Exhibit F-12: Roccatano

An article entitled, "Development of a Parallel Molecular Dynamics Code on SIMD Computers: Algorithm for U
Criterion," by Roccatano et al. ("Roccatano") was published in the Journal of Computational Chemistry, vol. 19,
1998 and is therefore prior art to U.S. Patent No. 7,620,800 ("'800 Patent") at least under 35 U.S.C. §§ 102(a) an

As described in detail below, Roccatano anticipates the asserted claim(s) of the '800 Patent. To the extent it is fo
does not expressly disclose certain limitations in the asserted claim, such limitations are inherent. Furthermore, t
found that Roccatano does not anticipate the asserted claim, Roccatano renders the asserted claim obvious, either
combination with other prior art identified in the cover pleading or herein.

This chart is subject to all reservations, objections, and disclaimers in Microsoft's Invalidity Contentions and any
supplement, or modification thereof, which are incorporated herein by reference in their entirety.

Asserted Claim of '800 Patent	**Exemplary Disclosure of Roccatano**
[1A] A method for data processing in a reconfigurable computing system, the reconfigurable computing system comprising at least one reconfigurable processor, the reconfigurable processor comprising a plurality of functional units, said method comprising:	At least under Plaintiff's apparent theories of infringement and interpretations alleging that any of Defendant's accused products satisfy this claim limitation in combination with one or more references, discloses: Roccatano at Abstract: "In recent years several implementations of molecular have been reported on multiple instruction multiple data MIMD machines. Ho implementations of MD codes on single instruction multiple data SIMD mach reported. The difficulty in using pair lists of nonbonded interactions is the ma codes for SIMD machines, such that, generally, the full connectivity computa We present an algorithm, the global cut-off algorithm GCA, which permits th SIMD machines. GCA is based on a probabilistic approach and requires the c simultaneously verified on all nodes of the machine. The MD code used was t GROMOS package; only the routines involved in the pair lists and in the com interactions were rewritten for a parallel architecture. The remaining calculati the host computer. The algorithm has been tested on Quadrics computers for c 128, and 512 processors and for systems of 4000, 8000, 15,000, and 30,000 pa Roccatano at 686: "Classical molecular dynamics MD is used to study the pro solids, and molecules. The Newton equation of motion for each particle of the numerical integration and its trajectory is obtained. From this microscopic poi

	microscopic and macroscopic properties can be obtained. The need for numer the time step to the femtosecond scale and makes MD simulation a very time Therefore, considerable efforts have been concentrated on optimizing MD coc computers of different architectures." Roccatano at 686: "Less work has been done using SIMD systems. In general full connectivity computation; that is, all atom pair interactions are calculated long-range force systems. This is due to the difficulty of using pair lists of nor SIMD machines with no local addressing. In the present study we propose an algorithm that permits the use of pair lists SIMD machine with no local addressing. The algorithm requires simultaneous step and geometric decomposition methods. In addition, the systolic loop met reduce computation time. The method was tested on Quadrics computers, a class of SIMD machines dev Alenia Spazio, for configurations of 32, 128, and 512 processors." To the extent Plaintiff asserts this limitation is not expressly or inherently disc apparent claim construction, or any other claim construction, the claimed subj been obvious to a person of ordinary skill in the art considering this reference the knowledge of one of ordinary skill in the art at the time of the alleged inve disclosures in one or more of the references identified in Section I.B.2 of the c
[1B] transforming an algorithm into a data driven calculation that is implemented by said reconfigurable computing system at the at least one reconfigurable processor;	At least under Plaintiff's apparent theories of infringement and interpretations alleging that any of Defendant's accused products satisfy this claim limitation in combination with one or more references, discloses: Roccatano at 688: "GEOMETRIC DECOMPOSITION The assignment of the atoms to the nodes is obtained by a dynamically geome such a way that the same number of atoms is assigned to each node. In what f decomposition for a bidimensional case; the extension to a third dimension is the bidimensional box of Figure 1a and a 2D parallel topology of $n = n_x \times n_y$

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$n_y = 2$, the box is first divided into n_x boxes along the x-axis, as shown in Fig
containing the same number of atoms. Each box is successively divided into r
axis in such a way that each one of the $n_x = n_y$ boxes contains the same numb
When, as in a real case, a third dimension exists, a successive division along t
performed.

It is obvious that, before performing any division along a given axis, it is nece
atoms of each box along that axis. The density of a molecular system, such as
uniform; thus, the boxes do not have the same axis lengths. However, these di
significantly reduce the efficiency of the GCA described in what follows."

Roccatano at Figure 1:

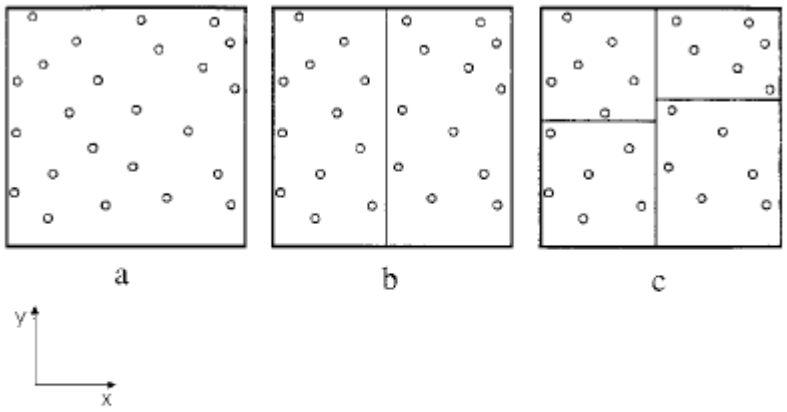

FIGURE 1. Domain decomposition of the molecular system in boxes with the same number of atoms, for a bidimensional case.

Roccatano at 688: "Quadrics topology makes it possible to use a systolic loop
nonbonded interactions between the atoms assigned to the different nodes. Th
is one of the most efficient algorithms for calculation of two-body interaction

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	machines.14, 16, 24, 25 The systolic loop algorithm passes the coordinates of ring of P processors in P/2 steps, such that half of the coordinates passes every once transient atoms. Each node also stores the coordinates of a group of aton system resident atoms. During the systolic cycle each processor evaluates and interactions of the resident atoms with the transient ones. Only half of the ato computational node as a consequence of the reciprocity of the interactions. The systolic loop path for a 32-node Quadrics machine is shown in Figure 2. two nodes along the y and z directions and eight along the x direction. The geometric decomposition of the system permits limitation of the search fo interactions only to the neighboring processors nearer than the cut-off radius, the number of nodes and on the system size, it is generally not necessary to pe systolic loop. The computed forces are passed back to the owning processor t force." Roccatano at Figure 2:

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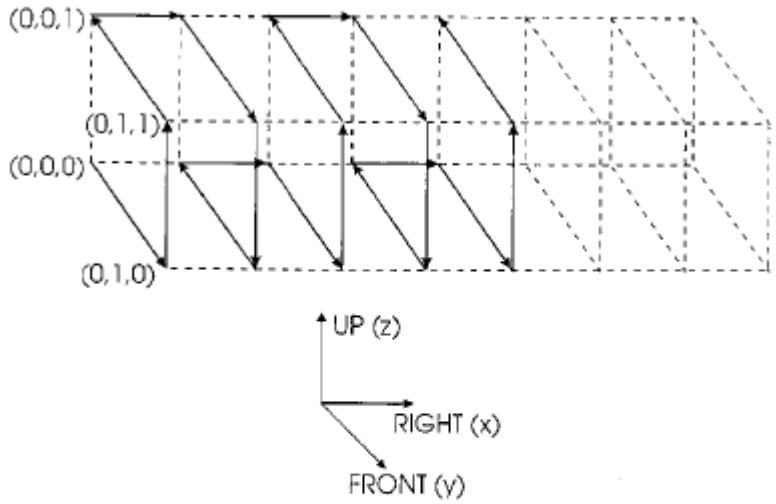

FIGURE 2. Systolic loop path for node (0, 0, 0) of a 32-node Quadrics machine. The transient groups of atoms visit only four neighboring $y-z$ planes, based on Newton's third law.

Roccatano at Figure 3:

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