

gi	17511255	ref	NP_006442.2	-----	MSDGFDRAPGACGRGRERGLGRGGGGPEGGGFNAGAPAEARARHQP- QPKAPGFLG	55
gi	157279853	ref	NP_001098441.1	-----	MSDGFDRAP	9
gi	57085297	ref	XP_536482.1	-----	MSDGFDRAP	9
gi	21703908	ref	NP_663432.1	-----	MSDSFDRAP	9
gi	109464360	ref	XP_345161.3	-----	MSDSFDRAPGACGRGRERGLGRGGGGPEGGGFNAGAPAEARARHQP- QPKAPGFLG	56
gi	51011097	ref	NP_001003504.1	-----	MNNNNSSAPSSSSSEAG	19
gi	19922420	ref	NP_611180.1	MSCRAPFPDDQVEQLRRPNVGGAGGVAMPGLDQAHLFGEYAGACAYGVVGNFVQCAMPQQAQLSDASNLASATAIFIPRGAAPPQQQRHQYQQAGGAGGGGAFYQQQPRFVNGFKHHHQHQQPQPHYNHHNHQOKFNNDMQKL	150	
gi	58394672	ref	XP_320878.2	-----		

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi	17511255	ref	NP_006442.2	PPPLRQPRTPPPGACCEVPASPORPSRPGALPEQTRPLRAPSSG	DKIPOONSESAMAKPQVVVAVPLMSKLSVNAPEFYPSGYSSSYTESYEDGCEY	PTLSEYVODFLNHLTEOPGSFETEIQFAETLNG	189
gi	157279853	ref	NP_001098441.1	EQTRPLRAPSSP	DNIPQONSESAMAKPQVVVAVPLMSKLSVNAPEFYPSGYSSSYTESYEDGCEY	PTLSEYVODFLNHLTEOPGSFETEIQFAETLNG	110
gi	57085297	ref	XP_536482.1	EPTRPORAPSSG	DNIPQONSESAMAKPQVVVAVPLMSKLSVNAPEFYPSGYSSSYTESYEDGCEY	PTLSEYVODFLNHLTEOPGSFETEIQFAETLNG	110
gi	21703908	ref	NP_663432.1	EOTKPORAPSSG	DKIPOONSESAMAKPQVVVAVPLMSKLSVNAPEFYPSGYSSSYTESYEDGCEY	PTLSEYVODFLNHLTEOPGSFETEIQFAETLNG	110
gi	109464360	ref	XP_345161.3	PPPLRQPRTPPPGACCEVPASPORPSRPGALPEQTRPLRAPSSG	DKIPOONSESAMAKPQVVVAVPLMSKLSVNAPEFYPSGYSSSYTESYEDGCEY	PTLSEYVODFLNHLTEOPGSFETEIQFAETLNG	190
gi	51011097	ref	NP_001003504.1	DARSSAFNCEPLRQPRTPSPVSD	CGSGSPVSSNSGNSSSVADALVKNKLSAAAEEFIPGGYSSVQDDSYSDGSEGYAEPPLADVFVSHLNSSPGSFESIEIYITDILNE		135
gi	19922420	ref	NP_611180.1	TNSVQNRHLHNSQCGSAGNYQQVHQNTHHQHQHQHQHPHNOHAKFDRHFHLNNSFQQLVQQTOHNOQQPHHQHNOQQQYIQNONQOPQSTTAASSSSNSSPDMATIALEYLDTVIHLCLNPNPQFDSIASRFLTIFDG			300
gi	58394672	ref	XP_320878.2	-----			

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi	17511255	ref	NP_006442.2	CVTDDALQELVELIYQAAISIPNFYSYMGARLCNYLSHHLISIPSGNFRQLLQRCRTEYEYVKDQAAKGDEVTRKRHFHFVFLFGLGELYLNLEIKGTNGOVRTADILQVGLRELLNALFSNPMDNLI	CAVKLLKLTGSLVLEDAWKEKGG	339	
gi	157279853	ref	NP_001098441.1	WVTTDDALQELMELIYQAAISIPNFYSYMGARLCNYLSHHLISIPSGNFRQLLQRCRTEYEYVKDQAAKGDEVTRKRHFHFVFLFGLGELYLNLEIKGTNGOVRTADILQVGLRELLNALFSNPMDNLI	CAVKLLKLTGSLVLEDAWKEKGG	260	
gi	57085297	ref	XP_536482.1	WVTDDALQELVELIYQAAISIPNFYSYMGARLCNYLSHHLISIPSGNFRQLLQRCRTEYEYVKDQAAKGDEVTRKRHFHFVFLFGLGELYLNLEIKGTNGOVRTADILQVGLRELLNALFSNPMDNLI	CAVKLLKLTGSLVLEDAWKEKGG	260	
gi	21703908	ref	NP_663432.1	WVTDDALQELVELIYQAAISIPNFYSYMGARLCNYLSHHLISIPSGNFRQLLQRCRTEYEYVKDQAAKGDEVTRKRHFHFVFLFGLGELYLNLEIKGTNGOVRTADILQVGLRELLNALFSNPMDNLI	CAVKLLKLTGSLVLEDAWKEKGG	260	
gi	109464360	ref	XP_345161.3	WVTDDALQELVELIYQAAISIPNFYSYMGARLCNYLSHHLISIPSGNFRQLLQRCRTEYEYVKDQAAKGDEVTRKRHFHFVFLFGLGELYLNLEIKGTNGOVRTADILQVGLRELLNALFSNPMDNLI	CAVKLLKLTGSLVLEDAWKEKGG	340	
gi	51011097	ref	NP_001003504.1	WVTTEILQELVELIYVCSISIPNFAYTGARLCNHLRHRLSPANRFRNLLQRCOTEVHQNRQAVQGDPEIKKKFHSYVFLFGLGELYLNLEIKGTNGOVRTADILQVGLRELLNALFSNPMDNLI	CAVKLLKLTGSLVLEDAWKEKGG	285	
gi	19922420	ref	NP_611180.1	MENNQVFLSIAMEDIFEKSTEQPNFRYMGAKLYNLLHMLNPKDLSLFHLLKCKLDVHQEVYKYMRSNEQVRETFALFLAELVMQLRGDDDSRIQLTAVNIVYLSKLLASESNENVRCLCOTLKLAGYDLTADCP		438	
gi	58394672	ref	XP_320878.2	-----	-----	-----	110

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi	17511255	ref	NP_006442.2	MDMEIIRQIENNVLDANC SRDVKQMLLKLVELRSSNWGRVHAATSTYREATPENDPNY	FMNEPFIYTS DGVPFTAADPDYQEKYQELLEREDFFPD	YEENGDLGAGDPVLDIDDEMDPEIEAYEKFCLESER	475			
gi	157279853	ref	NP_001098441.1	MDMEIIRQIENNVLDANC SRDVKQMLLKLVELRSSNWGRVHAATSTYREATPENDPNY	FMNEPFIYTS DGVPFTAADPDYQEKYQELLEREDFFPD	YEENGDLGAGDPVLDIDDEMDPEIEAYEKFCLESER	396			
gi	57085297	ref	XP_536482.1	NDMEIIRQIENNVLDANC SRDVKQMLLKLVELRSSNWGRVHAATSTYREATPENDPNY	FMNEPFIYTS DGVPFTAADPDYQEKYQELLEREDFFPD	YEENGDLGAGDPVLDIDDEMDPEIEAYEKFCLESER	396			
gi	21703908	ref	NP_663432.1	MDMEIIRQIENNVLDANC SRDVKQMLLKLVELRSSNWGRVHAATSTYREATPENDPNY	FMNEPFIYTS DGVPFTAADPDYQEKYQELLEREDFFPD	YEENGDLGAGDPVLDIDDEMDPEIEAYEKFCLESER	396			
gi	109464360	ref	XP_345161.3	MDMEIIRQIENNVLDANC SRDVKQMLLKLVELRSSNWGRVHAATSTYREATPENDPNY	FMNEPFIYTS DGVPFTAADPDYQEKYQELLEREDFFPD	YEENGDLGAGDPVLDIDDEMDPEIEAYEKFCLESER	474			
gi	51011097	ref	NP_001003504.1	SDMDLKVKKIEILLDAKCSRDVQMLLKLVELRSSNWGRVHTAAVSDATPDNDPNY	FMNEPFIYTVGDPFTAADPEYSEKYQELLEREDFFPD	YEENGDLGAGDPVLDIDDEMDPEIEAYEKFCLESER	415			
gi	19922420	ref	NP_611180.1	KDIEIITALQAEIKSP	GKYPMAASVIALQNNWGR	KVSNALGDDEDTVKEPF	RLSDEPFVYGPDRGLTAEETDFLAG	GNDDGDDDFDGDGAD	LEIDAEMDEETERAYKEFCRQGGK	557
gi	58394672	ref	XP_320878.2	DKVDQIMKNLDQARSSVPS	AAEKLIQSVIELRKIAGRSEIIPSAALPPMPVSVGAMGGGPIGAGEYQNNPFVYGPDQVLTVEEESFLETNVKNKAQAQAFSGYDDDEY				GLVDPDDPEVQAFVEFLQSNPQ	249

.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

gi	17511255	ref	NP_006442.2	KRKC	479
gi	157279853	ref	NP_001098441.1	KRKC	400
gi	57085297	ref	XP_536482.1	KRKC	400
gi	21703908	ref	NP_663432.1	KRKC	400
gi	109464360	ref	XP_345161.3	KRKC	478
gi	51011097	ref	NP_001003504.1	RRKC	419
gi	19922420	ref	NP_611180.1	KT	559
gi	58394672	ref	XP_320878.2	NRCPHPYRPDV	261

.....610..