

## Physicochemical and Structural Investigation of L-Threonine/Glycerol-based Deep Eutectic Solvent Using Experimental and Molecular Modelling Approaches.

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### List of Supporting Tables

**Table S1.** IR wavenumbers and intensities of L-threonine, Glycerol, and four cluster conformers (A, B, C, D) of 1:3 Thr: Gly DES clusters

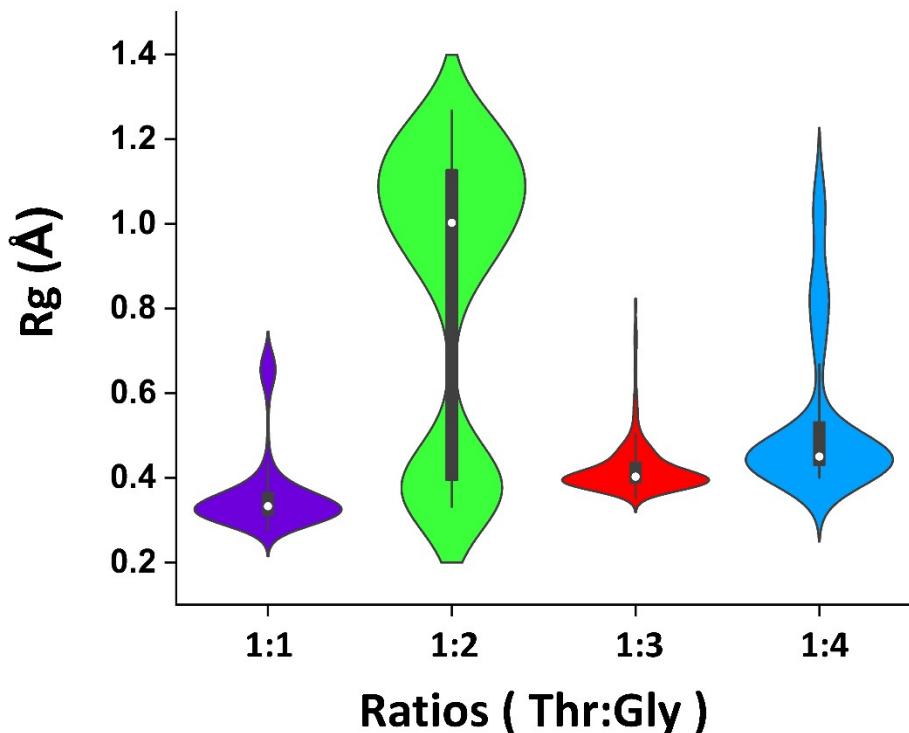
	Gly	Intensity		Thr	Intensity		A	Intensity		B	Intensity		C	Intensity		D	Intensity
u (OH - free )	3410	48.21	u (OH-free)	3306	87.71	u (OH-free)	3380	55.27	u (OH-free)	3386	42.54	u (OH-free)	3363	78.2	u (OH-free)	3409	41.58
						u (OH-bond.)	3200	355.86	u (OH-bond.)	3277	244.8	u (OH-bond.)	3193	396.88	u (OH-bond.)	3257	323.26
															u (OH-bond.)	2912	666.17
		uas (NH)	3156	9.44	uas (NH)	N/A		uas (NH)	3138	29.86	uas (NH)	N/A		uas (NH)	3137	30.94	
		us (NH)	3077	7.29	us (NH)	3105	76.53	us (NH)	3076	17.2	us (NH)	3080	29.32	us (NH)	3069	61.81	
uas (CH)	2867	50.38	uas (CH)	3013	22.66	uas (CH)	2977	28.39	uas (CH)	2976	32.77	uas (CH)	2969	29.76	uas (CH)	2982	28.85
us (CH)	2920	62.36	us (CH)	2839	50.48	us (CH)	2887	43.39	us (CH)	2891	43.31	us (CH)	2899	37.46	us (CH)	2899	43.92
		u (C=O)	1780	41.77	u (C=O)	1754	525.27	u (C=O)	1787	290.8	u (C=O)	1749	320.12	u (C=O)	1732	334.11	
		S (NH2)	1602	33.71	S (NH2)	1611	45.46	S (NH2)	1624	32.98	S (NH2)	1618	31.85	S (NH2)	1626	20.46	
u(C-C) + u(C-O) + S (C-C)	1059	66.71	u (C-C)	1048	60.93	u (C-C)	1440	27.21	u (C-C)	1408	29.07	u (C-C)	1390	56.65	u (C-C)	1417	33.38
			δ (COOH)	1105 - 1384	49.61	δ (COOH)	1157 - 1418	28.07	δ (COOH)	1118 - 1336	29.37	δ (COOH)	1173 - 1397	24.42	δ (COOH)	1214 - 1446	28.76
β (OH)	1033 - 1397	37.51	β (OH)	1048 - 1287	54.78	β (OH)	1013 - 1474	33.15	β (OH)	1023 - 1441	35.79	β (OH)	1017 - 1463	33.69	β (OH)	1024 - 1446	35.07

			$\nu$ (C-O) + $\nu$ (C-N)	1107	21.08	$\nu$ (C-N)	1160	292.06	$\nu$ (C-N)	1118	202.94	$\nu$ (C-N)	1132	56.657	$\nu$ (C-N)	1176	26.65
						$\nu$ (C-O)	1052	130.71	$\nu$ (C-O)	1076	254.07	$\nu$ (C-O)	1060	57.82	$\nu$ (C-O)	1066	54.37
			W (NH <sub>2</sub> )	888	56.21	W (NH <sub>2</sub> )	847	30.95	W (NH <sub>2</sub> )	872	25.27	W (NH <sub>2</sub> )	848	57.1	W (NH <sub>2</sub> )	882	41.58
$\gamma$ (OH)	544	55.04	$\gamma$ (OH)	535- 724	58.61	$\gamma$ (OH)	529- 874	74.86	$\gamma$ (OH)	519- 860	79.91	$\gamma$ (OH)	523- 862	77.2	$\gamma$ (OH)	524- 915	61.04

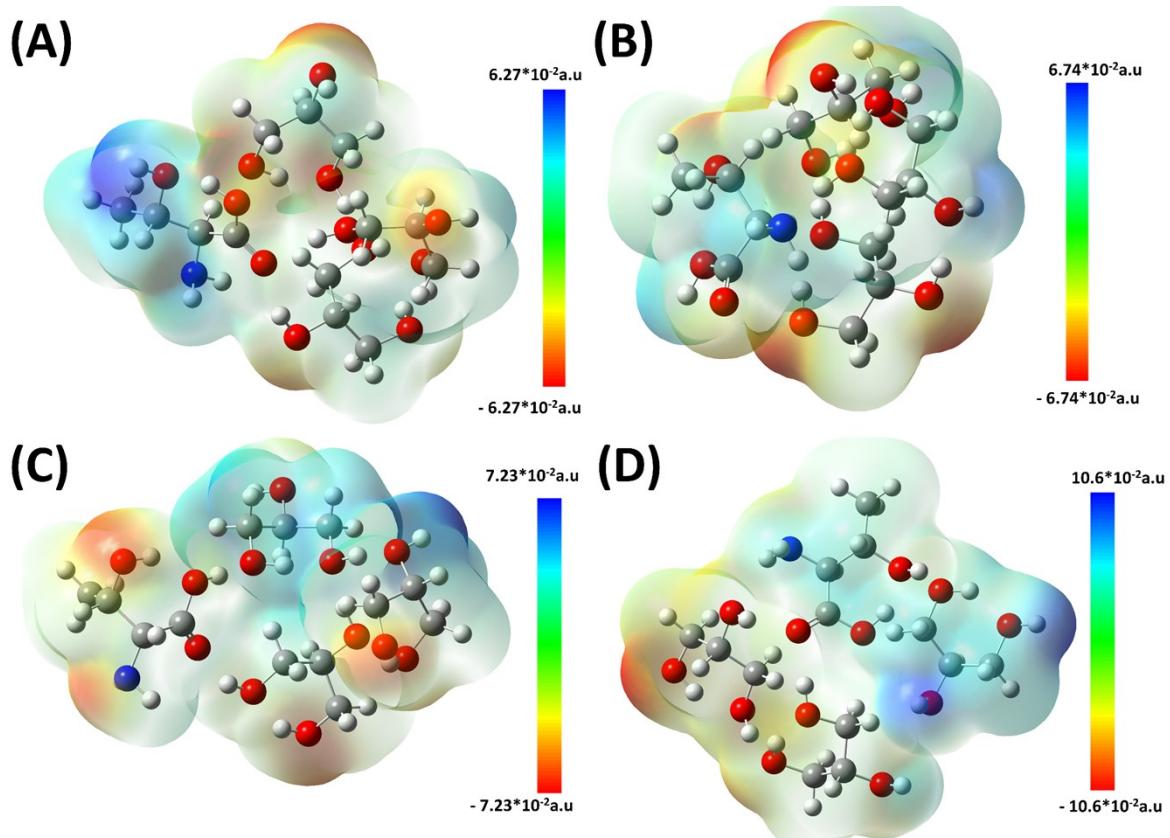
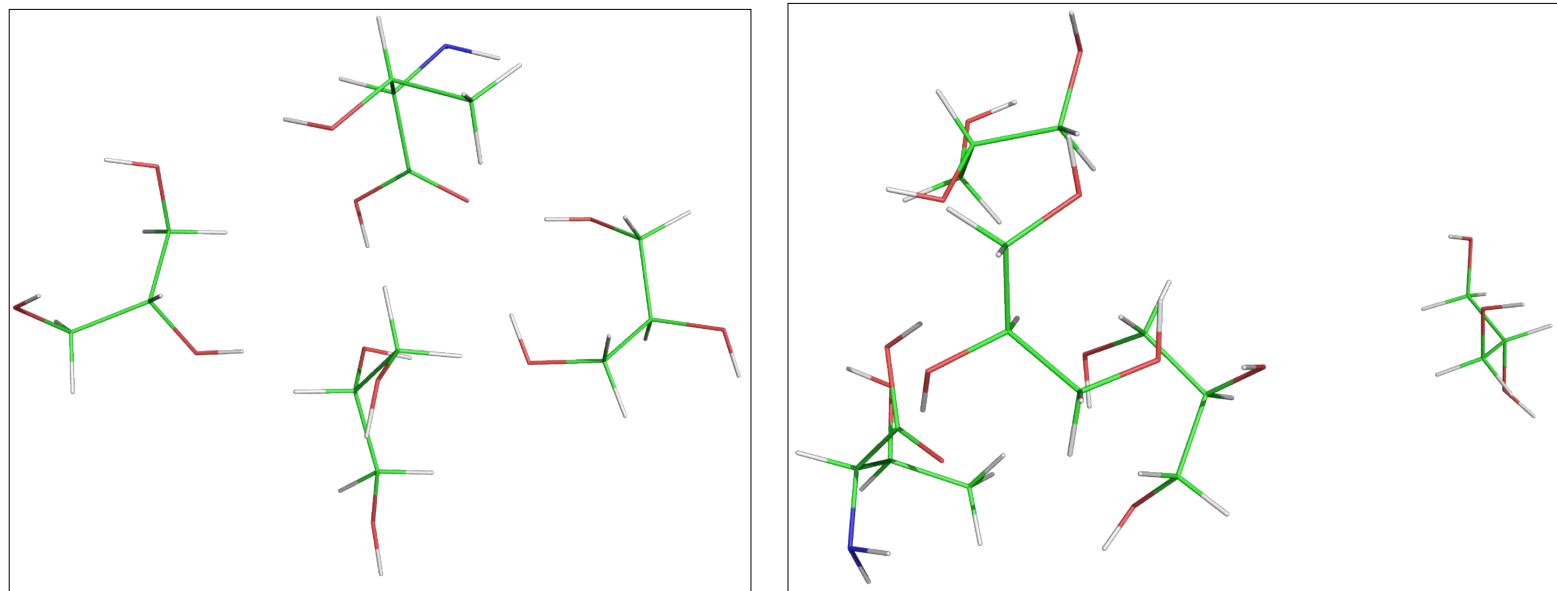
$\nu_{as}$  = asymmetric stretching;  $\nu_s$  = symmetric stretching;  $\beta$  = In-plane bending;  $\gamma$  = out-plane bending;  $\delta$  = deformation; W = wagging; S = scissoring

**Table S2.** Gibbs free energy change  $\Delta G$  and electronic energy change  $\Delta E$  (in kJ/mol) of L-Threonine, Glycerol and the DES's Conformers Calculated using the  $\omega$ B97xD/6-311G(d,p) Level of Theory in the Gas Phase and with Standard Conditions

Parameter	Conformer A	Conformer B	Conformer C	Conformer D
$\Delta G$ (kJ/mol)	-53.9908	-43.6043	-50.2074	-48.0046
$\Delta E$ (kJ/mol)	-241.882	-231.711	-241.129	-224.869



**Figure S1.** The radius of gyration of different pairs of threonine and glycerol

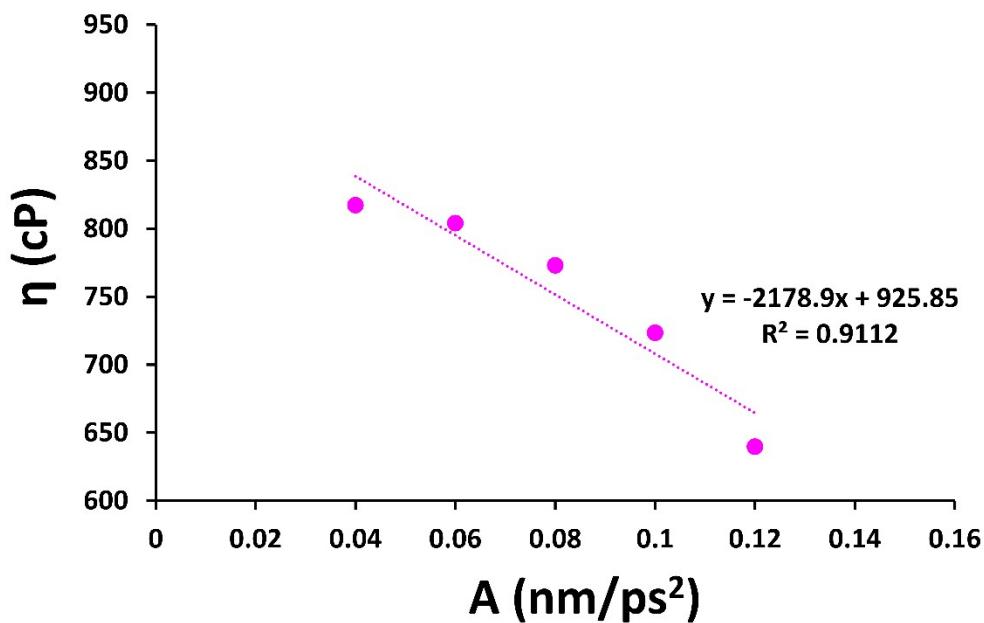


**Figure S2.** Representative conformers of 1:3 (left) and 1:4 pair (right)

**Figure S3.** The surface electrostatic potential is created by mapping the total density onto the electrostatic potential of conformers (A-D). The color code determines the electrostatic potential where: red= the most negative, blue = the most positive, and green = zero-potential region.

### S1.1 The Surface Electrostatic Potential

The surface electrostatic potential gives information regarding the density of electrons in space around the molecule and eventually plays an important role in unrevealing the prominent non-covalent interaction sites<sup>1,2</sup>. The surfaces were generated and plotted in Gauss View 5. In clusters A and B, the doubly bonded oxygen atom of Threonine is shown in yellow, indicating a strong negative electrostatic potential, while in clusters C and D, it is light yellow, suggesting a moderate negative potential. Nearby hydrogen atoms of Glycerol are very light blue, representing a very low positive potential. This facilitates bonding between these atom pairs from both molecules, which can endure steric hindrance<sup>3</sup>. The hydrogen atoms attached to the oxygen of Threonine are light blue in clusters A, C, and D. In contrast, the oxygens of Glycerol are red in cluster A and very light yellow in the other two clusters, reflecting strong non-bonding interactions in the first type and moderate interactions in the second. In cluster B, the single-bonded oxygen on Threonine is red, and the corresponding hydrogen atoms (attached to carbon) are mostly very light blue, suggesting that the bonding here would be of moderate to low intensity. The nitrogen atom's surface in cluster B is light blue, with nearby hydrogens (attached to O or C) also very light blue, indicating that any potential non-bonding interactions between these atoms would be very weak. For Glycerol bonding interactions, atoms C-H, O-H, and O exhibit various patterns, allowing for a range of non-bonding interactions from low to strong.



**Figure S4.** Extrapolated Viscosity of glycerol (NEMD)

**Modified Force field Parameters of L-threonine.**

;  
; GENERATED BY LigParGen Server  
; Jorgensen Lab @ Yale University  
; Scaled by a factor of 0.8 by The Red-Green Research Center  
; rgrcdhakalab@gmail.com

[ moleculetype ]

; Name nrexcl

THM 3

[ atoms ]

; nr type resnr residue atom cgnr charge mass

1	opls_800	1	THM	C00	1	0.36448	12.0110
2	opls_801	1	THM	C01	1	0.07144	12.0110
3	opls_802	1	THM	C02	1	0.152	12.0110
4	opls_803	1	THM	C03	1	-0.19712	12.0110
5	opls_804	1	THM	O04	1	-0.3972	15.9990
6	opls_805	1	THM	O05	1	-0.43264	15.9990
7	opls_806	1	THM	O06	1	-0.54768	15.9990
8	opls_807	1	THM	N07	1	-0.75336	14.0070
9	opls_808	1	THM	H08	1	0.28984	1.0080
10	opls_809	1	THM	H09	1	0.28984	1.0080
11	opls_810	1	THM	H0A	1	0.35144	1.0080
12	opls_811	1	THM	H0B	1	0.36208	1.0080
13	opls_812	1	THM	H0C	1	0.0808	1.0080

14 opls\_813 1 THM HOD 1 0.0808 1.0080  
15 opls\_814 1 THM HOE 1 0.1208 1.0080  
16 opls\_815 1 THM HOF 1 0.08208 1.0080  
17 opls\_816 1 THM HOG 1 0.0808 1.0080

[ bonds ]

2 1 1 0.1522 265265.600  
3 2 1 0.1529 224262.400  
4 3 1 0.1529 224262.400  
5 1 1 0.1229 476976.000  
6 1 1 0.1364 376560.000  
7 3 1 0.1410 267776.000  
8 2 1 0.1448 319657.600  
9 8 1 0.1010 363171.200  
10 8 1 0.1010 363171.200  
11 7 1 0.0945 462750.400  
12 6 1 0.0945 462750.400  
13 4 1 0.1090 284512.000  
14 4 1 0.1090 284512.000  
15 2 1 0.1090 284512.000  
16 3 1 0.1090 284512.000  
17 4 1 0.1090 284512.000

[ angles ]

; ai aj ak funct c0 c1 c2 c3  
1 2 3 1 111.100 527.184  
2 3 4 1 112.700 488.273  
2 1 5 1 120.400 669.440  
2 1 6 1 108.000 585.760  
2 3 7 1 109.500 418.400  
1 2 8 1 111.200 669.440

2	8	9	1	109.500	292.880
2	8	10	1	109.500	292.880
3	7	11	1	108.500	460.240
1	6	12	1	113.000	292.880
3	4	13	1	110.700	313.800
3	4	14	1	110.700	313.800
1	2	15	1	109.500	292.880
2	3	16	1	110.700	313.800
3	4	17	1	110.700	313.800
14	4	17	1	107.800	276.144
13	4	14	1	107.800	276.144
9	8	10	1	106.400	364.845
3	2	15	1	110.700	313.800
7	3	16	1	109.500	292.880
4	3	7	1	109.500	418.400
13	4	17	1	107.800	276.144
3	2	8	1	109.470	470.282
5	1	6	1	121.000	669.440
8	2	15	1	109.500	292.880
4	3	16	1	110.700	313.800

[ dihedrals ]

; IMPROPER DIHEDRAL ANGLES

;	ai	aj	ak	al	funct	c0	c1	c2	c3	c4	c5
6	1	2	5	4		180.000	43.932	2			

[ dihedrals ]

; PROPER DIHEDRAL ANGLES

;	ai	aj	ak	al	funct	c0	c1	c2	c3	c4	c5
4	3	2	1	3		-4.960	6.286	1.310	-2.636	-0.000	0.000

10	8	2	1	3	-1.268	3.021	1.745	-3.498	-0.000	0.000
9	8	2	1	3	-1.268	3.021	1.745	-3.498	-0.000	0.000
9	8	2	3	3	-1.268	3.021	1.745	-3.498	-0.000	0.000
10	8	2	3	3	-1.268	3.021	1.745	-3.498	-0.000	0.000
15	2	1	5	3	0.000	0.000	0.000	-0.000	-0.000	0.000
15	2	1	6	3	0.000	0.000	0.000	-0.000	-0.000	0.000
16	3	2	1	3	-0.209	-0.628	0.000	0.837	-0.000	0.000
17	4	3	2	3	0.628	1.883	0.000	-2.510	-0.000	0.000
13	4	3	2	3	0.628	1.883	0.000	-2.510	-0.000	0.000
14	4	3	2	3	0.628	1.883	0.000	-2.510	-0.000	0.000
15	2	3	4	3	0.628	1.883	0.000	-2.510	-0.000	0.000
16	3	4	14	3	0.628	1.883	0.000	-2.510	-0.000	0.000
16	3	2	15	3	0.628	1.883	0.000	-2.510	-0.000	0.000
16	3	4	13	3	0.628	1.883	0.000	-2.510	-0.000	0.000
17	4	3	16	3	0.628	1.883	0.000	-2.510	-0.000	0.000
16	3	2	8	3	-4.096	5.088	2.966	-3.958	-0.000	0.000
14	4	3	7	3	0.979	2.937	0.000	-3.916	-0.000	0.000
13	4	3	7	3	0.979	2.937	0.000	-3.916	-0.000	0.000
17	4	3	7	3	0.979	2.937	0.000	-3.916	-0.000	0.000
15	2	3	7	3	0.979	2.937	0.000	-3.916	-0.000	0.000
15	2	8	9	3	0.837	2.510	0.000	-3.347	-0.000	0.000
15	2	8	10	3	0.837	2.510	0.000	-3.347	-0.000	0.000
16	3	7	11	3	0.736	2.209	0.000	-2.946	-0.000	0.000
12	6	1	2	3	26.150	-3.138	-23.012	-0.000	-0.000	0.000
12	6	1	5	3	23.012	0.000	-23.012	-0.000	-0.000	0.000
11	7	3	4	3	-0.444	3.833	0.728	-4.117	-0.000	0.000
11	7	3	2	3	-0.444	3.833	0.728	-4.117	-0.000	0.000
8	2	1	5	3	0.000	0.000	0.000	-0.000	-0.000	0.000
8	2	1	6	3	14.435	-11.004	-3.431	-0.000	-0.000	0.000
8	2	3	4	3	3.335	-1.552	2.820	-4.602	-0.000	0.000

8	2	3	7	3	16.736	-16.736	0.000	-0.000	-0.000	0.000
5	1	2	3	3	0.000	0.000	0.000	-0.000	-0.000	0.000
6	1	2	3	3	5.318	0.732	-2.284	-3.766	-0.000	0.000
7	3	2	1	3	-12.929	12.929	0.000	-0.000	-0.000	0.000

[ pairs ]

1	4	1
3	5	1
1	7	1
3	6	1
1	9	1
1	10	1
4	8	1
3	9	1
5	8	1
3	10	1
2	11	1
6	8	1
2	12	1
7	8	1
4	11	1
2	13	1
2	14	1
5	12	1
1	16	1
4	15	1
2	17	1
7	13	1
5	15	1
7	14	1

6 15 1  
7 15 1  
9 15 1  
8 16 1  
7 17 1  
10 15 1  
11 16 1  
13 16 1  
14 16 1  
15 16 1  
16 17 1

## DATA AND SOFTWARE AVAILABILITY

Server/Software	Function	Website
Gaussian09	Optimization, frequency and Gibbs free energy calculation	<a href="https://gaussian.com/glossary/g09/">https://gaussian.com/glossary/g09/</a>
Biovia Discovery Studio 2024	Visualization of compound models and interactions	<a href="https://www.3ds.com/products/biovia/discovery-studio/">https://www.3ds.com/products/biovia/discovery-studio/</a>
Chimera X 1.3	Visualization of complexes	<a href="https://www.cgl.ucsf.edu/chimerax/download.html">https://www.cgl.ucsf.edu/chimerax/download.html</a>
Origin Pro (2021)	Plotting data, PCA	<a href="https://www.originlab.com/2021">https://www.originlab.com/2021</a>
Microsoft Excel	Plotting data	<a href="https://www.microsoft.com/en-us/microsoft-365/microsoft-office">https://www.microsoft.com/en-us/microsoft-365/microsoft-office</a>
GROMACS 2022.4	Molecular Dynamics Simulation And data analysis	<a href="https://manual.gromacs.org/documentation/2022.4/index.html">https://manual.gromacs.org/documentation/2022.4/index.html</a>
LigParGen server	Forcefield parameters of L-threonine	<a href="https://zarbi.chem.yale.edu/lipgargen">https://zarbi.chem.yale.edu/lipgargen</a>
Peer Reviewed Article	Forcefield parameters of Glycerol	<a href="https://pubs.acs.org/doi/10.1021/acs.jpcb.8b06647">https://pubs.acs.org/doi/10.1021/acs.jpcb.8b06647</a>

Travis code	Analyzing RDF, CDF, SDF and MSD	<a href="http://www.travis-analyzer.de">http://www.travis-analyzer.de</a>
VMD 1.9.3	Analyzing interactions and SDF	<a href="https://www.ks.uiuc.edu/Research/vmd">https://www.ks.uiuc.edu/Research/vmd</a>

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- 3 M. K. Chaudhary, A. Srivastava, K. K. Singh, P. Tandon and B. D. Joshi, *Comput. Theor. Chem.*, 2020, **1191**, 113031.