	FM-H	FM- HF - BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	
DBLPXML	0.651	70	1.192	32	1.642	34	1.770	17	
DNA	0.233	29	0.601	28	1.112	79	1.330	24	
ENGLISH	0.598	61	1.247	38	1.684	69	2.239	27	
PROTEINS SOURCES	$0.545 \\ 0.747$	56 73	1.362 1.435	53 39	1.559 1.761	89 53	2.805 2.439	$\frac{48}{26}$	

Table 1: Time in μ sec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -DUSE_HP -msse4.2 -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

	FM-H	FM-HF-BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	
DBLPXML	0.923	70	1.158	32	2.660	34	1.765	17	
DNA	0.321	29	0.606	28	1.268	79	1.334	24	
ENGLISH	0.783	61	1.306	38	1.995	69	2.242	27	
PROTEINS SOURCES	$0.708 \\ 0.955$	56 73	1.387 1.501	53 39	1.891 2.205	89 53	2.774 2.424	48 26	

Table 2: Time in μ sec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -DPOPCOUNT_TL -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

	FM-H	FM-HF-BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	
DBLPXML	0.730	70	1.151	32	2.006	34	1.753	17	
DNA	0.271	29	0.620	28	1.266	79	1.377	24	
ENGLISH	0.663	61	1.268	38	1.863	69	2.232	27	
PROTEINS SOURCES	$0.595 \\ 0.839$	56 73	1.331 1.512	53 39	1.766 2.044	89 53	2.782 2.472	$\frac{48}{26}$	

Table 3: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

	FM-H	FM-HF-BV		$FM-HF-R^3-15$		FM-RLMN		$F-R^3-63$
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)
DBLPXML	1.390	70	2.125	32	5.490	34	4.379	17
DNA	0.559	29	1.183	28	2.112	79	3.165	24
ENGLISH	1.216	61	2.285	38	3.073	69	5.301	27
PROTEINS	1.100	56	2.493	53	2.941	89	5.945	48
SOURCES	1.478	73	2.614	39	3.413	53	5.921	26

Table 4: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -00 -DNDEBUG.

	FM-H	FM- HF - BV		$FM-HF-R^3-15$		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	
DBLPXML	0.773	70	1.188	32	2.204	34	1.786	17	
DNA	0.277	29	0.621	28	1.215	79	1.352	24	
ENGLISH	0.686	61	1.300	38	1.874	69	2.238	27	
PROTEINS SOURCES	$0.611 \\ 0.839$	56 73	1.388 1.494	53 39	1.795 1.982	89 53	2.714 2.467	$\frac{48}{26}$	

Table 5: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -01 -DNDEBUG.

	FM-H	FM-HF-BV		FM - HF - R^3 - 15		FM-RLMN		$FM-HF-R^3-63$	
	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	Time (μs)	Space (%)	
DBLPXML	0.639	70	1.161	32	1.620	34	1.746	17	
DNA	0.233	29	0.599	28	1.099	79	1.337	24	
ENGLISH	0.598	61	1.243	38	1.669	69	2.231	27	
PROTEINS	0.537	56	1.360	53	1.568	89	2.768	48	
SOURCES	0.738	73	1.489	39	1.796	53	2.486	26	

Table 6: Time in μsec per pattern symbol in a count query. Index space as fraction of original file size. Compile options: -msse4.2 -09 -funroll-loops -fomit-frame-pointer -ffast-math -DNDEBUG.

Identifier	sdsl class
FM-HF-BV	csa_wt <wt.huff<bit.vector, rank_support_v5<="">, select_support_scan<>, select_support_scan<0>>, 1<<20, 1<<20></wt.huff<bit.vector,>
FM-HF-R ³ -15	csa_wt <wt_huff<rrr_vector<15> >, 1<<20, 1<<20></wt_huff<rrr_vector<15>
$FM-HF-R^3-63$	csa_wt <wt_huff<rrr_vector<63> >, 1<<20, 1<<20></wt_huff<rrr_vector<63>
FM-RLMN	csa_wt <wt_rlmn<>>, 1<<20, 1<<20></wt_rlmn<>

Table 7: Index identifier and corresponding sdsl-type.