

gi | 189571638 | ref | NP_001121676.1 | -----MKYSCCALVLAVLGTELLGSLCSVTRSPRFRGRIOQERKNIRPN IILVLTDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 139
gi | 73999469 | ref | XP_544115.2 | -----MKYSCCALVLAVLATELLGGCSVTRSPRFRGRIOQERKNIRPN IILVLTDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 139
gi | 26986617 | ref | NP_758498.1 | -----MKYSLWALLLAVLGTELLGSLCSVTRSPRFRGRIOQERKNIRPN IILVLTDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 139
gi | 19705485 | ref | NP_599205.1 | -----MKNSCWALLLAVLGAELLGGFCSTRSPRFRGRIOQERKNIRPN IILVLTDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 139
gi | 51467917 | ref | NP_001003846.1 | -----MMQLVSLAWMMVLAAPLV-CFGFTIRGCGLLRGRVQDRRNRIRPN IILVLTDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 138
gi | 17568795 | ref | NP_508560.1 | -----MISNLRISNMFILIFVLEFLIPIKVTG IHFVDSQH-----NVILLITDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 131
gi | 24647401 | ref | NP_524987.1 | -----MNRHSSLRLIIGLLILLFLVNLVFSKQSGSHHKKRSHAKRFSRDSNSARERPN IILVLTDDQVDELGSLQVMNKRKIMEHGGAFTINAFVITPMCCPFRSSMLTGKVVHNHNYTNNENCSSPFWQAMHEPRITFAVYLNNTGYRTAF 150
gi | 158292967 | ref | XP_314283.4 | -----LVHNHNVFTNNDCSSTWQTHETRSFATYLSNAGYRTGY 41



gi | 189571638 | ref | NP_001121676.1 | FGKYLNEYNGSYIIPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 289
gi | 73999469 | ref | XP_544115.2 | FGKYLNEYNGSYIIPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 289
gi | 26986617 | ref | NP_758498.1 | FGKYLNEYNGSYIIPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 289
gi | 19705485 | ref | NP_599205.1 | FGKYLNEYNGSYIIPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 289
gi | 51467917 | ref | NP_001003846.1 | FGKYLNEYNGSYIIPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 288
gi | 17568795 | ref | NP_508560.1 | LGKYLNEYDGSYIIPGWDEWHAIFNNSKRFYNYTVCRNGIKEKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 281
gi | 24647401 | ref | NP_524987.1 | FGKYLNEYNGSYIIPGWREWGLIMNSKYYNSINLNGQIKKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 300
gi | 158292967 | ref | XP_314283.4 | FGKYLNEYNGSYIIPGWREWGLIMNSKYYNSINLNGQIKKHGFDYAKDYFDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPNASQHI TFSYNYAPNMDKHWIMQYTGPMLP IHMEFTNLVLRKRRLQTLMSV 191



gi | 189571638 | ref | NP_001121676.1 | DDSVERLYNMLVEIGELNTYIIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 416
gi | 73999469 | ref | XP_544115.2 | DDSVERLYNMLVEIGELNTYIIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 416
gi | 26986617 | ref | NP_758498.1 | DDSVERLYNMLVEIGELNTYIIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 416
gi | 19705485 | ref | NP_599205.1 | DDSVERLYNMLVEIGELNTYIIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 416
gi | 51467917 | ref | NP_001003846.1 | DDSVEKVNALVDIGELNTYIIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 415
gi | 17568795 | ref | NP_508560.1 | DDEIERLRLNLLRELNLWNTYIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 406
gi | 24647401 | ref | NP_524987.1 | DVAVERVVQELKALGELDNTYIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 446
gi | 158292967 | ref | XP_314283.4 | DVAVERVVQELKALGELDNTYIYIYADGHYHIGQFGLVKGKSMYPDFDIRVPPFFIRGPEVEPGSVIPQIVLNLIDLAP IILDIAGLDTPPDVVGKSVLKLLE-----LEKPGNRFRNKKAKIWRDIFLVERG 340



gi | 189571638 | ref | NP_001121676.1 | -----KFLRKKEE-----SSKNIQOSNHLPKYERVKELCOQARYQTACEPGQKWCIEDTSGKLRHK 475
gi | 73999469 | ref | XP_544115.2 | -----KFLRKKEE-----SSKNIQOSNHLPKYERVKELCOQARYQTACEPGQKWCIEDTSGKLRHK 475
gi | 26986617 | ref | NP_758498.1 | -----KFLRKKEE-----SSKNIQOSNHLPKYERVKELCOQARYQTACEPGQKWCIEDTSGKLRHK 475
gi | 19705485 | ref | NP_599205.1 | -----KFLRKKEE-----SSKNIQOSNHLPKYERVKELCOQARYQTACEPGQKWCIEDTSGKLRHK 475
gi | 51467917 | ref | NP_001003846.1 | -----KILRKHDSAE-----SSLNITQHSNLSLKYKKEVCOQAEFOTCEPGQKWHCVBEVSGKWRLOK 476
gi | 17568795 | ref | NP_508560.1 | -----KMPLKKIR-----DRYIKOKKKNENKRLSKECKRRKWRDQVH-GQLWKCYYTVEDRWRIYK 464
gi | 24647401 | ref | NP_524987.1 | -----CPDGEVEEVTNEEDDVGDCGAMSSAAALEEDDDAAFEEDDEILD-----QFQONNDLPAFYITKMMRLNSECSDPALLKNCLEP-GOKWCVNE-EGRWKXK 582
gi | 158292967 | ref | XP_314283.4 | -----NSSLLEDFLEGAGES-FTIVSSSSTAAATLMSSTAQ-----CPDGEVEEVTNEEDDVGDCGAMSSAAALEEDDDAAFEEDDEILD-----QFQONNDLPAFYITKMMRLNSECSDPALLKNCLEP-GOKWCVNE-EGRWKXK 488



gi | 189571638 | ref | NP_001121676.1 | CKGSPDLLIVRQSRNLYARGFHDKDKE-----CSCRESGYRASRSQRKSRQFLRNQGTPKYKPRFVHTROTSLRSLVEFEFEGEYIDINLEEEELQVLQP-----RNIAKRHDEHGKGR-DLQASSGCNCRMLADSSN--- 604
gi | 73999469 | ref | XP_544115.2 | CKGSPDLLIVRQSRNLYARGFHDKDKE-----CSCRESGYRASRSQRKSRQFLRNQGTPKYKPRFVHTROTSLRSLVEFEFEGEYIDINLEEEELQVLQP-----RNIAKRHDEHGKGR-GHQAPQGD--VMLADRD--- 603
gi | 26986617 | ref | NP_758498.1 | CKGSPDLLIVRQSRNLYARGFHDKDKE-----CSCRESGYRASRSQRKSRQFLRNQGTPKYKPRFVHTROTSLRSLVEFEFEGEYIDINLEEEELQVLQP-----RNIAKRHDEHGKGR-GHQAAAGDTRNEMLADSSN--- 603
gi | 19705485 | ref | NP_599205.1 | CKGSPDLLIVRQSRNLYARGFHDKDKE-----CSCRESGYRASRSQRKSRQFLRNQGTPKYKPRFVHTROTSLRSLVEFEFEGEYIDINLEEEELQVLQP-----RNIAKRHDEHGKGR-GHQAAAGDTRNEMLADSSN--- 603
gi | 51467917 | ref | NP_001003846.1 | CKG-SLKGSGSKRRLSRSRSDNREK-----CSCGGERPKAARARRAHRQFGS-SNPRYRPRFVHTROTSLRSLVEFEFEGEYIDINLEEEELQVLQP-----RNIAKRHDEHGKGR-DLQASSGCNCRMLADSSN--- 603
gi | 17568795 | ref | NP_508560.1 | CRDNWSDCSCRKRREISN-----VDDIDID-----RPTSKRHYEPPEGFDSDFGLESDDGSEEMQSDDTN--- 494
gi | 24647401 | ref | NP_524987.1 | CKFHLLQLEHQLAAMPKQ-----YQRNCACTPDGVVYIKIRAPASAGLHRVNRKT-----HNGPQRNRNKREVFHTELPEMEELLDLHGVVDQVLD-----HTHRSKRDLPASSNETTAQVIQQIQSLLELLELKFN--- 705
gi | 158292967 | ref | XP_314283.4 | CKFHGLQHLAEMARKTNGQANRNCACFPQDNFFYIKITKRDHTKWQPMATQPMATHQHRRRRTQKRSVLTGLGPTMBSLVQVAARDALQRSLYEGELEEEHESGKRTTRSKRDTTSSPSHLADVHLELQQLVLEIEREYETA 638



gi	189571638	ref	NP_001121676.1	-----	AVGPPPTVTRVTHKCFILPNDTIHCERELYOSARAWKDHKAYIDKEIEALQDKIKNLEVRVGHLLKRRKPPECSCFKOSYNNKEKGVK-----KQEKLKS-----HLHPFKAAA	706
gi	73999469	ref	XP_544115.2	-----	ALGLPTTVTRVTHKCFILPNDTIHCERELYOSARAWKDHKAYIDKEIEALQDKIKNLEVRVGHLLKRRKPPECACSKOSYNNKEKGVK-----KQEKVKS-----HLHPFKAAA	705
gi	26986617	ref	NP_758498.1	-----	AVGLPATVTRVTHKCFILPNDTIHCERELYOSARAWKDHKAYIDKEIEVLQDKIKNLEVRVGHLLKRRKPPECAGDQOSYNNKEKGVK-----RQEKLKS-----HLHPFKAAA	706
gi	19705485	ref	NP_599205.1	-----	AVGLPTTVTRVTHKCFILPNDTIHCERELYOSARAWKDHKAYIDKEIEVLQDKIKNLEVRVGHLLKRRKPPECSCFKOSYNNKEKGVK-----KQEKLKS-----HLHPFKAAA	706
gi	51467917	ref	NP_001003846.1	-----	AVGVPNLSLKVTHKCFILINDTVRCEREIYOSRAWKDHKNVVDHEIEQLQDKMKLREVRVGHLLKRRPDECDCKKSYFSKEREQKN-----KPERLKNRNDHLHPFKBAM	709
gi	17568795	ref	NP_508560.1	-----	-----MADRENFESEGHEWYQGEFEDSGEVG-----EELDGHRSKRGLSK-----CSCSRN-----VSHPIKLE-----	549
gi	24647401	ref	NP_524987.1	-----	-----EHELHASNSSGNSVERGEKYTEGGHRCFVDATTAKVNCNVIIDDEKLTWRTSRQIDMLIKLLKDKIGLKEKMKQLRESNKAALAAARR-----NDRNRNDQSLVDSGAGPEFN-----MSYFTEISSPFRNVVGQTEVFGCYGS	844
gi	158292967	ref	XP_314283.4	-----	VEGRDDHTINDSNGSNTASGEVGVFVGVVTKRCSVLAADKINCSNVVIDEVSWRNRMRKVDQLIRVLKDKINALKDKIRLLREHRPAGVRGDSLEDNNEEENEIIGSGGMEERTLSSSTVSSAAATPAATEPSEAVQTPSG	788
				760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900	



gi	189571638	ref	NP_001121676.1	-----	OEVDSKLOLFKKNRRRKRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLFCFEFATGFLEYFDMNTDPYQLTNTVHT	816
gi	73999469	ref	XP_544115.2	-----	OEVDSKLOLFKEN-----RRRKRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLFCFEFATGFLEYFDMNTDPYQLTNAVHT	814
gi	26986617	ref	NP_758498.1	-----	OEVDSKLOLFKEH-----RRRKRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLFCFEFATGFLEYFDMNTDPYQLTNTVHT	815
gi	19705485	ref	NP_599205.1	-----	OEVDSKLOLFKEH-----RRRKRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLFCFEFATGFLEYFDMNTDPYQLTNTVHT	815
gi	51467917	ref	NP_001003846.1	-----	OEVDSKAOLYNEI-----RRRKRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLFCFEFATGFLEYFDMNTDPYQLTNAVHT	818
gi	17568795	ref	NP_508560.1	-----	CKMSKHKYLYKYYK-----KPNGLSKPKDCSLPQMNCFTHTASHWKPPLPWPBEGFCFCQNCNNTYWCLRTVNETHNFLYCFEYVIEFISFYDFNTDPDQLINAVYS	653
gi	24647401	ref	NP_524987.1	-----	AAAFDLEIQOSHRFVPRACVYCEPDVNGN-----HADSEKEMAREARKLKEERQRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLYCFEYVIEFISFYDFNTDPDQLINRAAG	988
gi	158292967	ref	XP_314283.4	-----	SAGPRRVVAVAKLLCWRRFRWSPSSSYPHSPVPDEKELARERRRLKEERQRKKEKRRQRKGECSLPGLTCTHDDNNHWQTAPFW-----NLGSFCACTSSNNNTYWCLRTVNETHNFLYCFEYVIEFISFYDFNTDPDQLINRAAG	936
				910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050	



gi	189571638	ref	NP_001121676.1	-----	VERGILNQLHVQLMELRSCQGYKQCNPRPKNLDVGNKD---GGSYDLHRGQLWDGWEG-----	871
gi	73999469	ref	XP_544115.2	-----	VERGILNQLHVQLMELRSCQGYKQCNPRPKGLVEDSYG---MDGKVNLPSTTVDVNNQGLDLYSVNASVVEYRQNYLSLVDWTNYLKDVDVRFALLNSRHEQKTKNKTKNAQSDGFLAGSAELVPAETASAESDEDPRLVGEAPHLE	963
gi	26986617	ref	NP_758498.1	-----	VERGILNQLHVQLMELRSCQGYKQCNPRPKSLDIDGAKG---GGNYDPHRGQLWDGWEG-----	870
gi	19705485	ref	NP_599205.1	-----	VERGILNQLHVQLMELRSCQGYKQCNPRPKSLDIDGAKG---GGNYDPHRGQLWDGWEG-----	870
gi	51467917	ref	NP_001003846.1	-----	VEKDIILSOLHSOLMEMRSCQCHKQCNPRPKSDAEHSQPGTSTKVKLPNFTEDVDWQGLADLYSMNEELYEHRHNYSPVLDQDMNFWKVDVSMFALLRNKTLNQTDKLDPVLEGL-----EGVLVEASGAGSLILENLATAGPSVD	960
gi	17568795	ref	NP_508560.1	-----	LIDIGVLEQLSEQLRNLKCK---NRCCIEWSTSQMLRSPK---LVDLRLVNEKSFITYQPEKT	709
gi	24647401	ref	NP_524987.1	-----	LTPGERSHMDALDOLKSCR---GRSCSIRRHQNHLEGGSSAPLLPINCQVHRNKRKHSPLAGAVGNVAFVGPRLDMEALPPIKRKLKSKYRNLGSGQQSHMKRRPQKQTPQQSPRFLRHSVTPAQA	1114
gi	158292967	ref	XP_314283.4	-----	LTAEEKTVLHETLEEMKRCR---GKGCTLPRHQNV	969
				1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200	



gi	189571638	ref	NP_001121676.1	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	871
gi	73999469	ref	XP_544115.2	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	1113
gi	26986617	ref	NP_758498.1	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	870
gi	19705485	ref	NP_599205.1	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	870
gi	51467917	ref	NP_001003846.1	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	1093
gi	17568795	ref	NP_508560.1	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	709
gi	24647401	ref	NP_524987.1	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	1114
gi	158292967	ref	XP_314283.4	-----	LPADLRLHLNQPFSFPEKLEWNNDIPEVSRNLSEHWRNHTKWLKHEERHLEIDFSGNGLTELVLKPRRPPGSRQHKELPQGGPGEDVFEDQLHLPVHSDVDVHQTINTAAVEPPNSSSEKRMNLKVKNHKMGSLQSLGSG	969
				1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350	



gi	189571638	ref	NP_001121676.1	-----	871
gi	73999469	ref	XP_544115.2	-----	AVFPLSSD 1121
gi	26986617	ref	NP_758498.1	-----	870
gi	19705485	ref	NP_599205.1	-----	870
gi	51467917	ref	NP_001003846.1	-----	AVGLSH 1099
gi	17568795	ref	NP_508560.1	-----	709
gi	24647401	ref	NP_524987.1	-----	1114
gi	158292967	ref	XP_314283.4	-----	969
				