PTM,CARBOHYL MOLECULE_PROCESSING,CHAIN,T

 ${\tt MOLECULE_PROCESSING,CHAIN,Ceramide-1}$

MOLECULE_PROCESSING, CHAIN, Arf-GAP with coiled-coil, ANK repeat and PH doma

SCNN1D | SCNN1D-201

SCNN1D | SCNN1D-007 SCNN1D | SCNN1D-003

SCNN1D | SCNN1D-006 SCNN1D | SCNN1D-001

SCNN1D | SCNN1D-002

SCNN1D | SCNN1D-008

UBE2J2 | UBE2J2-013

UBE2J2 | UBE2J2-201___

UBE2J2 | UBE2J2-011 UBE2J2 | UBE2J2-012 UBE2J2 | UBE2J2-004

UBE2J2 | UBE2J2-019 UBE2J2 | UBE2J2-018

UBE2J2 | UBE2J2-005

UBE2J2 | UBE2J2-010, UBE2J2 | UBE2J2-003, UBE2J2 | UBE2J2-002

UBE2J2 | UBE2J2-006, UBE2J2 | UBE2J2-202

UBE2J2 | UBE2J2-016, UBE2J2 | UBE2J2-007,

UBE2J2 | UBE2J2-001

TOPOLOGY TOPO, DOM Cytoplasmic ENST0000360466 — 5 EYAU TOPAL HE W. ENST0000360466 — piquitin-conjugating enzyme EZ J2JENST0000360466 —

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

TOPOLOGY, TRANSMEM, Helicalien, ST00000379116

TOPOLOGY, TRANSMEM, Helicalien, ST00000379116

TOPOLOGY, TO

MOLECULE PROCESSING, CHAIN, Ubiquitin-cor

MOLECULE_PROCESSING,CHAIN,Ubiquitin-conju

1275000 1200000 1225000 1250000 1300000 Genomic coordinate (chr1), "+" strand polyAS 1111111 MXRA8 | MXRA8-005 MXRA8 | MXRA8-006 MXRA8 | MXRA8-009 MXRA8 | MXRA8-008 MXRA8 | MXRA8-007 MXRA8 | MXRA8-201 MXRA8 | MXRA8-003 MXRA8 | MXRA8-002 MXRA8 | MXRA8-001 MXRA8 | MXRA8-004 DVL1 | DVL1-005 DVL1 | DVL1-001 DVL1 | DVL1-004 TAS1R3 | TAS1R3-001 GLTPD1 | GLTPD1-003 STRUCTURAL STRAND, ENSTROBBORG 43938 ä GLTPD1 | GLTPD1-001 GLTPD1 | GLTPD1-002 CPSF3L | CPSF3L-035 CPSF3L | CPSF3L-036 CPSF3L | CPSF3L-025 **⊭-1**1< CPSF3L | CPSF3L-031 CPSF3L | CPSF3L-014 CPSF3L | CPSF3L-033 CPSF3L | CPSF3L-027 CPSF3L | CPSF3L-032 CPSF3L | CPSF3L-015 CPSF3L | CPSF3L-003 CPSF3L | CPSF3L-002 CPSF3L | CPSF3L-016 RP5-890O3.9 | RP5-890O3.9-001 CPSF3L | CPSF3L-026 CPSF3L | CPSF3L-039 CPSF3L | CPSF3L-040 CPSF3L | CPSF3L-034 CPSF3L | CPSF3L-030 CPSF3L | CPSF3L-013 CPSF3L | CPSF3L-038 CPSF3L | CPSF3L-037 CPSF3L | CPSF3L-018 CPSF3L | CPSF3L-041 CPSF3L | CPSF3L-045 \boldsymbol{H} CPSF3L | CPSF3L-017 CPSF3L | CPSF3L-019 #+4+ CPSF3L | CPSF3L-044 | | | CPSF3L | CPSF3L-043 ### H CPSF3L | CPSF3L-042 CPSF3L | CPSF3L-047 CPSF3L | CPSF3L-046 CPSF3L | CPSF3L-048 CPSF3L | CPSF3L-020 CPSF3L | CPSF3L-022 CPSF3L | CPSF3L-202 CPSF3L | CPSF3L-024 CPSF3L | CPSF3L-023 CPSF3L | CPSF3L-029 CPSF3L | CPSF3L-006 CPSF3L | CPSF3L-201 CPSF3L | CPSF3L-007 CPSF3L | CPSF3L-012 CPSF3L | CPSF3L-009 ######### *** * * * * *** | CPSF3L | CPSF3L-005 CPSF3L | CPSF3L-011 CPSF3L | CPSF3L-004 CPSF3L | CPSF3L-021 STRUCTURAL TURN, IENST00000435064 STRUCTURAL THEN INST80000435064 MOLECULE_PROCESSING, CHAIN, Integrator complex submit TJENST00000435064 CPSF3L | CPSF3L-001 ###### **- 4 | k - < |** CPSF3L | CPSF3L-008 PUSL1 | PUSL1-002 PUSL1 | PUSL1-003 PUSL1 | PUSL1-004 PUSL1 | PUSL1-005 PTM,MOD. RES.PhosphoserinelENST00000379031
MOLECULE_PROCESSING,CHAIN,tRNA pseudouridine synthase-like 1|ENST00000379031 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

PTM,CARBOHYDLECKES,PIOS PTM,CARBOHYDLECKES, MON MOLECULE PROCESSING,CHAIN,Matrix remodeling-associated