A structural determinant of mycophenolic acid resistance in eukaryotic inosine 5'-monophosphate dehydrogenases

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Supporting Information

Alignment S1. Alignment of MPA sensitive and resistant enzymes. Residues that contact MPA are highlighted in yellow. Residue 267 (*Pb*IMPDHA numbering) is highlighted in cyan.

Organism	**Abbreviation**	**Sequence**	**Comments**
Aspergillus nidulans	*An*IMPDH	AspGB An12478 [a]	MPA sensitive
Candida albicans	*Ca*IMPDH	UniProt O00086	MPA sensitive
Cricetulus griseus	*Cg*IMPDH	UniProt G3GZ89	MPA sensitive; structure of E-XMP*MPA complex 1JR1
Penicillium brevicompactum	*Pb*IMPDHA	UniProt AEP94206.1	MPA resistant; note: partial coding sequence missing N-terminal MPITASDAAP
Penicillium brevicompactum	*Pb*IMPDHB	UniProt A0A0B5L585	MPA resistant
P. rubens Wisconsin	*Pr*IMPDHA	UniProt B6HC24	formerly *P. chrysenogenum;* MPA sensitive
P. rubens Wisconsin	*Pr*IMPDHB	UniProt B6H451	formerly *P. chrysenogenum;* MPA sensitive
Saccharomyces cerevisiae	*Sc*IMPDH2	UniProt P38697	MPA resistant
Saccharomyces cerevisiae	*Sc*IMPDH3	UniProt A7A1V2	MPA sensitive
Saccharomyces cerevisiae	*Sc*IMPDH4	UniProt P50094	MPA sensitive

[a] AspGB: Aspergillus Genome Database

Percent identity matrix

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1: CgIMPDH     100.00   60.59   59.79   61.66   61.39   59.18   64.61   64.08   62.73   61.13
2: PrIMPDHB     60.59  100.00   91.62   79.62   78.48   78.88   64.16   63.34   63.34   61.42
3: PbIMPDHB     59.79   91.62  100.00   80.23   79.28   79.88   62.50   63.03   62.84   61.49
4: AnIMPDH      61.66   79.62   80.23  100.00   89.17   87.50   64.30   63.93   62.72   60.99
5: PrIMPDHA     61.39   78.48   79.28   89.17  100.00   91.81   64.68   64.89   63.48   61.95
6: PbIMPDHA     59.18   78.88   79.88   87.50   91.81  100.00   62.89   63.69   62.26   62.06
7: CaIMPDH      64.61   64.16   62.50   64.30   64.68   62.89  100.00   75.43   74.28   71.98
8: ScIMPDH4     64.08   63.34   63.03   63.93   64.89   63.69   75.43  100.00   88.91   84.13
9: ScIMPDH3     62.73   63.34   62.84   62.72   63.48   62.26   74.28   88.91  100.00   92.54
10: ScIMPDH2    61.13   61.42   61.49   60.99   61.95   62.06   71.98   84.13   92.54  100.00
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CLUSTAL O(1.2.4) multiple sequence alignment

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CgIMPDH        ------------------------------------------------------------      0
PrIMPDHB       --------------MVEVLDYTKALEVL-KEYP-GDGLHVDTLLDSDSHGALTYNDFLIL      44
PbIMPDHB       --------------MVEILDYTKALEVL-KEYPSGDGLHVDTLLDSDNHGALTYNDFLIL      45
AnIMPDH        MPIANGDA-LGRAMKAEFQDHTKALEVLEKEYPIKDGLDVDTLLDSDKHGALTYNDFLIL      59
PrIMPDHA       MPITAGDAAPGAAMKAEITDYAKALEVV-KTYTTADGLDADTLLDSDKHGALTYNDFLIL      59
PbIMPDHA       MPITASDAAPGAAMKAEITDYAKALEVV-ETYKTRDGLDVDTLIDSDKHGALTYNDFLIL      59
CaIMPDH        ----------------MVFETSKATSYL-KDYPKKDGLSVKELIDSTNFGGLTYNDFLIL      43
ScIMPDH4       -------------MSAAPLDYKKALEHL-KTYSSKDGLSVQELMDSTTRGGLTYNDFLVL      46
ScIMPDH3       --------------MAAVRDYKTALEFA-KSLPRLDGLSVQELMDSKTRGGLTYNDFLVL      45
ScIMPDH2       --------------MAAIRDYKTALDFT-KSLPRPDGLSVQELMDSKIRGGLTYNDFLIL      45


CgIMPDH        ------------------------------------------------------------      0
PrIMPDHB       PGSITFPASDVSLETKVTRRFTIKAPLLSSPMDTVTEHSMAIHMALLGGLGVIHNNCPPD      104
PbIMPDHB       PGSITFSAADVSLDTKVTRRFTIKAPLLSSPMDTVTEHNMAIHMALLGGLGVIHNNCPPD      105
AnIMPDH        PGYIGFPASDVTLDTPVTKRVTLKAPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPE      119
PrIMPDHA       PGYIGFPASDVSLDTPVTKRISLKTPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPE      119
PbIMPDHA       PGYIGFPASDVSLDTPVTKRISLKTPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPE      119
CaIMPDH        PGLINFPSSAVSLETKLTKKITLKSPFVSSPMDTVTEENMAIHMALLGGIGIIHHNCTSE      103
ScIMPDH4       PGLVNFPSSAVSLQTKLTKKITLNTPFVSSPMDTVTEADMAIYMALLGGIGFIHHNCTPK      106
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ScIMPDH3      PGLVDFPSSEVSLQTKLTRNITLNTPFVSSPMDTVTESEMAIFMALLGGIGFIHHNCTPE      105
ScIMPDH2      PGLVDFASSEVSLQTKLTRNITLNIPLVSSPMDTVTESEMATFMALLGGIGFIHHNCTPE      105


CgIMPDH       ---------------------------------------GFSGIPITA------------      9
PrIMPDHB      EQAEMVRKVKRYENGFIQDPIVLSPETTVGEAKELKTKWGFGGFPVTE------------      152
PbIMPDHB      DQAEMVRKVKRYENGFILDPVVLSPSTTVAEAKELKTKWNFGGFPVTGKTHYLSSFGKLA      165
AnIMPDH       DQAEMVRKVKRYENGFILDPVVLSPRATVREAKELKAKWGFGGFPVTE------------      167
PrIMPDHA      DQAEMVRKVKRYENGFILDPVVISPKATVGEVKELKAKWGFGGFPVTE------------      167
PbIMPDHA      AQAEMVRKVKRYENGFILDPVVLSPQATVGEAKELKAKWGFGGFPVTE------------      167
CaIMPDH       EQAEMVRKVKKYENGFINDPVVISPEVTVGEVKKMGEVLGFTSFPVTE------------      151
ScIMPDH4      EQASMVKKVKMFENGFINSPIVISPTTTVGEVKVMKRKFGFSGFPVTE------------      154
ScIMPDH3      DQADMVRRVKNYENGFINNPIVISPTTTVGEAKSMKERFGFSGFPVTE------------      153
ScIMPDH2      DQADMVRRVKNYENGFINNPIVISPTTTVGEAKSMKEKYGFAGFPVTT------------      153
                                                     .* .:*:*

CgIMPDH       ---------TGTMGSKLVGIVTSRDIDFLAEKDHTTLLSEVMTPRIELVVAPAGVTLKEA      60
PrIMPDHB      ---------KGTLLSKLLGIVTSRDIQFHKNHE--DPVTAVMM--TDLVTAPAGTTLAEA      199
PbIMPDHB      SSDSFSLLEKGTLHSKLLGIVTSRDIQFHKTPE--DPVTAVMS--TELVTAPAGTTLAEA      221
AnIMPDH       ---------NGTLRSKLVGIVSTRDIQFHNNLD--DSVTAIMS--TDLVTAPAGTTLAEA      214
PrIMPDHA      ---------NGTLKSKLVGMVTSRDIQFHTDLN--EPVTAVMA--TDLVTAPAGTTLTEA      214
PbIMPDHA      ---------NGTLRSKLVGMVTSRDIQFHHNLS--DPVTAIMA--TDLVTAPAGTTLAEA      214
CaIMPDH       ---------NGKVGGKLVGIITSRDIQFHEDNK--SPVSEVMT--KDLVVGKKGISLTDG      198
ScIMPDH4      ---------DGKCPGKLVGLVTSRDIQFLEDDS--LVVSEVMT--KNPVTGIKGITLKEG      201
ScIMPDH3      ---------DGKRNGKLMGIVTSRDIQFVEDNS--LLVQDVMT--KNPVTGAQGITLSEG      200
ScIMPDH2      ---------DGKRNAKLVGVITSRDIQFVEDNS--LLVQDVMT--KNPVTGAQGITLSEG      200
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CgIMPDH       NEILQRSKKGKLPIVNDQDELVAIIARTDLKKNRDYPLASKDSH-KQLLCGAAVGTREDD      119
PrIMPDHB      NEVLRSSKKGKLPIVDKDGSLISLLSRSDLMKNIHYPLASKLPS-KQLLCAAAISTHDAD      258
PbIMPDHB      NEVLRSSKKGKLPIVDKDGLLVSLLSRSDLMKNIHYPLASKLPS-KQLLCAAAISTHDAD      280
AnIMPDH       NEVLRSSKKGKLPIVDENGSLVSLLSRSDLMKNLHYPLASKLPASKQLICAAAIGTREED      274
PrIMPDHA      NQVLRQSKKGKLPIVDANGNIVSLLSRSDLMKNLHYPLASKLPDSKQLICAAAIGTREED      274
PbIMPDHA      NEVLRQSKKGKLPIVDASGNIVSLLSRSDLMKNLHYPLASKLPDSKQLICAASIGTREED      274
CaIMPDH       NELLRSSKKGKLPIVDAEGNLVSLISRTDLQKNQDYPNASKSFHSKQLLCGAAIGTIDAD      258
ScIMPDH4      NEILKQTKKGKLLIVDDNGNLVSMLSRADLMKNQNYPLASKSATTKQLLCGAAIGTIEAD      261
ScIMPDH3      NEILKKIKKGKLLIVDDNGNLVSMLSRTDLMKNQNYPLASKSATTKQLLCGAAIGTIDAD      260
ScIMPDH2      NEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNQNYPLASKSANTKQLLCGASIGTMDAD      260
              *::*:  ***:* :*: .. ::::::*:** ** .** ***    ***:*.*::.* : *

CgIMPDH       KYRLDLLTQAGADVIVLDSSQGNSVYQIAMVHYIKQKYPHLQVIGGNVVTAAQAKNLIDA      179
PrIMPDHB      KVRLEKLVDAGLDIVVVDSSQGHSIFQIAMIKYIKQTFPDIDVIGGNIVTREQAAALIAA      318
PbIMPDHB      KVRLQKLVDAGLDIVVVDSSQGNSMYQIAMIKWIKSTFPDIDIIAGNIVTREQAAALIAA      340
AnIMPDH       KHRLKLLVEAGLDIVILDSSQGNSMYQIEMIKYIKKTYPEIDVIGGNVVTRDQAAALIAA      334
PrIMPDHA      KKRLQLLVEAGLDIVILDSSQGNSMYQIEMIKYIKKNMPEIDVIGGNVVTREQAAALIAA      334
PbIMPDHA      KRRLQLLVDAGLDIVILDSSQGNSMYQIEMIKYVKKELPQIDVIGGNVVTREQAAALIAA      334
CaIMPDH       RERLDKLVEAGLDVVVLDSSNGSSVFQLNMIKWIKEKYPELQVIAGNVVTREQAALLIEA      318
ScIMPDH4      KERLRLLVEAGLDVVILDSSQGNSVFQLNMIKWIKETFPDLEIIAGNVATREQAANLIAA      321
ScIMPDH3      KERLRLLVEAGLDVVILDSSQGNSIFQLNMIKWIKETFPDLEIIAGNVATREQAANLIAA      320
ScIMPDH2      KERLRLLVKAGLDVVILDSSQGNSIFELNMLKWVKESFPGLEVIAGNVVTREQAANLIAA      320
              : **  *..** *::::***:* *:::: *::::*.  * :::*.**:.*  **  ** *

CgIMPDH       GVDGLRVGMGCGSICITQEVMACGRPQGTAVYKVAEYARRFGVPVIADGGIQTVGHVVKA      239
PrIMPDHB      GADGLRIGMGSGSACITQEVMAAGRPQAAAVRSVSAFAARFGVPTIADGGVQNLGHIVKG      378
PbIMPDHB      GADGLRIGMGSGSACITQEVMAVGRPQAASVRSVSAFAARFGVPTIADGGVQNLGHIVKG      400
AnIMPDH       GVDGLRIGMGSGSACITQEVMAVGRPQALSVRRVTQFAARFGVPCIADGGIQNVGHIVKG      394
PrIMPDHA      GVDGLRIGMGSGSACITQEVMAVGRPQAASVRSVASFAARFGVPCIADGGIQNVGHIVKG      394
PbIMPDHA      GVDGLRIGMGSGSACITQEVMAVGRPQAASVRSVSSFAARFGVPCIADGGVQNLGHIVKG      394
CaIMPDH       GADALRIGMGSGSICITQEVMACGRPQGTAVYGVTEFANKFGVPCIADGGIGNIGHITKA      378
ScIMPDH4      GADGLRIGMGSGSICITQEVMACGRPQGTAVYNVCQFANQFGVPCMADGGVQNIGHITKA      381
ScIMPDH3      GADGLRIGMGSGSICITQEVMACGRPQGTAVYNVCEFANQFGIPCMADGGVQNIGHITKA      380
ScIMPDH2      GADGLRIGMGTGSICITQEVMACGRPQGTAVYNVCEFANQFGVPCMADGGVQNIGHITKA      380
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CgIMPDH       LALGASTVMMGSLLAATTEAPGEYFFS-DGVRLKKYRGMGSLDAMEKSS-----------      287
PrIMPDHB      LALGASAVMMGSLLAGTTESPGEYFMSSEGQLVKAFRGMGSIAVMEDKSKSGAGN-----      433
PbIMPDHB      LALGASAVMMGSLLAGTTESPGEYYVSNEGQLVKAFRGMGSIAVMEDKGKSGGGK-----      455
AnIMPDH       LAMGATTVMMGGLLAGTTESPGEYFVSNEGQLVKAYRGMGSIAAMEDKKAGGNGKDSKAS      454
PrIMPDHA      LAMGASTIMMGGLLAGTTESPGEYFVSNEGQLVKAYRGMGSIAAMEDKKAGGDGKDSKAS      454
PbIMPDHA      LAMGASTVMMGGLLAGTTESPGEYYVSNEGQLVKAYRGMGSIAAMEDKKAGNGAKDSKAS      454
CaIMPDH       LALGASCVMMGGLLAGTAETPGDYFYR-DGKRLKTYRGMGSIDAMQQTNTNA--------      429
ScIMPDH4      LALGSSTVMMGGMLAGTTESPGEYFYK-DGKRLKAYRGMGSIDAMQKTGNKG--------      432
ScIMPDH3      LALGSSTVMMGGMLAGTTESPGEYFYQ-DGKRLKAYRGMGSIDAMQKTGTKG--------      431
ScIMPDH2      LALGSSTVMMGGMLAGTTESPGEYFYQ-DGKRLKAYRGMGSIDAMQKTGTKG--------      431
              **:*:: :***.:**.*:*:**:*:   :*  :* :*****: .*:..

CgIMPDH       -SSQKRYFSEGDKVKIAQGVSGSIQDKGSIQKFVPYLIAGIQHGCQDIGAQSLSVLRSMM      346
PrIMPDHB      NAGASRYFSENDKVKVAQGVAGSVIDRGSITQYVPYLVAGVQHSLQDIGVQNLDALRDGV      493
PbIMPDHB      NAGASRYFSENDKVKVAQGVAGSVVDRGSITQYVPYLVAGIQHSLQDIGVQDLEALHNGV      515
AnIMPDH       NAGTARYFSEKDRVLVAQGVAGSVLDRGSVTKFVPYLVAGVQHSLQDIGVSSLQQLHEGV      514
PrIMPDHA      NAGTARYFSEKDRVLVAQGVAGSVLDRGSVTKFVPYLVAGVQHSLQDIGVKSLADLHDGV      514
PbIMPDHA      NAGTARYFSEKSNVLVAQGVAGSVLDRGSVTKFIPYLVAGVQHSLQDIGVPSLSAMHAGV      514
CaIMPDH       NASTSRYFSEADKVLVAQGVSGSVVDKGSITKFVPYLYNGLQHSLQDIGIKSIDELRENV      489
ScIMPDH4      NASTSRYFSESDSVLVAQGVSGAVVDKGSIKKFIPYLYNGLQHSCQDIGCESLTSLKENV      492
ScIMPDH3      NASTSRYFSESDSVLVAQGVSGAVVDKGSIKKFIPYLYNGLQHSCQDIGYKSLTLLKENV      491
ScIMPDH2      NASTSRYFSESDSVLVAQGVSGAVVDKGSIKKFIPYLYNGLQHSCQDIGCRSLTLLKNNV      491
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CgIMPDH       YSGELKFEKRTMSAQIEGGVHGLHSYEKRLY--      377
PrIMPDHB      NNGTVRFEMRSASAQTEGNVHGLHTHEKKLYS-      525
PbIMPDHB      NNGQVRFEMRSASAQTEGNVHGLHSHEKKLYSS      548
AnIMPDH       NNGTVRFEVRSASAMAEGNVHGLHSYDKKLYS*      546
PrIMPDHA      NKGTVRFEMRSASAMTEGNVHGLHSYDKKLYS-      546
PbIMPDHA      DNGTVRFEMRSASAMTEGNVHGL----------      537
CaIMPDH       DNGEIRFEFRTASAQFEGGVHGLHSYEKRLHN-      521
ScIMPDH4      QNGEVRFEFRTASAQLEGGVHNLHSYEKRLYN-      524
ScIMPDH3      QSGKVRFEFRTASAQLEGGVHNLHSYEKRLHN-      523
ScIMPDH2      QRGKVRFEFRTASAQLEGGVHNLHSYEKRLHN-      523
                * ::** *: **  **.**.*
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Alignment S1. Alignment of Aspergillus IMPDHs. Residue 267 (*Pb*IMPDHA numbering) is highlighted in yellow.

Species	**IMPDH sequence**	**Comment**
Aspergillus aculeatinus	XP_025509000.1	
Aspergillus bombycis	XP_022386829.1	
Aspergillus brunneoviolaceus	XP_025436855.1	
Aspergillus campestris	XP_024695056.1	
Aspergillus candidus	XP_024671855.1	Silage (1); optimal temperature 20-24 C (1)
Aspergillus clavatus	XP_001272822.1	Wheat silage (1); optimal temperature 24-25 C (1)
Aspergillus eucalypticola	XP_025391094.1	
Aspergillus fischeri	XP_001265922.1	
Aspergillus fumigatus	XP_749494.1	Corn silage (2) ; optimal temperature 37 C (1)
Aspergillus glaucus	XP_022403647.1	Pioneer species in grain silage (1); optimal temperature 24-25 C (1)
Aspergillus heteromorphus	XP_025403602.1	
Aspergillus homomorphus	XP_025550436.1	
Aspergillus ibericus	XP_025572109.1	
Aspergillus japonicus	XP_025522930.1	
Aspergillus lacticoffeatus	XP_025451440.1	
Aspergillus neoniger	XP_025478868.1	
Aspergillus niger	XP_001391892.2	Wheat silage (1); optimal temperature 35-37 C (1)
Aspergillus nomius	XP_015408913.1	
Aspergillus novofumigatus	XP_024686877.1	
Aspergillus oryzae	XP_001823965.1	Corn silage (3); optimal temperature 35-37 C (1)
Aspergillus piperis	XP_025510507.1	
Aspergillus saccharolyticus	XP_025435086.1	
Aspergillus sclerotionige	XP_025464902.1	
Aspergillus steynii	XP_024700898. 1	Does not grow at 37 C (4)
Aspergillus terreus	XP_001218150.1	Silage (1; 2)
Aspergillus uvarum	XP_025490880.1	
Aspergillus vadensis	XP_025560215.1	
Penicilliopsis zonata	XP_022581501.1	formerly *A. zonata;* optimal temperature 24-25 C (ATCC 16867 product sheet)

References

1. Panasenko VT (1967) Ecology of microfungi. Bot Rev 33:189-215.
2. Wambacq E, Vanhoutte I, Audenaert K, De Gelder L, Haesaert G (2016) Occurrence, prevention and remediation of toxigenic fungi and mycotoxins in silage: a review. J Sci Food Agric 96:2284-2302. PMID: 26676761 {Medline}
3. Zulkifli NA, Zakaria L (22017) Morphological and Molecular Diversity of Aspergillus From Corn Grain Used as Livestock Feed. HAYATI Journal of Biosciences 24:26-34.
4. Frisvad JC, Frank JM, Houbraken JAMP, Kuijpers AFA, Samson RA (2004) New ochratoxin A producing species of Aspergillus section Circumdati. Stud Mycol 50:23-43.

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CLUSTAL O(1.2.4) multiple sequence alignment


XP_022581501.1      ------------MKAEIQDHTKALEVL-KEYKTQDGLDVDTLLDSDKHGALTYNDFLILP    47
XP_024695056.1      MPISKGDSLGMAMPAEIQDYSKALDVLEKDYSSRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_024671855.1      MPISKGDSLGMAMPAEIQDYSKALDVLEKDYSSRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_022403647.1      MTLGQGDNQGLAMKAEIQDYSKALDVLEKDYPTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_025403602.1      MPIANGDSLGRAMKAEIQDHTKALEVLEKDYQTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_025435086.1      MTFANGDIPGPAMKAEIQDYTKAVEVLKNEYKVSDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_025550436.1      MTFANGDIPGPAMKAEIQDYTKALEVLKQEYTTSDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_025436855.1      MTFANGDIPGPAMKAEIQDYTKALEVLQKEYTTSDGLDIDTLLDSDKHGALTYNDFLILP    60
XP_025509000.1      MTFANGDIPGPAMKAEIQDYTKALEVLQKEYTTSDGLDIDTLLDSDKHGALTYNDFLILP    60
XP_025490880.1      ------------------------------------------------------------    0
XP_025522930.1      MTFANGDIPGPAMKAEIQDYTKALEVLQKEYTTSDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_025451440.1      ------------------------------------------------------------    0
XP_001391892.2      MPISNGDSLGRAMQAEIQDHTKALEVL-KTYTTQDGLDVDTLLDSDKHGALTYNDFLILP    59
XP_025560215.1      ------------------------------------------------------------    0
XP_025391094.1      MPISNGDSLGRAMQAEIQDHTKALEVL-KTYTTQDGLDVDTLLDSDKHGALTYNDFLILP    59
XP_025510507.1      MPISNGDSLGRAMQAEIQDHTKALEVL-KTYTTQDGLDVDTLLDSDKHGALTYNDFLILP    59
XP_025478868.1      ------------------------------------------------------------    0
XP_025464902.1      ------------------------------------------------------------    0
XP_025572109.1      MPISNGDSLGRAMQAEIQDHTKALEVLAQEYTTGDGLDIDTLLDSDKHGALTYNDFLILP    60
XP_024700898.1      MPISNGDALGRAMKAEIQDHTKALEVLEKEYPSRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_001218150.1      MPISNGDSLGRAMHAEIQDYTKALEVLEKDYTTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_001823965.1      MPISNGDALGRAMKAEIEDHTKALEVLEKDYTTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_022386829.1      MPISNGDALGRAMKAEIQDHTKALEVLEKDYTSRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_015408913.1      MPISNGDALGRAMKAEIQDHTKALEVLEKDYTSRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_001272822.1      MPIANGDALGRAMKAEIQDHTKALEVLEKEYSTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_749494.1         MPIANGDSLGCAMKADIQDYTKALEILEKEYTTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_024686877.1      MPIANRDSLGRAMKAEIQDYTKALEVLEKEYTTRDGLDVDTLLDSDKHGALTYNDFLILP    60
XP_001265922.1      MPIANGDSLGRAMKAEIQDHTKALEVLEKEYTTRDGLDVDTLLDSDKHGALTYNDFLILP    60


XP_022581501.1      GYIGFAASEIALDSPITKRITLKAPLVSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPED    107
XP_024695056.1      GYIGFPASDVVLDTPVTKRVTLKTPLVSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPDE    120
XP_024671855.1      GYIGFPASDVVLDTPVTKRVTLKTPLVSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPDE    120
XP_022403647.1      GHVGFTASDVTLDTPVTKRITLKAPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSAED    120
XP_025403602.1      GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPEA    120
XP_025435086.1      GYIGFPASDVTLDTAVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPQD    120
XP_025550436.1      GYIGFPASDVTLDTAVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPQD    120
XP_025436855.1      GYIGFPASDVTLDTAVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPQD    120
XP_025509000.1      GYIGFPASDVTLDTAVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPQD    120
XP_025490880.1      ------------------------------MDTVTEHNMAIHMALLGGLGIIHHNCSPQD    30
XP_025522930.1      GYIGFPASDVTLDTAVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGIIHHNCSPQD    120
XP_025451440.1      ------------------------------MDTVTEHNMAIHMALLGGLGVIHHNCAPEE    30
XP_001391892.2      GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCAPEE    119
XP_025560215.1      ------------------------------MDTVTEHNMAIHMALLGGLGVIHHNCAPED    30
XP_025391094.1      GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCAPEE    119
XP_025510507.1      GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCAPEE    119
XP_025478868.1      ------------------------------MDTVTEHNMAIHMALLGGLGVIHHNCAPEE    30
XP_025464902.1      -MTGFPASDVSLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCAPAE    59
XP_025572109.1      GYIGFPASDVSLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCAPAE    120
XP_024700898.1      GYIGFPASDVSLDTPVTKRIGLKAPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSAED    120
XP_001218150.1      GYIGFPASEVTLDTPVTKRVSLKAPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPEA    120
XP_001823965.1      GYIGFPASDVTLDTPVTKRVSLKAPLLSSPMDTVTEHNMAIHMALLGGLGIIHHNCSPED    120
XP_022386829.1      GYIGFPASDVTLDTPVTKRVSLKAPLLSSPMDTVTEHNMAIHMALLGGLGIIHHNCSPED    120
XP_015408913.1      GYIGFPASDVTLDTPVTKRVSLKAPLLSSPMDTVTEHNMAIHMALLGGLGIIHHNCSPED    120
XP_001272822.1      GYIGFAASDVSLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCAPED    120
XP_749494.1         GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPED    120
XP_024686877.1      GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPED    120
XP_001265922.1      GYIGFPASDVTLDTPVTKRVSLKVPLLSSPMDTVTEHNMAIHMALLGGLGVIHHNCSPED    120
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XP_022581501.1      QAEMVRKVKRYENGFISDPVVLSPTATVADAKELKAKWGFGGFPVTENGTLRSKLIGIIT    167
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XP_024695056.1      QAEMVRKVKRYENGFILDPVVLAPTATVGEAKELKAKWGFGGFPVTENGTLRSKIIGMVT    180
XP_024671855.1      QAEMVRKVKRYENGFILDPVVLAPTATVGEAKELKAKWGFGGFPVTENGTLRSKIIGMVT    180
XP_022403647.1      QAEMVRKVKRYENGFILDPVVLSPNATVGEAKDLKARWGFGGFPVTENGTLRSKLVGMVT    180
XP_025403602.1      QAEMVRKVKRYENGFILDPVVLSPKATVAEAKELKAKWGFGGFPVTENGTLRSKLVGIVT    180
XP_025435086.1      QAEMVRKVKRYENGFILDPVVLAPTATVREAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_025550436.1      QAEMVRKVKRYENGFILDPVVLAPTATVREAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_025436855.1      QAEMVRKVKRYENGFILDPVVLSPTATVREAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_025509000.1      QAEMVRKVKRYENGFILDPVVLSPTATVREAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_025490880.1      QAEMVRKVKRYENGFILDPVVLSPTATVQEAKELKAKWGFGGFPVTENGTLRSKLVGMVT    90
XP_025522930.1      QAEMVRKVKRYENGFILDPVVLSPTATVQEAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_025451440.1      QAEMVRKVKRYENGFISDPVVLSPKATVREAKELKAKWGFGGFPVTENGTLRSKLVGIVT    90
XP_001391892.2      QAEMVRKVKRYENGFISDPVVLSPKATVREAKELKAKWGFGGFPVTENGTLRSKLVGIVT    179
XP_025560215.1      QAEMVRKVKRYENGFISDPVVLSPKASVREAKELKAKWGFGGFPVTENGTLRSKLVGIVT    90
XP_025391094.1      QAEMVRKVKRYENGFISDPVVLSPKATVREAKELKAKWGFGGFPVTENGTLRSKLVGIVT    179
XP_025510507.1      QAEMVRKVKRYENGFISDPVVLSPKATVREAKELKAKWGFGGFPVTENGTLRSKLVGIVT    179
XP_025478868.1      QAEMVRKVKRYENGFISDPVVLSPKATVREAKELKAKWGFGGFPVTENGTLRSKLVGIVT    90
XP_025464902.1      QAEMVRKVKRYENGFISDPVVLSPKATVSEAKELKAKWGFGGFPVTENGTLRSKLVGIVT    119
XP_025572109.1      QAEMVRKVKRYENGFISDPVVLSPKATVSEAKELKAKWGFGGFPVTENGTLRSKLVGIVT    180
XP_024700898.1      QAEMVRKVKRYENGFILDPVVLSPSATVGEAKDLKTKWGFGGFPVTENGTLRSKLVGMVT    180
XP_001218150.1      QAEMVRKVKRYENGFILDPVVLSPKATVGEAKDLKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_001823965.1      QAEMVRKVKRYENGFILDPVVLSPKATVGEAKELKSKWGFGGFPVTESGNLRSKLVGIVT    180
XP_022386829.1      QAEMVRKVKRYENGFILDPVVLSPNATVGEAKELKSKWGFGGFPVTESGNLRSKLVGIVT    180
XP_015408913.1      QAEMVRKVKRYENGFILDPVVLSPKATVGEAKELKSTWGFGGFPVTESGNLRSKLVGIVT    180
XP_001272822.1      QAEMVRKVKRYENGFILDPVVLSPKATVGEAKELKAQWGFGGFPVTENGTLRSKLVGMVT    180
XP_749494.1         QAEMVRKVKRYENGFILDPVVLSPKATVGEAKALKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_024686877.1      QAEMVRKVKRYENGFILDPVVLSPKATVGEAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
XP_001265922.1      QAEMVRKVKRYENGFILDPVVLSPKATVGEAKELKAKWGFGGFPVTENGTLRSKLVGMVT    180
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XP_022581501.1      TRDIQFHPNPEDPVTAVMATDLVTAPAGTTLAEANDVLRSSKKGKLPIVDENGNLISLLS    227
XP_024695056.1      SRDIQFHNNSSDPVTNVMSTDLITAPAGTTLAEANDVLRSSKKGKLPIVDDNGNIVSLLS    240
XP_024671855.1      SRDIQFHNNSSDPVTNVMSTDLITAPAGTTLAEANDVLRSSKKGKLPIVDDNGNIVSLLS    240
XP_022403647.1      SRDIQFHPSLDDPVTAIMATDLVTAPAGTTLAEANDVLRSSKKGKLPIVDGEGNLVSLLS    240
XP_025403602.1      SRDIQFHPNGEDSVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNIVSLLS    240
XP_025435086.1      SRDIQFHRDLDAPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNIVSLLS    240
XP_025550436.1      TRDIQFHCDLDAPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIIDENGNIVSLLS    240
XP_025436855.1      SRDIQFHRDLDAPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDTNGNLVSLLS    240
XP_025509000.1      SRDIQFHRDLDAPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDTNGNIVSLLS    240
XP_025490880.1      SRDIQFHRDLDAPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDTNGNLVSLLS    150
XP_025522930.1      SRDIQFHRDLDAPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDTNGNLVSLLS    240
XP_025451440.1      SRDIQFHHDLDDSVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNLVSLLS    150
XP_001391892.2      SRDIQFHHDLDDSVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNLVSLLS    239
XP_025560215.1      SRDIQFHGDLDDSVTAIMSTDLITAPAGTTLAEANEVLRSSKKGKLPIVDENGNLVSLLS    150
XP_025391094.1      SRDIQFHRDLDDSVTAIMSTDLITAPAGTTLAEANEVLRSSKKGKLPIVDENGHLVSLLS    239
XP_025510507.1      SRDIQFHRDLDDSVTAIMSTDLITAPAGTTLAEANEVLRSSKKGKLPIVDENGHLVSLLS    239
XP_025478868.1      SRDIQFHRDLDDSVTAIMSTDLITAPAGTTLAEANEVLRSSKKGKLPIVDENGHLVSLLS    150
XP_025464902.1      SRDIQFHNNVNDPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNLISLLS    179
XP_025572109.1      SRDIQFHNNLEDPVTVIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNLVSLLS    240
XP_024700898.1      SRDIQFHHKLDDPVTAIMATDLVTAPAGTTLAEANEVLRSSKKGKLPIVDESGNLVSLLS    240
XP_001218150.1      SRDIQFHPNLDDPVTAIMTTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDENGNLVSLLS    240
XP_001823965.1      SRDIQFHPNLEDPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDNDGNLVSLLS    240
XP_022386829.1      SRDIQFHPKPEDPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDKDGNLVSLLS    240
XP_015408913.1      SRDIQFHPNLDDPVTAIMSTDLVTAPAGTTLAEANEVLRSSKKGKLPIVDKDGNLVSLLS    240
XP_001272822.1      SRDIQFYPNLDDPVTAIMSTDLVTAPAGTTLAEANNVLRSSKKGKLPIVDENGHLVSLLS    240
XP_749494.1         SRDIQFHTNLDDPVTAIMSTDLVTAPAGTTLAEANDVLRSSKKGKLPIVDADGNLVSLLS    240
XP_024686877.1      SRDIQFHTNLNDPVTAIMSTDLVTAPAGTTLAEANNVLRSSKKGKLPIVDANGNLVSLLS    240
XP_001265922.1      SRDIQFHTNLNDPVTAIMSTDLVTAPAGTTLAEANNVLRSSKKGKLPIVDANGNLVSLLS    240
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XP_022581501.1      RSDLMKNLHYPLASKLPDSKQLICAASIGTRDEDKHRLQLLVNAGLDIVILDSSQGNSIY    287
XP_024695056.1      RSDLMKNLHYPLASKLPQSKQLICAAAIGTREEDKSRLKLLVEAGLDIVVLDSSQGNSLY    300
XP_024671855.1      RSDLMKNLHYPLASKLPQSKQLICAAAIGTREEDKNRLKLLVEAGLDIVVLDSSQGNSLY    300
XP_022403647.1      RSDLMKNLHYPLASKLPQSKQLVCSATIGTREEDKTRLKLLVEAGLDIVILDSSQGNSIF    300
XP_025403602.1      RSDLMKNLHYPLASKLPQSKQLICAASIGTREEDKTRLRLLVEAGLDIVILDSSQGNSLF    300
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XP_025435086.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    300
XP_025550436.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    300
XP_025436855.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREEDKNRLKLLVEAGLDIVILDSSQGNSMY    300
XP_025509000.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    300
XP_025490880.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    210
XP_025522930.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREEDKTRLKLLVEAGLDIVVLDSSQGNSMY    300
XP_025451440.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREQDKTRLKLLVDAGLDIVILDSSQGNSMY    210
XP_001391892.2      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREQDKTRLKLLVDAGLDIVILDSSQGNSMY    299
XP_025560215.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREQDKTRLKLLVDAGLDIVILDSSQGNSMY    210
XP_025391094.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREQDKTRLKLLVDAGLDIVILDSSQGNSMY    299
XP_025510507.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREQDKTRLKLLVDAGLDIVILDSSQGNSMY    299
XP_025478868.1      RSDLMKNLHYPLASKLPQSKQLIAAAAIGTREQDKTRLKLLVDAGLDIVILDSSQGNSMY    210
XP_025464902.1      RSDLMKNLHYPLASKLPQSKQLICAAAIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    239
XP_025572109.1      RSDLMKNLHYPLASKLPQSKQLICAAAIGTREEDKARLKLLVEAGLDIVILDSSQGNSMY    300
XP_024700898.1      RSDLMKNLHYPLASKLPESKQLICAATIGTRDADKERLAQLVEAGLDIVILDSSQGNSLY    300
XP_001218150.1      RSDLMKNLHYPLASKLPQSKQLICAASIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    300
XP_001823965.1      RSDLTKNLHYPLASKLPHSKQLICAAAIGTREEDKRRLQLLADAGLDIVVLDSSQGNSMY    300
XP_022386829.1      RSDLMKNLHYPLASKLPQSKQLICAAAIGTREEDKRRLQLLADAGLDIVVLDSSQGNSMY    300
XP_015408913.1      RSDLMKNLHYPLASKLPQSKQLICAAAIGTREEDKRRLQLLVDAGLDIVVLDSSQGNSMY    300
XP_001272822.1      RSDLMKNLHYPLASKLPDSKQLICAASIGTREEDKTRLKLLVEAGLDIVILDSSQGNSMY    300
XP_749494.1         RSDLMKNLHYPLASKLPDSKQLICAAAIGTREEDKHRLKLLVEAGLDIVVLDSSQGNSIY    300
XP_024686877.1      RSDLMKNLHYPLASKLPDSKQLICAAAIGTREEDKHRLKLLVEAGLDIVILDSSQGNSIY    300
XP_001265922.1      RSDLMKNLHYPLASKLPDSKQLICAAAIGTREEDKHRLKLLVEAGLDIVILDSSQGNSIY    300
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XP_022581501.1      QIEMLKWVKETFPKLDVIAGNVVTREQAASLIAAGADGLRIGMGSGSACITQEVMAVGRP    347
XP_024695056.1      QMEMIKYIKQAFPEIDVIGGNVVTREQAASLIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_024671855.1      QMEMIKWVKQAFPEIDVIGGNVVTREQAASLIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_022403647.1      QIEMIKYTKENFPDIDVIGGNVVTREQAASLIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025403602.1      QIEMIKWTKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025435086.1      QIEMIKWIKKEIPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025550436.1      QIEMIKWIKQNIPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025436855.1      QIEMIKWIKQNIPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025509000.1      QIEMIKWIKQNIPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025490880.1      QIEMIKWIKQNIPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    270
XP_025522930.1      QIEMIKWIKQNIPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_025451440.1      QIEMIKWIKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    270
XP_001391892.2      QIEMIKWIKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    359
XP_025560215.1      QIEMIKWIKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    270
XP_025391094.1      QIEMIKWIKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    359
XP_025510507.1      QIEMIKWIKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    359
XP_025478868.1      QIEMIKWIKQNFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    270
XP_025464902.1      QIQMIRWVKENFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    299
XP_025572109.1      QIQMIRWVKENFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_024700898.1      QIEMIKWVKKTFPEIDVIGGNVVTREQAAALIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_001218150.1      QIEMIKYAKKTYPEIDVIGGNVVTREQAASLIAAGVDGLRIGMGSGSACITQEVMAVGRP    360
XP_001823965.1      QIEMIKYIKKTHPEIDVIAGNVVTREQAAPLIAAGADGLRIGMGSGSACITQEVMAVGRP    360
XP_022386829.1      QIEMIKYVKKTHPDIDVIAGNVVTREQAAPLIAAGADGLRIGMGSGSACITQEVMAVGRP    360
XP_015408913.1      QIEMIKYIKKTHPDIDVIAGNVVTREQAAPLIAAGADGLRIGMGSGSACITQEVMAVGRP    360
XP_001272822.1      QIEMIKWVKKTFPEIDVVAGNVVTREQAAALIAAGADGLRIGMGSGSACITQEVMAVGRP    360
XP_749494.1         QIEMIKWVKKTFPEIDVIAGNVVTREQAAALIAAGADGLRIGMGSGSACITQEVMAVGRP    360
XP_024686877.1      QIEMIKWVKKTFPEIDVIAGNVVTREQAAALIAAGADGLRIGMGSGSACITQEVMAVGRP    360
XP_001265922.1      QIEMIKWVKKTFPEIDVIAGNVVTREQAAALIAAGADGLRIGMGSGSACITQEVMAVGRP    360
                    *::*::: *:  *.:**:.********** *****.************************

XP_022581501.1      QALAVRRVAQFASRFGVPCIADGGIQNIGHIVKGLAMGASTIMMGGLLAGTSESPGEYFV    407
XP_024695056.1      QAVAVRSVTSFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
XP_024671855.1      QAVAVRSVTSFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
XP_022403647.1      QALSVRSVSHFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
XP_025403602.1      QAAAVRSVSSFAARFGVPCIADGGVQNLGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
XP_025435086.1      QAASVRSVSNFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM    420
XP_025550436.1      QAASVRSVSHFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
XP_025436855.1      QAASVRSVSNFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
XP_025509000.1      QAASVRSVSNFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV    420
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XP_025490880.1      QAASVRSVSNFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   330
XP_025522930.1      QAASVRSVSNFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_025451440.1      QAIAVRSVTAFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM   330
XP_001391892.2      QAIAVRSVTAFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM   419
XP_025560215.1      QAIAVRSVTAFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM   330
XP_025391094.1      QAIAVRSVTAFAARFGVPCIADGGIQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM   419
XP_025510507.1      QAIAVRSVTAFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM   419
XP_025478868.1      QAIAVRSVTAFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFM   330
XP_025464902.1      QAAAVRSVTSFAARFGVPCIADGGIQNIGHIVKGLAAGASTVMMGGLLAGTTESPGEYFV   359
XP_025572109.1      QAAAVRSVTSFAARFGVPCIADGGIQNVGHIVKGLAAGASTVMMGGLLAGTTESPGEYFV   420
XP_024700898.1      QAASVRSVSSFAARFGVPCIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_001218150.1      QAAAVRSVTSFASRFGVPCIADGGIQNIGHIVKGLAMGASTIMMGGLLAGTTESPGEYFV   420
XP_001823965.1      QAISVRSVSSFAARFGVPTIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_022386829.1      QAISVRSVSSFAARFGVPTIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_015408913.1      QAISVRSVSSFAARFGVPTIADGGVQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_001272822.1      QAVAVRSVASFAARFGVPCIADGGVQNIGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_749494.1         QAVAVRSVASFAARFGVPCIADGGIQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_024686877.1      QAVAVRSVASFAARFGVPCIADGGIQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
XP_001265922.1      QAVAVRSVAAFAARFGVPCIADGGIQNVGHIVKGLAMGASTVMMGGLLAGTTESPGEYFV   420
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XP_022581501.1      SSEGQLVKAYRGMGSIAAMEDKKAGKGGKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   467
XP_024695056.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDAKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_024671855.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_022403647.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_025403602.1      SKEGQLVKAYRGMGSIAAMEDKKAGGDG---KASNAGTARYFSEKANVLVAQGVAGSVLD   477
XP_025435086.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGAKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   480
XP_025550436.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGAKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   480
XP_025436855.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGAKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   480
XP_025509000.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGAKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   480
XP_025490880.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGAKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   390
XP_025522930.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGAKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   480
XP_025451440.1      SKEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDGVLVAQGVAGSVLD   390
XP_001391892.2      SKEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDGVLVAQGVAGSVLD   479
XP_025560215.1      SKEGQLVKSYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDGVLVAQGVAGSVLD   390
XP_025391094.1      SKEGQLVKSYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDGVLVAQGVAGSVLD   479
XP_025510507.1      SKEGQLVKSYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDGVLVAQGVAGSVLD   479
XP_025478868.1      SKEGQLVKSYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDGVLVAQGVAGSVLD   390
XP_025464902.1      SKEGQLVKAYRGMGSIAAMEDRKAGAGNKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   419
XP_025572109.1      SKEGQLVKAYRGMGSIAAMEDRKAGAGSKDSKASNAGTARYFSEKDSVLVAQGVAGSVLD   480
XP_024700898.1      SNEGQLVKAYRGMGSIAVMEDKKTGKAG---KAGNAGTARYFSEKDNVLVAQGVAGSVLD   477
XP_001218150.1      SSEGQLVKAYRGMGSIAAMEDKKAAAGAKDSKASNAGTARYFSEKSGVLVAQGVAGSVLD   480
XP_001823965.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVSGSVLD   480
XP_022386829.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_015408913.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_001272822.1      SNEGQLVKAYRGMGSIAAMEDKKASAGNKDTKASNAGTARYFSEKDRVLIAQGVAGSVLD   480
XP_749494.1         SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_024686877.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
XP_001265922.1      SNEGQLVKAYRGMGSIAAMEDKKAGAGSKDSKASNAGTARYFSEKDRVLVAQGVAGSVLD   480
                    *.******:********.***:*:.      **.***********  **:****:*****

XP_022581501.1      RGSITKFVPYLITGVQHSLQDIGVRSIDALHEGVDNGTVRFEVRSASAMAEGNVHGLHSY   527
XP_024695056.1      RGSVTKFIPYLVAGVQHSLQDIGVESLDALHKGVDGGVVRFEVRSASAQTEGNVHGLHSY   540
XP_024671855.1      RGSVTKFIPYLVAGVQHSLQDIGVESLDALHKGVDGGVVRFEVRSASAMTEGNVHGLHSY   540
XP_022403647.1      RGSVTKFIPYLVTGIQHSLQDIGVKSLEAFHDGVNEGTVRFEVRSASAQTEGNVHGLHSY   540
XP_025403602.1      RGSITKFVPYLIAGVQHSLQDIGVTSLQALHDGVNQGVVRFEMRSASAMTEGNVHGLHSY   537
XP_025435086.1      RGSVTKFVPYLTAGIQHSLQDIGVQSLKALHDGVNQGTVRFEMRSASAMAEGNVHGLHSY   540
XP_025550436.1      RGSVTKFVPYLTAGVQHSLQDIGVKSLKDLHDGVNQGKVRFEMRSASAMTEGNVHGLHSY   540
XP_025436855.1      RGSVTKFVPYLTAGVQHSLQDIGVKSLKDLHDGVNQGKVRFEMRSASAMAEGNVHGLHSY   540
XP_025509000.1      RGSVTKFVPYLTAGVQHSLQDIGVKSLKDLHDGVNQGKVRFEMRSASAMAEGNVHGLHSY   540
XP_025490880.1      RGSVTKFVPYLTAGVQHSLQDIGVKSLKDLHDGVNQGKVRFEMRSASAMAEGNVHGLHSY   450
XP_025522930.1      RGSVTKFVPYLTAGVQHSLQDIGVKSLKDLHDGVNQGKVRFEMRSASAMAEGNVHGLHSY   540
XP_025451440.1      RGSVTKFVPYLVAGVQHSLQDIGVKSLKALHEGVDNGTVRFEMRSASAMAEGNVHGLHSY   450
XP_001391892.2      RGSVTKFVPYLVAGVQHSLQDIGVKSLKALHEGVDNGTVRFEMRSASAMAEGNVHGLHSY   539
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XP_025560215.1      RGSVTKFVPYLVAGVQHSLQDIGVPSLKALHEGVNNGTVRFEMRSASAMAEGNVHGLHSY    450
XP_025391094.1      RGSVTKFVPYLVAGVQHSLQDIGVPSLKALHQGVNNGTVRFEMRSASAMAEGNVHGLHSY    539
XP_025510507.1      RGSVTKFVPYLVAGVQHSLQDIGVPSLKALHEGVNNGTVRFEMRSASAMAEGNVHGLHSY    539
XP_025478868.1      RGSVTKFVPYLVAGVQHSLQDIGVPSLKALHEGVNNGTVRFEMRSASAMAEGNVHGLHSY    450
XP_025464902.1      RGSITKFVPYLVAGIQHSLQDIGVPSLQALHDGVNKGTVRFEMRSASAMAEGNVHGLHSY    479
XP_025572109.1      RGSITKFVPYLVAGIQHSLQDIGVPSLQALHDGVNNGSVRFEMRSASAMAEGNVHGLHSY    540
XP_024700898.1      RGSVTKFIPYLVAGVQHSLQDIGVPSLEALHDGVNKGLVRFEMRSASAQTEGNVHGLHSY    537
XP_001218150.1      RGSVTKFIPYLVTGVQHSLQELGCRNLQELHDNVNKGVIRFEMRSASAMAEGNVHGLHSY    540
XP_001823965.1      RGSVTKFVPYLVAGVQHSLQDIGVQSLDALHEGVNNGTVRFEMRSASAMAEGNVHGLHSF    540
XP_022386829.1      RGSVTKFVPYLVAGVQHSLQDIGVQSLEALHEGVNKGTVRFEMRSASAMAEGNVHGLHSF    540
XP_015408913.1      RGSVTKFVPYLVAGVQHSLQDIGVQSLDALHEGVNNGTVRFEMRSASAMAEGNVHGLHSF    540
XP_001272822.1      RGSVTKFVPYLAAGVQHSLQDIGVKSLEALHDGVNKGIVRFEMRSASAMAEGNVHGLHSY    540
XP_749494.1         RGSVTKFVPYLVAGVQHSLQDIGVKSLDELHDGVNKGIVRFEMRSASAMAEGNVHGLHSY    540
XP_024686877.1      RGSVTKFIPYLVAGVQHSLQDIGVKSLDELHDGVNKGIVRFEMRSASAMAEGNVHGLHSY    540
XP_001265922.1      RGSVTKFVPYLVAGVQHSLQDIGVKSLDELHDGVNKGIVRFEMRSASAMAEGNVHGLHSY    540
                    ***:***:*** :*:*****::*  .:. :*..*: * :***:***** :*********:

XP_022581501.1      DKKLYV    533
XP_024695056.1      DKKLYS    546
XP_024671855.1      DKKLYS    546
XP_022403647.1      DKKLYS    546
XP_025403602.1      DKKLYA    543
XP_025435086.1      DKKLYS    546
XP_025550436.1      DKKLYS    546
XP_025436855.1      DKKLYS    546
XP_025509000.1      DKKLYS    546
XP_025490880.1      DKKLYS    456
XP_025522930.1      DKKLYS    546
XP_025451440.1      DKKLYS    456
XP_001391892.2      DKKLYS    545
XP_025560215.1      DKKLYS    456
XP_025391094.1      DKKLYS    545
XP_025510507.1      DKKLYS    545
XP_025478868.1      DKKLYS    456
XP_025464902.1      DKKLYA    485
XP_025572109.1      DKKLYA    546
XP_024700898.1      DKKLYS    543
XP_001218150.1      DKKLYA    546
XP_001823965.1      DKKLYS    546
XP_022386829.1      DKKLYS    546
XP_015408913.1      DKKLYS    546
XP_001272822.1      DKKLYS    546
XP_749494.1         DKKLYS    546
XP_024686877.1      DKKLYS    546
XP_001265922.1      DKKLYS    546
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