

SUPPLEMENTAL FIGURE 1. Steap family amino acid sequence alignment. All complete Steap family amino acid sequences were collected from the NCBI nr database and aligned with Clustal Omega software. Sequences under the same panel number are aligned with each other. The strictly-conserved residues in the oxidoreductase domain of Steap2, 3, and 4 are indicated by blue boxes (panels 3.B-F, 4.B-F, 5.B-F). Strictly-conserved residues in the transmembrane domain of Steap1, 2, 3, and 4 are indicated by red boxes (panels 6.A-F, 7.A-F, 8.A-F). Conserved residue numbers are given at the bottom of each panel according to human Steap3 numbering. Species name and identification of Steap member subtype can be found by sequence accession number in the supplemental spreadsheet.

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 gi|635114985|ref|XP_007980441.1|
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 gi|640797078|ref|XP_008054657.1|
 gi|284005327|ref|NP_001164745.1|
 gi|47523676|ref|NP_999470.1|
 gi|465984745|ref|XP_004265676.1|
 gi|602733452|ref|XP_007452111.1|
 gi|532098195|ref|XP_005334745.1|
 gi|488586809|ref|XP_004478735.1|
 gi|472348935|ref|XP_004394171.1|
 gi|593759248|ref|XP_007118379.1|
 gi|585167015|ref|XP_006735605.1|
 gi|471395595|ref|XP_004381562.1|
 gi|548463586|ref|XP_005679360.1|
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 gi|564230520|ref|XP_006259687.1|
 gi|557325124|ref|XP_006035579.1|
 gi|695138615|ref|XP_009510760.1|
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 gi|677460376|gb|KFK49790.1|
 gi|676240922|gb|KFO04794.1|
 gi|327274492|ref|XP_003222011.1|
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 gi|677536446|gb|KFO98355.1|
 gi|675309850|gb|KFM05112.1|
 gi|677485789|gb|KFK75194.1|
 gi|677065660|gb|KFP25666.1|
 gi|677385324|gb|KFO06625.1|
 gi|678999197|gb|KFW02769.1|
 gi|683460598|gb|KFP25531.1|
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 gi|677306180|gb|KFP88608.1|

Panel 1.B

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gi|677240187|gb|KFP55213.1|
gi|602634684|ref|XP_007424213.1|
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gi|676772626|gb|KFP01083.1|
gi|678171735|gb|KFV39739.1|
gi|677419357|gb|KFQ23881.1|
gi|677154760|gb|KFP42681.1|
gi|529418081|ref|XP_005228921.1|
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gi|676700994|gb|KFO83399.1|
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gi|677386179|gb|KFQ07179.1|
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gi|669272197|ref|XP_008628114.1|
gi|696975798|ref|XP_009557373.1|
gi|543727822|ref|XP_005505003.1|
gi|541950812|ref|XP_005432194.1|
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gi|694922370|ref|XP_009451808.1|
gi|426356830|ref|XP_004045756.1|
gi|677449625|gb|KFQ41817.1|
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gi|602634686|ref|XP_007424214.1|
gi|677415485|gb|KFQ21444.1|
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gi|281183125|ref|NP_001162460.1|
gi|195977102|gb|ACG63652.1|
gi|100913194|ref|NP_001035755.1|
gi|640797080|ref|XP_008054658.1|
gi|677364635|gb|KFP94340.1|
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gi|157822623|ref|NP_001101316.1|
gi|585679651|ref|XP_006891518.1|
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gi|697032336|ref|XP_009578311.1|
gi|677370074|gb|KFP96995.1|
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gi|678183296|gb|KFV51018.1|
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gi|690459529|ref|XP_009328805.1|
gi|514739113|ref|XP_005017952.1|
gi|472348933|ref|XP_004394170.1|
gi|529418083|ref|XP_005228922.1|
gi|395540030|ref|XP_003771965.1|

Panel 1.E

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gi 591384664 ref XP_007066785.1					
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gi 591299567 ref XP_007076799.1					
gi 642101771 emb CDQ76188.1					
gi 558213257 ref XP_006134172.1			MKPL		SYYYLLC 11
gi 586554628 ref XP_006925771.1					
gi 617463244 ref XP_00572760.1					
gi 585154586 ref XP_006729650.1					
gi 593730883 ref XP_007111076.1					
gi 560979331 ref XP_006211922.1					
gi 560925797 ref XP_006189080.1					
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gi 301756344 ref XP_002914022.1					
gi 326921724 ref XP_003207106.1					
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gi 109067578 ref XP_001104041.1					
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gi 663261998 ref XP_008492349.1					
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gi 679216243 gb KFN94833.1					
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gi 521032115 gb EPQ13901.1					
gi 554563717 ref XP_005876182.1					
gi 686595796 ref XP_009273959.1					
gi 558171384 ref XP_006099145.1			MP		2
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gi 678192031 gb KFW59725.1					
gi 677380957 gb KFO03816.1					
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gi 292617388 ref XP_002663339.1					
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gi 677399646 gb KFO14863.1					
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Panel 2.A

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gi 675704305 ref XP_008960306.1					
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gi 562883058 ref XP_006169062.1					
gi 640797078 ref XP_008054657.1					
gi 284005327 ref NP_001164785.1					
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gi 465984745 ref XP_004265676.1					
gi 602733452 ref XP_007452111.1					
gi 532098195 ref XP_005334745.1					
gi 488586809 ref XP_004478735.1					
gi 472348935 ref XP_004394171.1					
gi 593759248 ref XP_007118379.1					
gi 585167015 ref XP_006735605.1					
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gi 478514256 ref XP_004431379.1					
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gi 301769711 ref XP_002920273.1					
gi 674094851 ref XP_008820733.1					
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gi 589949124 ref XP_006987220.1					
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gi 157817514 ref NP_001100099.1					
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gi 524968285 ref XP_005084028.1					
gi 504139794 ref XP_004582345.1					
gi 532030830 ref XP_005358357.1					
gi 617633976 ref XP_007530280.1					
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gi 505775878 ref XP_004602338.1					
gi 395540028 ref XP_003771964.1					
gi 126341322 ref XP_001368631.1					
gi 591381645 ref XP_007065358.1					
gi 558122566 ref XP_006114505.1					
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gi 530577003 ref XP_005282462.1					
gi 564230520 ref XP_006259687.1					
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gi 690459531 ref XP_009328807.1					
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gi 524985846 ref XP_005040881.1					
gi 694847615 ref XP_009464897.1					
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gi 679187928 gb KFW78811.1					
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gi 679144654 gb KFW71726.1					
gi 677478626 gb KFO68031.1					
gi 677536446 gb KFO98355.1					
gi 675309850 gb KFO51112.1					
gi 677485789 gb KFO75194.1					
gi 677065660 gb KFO25666.1					
gi 677385324 gb KFO06625.1					
gi 678999197 gb KFO2769.1					
gi 683460598 gb KFO25531.1					
gi 678186697 gb KFO54419.1					
gi 677306180 gb KFO88608.1					


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      gi|9558759|ref|NP_036581.1| ..... 200 Panel 3.A ..... 240 ..... 260
gi|114614402|ref|XP_001164872.1| .....
gi|109067567|ref|XP_001103605.1| .....
gi|297681115|ref|XP_002818311.1| .....
gi|635114985|ref|XP_007980441.1| .....
gi|281183115|ref|NP_001162459.1| .....
gi|332206685|ref|XP_003252427.1| .....
gi|675704305|ref|XP_008960306.1| .....
gi|355747866|gb|EHH52363.1| .....
gi|403257228|ref|XP_003921231.1| .....
gi|167427288|gb|ABZ80265.1| .....
gi|296209751|ref|XP_002751667.1| .....
gi|168986657|gb|ACA35052.1| .....
gi|545522297|ref|XP_005628542.1| .....
gi|562883058|ref|XP_006169062.1| .....
gi|640797078|ref|XP_008054657.1| .....
gi|284005327|ref|NP_001164745.1| .....
gi|47523676|ref|NP_999470.1| .....
gi|465984745|ref|XP_004265676.1| .....
gi|602733452|ref|XP_007452111.1| .....
gi|532098195|ref|XP_005334745.1| .....
gi|488586809|ref|XP_004478735.1| .....
gi|472348935|ref|XP_004394171.1| .....
gi|593759248|ref|XP_007118379.1| .....
gi|585167015|ref|XP_006735605.1| .....
gi|471395595|ref|XP_004381562.1| .....
gi|548463586|ref|XP_005679360.1| .....
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gi|594104641|ref|XP_006075297.1| .....
gi|634845395|ref|XP_007938026.1| .....
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gi|667308743|ref|XP_008583828.1| .....
gi|344270750|ref|XP_003407206.1| .....
gi|410952218|ref|XP_003982780.1| .....
gi|560979325|ref|XP_006211919.1| .....
gi|560936071|ref|XP_006193855.1| .....
gi|533147257|ref|XP_005388040.1| .....
MSA YYLESRES VF 13
gi|177773086|gb|ACB73280.1| .....
gi|556762767|ref|XP_005976676.1| .....
gi|594697428|ref|XP_007195873.1| .....
gi|194209596|ref|XP_001492607.2| .....
gi|329663204|ref|NP_001192735.1| .....
gi|670986759|ref|XP_008684436.1| .....
gi|507646395|ref|XP_004702858.1| .....
gi|586554622|ref|XP_006925768.1| .....
gi|507930961|ref|XP_004676724.1| .....
gi|478514256|ref|XP_004431379.1| .....
gi|395818574|ref|XP_003782699.1| .....
gi|558107925|ref|XP_006084992.1| .....
gi|281350064|gb|EFB25648.1| .....
gi|641692779|ref|XP_008147526.1| .....
gi|514471127|ref|XP_003475031.2| .....
gi|554563711|ref|XP_005876179.1| .....
gi|512867117|ref|XP_004891357.1| .....
gi|586451062|ref|XP_006878402.1| .....
M I G 3
gi|584041388|ref|XP_006779245.1| .....
gi|301769711|ref|XP_002920273.1| .....
MFVPREI NE SGR SRPLAEDG SLKENRERPG CNVGKPLVRP LGPPRTVPPR 50
gi|674094851|ref|XP_008820733.1| .....
gi|354484535|ref|XP_003504442.1| .....
gi|589949124|ref|XP_006987220.1| .....
gi|507575190|ref|XP_004671140.1| .....
gi|254553462|ref|NP_081675.2| .....
gi|157817514|ref|NP_001100099.1| .....
gi|511830092|ref|XP_004739744.1| .....
gi|524968285|ref|XP_005084028.1| .....
gi|504139794|ref|XP_004582345.1| .....
gi|532030830|ref|XP_005358357.1| .....
gi|617633976|ref|XP_007530280.1| .....
gi|585679781|ref|XP_006891553.1| .....
gi|505775878|ref|XP_004602338.1| .....
gi|395540028|ref|XP_003771964.1| .....
gi|126341322|ref|XP_001368631.1| .....
gi|591381645|ref|XP_007065358.1| .....
gi|558122566|ref|XP_006114505.1| .....
gi|465965470|gb|EMP30673.1| .....
gi|530577003|ref|XP_005282462.1| .....
gi|564230520|ref|XP_006259687.1| .....
gi|557325124|ref|XP_006035579.1| .....
gi|695138615|ref|XP_009510760.1| .....
gi|514739109|ref|XP_005017951.1| .....
gi|543346262|ref|XP_005518840.1| .....
gi|675407222|ref|XP_008932023.1| .....
gi|677239856|gb|KFP55094.1| .....
gi|686595794|ref|XP_009273958.1| .....
gi|690459531|ref|XP_009328807.1| .....
gi|326921728|ref|XP_003207108.1| .....
gi|118085789|ref|XP_418642.2| .....
gi|527270061|ref|XP_005153000.1| .....
gi|524985846|ref|XP_005040881.1| .....
gi|694847615|ref|XP_009464897.1| .....
SLSET FLPNGI N GI K DAR KVTVGVI G S G D FAKSLTI RL I RCGYHVVI G SRNPKFAS E 65
gi|676264854|gb|KFO21189.1| .....
gi|679187928|gb|KFW78811.1| .....
gi|677444859|gb|KFO39506.1| .....
gi|675607450|ref|XP_008947618.1| .....
gi|663262001|ref|XP_008492350.1| .....
gi|678213943|gb|KFV80922.1| .....
gi|678117094|gb|KFU92570.1| .....
gi|677460376|gb|KFQ49790.1| .....
gi|676240922|gb|KFO04794.1| .....
gi|327274492|ref|XP_003222011.1| .....
gi|697035938|ref|XP_009580305.1| .....
gi|679144654|gb|KFW71726.1| .....
gi|677478626|gb|KFO68031.1| .....
gi|677536446|gb|KFO98355.1| .....
gi|675309850|gb|KFM05112.1| .....
gi|677485789|gb|KFQ75194.1| .....
gi|677065660|gb|KFP25666.1| .....
gi|677385324|gb|KFO06625.1| .....
gi|678999197|ref|XP_00792769.1| .....
gi|683460598|gb|KFP25531.1| .....
gi|678186697|gb|KFW54419.1| .....
gi|677306180|gb|KFP88608.1| .....

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Panel 3.D

Table with columns for identifiers (e.g., gi|556769052), gene names (e.g., KMDKP, EMDKP), protein domains (e.g., S DGS LAEAPSE), amino acid positions (e.g., VPKVGI LGS G), and accession numbers (e.g., SRNP KRMA-G 132).

Panel 3.F

gi 678203614 gb KFV70595.1	----- RNS -	SNTMALAP -	-----	STANK	KEVVCI	FGTG	DFGRALGQKL	I QSGYRVVFG	SRRSTKLS -	S	54	
gi 449492447 ref XP_002193727.2	-----	MMALAP -	-----	NTSNK	RETVCI	FGTG	DFGRALGHKM	I QSGYRVVYG	SRRSTQIS -	N	49	
gi 677488410 gb RFQ77815.1	-----	MSKNS -	SNI MALAP -	-----	NTSSK	RETVCI	DFGRALGHKL	I QSGYRVVFG	SRRSTQTS -	T	56	
gi 551506445 ref XP_005804755.1	-----	EVKPE S -	MSLYPAS A -	-----	AAANPE	QEAVCI	DLGRSLGQRL	LQSGYRLVYG	SRRRPHSC -	G	60	
gi 676412338 gb KFO56232.1	-----	MNKNS -	SNI MALAP -	-----	NTSNK	RETVCI	DFGRALGHKM	I QSGYRVVYG	SRRSTQIS -	N	56	
gi 291190416 ref NP_001167369.1	-----	EEKS EC -	VSMS P MMEA -	-----	DPALPE	SERVCFVFTG	DLGHSGLRL	LQAGYGVVFG	SRRRPHSC -	S	66	
gi 669272195 ref XP_008628113.1	-----	MNKNS -	SNI MALAP -	-----	NTSNK	RETVCI	DFGRALGHKM	I QSGYRVVYG	SRRSTQIS -	N	56	
gi 543346256 ref XP_005518838.1	-----	MTKNS -	SNI MALAP -	-----	NTSNK	RETVCI	DFGRALGHKM	I QSGYRVVYG	SRRSTQIS -	N	56	
gi 542142451 ref XP_005480330.1	-----	MNKNS -	SNTMALAP -	-----	NTSNK	RETVCI	DFGRALGHKM	I QSGYRVVYG	SRRSTQIS -	N	56	
gi 327274760 ref XP_003222144.1	-----	MEKN	STI I PLTS -	-----	DLLNK	KETVCI	DFGRSLGYKM	LQCGYSI VYG	SRRNPQAS -	G	55	
gi 513168239 ref XP_001235257.3	-----	MNKNS -	SNI MALAP -	-----	KTSNK	RETVCI	DFGRALGHKL	I QSGYRVVFG	SRRSPPWS -	S	56	
gi 565316654 gb ETE68273.1	-----	MSGLEKV	NAMI PLTS -	-----	DMPNK	KEI VCI	DFGRSLGYKL	MQCGYSI VYG	SRRSTQNS -	G	58	
gi 683467094 gb RFZ61303.1	-----	MNKNS -	SNI MALAP -	-----	NTSNK	RETVCI	DFGRALGHKM	I QSGYRVVFG	SRRSTQKS -	S	56	
gi 683900635 ref XP_009084178.1	-----	MNKNP -	SNTMALAP -	-----	NTSNK	RETVCI	DFGRALGHKM	I QAGYRVVYG	SRRSTQIS -	N	56	
gi 505775871 ref XP_004602336.1	-----	MEKS	TDAI ALTM -	-----	NSSEK	LETI CI	DFGRSLGLKM	LQCGYSI I F G	SRRNPQKC -	N	55	
gi 676275116 gb KFO29573.1	-----	GMENPC -	PNVLP LNM -	-----	NSSRK	QETVCI	DFGRSLGLKM	LHCYGS VVFG	SRRNPQMS -	S	82	
gi 696975795 ref XP_009557372.1	-----	MNRNS -	YNI MALAP -	-----	NTSKK	RETVCI	DFGRALGHKM	I QSGYRVVFG	SRRSAQTS -	S	56	
gi 676586017 gb KFO74821.1	-----	MNRNS -	YNI MALAP -	-----	NTSKK	RETVCI	DFGRALGHKM	I QSGYRVVFG	SRRSAQTS -	S	56	
gi 679006701 gb KFW07166.1	-----	MNKNS -	SNI MALAP -	-----	NTPNK	RETVCI	DFGRALGHKI	I QAGYRVVFG	SRRSTQTS -	S	56	
gi 676813260 gb KFP09648.1	-----	MNKNS -	SNTMALAP -	-----	NTSNK	RQTVCFVFTG	DFGRALGHKM	I QSGYRVVFG	SRRSAQTS -	S	56	
gi 697032879 ref XP_009578615.1	-----	QMNKNS -	SNI MALAP -	-----	NTPNK	RETVCI	DFGRALGHKI	I QAGYRVVFG	SRRSTQTS -	S	108	
gi 354488334 ref XP_003506325.1	-----	MEKTC -	ADALPLTV -	-----	NSSEK	QETVCI	DFGKSF GFKM	LQCGYS VVLG	SRRNPQMS -	S	56	
gi 507713563 ref XP_004647823.1	-----	MENSC -	TNAFPLTM -	-----	NSSQK	QETVCI	DFGRSLGLKM	LQCGYAVVFG	SRRNPQMS -	S	56	
gi 524968279 ref XP_005084025.1	-----	MEKTG -	ADALPLTV -	-----	NSTEK	QETI CI	DFGKSLGFKM	LQCGYS VVFG	SRRNPQMS -	S	56	
gi 410905463 ref XP_003966211.1	-----			-----		MGI	FGTG	DLGRSLGLRL	LQSGYRVVYG	SRRRPHSC -	G	35
gi 548400752 ref XP_005738595.1	-----	MKTEG -	A - - MLHQLA	-----	S GDGPE	PELMCI	FGTG	DLGRSLGLCL	LQSGYRVVYG	SRRRPHSC -	G	56
gi 498938966 ref XP_004541746.1	-----	MKTEG -	A - - MLHPLA	-----	S GDGPE	PELMCI	FGTG	DLGRSLGLCL	LQSGYRVVYG	SRRRPHSC -	G	56
gi 675614756 ref XP_008936236.1	-----	MTKNS -	SNI MALSP -	-----	NTSNK	RETVCI	DFGRALGLKM	I QSGYRVVFG	SRRSTQTS -	S	56	
gi 348578509 ref XP_003475025.1	-----	MENPC -	MNALPLTM -	-----	TSSQK	QVTVCI	DFGRSLGLKM	LQCGHVVVYG	SRRNPQMS -	S	56	
gi 548400757 ref XP_005738596.1	-----	EVNS ES -	VS LCP LST -	-----	AAATE	QEMLCI	FGTG	DLGRSLGQRL	FQTGYKVVYG	SRRRPHSC -	G	60
gi 554854825 ref XP_005937599.1	-----	EVNS ES -	VS LCP LST -	-----	PAATE	QEMLCI	FGTG	DLGRSLGQRL	FQTGYKVVYG	SRRRPHSC -	G	60
gi 584013191 ref XP_006801411.1	-----	EVNS ES -	VS LCP LST -	-----	AAATE	QEMLCI	FGTG	DLGRSLGQRL	LQTGYKVVYG	SRRRPHSC -	G	60
gi 498937702 ref XP_004541468.1	-----	EVNS ES -	VS LCP LST -	-----	PAATE	QEMLCI	FGTG	DLGRSLGQRL	FQTGYKVVYG	SRRRPHSC -	G	60
gi 664765458 ref XP_008540415.1	-----	EMDKP -	LI SRRLLV D	-----	S	DGSLAEAPSE	APKVG I LGS G	DFARSLATRL	VGS GFVVVYG	SRRNPKRMA -	G	102

G57 R59

S58

Panel 4.C

Table with columns: gi, ref, protein names (e.g., FFPFHVVDDTH, HEDALTKTN), amino acid sequences, and UniProt IDs (e.g., SNNMVRVN, SNNMRI). The table lists protein entries and their corresponding UniProt identifiers.

Panel 4.F

gi 678203614 gb KFV70595.1	LI P AGAEVLS	HAEAAQRAA	-- I I I VAVQR	QHYSFL	-----	LPLAEA	LQGKVL	-----	VDI	SNLKI D	-	Q	YPESNAQHLA	120
gi 449492447 ref XP_002193727.2	LI P KDAEVLG	HAEAAQKAA	-- I I I AI PR	QHYNFL	-----	TPLAEV	LHGKVL	-----	VDI	SNLKL N	-	Q	YPSNAEHLA	115
gi 677488410 gb RFQ77815.1	LI P KGAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TS LAEI	LHGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	122
gi 551506445 ref XP_005804755.1	PVP P GAQVMS	HEVAAQAS	-- LVFVCVQR	EHYDFL	-----	ETLAPQ	LNGKVL	-----	VDV	SNLKK N	-	M	YPEANA EYLQ	126
gi 676412338 gb RFQ56232.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	I PLAEI	LHGKVL	-----	VDI	SNLKL N	-	Q	YPESNAEYLA	122
gi 291190416 ref NP_001167369.1	RLP HGAQVLG	HAAAAQSAH	-- LI FI AVQR	EHYDFL	-----	VPLANQ	LKGKVL	-----	VDL	SNLRR N	-	Q	YPEANA EYLQ	132
gi 669272195 ref XP_008628113.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	I PLAEI	LHGKVL	-----	VDI	SNLKL N	-	Q	YPESNAEYLA	122
gi 543346256 ref XP_005518838.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AVQR	QHYNFL	-----	I PLAEV	LRGKVL	-----	VDI	SNLKL N	-	Q	YPESNAEYLA	122
gi 542142451 ref XP_005480330.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEV	LRGKVL	-----	VDI	SNLKL N	-	Q	YPESNAEHLA	122
gi 327274760 ref XP_003222144.1	LI P EGATI SS	HAEAAQMAN	-- VI I I AI HR	GHYNFL	-----	ESLGEV	LHGKVL	-----	VDV	SNLKT N	-	Q	YPESNAEYLA	121
gi 513168239 ref XP_001235257.3	LI P KDAEVLN	HAEAAQKAA	-- I I I AI QR	QHYDFL	-----	ASLEET	LHGKVL	-----	VDI	SNLKI N	-	Q	YPESNAKYLA	122
gi 565316654 gb ETE68273.1	LI P QGATI LS	HAEAAETS E	-- VI I VAVHR	AHYSFL	-----	GSLREI	LNGKVL	-----	VDV	SNLKI N	-	Q	YAESNAEYLA	124
gi 683467094 gb RFZ61303.1	LI P NDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEI	LHGKVL	-----	VDI	SNLKI N	-	Q	YPESNAEYLA	122
gi 683900635 ref XP_009084178.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEV	LRGKVL	-----	VDI	SNLKL N	-	Q	YAESNAEHLA	122
gi 505775871 ref XP_004602336.1	LLP SGTELLS	YSEAAQKS D	-- I I I AI HR	EHYHFL	-----	TELTEF	LNGKI L	-----	VDV	SNLVRT N	-	Q	YAESNAEYLA	121
gi 676275116 gb KFO29573.1	QMP NGAEVLS	YSEAAQKS D	-- I I I AI HR	DHYNFF	-----	I ELTEV	LHEKI L	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	148
gi 696975795 ref XP_009557372.1	LI P KDAEVLG	HTEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEV	LRGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	122
gi 676586017 gb KFO74821.1	LI P KDAEVLG	HTEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEV	LRGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	122
gi 679006701 gb RFW07166.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEI	LHGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	122
gi 676813260 gb KFP09648.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEI	LQGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	122
gi 697032879 ref XP_009578615.1	LI P KDAEVLG	HAEAAQKAA	-- I I I AI QR	QHYNFL	-----	TPLAEI	LHGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	174
gi 354488334 ref XP_003506325.1	LLP RGAEVLS	YSEAAQKS D	-- I I I LAI HR	EHYDFL	-----	TELVDP	LNGKI L	-----	VDV	SNLRR KI	-	Q	YPESNAEYLA	122
gi 507713563 ref XP_004647823.1	LLP SGAEVLS	YSEAAQKS D	-- I I FVAI HR	DHYNFF	-----	I DLTEV	LKGKI L	-----	VDV	SNLKI N	-	Q	YPESNAEHLA	122
gi 524968279 ref XP_005084025.1	LLP RGAEVLN	YSEAAQKS D	-- I I I LAMHR	EHYDCL	-----	TELVDP	LNGKI L	-----	VDV	SNLRR KI	-	Q	YPESNAEYLA	122
gi 410905463 ref XP_003966211.1	PVP QGAEVAS	HAEAAKEAS	-- LI FVCVHR	EHYEFL	-----	TTLTPH	LKGKVL	-----	VDL	SNLKKG	-	I	YPEANAAYLQ	101
gi 548400752 ref XP_005738595.1	PLP EGAQVMT	HEESARS AK	-- MI FVCVHR	EHYEFL	-----	EKMAPQ	LERKVL	-----	VDL	SNLKKD	-	M	YMEANAVYLQ	122
gi 498938966 ref XP_004541746.1	PLP EGAQVMT	HEESARS AK	-- MI FVCVHR	EHYEFL	-----	EKMAPQ	LERKVL	-----	VDL	SNLKKD	-	M	YMEANAVYLQ	122
gi 675614756 ref XP_008936236.1	LI P KDAEVLG	HAEAAQKAA	-- I I I ALQR	QHYNFL	-----	I PLAEV	LHGKVL	-----	VDV	SNLKI N	-	Q	YPESNAEYLS	122
gi 348578509 ref XP_003475025.1	LLP SGAEVLS	YSEAAQKS D	-- I I I VAI HR	DHYNFF	-----	I DLTEV	LNGKI L	-----	VDV	SNLKI N	-	Q	YPESNAEYLA	122
gi 548400757 ref XP_005738596.1	PLP PGTQAMS	HVAAAQARS	-- LVFVCI HR	ENYNFL	-----	ETLAPQ	LKGKVL	-----	VDV	SNLKK N	-	M	YPEANA EYLQ	126
gi 554845425 ref XP_005937599.1	PLP PGTQAMS	HVAAAQARS	-- LVFVCI HR	ENYNFL	-----	ETLAPQ	LKGKVL	-----	VDV	SNLKK N	-	M	YPEANA EYLQ	126
gi 584013191 ref XP_006801411.1	PLP PGTQAMS	HVAAAQARS	-- LVFVCI HR	ENYNFL	-----	ETLAPQ	LKGKVL	-----	VDV	SNLKK N	-	M	YPEANA EYLQ	126
gi 498937702 ref XP_004541468.1	PLP PGTQAMS	HVAAAQARS	-- LVFVCI HR	ENYNFL	-----	ETLAPQ	LKGKVL	-----	VDV	SNLKK N	-	M	YPEANA EYLQ	126
gi 664765458 ref XP_008540415.1	LFP SAAQVTF	QEEAVGSP E	-- VI FVAMFR	EHYSSL	-----	CSLSSQ	LAGKI L	-----	VDV	SNPTEQHLQ	-	-	HRESNAEYLA	170

D113 N116
S115

Panel 5.A

Table with columns for ID, reference, sequence, and protein name. Includes entries like g1|9558759|ref|NP_036581.1|KMKP R R N L - - E E D D - - - - - Y L H K D T - - - - - G E T S M L K R P V L L H L H Q T A H A - - - - - D E F D C P S E L - Q H T Q E L F P Q W H L P I K I A A 79.

Panel 5.D

Table with columns for ID, Reference, Abbreviation, and Page Number. The table lists numerous entries, many of which are truncated on the right side. The first few rows include IDs like 'gi|556769052|ref|XP_005979736.1' and 'gi|50768587|ref|XP_004711963.1'. The table ends with IDs like 'gi|548463578|ref|XP_005679356.1' and 'gi|548463578|ref|XP_005679356.1'.

Panel 5.F

gi 678203614 gb KFV70595.1	QLLPA	AAKVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKRLV-	MD	LVRALGLTPL	DQGS	LLAAARE	I ENYPLQLFP	SWRFPI	LLSL	206					
gi 449492447 ref XP_002193727.2	QLLPG	KVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	VEAKQMV-	MN	I VRALGLTPL	DKGS	LLAAQE	I ENYPLQLFP	MWKFPI	FLSL	201					
gi 677488410 gb KFQ77815.1	QLVPG	AAKVV-	- KALNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKQMV-	MD	I VRALGLTPL	DQGS	LLAAQE	I ENYPLQLFP	MWKFPI	LLSL	208					
gi 551506445 ref XP_005804755.1	KLIPG	AHV-	- KAFNTL	SAW	ALQ-	NGPSDA	NRQVY	LCGNN	PEAKQAV-	AV	I STKLGLTPV	DRGS	LSAARE	LEDFPLQLFP	EWRPL	MLRTI	212					
gi 676412338 gb KFO56232.1	QLLPG	RVV-	- KAFNTL	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	VEAKQMV-	MN	I VRALGLTPL	DKGS	LLAAQE	I ENYPLQLFP	I WKFPI	FLSL	208					
gi 291190416 ref NP_001167369.1	SLVPG	AEEV-	- KGFNTL	SAW	SLQ-	NGPSDA	NRQVY	ICGES	AEAKQAV-	I A	VATKLGFSAL	DRGS	ISVARE	LEDFPLQLFP	QWRPL	PLRI	218					
gi 669272195 ref XP_008628113.1	QLLPG	RVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	VEAKQMV-	MN	I VRALGLTPL	DKGS	LLAAQE	I ENYPLQLFP	I WKFPI	FLSL	208					
gi 543346256 ref XP_005518838.1	QLLPG	KVV-	- KGFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	VEAKQMV-	MN	I VRALGLTPL	DKGS	LLAAQE	I ENYPLQLFP	MWKFPI	FLSL	208					
gi 542142451 ref XP_005480330.1	QLLPG	KVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	VAAKEMV-	MN	I VRALGLTPL	DKGS	LLAAQE	I ENYPLQLFP	MWKFPI	FLSL	208					
gi 327274760 ref XP_003222144.1	QLMPS	KVV-	- KAFNTV	SAW	ALQ-	SGGLDA	SRQVF	VCGDD	HKS	KDKV-	ME	I VRSLGLTTPV	DKGS	LLAATE	I ENYPLRFLFP	MWKYPI	LLSL	207				
gi 513168239 ref XP_001235257.3	QLVPG	ARVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	TEAKQMV-	MD	I I RALGLTPL	DQGS	LLAAARE	I ENYPLQLFP	MWKI	PI	FLSL	208				
gi 565316654 gb ETE68273.1	QLLPG	KVV-	- KAFNTV	SAW	ALQ-	SGGLDA	NRQVFI	CGDD	RKAKE	KV-	I E	I VRSLGLTPL	DKGS	LLASKE	I ENYPLQLFP	MWFPI	YLSF	210				
gi 683900635 ref XP_009084178.1	QLLPG	KVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKQMV-	MD	I VRALGLTPL	DQGS	LLAAQE	I ENYPLQLFP	MWKFPI	LLSL	208					
gi 683467094 gb KFZ61303.1	QLLPG	KVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	VEAKQMV-	MN	I VRALGLTPL	DKGS	LLAAQE	I ENYPLQLFP	MWFPI	MYLSL	208					
gi 505775871 ref XP_004602336.1	QLVPG	VHV-	- KAFNTI	SAW	ALQ-	SGALDA	SRQVF	VCGDD	S	KAKQRV-	I A	I VSSLGLTPL	DQGS	PLKAAKE	I ENYPLQLFP	MWKFPI	YLSA	207				
gi 676275116 gb KFO29573.1	QLVPG	AHV-	- KAFNTI	SAW	ALQ-	SGALDA	SRQVF	VCGND	I	KAKQRV-	MD	I VRTLGLTPL	DQGS	LVAAKE	I ENYPLQLFP	MWFPI	YLSA	234				
gi 696975795 ref XP_009557372.1	QLVPG	ARVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKQMV-	MD	I VRALGLTPL	DQGS	LLAAQE	I ENYPLQLFP	MWKFPI	FLSL	208					
gi 676586017 gb KFO74821.1	QLVPG	ARVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKQMV-	MD	I VRALGLTPL	DQGS	LLAAQE	I ENYPLQLFP	MWKFPI	FLSL	208					
gi 679006701 gb KFW07166.1	QLVPG	AHV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MGAKQMV-	MD	I VRALGLTPL	DQGS	LLAAQE	I ENYPLQLFP	MWKFPI	LLSL	208					
gi 676813260 gb KFP09648.1	QLVPG	AHV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKQMV-	MD	I ARALGLTPL	DRGS	LLAAQE	I ENYPLQLFP	MWKFPI	LLSL	208					
gi 697032879 ref XP_009578615.1	QLVPG	AHV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MGAKQMV-	MD	I VRALGLTPL	DQGS	LLAAQE	I ENYPLQLFP	MWKFPI	LLSL	260					
gi 354488334 ref XP_003506325.1	QLVPG	AHV-	- KAFNTI	SAW	ALQ-	SGLTDA	SRQVF	VCGND	S	KAKHRV-	MD	I ARTLGLTPL	DQGS	LVAANE	I ENYPLQLFP	MWRLP	FYLS	208				
gi 507713563 ref XP_004647823.1	QLVPG	AHV-	- KAFNTV	SAW	ALQ-	SGALDA	SRQVF	VCGND	T	KAKHRV-	MD	I VLTGLTPL	DQGS	LLAAKE	I ENYPLQLFP	MWRFPI	CLSA	208				
gi 524968279 ref XP_005084025.1	QLVPG	AHV-	- KAFNTI	SAW	ALQ-	SGLTDA	SRQVF	VCGND	S	KAKHRV-	MD	VARTLGLTPL	DQGS	LVAANE	I ENYPLQLFP	MWRLP	FYLS	208				
gi 410905463 ref XP_003966211.1	RLVPG	ADV-	- KGLNTLS	SAW	ALQ-	NGL- LA	GKQVY	LCGNS	ANAKQAV-	SE	MATKLGTLV	DRGS	LSAARE	LEDFPLRFLFP	EWRPL	LLVAA	186					
gi 548400752 ref XP_005738595.1	RLVPG	AAVV-	- KGLNTLS	TW	ALQ-	NGL- LA	GRQVY	LCGNN	GEAKRDV-	AE	MATKLGTLV	DKGS	LSAAKE	VEDFPLQLFP	EWRMP	LYVAF	207					
gi 498938966 ref XP_004541746.1	QLLPG	ARVV-	- KAFNTV	SAW	ALQ-	SGLTDA	SRQVF	VCGDD	MEAKQMV-	MD	I VRAVGLTPL	DKGS	LVAANE	I ENYPLQLFP	MWKFPI	FLSL	208					
gi 675614756 ref XP_008936236.1	QLVPG	AHV-	- KAFNTI	SAW	ALQ-	SGALDA	SRQVF	VCGND	T	NAKHRV-	MD	I VRTLGLTPL	DRGAL	VAAKE	I ENYPLQLFP	MWRFPI	CLSA	208				
gi 548400757 ref XP_005738596.1	RLVPG	AHV-	- KGFNTLS	SAW	ALQ-	NGPSDA	NRQVY	VCGNS	LEAKQAV-	I E	VATKLGFTVL	DRGS	LTAARE	LEDFPLQLFP	EWRPL	PLQAT	212					
gi 554854825 ref XP_005937599.1	RLVPG	AHV-	- KGFNTLS	SAW	ALQ-	NGPSDA	NRQVY	VCGNS	LEAKQAV-	I E	VATKLGFTVL	DRGS	LTAARE	LEDFPLQLFP	EWRPL	PLQAT	212					
gi 584013191 ref XP_006801411.1	RLVPG	AHV-	- KGFNTLS	SAW	ALQ-	NGPSDA	NRQVY	VCGNS	LEAKQAV-	I E	VATKLGFTVL	DRGS	LTAARE	LEDFPLQLFP	EWRPL	PLQAT	212					
gi 498937702 ref XP_004541468.1	RLVPG	AHV-	- KGFNTLS	SAW	ALQ-	NGPSDA	NRQVY	VCGNS	PEAKQAV-	I E	VATKLGFTVL	DRGS	LTAARE	LEDFPLQLFP	EWRPL	PLQAT	212					
gi 664765458 ref XP_008540415.1	SLFPT	CSVV-	- KAFNVI	SAW	TLQ-	S	SPR	RDG	NRQVPI	CS	DQ	PEAKRTV-	SE	MVHAMGFTPV	DMG	LVS	ARE	VEAMP	LRLLP	GWKVP	ALLTL	256

P138

S150

D191 G193

Panel 6.A

Table with 5 columns: ID, Ref, Description, Mutation, and Position. Contains a list of genetic variants with their corresponding reference sequences and positions.

Panel 6.C

Table with 4 columns: ID, Label, Content, and Page Number. The content is a dense list of alphanumeric strings, likely a codebook or data dictionary. The page number on the right side of each row varies, ranging from 309 to 326.

Panel 6.D

Table with 5 columns: ID, Reference, Text, and two column headers (likely GLLS and GLLS). The table contains 400 rows of data, including IDs such as gi|556769052 and various alphanumeric strings.

Panel 6.F

gi 678203614 gb KFV70595.1	GLTI FFFLYC	LALDVI YPYV	YQKKDLS - FL	I AVSI PNEVC	PVLALMLLGL	VYVPGVLAAI	LQLWRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	295
gi 449492447 ref XP_002193727.2	GLTAFYYYC	VLLDI I YTYI	YEKNDFS - FF	I AI TI PNRVC	PVMALI L LAL	VYLPGI FAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLI A	290
gi 677488410 gb KFQ77815.1	GLTAFYYYC	LI RDI I YPYV	YENKDYS - FF	I AI SI PNRI C	PI LALI L LAL	VYLPGLAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 551506445 ref XP_005804755.1	GLTAFYYYL	LTRDVI YAYV	DEGRDI - FR	I MMSLANKVF	PSVSLI L LSL	CYLPGVI AGF	F QLYRGT	KYK	RFPDWLDRWM	LCKKQLGLI A	301
gi 676412338 gb KFO56232.1	GLTAFYYYC	LALDVI YTYI	YERNNFS - FF	I AI TI PNRVC	PVMALI L LAL	VYLPGI FAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLI A	297
gi 291190416 ref NP_001167369.1	GLSAAFFYYL	LI RDI I YAYV	TQGGDI - FR	I MVSLANKVC	PI VSLI M LSL	CYLPGLASF	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLLA	307
gi 669272195 ref XP_008628113.1	GLTAFYYYC	LALDVI YTYI	YERNNFS - FF	I AI TI PNRVC	PVMALI L LAL	VYLPGI FAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLI A	297
gi 543346256 ref XP_005518838.1	GLTAFYYYC	VALDI I YTYI	YEKNNFS - FF	I AI TI PNRVC	PVMALI L LAL	VYLPGI FAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLI A	297
gi 542142451 ref XP_005480330.1	GLSAPVLYS	I I RDVVYNYV	EKDKKYF - FF	I AI SI PNRI C	PVVALVLLAL	VYLPGI FAAI	L QLYRGT	KYS	RFPDWLDRWM	LCKKQLGLVA	296
gi 327274760 ref XP_003222144.1	GLTAFYYYC	LTRDVI YPYV	YENKDYS - FF	I AI SI PNRI C	PI I ALVLLAL	VYLPGI LAAI	I QLYRGT	KYS	RFPDWLDRWM	LCKKQLGLVA	297
gi 513168239 ref XP_001235257.3	ALSAFI FLYS	VVRDVI YNHV	EKSKDYS - FF	I VVTI ANRI C	PVVALVLLAL	VYLPGI FAAI	L QLYRGT	KYS	RFPDWLDRWM	LCKKQLGLVA	299
gi 565316654 gb ETE68273.1	GLTAFYYYC	LTLDI I YPYV	YENKDFS - FF	I AI SI PNRI C	PI LALI L LAL	VYLPGLAAI	I QLYRGT	KYH	RFPDWLDRWM	LCKKQLGLVA	297
gi 683900635 ref XP_009084178.1	GLTAFYYYC	VALDI I YTYI	YEKNNFS - FF	I AI TI PNRVC	PVMALI L LAL	VYLPGI FAAI	I QLYRGT	KYH	RFPDWLDRWM	LCKKQLGLI S	297
gi 505775871 ref XP_004602336.1	ALFI FFFHYC	VI RDI I YFYV	SKKKDVT - FS	LAYS I PSHVC	PI VALI L LGL	VYLPGI I AAI	L QLYRGT	KYH	QFPNWLDRWM	LCKKQLGLI S	296
gi 676275116 gb KFO29573.1	ALCI FFFHYC	I I RDI I YPYV	NKKEDNT - FR	LAI SI PNRVF	PI TALVLLAL	VYLPGLS AI	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	323
gi 696975795 ref XP_009557372.1	GLTAFYYYC	LI RDVI YAYV	YEKNDYS - FF	I AI SI PNQI C	PI LALI L LAL	VYLPGLAAI	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 676586017 gb KFO74821.1	GLTAFYYYC	LI RDVI YAYV	YEKNDYS - FF	I AI SI PNQI C	PI LALI L LAL	VYLPGLAAI	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 679006701 gb KFW07166.1	GLTAFYYYC	LTRDVI YPYV	YENKDFS - FF	I VI SI PNRI C	PI LALI L LAL	VYFPGVLAAI	I QLYRGT	KYL	RFPDWLDRWM	LCKKQLGLVA	297
gi 676813260 gb KFP09648.1	GLTTFFFFY	LI REVI YAYV	YENKDFS - FF	I AI SI PNRI C	PV LALI L LAL	VYLPGLAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 697032879 ref XP_009578615.1	GLTAFYYYC	LTRDVI YPYV	YENKDFS - FF	I VI SI PNRI C	PI LALI L LAL	VYFPGVLAAI	I QLYRGT	KYL	RFPDWLDRWM	LCKKQLGLVA	349
gi 354488334 ref XP_003506325.1	VLCAPFFVYC	AI REVI YPYV	NGKTDTT - FR	LAI SI PNRVF	PI TALVLLAL	VYLPGLAAI	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 507713563 ref XP_004647823.1	ALCI FFFHYC	VI RDI I YPYV	SKKQDNT - FR	LAI SI PNRVF	PI TALVLLAL	VYLPGVI AAI	L QLYRGT	KYH	RFPDWLDRWM	LCKKQLGLVA	297
gi 524968279 ref XP_005084025.1	VLCVFFVYV	VI REVI YPYV	NEKTDTT - FR	LAI SI PNRVF	PI TALVLLAL	VYLPGLAAI	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 410905463 ref XP_003966211.1	CLMGFFYYL	LI RDVI YAYV	ETGQDI - YR	I MI SLANKVF	PI VSLVMLS L	CYLPGCI AAF	L QLYRGT	KYK	RFPDWLDRWM	LCKKQMLVA	275
gi 548400752 ref XP_005738595.1	GLAFFFLLYL	VI RDI I YAYV	ENEDI S - YR	I MI SLANKI T	PVVS LI M LSL	CYLPGAI AGF	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLLA	296
gi 498938966 ref XP_004541746.1	GLSAPVLYL	LI RDI I YAYV	ENEDI S - YR	I MI SLANKI T	PVVS LI M LSL	CYLPGAI AGF	L QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLLA	296
gi 675614756 ref XP_008936236.1	GLTAFYYYC	LALDVI YPYV	YQNKDFS - FF	I VI SI PNRI C	PI LALI L LAL	VYLPGLAAI	I QLYRGT	KYR	RFPDWLDRWM	LCKKQLGLVA	297
gi 348578509 ref XP_003475025.1	MLCI FFFHYC	VI RDI I YPYV	YKKE DNT - FR	LAI SI PNRVF	PI TALVLLAL	VYLPGVI AAI	L QLYRGT	KYF	RFPDWLDRWM	LCKKQLGLVA	297
gi 548400757 ref XP_005738596.1	GLTAFYYYL	LI RDVI YS YV	VNDKDI S - FR	I MASLANKVF	PI VSLI M LSL	CYLPGVI AAF	L QLYRGT	KYK	RFPDWLDRWM	LCKKQLGLVA	301
gi 554854825 ref XP_005937599.1	GLTAFYYYL	LI RDVI YS YV	VNDKDI S - FR	I MASLANKVF	PI VSLI M LSL	CYLPGVI AAF	L QLYRGT	KYK	RFPDWLDRWM	LCKKQLGLVA	301
gi 584013191 ref XP_006801411.1	GLTAFYYYL	LI RDVI YS YV	VNDKDI S - FR	I MASLANKVF	PI VSLI M LSL	CYLPGVI AAF	L QLYRGT	KYK	RFPDWLDRWM	LCKKQLGLVA	301
gi 498937702 ref XP_004541468.1	GLTAFYYYL	LI RDVI YS YV	VNDKDI S - FR	I MASLANKVF	PI VSLI M LSL	CYLPGVI AAF	L QLYRGT	KYK	RFPDWLDRWM	LCKKQLGLVA	301
gi 664765458 ref XP_008540415.1	GLLVFFAYN	FVRDVLHPYL	QE GKNKF - YK	LP VS VVNTTL	PCVAYVLLSL	VYLPGLAAA	L QLRRTG	KYR	RFPDWLDRWM	QHRKQI GLLS	345

Y229

Y271

Q281 K287

W298 K303

L295 R302

Panel 7.F

gi 678203614 gb KFV70595.1	LAFASVHVLV	TLVTP I RS YV	KWRASSQAVS	QAL - - S - NTT	Q - - PLNTTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NSVNWREFRF	379
gi 449492447 ref XP_002193727.2	LAFASLHVLF	TLVTP I RS FV	RWRTSTR I S	QVM - - N - NKT	E - - PLDHTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	374
gi 677488410 gb KFQ77815.1	LAFASLHVLY	TLVI P I RFFV	RWRI SSR I I S	QAL - - N - NKT	E - - PLNTSNA	WLSDSYVALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 551506445 ref XP_005804755.1	LALASLHVLY	TLVI P I RYFV	RFRLAGS T I S	QI K - - S - NKT	S - - PFDTTMA	WRTDSYYAI G	ALGFGLYLL	GI SSLPS - VS	NALS WREFSF	385
gi 676412338 gb KFO56232.1	LAFASLHVVF	TLVTPMR AFV	SWRTSKGI I S	QVL - - N - NKT	E - - PLSNTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 291190416 ref NP_001167369.1	LGF AFL HVLY	TLVI P I RYFV	RFKVTER TVS	VI R - - E - NRT	T - - EFDTTTA	WRSDSYLSLG	ILGFGLYLL	GI TSLPS - VI	NSLSWREFSF	391
gi 669272195 ref XP_008628113.1	LAFASLHVVF	TLVTPMR AFV	SWRTSKGI I S	QVL - - N - NKT	E - - PLSNTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 543346256 ref XP_005518838.1	LAFASLHVVF	TLVTPMR AFA	SWRTSKGI I S	QAL - - N - NKT	E - - PLNNTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 542142451 ref XP_005480330.1	LAFASLH AVF	TLVTP LRAFA	SWRTGKGI I S	QAL - - N - NKT	E - - PLDHTKA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 327274760 ref XP_003222144.1	LAY AFL HVLY	TLVI P I RYFV	RWRI GS Y TLE	QAL - - N - NRT	N - - PLNTENA	WLSDSYVALG	ILGFFLVLL	GI TSLPS - VS	NSVNWREFRF	380
gi 513168239 ref XP_001235257.3	LAFASLHV I Y	TLVI P I RYFV	RWRI EDRT I S	QAL - - N - NKT	T - - PFDNTNG	WLSDSYLALG	ILGFLLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 565316654 gb ETE68273.1	LAY AFL HV I Y	TLVI P I RYFV	RWRQNS YVLE	QAL - - K - NKT	D - - PFWGTGA	WHSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NSVNWREFRF	383
gi 683467094 gb KFZ61303.1	LAFASLHVLY	TLVI P I RS FV	RWRI SSS TVS	QAL - - N - NKT	E - - PLNNTYA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 683900635 ref XP_009084178.1	LAFASLHVVL	TLVSPRR AF T	KWKTGKGI I S	QVL - - N - NKT	E - - PLDHTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - I S	NNVNWREFRF	381
gi 505775871 ref XP_004602336.1	LGL ACL HVLF	I VSTPLRY I A	LWHFKNMT I S	QVA - - L - KKE	S - - PI STYRA	WNSDSYLT LG	VLGFFLVLL	GI TSLPS - VS	NLVNWREFRF	380
gi 676275116 gb KFO29573.1	LGF AFL HV I Y	TLVI P I RYFV	RWRLRNI TAT	QVI - - D - KKD	D - - PFI TSTA	WLSDSYVSLG	ILGFFLVLL	GI TSLPS - VS	NMVNWREFRF	407
gi 696975795 ref XP_009557372.1	LAFASLHVLY	TLVI P I RS FV	RWRI SSS TVS	QAL - - K - NAT	Q - - PLNTTYA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 676586017 gb KFO74821.1	LAFASLHVLY	TLVI P I RS FV	RWRI SSS TVS	QAL - - K - NAT	Q - - PLNTTYA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 679006701 gb KFW07166.1	LAFASLHVLY	TLVI P I RFFV	RWRI SSQ I I S	QAL - - N - NKT	E - - PLNTTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 676813260 gb KFP09648.1	LAFASLHVLY	TLVI P I RS FV	RWRI SSR TI A	LAL - - N - NKT	E - - PLNTTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 697032879 ref XP_009578615.1	LAFASLHVLY	TLVI P I RFFV	RWRI SSQ I I S	QAL - - N - NKT	E - - PLNTTNA	WLSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	433
gi 354488334 ref XP_003506325.1	LGF AFL HV I Y	TLVI P I RYFV	RWRLRNATVT	QAL - - A - NKD	N - - PFSSTA	WNSDSYLALG	ILGFFLVLL	GI TSVPS - VS	NMVNWREFRF	381
gi 507713563 ref XP_004647823.1	LGF AFL HV I Y	TLVI P I RYFV	RWRLRNATVT	QVI - - S - RKD	D - - PFSSTA	WYDSYMS LG	VLGFFLVLL	GI TSLPS - VS	NMVNWREFRF	381
gi 524968279 ref XP_005084025.1	LGF AFL HV I Y	TLVI P I RYFV	RWRLRNGT VT	QAL - - A - NRD	N - - PFSSTA	WNSDSYLALG	ILGFFLVLL	GI TSLPS - VS	NTVNWREFRF	381
gi 410905463 ref XP_003966211.1	LGL ALL HAI Y	TLVI P I RYFV	RHKL I SRVVD	EM - - - KNNKT	TPFYFDNKEA	WGTDSFYVLG	ILGFFLVLL	GLTSLPS - VG	GSLSWREFSF	361
gi 548400752 ref XP_005738595.1	LGF ALL HAI Y	TLVI P I RYFV	RQRVI SNVLN	EV - - - KKNKT	TPLYFDNTSA	WRTDSLYALG	ILGFFLVLL	GLTSLPS - VG	GTLWREFSF	382
gi 498938966 ref XP_004541746.1	LGF ALL HAI Y	TLVI P I RYFV	RQRVI SNVLN	EV - - - KKNKT	TPLYFDNTSA	WRTDSLYALG	ILGFFLVLL	GLTSLPS - VG	GTLWREFSF	382
gi 675614756 ref XP_008936236.1	LAFASVHVLV	TLVI P I RS YV	RWRI SSHT I S	QAL - - N - NKT	E - - PLNTTNA	WLSDSYVALG	ILGFFLVLL	GI TSLPS - VS	NNVNWREFRF	381
gi 348578509 ref XP_003475025.1	LGF AFL HV I Y	TLVI P I RYFV	RWRLRNI TVT	QAI - - N - KKD	D - - PFSI SLA	WLSDSYVSLG	ILGFFLVLL	GI TSLPS - VS	NMVNWREFRF	381
gi 548400757 ref XP_005738596.1	LALASLHVLY	TLVI P I RYFV	RYRLAAHT I S	QI K - - E - NKT	S - - PFDTTMA	WRTDSYYV I G	ILGFGLYLL	GI TSLPS - VS	NVLSWREFSF	385
gi 554854825 ref XP_005937599.1	LALASLHVLY	TLVI P I RYFV	RYRLAAHT I S	QI K - - E - NKT	S - - PFDTTMA	WRTDSYYV I G	ILGFGLYLL	GI TSLPS - VS	NVLSWREFSF	385
gi 584013191 ref XP_006801411.1	LALASLHVLY	TLVI P I RYFV	RYRLAAHT I S	QI K - - E - NKT	S - - PFDTTMA	WRTDSYYV I G	ILGFGLYLL	GI TSLPS - VS	NVLSWREFSF	385
gi 498937702 ref XP_004541468.1	LALASLHVLY	TLVI P I RYFV	RYRLAAHT I S	QI K - - E - NKT	S - - PFDTTMA	WRTDSYYV I G	ILGFGLYLL	GI TSLPS - VS	NVLSWREFSF	385
gi 664765458 ref XP_008540415.1	FFCAALH ALY	RGESE PAAAA	VLVLLWLKDT	KVL - - A - NKS	H - - LWVEEV	WRMEI YVSLG	VLALGTLSLL	AVTSLPS - I A	NSLNWREFSF	429

H316

W355

W388

E390

Panel 8.A

Table with columns for ID, Ref, Description, and other identifiers. The table is organized into two main columns, with a central header 'Panel 8.A' and column numbers 640, 660, 680, 700, 720 indicated at the top. The rows contain alphanumeric codes, reference numbers, and descriptive text, often including technical specifications or component names.

Panel 8.B

Table with 5 columns: ID, Reference, Key, Value, and Status. Rows include identifiers like 'g1|679184771', 'g1|694667236', and 'g1|677475561' paired with values like 'OS|KMGYAL|LLCT|V|HAL|VF' and 'AVL|VF'. The right side of the table lists various codes and status indicators such as 'PI|VLLCKC', 'PI|VLLCCK', and 'PI|VLLCCK'.

Panel 8.F

gi 678203614 gb KFV70595.1	VQS	KLGYLTL	VLCTAHTM	VY	GGKWLFPSS	YKWLPLPI	YMLSLII	-----	PCAVLVI	KFVLI	FPCLDKP	LTQIR	-	QGW	451		
gi 449492447 ref XP_002193727.2	VQS	KLGYLTL	ILSTAHTL	VY	GGKWFLSPST	YKWLPLNI	YLSLII	-----	PCSVL	VVKFLLI	FPVCDKP	LTQIR	-	QGW	446		
gi 677488410 gb RFQ277815.1	VQS	KLGYLTL	ILCTAHTL	VY	GGKQFLRPSS	YRWLPSAYM	LSSLVV	-----	PCI	VLVVKF	VLI	FPCLDKP	LTRI	-	QGW	453	
gi 551506445 ref XP_005804755.1	IQS	KLGYLTL	FFCTFHTY	LY	GWDRFLYISQ	YKWTTPPGYM	LCLVV	-----	PSLVL	VFRL	LLLLP	CVDKS	LSRI	-	QGW	457	
gi 676412338 gb RF056232.1	VQS	KLGYLAL	ILCTAHTL	VY	GGKWFLSPSA	YKWLPLNI	YLSLIV	-----	PCAVL	VVKF	VLI	FPVCDKP	LTQIR	-	QGW	453	
gi 291190416 ref NP_001167369.1	VQS	KLGHLLTL	LLCTAHTY	LY	GWNRFLSSST	YKWTTPPGYM	LCLVL	-----	PSVVL	LLKL	LLI	THTHHT	QNNTL	-	RGW	463	
gi 669272195 ref XP_008628113.1	VQS	KLGYLAL	ILCTAHTL	VY	GGKWFLSPSA	YKWLPLNI	YLSLIV	-----	PCAVL	VVKF	VLI	FPVCDKP	LTQIR	-	QGW	453	
gi 543346256 ref XP_005518838.1	VQS	KLGYLAL	ILCTAHTL	VY	GGKWFLSPSA	YKWLPLNI	YLSLIV	-----	PCAVL	VVKF	VLI	FPVCDKP	LTQIR	-	QGW	453	
gi 542142451 ref XP_005480330.1	VQS	KLGYLAL	ILCTAHTL	VY	GGKWFLSPSA	YKWLPLNI	YLSLIV	-----	PCAVL	VVKF	VLI	FPVCDKP	LTQIR	-	QGW	453	
gi 327274760 ref XP_003222144.1	VQS	YLGYLTL	ILCTAHTL	VY	GGKRFLRPSS	YPWGLPSI	YFSLII	-----	PCI	VLVMKF	VLI	LPCLDRP	LTQIR	-	QGW	452	
gi 513168239 ref XP_001235257.3	VQS	KLGYLTL	ILCTAHTL	VY	GGKRFLSPSA	YRWLPLNAYM	LSLII	-----	PCI	VLVVKF	VLI	LPCLDKQ	LTRI	-	QGW	453	
gi 565316654 gb ETE68273.1	VQS	YLGYLTL	VLCTAHTL	GY	GGKRFLYPHS	YPWFLPPVYL	LSLII	-----	PCI	VLFI	KFVLFV	PCIDRP	LTEIR	-	QGW	455	
gi 683467094 gb RFZ61303.1	VQS	KLGYLTL	VLCTAHTL	VY	GGNRFLNPSS	YRWLPLNAYM	LSLIV	-----	PCI	VLVVKF	VLFV	PCIDRP	LTQIR	-	QGW	453	
gi 683900635 ref XP_009084178.1	VQS	KLGYLAL	ILCTAHTL	VY	GGKWFLSPSA	YKWLPLNI	YLSLIV	-----	PCAVL	VVKF	VLI	FPVCDKP	LTQIR	-	QGW	453	
gi 505775871 ref XP_004602336.1	VQS	KLGYLTL	VLCTAHTL	VY	GGKWFLSPSA	YKWLPLNI	YLSLIV	-----	PCAVL	VVKF	VLI	FPVCDKP	LTQIR	-	QGW	453	
gi 676275116 gb KFO29573.1	VQS	KLGYLTL	ILCTAHTL	VY	GGKRFLSPAA	LRWYLPSTYL	IALTI	-----	PCT	VLVI	KCILI	LPICDRT	LNRI	-	QGW	452	
gi 696975795 ref XP_009557372.1	VQS	KLGYLTL	ILCTAHTL	VY	GGKRFLSPAA	LRWYLPSTYL	IALTI	-----	PCT	VLVI	KCILI	LPICDRT	LNRI	-	QGW	452	
gi 676586017 gb KFO74821.1	VQS	KLGYLTL	ILCTAHTL	VY	GGNRFLSPSS	YKWLPSAYM	LSLIV	-----	PCI	VLVVKF	VLFV	PCIDRP	LTEIR	-	QGW	453	
gi 679006701 gb RFW07166.1	VQS	KLGYLTL	ILCTAHTL	VY	GGKRFLSPSS	YKWLPSAYM	LSLIV	-----	PCI	VLVVKF	VLFV	PCIDRP	LTEIR	-	QGW	453	
gi 676813260 gb KFP09648.1	VQS	KLGYLTL	ILCTAHTL	VY	GGNRFLSPSS	YRWLPLNAYM	LALVV	-----	PCI	VLVVKF	VLFV	PCIDRP	LTEIR	-	QGW	453	
gi 697032879 ref XP_009578615.1	VQS	KLGYLTL	ILCTAHTL	VY	GGKRFLSPSS	YRWLPLNAYM	LALVV	-----	PCI	VLVVKF	VLFV	PCIDRP	LTEIR	-	QGW	453	
gi 354488334 ref XP_003506325.1	VQS	KLGYLTL	VLCTAHTL	VY	GGKRFLSPGI	LRWYLPSTYL	IALTI	-----	PCT	VLVI	KCILI	LPICDRT	LNRI	-	QGW	452	
gi 507713563 ref XP_004647823.1	VQS	KLGLFTL	ILCTAHTL	VAY	GGKFLPSPGI	LRWYLPSTYL	IALTI	-----	PCT	VLVI	KCILI	LPICDRT	LNRI	-	QGW	452	
gi 524968279 ref XP_005084025.1	VQS	KLGYLTL	VLCTAHTL	MY	GGKRFLSPGI	LRWYLPSTYL	IALTI	-----	PCT	VLVI	KCILI	LPICDRT	LNRI	-	QGW	452	
gi 410905463 ref XP_003966211.1	VQS	KLGHLLTL	SICTAHGY	IY	GWNRFLRPST	YKWTTPPGYM	LCLIV	-----	PSVVL	VLKI	LLLLP	CVDRA	LTRI	-	QGW	433	
gi 548400752 ref XP_005738595.1	VQS	TLGYLTL	FLSTAHCY	IY	AWDKFLRKS	YKWTTPPDSM	LCLIV	-----	PSVTL	VLKL	VLLP	CVNRP	LMRI	-	QGW	454	
gi 498938966 ref XP_004541746.1	VQS	TLGYLTL	FLSTAHCY	IY	AWDKFLRKS	YKWTTPPDSM	LCLIV	-----	PSVTL	VLKL	VLLP	CVNRP	LMRI	-	QGW	454	
gi 675614756 ref XP_008936236.1	VQS	KLGYLTL	ILCTAHTL	VY	GGKWFLNLSL	YKWLPHAYM	LSLIV	-----	PCI	VLVI	KFVLI	FPCLDKP	LTQIR	-	QGW	453	
gi 348578509 ref XP_003475025.1	VQS	KLGYLTL	TLCTAHTL	VY	GGKRFLTPSA	LRWYLPSTYL	IALTI	-----	PCT	VLVVKF	VLI	MPICDRT	LTRI	-	QGW	453	
gi 548400757 ref XP_005738596.1	IQS	KLGYLTL	FFCTFHTY	LY	GWDFLQPS	YKWFMLPGYM	LSLVV	-----	PSVVL	VLKL	LLLLP	CVDS	T	LTRI	-	QGW	457
gi 554854825 ref XP_005937599.1	IQS	KLGYLTL	FFCTFHTY	LY	GWDFLQPS	YKWFMLPGYM	LSLVV	-----	PSVVL	VLKL	LLLLP	CVDS	T	LTRI	-	QGW	457
gi 584013191 ref XP_006801411.1	IQS	KLGYLTL	FFCTFHTY	LY	GWDFLQPS	YKWFMLPGYM	LSLVV	-----	PSVVL	VLKL	LLLLP	CVDS	T	LTRI	-	QGW	457
gi 498937702 ref XP_004541468.1	IQS	KLGYLTL	FFCTFHTY	LY	GWDFLQPS	YKWFMLPGYM	LSLVV	-----	PSVVL	VLKL	LLLLP	CVDS	T	LTRI	-	QGW	457
gi 664765458 ref XP_008540415.1	VQS	TLGFVAL	VLSTLHTL	TY	GWTRAFEE	SR	YKFLPPTFT	LTLV	-----	PCVVI	LARG	LFLLP	CVSRR	LSKIR	-	RGW	501

Q395

H409

P439

Panel 9.C

gi 126341326 ref XP_001368664.1	EKS QFLEV - A	S	GI - I P H L S	PERVTVM	489
gi 532098193 ref XP_005334744.1	EKS QFLEEGT	G	GT - I P H L S	PERVTVM	490
gi 617633979 ref XP_007530281.1	EKS QFLEEGM	R	- A - V P H L S	PERVTVM	489
gi 556762769 ref XP_005976677.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 118150810 ref NP_001071315.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 426227824 ref XP_004008015.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 560936067 ref XP_006193853.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 558107932 ref XP_006084994.1	EKS QFPEEGV	G	GA - V P H F S	PERVTVM	490
gi 678117095 gb KFU92571.1	EKS HGI - EEA	S	GS - V P H L S	PERI T V M	489
gi 698447595 ref XP_009700180.1	EKS HVI - EEA	S	GS - V P H L S	PERI T V M	489
gi 594104639 ref XP_006081037.1	EKS QFLEEGI	G	GA - V P H L L	PERVTVM	502
gi 585167019 ref XP_006735607.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 521032109 gb EPQ13895.1	EKS QFPEEGV	G	GA - V P H F S	PERVTVM	587
gi 594697418 ref XP_007195868.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 478514258 ref XP_004431380.1	EKS QFLEEGI	G	GG - V P H L S	PERVTVM	490
gi 586450893 ref XP_006834377.1	EKNQFLEEGI	G	GA - I P H L S	PERVTVM	490
gi 634845392 ref XP_007938025.1	EKS QFLEEGI	G	GA - I P H L S	PERVTVM	490
gi 675606498 ref XP_008947094.1	EKS HVT - EEA	S	GS - V P H L S	PERI T V M	489
gi 593759238 ref XP_007118374.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 697818105 ref XP_009639962.1	EKS HVI - EEA	S	GS - V P H L S	PERI T V M	489
gi 667308740 ref XP_008583827.1	EKS QFLEEGI	G	GT - I P H L S	PERVTVM	490
gi 602733454 ref XP_007452112.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 678002015 ref XP_009077875.1	EKRHV - I EEI	S	GS - V P H L S	PERI T I M	489
gi 557265001 ref XP_006017953.1	EKGRYVKFT	LPS ATG	- E F S S G E T S S N V	488	
gi 564242436 ref XP_006278018.1	EKGRYVKFT	LPS ATG	- E F S S G E T S S N V	488	
gi 591381643 ref XP_007065357.1	EKS QVMEEG	G	GT - V P H L S	PERI T V M	489
gi 470653227 ref XP_004329513.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 573893198 ref XP_006634352.1	ENS - - - QYK	- EETM	GS - A T H V S	PERVTI M	490
gi 676581571 gb KFO71606.1	EKGRYVKFI	LPS ATG	- E Y S S G E T S S N V	459	
gi 465984730 ref XP_004265673.1	EKS QFLEEGI	G	GA - V P H L S	PERVTVM	490
gi 530577007 ref XP_005282464.1	EKS QVMEEG	G	GT - I P H L S	PERI T V M	489
gi 676724330 gb KFO91432.1	EKS HV - I EEA	S	GS - V P H L S	PERI T V M	489
gi 696963642 ref XP_009569809.1	EKGRYVKFI	LPS ATG	- E Y S S G E T S S N V	488	
gi 59773387 ref XP_007250435.1	ESS - - - QRY	- SDHE	RP - A A H V S	PERVTI M	492
gi 532008995 ref XP_005348316.1	EKDGAVKFM	LPADH	- - MQG E K T S H V	488	
gi 512848845 ref XP_004915480.1	EKS HF KENTS	G	GS - A A H V S	PERVTVM	488
gi 530566743 ref XP_005279909.1	EKGRYVKFT	LPS ATG	- E Y S S G E S S S N V	494	
gi 677540716 gb KFR02250.1	EKGRYVKFV	LPS AAG	- E Y S S G E T S S N V	459	
gi 542158470 ref XP_005487985.1	EKGRYVKFV	LPS ATG	- E F S S G E T S S N V	489	
gi 694847613 ref XP_009464896.1	EKS HVVI EAA	S	GS - V P H L S	PERI T V M	490
gi 678182455 gb KFV50177.1	EKGRYVKFV	LPS ATG	- D Y S S G E T S S N V	455	
gi 679011487 gb KFW09927.1	EKGRYVKFV	LPS ATG	- E Y A S G E T S S N V	459	
gi 669287235 ref XP_008636445.1	EKGRYVKFV	LPS TTG	- E F S S G E T S S N V	483	
gi 677406991 gb KFO17415.1	EKGRYVKFI	LPS PTG	- E F S S G E T S S N V	459	
gi 679204949 gb KFW09615.1	EKGRYVKFV	LPS TTS	- G - - - E T S S N V	455	
gi 676419860 gb KFO62638.1	EKGRYVKFV	LPS TTG	- E F S S G E T S S N V	459	
gi 675608719 ref XP_008948321.1	EKGRYVKFI	LPS PTG	- E F S S G E T S S N V	487	
gi 695149311 ref XP_009502251.1	EKGRYVKFV	LPS TTS	- G - - - E T S S N V	484	
gi 657741051 ref XP_008305597.1	DSS - - - LYQF	RRLEPV	- - - GL - A A H V S	PVKVTI M	516
gi 676250196 gb KFO14068.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 677275314 gb KFP66632.1	EKGRYVKFV	LPS TTG	- E Y S S G E T S S N V	459	
gi 683470305 gb KF264514.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 677495685 gb KFO85090.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 678215546 gb KFV82525.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 679012261 gb KFW10387.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 678203332 gb KFV70313.1	EKGRYVKFV	LPS ATG	- E F S S G E T S S N V	459	
gi 677360974 gb KFP92909.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 591364413 ref XP_007057107.1	EKGRYVKFT	LPS ATG	- E Y S S G E S S S N V	488	
gi 642059449 emb CDQ90921.1	ESS - - - QLR	- QDPV	- - - GA - A A H V S	PERVTI M	508
gi 514790431 ref XP_005029984.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S H V	464	
gi 697039297 ref XP_009582166.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	488	
gi 683466853 gb KF261062.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 445990260 gb EMP38328.1	EKGS CGPTQT	MPHI VE	- E R L L T R V S G G L E E L H P A T E D A	- I T W L D D	505
gi 449279972 gb EMC87394.1	EKGRYVKFV	LPS TTE	- E Y S S G E T S S N V	459	
gi 683905829 ref XP_009086054.1	EKGRYVKFV	LPS ATG	- E F S S G E T S S N V	489	
gi 189537018 ref XP_001921185.1	DSH - - - QSR	- TNHE	RP - A A H V S	PERVTI M	492
gi 677528574 gb KFO91682.1	EKGRYVKFV	LPS TTG	- E Y S S G E T S S N V	459	
gi 54220465 ref XP_003440973.2	EKS RHI RFI L	- - - PDDDCR	NG - L E N V S N V	542	
gi 505775464 ref XP_004602222.1	EKS QFLEEGN	R	GT - V P H L S	PERVTVM	490
gi 543728167 ref XP_005505171.1	EKGRYVKFV	LPS TTE	- E Y S S G E T S S N V	488	
gi 694832483 ref XP_009470120.1	EKGRYVKFV	LPS TTG	- E Y S S G E T S S N V	488	
gi 121717655 ref NP_579848.1	ERDGAVKFM	LPAGH	- - - T Q G E K T S H V	488	
gi 543348556 ref XP_005519686.1	EKGRYVKFV	LPS TTG	- E F S S G E T S S N V	483	
gi 529422017 ref XP_005230862.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	488	
gi 678127582 gb KFU96770.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 675307570 gb KFM02832.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 551522965 ref XP_005812970.1	ERNRHI RFML	- - - PAEDCR	NE - V E D V S N V	490	
gi 677996453 ref XP_009076494.1	EKGRYVKFV	LPS ATG	- E Y S S W E T S S N V	488	
gi 449507517 ref XP_002193303.2	EKGRYVKFV	LPS ATG	- E F S S G E T S S N V	483	
gi 686589478 ref XP_009289253.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	488	
gi 641705622 ref XP_008141672.1	EKDS AVKFM	LPMDH	- - - A L G Q K T S H L	488	
gi 67811918 gb KFO88398.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	461	
gi 657587052 ref XP_008297799.1	DNM - - - QYRC	QRLEPV	- - - GS - A A H S	PERVTI M	514
gi 525004174 ref XP_005049782.1	EKGRYVKFV	LPS ATG	- E F S S G E T S S N V	573	
gi 326923015 ref XP_003207737.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	483	
gi 548407520 ref XP_005739903.1	EKS RHI RFI L	- - - PDDDCR	NG - L E N V S N V	489	
gi 498991970 ref XP_004552642.1	EKS RHI RFI L	- - - PDDDCR	NG - L E N V S N V	489	
gi 556961687 ref XP_005991123.1	EKGQRWCSFP	- - - GQNQYS DA	PA - S Q N T S M L	488	
gi 679141247 gb KFW69266.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 602637514 ref XP_007425602.1	ERS RYVNF	LP RAS G	- E F S S G E S S S T V	488	
gi 181900480 asp Q8C159.1 STEA3_MOUSE	EKDGAVKFM	LP GDH	- - - T Q G E K T S H V	488	
gi 637354672 ref XP_008118990.1	ERGRYVKFT	LP RAS G	- E F S S G E S S S I V	488	
gi 658907460 ref XP_008436460.1	DTS - - - PCKA	RRLEPV	- - - GS - A A N I S	PERVTI M	509
gi 478499252 ref XP_004423952.1	EKDGAVKFT	LPMDH	- - - A L A Q K T S H V	488	
gi 554847391 ref XP_005934004.1	EKS RHI RFI L	- - - PDDDCR	NG - L E N I D A R	RCSI QASE - MHV	500
gi 617482021 ref XP_007576620.1	DTS - - - PCKA	RRLEPV	- - - GS - A A N I S	PERVTI M	509
gi 499043063 ref XP_004572136.1	DSS - - - EMRG	KRMEPV	- - - GS - A A H V S	PERVTVM	511
gi 677457755 gb KFO47169.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 548538803 ref XP_005752751.1	DSS - - - EMRG	KRMEPV	- - - GS - A A H V S	PERVTVM	511
gi 690451678 ref XP_009325389.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	488	
gi 527271964 ref XP_005153835.1	EKGRYVKFV	LPS ATG	- E Y S S K E N S S N V	488	
gi 554858454 ref XP_005939371.1	DSS - - - EMRG	KRMEPV	- - - GS - A A H V S	PERVTI M	511
gi 584021062 ref XP_006805209.1	DSS - - - EMRG	KRMEPV	- - - GS - A A H V S	PERVTI M	511
gi 348540180 ref XP_003457566.1	DSS - - - EMRG	KRMEPV	- - - GS - A A H I S	PERVTI M	512
gi 676775583 gb KFP03399.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 146134446 ref NP_573449.2	EKDGAVKFM	LP GDH	- - - T Q G E K T S H V	488	
gi 560947457 ref XP_006196306.1	EKDGAI NFT	RPVDH	- - - A L A Q K T S H V	502	
gi 663271948 ref XP_008495247.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	488	
gi 504154911 ref XP_004589401.1	ERGS AVRFM	MPTDP	- - - A L V E K T S H V	488	
gi 678138311 gb KFOV07483.1	EKGRYVKFV	LPS ATG	- E Y S S G E T S S N V	459	
gi 655827020 ref XP_008256700.1	EKGS AL KFT	PTPTDN	- - - A P V E K T S H V	526	
gi 558227294 ref XP_006137688.1	EKGRYVKFT	LPAATG	- - - E Y S S G E S C S N V	488	
gi 488558203 ref XP_004469496.1	ESE GALRGV	PAAARG	- - - A L A E K T S H V	526	
gi 584001444 ref XP_006795762.1	EKS RHI RFI L	- - - PDDDCR	NG - L E N V S N V	489	
gi 194222160 ref XP_001488330.2	EKDGAI KFT	LPMDH	- - - T L A Q K T S H V	484	

Panel 9.D

gi 556769052 ref XP_005979736.1	EKDGS VRFT	LPVDH	ALAQKTS HV	554	
gi 507686587 ref XP_004711963.1	EKD TI QFV	LPADH	TQAQKTS QV	487	
gi 335302527 ref XP_003359484.1	EKEGAI KFT	LPGDH	ALAQKTS HV	526	
gi 524932352 ref XP_005070358.1	EKDS AVKFL	LP AEH	TQREKTS HV	525	
gi 117646612 emb CAL37421.1	ERES TI KFT	LPTGH	ALAEKTS HV	488	
gi 440900774 gb ELR51839.1	EKDDGVRFT	LPVDH	ALAQKTS HV	492	
gi 156549145 ref NP_878919.2	ERES TI KFT	LPTDH	ALAEKTS HV	498	
gi 528900695 ref XP_580320.4	EKDGS VRFT	LPVDH	ALAQKTS HV	521	
gi 594066504 ref XP_006057222.1	EKDGS VRFT	LPVDH	ALAQKTS HV	521	
gi 402892086 ref XP_003909253.1	ERDGA I KFT	LPTDH	ALAEKTS HV	488	
gi 297668475 ref XP_002812462.1	ERDGA I KFT	LPTDH	ALAEKTS HV	498	
gi 544474563 ref XP_005573007.1	ERDGA I KFT	LPTDH	ALAEKTS HV	488	
gi 296490495 tpg DAA32608.1	EKDDG VRFT	LPVDH	ALAQKTS HV	541	
gi 602688388 ref XP_007456415.1	EKDDG VRFT	LPVDC	ALAQKTS HV	524	
gi 635057451 ref XP_007962925.1	ERDGA I KFT	LPTDH	ALAEKTS HV	488	
gi 114580636 ref XP_515757.2	ERDGTI KFT	LPTDH	ALAEKTS HV	498	
gi 47208402 emb CAG12826.1	EKTRHI RFTL	PEDDGCH	NG LEDI SHV	491	
gi 332265514 ref XP_003281765.1	ERDGA I RFT	LPTDH	SLAEKTS HV	498	
gi 355751640 gb EHH55895.1	ERDGA I KFT	LPTDH	ALAEKTS HV	498	
gi 355566041 gb EHH22470.1	ERDGA I KFT	LPTDH	ALAEKTS HV	498	
gi 507625590 ref XP_004626461.1	EKDDGVRKFM	LPVDS	VLAEKTS HV	583	
gi 426336960 ref XP_004031719.1	ERDGTI KFT	LPTDH	ALAEKTS HV	488	
gi 466042113 ref XP_004276550.1	EKDDGVRKFM	LPVDC	ALAQKTS HV	484	
gi 348586053 ref XP_003478785.1	EKDS AVKFM	LPNDS	ILTEKTS HV	498	
gi 678203611 gb KFV70592.1	EKDDG VRFT	LPVDH	TLAQKTS HV	448	
gi 548454266 ref XP_005676308.1	EKDDG VRFT	LPVDH	TLAQKTS HV	521	
gi 403257231 ref XP_003921232.1	EKDDG VRFT	LPVDH	TLAQKTS HV	454	
gi 584050028 ref XP_006769725.1	EKDS AVKFT	LPGDH	ALGQKTS HL	484	
gi 466042108 ref XP_004276549.1	EKDDGVRKFM	LPVDC	ALAQKTS HV	524	
gi 589936480 ref XP_006981008.1	EKDRAVKFM	LTADH	TQGEKTS HV	526	
gi 470636779 ref XP_004323715.1	EKDDGVRKFM	LPVDC	ALAQKTS HV	524	
gi 617610093 ref XP_007524819.1	EKDDGVRKFM	LPAS Q	ALAQKTS HV	488	
gi 345784138 ref XP_541005.3	EKDDG VRFT	LPMDH	ALAQKTS HV	488	
gi 558170211 ref XP_006098885.1	EKDS AVKFT	LPVDH	ALGQKTS HL	484	
gi 426356824 ref XP_004045753.1	EKDDG VRFT	LPVDC	ALAQKTS HV	454	
gi 573897177 ref XP_006636326.1	ERGQI RFRL	PEDG	AA LEDVSNV	484	
gi 635114983 ref XP_007980440.1	EKDDG VRFT	LPVDC	ALAQKTS HV	452	
gi 545532013 ref XP_005631969.1	EKDDG VRFT	LPVDC	ALAQKTS HV	522	
gi 555980326 ref XP_005902090.1	EKDDG VRFT	LPVDC	ALAQKTS HV	627	
gi 554564434 ref XP_005876534.1	EKDS TVKFT	LPVDH	ALGQKTS HL	517	
gi 677471114 gb KFO60528.1	EKGRYVKFV	LPSATG	E YSSGETS SNV	459	
gi 625234438 ref XP_007608377.1	EKDDGVRKFM	LPADH	RQGEKTS HV	503	
gi 594631581 ref XP_007169320.1	EKDDGVRKFM	LPVDR	ALAQKTS HV	524	
gi 444513159 gb ELV10282.1	EKDDGVRKFM	LPVDH	VLAEKTS HV	488	
gi 617416661 ref XP_007557133.1	ERNRHI RFML	PAEDCR	NG VENVSNV	490	
gi 403280150 ref XP_003931594.1	ERDGA I KFM	LPTDN	ALAEKTS HV	488	
gi 65836963 ref XP_008259713.1	EKDDG VRFT	LPVDC	ALAQKTS HV	456	
gi 674056440 ref XP_008839619.1	EKDDGVRKFM	LPADH	VQGEKTS HV	488	
gi 694643962 ref XP_009479681.1	EKGRYVKFV	LPSATG	E YSSGETS SNV	488	
gi 676823415 gb KFP17617.1	EKGRYVKFV	LPSATG	E YLSRETSS NV	459	
gi 512947279 ref XP_004836120.1	EKDDGVRKFM	LPADS	ILAEKTS HV	520	
gi 562884237 ref XP_006169609.1	EKDDGVRKFM	LPVDH	VLAEKTS HV	526	
gi 533168218 ref XP_005397737.1	EKDDGVRKFM	LPTDS	VLTEKTS HV	520	
gi 511879767 ref XP_004759809.1	EKDDGVRKFM	LPVDH	TLAQKTS HV	522	
gi 677163112 gb KFP44655.1	EKGRYVKFV	LPSATG	E YSSGETS SNV	434	
gi 326921734 ref XP_003207111.1	EGS QF KVQCS	TANMTS WAHR	RA VSHSL	504	
gi 593713838 ref XP_007103422.1	EKDDGVRKFM	LPVDH	ALAQKTS HV	635	
gi 586476470 ref XP_006868786.1	EETDS I QFL	LPADH	ALAEKTS HV	488	
gi 677375060 gb KFO00083.1	EKGRYVKFV	LPSATG	E YSSGETS SNV	459	
gi 667335164 ref XP_008592848.1	EKDDGVRKFM	LPADH	TLVEKTS LV	555	
gi 586532353 ref XP_006921073.1	EKDS AVKFT	LPMDH	ALAEKTS HV	484	
gi 560930861 ref XP_006191567.1	EKDDGVRKFM	LPVDR	ALAEKTS HV	512	
gi 472370587 ref XP_004404804.1	EKDDGVRKFM	LPMDH	ALAEKTS HV	522	
gi 431894760 gb ELK04553.1	EKDS AVKFT	LPMDH	ALAEKTS HV	518	
gi 676711062 gb KFO66351.1	EKGRYVKFV	LPSATG	E YASGETS SNV	459	
gi 675664592 ref XP_008997264.1	ERDGA I KFT	LPTDN	SLAEKTS HV	498	
gi 126326172 ref XP_001368064.1	EKETT VKFL	LPADY	PHTKTS HV	488	
gi 410968534 ref XP_003990757.1	EKDDGVRKFM	LPMDH	ALAEKTS HV	488	
gi 410966137 ref XP_003966548.1	EKTRHI RFTL	PEVVSH	V	483	
gi 676275422 gb KFO29854.1	EKDDGVRKFM	LPTDS	ILAEKTS HV	613	
gi 657561192 ref XP_008284251.1	EKS RHI RFI L	PPDDCR	NG LEDVSNV	491	
gi 640809324 ref XP_008061223.1	ERDGA VRFT	QPTDH	ALVEKTS HV	488	
gi 557017631 ref XP_006009219.1	EQS QFLEE I T		GA VLQLS	PERVTVM	489
gi 554563703 ref XP_005876175.1	EKDDG VRFT	LPVDC	ALAQKTS HV	449	
gi 505800938 ref XP_004608216.1 PREDICTED	EKDDGVRKFM	VPNMN	TLAEKTS HV	488	
gi 344289984 ref XP_003416720.1	EKAGATRF P	LCEDH	TVAQKTS HV	488	
gi 395519413 ref XP_003763844.1	EKKT TVKFL	LPTDY	PHTKTS HV	485	
gi 187607545 ref NP_001120430.1	EKS PTGK P SE	N	G DVPLQ K	CKL	473
gi 471416430 ref XP_004389738.1	EKAGAAQFP	LPEDH	SFAQKTS HV	488	
gi 1301764381 ref XP_002917160.1	EKDDGVRKFM	LPTDH	ALAEKTS HV	488	
gi 677437107 gb KFO35295.1	EKGRYVKFV	LPSATG	E YSSGETS SNV	456	
gi 177773087 gb ACB73281.1	QQATAPS QEP	G	GR TKSS S	PRQI P VV	492
gi 657793049 ref XP_008323412.1	ETS QHVRFMS	LEEEDDCR	GG LEDVSNV	493	
gi 432964301 ref XP_004086917.1	DRS LHGC	RRLEP V	GS AANVS	PERVTI M	515
gi 532060180 ref XP_005315977.1	EKDDG VRFT	LPTDH	ILVEKTS HV	487	
gi 507927026 ref XP_004674772.1	EKDS TVRFT	LPTNP	ALAEKTS HV	488	
gi 507551826 ref XP_004659712.1	EKDRAVKFM	PPTDQ	VLVEKTS HV	541	
gi 395839610 ref XP_003792679.1	ERDGA VRFT	LP LGH	MLAEKTS CV	488	
gi 573896941 ref XP_006636209.1	ERRS VKVPNI	T D	S KNRRKTL I	474	
gi 62751817 ref NP_001015852.1	ERN S KS			458	
gi 585679639 ref XP_006891515.1	ERNPKI S SA	L N	G KTDI	469	
gi 634822528 ref XP_007935951.1	EKADSI QFI	LPEDH	TLAQKTS CV	484	
gi 1642077565 emb CDQ86899.1	EKS RAI RFTL	PEDER NG	PS QEDI SNV	506	
gi 632986455 ref XP_007910248.1	ERN S KSE TE	A L	T NS APVI	467	
gi 148230759 ref NP_001083586.1	EKS S S AGKE P	E N	G DVPLQ T K M	474	
gi 657582034 ref XP_008295059.1	EST QYWP VNN	QE PGGG RE	AH PQQNFD D	V	492
gi 530577035 ref XP_005282478.1	ERN S KDS KQS	YND	S KSAV	472	
gi 674094847 ref XP_008820731.1	ERN S KCS KSA	L N	G KSDL	470	
gi 148223547 ref NP_001083283.1	ERN S KH			458	
gi 658835831 ref XP_008426519.1	ERNRHI RFML	PAEDCC	NG VEDVSNV	486	
gi 76691767 ref XP_583351.2	ERNPKYESS	L N	G KTDI	470	
gi 594062502 ref XP_006055307.1	ERNPKYESS	L N	G KTDI	470	
gi 634845398 ref XP_007938027.1	ERN S KTS SA	L N	G KADI	469	
gi 507645744 ref XP_004702703.1	ERS S KS A SA	L N	R KTDI	469	
gi 555978956 ref XP_005901413.1	ERNPKYESS	L N	G KTDI	470	
gi 488585569 ref XP_004478137.1	ERN S KMS KSA	L N	G KTDI	470	
gi 511830077 ref XP_004739737.1	ERTS KPTS NG	Q Y	L KQNS	I CMDS Q L	477
gi 291394853 ref XP_002713875.1	ERN TDFS KSA	V N	G KSDI	470	
gi 395818569 ref XP_003782697.1	ERN S KI S KSA	L N	G KTDI	470	
gi 664746520 ref XP_008530613.1	ERN S KFS KLA	L N	V KTHI	470	
gi 641692785 ref XP_008147562.1	ERN S KFS KSA	L N	G QTDI	470	
gi 149705913 ref XP_001492269.1	ERN S KFS KLA	L N	V KTHI	470	
gi 562886193 ref XP_006170537.1	ERN S KHS KSA	L N	A KSDI	470	
gi 410952214 ref XP_003982778.1	ERN AKP TLNG	E R	Y LKQSS VHV	L DSE L	478
gi 548463578 ref XP_005679356.1	ERNPKYESS A	L N	G KTDI	470	

Panel 9.E

gi 426227818 ref XP_004008012.1	ERNPKYSESA	L - N - - - -	- G - KTDI - - - - -	470
gi 556762761 ref XP_005976673.1	ERNPKYSESA	L - N - - - -	- G - KTDI - - - - -	470
gi 478514250 ref XP_004431376.1	ERNSSKSKSA	L - N - - - -	- G - KTDI - - - - -	470
gi 504139789 ref XP_004582343.1	ERDTAVVKPA	V - N - - - -	- G - KPDM - - - - -	470
gi 591384664 ref XP_007066785.1	ERNSSKSKSA	NYND - - - -	- S - KSAV - - - - -	472
gi 431839048 gb ELK00976.1	ERHSSKSNWH	- - - - -	- - - - -	462
gi 591299567 ref XP_007076799.1	ERNAKPTLNG	E - R - - - -	- Y - LKQSSVH - - - - - LDSE L - - - -	478
gi 164210771 emb CDQ76188.1	ESPCHHPPQT	QE - - DTANG -	- VL - PRDLSGD VTI FTCKN - - - -	549
gi 558213257 ref XP_006134172.1	ERNSSKSEQS	HYND - - - -	- S - KSAV - - - - -	472
gi 586554628 ref XP_006925771.1	ERHSSKXKLKA	L - N - - - -	- R - KTDI - - - - -	469
gi 617463244 ref XP_007572760.1	ERTQPKEMD -	E - I - - - -	- K - TTNL - - - - -	481
gi 585154586 ref XP_006729650.1	ERNSSKQTSKG	Q - Y - - - -	- L - KQSS - - - - - I YLDSQ L - - - -	477
gi 593730883 ref XP_007111076.1	ERNPKYSESA	L - N - - - -	- G - KTDI - - - - -	469
gi 560979331 ref XP_006211922.1	ERNPKYSDSA	L - N - - - -	- G - KTDI - - - - -	470
gi 560925797 ref XP_006189080.1	ERNPKYSDSA	L - N - - - -	- G - KTDI - - - - -	470
gi 617642095 ref XP_007531980.1	ERD - - - - -	- - - - -	- - - - -	454
gi 281347098 gb EFB22682.1	ERNSSK - - - -	- - - - -	- - - - -	458
gi 472383394 ref XP_004411076.1	ERNSSKPTSNG	Q - Y - - - -	- L - KQSS - - - - - I YLDSQ L - - - -	477
gi 301756344 ref XP_002914022.1	ERNSSKFVQES	L - G - - - -	- A - ETTGNKQ VTNQRHLQAT LGVALKKD - - - -	491
gi 326921724 ref XP_003207106.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 602704474 ref XP_007446805.1	ERNPKYSESA	L - N - - - -	- G - KTDI - - - - -	469
gi 532110716 ref XP_005340062.1	ERDSSKSESA	L - N - - - -	- G - KSDI - - - - -	470
gi 670986751 ref XP_008684432.1	ERNSSKPTSNG	Q - Y - - - -	- L - K - - - - QS SI HLDSQ L - - - -	476
gi 544421694 ref XP_005550352.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 471395586 ref XP_004381559.1	ERNSSKISSA	L - N - - - -	- G - KTDI - - - - -	468
gi 332206641 ref XP_003252407.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 635115010 ref XP_007980452.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 109067578 ref XP_001104041.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 483515133 gb E0B02513.1	ERNPQY - - - -	- - - - -	- - - - -	459
gi 402864294 ref XP_003896407.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 679009785 gb KFW08962.1	YRNPQYSE - -	- - - - -	- - - - -	461
gi 657790068 ref XP_008321837.1	ERTDPEDASK	Q - A - - - -	- L - LM - - - - -	472
gi 344270753 ref XP_003407207.1	ERNSSKISSA	L - N - - - -	- G - KTDI - - - - -	468
gi 465984774 ref XP_004265679.1	ERNPKYSESA	L - N - - - -	- G - KSDI - - - - -	469
gi 100815815 ref INP_078912.2	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 426356807 ref XP_004045745.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 55628944 ref XP_527809.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 296209755 ref XP_002751668.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 297681122 ref XP_002818315.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 403257216 ref XP_003921225.1	ERNSSKH - - - -	- - - - -	- - - - -	459
gi 564244487 ref XP_006261377.1	ERNPQEFKNS	NYNS - - - -	- A - V - - - -	469
gi 586450897 ref XP_006834379.1	ERNSSKMS - SV	L - N - - - -	- G - KTDI - - - - -	469
gi 557260663 ref XP_006015971.1	ERNPQEFKNS	NYNG - - - -	- S - NSAV - - - - -	472
gi 667273517 ref XP_008571690.1	ERSSKYSKSA	L - N - - - -	- G - KTYMK - - - - -	484
gi 507930953 ref XP_004676720.1	ERDSSKSKSA	L - N - - - -	- G - KTDI - - - - -	470
gi 514739105 ref XP_005017950.1	ERNPQYSEQS	HYI I - - - -	- N - KSAV - - - - -	524
gi 677057004 gb KFP23881.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 470640506 ref XP_004325219.1	ERNPKYSESA	L - N - - - -	- G - KTDI - - - - -	469
gi 678145287 gb KFV14453.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 657789586 ref XP_008321572.1	ERNQSKETVG	D - N - - - -	- K - ATNL - - - - -	473
gi 640815258 ref XP_008064391.1	ERNSSKYSTLN	- - - - -	- K - KSDV - - - - -	468
gi 543727826 ref XP_005505005.1	ERNPQYDPS	NYI I - - - -	- N - KSAV - - - - -	524
gi 594636285 ref XP_007171542.1	ERNPKYSESA	L - N - - - -	- G - KTDI - - - - -	469
gi 262063564 ref INP_001159961.1	ERNPKFLESA	L - N - - - -	- G - KTDL - - - - -	470
gi 584041383 ref XP_006779243.1	ERNSSKSKSA	L - N - - - -	- G - QTDI - - - - -	470
gi 677482698 gb KFP72103.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 126341543 ref XP_001377787.1	ERNSSKVS KA	QLEN - - - -	- G - KSEV - - - - -	474
gi 597799143 ref XP_007261108.1	ERI RKCPVPQ	HH - - HAGDNG	- TL - PEV - - - - -	502
gi 507557180 ref XP_004662336.1	ERNPRNSKST	L - H - - - -	- G - KSDI - - - - -	469
gi 597748725 ref XP_007236319.1	ERPAKGGTAG	K - D - - - -	- A - KSSRPLI L - - - -	472
gi 676772623 gb KFP01080.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 658895934 ref XP_008430820.1	ERAQPKQMD -	E - I - - - -	- K - TTNL - - - - -	470
gi 663261998 ref XP_008492349.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 678214307 gb KFV81286.1	ERNPRHSE - -	- - - - -	- - - - -	461
gi 675309853 gb KFM05115.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 62955445 ref INP_001017734.1	ERQSKTSANC	I - - D - - - -	- G - KTNQPLM A - - - -	464
gi 602643791 ref XP_007428353.1	ERKPKYI NHS	NSNQ - - - -	- S - TKEMSSV - - - -	522
gi 676720236 gb KFO89856.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 679216243 gb KFN94833.1	ERKPKYSE - -	- - - - -	- - - - -	461
gi 695163616 ref XP_009510156.1	ERKPKYSEEP	NYI V - - - -	- N - KTAV - - - - -	472
gi 521032115 gb EPQ13901.1	ERNSSKCSKA	V - N - - - -	- G - QTDI - - - - -	470
gi 554563717 ref XP_005876182.1	ERNSSKCSKA	V - N - - - -	- G - QTDI XSN VQCTQSSSELY VSR - - - -	486
gi 685595796 ref XP_009273959.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	524
gi 558171384 ref XP_006099145.1	ERNNAKCSKA	L - N - - - -	- G - QTDI XSN VQCI QSSSELY V - - - -	484
gi 677536450 gb KFO98359.1	ERKPKYSE - -	- - - - -	- - - - -	461
gi 679144657 gb KFW71729.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 677222689 gb KFP50613.1	ERNPQHSE - -	- - - - -	- - - - -	461
gi 694847617 ref XP_009464898.1	ERKPKYSEQS	NYI I - - - -	- N - KSAV - - - - -	524
gi 677302700 gb KFP85128.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 678192031 gb KFW59725.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 677380957 gb KFO3816.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 690459533 ref XP_009328808.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	524
gi 292617388 ref XP_002663339.1	ESKRNCPLVQ	HH - - HLQANG	- VP - - - - -	481
gi 527270063 ref XP_005153001.1	ERNPQYSEQS	HYI I - - - -	- N - KSAV - - - - -	523
gi 410905459 ref XP_003966209.1	ERNAGDSDSR	K - A - - - -	- L - LT - - - - -	479
gi 678117091 gb KFO92567.1	ERNPPYSE - -	- - - - -	- - - - -	461
gi 678173365 gb KFW41361.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 432908525 ref XP_004077904.1	ERTDPEEST	K - S - - - -	- L - LR - - - - -	472
gi 529418079 ref XP_005228920.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 677399646 gb KFO14863.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 541950816 ref XP_005432195.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 678144582 gb KFW13748.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 112984288 ref XP_001037730.1	ERKSKYAQST	L - N - - - -	- G - KSDI - - - - -	470
gi 532030822 ref XP_005358353.1	ERNSSKSKSA	L - N - - - -	- G - KPDI - - - - -	470
gi 677769649 ref XP_009082926.1	ERNPKYSEQS	NYI I - - - -	- N - KSAV - - - - -	468
gi 676251117 gb KFO14989.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 543253204 ref XP_005418648.1	ERNPKYTKQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 677147066 gb KFP40888.1	ERKPKYK - - -	- - - - -	- - - - -	461
gi 642120318 emb CDQ64940.1	ERGADQRN - P	K - D - - - -	- S - QPLIP - - - -	481
gi 677553655 gb KFR13417.1	ERNPQHS - - -	- - - - -	- - - - -	460
gi 677457512 gb KFO46926.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 589949118 ref XP_006987217.1	ERNSSKSKSA	L - N - - - -	- G - KSDI - - - - -	470
gi 632986449 ref XP_007910245.1	ERKLSKGNDR	V - - - - -	- - - - -	460
gi 677417976 gb KFO23007.1	ERNPKYSE - -	- - - - -	- - - - -	461
gi 677469944 gb KFO59358.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 31981509 ref INP_473439.2	ERNSSKYTQSA	L - N - - - -	- G - KSDI - - - - -	470
gi 524985734 ref XP_005040826.1	ERKPRYSEQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 47225470 emb CAG11953.1	ERN - - - - -	- - - - -	- - - - -	463
gi 657537742 ref XP_008275282.1	DRTDKAEDSE	K - S - - - -	- L - LT - - - - -	470
gi 677274891 gb KFP66209.1	ERNPQYSE - -	- - - - -	- - - - -	461
gi 679184773 gb KFW6184.1	ERNPKSE - - -	- - - - -	- - - - -	461
gi 694637176 ref XP_009477232.1	ERNPQYSEQS	NYI I - - - -	- N - KSAV - - - - -	524
gi 345307590 ref XP_001509103.2	ERNSSKAKKA	QYEN - - - -	- G - RADM - - - - -	469
gi 675407224 ref XP_008932024.1	ERNPKSEQS	NYI I - - - -	- N - KSAV - - - - -	472
gi 658895943 ref XP_008430825.1	ERTDPENDSK	K - K - - - -	- S - LLA - - - - -	473

Panel 9.F

gi 678203614 gb KFV70595.1	ERNPRYSE--	----	----	----	----	----	459
gi 449492447 ref XP_002193727.2	ERNPKYSEQS	NYI I	----	-N- KSAV-	----	----	465
gi 677488410 gb KFQ77815.1	ERNPQYSE--	----	----	----	----	----	461
gi 551506445 ref XP_005804755.1	ERTDTENDSK	K - S	----	-L- LA-	----	----	472
gi 676412338 gb KFO56232.1	ERNPKHSE--	----	----	----	----	----	461
gi 291190416 ref NP_001167369.1	LPPNHRLPCF	W - D	----	-Q- KP TI TFH	----	----	483
gi 669272195 ref XP_008628113.1	ERNPKHSEQS	NYI I	----	-N- KSAV-	----	----	472
gi 543346256 ref XP_005518838.1	ERKPKYSEQS	NYVI	----	-N- KSAV-	----	----	472
gi 542142451 ref XP_005480330.1	ERNPKYSKQS	NYVI	----	-N- KSAV-	----	----	472
gi 327274760 ref XP_003222144.1	ERKS KYVNI	NNDE	----	-T- MKES SAV	----	----	474
gi 513168239 ref XP_001235257.3	ERNPQYSEQS	NYVI	----	-N- KSAV-	----	----	472
gi 565316654 gb ETE68273.1	ERKPKNMSHS	NSNQ	----	-N- TKEMS SV	----	----	477
gi 683467094 gb KFZ61303.1	ERNPKYSK-	----	----	----	----	----	461
gi 683900635 ref XP_009084178.1	ERNPKYAKQT	NYI I	----	-N- KSAV-	----	----	472
gi 505775871 ref XP_004602336.1	DRNSES SKPS	L - N	----	-R- KTKI-	----	----	469
gi 676275116 gb KFO29573.1	ERNS KYSKSA	L - F	----	-R- KSDVSSK	AECTWAS EL-	----	508
gi 696975795 ref XP_009557372.1	ERNPQYSEQS	NYI T	----	-N- KSAV-	----	----	472
gi 676586017 gb KFO74821.1	ERNPQYSE--	----	----	----	----	----	461
gi 679006701 gb KFW07166.1	ERNPQYSE--	----	----	----	----	----	461
gi 676813260 gb KFP09648.1	ERKPKYSE--	----	----	----	----	----	461
gi 697032879 ref XP_009578615.1	ERNPQYSEQS	NYI I	----	-N- KSAV-	----	----	524
gi 354488334 ref XP_003506325.1	ERDS QYSKSA	L - N	----	-G- KSDI-	----	----	470
gi 507713563 ref XP_004647823.1	ERNS KYSKSL	S - F	----	-G- KSNVSSN	VECTWAS EI-	----	482
gi 524968279 ref XP_005084025.1	ERS SQHSKSA	M - N	----	-G- KSDI-	----	----	470
gi 410905463 ref XP_003966211.1	ERNPPLIEVN	K - A	----	-S- SL-	----	----	448
gi 548400752 ref XP_005738595.1	ERNRLKDEMG	E - L	----	-K- ATNM-	----	----	471
gi 498938966 ref XP_004541746.1	ERNRLKDEMG	E - L	----	-K- ATNM-	----	----	471
gi 675614756 ref XP_008936236.1	ERNPKYSEQS	NYI I	----	-N- KSAV-	----	----	472
gi 348578509 ref XP_003475025.1	EKNS KSKPL	L - F	----	-R- KSDVSNK	AECTWAS EI-	----	482
gi 548400757 ref XP_005738596.1	ERTDPEQERK	K - L	----	-L- LT-	----	----	472
gi 554854825 ref XP_005937599.1	ERTDPEQERK	K - L	----	-L- LT-	----	----	472
gi 584013191 ref XP_006801411.1	ERTDPEQERK	K - L	----	-L- LT-	----	----	472
gi 498937702 ref XP_004541468.1	ERTDPEQERK	K - L	----	-L- LT-	----	----	472
gi 664765458 ref XP_008540415.1	EKDGAI KFT-	LPMDH-	----	-TLAQKTS HV	----	----	524