

gi	21361095	ref	NP_004447.2	-----MGOTGKKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	129
gi	114616631	ref	XP_001166174.1	-----MIYFIRITMGOTGKKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	137
gi	119891668	ref	XP_870752.2	-----MGOTGKKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	129
gi	73978423	ref	XP_532733.2	-----MGOTGKKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	129
gi	118086295	ref	XP_418879.2	MFICDNNNASSEGLVMGOTGKKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	144
gi	6679721	ref	NP_031997.1	-----MGOTGKKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	129
gi	109471996	ref	XP_231705.4	-----MTIGTLR-----LALGPVAVDTWDI-----EGSSVPAATAAAARWGGAREKRGAL-RGT-KCSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	97
gi	116267951	ref	NP_001070747.1	-----MGLTGRKSEKGPVWCWRKRVKSEYMLRQLKFRRADEVKSMFSSNRQKIL-----ERTEILNQEWKORRIQPVHILTSVSSLRGTRECSVTSDDLDFPTQVIPLKTLNAVASVPIYMSWSPLOQNFVMEDEVTLV	130
gi	24662251	ref	NP_524021.2	-----MNTKVPPEWKRVRKSEYIKIRQKRYKRADEIKAEWIRNWDEN-----HNVLDLYCESEKVVWAKPYPDP-HVDCVKRAEVTIYNGIP-----SGPKVPICVINAVTPIPTMYTWAPIQQNFVMEDEVTLV	122
gi	58375633	ref	XP_307419.2	-----MLKQKVSLEWKRVRKSEYMKIRLKRHKVDDVRSAWNRRGALGLMVAENDAWLSTNATWLGCEVEQLP-HVNCMKKAVVLDHEGN-----HNVNIRVVNAVITPIPTMYTWAPIQQNFVMEDEVTLV	124



gi	21361095	ref	NP_004447.2	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YNDD-----DDDDDDGDDPDEREEK-----KDLEDHRDDKESR-----PPRKFPSDKIFEAISS	229
gi	114616631	ref	XP_001166174.1	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YNDD-----DDDDDDGDDPDEREEK-----KDLEDHRDDKESR-----PPRKFPSDKIFEAISS	237
gi	119891668	ref	XP_870752.2	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YNDD-----DDDDDDGDDPDEREEK-----KDLESREDDKESR-----PPRKFPSDKIFEAISS	229
gi	73978423	ref	XP_532733.2	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YNDD-----DDDDDDGDDPDEREEK-----KDLENRDDKESR-----PPRKFPSDKIFEAISS	229
gi	118086295	ref	XP_418879.2	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YSDD-----EDDDGDDNIEKESH-----KDRGNRIEKESH-----PPRRFESDKIFEAISS	244
gi	6679721	ref	NP_031997.1	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YNDD-----DDDDDDGDDPDEREEK-----KDLEDNRDDKETS-----PPRKFADKIFEAISS	229
gi	109471996	ref	NP_231705.4	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YNDD-----DDDDDDGDDPDEREEK-----KDLEDNRDDKETS-----PPRKFADKIFEAISS	197
gi	116267951	ref	NP_001070747.1	NIPYMGDEVLDODGTFFIEELIKNYDGKVGHDRECGFINDEIFVELVNALGQ-YSDN-----EDDEEDDHDYKFEK-----MDLCDGKDDADHKEQLSSESHNDGSKKFPDKIFEAISS	242
gi	24662251	ref	NP_524021.2	NIPYMGDEVLDKDGKFFIEELIKNYDGKVGHDKDPDFMDDAIFVELVHALMRSYSKELEAAPGTAATAIKTEFLAKSKGQEDDGVVDADGESPMKLEKTD-SKGLDTEVEKKEEPELLEDADVKPVEEVKDKLFPFAPITFOAISA	271
gi	58375633	ref	XP_307419.2	NIPYMGDEVLDKDGKFFIEELIKNYDGKVGHDKEDS-IDDDAMFVELVHTLMQ-YTNQESNIDEKLAHS-KSEIGKSPITSHN--FDQSTGKASSKMKKDNCDENLTCNDLNTNKELRLLQPNAMKKNRLNVK--AFPAPITFOAISA	266



gi	21361095	ref	NP_004447.2	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLHRCNYSFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIN	376
gi	114616631	ref	XP_001166174.1	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLH-----PFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIN	379
gi	119891668	ref	XP_870752.2	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLH-----PFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIN	376
gi	73978423	ref	XP_532733.2	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLHRCNYSFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIN	376
gi	118086295	ref	XP_418879.2	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLHRCNYSFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIN	391
gi	6679721	ref	NP_031997.1	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLH-----PFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIS	371
gi	109471996	ref	XP_231705.4	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLH-----PFHATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIS	339
gi	116267951	ref	NP_001070747.1	MFPDKGTAEBELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLH-----PFQATPNTYKRNKTEALDNKPCGPGCYOHLG-----AKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTIN	387
gi	24662251	ref	NP_524021.2	NFPDKGTAEBELKEKYKELTEHODP-ERPQECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLH--LQG-HAGPNLQKRRYPBLKFAEPQCSNSCYMLIDG-----MKEKLAADSKTTP--ID	388
gi	58375633	ref	XP_307419.2	LFPENGTGEELRDKYIELTERVDP-ERPPECTPNIDGPNRAESVREQTLHSYHTLFCRRCFKYDCFLH--LQACHPGPIQRRRYPBLKPPGKPCGEACVHLIDG-----VKQLSFDNIGKSVMLD	387



gi	21361095	ref	NP_004447.2	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	526
gi	114616631	ref	XP_001166174.1	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	529
gi	119891668	ref	XP_870752.2	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	521
gi	73978423	ref	XP_532733.2	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	526
gi	118086295	ref	XP_418879.2	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	526
gi	6679721	ref	NP_031997.1	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	521
gi	109471996	ref	XP_231705.4	VLESKDTSDREAGTEFGGENNDKBEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEVWSGAEASMFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	489
gi	116267951	ref	NP_001070747.1	S-ETKDTSDREGGAD-GNDSNDKDDKDETSSSSEANSRCQTPVKLKLSEPPENVDWSGAEASLFRVLIGTYDNCFAIARLIGTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	535
gi	24662251	ref	NP_524021.2	SONEASSEDSNDSNCFNSKDFNH--ENSKDNLGLVNSAAVAEINSIMAGMNNITSTQCWVIGADQALYRVLHKVYLKNYCAIAHNLTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	536
gi	58375633	ref	XP_307419.2	SONEASSEDSNDSNCFNSKDFNH--ENSKDNLGLVNSAAVAEINSIMAGMNNITSTQCWVIGADQALYRVLHKVYLKNYCAIAHNLTKTCROYVEFRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQLKKGSSNHVNYQ	519



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gi | 21361095 | ref | NP_004447.2 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 676
gi | 114616631 | ref | XP_001166174.1 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 679
gi | 119891668 | ref | XP_870752.2 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 671
gi | 73978423 | ref | XP_532733.2 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 676
gi | 118086295 | ref | XP_418879.2 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 691
gi | 6679721 | ref | NP_031997.1 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 671
gi | 109471996 | ref | XP_231705.4 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 639
gi | 116267951 | ref | NP_001070747.1 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGAKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 685
gi | 24662251 | ref | NP_524021.2 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGAKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 685
gi | 58375633 | ref | XP_307419.2 | PCDHPRQPCDSSCPVIAQNFCEKFCQCSSECONRFFPGCRCKAQCNTKQPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGAKKHLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIIISQDEADRRGKVYDKYMC SFLFNLNN 667
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi | 21361095 | ref | NP_004447.2 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 751
gi | 114616631 | ref | XP_001166174.1 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 754
gi | 119891668 | ref | XP_870752.2 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 746
gi | 73978423 | ref | XP_532733.2 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 751
gi | 118086295 | ref | XP_418879.2 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 766
gi | 6679721 | ref | NP_031997.1 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 746
gi | 109471996 | ref | XP_231705.4 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 714
gi | 116267951 | ref | NP_001070747.1 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 760
gi | 24662251 | ref | NP_524021.2 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 760
gi | 58375633 | ref | XP_307419.2 | DFVVDATRKGKIRFANHSVNPNCYAKVMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIP 742
.....760.....770.....780.....790.....800.....810.....820.....

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