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gi | 115481600 | ref | NP_001064393.1 | GELPLAGASLAIISLANVIGFSLLLFGMASALDILCGOAVGARQVHLLGVYKORAMLVLAVAAPVIALWASA-GEILLLLFGODPAIAAEAGAVARWLPVSLVFPVPLVCHIRFLQASAVLVPVMAACGVTAASHVAVCWALVVR--AGMGS 450
gi | 115481602 | ref | NP_001064394.1 | GELPLAGASLAIISLANVIGFSLLLFGMATAMDILCGOAVGARQVHLLGVYKORAMVLAACVPIALWASA-GRILLLLFGODAGIAAEAGAVARWMLPSLAAYVPLVCHIRFLQASAVLVPVMAASAAATALLHPLVCWLVVFR--AGMGS 450
gi | 115481598 | ref | NP_001064392.1 | -----SDQFGMSSALDILCGOAVGAGQHRLLGVYKORAMVLAACVPIALWASA-GEILLLLFGODPAIAAEAGAVARWMLPSLAAYVPLVCHIRFLQASAVLVPVMAASGVAAYGHVAVCWALVVK--AGMGS 450
gi | 115457946 | ref | NP_001052573.1 | GELPLSSASIAISFAGVTGFSLLLAGMASALDILCGOAFGARQVHLLGVYKORAMVLLGLASVCAAVWAYT-GEILLLLFGODPEIAAAAGSVIRWMLPALLAYGPLVCHVRFLQASAVLVPVMAASGAAAACHLFPVCWLLVYG--AGLGS 450
gi | 115468176 | ref | NP_001057687.1 | GELPLAGASMASSFAAVTGLSLLLLGMASALDILCGOAFGARQVHLLGVYKORAMLLTAVSVPLVVWFYI-GDILVAFGODADIAAEAGAVARWMLPALFAYGPLVCHVRFLQASAVLVPVMAASGAAAACHLFPVCWLVVYA--AGMGS 450
gi | 115468182 | ref | NP_001057690.1 | GELPLAGASMASSFAAVTGLSLLLLGLASALDILCGOAFGARQVHLLGVYKORAMLLTAVSVPLAVAWYI-GDILLLLFGODADIAAEAGAVARWMLPALFAYGPLVCHVRFLQASAVLVPVMAASGAAAACHLFPVCWLVVYA--AGMGS 450
gi | 115468180 | ref | NP_001057689.1 | -----MASLADILCGOAFGARQVHLLGVYKORAMLLTAVSVPLAVAWYI-GDILLRFGODADIAAEAGAVARWMLPALFAYGPLVCHVRFLQASAVLVPVMAASGAAAACHLFPVCWLVVYA--AGMGN 450
gi | 15237158 | ref | NP_200058.1 | GSLPLSAASIAISFASVTGFSFLMGTASALDILCGOAVGARQVHLLGVYKORAMVLLTASVPLIIVWANT-EHLLVFFGQDKSIATLHSGSVARFMPISIFAYGLLCLNRFLOASAVLVPVMAASGAAAACHLFPVCWLVVYK--SGLGF 450
gi | 240254581 | ref | NP_180983.4 | GSLPLSAASIAISFASVTGFSFLMGTASALDILCGOAVGARQVHLLGVYKORAMVLLTASVPLIIVWANT-EHLLVFFGQDKSIATLHSGSVARFMPISIFAYGLLCLNRFLOASAVLVPVMAASGAAAACHLFPVCWLVVYK--SGLGF 450
gi | 15219524 | ref | NP_177511.1 | GSLPLSAASIAISFASVTGFSFLMGTASALEILCGOAVGARQVHLLGVYKORAMVLLTASVPLIIVWANT-EQILVLVHODKSIASVAGSVAKYMIPLSFLAYGLLCLNRFLOASAVLVPVMAASGAAAACHLFPVCWLVVYK--SGLGF 450
gi | 50312043 | ref | NP_456053.1 | GSNELGAVITLGMSTASITGFPAIQGLCTCLDILCAOAVGGNHVHLVGLFORCAIITIIISLPVLFITWQWSEQILALFIPERELCALAAKYLQVSLGIPAFILFECGKRFLQCGGIFHASSIVLLVCAPIALNALMNVLVWDKNTIGIY 450
gi | 45190837 | ref | NP_985091.1 | GTKELGGITLGMSTASITGFPAIQGLCTCLDILCAOAVGARNYTLVGLLQRCIIISLIVFAPVVLWVVCYS-EQVLYLVSDELCLFAAKVLRVAAGLPAFILFECGKRFLQCGGIFHASSIVLLVCAPIALNALMNVLVWDKNTIGIY 450
gi | 145608424 | ref | XP_360580.2 | GMVELAANLAIMTASITCYVFPQGLATCLDILCAOAVGSGHKLHVLQAOQRMVFLWILMVPVIAVLWVFE-GPIIEKLVPGEEITAGLSSLVLRVLLGMPGVAALLESKGRFVQAQGLFHATIVYLLITAPLSFFLNLVLFVFR--FGWGF 450
gi | 22907060 | ref | NP_060712.2 | GKLELDAVTLAIAVINVTGVSVGFGLSSACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-CHILLFRDDPDVSRLLTQTVTTFIPALPATFLYMLQVKYLLNQGIVLPQIVTGAANLVNALANVFLHQ--LHLGV 450
gi | 114668714 | ref | NP_001144887.1 | GKLELDAVTLAIAVINVTGVSVGFGLSSACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-CHILLFRDDPDVSRLLTQTVTTFIPALPATFLYMLQVKYLLNQGIVLPQIVTGAANLVNALANVFLHQ--LHLGV 450
gi | 119912025 | ref | NP_873599.2 | GKLELDAVTLAIAVINVTGVSVGFGLSSACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-QLILLFRDDPAVSRLLTQVTVMIFIPALPATFLYMLQVKYLLNQGIVLPQIVTGAANLVNALANVFLHQ--LHLGV 450
gi | 13385694 | ref | NP_080459.1 | -----MSDPSQAGVLSRARLLQLRRHSSQ-----RPERSGLAG-----LLERVGIVLPQIVTGAANLVNALANVFLHQ--LHLGV 450
gi | 62078965 | ref | NP_001014140.1 | GKLELDAVTLAIAVINVTGVSVGFGLSSACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-EQILLFRDDPDVSRLLTQVTVMIFIPALPATFLYMLQVKYLLNQGIVLPQIVTGAANLVNALANVFLHQ--LHLGV 450
gi | 73956142 | ref | NP_546648.2 | GKLELDVTLAIAIAINVTGVSVGFGLSSACDILMSOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-ETILLFRDDPDVSRLLTQVTVMIFIPALPATFLYMLQVKYLLNQGIVLPQIVTGAANLVNALANVFLHQ--LHLGV 450
gi | 189534168 | ref | NP_688576.2 | GKTELAVTALIAIAVINVTGISIGSGLASACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-EPILLAVRQSPNVASLSQLVVKIFMPALPATFMYLQGLYLLNQGIIWPOVITGAAGNTILNALINVFLYL--LDLGV 450
gi | 122114563 | ref | NP_001073648.1 | GKTELAVTALIAIAVINVTGISIGSGLASACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-EPILLAVRQSPNVASLSQLVVKIFMPALPATFMYLQGLYLLNQGIIWPOVITGAAGNTILNALINVFLYL--LHLGV 450
gi | 118100277 | ref | NP_415860.2 | KVVELASVTLAIAVINVTGISVGFGLSSACDILISOTYGSQNLKHVGVILQRSALVLLCCFPCCWALFLNT-EQILLFRDDPDVSRLLTQVTVMIFIPALPATFLYMLQVKYLLNQGIVLPQIVTGAANLVNALANVFLHQ--LHLGI 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi | 115481600 | ref | NP_001064393.1 | RGAALANAVSYGVNLTIMSLYVRLRS--CEKLTWGFSS--MEAFRELRYAELAIIPAAMMVC--LEWWS-----FEFLVMLSG-----LLPNPK-----LEIS--VLICLNTGALLVMV 600
gi | 115481602 | ref | NP_001064394.1 | KGAALANAVSYAVNLAIVYVRSANT--CKGRNSGFS--GEAFKELRQFAALAMPSAMMIC--LEWWS-----FEILVLLSG-----LLPNPQ-----LEIS--VLICLNTGALLVMV 600
gi | 115481598 | ref | NP_001064392.1 | KGAALSGAVTYWNLAVLALVYVRLSQA--CETTWTGFS--IDAFRELRFTELAVPSAMMVC--LEWWS-----FEILVLLSG-----LLPNPQ-----LEIS--VLICLNTSLLFMV 600
gi | 115457946 | ref | NP_001052573.1 | KGAALANAVAYLANAALAAVYVRLSPA--CRSTWTGFS--SEAFHDLVGFMR LAVPSALMVC--LEWWS-----FELLVLLSG-----LLPNPK-----LEAS--VLICLNSGSLAFMI 600
gi | 115468176 | ref | NP_001057687.1 | KGAALSNVSYWINVAILAVYVRSVSS--CKKTWTGFS--MEAFHDLPSFFRLAIPALMVC--LEWWS-----FELIVLLSG-----LLPNPK-----LEIS--VLSISLNTAAFWMI 600
gi | 115468182 | ref | NP_001057690.1 | RGAALGNVSYWINVGLAVYVRSVRS--CKKTWTGFS--MEAFRDLPSFFRLAIPALMVC--LEWWS-----FELLVLLSG-----LLPNPK-----LEIS--VLSITLNTANCLFMI 600
gi | 115468180 | ref | NP_001057689.1 | RGAALSNVSYWINVAILAVYVRSVSS--CKKTWTGFS--TEAFRDALGFFRLAVPSALMVW--SSQPKAADVRAINQPOHCFGLVDDPLWRPRLCHKSKGRIERDGRWPIILRRPKSGGWIGAAIAITIGNHRLVTAISTHAIFTI 600
gi | 15237158 | ref | NP_200058.1 | QGAALANSISYWLNVLLFCYVKFSPS--CSLTWTGFS--KEALRDILPFLRLAVPSALMVC--LEWWS-----FELLVLLSG-----LLPNPV-----LEIS--VLSICLNTSGMWMMI 600
gi | 240254581 | ref | NP_180983.4 | RGAAVANAVSYWLNVLLFCYVKFSPS--CSLTWTGFS--KEARRDIPFMRKLVIPSAFMVCSLEWWS-----FELLVLLSG-----LLPNPV-----LEIS--CE-----RTWMMI 600
gi | 15219524 | ref | NP_177511.1 | RGAALAVSYWNVLLFCYVKFSPS--CSHSWTGFS--KEAFQELYDFSKIAFSPAMMVC--LEWWS-----FELLVLLSG-----LLPNPV-----LEIS--VLSICLNTSLTIWQI 600
gi | 50312043 | ref | NP_456053.1 | LGAPISVVLNLYWMLGLFAYLITKNEKNPMKCNWGFKPHQILKNSRMRMFLNLPGLIIMVE-AEFLG-----FEILTIFAS-----HICPHELAOSIITIASLAYQV 600
gi | 45190837 | ref | NP_985091.1 | LGAPISVVLNLYWMLGLLFLYIFKSEIQRKCVGWIKPHQIFKNDKMLGLALPGIIMVE-AEFLG-----FEILTIFAS-----HISVNALAASITATIASLAYQI 600
gi | 145608424 | ref | XP_360580.2 | AGSASAMAVQNLIPILLVLYVVFPEG--RECWSGFS--WKAFRNWGPMIKLALPGMIMIE-AQFV-----LEILTIAAG-----QLGTAHAAASVLTVTSTFNI 600
gi | 22907060 | ref | NP_060712.2 | IGSALANLISQYTLALLFLYLILGKKLH--QATWGGWS--LECLQDWSFRLAIPSMMLC-MEWWA-----YEVGSFSLG-----ILGMVELGAOSIVVELAIVYMV 600
gi | 114668714 | ref | NP_001144887.1 | IGSALANLISQYTLALLFLYLILGKKLH--QATWGGWS--LECLQDWSFRLAIPSMMLC-MEWWA-----YEVGSFSLG-----ILGMVELGAOSIVVELAIVYMV 600
gi | 119912025 | ref | NP_873599.2 | MGSALANLISQYTLALLFLYLILAKRLH--QDTWGGWS--WECLQDWPFFRLAIPSMMLC-IEWWA-----YEIGSFSLG-----ILGMVELGAOSIAYELAVIYMV 600
gi | 13385694 | ref | NP_080459.1 | MGSALANLISQFALAIPLFLYLILWRRLE--QATWGGWS--WECLQDWSFRLAIPSMMLC-IEWWA-----YEVGSFSLG-----ILGMVELGAOSIVVELAIVYMI 600
gi | 62078965 | ref | NP_001014140.1 | MGSALANLISQFALAIPLFLYLILWRRLE--HATWGGWS--WECLQDWSFRLAIPSMMLC-IEWWA-----YEVGSFSLG-----ILGMVELGAOSIYVELAIVYMI 600
gi | 73956142 | ref | NP_546648.2 | MGSALANLISQFALVLFHYIISGKLEH--EATWGGWS--LECLQDWSFFNLAIIPSMMLC-MEWWA-----YEIGSFSLG-----ILGMVELGAOSVVELTVILYMI 600
gi | 189534168 | ref | NP_688576.2 | PGSAAAANISQYSLAVILYTYIRCMGLE--KATWDGWS--WDCLEWGSFIRLALPSMMLC-AEWWT-----YEIGGFLAG-----LISEVELGAOSIVVELASVMYMF 600
gi | 122114563 | ref | NP_001073648.1 | AGSAAAANTISQYSLAVFLYVYIRWKNLE--KATWDGWS--RDCLEWGFIRLALPSMMLC-VEWWT-----YEIGGFLAG-----LISEVELGAOSVVELATAYMF 600
gi | 118100277 | ref | NP_415860.2 | VGSAAWANTIAQYSCYIFFLYIYVGGKLEH--VKTWGGWS--RECLLEWDSFSLAIPSMMLC-IEWWT-----YEIGSFSLG-----LLSVVELGAOSVYVELSVYAFMI 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi	115481600	ref	NP_001064393.1	P	-----TGLTATIS-----	TRVWNELGAGNPQAAKLAIRVVVICMAMTEGSSVAFIMILLR-NSWGHMYSDEAEVVVYIARMIPLVLAISFFFDGMHSAL-----SGVL	750
gi	115481602	ref	NP_001064394.1	P	-----LGLCSSTIS-----	TRVSNELGAGQPOAAKRAIRVVMMALEGLVIFIMFLLR-NVWGYMYSNEQEVVYIARMLPILDISFFIDGLHSSL-----SGVL	750
gi	115481598	ref	NP_001064392.1	P	-----RGTGSSLS-----	TRVSNELGGHPRAARMAARVAIAMTVLVCLVIVIAMIFLR-NVWGNAYSSEEEVVVYIASMLPVLAVSFFFDGINGAL-----SGVL	750
gi	115457946	ref	NP_001052573.1	P	-----FGLGSAIS-----	TRVSNELGAGRPEAARLASRVVMALGLVVGVATGLAMILVR-HLWGYAYSNEEEVVVQVAKMMPILAVSFLFDLQCVLISVRDS-SGVA	750
gi	115468176	ref	NP_001057687.1	P	-----FGLGSAIS-----	TRVSNELGAGRPEAARLASRVVVFMAVSEGLVIGLVLVGVR-YIWHGAYSDEEEVVVYVAKMMLVIAVSNFFDGIQCVL-----SGVA	750
gi	115468182	ref	NP_001057690.1	P	-----FGLGSAIS-----	TRVSNELGAGRPEAARLASRVVLLALEGLGMALVLCVR-YVWGHAYSNEEEVVVAVAKMMLVIAVSNFFDGIQCVL-----SGVA	750
gi	115468180	ref	NP_001057689.1	P	RGDENIGGFVQLGVIFDKYGERFINRDNHHEVFLLGVQTFEHVVGRLIEVSVLELAITFNRR	TRVSNELGAGRPHAACLAVRVVFMVAEGLVIGLVLLISVR-NIWHGAYSNEEEVVVKVQVLLVIAVSNFFDGIQCVL-----SGVA	750
gi	15237158	ref	NP_200058.1	P	-----FGLGSAAS-----	TRISNELGAGNPKVAKLAVRVVICIAVAESIVIGVLLILIR-NIWGLAYSSEEEVVSVASMMPIALGNFLDSQCVL-----SGVA	750
gi	240254581	ref	NP_180983.4	P	-----FGLGSAAS-----	TRVSNELGSGNPKGAKLAVRVVLFIVESILVGTVLILIR-KIWGFAYSDDPEVVSHVASMLPILALGHSLLDSFQVIL-----SGVA	750
gi	15219524	ref	NP_177511.1	S	-----VGLGGAAS-----	IRVSNELGAGNPQVAKLAVYIVIGIAVAEIGVVVTVLLSIR-KILGHAFSSDPKIIAVAASMLPITVACGNFLDGLQCVL-----SGVA	750
gi	50312043	ref	XP_456053.1	P	-----FSIISTIS-----	TRVANFIGASLRVRSCTIICKVSLLSLFIISLNMAMIVKAR-YLIARLFSSEPDVRLVSSSLPILAFMQIFDAPNASI-----AGCL	750
gi	45190837	ref	NP_985091.1	P	-----FSIISTIS-----	TRVANFIGASLRVRSCTIICKVSLLSLFGVSLTSMALIVFRNLAHLIFLNBAEVMILITETLPLILAVMQIFDAPNASI-----AGCL	750
gi	145608424	ref	XP_360580.2	P	-----FPLAIAIS-----	TRVANLIGANGDAARTIKVAIFAALAVGVFNMIMLISLR-RVLPVAVFDDERVVIDLASKTMIIVCGIMQIFDALAAYS-----HGIL	750
gi	22907060	ref	NP_060712.2	P	-----AGFVAAS-----	VRVGNALGAGDMEQARKSSTVSLLLIVLFAVAFSVLLLSCK-DHVGVIYFTDRDIINLVAQVVPPIYAVSHLFEALACTS-----GGVL	750
gi	114668714	ref	XP_001144887.1	P	-----AGFVAAS-----	VRVGNALGAGDMEQARKSSTVSLLLIVLFAVAFSVLLLSCK-DHVGVIYFTDRDIINLVAQVVPPIYAVSHLFEALACTS-----GGVL	750
gi	119912025	ref	XP_873599.2	P	-----AGFVAAS-----	VRVGNALGARDTEQAKTSVAALLVTLGLFAVIFCVLLLSCK-DVVGVIYFTKDDQIVSLVAQVVPPIYAVSHLFEALACTS-----GGIL	750
gi	13385694	ref	NP_080459.1	P	-----AGFVAAN-----	VRVGNALGAGNIDQAKKSASISLIVTELFVAVTFCVLLLSCK-DLVGYIYFTDRDIIVALVAQVVPPIYAVSHLFEALACTS-----GGIL	750
gi	62078965	ref	NP_001014140.1	P	-----AGFVAAN-----	VRVGNALGAGNIDQAKKSASISLIVTELFVAVTFCVLLLSCK-DLVGYIYFTDRDIIVALVAQVVPPIYAVSHLFEALACTS-----GGVL	750
gi	73956142	ref	XP_546648.2	P	-----SGFVAAS-----	VRVGNALGAGNIDQAKKSASVALLVTFGFFAVTFCVVMVLSCK-DLVGVIYFTDRDIIVLVAQVVPPIYAVSHLFEALACTS-----GGIL	750
gi	189534168	ref	XP_688576.2	P	-----LGFVAAG-----	VRVGNALGAGNIDQAKLSAKVSLVCGLLVSVVIAVVIAGTN-NIIGYIYFSKDEDIVLRVSVQVMVMYGFVHLFDALAGIIL-----GGIV	750
gi	122114563	ref	NP_001073648.1	P	-----LGFVAAS-----	VRVGNALGAGNIDQAKLSAKVSLVCGLLVSVVIAVVIAGTN-NIIGYIYFSKDEDIVLRVSVQVMVMYGFVHLFDALAGIIL-----GGIV	750
gi	118100277	ref	XP_415860.2	P	-----LGLGTAAS-----	VRVGNALGAGDIEVAKRSSTSMVLCITGAFCAVGAIIAAIK-DLVGYIYFTNKKKILLDLVAWVMPVIVVFLHFAEMCCAG-----GGVL	750



gi	115481600	ref	NP_001064393.1	T	TGCGKQK-IGARVNLGAFYLAGIPMAVFLAFVHLHNGMGLWLGIVCGSLKLLILLFWITMSIWEKESTRAKELVFSSSLFVA-----	900
gi	115481602	ref	NP_001064394.1	T	TGCGKQK-IGAAVNLGAFYLVGIPVAVLLAFVHLHNGMGLWLGIVCGSIIKLLVLLIIVSCCIDWEKEAILAKDRVFSSSLFVA-----	900
gi	115481598	ref	NP_001064392.1	T	TGCGKQK-IGAHVNLAAAFYLVGIPAVLLAFVHLHNGEGLWLGIVCGSIIKVMGLLFTLRITDQKGEVRKPSFYKHPG-----	900
gi	115457946	ref	NP_001052573.1	R	RGCGWQK-IGAIVNLGAYYLVGIPAALCFAFVYHLGGMGLWLGIMCALIVQMLLLLAITVCTNWEKEALKAKERVFSSSLPADMT-----	900
gi	115468176	ref	NP_001057687.1	R	RGCGWQK-IGACVNLGAYYIVGIPSAAYLIAFVHLVGGMGLWLGIIICGLLVQVLLMAITLCTNWDKEAANAKDRVFSSSLPADLAT-----	900
gi	115468182	ref	NP_001057690.1	R	RGCGWQK-IGACINLGAFFYVVGPPAAAYLAAFVLRAGGLGLWMGIICGVAVQTLFLLAITVSRDQWKEAKMAKDRVFSSSLPTDLAT-----	900
gi	115468180	ref	NP_001057689.1	R	RGCGWQK-IGACVNLGAYYIVGIPSAAYLIAFVHLHNGMGLWLGIIICGILVQVLLMAITLCTNWDKEAANAKHRALNSSLPSDTAT-----	900
gi	15237158	ref	NP_200058.1	R	RGCGWQK-IGAIINLGSYYLVGVPGLLLAFHFHVGGRGLWLGIIICALVQVFGGLGLVITFTNWDDEAKKATNRVIESSSSVKDFAVDDRSVVVF-----	900
gi	240254581	ref	NP_180983.4	R	RGCGWQK-IGAFVNLGSYYLVGVPGLLLGFHFHVGGRGLWLGIIICALIVQVGLSLITFTFTNWDDEEKKATSRKSSSEVKFAVDNGSILV-----	900
gi	15219524	ref	NP_177511.1	R	RGCGWQK-IGACVNLGSYYLVGVPGLLLGFHFHVGGRGLWLGIVTALSQQVLCVSLVITFTNWDKEAKKATNRVSS-DDKDGVDQ-----	900
gi	50312043	ref	XP_456053.1	R	RGQGQK-IGGYINVFAYFCIGIPVSYLLTFHYGFGVSGLWMGITSGLVFMISFQSVAVFHCMWNDIIRAARKSRNSEGAMV-----	900
gi	45190837	ref	NP_985091.1	R	RGQGQK-DWLLSNVFAFYCIGIPMSYFLSFHCDLGVKGLWYGITCALIVMSVCSQSVAVFNCSWEELVKAANLRITSEDVF-----	900
gi	145608424	ref	XP_360580.2	R	RGVGRQK-VGGYANLFSYFVALPVSLSTAFALGWKLSGLWAGLVSGLAVVSALELLLYLNSDWSAIAQAARMRSEEEVIVEPKAGN-----	900
gi	22907060	ref	NP_060712.2	R	RGSGNOK-VGAIVNTIGYYVVLGPIGIALMFATTLGVMLWSGIIICTVFOAVCFLGFIIQLNWKKAQQQAQVHANLKVNNVPRSGNSALPQDPLHPGCPENL-EGILINDVVGKTEGPOS-----DQQMRDEEPLPEHPQDGAKLS	900
gi	114668714	ref	XP_001144887.1	R	RGSGNOK-VGAIVNTIGYYVVLGPIGIVLMFATTLGVMLWSGIIICTVFOAVCFLGFIIQLNWKKAQQQAQVHANLKVNNVPRSGNSALPQDPLHPGCPENL-EGILINDVVGKTEGPOS-----DQQMRDEEPLPEHPQDGAKLS	900
gi	119912025	ref	XP_873599.2	R	RGTGNOK-AGAIINAVGYYVVLGPIGISLMAAGLGLLGLWSGIIICTISQAACFLGFIIARLNWKKAQQQAQVHANLKR--MAGNGMALPQDPLCPVGPENR-GGMLIRDVGVGKEETQS-----DQQMRDEEPLPEHPRAAWRLS	900
gi	13385694	ref	NP_080459.1	R	RGTGNOK-VGAIVNAIGYYVVLGPIGIALMFAAKLGVIGLWSGIIICTVCTCFLAFIARLNWKKAQQQAQVHANLKV--VALN--SAVSHEPAHPVCPESH-GEIMMTDLEKKDETQL-----DQPMNQOALPVRPKDSNKL	900
gi	62078965	ref	NP_001014140.1	R	RGTGNOK-VGAIVNAIGYYVVLGPIGISLMAAGLGLLGLWSGIIICTVCTCFVLFARLNWKKAQQQAQVHANLKV--VALN--SAVSHEPAHPVGPESH-GEIMMTDLEKKDETQL-----DQPMNQOALPVRPKDSNKL	900
gi	73956142	ref	XP_546648.2	R	RGTGNOK-VGAIVNAIGYYVVLGPIGIVLMFAAKLGVIGLWSGIIICTVCTCFLAFIARLNWKKAQEEAQQVHANLRLN-TTQDTSAAQDQHPVGPENR-GGISMQDVRKRVRAVGGQVCGPETHQPMHGEELHCVQPTGTATLI-----	900
gi	189534168	ref	XP_688576.2	R	RGAGKQK-IGALCNMVGYYVCGPPIGVSLMFAFNMGIVGLWIGFFVCFVLOSFFIILYRLDWWKKAQEAALIRAGVQLTEIKYESFGLNKGCTEEAAQEN--TEEGQTDINTDLEGLS-----KGGEGITDAVALVTGCVLL	900
gi	122114563	ref	NP_001073648.1	R	RGAGKQK-LGALCNMVGYYVCGPPIGVSLMFAFNMGIVGLWIGFFVCFVLOSFFIILYRLDWWKKAQEAALIRAGVQLTEIKYESFGLNKGCTEEAAQEN--TEEGQTDINTDLEGLS-----KGGEGITDAVALVTGCVLL	900
gi	118100277	ref	XP_415860.2	R	RGTGKQK-FGAILNAVSYVGLPPLGAVLLFVARIGVIGLWLSMLVCSMLCTCFLLIYICRMDWRKAEEEAQRAGVTPQPLEEQHNPPEHSGKPSLAPHTHLPAAAVRCVAGMDAANG-----VVLTITTRTEGANFREEPRGALPG	900



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gi|115481600|ref|NP_001064393.1|-----1050
gi|115481602|ref|NP_001064394.1|-----1050
gi|115481598|ref|NP_001064392.1|-----1050
gi|115457946|ref|NP_001052573.1|-----1050
gi|115468176|ref|NP_001057687.1|-----1050
gi|115468182|ref|NP_001057690.1|-----1050
gi|115468180|ref|NP_001057689.1|-----1050
gi|15237158|ref|NP_200058.1|-----1050
gi|240254581|ref|NP_180983.4|-----1050
gi|15219524|ref|NP_177511.1|-----1050
gi|50312043|ref|XP_456053.1|-----1050
gi|45190837|ref|NP_985091.1|-----1050
gi|145608424|ref|XP_360580.2|-----1050
gi|22907060|ref|NP_060712.2|-----1050
gi|114668714|ref|XP_001144887.1|-----1050
gi|119912025|ref|XP_873599.2|-----1050
gi|13385694|ref|NP_080459.1|-----1050
gi|62078965|ref|NP_001014140.1|-----1050
gi|73956142|ref|XP_546648.2|-----1050
gi|189534168|ref|XP_688576.2|-----1050
gi|122114563|ref|NP_001073648.1|-----1050
gi|118100277|ref|XP_415860.2|-----1050
---RKQLVLRRLGLLLLGVFLILLVGIIV-RFYVRIG
---RKQLVLRRLGLLLLGVFLILLVGIIV-RFYVRIG
---GKQLVLRRLGLLLLAVLVILLVGIIV-KVYVRFY
---GKQLALRRGLLLLGVVLVLVGGILV-RVYIRIE
---GKQLALRRGLLFLGVVLVLVGGILV-RVYIRIE
---GSCLLLRRGLLLVGVFSLVLLMGILV-RVYIRIKWYPSLPEYTSKRICPFSSGGPGIRMGDGGWCGGLISGPTLQAEECTPPPPPSAGNTFCNTPLLAQLMIFLIGVSSIFCGHLGKVELDAVTLAVSVVNVITGISVGTGLASACD
---AKQLAVRRGLAFFFMILLITGGIVLNEVLIRFVI
---TKQLVLRRLAVLLMLLILAGGIVLNEMLVRYLR
---AAPSRLILRRGLIAAAAI AVLALGVVIKLVTSKH
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050
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gi|115481600|ref|NP_001064393.1|-----1083
gi|115481602|ref|NP_001064394.1|-----1083
gi|115481598|ref|NP_001064392.1|-----1083
gi|115457946|ref|NP_001052573.1|-----1083
gi|115468176|ref|NP_001057687.1|-----1083
gi|115468182|ref|NP_001057690.1|-----1083
gi|115468180|ref|NP_001057689.1|-----1083
gi|15237158|ref|NP_200058.1|-----1083
gi|240254581|ref|NP_180983.4|-----1083
gi|15219524|ref|NP_177511.1|-----1083
gi|50312043|ref|XP_456053.1|-----1083
gi|45190837|ref|NP_985091.1|-----1083
gi|145608424|ref|XP_360580.2|-----1083
gi|22907060|ref|NP_060712.2|-----1083
gi|114668714|ref|XP_001144887.1|-----1083
gi|119912025|ref|XP_873599.2|-----1083
gi|13385694|ref|NP_080459.1|-----1083
gi|62078965|ref|NP_001014140.1|-----1083
gi|73956142|ref|XP_546648.2|-----1083
gi|189534168|ref|XP_688576.2|-----1083
gi|122114563|ref|NP_001073648.1|-----1083
gi|118100277|ref|XP_415860.2|-----1083
.....1060.....1070.....1080...
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