ENCFF718AWL					
120	0000	<b>I</b> 1225000	T 1250000  Genomic coordinate (chrl.) "+" strand	 1275000	1300000
			Genomic coordinate (chr1), "+" strand		
polyA:		1 11 11	1 11111111 1	1 1 1 1	1 111
MXRA8   MXRA8-005 MXRA8   MXRA8-006					
MXRA8   MXRA8-009					****
MXRA8   MXRA8-008					 ■#
MXRA8   MXRA8-007	7				<b>■</b> #
MXRA8   MXRA8-201	1				<b>■             </b>
MXRA8   MXRA8-003	3				<b>■-###</b> -+
MXRA8   MXRA8-002	2				**************************************
TOPOLOS / 100p 50st 27855   110m   120m   12	<u>s</u> 1				100 STATE OF THE S
MXRA8   MXRA8-004					<del></del>
DVL1   DVL1-00				B <del>   &lt; &lt; &lt;  </del>	
DVL1   DVL1-00  STRUCTURALSTRAIN, [ENSTRO0003378888] PTM MOD RULE PROCESSING, CHAIN, Segment polarity protein dishevelled normally by 11 [ENSTRO000378888] MOLECULE_PROCESSING, CHAIN, Segment polarity protein dishevelled normally by 11 [ENSTRO000378888]	1			<del>■ &lt;                                     </del>	
DVL1   DVL1-00	4				
TOBOLOGY, TRANSMEM, Helicalien ST0000333338.  PTM, CARBOHYD NAME OF THE STORY OF TH	1				
				<b>&gt;1==11==</b>	
GLTPD1   GLTPD1-003  STRUCTURAL STRAIN LENSTRONDS 333333  MOLECULE_PROCESSING,CHAIN.Ceramide-1-phosphate transfer protein NST00000333333			<del>** +   </del> : <u>"</u>		
GLTPD1   GLTPD1-00	1		™ * <del></del>		
GLTPD1   GLTPD1-002			* → ■		
CPSF3L   CPSF3L-035			■		
CPSF3L   CPSF3L-036			<del>∤  &lt; ■  </del>		
CPSF3L   CPSF3L-025 CPSF3L   CPSF3L-031			<del>                                      </del>		
CPSF3L   CPSF3L-014			<del>⊩                                      </del>		
CPSF3L   CPSF3L-033			<u> </u>		
CPSF3L   CPSF3L-027	,		<del>■                                      </del>		
CPSF3L   CPSF3L-032	!		<b>▶+</b>    <b>*</b>		
CPSF3L   CPSF3L-015	j		<b>■-!</b> *		
CPSF3L   CPSF3L-003	3				
CPSF3L   CPSF3L-002			■-■		
CPSF3L   CPSF3L-016			<del>■                                     </del>		
RP5-89003.9   RP5-89003.9-001			₩		
CPSF3L   CPSF3L-026 CPSF3L   CPSF3L-039			<del>-                                    </del>		
CPSF3L   CPSF3L-040			•		
CPSF3L   CPSF3L-034			<del>    &lt; -           </del>		
CPSF3L   CPSF3L-030	)		4 <del>   &lt;                                   </del>		
CPSF3L   CPSF3L-013	3		<del>                                    </del>		
CPSF3L   CPSF3L-038	3		<del>                                     </del>		
CPSF3L   CPSF3L-037			# <del>   &lt;            </del>		
CPSF3L   CPSF3L-018			<del>■#&lt; &lt;  &lt;  </del>		
CPSF3L   CPSF3L-041			<del>*1 1</del> 1		
CPSF3L   CPSF3L-045 CPSF3L   CPSF3L-017			н		
CPSF3L   CPSF3L-017			# <del>   &lt;                                  </del>		
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CPSF3L   CPSF3L-043			*# ** ·		
CPSF3L   CPSF3L-042			# <del># 4   &lt; &lt;  </del>		
CPSF3L   CPSF3L-047	,		<del>101 t</del>		
CPSF3L   CPSF3L-046			<del>₩   &lt;  </del>		
CPSF3L   CPSF3L-048			<del>MB 1</del>		
CPSF3L   CPSF3L-020			<b>■</b> +		
CPSF3L   CPSF3L-022			###		
CPSF3L   CPSF3L-202 CPSF3L   CPSF3L-024					
CPSF3L   CPSF3L-023			HHB -  - - - - - - - - - - - - - - - - -		
CPSF3L   CPSF3L-029			MHHH+1+		
CPSF3L   CPSF3L-006			**************************************		
CPSF3L   CPSF3L-201			MMM.H+1.8 - 4 1.8 1.5 -		
CPSF3L   CPSF3L-007	,		MINI 10 + 1 +		
CPSF3L   CPSF3L-012			######################################		
CPSF3L   CPSF3L-009			MHHH+114		
CPSF3L   CPSF3L-005			<del>M11:0+1 **</del>		
CPSF3L   CPSF3L-011			MH81-H+1-8		
CPSF3L   CPSF3L-004 CPSF3L   CPSF3L-021			#####################################		
CPSF3L   CPSF3L-U21 STRUCTURAL TURN LENGTHORS MOLECULE_PROCESSING, CHAIN, Integrator complex submit 11 [IRS 100000435064]			### ##################################		
MOLECULE_PROCESSING,CHAIN,Integrator cömplex sübünit TI [ENST00000435064 *  CPSF3L   CPSF3L-001			**************************************		
CPSF3L   CPSF3L-008			<del>910€9+ ≡</del>		
PUSL1   PUSL1-002			* <del>******</del>		
PUSL1   PUSL1-003			<del>##                                   </del>		
PUSL1   PUSL1-004	1		<b>/■</b>		

**■ + | <|| | < < < -|** 

<del>||| - |||</del>

PUSL1 | PUSL1-005

PUSL1 | PUSL1-001

ACAP3 | ACAP3-005 ACAP3 | ACAP3-006 ACAP3 | ACAP3-007

ACAP3 | ACAP3-012

ACAP3 | ACAP3-002

ACAP3 | ACAP3-008

ACAP3 | ACAP3-011 ACAP3 | ACAP3-009

ACAP3 | ACAP3-010 ACAP3 | ACAP3-003

ACAP3 | ACAP3-004

ACAP3 | ACAP3-201

ACAP3 | ACAP3-001

SCNN1D | SCNN1D-005

SCNN1D | SCNN1D-201

SCNN1D | SCNN1D-007

SCNN1D | SCNN1D-003

SCNN1D | SCNN1D-006

SCNN1D | SCNN1D-001

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UBE2J2 | UBE2J2-013

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UBE2J2 | UBE2J2-011

UBE2J2 | UBE2J2-005

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UBE2J2 | UBE2J2-006-1-1-1

UBE2J2 | UBE2J2-001

TOPOLOGY TOPO DOM Cytoplasmic FNST0000349431 TSP HID FORM THE IN FNST0000349431 biouitin-conjugating enzyme E2 J2JENST00000349431

TOPOLOGY TOPO DOM Cytoplasmic FNST0000360466 STS WILL TORAL BE IN IEST 10000360466 Significancy of the conjugating enzyme Ez JZ ENST0000360460

RP5-902P8.10 | RP5-902P8.10-002 RP5-902P8.10 | RP5-902P8.10-001

TOPOLOGY, TRANSMEM, HelicalleNST0000379116

TOPOLOGY, TRANSMEM, HelicalleNST0000379116

TOPOLOGY, TUPP, DOM, Cytargellular ENST0000379116

MOLECULE\_PROCESSING, CHAIN, Amilionide Sensitive Southing Hamiles Subarne (1880) ENST0000379111

MOLECULE\_PROCESSING,CHAIN,Ubiquitin-con

MOLECULE\_PROCESSING,CHAIN,Ubiquitin-conju

PTM, MOD. RES.PhosphoserineIENST00000379031
MOLECULE\_PROCESSING,CHAIN,tRNA pseudouridme synthase-like 1|ENST00000379031

MOLECULE\_PROCESSING,CHAIN,Arf-GAP with coiled-coil, ANK repeat and PH domain