TABLE S1 Comparison of Different Software Packages for Calculation of Volumes of Proteins

Software	Volume Type	Web-Server	vdW radii	vdW radii selectable	Explicit Hydrogens	Probe size adjustable	Algorithm	Issues
ProteinVolume	V_{MS} V_{Void} V_{VDW}	Yes [a]	All-atom	Yes	Yes	Yes	Flood-Filling	
MCVOL [1]	V_{MS} V_{VDW} V_{Void}	No	All-atom	Yes	Yes	Yes	Monte Carlo	Slight deviation per run (<0.5%)
VOIDOO [2]	V_{Vdw} V_{SA} V_{Void}	No	All-atom	Yes	Yes	Yes	3D-grid	No V_{MS}
AVP [3]	V_{Void}	No	United	No	Yes	Yes	3D-grid	No V_{MS} AVP produces V_{Void} volumes are 30% lower than all other programs.
^{3}V [4]	V_{MS} V_{VDW} V_{Void}	Yes [b]	All-atom	Yes (not for web-server)	Yes	Yes	3D-grid	Web server has a max grid resolution of 0.5A, which produces V_{MS} that is 10-15% larger than other software.
Voronoia [5]	V_{MS} V_{Void} V_{VDW}	Yes [c]	United	No [e]	No	Yes	3D-grid	Large overestimation of V_{MS} due to radii set. Some heavy atoms missing from volume calculation.
VADAR [6]	V_{MS} + parts of V_E	Yes [d]	United	No [f]	No	No	Voronoi/ Delaney	No V_{MS}
GEPOL [7]	V_{MS} V_{VDW}	No	All-atom	Yes	Yes	N/A	Numerical tessellation	Limit to 100,000 surface points
MSROLL [8]	V_{MS} V_{VDW} V_{Void}	No	All-atom	Yes	Yes	N/A	Analytical	Susceptible to geometrical degeneracies
VORLUME [9]	V_{Vdw} V_{SA}	No	United	No	No	N/A	Alpha-Shapes	No V_{MS}
ALPHAVOL [10]	V_{Vdw}, V_{SA}	No	United	No	Polar Only	N/A	Alpha-Shapes	No V_{MS} , limit 500 amino acid residues

a ProteinVolume - gmlab.bio.rpi.edu
b 3V - http://3vee.molmovdb.org/volumeCalc.php
c Voronoia - http://bioinformatics.charite.de/voronoia/index.php?site=input
d VADAR - http://vadar.wishartlab.com/
e selectable from ProtOr, or Stouten
f selectable from Chothia, Eisenberg, Richards or Shrake.

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