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## org.systemsbioinformatics.libs.apmlparser

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## Package org.systemsbioinformatics.libs.apmlparser

### Class Summary

<a href="#">AlignedFeature</a>	AlignedFeature is a class for single aligned feature.
<a href="#">Alignment</a>	Alignment is a class for a single alignment containing features from multiple LCMS runs
<a href="#">AlignmentHandler</a>	
<a href="#">APML</a>	APML is a container object for top apml elements in APML.
<a href="#">APMLElement</a>	APMLElement is a class for all APML element container classes.
<a href="#">APMLElementName</a>	APMLElementName contains all String type of APML Elements, therefore, if there is any update of element string name, APMLElementName is the only place to be updated.
<a href="#">APMLParser</a>	APMLParser is for parsing APML file.
<a href="#">APMLSAXHandler</a>	APMLSAXHandlerI should be implemented in all APML SAX Handler classes.
<a href="#">APMLValidator</a>	APMLValidator is a class to validate APML syntax based on more detailed schema.
<a href="#">Cluster</a>	Cluster is a container class for Cluster element which lists all the reference features used to make consensus cluster profile.
<a href="#">ClusterProfile</a>	ClusterProfile is a container class for Cluster element which is collection of an type of "theoretical" or "expected" trend profile.
<a href="#">ClusterProfileHandler</a>	ClusterProfileHandler is APMLSAXHandler for parse apml and create ClusterProfile object.
<a href="#">ClusterProfileParser</a>	Class is parsing Cluster element using STAX parser.
<a href="#">Coordinate</a>	Coordinate contains the coordinates of each feature
<a href="#">DataProcessing</a>	DataProcessing is a container class for dataProcessing element.
<a href="#">DataProcessingHandler</a>	DataProcessingHandler is APMLSAXHandler for parse apml and create DataProcessing object.
<a href="#">ElutionProfile</a>	ElutionProfile is a container class for elution_profile element which is collection of MS 1 elution profile given a feature and used for APML viewer.
<a href="#">Feature</a>	Feature is a single feature for a putative peptide.
<a href="#">FeatureSourceListParser</a>	Class is parsing feature_source_list element using STAX parser.
<a href="#">GenericAttribute</a>	GenericAttribute is a class for generic name, value and type attribute set.
<a href="#">Modification</a>	Modification is a class for information on amino acid modification
<a href="#">PeakList</a>	PeakList is a container of peak_list element which is a collection of peaks peaked by a single LCMS run.
<a href="#">PeakListHandler</a>	PeakListHandler is APMLSAXHandler for parse apml and create PeakList object.
<a href="#">ProfileData</a>	ProfileData is a container class for profile_data element in APML, which is collection of consists of cluster profile