

Summarizing Sequence Locations in a Patent Family [Patents PT-8]

In this example, we've used two new features in BizInt Smart Charts Reference Rows -- the "Create Subtable from Columns" tool and "Summarize All Values" rule -- to create a subtable summarizing key columns for sequences grouped by the Common Patent Family tool.

SUBTABLE SUMMARIZING RELATED SEQUENCES



Title	Database	Patent Assignee	Sequence Summary				
			Sequence ID	% Identity	Length	Location	
1. New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.	1.1 GENESEQ link	INCYTE CORP.	WO20040023973-5059	91.59	642	Claim 27; Page; 190pp; English.	1.1
	1.2 GPATPRT link		WO2004023973-5059	91.59	642	claim: 27; 28	1.2
1.1 GENESEQ		1.1 GENESEQ					
2. New isolated PRO nucleic acid, useful for diagnosing, treating, or preventing, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, systemic sclerosis, psoriasis, allergic disease, or asthma.	2.1 GENESEQ link	GENENTECH INC.	WO20050019258-1490	100.00	642	Claim 8; SEQ ID NO 1490; 158pp; English.	2.1
	2.2 GENESEQ link		WO20050016962-1490	100.00	642	Claim 8; SEQ ID NO 1490; 158pp; English.	2.2
	2.3 GPATPRT link		EP2014675-1490	100.00	642	probable disclosure (not found by automated parsing)	2.3
	2.4 GPATPRT link		US20070184444-1490	100.00	642	claim: 1; 2; 8; 19; 20; 21; 22; 23; 25; 26; 27	2.4
	2.5 GPATPRT link		US20110245090-1490	100.00	642	claim: 20; 23; 28; 31; 36; 38; 40	2.5
	2.6 GPATPRT link		WO2005016962-1490	100.00	642	claim: 2; 8; 19; 20; 21; 22; 23; 25; 26	2.6
	2.7 GPATPRT link		WO2005019258-1490	100.00	642	claim: 1; 2; 7; 19; 20; 21; 22; 23; 25; 26; 27	2.7
	2.8 GPATPRT link		EP2182006-1490	100.00	642	claim: 1; 3; 4; 5; 6; 7; 9; 10; 11	2.8
2.1 GENESEQ		2.1 GENESEQ					
3. Improved yeast cellular assay system for detecting e.g. polycyclic aromatic hydrocarbons, dioxins, PCBs comprising additional cellular proteins from the AHR signaling pathway which improve the sensitivity and maximal	3.1 GENESEQ link	WISCONSIN ALUMNI RES FOUND.		97.04	642	Example; Fig 6C; 26pp; English.	3.1
	3.2 GENESEQ link			99.84	642	Example; Fig 6C; 26pp; English.	3.2

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How did we create this?

SEARCHES:

- GenomeQuest – sequence search from GQPAT and/or GENESEQ.

BIZINT SMART CHARTS FOR PATENTS

1. Import each set of results into BizInt Smart Charts for Patents to create .chp files.
2. Use the **File | Combine** feature to create a single combined chart. Run the Identify Common Patent Families tool.
3. Display the Seq. ID Number, Percentage Identity, Subject Length, and Patent Sequence Location columns (**View | Columns**).
4. Change the title on the Patent Sequence Location column to “Location” (by double-clicking on the column header). Repeat to rename the Seq. ID Number column to “Sequence ID”, Percentage Identity to “% Identity”, and Subject Length to “Length”. *You need to give columns short names now, because you can't change them after creating the subtable in step 8, below.*
5. Save the .chp file.
6. Send the chart to Reference Rows using the toolbar icon (or **File | Send to Reference Rows**).

BIZINT SMART CHARTS REFERENCE ROWS

7. During the Create Reference Rows wizard, make GENESEQ the top-ranked database (if present). *This will cause the Derwent enhanced titles and normalized assignee to be preferred in the final report. This is faster than changing the database ranking in the columns one at a time*
8. When the wizard finishes, run **Tools | Create Subtable from Columns**.
9. Select the Sequence ID, % Identity, Length, and Location columns in that order and press Apply. A new column will be created.
10. Double click on the column header to rename the new column from Untitled Subtable to “Sequence Summary”.
11. Use **View | Columns** to hide the original Sequence ID, % Identity, Length, and Location columns.
12. Use **Reference Rows | Column Rules...** to set the rule for the new column to Summarize All Values.
13. Use **File | Export** to export the report to HTML and see the subtable column summarizing the sequence data.