Hierarchical clustering of features

Samples

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numberOfWords(Features) >= 24
numberOfChars(Features) >= 167
sum(numbers(Features)) >= 31.5
numberOfChars(Keywords) >= 197
Features contains alternative
wordFrequencies(Keywords) for splicing inRange (0.0458 to 0.36)
wordFrequencies(Features) for alternative inRange (0.0818 to 0.18)
Features contains (4).
wordFrequencies(Features) for modified inRange (0.0818 to 0.16)
wordFrequencies(Keywords) for phosphoprotein inRange (0.1 to 0.27)
slidingSubsets(Features) contains (residue, 1)
numericPairs(Features) for (chain) >= 1.5
Features contains (3).
Features contains 5
wordCounts(Gene ontology (GO)) for go >= 15.5
numberOfChars(Gene ontology (GO)) >= 972
sum(numbers(Gene ontology (GO))) >= 2345276.0
max(numbers(Gene ontology (GO))) >= 1901383.5
Gene ontology (GO) contains protein
slidingSubsets(Gene ontology (GO)) contains (go, regulation, of)
wordFrequencies(Gene ontology (GO)) for activity inRange (0.0019 to 0.15)
min(numbersUSFormat(Gene ontology (GO))) < 1528.5
wordCounts(Gene ontology (GO)) for binding >= 2.5
wordFrequencies(Features) for variant inRange (0.0818 to 0.22)
Features contains variant
slidingSubsets(Features) contains (1, natural)
wordCounts(Protein names) for protein >= 1.5
wordCounts(Gene ontology (GO)) for membrane >= 2.5
numericPairs(Gene ontology (GO)) for (membrane) notInRange (9,614 to 19,897.5)
Gene ontology (GO) contains 0016020
numberOfWords(Involvement in disease) >= 49
Involvement in disease contains disease is
numericPairs(Features) for (natural) >= 2.5
wordFrequencies(Features) for mutagenesis inRange (0.0807 to 0.16)
Features contains mutagenesis
slidingSubsets(Features) contains (mutagenesis, natural)
Post-translational modification contains 0000269
slidingSubsets(Features) contains (helix, residue)
numericPairs(Features) for (modified) >= 4.5
slidingSubsets(Keywords) contains (structure, alternative)
slidingSubsets(Features) contains (alternative, sequence, beta)
skipgramsAndBiGrams(Keywords) contains (alternative, splicing)
Keywords contains structure
Features contains 6).
Gene ontology (GO) contains 0005829
wordFrequencies(Keywords) for cytoplasm inRange (0.0458 to 0.23)
wordCounts(Gene ontology (GO)) for protein >= 3.5
Gene ontology (GO) contains signal
Gene ontology (GO) contains 0005925
Features does not contain modified
wordFrequencies(Gene ontology (GO)) for go < 0.761
Gene ontology (GO) does not contain regulation
Gene ontology (GO) does not contain binding
wordFrequencies(Keywords) for reference >= 0.263
The percent of W in (Sequence) notInRange (0.23 to 1.35)
Features contains (1)
skipgramsAndBiGrams(Features) contains (1, 1)
Features does not contain 2
The percent of L in (Sequence) >= 11.266
Length < 346
elementCount(Sequence) for D < 12.5
elementCount(Sequence) for K < 13.5
elementCount(Sequence) for E < 10.5
wordFrequencies(Features) for region >= 0.227
wordFrequencies(Features) for peptide >= 0.161
wordFrequencies(Keywords) for signal >= 0.283
wordFrequencies(Gene ontology (GO)) for 0005615 >= 0.055
wordFrequencies(Features) for disulfide >= 0.168
wordFrequencies(Features) for glycosylation >= 0.178
wordFrequencies(Gene ontology (GO)) for receptor >= 0.201
Keywords == Cell membrane. Disulfide bond. G-protein coupled receptor. Glycoprotein. Membrane. Olfaction. Receptor. Reference proteome. Sensory transduction. Transducer. Trans
Keywords contains host
Tissue specificity contains specificity: ubiquitous
skipgrams(Gene ontology (GO)) contains (granule, *, go)
stemmedWordsWithoutCommonTerms(Features) contains initi
Features contains initiation
wordFrequencies(Features) for initiation inRange (0.0814 to 0.16)
slidingSubsets(Features) contains (residue, natural, variant)
Tissue specificity contains placenta
Tissue specificity contains skeletal muscle
Tissue specificity contains widely expressed
slidingSubsets(Keywords) contains (acetylation, alternative)
Keywords contains acetylation. alternative
skipgramsAndBiGrams(Keywords) contains (acetylation, alternative)
numericPairs(Keywords) contains (acetylation.)
slidingSubsets(Features) contains (erroneous, helix)
Tissue specificity contains specificity: testis
Gene ontology (GO) contains rna
slidingSubsets(Gene ontology (GO)) contains (go, transcription)
Gene ontology (GO) contains factor
wordFrequencies(Keywords) for nucleus inRange (0.0458 to 0.25)
Gene ontology (GO) contains 0005654
Keywords contains ubl
wordFrequencies(Keywords) for isopeptide inRange (0.11 to 0.21)
Gene ontology (GO) contains 0000785
Features contains terminal