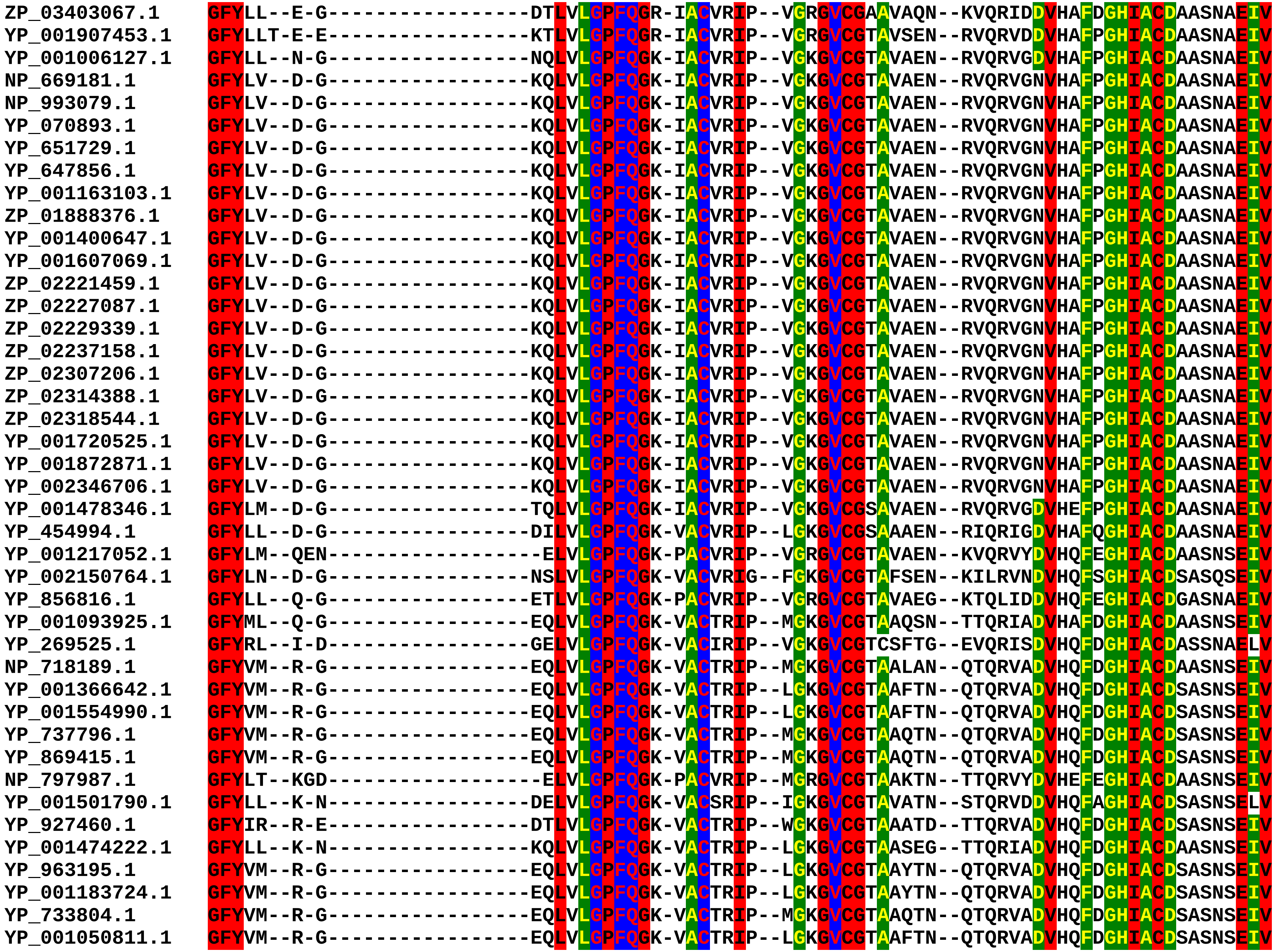

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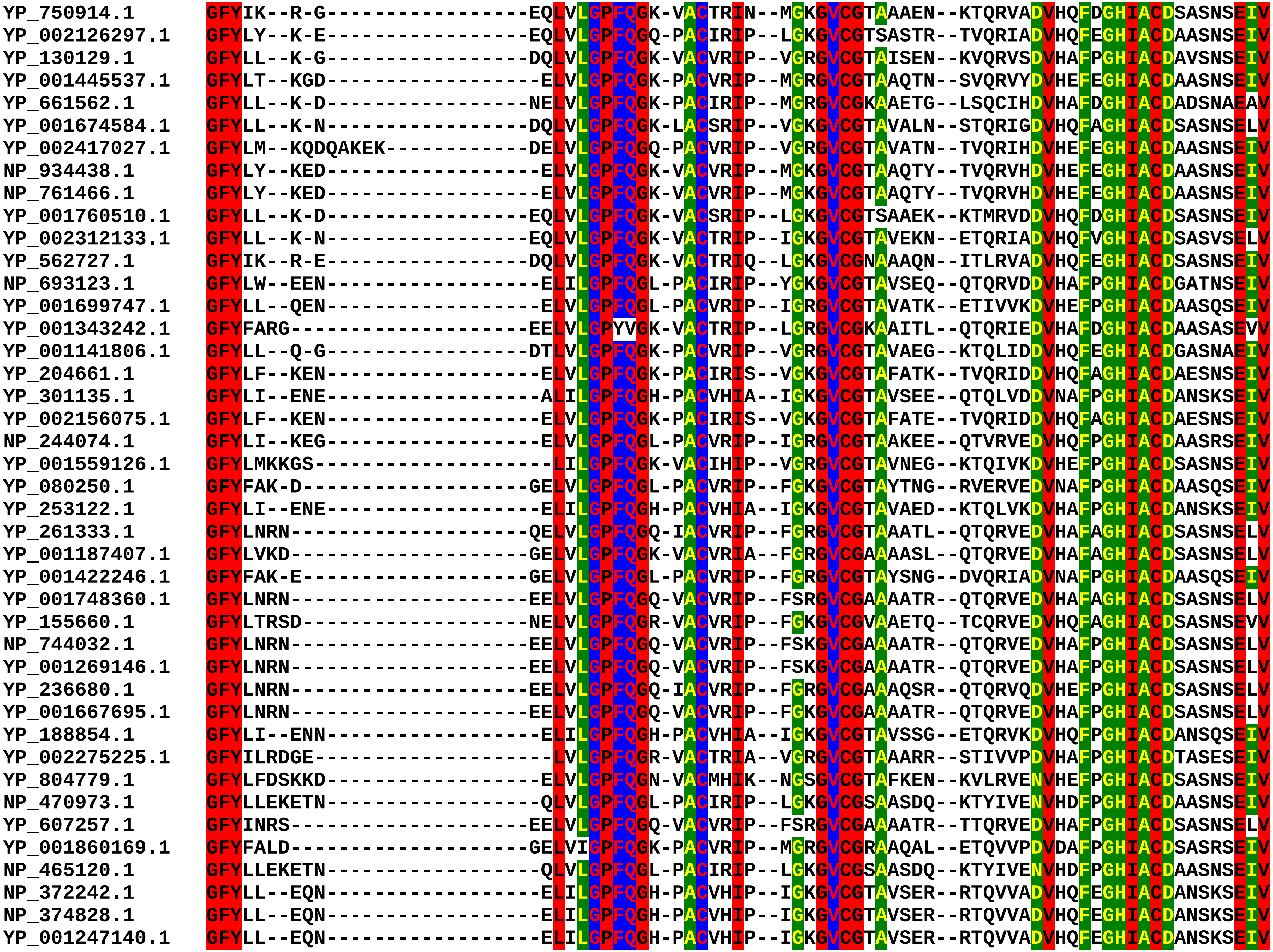

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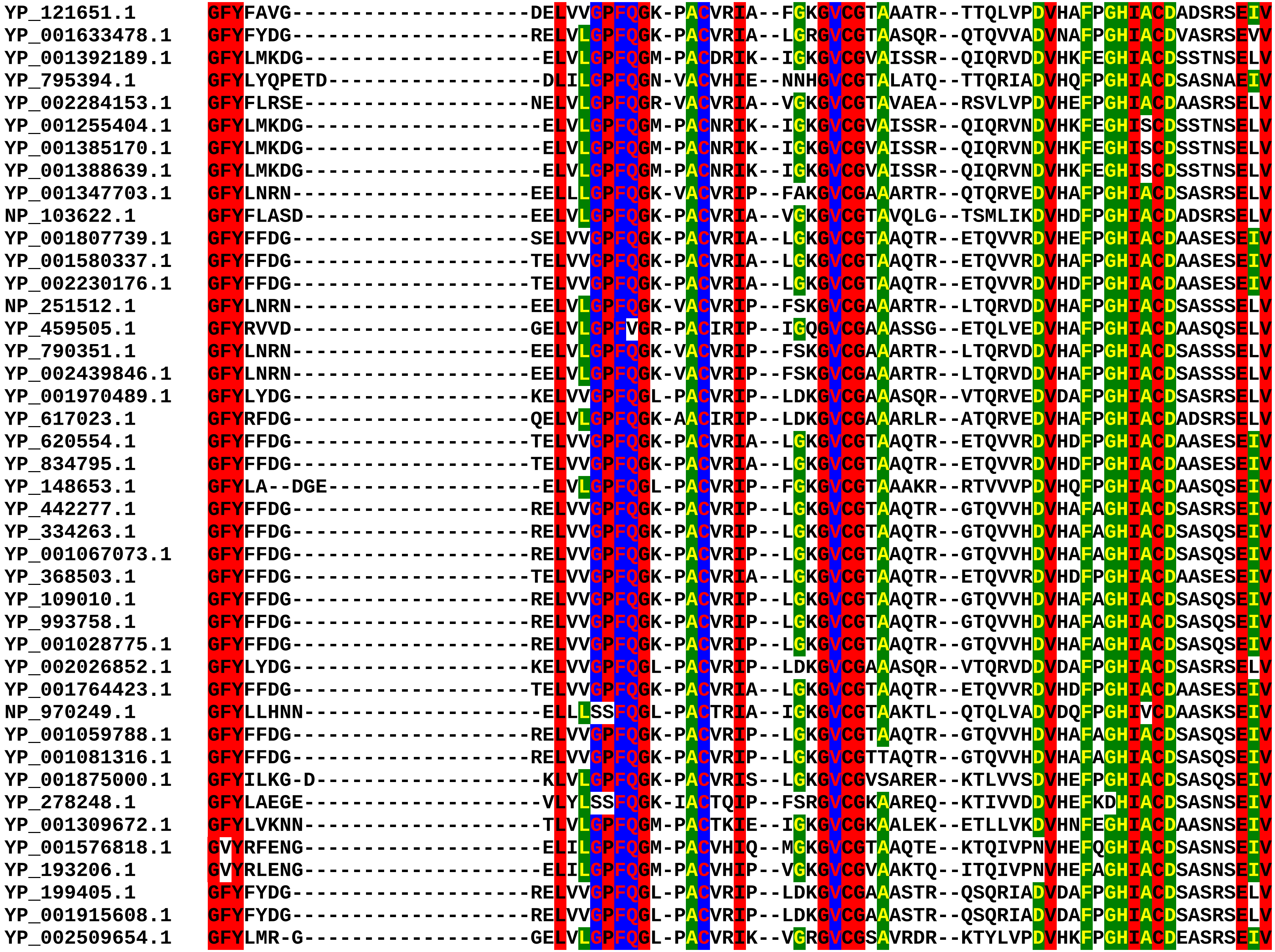

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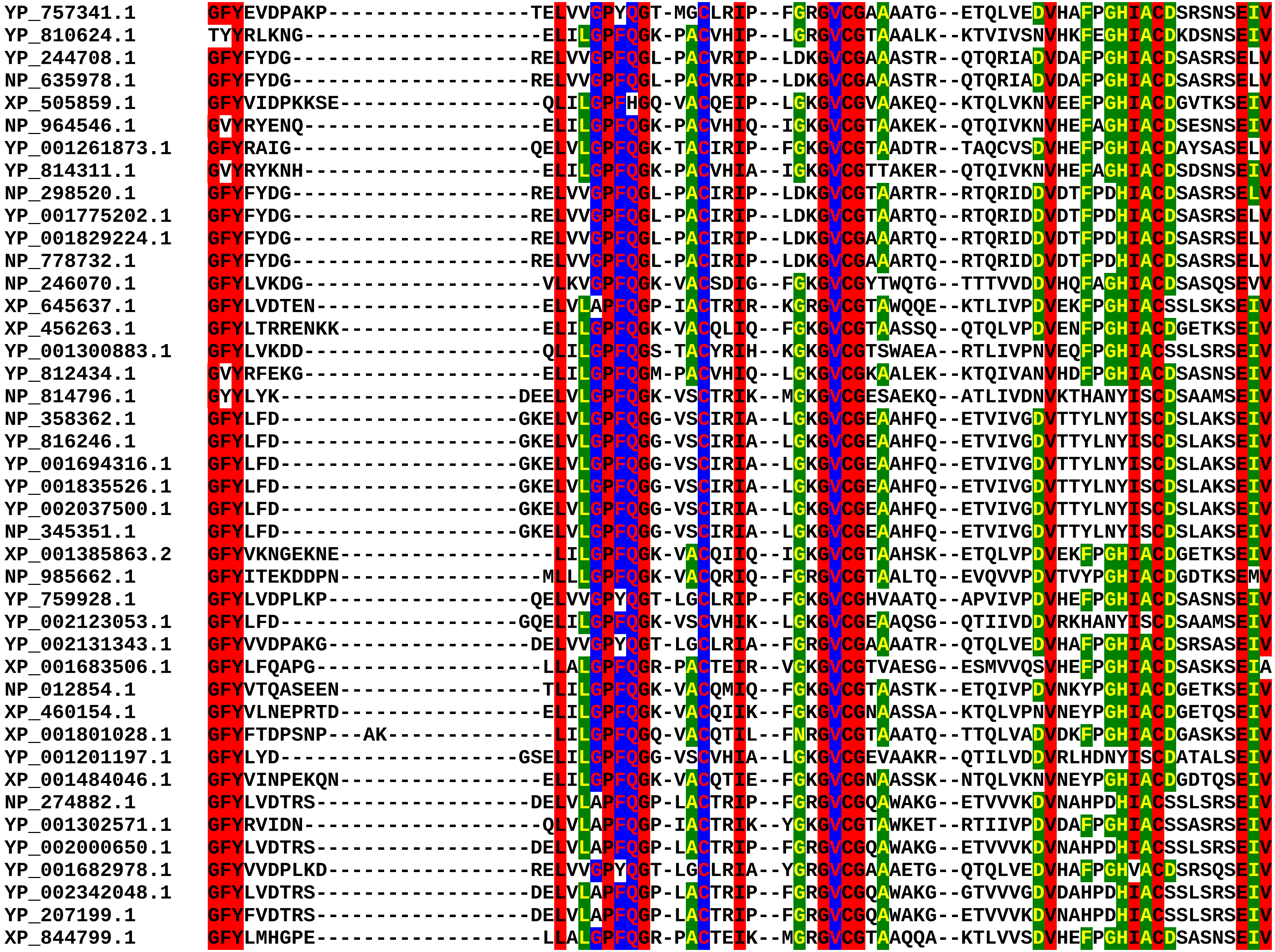

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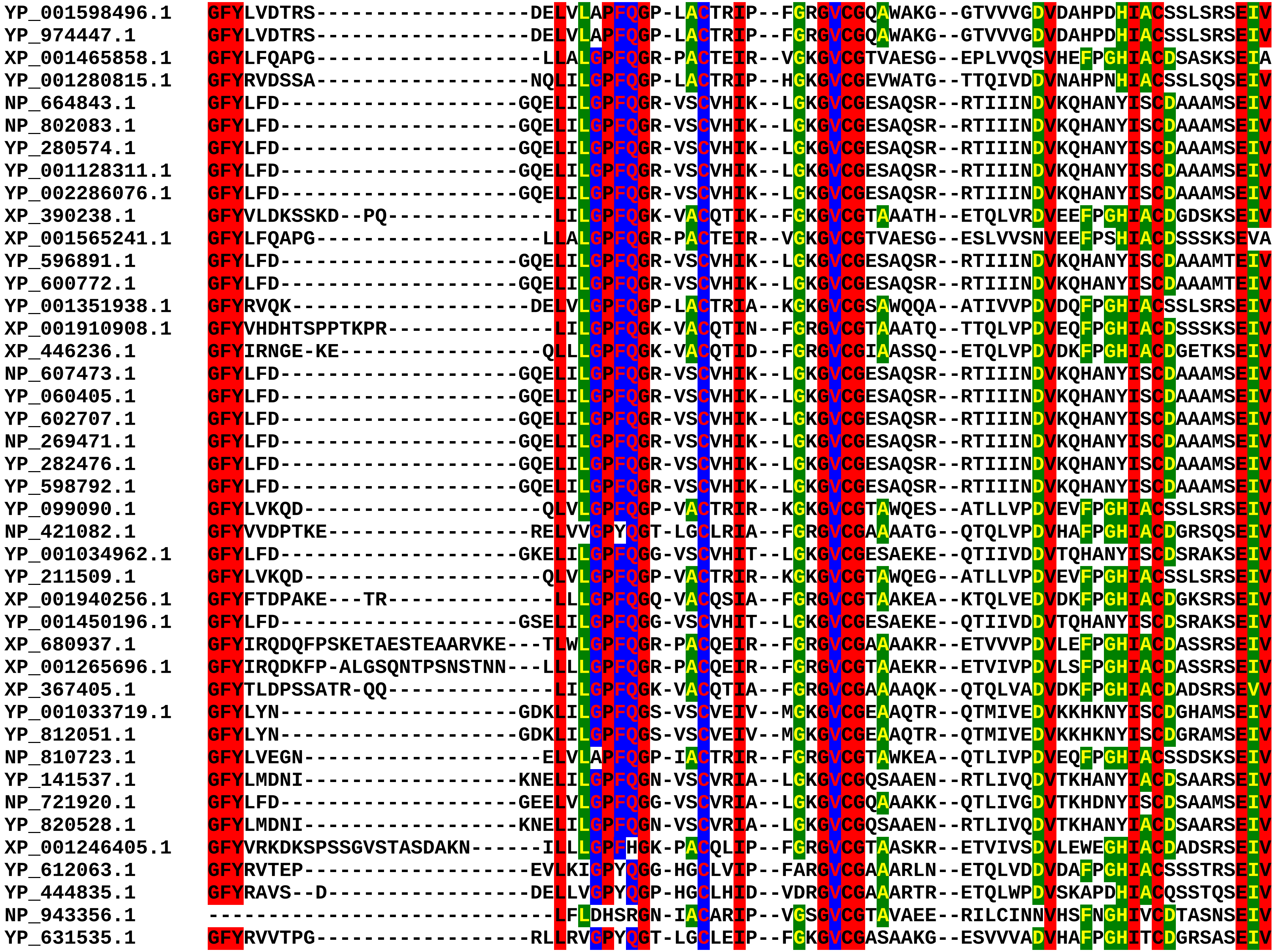

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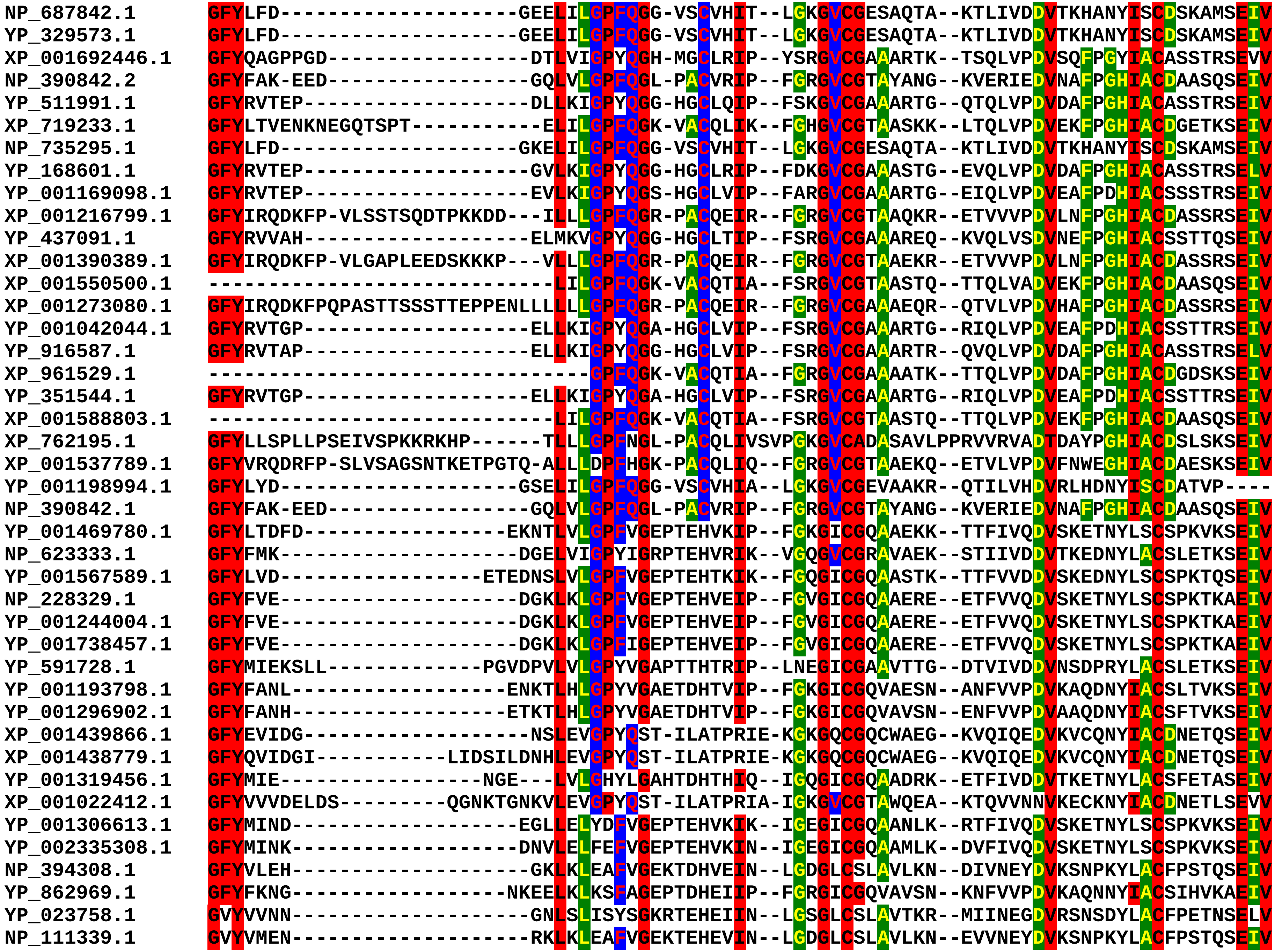

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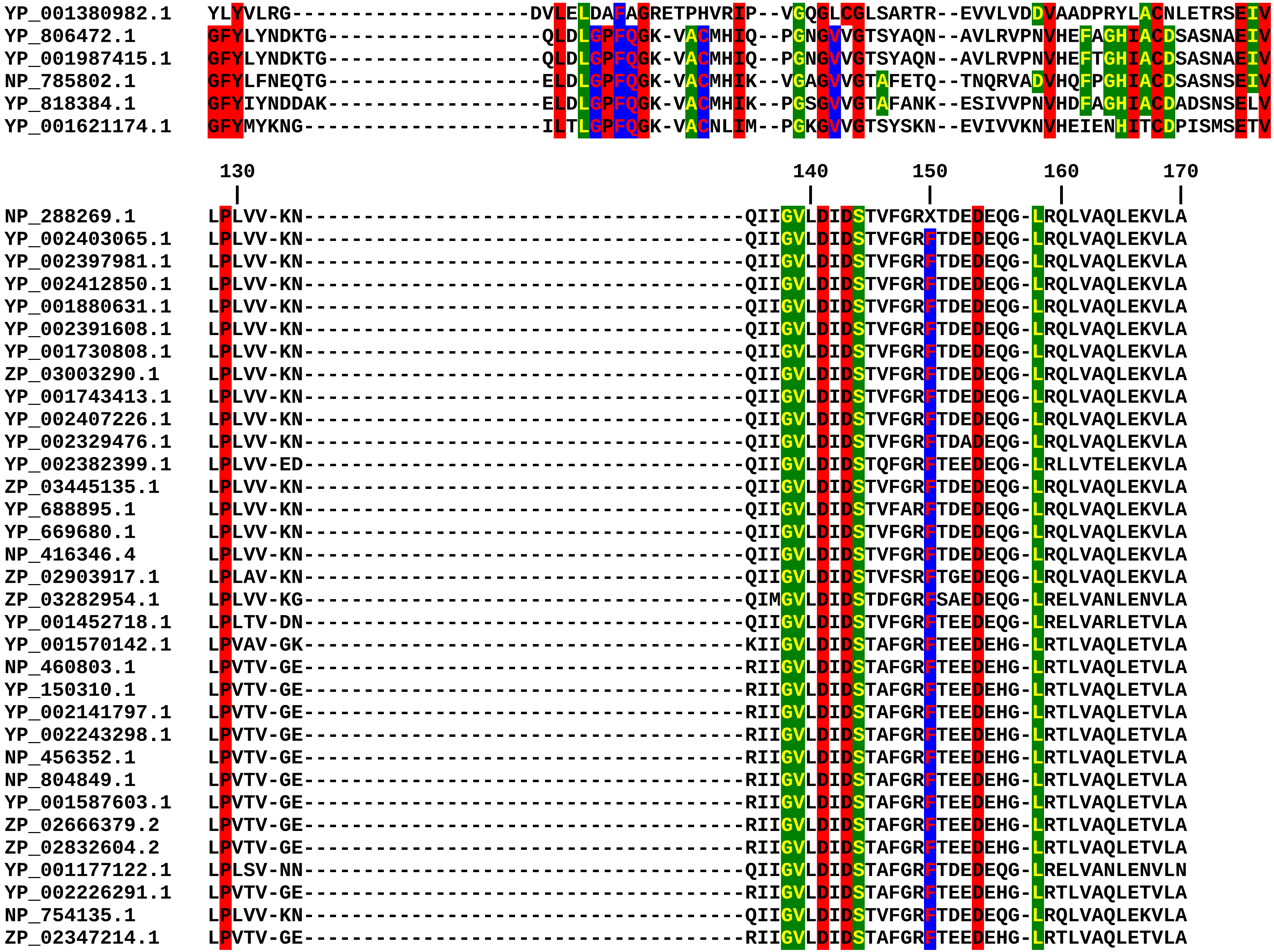

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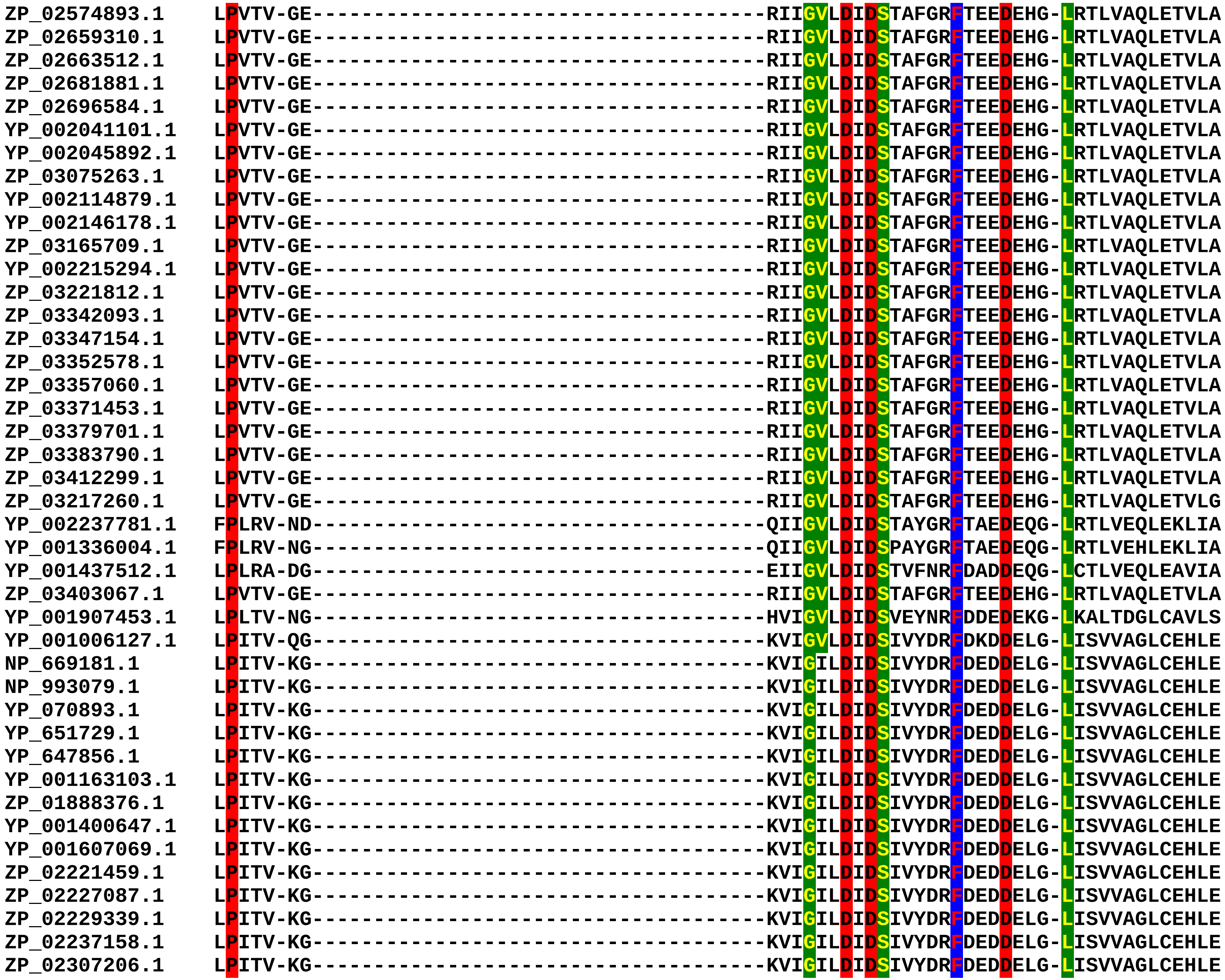

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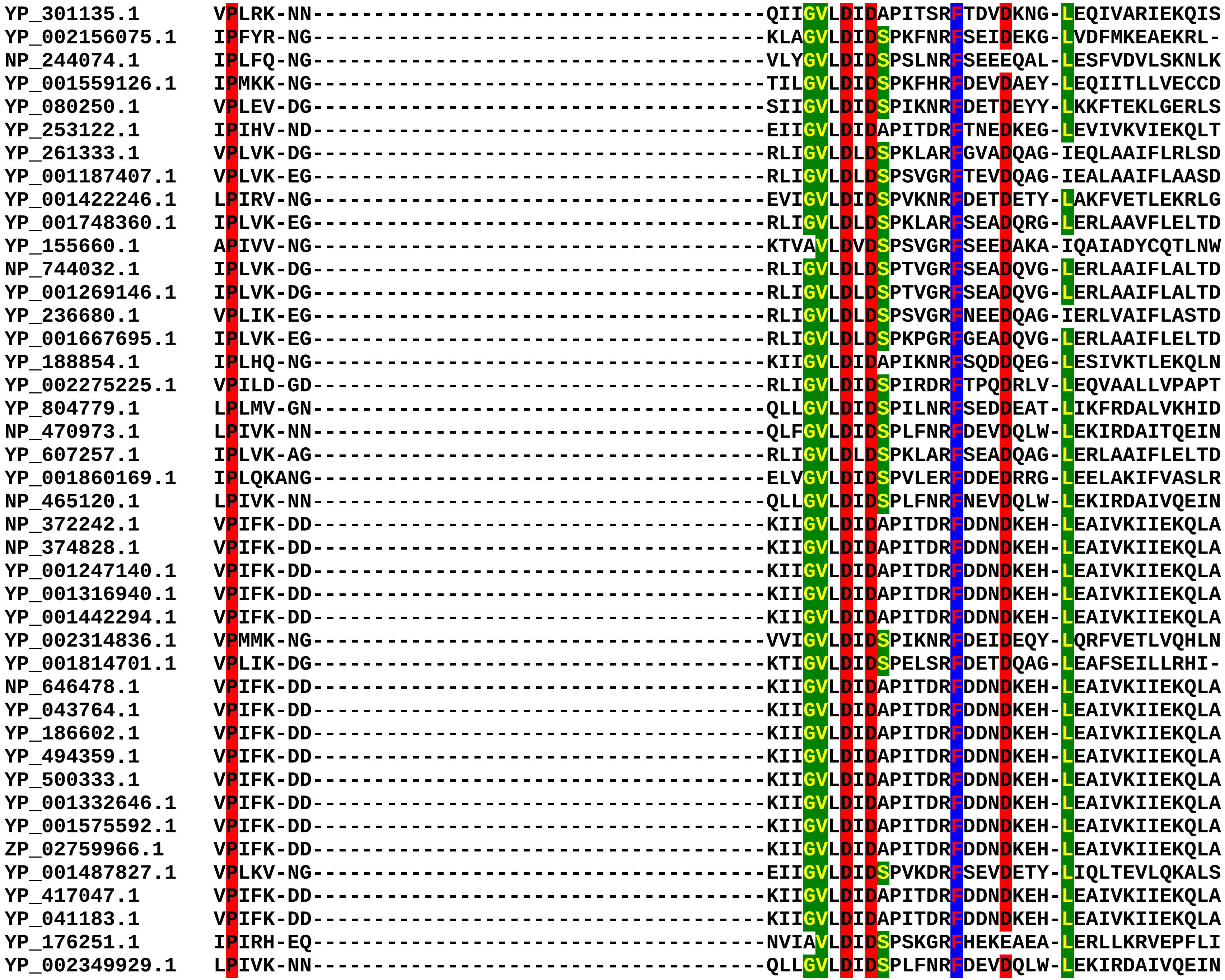

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YP_043764.1       VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_186602.1       VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_494359.1       VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_500333.1       VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_001332646.1    VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_001575592.1    VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
ZP_02759966.1     VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_001487827.1    VPLKV-NG-------------------------------------EIIGVLDIDSPVKDRFSEVDETY-LIQLTEVLQKALS
YP_417047.1       VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_041183.1       VPIFK-DD-------------------------------------KIIGVLDIDAPITDRFDDNDKEH-LEAIVKIIEKQLA
YP_176251.1       IPIRH-EQ-------------------------------------NVIAVLDIDSPSKGRFHEKEAEA-LERLLKRVEPFLI
YP_002349929.1    LPIVK-NN-------------------------------------QLLGVLDIDSPLFNRFDEVDQLW-LEKIRDAIVQEIN
```

Supplemental data

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YP_001376537.1   VPMIK-EG-------------------------------------NVIGVLDIDSPEKNRFDKVDQQY-LEKFVETLLKHM-
YP_784647.1      VPLLR-DG-------------------------------------QLLGVWDVDSPTPGRFDDADREG-MEALCQVFLHSLA
YP_557760.1      VPLVAPDG-------------------------------------TLIGVWDVDSPVVARFDEEDAKG-MEALCAVFIQAAL
YP_275769.1      VPLIK-DG-------------------------------------RLIGVLDLDSPSVGRFNEVDQAG-IERLAAIFLASTD
YP_001118914.1   VPLVAADG-------------------------------------TLIGVWDVDSPVAARFDDEDRSG-MEALCRVFVEHAW
YP_001782545.1   VPIIK-EN-------------------------------------KILGVLDLDSIEFGRFTELEEKY-FEKFVQILVENID
NP_882192.1      VPLVH-KG-------------------------------------SLLGVWDVDSPLPGRFDDEDRAG-MEALCEVFLHSLG
YP_001894915.1   VPLVAPDG-------------------------------------TLIGVWDVDSPSVARFDEEDAKG-MEALCAVFIEAAL
YP_001647268.1   VPIMK-EG-------------------------------------NIIGVLDIDSPEKNRFDEVDQHY-LEKFVETLLKHI-
NP_882465.1      VPLLH-KG-------------------------------------SLLGVWDVDSPLPGRFDDEDRAG-MEALCEVFLHSLG
YP_002448219.1   VPIVK-EG-------------------------------------AVIGVLDIDSPEKNRFDEVDQHY-LEKFVETLLKHM-
NP_834359.1      VPIVK-EG-------------------------------------AVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
YP_002369448.1   VPIVK-EG-------------------------------------AVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
YP_191278.1      LPVVA-RG-------------------------------------ALVGVLDIDSPVKDRFSDADRTR-LKEVVSLLVATLE
NP_886654.1      VPLVH-QG-------------------------------------SLLGVWDVDSPLPGRFDDEDRAG-MEALCEVFLHSLG
NP_847103.1      VPIIK-DG-------------------------------------NVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
YP_030799.1      VPIIK-DG-------------------------------------NVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
NP_981083.1      VPIIK-DG-------------------------------------NVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
YP_038702.1      VPIIK-DG-------------------------------------NVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
YP_002340711.1   VPIIK-DG-------------------------------------NVIGVLDIDSPEKKRFDEVDQRY-LEKFVETLLKHM-
YP_085975.1      VPIIK-DG-------------------------------------NVIGVLDIDSPEKNRFDEVDQRY-LEKFVETLLKHM-
YP_002453717.1   VPIIK-DG-------------------------------------NVIGVLDIDSPEKKRFDEVDQRY-LEKFVETLLKHM-
YP_772921.1      VPLVAADG-------------------------------------TLIGVWDVDSPVAARFDDEDRNG-MEALCRVFVEHAW
YP_001843726.1   VPIHQ-GD-------------------------------------KLWGVLDIDSPKLARFDQEDQAG-LERLAPLFLPGA-
YP_942902.1      LPISL-QG-------------------------------------APALLLDIDSPIKNRFTQNDQDG-LAYLVEQIQQHL-
YP_121651.1      VPLVR-DD-------------------------------------TVIGVLDLDSPRPGRFDTVDRDG-LEAVARVFLDAL-
YP_001633478.1   VPLVH-NG-------------------------------------ELIGVWDVDSPEPGRFDEDDRQG-MQALCAVFLASLA
YP_001392189.1   VPIIK-ED-------------------------------------KILGGLDLDSIEFGRFTELEEKY-FKKFVQILVENID
YP_795394.1      VPLTI-GE-------------------------------------TKFGVLDIDSPTKDRFTAADQQV-LEEFARVLLSHID
YP_002284153.1   IPLVK-DG-------------------------------------GIVGVLDLDSPTPHRFDAEDQAG-FEALAAIYVAASA
YP_001255404.1   VPIIK-ED-------------------------------------KVLGVLDLDSIEFGRFTGLEEKY-FKKFVQILVENID
YP_001385170.1   VPIIK-ED-------------------------------------KVLGVLDLDSIEFGRFTGLEEKY-FKKFVQILVENID
YP_001388639.1   VPIIK-ED-------------------------------------KVLGVLDLDSIEFGRFTGLEEKY-FKKFVQILVENID
YP_001347703.1   VPLLK-DG-------------------------------------RLIGVLDLDSPSEGRFSARDQAG-IERLVEIFLRLSD
NP_103622.1      VLLED-DE-------------------------------------GVFGVLDLDSPLPGRFDKADQAG-IETLAAIYAAASS
YP_001807739.1   VPLVAADG-------------------------------------TLIGVWDVDSPVAARFDDEDRNG-MEALCRVFVEHAW
YP_001580337.1   VPLVADDG-------------------------------------TLIGVWDVDSPVAARFDDEDRRG-MEALCRVFVEHAW
YP_002230176.1   VPLVAGDG-------------------------------------TLIGVWDVDSPVAARFDDEDRQG-MEALCRVFVEHAW
NP_251512.1      VPLIK-DG-------------------------------------RLVAVLDLDSPSVGRFSAEDQAG-IEGLVEIFLRLTD
YP_459505.1      VPVVR-DD-------------------------------------TVVAVIDLDAPTKARFARADAEG-IEELARRIAGRI-
YP_790351.1      VPLLK-DG-------------------------------------RLVAVLDLDSPSVGRFSAEDQAG-IEGLVEIFLRLTD
YP_002439846.1   VPLLK-DG-------------------------------------RLVAVLDLDSPSVGRFSAEDQAG-IEGLVEIFLRLTD
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Supplemental data

```
YP_001970489.1   VPLLR-GD-------------------------------------ELIGVFDIDSPKVGRFDADDQAG-LEAIARVFVEALG
YP_617023.1      VPVIA-ND-------------------------------------RLVGVLDLDSPLPARFTAADQAG-AEALVARIAGALA
YP_620554.1      VPLVADDG-------------------------------------TLIGVWDVDSPVAARFDDEDRKG-MEALCRVFVEHAW
YP_834795.1      VPLVADDG-------------------------------------TLIGVWDVDSPVAARFDDEDRKG-MEALCRVFVEHAW
YP_148653.1      VPLIK-DD-------------------------------------RVIGVLDIDSPVKNRFDDIDRRY-LEQFASVLISA--
YP_442277.1      VPLIARDG-------------------------------------ALIGVWDVDSPLIGRFDAEDATG-MEALCRVFVEVAW
YP_334263.1      VPLVARDG-------------------------------------ALIGVWDVDSPLVGRFDAEDATG-MEALCRVFVEVAW
YP_001067073.1   VPLVARDG-------------------------------------ALIGVWDVDSPLVGRFDAEDATG-MEALCRVFVEVAW
YP_368503.1      VPLVAADG-------------------------------------TLIGVWDVDSPVAARFDDEDRKG-MEALCRVFVESAW
YP_109010.1      VPLVARDG-------------------------------------ALIGVWDVDSPLVGRFDAEDAIG-MEALCRVFVEVAW
YP_993758.1      VPLVARDG-------------------------------------ALIGVWDVDSPLVGRFDAEDAIG-MEALCRVFVEVAW
YP_001028775.1   VPLVARDG-------------------------------------ALIGVWDVDSPLVGRFDAEDAIG-MEALCRVFVEVAW
YP_002026852.1   VPLLR-GD-------------------------------------ELIGVFDIDSPKVGRFDADDQAG-LEAIARVFVEALG
YP_001764423.1   VPLVADDG-------------------------------------TLIGVWDVDSPVAARFDDEDRTG-MEALCRVFVEHAW
NP_970249.1      VPLIHNG--------------------------------------KLLGVLDVDAPVLNRFDSEDQKG-LQGLVQILISKTV
YP_001059788.1   VPLVACDG-------------------------------------ALIGVWDVDSPLVGRFDAEDATG-MEALCRVFVEVAW
YP_001081316.1   VPLVARDG-------------------------------------ALIGVWDVDSPLVGRFDAEDAIG-MEALCRVFVEVAW
YP_001875000.1   VPIIK-NG-------------------------------------TLFGVLDIDSPIKNRFSDEDRIF-FEKVVGLFSKYSD
YP_278248.1      IPIIV-NS-------------------------------------KLYGVLDLDSPLKSNFKDKEIVLTLEKIATELANKIK
YP_001309672.1   IPIIK-EG-------------------------------------NLIGVLDLDSEEFERFTEVEKTY-LEKAVVILSKYIE
YP_001576818.1   VPIFK-DD-------------------------------------QLWGVFDFDSTKLDNFDETDKKY-LTEIANVIFA---
YP_193206.1      IPIFK-NR-------------------------------------KLWGVFDFDSTKLDDFDDMDKKY-LTRITKMVFA---
YP_199405.1      IPLVK-GD-------------------------------------TLIGVLDLDSPELDRFDADDQRG-LEAIAQLFVDALA
YP_001915608.1   IPLVK-GD-------------------------------------TLIGVLDLDSPELDRFDADDQRG-LEAIAQLFVDALA
YP_002509654.1   IPVEV-DG-------------------------------------DIIGVLDIDSPVKNRFDEIDKRY-LEEFVKKIINLSD
YP_757341.1      VPVRDA-------------------------------------AGALVAVLDIDSTEFGAFDEVDQAG-LEAICGEL-----
YP_810624.1      VPIFS-KN-------------------------------------EFWGVLDLDSTKFNYFDKNDQEY-LEKIGNYIFGI--
YP_244708.1      IPLVR-GD-------------------------------------TLIGVLDLDSPELDRFDADDQRG-LEAIAQVFVGALT
NP_635978.1      IPLVQ-GD-------------------------------------TLIGVLDLDSPELDRFDADDQRG-LEAIAQVFVGALT
XP_505859.1      VPIV-LNG-------------------------------------KLFGVIDIDCASLEGFDEVDQQG-LEKIALILAKSCE
NP_964546.1      VPIFKANG-------------------------------------DLWGVFDFDSTKLANFDELDQKY-LEKISKVFKF---
YP_001261873.1   VPIVH-EG-------------------------------------RLIGVLDLDSPIKGRFDEQDVVG-CAELMAVLGPRIA
YP_814311.1      IPIFKKNG-------------------------------------ELWGVFDFDSTKIANFDELDQKY-LEAISNIFKF---
NP_298520.1      VPLLK-DD-------------------------------------TLIGVLDLDSPTCARFDSDDQTG-IESLARVFVSSLR
YP_001775202.1   VPLLK-DD-------------------------------------TLIGVLDLDSPTCARFDSDDQTG-IESLARVFVSSLR
YP_001829224.1   VPLLK-DN-------------------------------------TLIGVLDLDSPTCARFDSDDQTG-IESLARVFVSNLR
NP_778732.1      VPLLK-DN-------------------------------------TLIGVLDLDSPTCARFDSDDQTG-IESLARVFVSNLR
NP_246070.1      VPIFQ-GG-------------------------------------EMIAELDVDSPRLARFSAEDVAF-LENCAALICIKE-
XP_645637.1      LPLYK--------------------------------------QGNIIGVLDVDSDKLNSFDEIDEKY-LTQILKLLDN---
XP_456263.1      VPIV-QNG-------------------------------------ETVGVIDIDCLDYNGFTKLDQEF-LEKLAASVSKTCV
YP_001300883.1   VPILA--------------------------------------NGQVKGVLDIDSNLLNFFDETDRRY-LEEVTAIVAKT--
YP_812434.1      VPVFNRDG-------------------------------------SLWGVYDFDSTNLDNFDDLDQKY-LEQIAASVLGN--
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Supplemental data

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NP_814796.1       VPMVKNHQ--------------------------------------LVGVLDIDSGVTNSYDAVDQLY-LEKFVTLLLEKSD
NP_358362.1       VPMMKNGQ--------------------------------------LLGVLDLDSSEIEDYDAMDRDY-LEQFVAILLEKTT
YP_816246.1       VPMMKNGQ--------------------------------------LLGVLDLDSSEIEDYDAMDRDY-LEQFVAILLEKTT
YP_001694316.1    VPMMKNGQ--------------------------------------LLGVLDLDSSEIEDYDAMDRDY-LEQFVAILLEKTT
YP_001835526.1    VPMMKNGQ--------------------------------------LLGVLDLDSSEIEDYDAMDRDY-LEQFVAILLEKTT
YP_002037500.1    VPMMKNGQ--------------------------------------LLGVLDLDSSEIEDYDAMDRDY-LEQFVAILLEKTT
NP_345351.1       VPMMKNGQ--------------------------------------LLGVLDLDSSEIEDYDAMDRDY-LEQFVAILLEKTA
XP_001385863.2    VPLV-KEG-------------------------------------KILAVLDIDCLALDGFDESDKKF-LEELAVLIVRTCE
NP_985662.1       VPIL-QDN-------------------------------------RTVAIMDLDCSEHNGFTDLDKKY-LEKLAQEISRTCK
YP_759928.1       LPVFRA-------------------------------------DGSLAAVLDVDSTQFDAFDAVDQAG-LTAICESL-----
YP_002123053.1    VPMLKAGR--------------------------------------LVGVLDLDSSLVADYDQIDQDY-LEQFVALLLENTS
YP_002131343.1    VPVLDA-------------------------------------GGELIAVFDVDSETKAAFDSTDREW-LERILSET-----
XP_001683506.1    VPVLIENG-------------------------------------SVVAVIDVDSTELGHFSEEDREG-LERMAAVLAQHLD
NP_012854.1       VPIISNDG-------------------------------------KTLGVIDIDCLDYEGFDHVDKEF-LEKLAKLINKSCV
XP_460154.1       VPIV-NKG-------------------------------------QVVGVLDIDCLTLEGFDDIDVKY-LEQLATLIGNTCD
XP_001801028.1    VPIVQGG--------------------------------------RTVAIIDVDCAELSGFDGEDQRA-LEELACMLGEACD
YP_001201197.1    VPMVKNDQ--------------------------------------LLGVLDLDSRLVADYDTIDQDY-LEKFVALLVEKTD
XP_001484046.1    VPIV-YEN-------------------------------------KVVGVLDIDCLDLNGFDKVDQKY-LERLVEMISSSCK
NP_274882.1       VPLFS--------------------------------------DGRCIGVLDADSEHLAQFDETDALY-LGELAKILEKR--
YP_001302571.1    VPVIW--------------------------------------ADKVIAVLDIDSDQPDSFDETDQIF-LEKIVELLPHQ--
YP_002000650.1    VPLFS--------------------------------------DGRCIGVLDADSEHLAQFDEADALY-LGELAKILERR--
YP_001682978.1    VPVFDA-------------------------------------AGTLLAVFDVDSDQPAAFDAVDQHG-IEIILKAT-----
YP_002342048.1    VPLFS--------------------------------------DGRCIGVLDADSEYLAQFDETDALY-LGELAKILEKR--
YP_207199.1       VPLFS--------------------------------------DGRCIGVLDADSEHLAQFDEADALY-LGELAKILERR--
XP_844799.1       VPIKSAAG-------------------------------------EVVGIIDVDSTQLNFFDDVDAQG-LQEVAEIVARHVD
YP_001598496.1    VPLFS--------------------------------------DGRCIGVLDADSEHLAQFDETDALY-LGELAKILEKR--
YP_974447.1       VPLFS--------------------------------------DGRCIGVLDADSEHLAQFDETDALY-LGELAKILEKR--
XP_001465858.1    VPVLIENG-------------------------------------SVVAVIDVDSTELDHFSEEDKEG-LERMAAVLAQHLD
YP_001280815.1    VPITDE-------------------------------------AGEIIAVLDIDSDTLATFDEVDGEY-LQQLVDLLK----
NP_664843.1       VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
NP_802083.1       VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_280574.1       VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_001128311.1    VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_002286076.1    VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
XP_390238.1       VPILVAQDDGT---------------------------------KKLVAIIDIDCAELNGFDEVDKAH-LEQLAALLATSCD
XP_001565241.1    VPVLIENG-------------------------------------SVVAVIDVDSTELGYFSEEDKEG-LERVAAVLEQHLN
YP_596891.1       VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_600772.1       VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_001351938.1    VPYFDR-------------------------------------NGEVAGVLDVDSEYPDAFSAVDQLW-LEKIAALLS----
XP_001910908.1    VPIMVEGK-------------------------------------GVVGIIDIDCTVENGFDQIDKEY-LEKLADFLAKSSD
XP_446236.1       VPIVSQSG-------------------------------------KTLGVIDLDCLDFEGFTDVDKEY-LEKLALAITKSCD
NP_607473.1       VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LETFVDLLLEKTT
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Supplemental data

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YP_060405.1      VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LETFVDLLLEKTT
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NP_269471.1      VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_282476.1      VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_598792.1      VPMVKEGH--------------------------------------LIGVLDLDSSLVADYDEVDQEY-LEAFVDLFLEKTT
YP_099090.1      VPLIK--------------------------------------DGEVWGVLDIDSDLLNFFDETDRKY-LEEMCGYLSK---
NP_421082.1      VPVFDP-------------------------------------DGRLIAVFDVDSDKPAAFDEIDQAW-LEKILKAT-----
YP_001034962.1   VPMVKVGR--------------------------------------LLGVLDLDSSLTGDYDKVDQEY-LEKFVQILLEKTT
YP_211509.1      VPLIK--------------------------------------DGEVWGVLDIDSDLLNFFDETDRKY-LEEMCGYLSK---
XP_001940256.1   VPVVQDG--------------------------------------KVVAIIDIDCAELNGFTEEDQEA-LEELAELLSQSCD
YP_001450196.1   VPMVKDGR--------------------------------------LLGVLDLDSALTGDYDKIDQEY-LEKFVQILLEKTI
XP_680937.1      VPILAGG--------------------------------------ETVAIIDIDCAEPSGFDDEDKEY-LEELAALLSESCD
XP_001265696.1   VPILVGG--------------------------------------ETVAIIDVDCTEPAGFDDEDKKW-LEELASLLSECCD
XP_367405.1      VPVLDSEG-------------------------------------QLRAIIDVDCALPDGFDEVDRVW-LESLAALVGRSCD
YP_001033719.1   VPMVKDGN--------------------------------------LVGVLDLDSSEVGFYDEIDQKY-LEEFASILCDMTD
YP_812051.1      VPMVKDGN--------------------------------------LVGVLDLDSSEVGFYDEIDQKY-LEEFASILCDMTD
NP_810723.1      VPIIK--------------------------------------EGNVIGVLDIDSDTPDSFDETDARY-LEEICTYIG----
YP_141537.1      VPMEKGGK--------------------------------------LVGVLDLDSHQVEDYNQVDQDY-LEAFVKILLEKTD
NP_721920.1      IPMVKDGQ--------------------------------------LIGVLDLDSHLVGDYDVIDQGY-LEQFVTILLEKTN
YP_820528.1      VPMEKGGK--------------------------------------LVGVLDLDSHQVEDYNQVDQDY-LEAFVKILLEKTD
XP_001246405.1   VPIVVDG--------------------------------------ETLALIDIDCTQPSGFDEIDKKG-LEHLAKLLAENCD
YP_612063.1      LPVRNR-------------------------------------AGEVIGVLDIDSNQPAAFDRDDQDA-LETLLHAV-----
YP_444835.1      VPVL----------TP---------------------------DDALLAVLDVDSDTLGAFDPTDREH-LEALCRDLG----
NP_943356.1      LPVRI-NN-------------------------------------TVVGALDIDSPAFSRFSSEDEL---------------
YP_631535.1      VPVFGR-------------------------------------NRELLAVLDIDSEHKNAFDEVDRRE-LEELVRWF-----
NP_687842.1      VPMFKNGK--------------------------------------LLGVLDLDSSLVADYDEIDQEY-LEKFVGILVEHTI
YP_329573.1      VPMFKNGK--------------------------------------LLGVLDLDSSLVADYDEIDQEY-LEKFVGILVEHTI
XP_001692446.1   VPVVRSHISFNDGRTPSI-------------------------PEKLVAVLDVDSDHPAAFTEVDQEC-LEELCEWLGDHLQ
NP_390842.2      LPIRV-DG-------------------------------------KIVGVLDIDSPVKNRFDEIDEKY-LTQFAETLEKALA
YP_511991.1      LPVRDA-------------------------------------SGAIIAVLDIDSNQPDAFTQDDATA-LESILRAT-----
XP_719233.1      VPIV-KNG-------------------------------------ETKGVIDLDCLDLEGFDQVDQKY-LEKLAELIAQSL-
NP_735295.1      VPMFKNGK--------------------------------------LLGVLDLDSSLVADYDEIDQEY-LEKFVGILVEHTI
YP_168601.1      LPVFGR-------------------------------------TGALIAVFDIDSDLPDAFTVADAEA-LGAILEQV-----
YP_001169098.1   LPVRNG-------------------------------------EGRLLGVLDLDSNTPAAFTEEDARR-LQALLDRT-----
XP_001216799.1   VPILAGG--------------------------------------ETVAIIDIDCTEPDGFDETDKKY-LEELAALLADSCD
YP_437091.1      LPLFNA-------------------------------------NGDVAAVLDIDSDHIDAFDAVDERF-LAELLTDL-----
XP_001390389.1   VPILSKG--------------------------------------ETVAIIDIDCAEPDGFDDEDKKY-LEELAALLAECCD
XP_001550500.1   VPIVVDG--------------------------------------VVKAIIDVDCGVKEGFDEVDRKW-LEELAGVLAEGCD
XP_001273080.1   VPVLVGG--------------------------------------ETVAIIDVDCTEPSGFDEVDRKY-LEELAALLAECCD
YP_001042044.1   LPVRNG-------------------------------------EGRLLGVLDLDSNTPAAFTEEDAAR-LQALLDRT-----
YP_916587.1      IPVIGG-------------------------------------GERLIGVLDIDSDQPDAFTRDDADR-LQEILDAT-----
XP_961529.1      VPIVVDD--------------------------------------RVVAIIDVDCAELNGFDEVDKVW-LEKLADLVGRSCD
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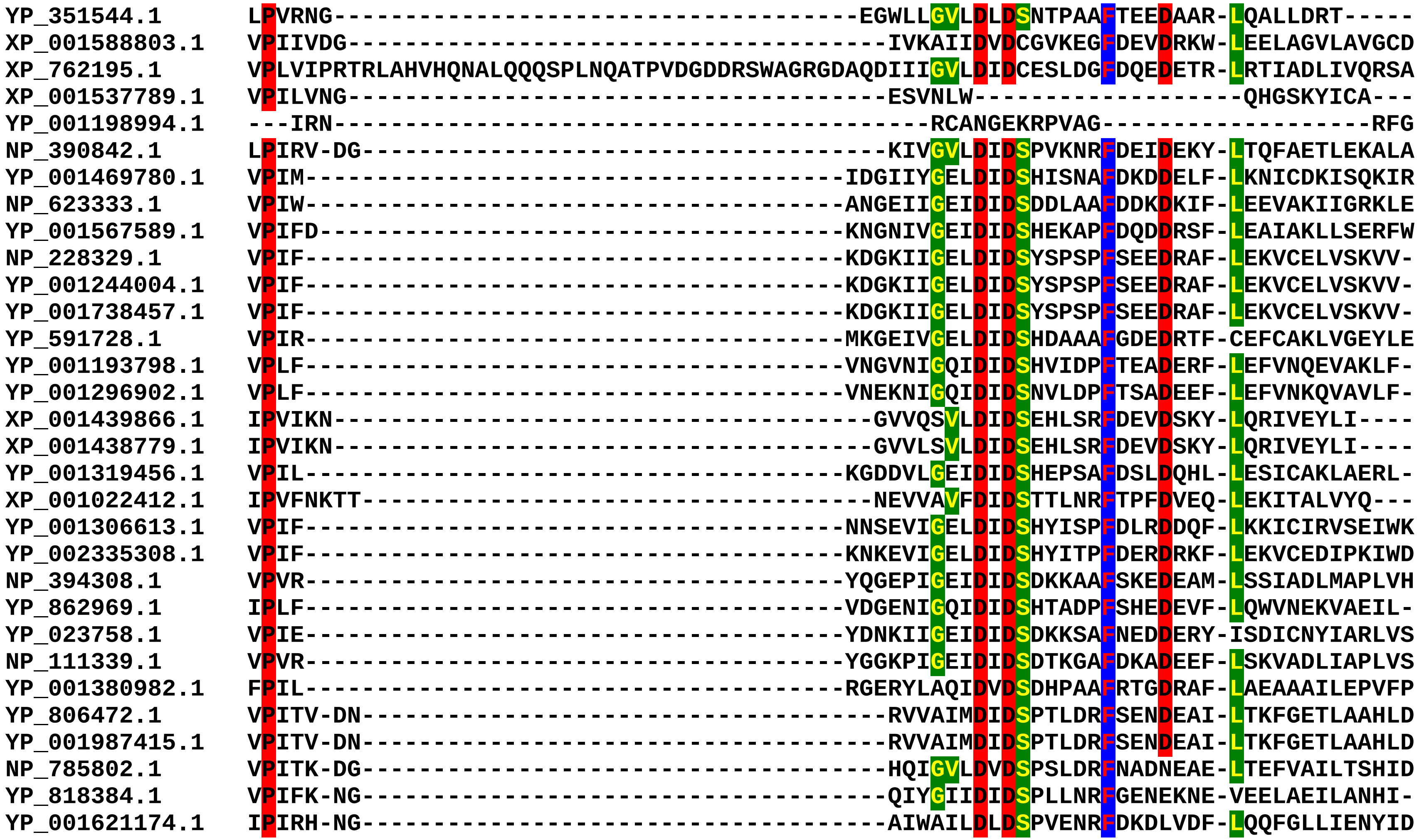
Supplemental data



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YP_351544.1        LPVRNG-------------------------------------EGWLLGVLDLDSNTPAAFTEEDAAR-LQALLDRT-----
XP_001588803.1     VPIIVDG--------------------------------------IVKAIIDVDCGVKEGFDEVDRKW-LEELAGVLAVGCD
XP_762195.1        VPLVIPRTRLAHVHQNALQQQSPLNQATPVDGDDRSWAGRGDAQDIIIGVLDIDCESLDGFDQEDETR-LRTIADLIVQRSA
XP_001537789.1     VPILVNG--------------------------------------ESVNLW-------------------QHGSKYICA---
YP_001198994.1     ---IRN------------------------------------------RCANGEKRPVAG-------------------RFG
NP_390842.1        LPIRV-DG-------------------------------------KIVGVLDIDSPVKNRFDEIDEKY-LTQFAETLEKALA
YP_001469780.1     VPIM--------------------------------------IDGIIYGELDIDSHISNAFDKDDELF-LKNICDKISQKIR
NP_623333.1        VPIW--------------------------------------ANGEIIGEIDIDSDDLAAFDDKDKIF-LEEVAKIIGRKLE
YP_001567589.1     VPIFD-------------------------------------KNGNIVGEIDIDSHEKAPFDQDDRSF-LEAIAKLLSERFW
NP_228329.1        VPIF--------------------------------------KDGKIIGELDIDSYSPSPFSEEDRAF-LEKVCELVSKVV-
YP_001244004.1     VPIF--------------------------------------KDGKIIGELDIDSYSPSPFSEEDRAF-LEKVCELVSKVV-
YP_001738457.1     VPIF--------------------------------------KDGKIIGELDIDSYSPSPFSEEDRAF-LEKVCELVSKVV-
YP_591728.1        VPIR--------------------------------------MKGEIVGELDIDSHDAAAFGDEDRTF-CEFCAKLVGEYLE
YP_001193798.1     VPLF--------------------------------------VNGVNIGQIDIDSHVIDPFTEADERF-LEFVNQEVAKLF-
YP_001296902.1     VPLF--------------------------------------VNEKNIGQIDIDSNVLDPFTSADEEF-LEFVNKQVAVLF-
XP_001439866.1     IPVIKN--------------------------------------GVVQSVLDIDSEHLSRFDEVDSKY-LQRIVEYLI----
XP_001438779.1     IPVIKN--------------------------------------GVVLSVLDIDSEHLSRFDEVDSKY-LQRIVEYLI----
YP_001319456.1     VPIL--------------------------------------KGDDVLGEIDIDSHEPSAFDSLDQHL-LESICAKLAERL-
XP_001022412.1     IPVFNKTT------------------------------------NEVVAVFDIDSTTLNRFTPFDVEQ-LEKITALVYQ---
YP_001306613.1     VPIF--------------------------------------NNSEVIGELDIDSHYISPFDLRDDQF-LKKICIRVSEIWK
YP_002335308.1     VPIF--------------------------------------KNKEVIGELDIDSHYITPFDERDRKF-LEKVCEDIPKIWD
NP_394308.1        VPVR--------------------------------------YQGEPIGEIDIDSDKKAAFSKEDEAM-LSSIADLMAPLVH
YP_862969.1        IPLF--------------------------------------VDGENIGQIDIDSHTADPFSHEDEVF-LQWVNEKVAEIL-
YP_023758.1        VPIE--------------------------------------YDNKIIGEIDIDSDKKSAFNEDDERY-ISDICNYIARLVS
NP_111339.1        VPVR--------------------------------------YGGKPIGEIDIDSDTKGAFDKADEEF-LSKVADLIAPLVS
YP_001380982.1     FPIL--------------------------------------RGERYLAQIDVDSDHPAAFRTGDRAF-LAEAAAILEPVFP
YP_806472.1        VPITV-DN-------------------------------------RVVAIMDIDSPTLDRFSENDEAI-LTKFGETLAAHLD
YP_001987415.1     VPITV-DN-------------------------------------RVVAIMDIDSPTLDRFSENDEAI-LTKFGETLAAHLD
NP_785802.1        VPITK-DG-------------------------------------HQIGVLDVDSPSLDRFNADNEAE-LTEFVAILTSHID
YP_818384.1        VPIFK-NG-------------------------------------QIYGIIDIDSPLLNRFGENEKNE-VEELAEILANHI-
YP_001621174.1     IPIRH-NG-------------------------------------AIWAILDLDSPVENRFDKDLVDF-LQQFGLLIENYID
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FIGURE SI: Sequence alignment of all putative fRMsr proteins.
The sequences of 358 putative fRMsrs were generated by PEDANT database (http://pedant.gsf.de/) and aligned with Bioedit software. The numbering of amino acid residues is based on the *E. coli* fRMsr sequence. For reason of clarity, only the alignment between residues 19 and 170 is represented. The residues conserved at least at 95 % are indicated in black on red boxes (such as Y66, C94, C118, E125, D141 and D143), those conserved at least at 90% in red on blue boxes (such as F78, and C84), and finally, in yellow on green boxes (for example W62) those conserved at 80%.

Supplemental data

The name of each sequence correspond to NCBI reference:

C84/C94/C118 signature (333 sequences, 93%) :
NP_288269.1: *Escherichia coli O157:H7 EDL933*; YP_002403065.1: *Escherichia coli 55989*; YP_002397981.1 : *Escherichia coli ED1a* ; YP_002412850.1: *Escherichia coli UMN026*; YP_001880631.1: *Shigella boydii CDC 3083-94*; YP_002391608.1: *Escherichia coli S88*; YP_001730808.1: *Escherichia coli str. K12 substr. DH10B*; ZP_03003290.1 : *Escherichia coli 53638*; YP_001743413.1: *Escherichia coli SMS-3-5*; YP_002407226.1 : *Escherichia coli IAI39*; YP_002329476.1: *Escherichia coli O127:H6 str. E2348/69*; YP_002382399.1: *Escherichia fergusonii ATCC 35469*; ZP_03445135.1*: Escherichia coli O157:H7 str. TW14588*; YP_688895.1: *Shigella flexneri 5 str. 8401*; YP_669680.1: *Escherichia coli 536*; NP_416346.4: *Escherichia coli str.K-12 substr. MG1655*; ZP_02903917.1: *Escherichia albertii TW07627*; ZP_03282954.1: *Enterobacter cancerogenus ATCC 35316*; YP_001452718.1: *Citrobacter koseri ATCC BAA-895*; YP_001570142.1: *Salmonella enterica subsp. arizonae serovar 62:z4,z23*; NP_460803.1: *Salmonella typhimurium LT2*; YP_150310.1: *Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150*; YP_002141797.1: *Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601*; YP_002243298.1: *Salmonella enterica subsp. enterica serovar Enteritidis str. P125109*; NP_456352.1: *Salmonella enterica subsp. enterica serovar Typhi str. CT18*; NP_804849.1: *Salmonella enterica subsp. enterica serovar Typhi str. Ty2*; YP_001587603.1*: Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7*; ZP_02666379.2: *Salmonella enterica subsp. enterica serovar Heidelberg str. SL486*; ZP_02832604.2: *Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537*; YP_001177122.1: *Enterobacter sp.* 638; YP_002226291.1: *Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91*; YP_216830.1: *Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67*; NP_754135.1: *Escherichia coli CFT073*; ZP_02347214.1: *Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29*; ZP_02574893.1: *Salmonella enterica subsp. enterica serovar 4,- str. CVM23701*; ZP_02659310.1: *Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191*; ZP_02663512.1: *Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480*; ZP_02681881.1: *Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066*; ZP_02696584.1: *Salmonella enterica subsp. enterica serovar Newport str. SL317*; YP_002041101.1: *Salmonella enterica subsp. enterica serovar Newport str. SL254*; YP_002045892.1: *Salmonella enterica subsp. enterica serovar Heidelberg str. SL476*; ZP_03075263.1: *Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188*; YP_002114879.1: *Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633*; YP_002146178.1: *Salmonella enterica subsp. enterica serovar Agona str. SL483*; ZP_03165709.1: *Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23*; YP_002215294.1: *Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853*; ZP_03221812.1: *Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433*; ZP_03342093.1: *Salmonella enterica subsp. enterica serovar Typhi str. 404ty*; ZP_03347154.1*: Salmonella enterica subsp. enterica serovar Typhi str. E00-7866*; ZP_03352578.1: *Salmonella enterica subsp. enterica serovar Typhi str. E01-6750*; ZP_03357060.1: *Salmonella enterica subsp. enterica serovar Typhi str. E02-1180*; ZP_03371453.1: *Salmonella enterica subsp. enterica serovar Typhi str. E98-2068*; ZP_03379701.1: *Salmonella enterica subsp. enterica serovar Typhi str. J185*; ZP_03383790.1: *Salmonella enterica subsp. enterica serovar Typhi str. M223*; ZP_03412299.1: *Salmonella enterica subsp. enterica serovar Typhi str. E98-3139*; ZP_03217260.1: *Salmonella enterica subsp. enterica serovar Virchow str. SL491*; YP_002237781.1: *Klebsiella pneumoniae 342;* YP_001336004.1: *Klebsiella pneumoniae subsp. pneumoniae MGH 78578*; YP_001437512.1: *Enterobacter sakazakii ATCC BAA-894*; ZP_03403067.1: *Salmonella enterica subsp. enterica serovar Typhi str. AG3*; YP_001907453.1: Erwinia tasmaniensis Et1/99; YP_001006127.1: Yersinia enterocolitica subsp. enterocolitica 8081; NP_669181.1: Yersinia pestis KIM; NP_993079.1: Yersinia pestis biovar Microtus str. 91001; YP_070893.1: Yersinia pseudotuberculosis IP 32953; YP_651729.1: Yersinia pestis Antiqua; YP_647856.1: Yersinia pestis Nepal516; YP_001163103.1: Yersinia pestis Pestoides F; ZP_01888376.1: Yersinia pestis CA88-4125; YP_001400647.1: Yersinia pseudotuberculosis IP 31758; YP_001607069.1: Yersinia pestis Angola; ZP_02221459.1: Yersinia pestis

biovar Orientalis str. F1991016; ZP_02227087.1: Yersinia pestis biovar Orientalis str. IP275; ZP_02229339.1: Yersinia pestis biovar Antiqua str. E1979001; ZP_02237158.1: Yersinia pestis biovar Antiqua str. B42003004; ZP_02307206.1: Yersinia pestis biovar Antiqua str. UG05-0454; ZP_02314388.1: Yersinia pestis biovar Orientalis str. MG05-1020; ZP_02318544.1: Yersinia pestis biovar Mediaevalis str. K1973002; YP_001720525.1: Yersinia pseudotuberculosis YPIII; YP_001872871.1: Yersinia pseudotuberculosis PB1/+; YP_002346706.1: Yersinia pestis CO92; YP_001478346.1: Serratia proteamaculans 568; YP_454994.1: Sodalis glossinidius str. 'morsitans'; YP_001217052.1: Vibrio cholerae O395; YP_002150764.1: Proteus mirabilis HI4320; YP_856816.1: Aeromonas hydrophila subsp. hydrophila ATCC 7966; YP_001093925.1: Shewanella loihica PV-4; YP_269525.1: Colwellia psychrerythraea 34H; NP_718189.1: Shewanella oneidensis MR-1; YP_001366642.1: Shewanella baltica OS185; YP_001554990.1: Shewanella baltica OS195; YP_737796.1: Shewanella sp. MR-7; YP_869415.1: Shewanella sp. ANA-3; NP_797987.1: Vibrio parahaemolyticus RIMD 2210633; YP_001501790.1: Shewanella pealeana ATCC 700345; YP_927460.1: Shewanella amazonensis SB2B; YP_001474222.1: Shewanella sediminis HAW-EB3; YP_963195.1: Shewanella sp. W3-18-1; YP_001183724.1: Shewanella putrefaciens CN-32; YP_733804.1: Shewanella sp. MR-4; YP_001050811.1: Shewanella baltica OS155; YP_750914.1: Shewanella frigidimarina NCIMB 400; YP_002126297.1: Alteromonas macleodii 'Deep ecotype'; YP_130129.1: Photobacterium profundum SS9; YP_001445537.1: Vibrio harveyi ATCC BAA-1116; YP_661562.1: Pseudoalteromonas atlantica T6c; YP_001674584.1: Shewanella halifaxensis HAW-EB4; YP_002417027.1: Vibrio splendidus LGP32; NP_934438.1: Vibrio vulnificus YJ016; NP_761466.1: Vibrio vulnificus CMCP6; YP_001760510.1: Shewanella woodyi ATCC 51908; YP_002312133.1: Shewanella piezotolerans WP3; YP_562727.1: Shewanella denitrificans OS217; NP_693123.1: Oceanobacillus iheyensis HTE831; YP_001699747.1: Lysinibacillus sphaericus C3-41; YP_001343242.1: Marinomonas sp. MWYL1; YP_001141806.1: Aeromonas salmonicida subsp. salmonicida A449; YP_204661.1: Vibrio fischeri ES114; YP_301135.1: Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305; YP_002156075.1: Vibrio fischeri MJ11; NP_244074.1: Bacillus halodurans C-125; YP_001559126.1: Clostridium phytofermentans ISDg; YP_080250.1: Bacillus licheniformis ATCC 14580; YP_253122.1: Staphylococcus haemolyticus JCSC1435; YP_261333.1: Pseudomonas fluorescens Pf-5; YP_001187407.1: Pseudomonas mendocina ymp; YP_001422246.1: Bacillus amyloliquefaciens FZB42; YP_001748360.1: Pseudomonas putida W619; YP_155660.1: Idiomarina loihiensis L2TR; NP_744032.1: Pseudomonas putida KT2440; YP_001269146.1: Pseudomonas putida F1; YP_236680.1: Pseudomonas syringae pv. syringae B728a; YP_001667695.1: Pseudomonas putida GB-1; YP_188854.1: Staphylococcus epidermidis RP62A; YP_002275225.1: Gluconacetobacter diazotrophicus PAl 5; YP_804779.1: Pediococcus pentosaceus ATCC 25745; NP_470973.1: Listeria innocua Clip11262; YP_607257.1: Pseudomonas entomophila L48; YP_001860169.1: Burkholderia phymatum STM815; NP_465120.1: Listeria monocytogenes EGD-e; NP_372242.1: Staphylococcus aureus subsp. aureus Mu50; NP_374828.1: Staphylococcus aureus subsp. aureus N315; YP_001247140.1: Staphylococcus aureus subsp. aureus JH9; YP_001316940.1: Staphylococcus aureus subsp. aureus JH1; YP_001442294.1: Staphylococcus aureus subsp. aureus Mu3; YP_002314836.1: Anoxybacillus flavithermus WK1; YP_001814701.1: Exiguobacterium sibiricum 255-15; NP_646478.1: Staphylococcus aureus subsp. aureus MW2; YP_043764.1: Staphylococcus aureus subsp. aureus MSSA476; YP_186602.1: Staphylococcus aureus subsp. aureus COL; YP_494359.1: Staphylococcus aureus subsp. aureus USA300; YP_500333.1: Staphylococcus aureus subsp. aureus NCTC 8325; YP_001332646.1: Staphylococcus aureus subsp. aureus str. Newman; YP_001575592.1 : Staphylococcus aureus subsp. aureus USA300_TCH1516; ZP_02759966.1: Staphylococcus aureus subsp. aureus USA300_TCH1516; YP_001487827.1: Bacillus pumilus SAFR-032; YP_417047.1: Staphylococcus aureus RF122; YP_041183.1: Staphylococcus aureus subsp. aureus MRSA252; YP_176251.1: Bacillus clausii KSM-K16; YP_002349929.1: Listeria monocytogenes HCC23; YP_001376537.1: Bacillus cereus subsp. cytotoxis NVH 391-98; YP_784647.1: Bordetella avium 197N; YP_557760.1: Burkholderia xenovorans LB400; YP_275769.1: Pseudomonas syringae pv. phaseolicola 1448A; YP_001118914.1: Burkholderia vietnamiensis G4; YP_001782545.1: Clostridium botulinum B1 str. Okra; NP_882192.1: Bordetella pertussis Tohama I; YP_001894915.1: Burkholderia phytofirmans PsJN; YP_001647268.1: Bacillus weihenstephanensis KBAB4; NP_882465.1: Bordetella parapertussis 12822; YP_002448219.1: Bacillus cereus G9842; NP_834359.1: Bacillus cereus ATCC 14579; YP_002369448.1:

Bacillus cereus B4264; YP_191278.1: Gluconobacter oxydans 621H; NP_886654.1: Bordetella bronchiseptica RB50; NP_847103.1: Bacillus anthracis str. Ames; YP_030799.1: Bacillus anthracis str. Sterne; NP_981083.1: Bacillus cereus ATCC 10987; YP_038702.1: Bacillus thuringiensis serovar konkukian str. 97-27; YP_002340711.1: Bacillus cereus AH187; YP_085975.1: Bacillus cereus E33L; YP_002453717.1: Bacillus cereus AH820; YP_772921.1: Burkholderia ambifaria AMMD; YP_001843726.1: Lactobacillus fermentum IFO 3956; YP_942902.1: Psychromonas ingrahamii 37; YP_121651.1: Nocardia farcinica IFM 10152; YP_001633478.1: Bordetella petrii DSM 12804; YP_001392189.1: Clostridium botulinum F str. Langeland; YP_795394.1: Lactobacillus brevis ATCC 367; YP_002284153.1: Rhizobium leguminosarum bv. trifolii WSM2304; YP_001255404.1: Clostridium botulinum A str. ATCC 3502; YP_001385170.1: Clostridium botulinum A str. ATCC 19397; YP_001388639.1: Clostridium botulinum A str. Hall; YP_001347703.1: Pseudomonas aeruginosa PA7; NP_103622.1: Mesorhizobium loti MAFF303099; YP_001807739.1: Burkholderia ambifaria MC40-6; YP_001580337.1: Burkholderia multivorans ATCC 17616; YP_002230176.1: Burkholderia cenocepacia J2315; NP_251512.1: Pseudomonas aeruginosa PAO1; YP_459505.1: Erythrobacter litoralis HTCC2594; YP_790351.1: Pseudomonas aeruginosa UCBPP-PA14; YP_002439846.1: Pseudomonas aeruginosa LESB58; YP_001970489.1: Stenotrophomonas maltophilia K279a; YP_617023.1: Sphingopyxis alaskensis RB2256; YP_620554.1: Burkholderia cenocepacia AU 1054; YP_834795.1: Burkholderia cenocepacia HI2424; YP_148653.1: Geobacillus kaustophilus HTA426; YP_442277.1: Burkholderia thailandensis E264; YP_334263.1: Burkholderia pseudomallei 1710b; YP_001067073.1: Burkholderia pseudomallei 1106a; YP_368503.1: Burkholderia sp. 383; YP_109010.1: Burkholderia pseudomallei K96243; YP_993758.1: Burkholderia mallei SAVP1; YP_001028775.1: Burkholderia mallei NCTC 10229; YP_002026852.1: Stenotrophomonas maltophilia R551-3; YP_001764423.1: Burkholderia cenocepacia MC0-3; NP_970249.1: Bdellovibrio bacteriovorus HD100; YP_001059788.1: Burkholderia pseudomallei 668; YP_001081316.1: Burkholderia mallei NCTC 10247; YP_001875000.1: Elusimicrobium minutum Pei191; YP_278248.1: Mycoplasma synoviae 53; YP_001309672.1: Clostridium beijerinckii NCIMB 8052; YP_001576818.1: Lactobacillus helveticus DPC 4571; YP_193206.1; Lactobacillus acidophilus NCFM; YP_199405.1: Xanthomonas oryzae pv. oryzae KACC10331; YP_001915608.1: Xanthomonas oryzae pv. oryzae PXO99A; YP_002509654.1: Halothermothrix orenii H 168; YP_757341.1: Maricaulis maris MCS10; YP_810624.1: Oenococcus oeni PSU-1; YP_244708.1: Xanthomonas campestris pv. campestris str. 8004; NP_635978.1: Xanthomonas campestris pv. campestris str. ATCC 33913; XP_505859.1: Yarrowia lipolytica; NP_964546.1: Lactobacillus johnsonii NCC 533; YP_001261873.1: Sphingomonas wittichii RW1; YP_814311.1: Lactobacillus gasseri ATCC 33323; NP_298520.1: Xylella fastidiosa 9a5c; YP_001775202.1: Xylella fastidiosa M12; YP_001829224.1: Xylella fastidiosa M23; NP_778732.1: Xylella fastidiosa Temecula1; NP_246070.1: Pasteurella multocida subsp. multocida str. Pm70; YP_001997158.1: Chloroherpeton thalassium ATCC 35110; XP_645637.1: Dictyostelium discoideum AX4; XP_456263.1: Kluyveromyces lactis; YP_001300883.1: Bacteroides vulgatus ATCC 8482; YP_812434.1: Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365; NP_814796.1: Enterococcus faecalis V583; NP_358362.1: Streptococcus pneumoniae R6; YP_816246.1: Streptococcus pneumoniae D39; YP_001694316.1: Streptococcus pneumoniae Hungary19A-6; YP_001835526.1: Streptococcus pneumoniae CGSP14; YP_002037500.1: Streptococcus pneumoniae G54; NP_345351.1: Streptococcus pneumoniae TIGR4; XP_001385863.2: Pichia stipitis CBS 6054; NP_985662.1: Ashbya gossypii ATCC 10895; YP_759928.1: Hyphomonas neptunium ATCC 15444; YP_002123053.1: Streptococcus equi subsp. zooepidemicus MGCS10565; YP_002131343.1: Phenylobacterium zucineum HLK1; XP_001683506.1: Leishmania major strain Friedlin; NP_012854.1: Saccharomyces cerevisiae; XP_460154.1: Debaryomyces hansenii CBS767; XP_001801028.1: Phaeosphaeria nodorum SN15; YP_001201197.1: Streptococcus suis 98HAH33; XP_001484046.1: Pichia guilliermondii ATCC 6260; NP_274882.1: Neisseria meningitidis MC58; YP_001302571.1: Parabacteroides distasonis ATCC 8503; YP_002000650.1: Neisseria gonorrhoeae NCCP11945; YP_001682978.1: Caulobacter sp. K31; YP_002342048.1: Neisseria meningitidis Z2491; YP_207199.1: Neisseria gonorrhoeae FA 1090; XP_844799.1: Trypanosoma brucei TREU927; YP_001598496.1: Neisseria meningitidis 053442; YP_974447.1: Neisseria meningitidis FAM18; XP_001465858.1: Leishmania infantum JPCM5; YP_001280815.1: Psychrobacter sp. PRwf-1; NP_664843.1: Streptococcus pyogenes MGAS315; NP_802083.1: Streptococcus pyogenes SSI-1;

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YP_280574.1: Streptococcus pyogenes MGAS6180; YP_001128311.1: Streptococcus pyogenes str. Manfredo; YP_002286076.1: Streptococcus pyogenes NZ131; XP_390238.1: Gibberella zeae PH-1; XP_001565241.1: Leishmania braziliensis MHOM/BR/75/M2904; YP_596891.1: Streptococcus pyogenes MGAS9429; YP_600772.1: Streptococcus pyogenes MGAS2096; YP_001351938.1: Janthinobacterium sp. Marseille; XP_001910908.1: Podospora anserina DSM 980; XP_446236.1: Candida glabrata CBS 138; NP_607473.1: Streptococcus pyogenes MGAS8232; YP_060405.1: Streptococcus pyogenes MGAS10394; YP_602707.1: Streptococcus pyogenes MGAS10750; NP_269471.1: Streptococcus pyogenes M1 GAS; YP_282476.1: Streptococcus pyogenes MGAS5005; YP_598792.1: Streptococcus pyogenes MGAS10270; YP_099090.1: Bacteroides fragilis YCH46; NP_421082.1: Caulobacter crescentus CB15; YP_001034962.1: Streptococcus sanguinis SK36; YP_211509.1 : Bacteroides fragilis NCTC 9343; XP_001940256.1: Pyrenophora tritici-repentis Pt-1C-BFP; YP_001450196.1: Streptococcus gordonii str. Challis substr. CH1; XP_680937.1: Aspergillus nidulans FGSC A4; XP_001265696.1: Neosartorya fischeri NRRL 181; XP_367405.1: Magnaporthe grisea 70-15; YP_001033719.1: Lactococcus lactis subsp. cremoris MG1363; YP_812051.1: Lactococcus lactis subsp. cremoris SK11; NP_810723.1: Bacteroides thetaiotaomicron VPI-5482; YP_141537.1: Streptococcus thermophilus CNRZ1066; NP_721920.1: Streptococcus mutans UA159; YP_820528.1: Streptococcus thermophilus LMD-9; XP_001246405.1: Coccidioides immitis RS; YP_612063.1: Silicibacter sp. TM1040; YP_001727726.1: Leuconostoc citreum KM20;YP_444835.1: Salinibacter ruber DSM 13855; NP_943356.1: Klebsiella pneumoniae; YP_631535.1: Myxococcus xanthus DK 1622; YP_809822.1: Oenococcus oeni PSU-1; NP_687842.1: Streptococcus agalactiae 2603V/R; YP_329573.1: Streptococcus agalactiae A909; XP_001692446.1: Chlamydomonas reinhardtii; YP_511991.1: Jannaschia sp. CCS1; XP_719233.1: Candida albicans SC5314; NP_735295.1: Streptococcus agalactiae NEM316; YP_168601.1: Silicibacter pomeroyi DSS-3; YP_001169098.1: Rhodobacter sphaeroides ATCC 17025; XP_001216799.1: Aspergillus terreus NIH2624; YP_437091.1: Hahella chejuensis KCTC 2396; XP_001390389.1: Aspergillus niger CBS 513.88;XP_001550500.1: Botryotinia fuckeliana B05.10; XP_001273080.1: Aspergillus clavatus NRRL 1; YP_001042044.1: Rhodobacter sphaeroides ATCC 17029; YP_916587.1: Paracoccus denitrificans PD1222; XP_961529.1: Neurospora crassa OR74A; YP_351544.1: Rhodobacter sphaeroides 2.4.1; XP_001588803.1: Sclerotinia sclerotiorum 1980; XP_762195.1: Ustilago maydis 521; XP_001537789.1: Ajellomyces capsulatus NAm1; YP_001198994.1: Streptococcus suis 05ZYH33; NP_390842.1: Bacillus subtilis subsp. subtilis str. 168.

C94/C118 signature (20 sequences, 5.6%):
NP_288269.1: *Escherichia coli O157:H7 EDL933；* YP_001469780.1: *Thermotoga lettingae TMO*; NP_623333.1: *Thermoanaerobacter tengcongensis MB4*; YP_001567589.1: Petrotoga mobilis SJ95； NP_228329.1: Thermotoga maritima MSB8； YP_001244004.1: Thermotoga petrophila RKU-1; YP_001738457.1: Thermotoga sp. RQ2; YP_591728.1: Acidobacteria bacterium Ellin345； YP_001193798.1: Flavobacterium johnsoniae UW101； YP_001296902.1: Flavobacterium psychrophilum JIP02/86; XP_001439866.1: Paramecium tetraurelia strain d4-2; XP_001438779.1: Paramecium tetraurelia strain d4-2; YP_001319456.1: Alkaliphilus metalliredigens QYMF； XP_001022412.1: Tetrahymena thermophila SB210； YP_001306613.1: Thermosipho melanesiensis BI429； YP_002335308.1: Thermosipho africanus TCF52B; NP_394308.1: Thermoplasma acidophilum DSM 1728; YP_862969.1: Gramella forsetii KT0803; YP_023758.1: Picrophilus torridus DSM 9790; NP_111339.1: Thermoplasma volcanium GSS1; YP_001380982.1: Anaeromyxobacter sp. Fw109-5.

C84/C118 signature (5 sequences, 1.4%):
YP_806472.1: Lactobacillus casei ATCC 334; YP_001987415.1: Lactobacillus casei BL23; NP_785802.1: Lactobacillus plantarum WCFS1;YP_818384.1: Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293; YP_001621174.1: Acholeplasma laidlawii PG-8A