

gi | 24658585 | ref | NP_647984.1 | -----MADVKEK-PEKTAEDLVVTKYKLAGIVNKTLKAVIGLCVVDASVREICTQGDNQLFEETGKVIKK--EKDLKGGIAPF--CLVSNVNCVCHFSPAKNDADYTLKA--GDVVKIDLGAGHIDGFIAVAARTIVVG--AAA 131
gi | 158292575 | ref | XP_313985.4 | -----MAPVFKQTDQELITIEDPTVIEKVRIAGDVVNRLLQAIIVKECVAGASVKETICQGDNMLMHDGKKYKH--DEDMKKGIAFP--CLVSNVNCVCHFSPAKNDADYTLKE--NDVVKIDMGAHIDGFIAVAARTIVVG--ATP 133
gi | 189536377 | ref | XP_001918902.1 | -----MSGDDDD-DEQTIADDLVVTKYKMGADIANLALKTIVIEAAPGVSVLTIKCEKGDFTFAAEKSKVFKK--EKIKKGIAPFP--CVSNVNCVCHFSPAKNDADYTLK--GDLVKIDLVGHVVDGFIANVAHRTIVVG--ATK 131
gi | 47086757 | ref | NP_997806.1 | -----MSGDDDD-DEQTIADDLVVTKYKMGADIANLALKTIVIEAAPGVSVLTIKCEKGDFTFAAEKSKVFKK--EKIKKGIAPFP--CVSNVNCVCHFSPAKNDADYTLK--GDLVKIDLVGHVVDGFIANVAHRTIVVG--ATK 131
gi | 50344794 | ref | NP_001002070.1 | -----MS-DDEQ-DEQTIADDLVVTKYKMGADIANLALKTIVIEAAPGVSVLTIKCEKGDFTFAAEKSKVFKK--EKDMKKGIAFP--CVSNVNCVCHFSPAKNDADYTLK--GDLVKIDLVGHVVDGFIANVAHRTIVVG--ATK 130
gi | 6755100 | ref | NP_035249.1 | -----MSGEDEQ-DEQTIADDLVVTKYKMGADIANRVLRSLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--VAQ 131
gi | 51948384 | ref | NP_001004206.1 | -----MSGEDEQ-DEQTIADDLVVTKYKMGADIANRVLRSLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--VAQ 131
gi | 124494254 | ref | NP_006182.2 | -----MSGEDEQ-DEQTIADDLVVTKYKMGADIANRVLRSLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--VAQ 131
gi | 114644286 | ref | XP_001169403.1 | -----MSGEDEQ-DEQTIADDLVVTKYKMGADIANRVLRSLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--VAQ 131
gi | 73968311 | ref | XP_531629.2 | -----MSGEDEQ-DEQTIADDLVVTKYKMGADIANRVLRSLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--VAQ 131
gi | 77736343 | ref | NP_001029871.1 | -----MSGEDEQ-DEQTIADDLVVTKYKMGADIANRVLRSLSVEASSSGVSVLSLCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--VAQ 131
gi | 118129651 | ref | XP_423059.2 | -----VLRVAVVEANSASVLCCEKGDAMIMEETGKIFKK--EKEMKKGIAFP--TSVSNVNCVCHFSPAKNDADYTLKE--GDLVKIDLVGHVVDGFIANVAHRTIVVG--ASK 101
gi | 15231039 | ref | NP_190748.1 | -----MSDDDE-RDEKELSLTSPEVVTKYKSAEIVNKALQVVLAECKPKAKIVDIKCEGDSFIREQIASMYKNS--KKIKERGVAFPT--CISVNNTVGHFSPKASD--ESVLED--GDMVKIDMCHIDGFIALVGHVTHVLQ--EGP 133
gi | 115463349 | ref | NP_001055274.1 | -----MSDDDEVREKELDSSDQVTKYKDAADLIINNALKLVSLCKPKAKIVDIKCEGDSFIREQIASMYKNS--KKIKERGVAFPT--CISVNNTVGHFSPKASD--ESVLED--NDMKVIMDCGHIDGFIALVGHVTHVLQ--DGA 134
gi | 17542840 | ref | NP_500311.1 | -----MVRKDSSESSCSDDGSHTHEDYTLANDAVVTKYQVAAEIINAVLKEVLANIKEGAIAGDLCKDGLKILKGLKLYKK--EKNFTKGIAPFP--CISVNNTVGHFSPKASD--ESVLED--GDMVKIDMCHIDGFIALVGHVTHVLQ--EGP 142
gi | 124808890 | ref | XP_001348435.1 | -----MEFTTETKTEEIDLEKYSSTSSLANTLKKVIEKCVHGAKIGELCYEYGEKFMKDELKDYVTKKRNKVEKGIFFPVINNV--EICNNYAPSLDVEI--EIKN--GDVVKISLGCCHIDGHISIVGHVTHVLQ--AEN 129
gi | 145608860 | ref | XP_369801.2 | -----MASE---DKIEDYILNNDPDLTKYKAAQISEKVLKDVSLCVAAGAKIVDIKCEGDLQIEELVAKVYRG--KKITKGFSPHT--TVSPSSVYVYPLKTLDEAAAEATELKAEGAVKIQLAGQIDGFSIVCDVILVPKGE-- 134
gi | 32403790 | ref | XP_322508.1 | -----MASETT--KQIDYSLNNDPDLTKYKAAQISEKVLAEVSKLVAAGEKIVDIKCEGDLQIEELVAKVYRG--KKITKGFSPHT--TVSPSSVYVYPLKTLDEAAAEATELKAEGAVKIQLAGQIDGFSIVCDVILVPAKDDQT-- 137
gi | 19114309 | ref | NP_593397.1 | -----MSIKKATSETAVDYSLNNDPDLTKYKAAQISEKVLAEVSKLVAAGEKIVDIKCEGDLQIEELVAKVYRG--KKITKGFSPHT--TVSPSSVYVYPLKTLDEAAAEATELKAEGAVKIQLAGQIDGFSIVCDVILVPAKDDQT-- 133



gi | 24658585 | ref | NP_647984.1 | DQKISGRQADVILAAVAVQAAALRLRLKSG--ANNYSLTDVAVQIIESYKCKPIEGMLSHQLQKFKIDGKETTIIQNPSEAORKEHEKCFEFTYEVYVIDVIVSTG--EGVGRKEDTK--VSIYKK--SEENVMLKMK 259
gi | 158292575 | ref | XP_313985.4 | ENKCKGRAADVILAAVAVQAAALRLRLKSG--TGNVAVTDVAVQIIASDFKCPPIEGMLSHQLQKFKIDGKETTIIQNPSEAORKEHEKCFEFTYEVYVIDVIVSTG--EGLGKEHDTN--VAIYKK--TDENVMLKMK 261
gi | 189536377 | ref | XP_001918902.1 | DAPVGRKADVILAAVAVQAAALRLRLKSG--NONSQVTDAWNKIAQSFKCMPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKARSGQR--TIIVYKRDPKQYGLKMK 260
gi | 47086757 | ref | NP_997806.1 | DAPVGRKADVILAAVAVQAAALRLRLKSG--NONSQVTDAWNKIAQSFKCMPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKARSGQR--TIIVYKRDPKQYGLKMK 260
gi | 50344794 | ref | NP_001002070.1 | EAPVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFKCNPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKARSGQR--TIIVYKRDPKQYGLKMK 259
gi | 6755100 | ref | NP_035249.1 | GTQVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 260
gi | 51948384 | ref | NP_001004206.1 | GSQVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 260
gi | 124494254 | ref | NP_006182.2 | GTQVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 260
gi | 114644286 | ref | XP_001169403.1 | GTQVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 260
gi | 73968311 | ref | XP_531629.2 | GTQVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 260
gi | 77736343 | ref | NP_001029871.1 | GTQVGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 260
gi | 118129651 | ref | XP_423059.2 | EKPVSGRKADVILAAVAVQAAALRLRLKSG--NONTQVTEAWNKAIAHSFNCTPIEGMLSHQLQKFKIDGKETTIIQNPPTDQKKDHEKAFFVEVHYAVDVLVSTG--EGKAKDAGOR--TIIVYKRDPKQYGLKMK 230
gi | 15231039 | ref | NP_190748.1 | ---LSGRKADVILAAVAVQAAALRLRLKSG--KKNKVDVTEAIOKVAAADCKIIVEGVLSHQLQKFKIDGKVVLS--VSSPETTVDVEFEENEVYADIVASTG--DGPKKLLDDEKOTIIVYKRDPKQYGLKMK 258
gi | 115463349 | ref | NP_001055274.1 | ---VTKAADVILAAVAVQAAALRLRLKSG--KKNKVDVTEAIOKVAAADCKIIVEGVLSHQLQKFKIDGKVVLS--VSNADTKVDEFEENEVYADIVASTG--EGKPKLLDDEKOTIIVYKRDPKQYGLKMK 259
gi | 17542840 | ref | NP_500311.1 | DNKVTCKLADLLRCVDALEIAIRSLRPP--TENTITIKNIDKIAAEFGLTPIENMLSHOLERNEIDGKETTIIQNPSEKKEGTEIKIKDKHEAYVIDILFSTG--KGGPKDMDTN--TIIVYKRDPKQYGLKMK 271
gi | 124808890 | ref | XP_001348435.1 | ES-IEGVKADVILAAVAVQAAALRLRLKSG--INASDITKNIQKACEELKCNVSNCTVYIQQIYKILEGSKYIFLKNIN--KIDDFQIEADDIYIIVDMVTSG--DGRKIKESDHK--TIIVYKRDPKQYGLKMK 255
gi | 145608860 | ref | XP_369801.2 | -GVVTCRDAVILAAVAVQAAALRLRLKSG--SLEEKVAAAEVNLVSEITSWLFDNREIEGKTKVIVIAPGEGAKGEG--VPEVGEVWVGVEMVSLG--SGKVKQLDR--ATLHRRRTIIVYKRDPK 277
gi | 32403790 | ref | XP_322508.1 | DDVTEGRNADLMLLANYANELLRLMVPVGLLAQTDEEKAKAASAKPPSQAKITELLQVVQVAAQDNCLVSEITSWLFDNREIEGKTKVIVIAPGEGAKGEG--VPEVGEVWVGVEMVSLG--SGKVKQLDR--ATLHRRRTIIVYKRDPK 281
gi | 19114309 | ref | NP_593397.1 | EEPVTPAADVILAAVAVQAAALRLRLKSG--INNVVIVDQKVIATSYGCKPVGMLSHQKEREVIDGKQVILNPSDSRSEMDTFTFEEGEVYGVVLDLVSITSPSGKVKRSIDIA--TRIYKKIDTIVYKRDPK 262



gi | 24658585 | ref | NP_647984.1 | ASRALLAEVTKYGNMFFNIRSEETKARMGVVECVGHKMIPEFQVLYEKPSEIVAQFKHIVLMLPAGVNLVITGIPFEAENVSEYVSAQ--EELKTLIAQPLGF--VKGKGGK--ATAGA--ATKVE--LAP 385
gi | 158292575 | ref | XP_313985.4 | ASRAFIGEYVKKKYGTMPFNLRNFEBAKAKLVNCEVTHKMVEPFQVLYEKNHNVVAQFKYIVLITANGKVVVGHPPFDENCSSEHSVOD--BEMKNLLAGKVAQEGAKAKKRNKRKKNKGAAGA--ADEEGSGEDAPAATAD 407
gi | 189536377 | ref | XP_001918902.1 | TSRMFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFVLSHEKEGEHVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KAQKKKKKASKNAES--ATGQP--VEA 388
gi | 47086757 | ref | NP_997806.1 | TSRMFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFVLSHEKEGEHVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KAQKKKKKASKNAES--ATGQP--VEA 388
gi | 50344794 | ref | NP_001002070.1 | TSRMFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFVLSHEKEGEHVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KAQKKKKKASKNAES--ATGQP--AEN 387
gi | 6755100 | ref | NP_035249.1 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 388
gi | 51948384 | ref | NP_001004206.1 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 388
gi | 124494254 | ref | NP_006182.2 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 388
gi | 114644286 | ref | XP_001169403.1 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 388
gi | 73968311 | ref | XP_531629.2 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 388
gi | 77736343 | ref | NP_001029871.1 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 388
gi | 118129651 | ref | XP_423059.2 | TSRAFFSEVERRRFDAMPFLLRAFEDSKARLVGVECAKHELLPPFNVLVYEKEGEFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KTOKKKKKASKTAE--ATSGE--TLE 343
gi | 15231039 | ref | NP_190748.1 | ASRFIIEIKNFRMPFARSLE--EKRARLGLVCEVNHGLOPPVLYEKEGDFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KKGKGGK--AKAGEGK--EASLEAP--MDA 386
gi | 115463349 | ref | NP_001055274.1 | ASRFIIEIKNFRMPFARSLE--EKRARLGLVCEVNHGLOPPVLYEKEGDFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KKGKGGK--AKAGEGK--EASLEAP--MDA 386
gi | 17542840 | ref | NP_500311.1 | ASRVFFSDVNKVVHGMPPFLRSFEEVAKARMGVVECEKYGILLVPPVLYEKEGDFVAQKFKVLLMANGPLRITISGLFEPPELKKSEYEVOD--PELKALLOSSASR--KKGKGGK--AKAGEGK--EASLEAP--MDA 391
gi | 124808890 | ref | XP_001348435.1 | LGRSFINELNKKFVPLPFHVKLEDRQAAALIGIPALRHNLIKPYSVYIEKKEGVAAEFKVVVMKVEDGKQVFTGLKFAQLNNCKTDSIQDETLKNILSLPSG--KKNKKNK--NEEENANQEN-- 377
gi | 145608860 | ref | XP_369801.2 | TSRKILSEVQKFKFTFFPSLRQLEDERDAKSGVVECVGRVNFVGRYELVGDGDGAARVALLTVAITKNGIKLGAAPPLDLSKYQTDKKIEDEEVLKLLAQPLSRNT--GNKKKKPKKTKKPA--KKEGEE--EESDE 413
gi | 32403790 | ref | XP_322508.1 | SSKRLLSEVQKFKFTFFPSLRQLEDERDAKSGVVECVGRVNFVGRYELVGDGDGAARVALLTVAITKNGIKLGAAPPLDLSKYQTDKKIEDEEVLKLLAQPLSRNT--GNKKKKPKKTKKPA--KKEGEE--EESDE 410
gi | 19114309 | ref | NP_593397.1 | ASRKVYSEIKTKGFPPFSRNTISFDSRINMGLNCS--SKHLFPYEVLLDKDGGIVAEFYSIALIKKGTIILDSEPKEDF--IKSDKIKVEDPEIVALLE--PIK--VTNKKKSKK--PSKANE-- 381



gi		24658585		ref		NP_647984.1		AVE	KA--	391
gi		158292575		ref		XP_313985.4		KAE	KA--	413
gi		189536377		ref		XP_001918902.1		ESE	AAA--	394
gi		47086757		ref		NP_997806.1		ESE	AAA--	394
gi		50344794		ref		NP_001002070.1		EVA	AK---	392
gi		6755100		ref		NP_035249.1		ENG	AGD--	394
gi		51948384		ref		NP_001004206.1		ENG	AGD--	394
gi		124494254		ref		NP_006182.2		ENE	AGD--	394
gi		114644286		ref		XP_001169403.1		ENE	AGD--	394
gi		73968311		ref		XP_531629.2		ENE	AGD--	394
gi		77736343		ref		NP_001029871.1		ENE	AGD--	394
gi		118129651		ref		XP_423059.2		-----	-----	343
gi		15231039		ref		NP_190748.1		SSN	ACE--	392
gi		115463349		ref		NP_001055274.1		S	SNDANKE	393
gi		17542840		ref		NP_500311.1		-----	-----	391
gi		124808890		ref		XP_001348435.1		-----	-----	377
gi		145608860		ref		XP_369801.2		-----	-----	413
gi		32403790		ref		XP_322508.1		-----	-----	410
gi		19114309		ref		NP_593397.1		-----	-----	381
									
