

# Leukaemia Section

## Short Communication

### t(2;5)(p23;q35) SQSTM1/ALK

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## Identity

### Note

Not to be confused with the t(2;5)(p23;q35) with NPM1-ALK involvement.

## Clinics and pathology

### Disease

ALK-positive large B-cell lymphoma (ALK+ LBCL)

### Phenotype/cell stem origin

One case to date, a 67-year-old male patient (Takeuchi et al., 2011).

### Cytology

Anti-ALK immunohistochemistry showed a diffuse cytoplasmic staining pattern, in contrast with the nuclear and cytoplasmic pattern usually seen in the NPM1-ALK fusion gene/protein.

### Prognosis

Complete remission was obtained, but the patient relapsed four months later.

## Genes involved and proteins

### ALK

#### Location

2p23

#### Protein

ALK is composed of an extracellular region (containing two MAM (meprin, A-5 protein, and receptor protein-tyrosine phosphatase mu) and one LDLa (low-density lipoprotein receptor) domains, and

one glycin-rich region), a transmembrane domain, and an intracellular region (composed of a tyrosine kinase domain). Membrane receptor tyrosine kinase.

### Germinal mutations

In familial neuroblastoma.

### Somatic mutations

Fusion proteins in anaplastic large cell lymphoma, some diffuse large B-cell lymphomas, inflammatory myofibroblastic tumours, and some non-small cell lung cancers. Somatic mutations in sporadic neuroblastoma (review in Allouche, 2010).

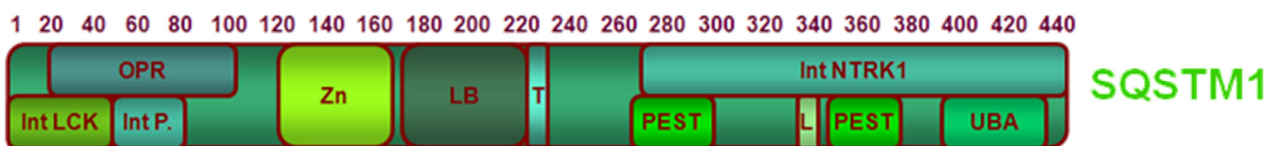
### SQSTM1

#### Location

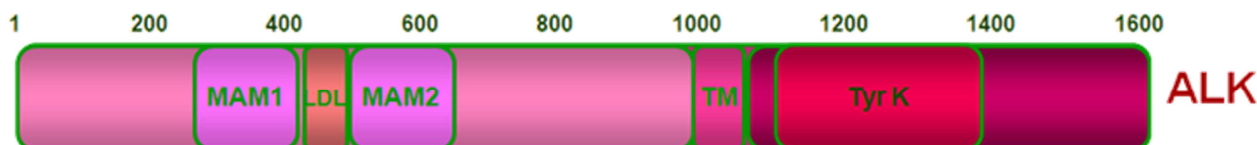
5q35.3

#### Protein

SQSTM1 (sequestosome1), also called p62, is a scaffolding protein with several interaction domains; it is composed of an OPR domain (octicosapeptide repeat (PB1 dimerization domain)), a Zn finger, a LIM protein-binding region, a TRAF6-binding motif, a PEST sequence (proline, glutamic acid, serine, and threonine rich), a LIR motif (LC3 interaction region, SGGDDDWTHLSS), a second PEST sequence, a KIR (keap1 interacting region), and an UBA (ubiquitin-associated) domain. Interacts with Caspase-8 and the apoptosis machinery, MAPK kinases such as MAP2K5 (15q23), LCK (1p34), NBR1 (17q21), PRKCI (3q26), PAWR (12q21), RIPK1 (6p25), TRAF6 (11p12) and NTRK1 (1q23) and the NF-kappaB pathway, KEAP1 (19p13), GABARAPL1 (12p13), MAP1LC3A/LC3 (20q11), and ubiquitin. Mediates the interaction between TRAF6 and CYLD (16q12). Implicated in the activation of the transcription factor NF-kappaB.



Note: in the first 2 rows, the two proteins are not on scale



**PB1 (OPR), Zinc finger and TRAF6-binding domains of SQSTM1 fused to the Tyrosine kinase domain of ALK**

Involved in the autophagy-lysosome pathway. Plays a role in the formation of cytoplasmic proteinaceous inclusions in various pathologic situations where autophagy is inactivated (Geetha and Wooten, 2002; Lamark et al., 2009; Moscat and Diaz-Meco, 2009; Moscat et al., 2009; Ichimura and Komatsu, 2010; Komatsu and Ichimura, 2010; Moscat and Diaz-Meco, 2011).

**Germinal mutations**

Mutated in Paget's disease of bone.

**Result of the chromosomal anomaly**

**Hybrid gene**

**Description**

Exon 5 of SQSTM1 fused to the ALK exon 20.

**Fusion protein**

**Description**

Fuses the PB1 dimerization domain of SQSTM1 to the tyrosine kinase domain of ALK, resulting in a constitutive activation of the ALK kinase domain.

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