Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2023 – 07:44 PM EDT

PDB ID	:	1PWH
Title	:	Rat Liver L-Serine Dehydratase- Complex with PYRIDOXYL-(O-METHYL-SERINE)-5-MONOPHOSPHATE
Authors	:	Yamada, T.; Komoto, J.; Takata, Y.; Ogawa, H.; Takusagawa, F.
Deposited on	:	2003-07-01
Resolution	:	2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

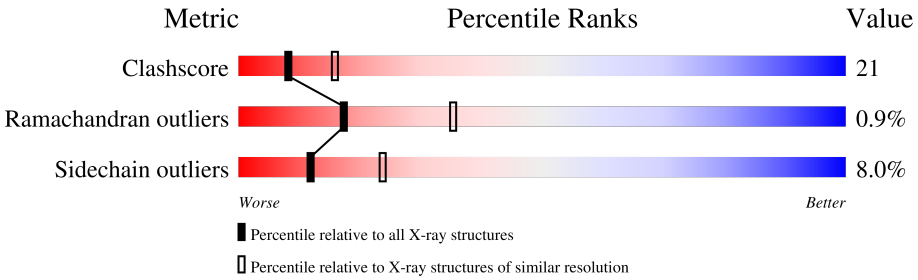
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	327	63% 31% 6%
1	B	327	67% 29% .
1	C	327	65% 31% .
1	D	327	65% 31% .

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9883 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

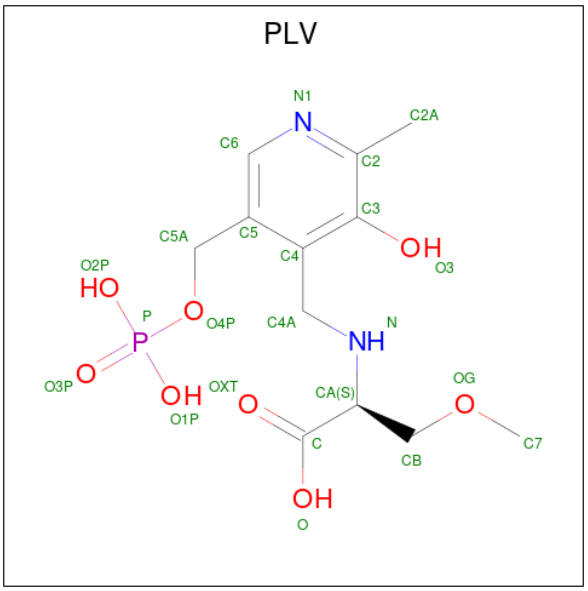
- Molecule 1 is a protein called L-serine dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2417	1540	410	453	14			
1	B	327	Total	C	N	O	S	0	0	0
			2417	1540	410	453	14			
1	C	327	Total	C	N	O	S	0	0	0
			2417	1540	410	453	14			
1	D	327	Total	C	N	O	S	0	0	0
			2417	1540	410	453	14			

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		
2	B	1	Total	K	0	0
			1	1		
2	C	1	Total	K	0	0
			1	1		
2	D	1	Total	K	0	0
			1	1		

- Molecule 3 is N-({3-HYDROXY-2-METHYL-5-[(PHOSPHONOOXY)METHYL]PYRIDIN-4-YL}METHYL)-O-METHYL-L-SERINE (three-letter code: PLV) (formula: $C_{12}H_{19}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	12	2	8	1		
3	B	1	Total	C	N	O	P	0	0
			23	12	2	8	1		
3	C	1	Total	C	N	O	P	0	0
			23	12	2	8	1		
3	D	1	Total	C	N	O	P	0	0
			23	12	2	8	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		
4	B	34	Total	O	0	0
			34	34		
4	C	21	Total	O	0	0
			21	21		
4	D	25	Total	O	0	0
			25	25		

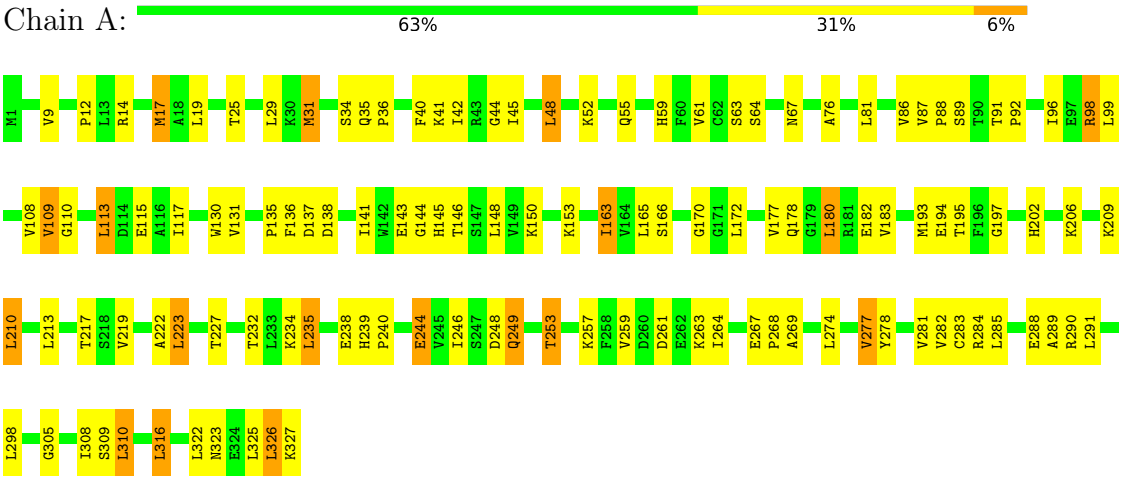
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

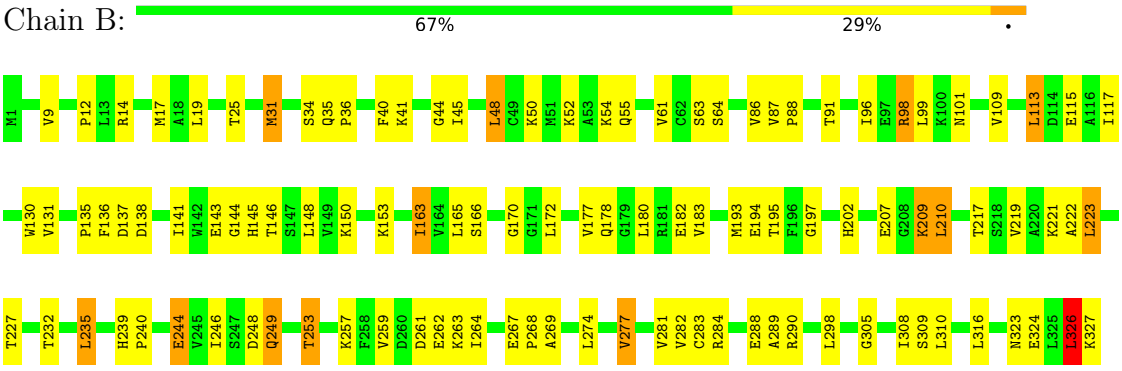
• Molecule 1: L-serine dehydratase

Chain A:



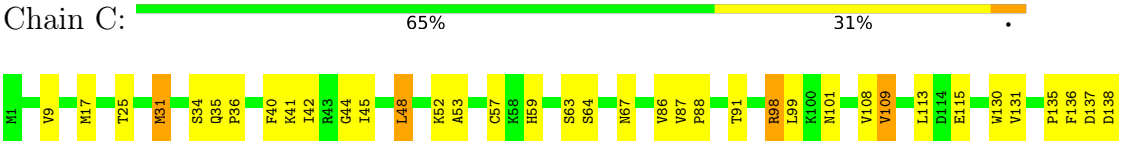
• Molecule 1: L-serine dehydratase

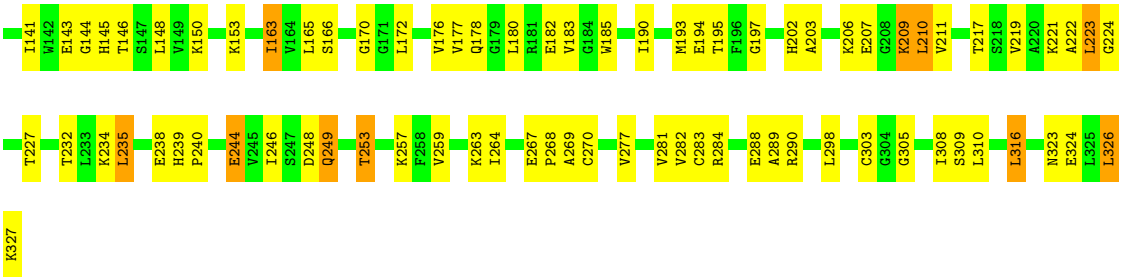
Chain B:



• Molecule 1: L-serine dehydratase

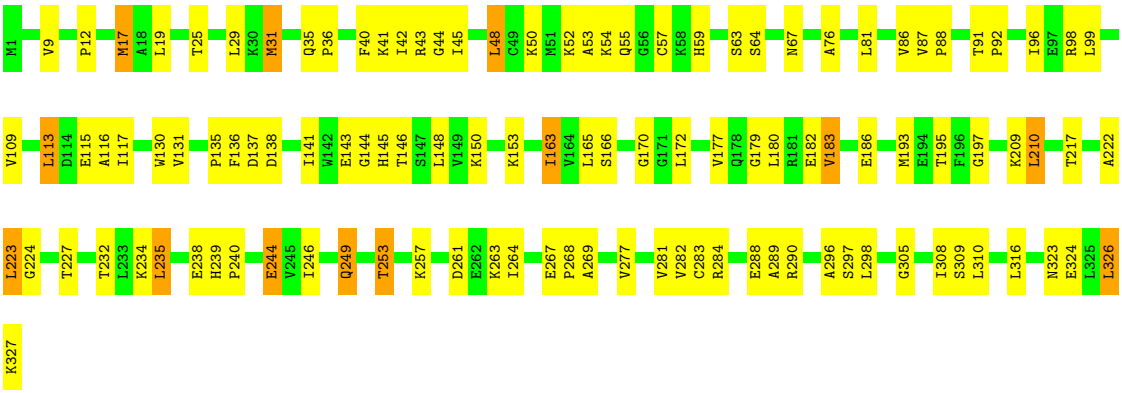
Chain C:





• Molecule 1: L-serine dehydratase

Chain D:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	62.24Å 109.26Å 98.94Å 90.00° 91.66° 90.00°	Depositor
Resolution (Å)	25.01 – 2.60	Depositor
% Data completeness (in resolution range)	92.5 (25.01-2.60)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.230 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9883	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PLV, K

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.45	0/2456	0.66	0/3327
1	B	0.45	0/2456	0.66	0/3327
1	C	0.45	0/2456	0.65	0/3327
1	D	0.45	0/2456	0.65	0/3327
All	All	0.45	0/9824	0.65	0/13308

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2417	0	2512	118	0
1	B	2417	0	2512	100	0
1	C	2417	0	2512	114	0
1	D	2417	0	2512	105	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	23	0	15	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	23	0	15	7	0
3	C	23	0	15	7	0
3	D	23	0	15	6	0
4	A	39	0	0	6	0
4	B	34	0	0	3	0
4	C	21	0	0	2	0
4	D	25	0	0	1	0
All	All	9883	0	10108	421	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (421) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:LYS:HG2	1:D:131:VAL:HG11	1.37	1.05
1:A:52:LYS:HG2	1:A:131:VAL:HG11	1.39	1.01
1:A:249:GLN:H	1:A:249:GLN:HE21	1.05	1.00
1:C:52:LYS:HG2	1:C:131:VAL:HG11	1.47	0.97
1:B:52:LYS:HG2	1:B:131:VAL:HG11	1.45	0.95
1:B:249:GLN:H	1:B:249:GLN:NE2	1.66	0.93
1:D:249:GLN:H	1:D:249:GLN:HE21	1.06	0.93
1:B:249:GLN:H	1:B:249:GLN:HE21	0.97	0.92
1:C:249:GLN:H	1:C:249:GLN:NE2	1.67	0.92
1:C:249:GLN:H	1:C:249:GLN:HE21	0.92	0.90
1:C:249:GLN:HE21	1:C:249:GLN:N	1.71	0.87
1:B:153:LYS:HD3	1:B:183:VAL:HG13	1.59	0.85
1:A:249:GLN:H	1:A:249:GLN:NE2	1.75	0.84
1:D:249:GLN:H	1:D:249:GLN:NE2	1.76	0.83
1:B:249:GLN:HE21	1:B:249:GLN:N	1.76	0.82
1:C:9:VAL:H	1:C:35:GLN:HE22	1.28	0.81
1:A:88:PRO:O	1:A:91:THR:HG22	1.82	0.80
1:B:9:VAL:H	1:B:35:GLN:HE22	1.26	0.80
1:D:88:PRO:O	1:D:91:THR:HG22	1.82	0.80
1:C:153:LYS:HD3	1:C:183:VAL:HG13	1.64	0.79
1:B:88:PRO:O	1:B:91:THR:HG22	1.83	0.78
1:A:153:LYS:HD3	1:A:183:VAL:HG13	1.66	0.78
1:D:153:LYS:HD3	1:D:183:VAL:HG13	1.67	0.76
1:C:88:PRO:O	1:C:91:THR:HG22	1.85	0.75
1:D:9:VAL:H	1:D:35:GLN:HE22	1.33	0.75
1:A:9:VAL:H	1:A:35:GLN:HE22	1.34	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:LEU:HD13	1:B:269:ALA:HB1	1.70	0.73
1:A:48:LEU:HD12	1:A:141:ILE:HD11	1.70	0.73
1:C:48:LEU:HD12	1:C:141:ILE:HD11	1.72	0.72
1:D:223:LEU:HD13	1:D:269:ALA:HB1	1.71	0.72
1:B:109:VAL:HG13	1:B:109:VAL:O	1.89	0.71
1:D:146:THR:HG22	1:D:150:LYS:HZ2	1.55	0.71
1:A:249:GLN:HE21	1:A:249:GLN:N	1.85	0.71
1:D:48:LEU:HD12	1:D:141:ILE:HD11	1.72	0.71
1:A:223:LEU:HD13	1:A:269:ALA:HB1	1.74	0.69
1:C:109:VAL:HG13	1:C:109:VAL:O	1.91	0.69
1:D:52:LYS:CG	1:D:131:VAL:HG11	2.20	0.69
1:C:223:LEU:HD13	1:C:269:ALA:HB1	1.75	0.69
1:A:109:VAL:HG13	1:A:109:VAL:O	1.93	0.69
1:D:249:GLN:HE21	1:D:249:GLN:N	1.86	0.68
1:A:146:THR:HG22	1:A:150:LYS:HZ2	1.59	0.68
1:B:48:LEU:HD12	1:B:141:ILE:HD11	1.74	0.68
1:B:327:LYS:HB3	1:B:327:LYS:NZ	2.09	0.68
1:C:52:LYS:CG	1:C:131:VAL:HG11	2.23	0.67
1:D:109:VAL:O	1:D:109:VAL:HG13	1.96	0.66
1:B:249:GLN:NE2	1:B:249:GLN:N	2.42	0.65
1:D:146:THR:HG22	1:D:150:LYS:NZ	2.11	0.65
1:D:288:GLU:OE2	1:D:290:ARG:NH1	2.29	0.65
1:A:177:VAL:HG21	1:A:235:LEU:HG	1.77	0.65
1:B:63:SER:O	1:B:135:PRO:HG3	1.97	0.65
1:C:63:SER:O	1:C:135:PRO:HG3	1.97	0.64
1:B:41:LYS:NZ	3:B:329:PLV:H4A1	2.12	0.64
1:C:177:VAL:HG21	1:C:235:LEU:HG	1.79	0.64
1:A:63:SER:O	1:A:135:PRO:HG3	1.96	0.64
1:A:108:VAL:HG12	4:A:336:HOH:O	1.96	0.64
1:B:35:GLN:HE21	1:B:36:PRO:HD2	1.62	0.64
1:D:177:VAL:HG21	1:D:235:LEU:HG	1.80	0.64
1:B:177:VAL:HG21	1:B:235:LEU:HG	1.81	0.63
1:D:63:SER:O	1:D:135:PRO:HG3	1.98	0.63
1:C:288:GLU:OE2	1:C:290:ARG:NH1	2.32	0.62
1:C:41:LYS:NZ	3:C:330:PLV:H4A1	2.14	0.62
1:D:163:ILE:HD11	1:D:165:LEU:HD23	1.81	0.62
1:A:288:GLU:OE2	1:A:290:ARG:NH1	2.33	0.62
1:B:136:PHE:HB3	4:B:334:HOH:O	2.00	0.62
1:A:41:LYS:HZ3	3:A:328:PLV:C4A	2.13	0.61
1:C:146:THR:HG22	1:C:150:LYS:HZ2	1.66	0.61
1:C:41:LYS:HZ1	3:C:330:PLV:C4A	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:ILE:HD13	1:C:141:ILE:HD12	1.82	0.61
1:B:41:LYS:NZ	3:B:329:PLV:C4A	2.63	0.61
1:D:40:PHE:CZ	1:D:41:LYS:HE3	2.36	0.61
1:C:136:PHE:CE1	1:C:137:ASP:HB3	2.36	0.61
1:C:35:GLN:HE21	1:C:36:PRO:HD2	1.65	0.61
1:C:41:LYS:NZ	3:C:330:PLV:C4A	2.63	0.61
1:A:40:PHE:CZ	1:A:41:LYS:HE3	2.36	0.60
1:C:136:PHE:HB3	4:C:337:HOH:O	2.01	0.60
1:D:136:PHE:CE1	1:D:137:ASP:HB3	2.35	0.60
1:C:64:SER:O	1:C:87:VAL:HG23	2.01	0.60
1:C:267:GLU:HB2	1:C:268:PRO:HD2	1.83	0.60
1:A:136:PHE:HB3	4:A:356:HOH:O	2.00	0.60
1:C:146:THR:HG22	1:C:150:LYS:NZ	2.16	0.60
1:B:52:LYS:CG	1:B:131:VAL:HG11	2.28	0.60
1:C:327:LYS:NZ	1:C:327:LYS:HB3	2.16	0.60
1:C:234:LYS:HE2	1:C:238:GLU:OE2	2.01	0.59
1:D:136:PHE:HB3	4:D:336:HOH:O	2.02	0.59
1:A:289:ALA:HB3	1:C:323:ASN:HA	1.83	0.59
1:C:44:GLY:H	1:C:145:HIS:CD2	2.20	0.59
1:B:288:GLU:OE2	1:B:290:ARG:NH1	2.34	0.59
1:C:223:LEU:HD13	1:C:269:ALA:CB	2.33	0.59
1:D:41:LYS:HZ3	3:D:331:PLV:C4A	2.16	0.59
1:C:40:PHE:CZ	1:C:41:LYS:HE3	2.39	0.58
1:C:138:ASP:HB3	1:C:141:ILE:HG12	1.85	0.58
1:A:64:SER:O	1:A:87:VAL:HG23	2.04	0.58
1:C:41:LYS:HZ1	3:C:330:PLV:H4A1	1.68	0.58
1:A:35:GLN:HE21	1:A:36:PRO:HD2	1.68	0.57
1:D:41:LYS:NZ	3:D:331:PLV:C4A	2.68	0.57
1:A:327:LYS:NZ	1:A:327:LYS:HB3	2.19	0.57
1:D:41:LYS:NZ	3:D:331:PLV:H4A1	2.19	0.57
1:A:52:LYS:CG	1:A:131:VAL:HG11	2.26	0.57
1:D:223:LEU:HD13	1:D:269:ALA:CB	2.33	0.57
1:B:41:LYS:HZ3	3:B:329:PLV:C4A	2.17	0.57
1:B:267:GLU:HB2	1:B:268:PRO:HD2	1.87	0.57
1:C:48:LEU:CD2	1:C:52:LYS:HD3	2.35	0.57
1:A:52:LYS:O	1:A:55:GLN:HB3	2.05	0.56
1:A:41:LYS:NZ	3:A:328:PLV:C4A	2.68	0.56
1:C:222:ALA:HB3	1:C:269:ALA:HB2	1.88	0.56
1:D:44:GLY:H	1:D:145:HIS:CD2	2.22	0.56
1:D:113:LEU:O	1:D:117:ILE:HG13	2.05	0.56
1:D:195:THR:HA	1:D:246:ILE:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:PHE:CE1	1:A:137:ASP:HB3	2.40	0.56
1:A:146:THR:HG22	1:A:150:LYS:NZ	2.20	0.56
1:B:35:GLN:HE21	1:B:36:PRO:CD	2.18	0.56
1:B:223:LEU:HD13	1:B:269:ALA:CB	2.34	0.56
1:D:249:GLN:NE2	1:D:249:GLN:N	2.50	0.56
1:D:327:LYS:NZ	1:D:327:LYS:HB3	2.20	0.56
1:C:35:GLN:HE21	1:C:36:PRO:CD	2.18	0.56
1:B:41:LYS:HZ3	3:B:329:PLV:H4A1	1.70	0.56
1:A:261:ASP:O	1:B:98:ARG:NH1	2.39	0.56
1:D:35:GLN:HE21	1:D:36:PRO:HD2	1.71	0.56
1:A:41:LYS:HZ3	3:A:328:PLV:H4A1	1.70	0.55
1:A:41:LYS:NZ	3:A:328:PLV:H4A1	2.20	0.55
1:B:64:SER:O	1:B:87:VAL:HG23	2.07	0.55
1:B:44:GLY:H	1:B:145:HIS:CD2	2.25	0.55
1:A:267:GLU:HB2	1:A:268:PRO:HD2	1.88	0.55
1:C:163:ILE:HD11	1:C:165:LEU:HD23	1.89	0.55
1:C:195:THR:HA	1:C:246:ILE:O	2.07	0.55
1:A:12:PRO:HG2	1:B:34:SER:HB3	1.87	0.55
1:A:44:GLY:H	1:A:145:HIS:CD2	2.24	0.55
1:A:298:LEU:C	1:A:298:LEU:HD12	2.27	0.55
1:C:53:ALA:HA	1:C:57:CYS:SG	2.47	0.54
1:D:64:SER:O	1:D:87:VAL:HG23	2.06	0.54
1:D:146:THR:CG2	1:D:150:LYS:NZ	2.69	0.54
1:D:267:GLU:HB2	1:D:268:PRO:HD2	1.88	0.54
1:B:45:ILE:HD13	1:B:141:ILE:HD12	1.89	0.54
1:C:249:GLN:NE2	1:C:249:GLN:N	2.40	0.54
1:C:146:THR:CG2	1:C:150:LYS:NZ	2.71	0.54
1:D:41:LYS:HZ3	3:D:331:PLV:H4A1	1.72	0.54
1:B:40:PHE:CZ	1:B:41:LYS:HE3	2.42	0.54
1:B:138:ASP:HB3	1:B:141:ILE:HG12	1.89	0.54
1:B:323:ASN:O	1:B:324:GLU:HG3	2.08	0.54
1:C:98:ARG:NH1	1:D:261:ASP:O	2.41	0.54
1:A:263:LYS:N	1:A:263:LYS:HD2	2.22	0.54
1:C:31:MET:CE	1:C:264:ILE:HG13	2.38	0.54
1:A:223:LEU:HD13	1:A:269:ALA:CB	2.38	0.54
1:D:263:LYS:HD2	1:D:263:LYS:N	2.23	0.54
1:C:267:GLU:HG2	1:C:305:GLY:HA3	1.91	0.53
1:B:170:GLY:HA3	1:B:232:THR:OG1	2.09	0.53
1:A:195:THR:HA	1:A:246:ILE:O	2.09	0.53
1:B:31:MET:CE	1:B:264:ILE:HG13	2.38	0.53
1:D:222:ALA:HB3	1:D:269:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:GLN:HE21	1:A:36:PRO:CD	2.21	0.53
1:B:263:LYS:HD2	1:B:263:LYS:N	2.23	0.53
1:B:195:THR:HA	1:B:246:ILE:O	2.09	0.53
1:D:143:GLU:O	1:D:146:THR:HB	2.08	0.53
1:D:67:ASN:OD1	1:D:305:GLY:HA2	2.08	0.53
1:C:263:LYS:HD2	1:C:263:LYS:N	2.24	0.53
1:D:35:GLN:HE21	1:D:36:PRO:CD	2.22	0.53
1:B:136:PHE:CE1	1:B:137:ASP:HB3	2.44	0.53
1:C:108:VAL:HG12	4:C:336:HOH:O	2.09	0.53
1:B:210:LEU:HD23	1:B:210:LEU:H	1.74	0.52
1:C:101:ASN:O	1:D:17:MET:CG	2.57	0.52
1:C:166:SER:HA	1:C:193:MET:O	2.10	0.52
1:D:53:ALA:HA	1:D:57:CYS:SG	2.49	0.52
1:C:44:GLY:H	1:C:145:HIS:HD2	1.57	0.52
1:D:52:LYS:O	1:D:55:GLN:HB3	2.09	0.52
1:B:44:GLY:HA2	1:B:144:GLY:HA3	1.92	0.52
1:C:146:THR:HG21	1:C:150:LYS:HZ1	1.75	0.52
1:D:109:VAL:HG22	1:D:115:GLU:CD	2.30	0.52
1:D:138:ASP:HB3	1:D:141:ILE:HG12	1.91	0.52
1:C:267:GLU:HB2	1:C:268:PRO:CD	2.39	0.52
1:A:163:ILE:HD11	1:A:165:LEU:HD23	1.92	0.52
1:A:249:GLN:NE2	1:A:249:GLN:N	2.49	0.51
1:C:146:THR:CG2	1:C:150:LYS:HZ1	2.23	0.51
1:D:267:GLU:HG2	1:D:305:GLY:HA3	1.92	0.51
1:A:143:GLU:O	1:A:146:THR:HB	2.11	0.51
1:D:63:SER:HA	1:D:86:VAL:O	2.10	0.51
1:A:323:ASN:HA	1:C:289:ALA:HB3	1.91	0.51
1:D:282:VAL:HG23	1:D:283:CYS:N	2.26	0.51
1:D:87:VAL:CG2	1:D:91:THR:HG21	2.41	0.51
1:B:253:THR:HG23	1:B:257:LYS:HE3	1.92	0.51
1:C:194:GLU:OE1	1:C:202:HIS:N	2.41	0.51
1:A:109:VAL:HG22	1:A:115:GLU:CD	2.31	0.50
1:A:148:LEU:C	1:A:148:LEU:HD23	2.32	0.50
1:A:166:SER:HA	1:A:193:MET:O	2.10	0.50
1:B:222:ALA:HB3	1:B:269:ALA:HB2	1.93	0.50
1:D:31:MET:CE	1:D:264:ILE:HG13	2.41	0.50
1:B:63:SER:HA	1:B:86:VAL:O	2.12	0.50
1:D:197:GLY:HA2	1:D:217:THR:HG23	1.94	0.50
1:C:197:GLY:HA2	1:C:217:THR:HG23	1.93	0.50
1:C:239:HIS:CG	1:C:240:PRO:HD2	2.46	0.50
1:A:138:ASP:HB3	1:A:141:ILE:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:244:GLU:HG2	1:C:281:VAL:CG1	2.42	0.50
1:B:41:LYS:NZ	3:B:329:PLV:N	2.60	0.50
1:B:267:GLU:HB2	1:B:268:PRO:CD	2.42	0.50
1:A:146:THR:CG2	1:A:150:LYS:NZ	2.75	0.49
1:C:44:GLY:HA2	1:C:144:GLY:HA3	1.93	0.49
1:C:57:CYS:HB3	1:C:131:VAL:HG21	1.93	0.49
1:B:267:GLU:HG2	1:B:305:GLY:HA3	1.93	0.49
1:A:44:GLY:H	1:A:145:HIS:HD2	1.60	0.49
1:B:87:VAL:HG23	1:B:88:PRO:HD2	1.95	0.49
1:B:166:SER:HA	1:B:193:MET:O	2.12	0.49
1:B:284:ARG:HD2	1:B:288:GLU:OE1	2.13	0.49
1:C:298:LEU:C	1:C:298:LEU:HD12	2.32	0.49
1:D:45:ILE:HD13	1:D:141:ILE:HD12	1.92	0.49
1:D:298:LEU:C	1:D:298:LEU:HD12	2.32	0.49
1:A:48:LEU:HD12	1:A:141:ILE:CD1	2.42	0.49
1:A:222:ALA:HB3	1:A:269:ALA:HB2	1.93	0.49
1:D:197:GLY:CA	1:D:217:THR:HG23	2.42	0.49
1:D:44:GLY:H	1:D:145:HIS:HD2	1.61	0.49
1:A:31:MET:CE	1:A:264:ILE:HG13	2.43	0.49
1:B:87:VAL:CG2	1:B:91:THR:HG21	2.43	0.49
1:C:40:PHE:CE1	1:C:172:LEU:HB2	2.48	0.49
1:D:41:LYS:NZ	3:D:331:PLV:N	2.60	0.49
1:A:308:ILE:HG13	1:A:309:SER:N	2.27	0.49
1:B:239:HIS:CG	1:B:240:PRO:HD2	2.47	0.49
1:D:210:LEU:H	1:D:210:LEU:HD23	1.78	0.49
1:B:197:GLY:CA	1:B:217:THR:HG23	2.43	0.49
1:D:87:VAL:CG2	1:D:91:THR:HB	2.43	0.49
1:D:146:THR:CG2	1:D:150:LYS:HZ1	2.26	0.49
1:A:63:SER:HA	1:A:86:VAL:O	2.13	0.48
1:A:87:VAL:CG2	1:A:91:THR:HB	2.43	0.48
1:A:194:GLU:OE1	1:A:202:HIS:N	2.45	0.48
1:C:101:ASN:O	1:D:17:MET:HG3	2.13	0.48
1:C:165:LEU:HD12	1:C:165:LEU:C	2.34	0.48
1:D:170:GLY:HA3	1:D:232:THR:OG1	2.13	0.48
1:A:34:SER:HB3	1:B:12:PRO:HG2	1.95	0.48
1:C:197:GLY:CA	1:C:217:THR:HG23	2.43	0.48
1:B:41:LYS:O	1:B:45:ILE:HB	2.14	0.48
1:A:89:SER:HB3	4:A:336:HOH:O	2.13	0.48
1:B:197:GLY:HA2	1:B:217:THR:HG23	1.95	0.48
1:A:59:HIS:HB3	1:A:130:TRP:CD1	2.49	0.48
1:A:165:LEU:HD12	1:A:165:LEU:C	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:VAL:HG23	1:A:283:CYS:N	2.27	0.48
1:A:290:ARG:NH1	1:C:249:GLN:HG2	2.28	0.48
1:B:109:VAL:HG22	1:B:115:GLU:CD	2.33	0.48
1:D:44:GLY:HA2	1:D:144:GLY:HA3	1.96	0.48
1:B:210:LEU:H	1:B:210:LEU:CD2	2.26	0.48
1:B:298:LEU:HD12	1:B:298:LEU:C	2.34	0.48
1:C:41:LYS:NZ	3:C:330:PLV:N	2.59	0.48
1:C:210:LEU:HD23	1:C:210:LEU:H	1.78	0.48
1:D:234:LYS:HE2	1:D:238:GLU:OE2	2.13	0.48
1:A:267:GLU:HG2	1:A:305:GLY:HA3	1.96	0.48
1:B:163:ILE:HD11	1:B:165:LEU:HD23	1.96	0.48
1:D:267:GLU:HB2	1:D:268:PRO:CD	2.43	0.48
1:A:322:LEU:O	1:A:323:ASN:HB2	2.14	0.48
1:C:63:SER:HA	1:C:86:VAL:O	2.14	0.48
1:D:308:ILE:HG13	1:D:309:SER:N	2.29	0.48
1:B:327:LYS:HB3	1:B:327:LYS:HZ3	1.77	0.48
1:D:163:ILE:O	1:D:163:ILE:HG13	2.14	0.48
1:A:259:VAL:O	1:A:263:LYS:HA	2.14	0.47
1:D:91:THR:HG23	1:D:96:ILE:HD11	1.96	0.47
1:A:67:ASN:OD1	1:A:305:GLY:HA2	2.13	0.47
1:A:170:GLY:HA3	1:A:232:THR:OG1	2.14	0.47
1:C:34:SER:HB3	1:D:12:PRO:HG2	1.95	0.47
1:A:278:TYR:HB3	4:A:365:HOH:O	2.14	0.47
1:C:87:VAL:CG2	1:C:91:THR:HB	2.44	0.47
1:D:146:THR:HG21	1:D:150:LYS:HZ1	1.79	0.47
1:C:52:LYS:O	1:C:57:CYS:SG	2.73	0.47
1:D:40:PHE:CE1	1:D:172:LEU:HB2	2.49	0.47
1:B:308:ILE:HG13	1:B:309:SER:N	2.30	0.47
1:D:87:VAL:HG21	1:D:91:THR:CB	2.44	0.47
1:A:41:LYS:NZ	3:A:328:PLV:N	2.59	0.47
1:A:45:ILE:HD13	1:A:141:ILE:HD12	1.97	0.47
1:D:48:LEU:CD2	1:D:52:LYS:HD3	2.44	0.47
1:C:327:LYS:HB3	1:C:327:LYS:HZ3	1.80	0.47
1:D:48:LEU:HD12	1:D:141:ILE:CD1	2.43	0.47
1:A:244:GLU:HG2	1:A:281:VAL:CG1	2.45	0.47
1:A:253:THR:HG23	1:A:257:LYS:HE3	1.96	0.47
1:D:239:HIS:CG	1:D:240:PRO:HD2	2.50	0.47
1:B:146:THR:HG22	1:B:150:LYS:HZ2	1.80	0.46
1:B:288:GLU:O	1:B:289:ALA:HB3	2.16	0.46
1:C:219:VAL:HG22	1:C:248:ASP:CG	2.36	0.46
1:C:244:GLU:HG2	1:C:281:VAL:HG11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:LYS:HG3	1:C:217:THR:OG1	2.16	0.46
1:C:45:ILE:HD13	1:C:141:ILE:CD1	2.45	0.46
1:C:253:THR:HG23	1:C:257:LYS:HE3	1.97	0.46
1:B:44:GLY:H	1:B:145:HIS:HD2	1.62	0.46
1:B:61:VAL:HG22	1:B:130:TRP:CE3	2.50	0.46
1:C:323:ASN:O	1:C:324:GLU:HG3	2.16	0.46
1:A:210:LEU:HD23	1:A:210:LEU:H	1.81	0.46
1:C:170:GLY:HA3	1:C:232:THR:OG1	2.15	0.46
1:D:43:ARG:HG2	1:D:43:ARG:HH11	1.80	0.46
1:B:194:GLU:OE1	1:B:202:HIS:N	2.46	0.46
1:B:219:VAL:HG22	1:B:248:ASP:CG	2.36	0.46
1:B:282:VAL:HG23	1:B:283:CYS:N	2.29	0.46
1:B:327:LYS:HB3	1:B:327:LYS:HZ2	1.81	0.46
1:C:282:VAL:HG23	1:C:283:CYS:N	2.30	0.46
1:C:143:GLU:O	1:C:146:THR:HB	2.15	0.46
1:C:101:ASN:O	1:D:17:MET:HG2	2.15	0.45
1:A:44:GLY:HA2	1:A:144:GLY:HA3	1.97	0.45
1:A:298:LEU:HD12	1:A:298:LEU:O	2.16	0.45
1:D:148:LEU:C	1:D:148:LEU:HD23	2.37	0.45
1:A:14:ARG:HB2	4:B:340:HOH:O	2.16	0.45
1:D:166:SER:HA	1:D:193:MET:O	2.16	0.45
1:A:87:VAL:HG21	1:A:91:THR:CB	2.46	0.45
1:A:113:LEU:O	1:A:117:ILE:HG13	2.16	0.45
1:A:267:GLU:HB2	1:A:268:PRO:CD	2.46	0.45
1:A:180:LEU:HD23	1:A:239:HIS:CE1	2.51	0.45
1:C:259:VAL:O	1:C:263:LYS:HA	2.17	0.45
1:D:136:PHE:CD1	1:D:137:ASP:HB3	2.51	0.45
1:D:210:LEU:H	1:D:210:LEU:CD2	2.29	0.45
1:D:244:GLU:HG2	1:D:281:VAL:CG1	2.47	0.45
1:A:163:ILE:HG13	1:A:163:ILE:O	2.16	0.45
1:B:143:GLU:O	1:B:146:THR:HB	2.17	0.45
1:D:45:ILE:HD13	1:D:141:ILE:CD1	2.47	0.45
1:A:284:ARG:HD2	1:A:288:GLU:OE1	2.16	0.45
1:C:91:THR:O	1:C:91:THR:HG23	2.17	0.45
1:D:36:PRO:HD2	1:D:42:ILE:HG21	1.99	0.45
1:A:91:THR:HG23	1:A:96:ILE:HD11	1.97	0.44
1:A:19:LEU:HD22	1:A:29:LEU:HD21	1.98	0.44
1:B:45:ILE:HD13	1:B:141:ILE:CD1	2.47	0.44
1:C:109:VAL:O	1:C:109:VAL:CG1	2.63	0.44
1:A:325:LEU:HD23	1:C:289:ALA:O	2.16	0.44
1:B:48:LEU:CD2	1:B:52:LYS:HD3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:LEU:HD22	1:D:29:LEU:HD21	1.99	0.44
1:D:323:ASN:O	1:D:324:GLU:HG3	2.18	0.44
1:A:217:THR:O	1:C:206:LYS:HE3	2.18	0.44
1:C:41:LYS:CE	3:C:330:PLV:H4A1	2.47	0.44
1:C:87:VAL:CG2	1:C:91:THR:HG21	2.47	0.44
1:C:288:GLU:O	1:C:289:ALA:HB3	2.16	0.44
1:B:244:GLU:HG2	1:B:281:VAL:CG1	2.48	0.44
1:C:178:GLN:O	1:C:182:GLU:HG2	2.18	0.44
1:D:91:THR:HG23	1:D:91:THR:O	2.17	0.44
1:B:221:LYS:O	3:B:329:PLV:H71	2.18	0.44
1:C:148:LEU:C	1:C:148:LEU:HD23	2.37	0.44
1:D:76:ALA:HB1	1:D:81:LEU:O	2.18	0.44
1:D:288:GLU:O	1:D:289:ALA:HB3	2.17	0.44
1:D:59:HIS:HB3	1:D:130:TRP:CD1	2.52	0.44
1:C:163:ILE:O	1:C:163:ILE:HG13	2.17	0.44
1:B:326:LEU:O	1:B:327:LYS:HB2	2.18	0.43
1:A:239:HIS:CG	1:A:240:PRO:HD2	2.53	0.43
1:B:148:LEU:HD23	1:B:148:LEU:C	2.38	0.43
1:D:91:THR:HA	1:D:92:PRO:HD3	1.88	0.43
1:A:285:LEU:HB2	1:A:291:LEU:HD12	1.99	0.43
1:B:146:THR:HG22	1:B:150:LYS:NZ	2.33	0.43
1:C:284:ARG:HD2	1:C:288:GLU:OE1	2.17	0.43
1:A:87:VAL:HG23	1:A:88:PRO:HD2	2.01	0.43
1:A:91:THR:HG23	1:A:91:THR:O	2.18	0.43
1:B:55:GLN:HB2	4:B:358:HOH:O	2.18	0.43
1:D:41:LYS:CE	3:D:331:PLV:H4A1	2.49	0.43
1:A:136:PHE:CD1	1:A:137:ASP:HB3	2.54	0.43
1:A:197:GLY:CA	1:A:217:THR:HG23	2.49	0.43
1:B:178:GLN:O	1:B:182:GLU:HG2	2.18	0.43
1:A:87:VAL:CG2	1:A:91:THR:HG21	2.49	0.43
1:A:274:LEU:O	1:A:277:VAL:HG13	2.18	0.43
1:D:50:LYS:O	1:D:54:LYS:HG2	2.19	0.43
1:A:109:VAL:O	1:A:109:VAL:CG1	2.64	0.43
1:C:87:VAL:HG21	1:C:91:THR:CB	2.49	0.43
1:C:136:PHE:CD1	1:C:137:ASP:HB3	2.54	0.43
1:A:197:GLY:HA2	1:A:217:THR:HG23	2.01	0.43
1:A:234:LYS:HE2	1:A:238:GLU:OE2	2.19	0.43
1:C:87:VAL:HG23	1:C:88:PRO:HD2	2.01	0.43
1:D:87:VAL:HG21	1:D:91:THR:HG21	2.01	0.43
1:A:288:GLU:O	1:A:289:ALA:HB3	2.18	0.42
1:B:40:PHE:CE1	1:B:172:LEU:HB2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:VAL:CG2	1:B:91:THR:HB	2.50	0.42
1:D:298:LEU:HD12	1:D:298:LEU:O	2.20	0.42
1:A:110:GLY:N	4:A:336:HOH:O	2.52	0.42
1:A:219:VAL:HG22	1:A:248:ASP:CG	2.40	0.42
1:D:63:SER:HB3	1:D:116:ALA:O	2.19	0.42
1:D:244:GLU:HG2	1:D:281:VAL:HG11	2.01	0.42
1:B:48:LEU:HD12	1:B:141:ILE:CD1	2.48	0.42
1:C:109:VAL:HG22	1:C:115:GLU:CD	2.39	0.42
1:A:41:LYS:HA	1:A:41:LYS:HD3	1.90	0.42
1:B:91:THR:HG23	1:B:96:ILE:HD11	2.00	0.42
1:B:207:GLU:O	1:B:209:LYS:HD3	2.19	0.42
1:C:207:GLU:O	1:C:209:LYS:HD3	2.19	0.42
1:B:146:THR:HG21	1:B:182:GLU:OE2	2.20	0.42
1:B:163:ILE:O	1:B:163:ILE:HG13	2.19	0.42
1:D:253:THR:HG23	1:D:257:LYS:HE3	2.01	0.42
1:A:316:LEU:HD13	4:A:341:HOH:O	2.19	0.42
1:C:203:ALA:HB1	1:C:211:VAL:HG21	2.02	0.42
1:C:210:LEU:H	1:C:210:LEU:CD2	2.32	0.42
1:A:41:LYS:CE	3:A:328:PLV:H4A1	2.50	0.42
1:B:41:LYS:CE	3:B:329:PLV:H4A1	2.50	0.42
1:D:146:THR:HG21	1:D:182:GLU:OE2	2.19	0.42
1:D:327:LYS:HB3	1:D:327:LYS:HZ3	1.84	0.42
1:B:165:LEU:C	1:B:165:LEU:HD12	2.40	0.41
1:D:87:VAL:HG23	1:D:88:PRO:HD2	2.02	0.41
1:A:178:GLN:O	1:A:182:GLU:HG2	2.20	0.41
1:C:153:LYS:HA	1:C:185:TRP:CH2	2.55	0.41
1:D:296:ALA:O	1:D:297:SER:C	2.59	0.41
1:A:45:ILE:HD13	1:A:141:ILE:CD1	2.50	0.41
1:A:91:THR:HA	1:A:92:PRO:HD3	1.91	0.41
1:A:244:GLU:HG2	1:A:281:VAL:HG11	2.01	0.41
1:A:310:LEU:HD12	1:A:310:LEU:HA	1.87	0.41
1:B:19:LEU:HD23	1:B:277:VAL:HG11	2.02	0.41
1:B:210:LEU:HD23	1:B:210:LEU:N	2.35	0.41
1:C:270:CYS:HA	1:C:303:CYS:SG	2.60	0.41
1:B:259:VAL:O	1:B:263:LYS:HA	2.20	0.41
1:A:40:PHE:CE1	1:A:172:LEU:HB2	2.55	0.41
1:A:98:ARG:NH1	1:B:261:ASP:O	2.53	0.41
1:D:179:GLY:O	1:D:183:VAL:HB	2.20	0.41
1:B:274:LEU:O	1:B:277:VAL:HG13	2.19	0.41
1:A:17:MET:HG3	1:B:101:ASN:O	2.21	0.41
1:A:87:VAL:HG22	1:A:88:PRO:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:177:VAL:HG12	1:C:190:ILE:HD12	2.03	0.41
1:A:76:ALA:HB1	1:A:81:LEU:O	2.21	0.41
1:C:141:ILE:HG22	1:C:145:HIS:CE1	2.56	0.41
1:C:177:VAL:HG21	1:C:235:LEU:CG	2.49	0.41
1:A:210:LEU:H	1:A:210:LEU:CD2	2.33	0.41
1:C:221:LYS:O	3:C:330:PLV:H71	2.20	0.41
1:C:308:ILE:HG13	1:C:309:SER:N	2.35	0.41
1:D:284:ARG:HD2	1:D:288:GLU:OE1	2.21	0.41
1:A:91:THR:CG2	1:A:96:ILE:HD11	2.51	0.41
1:B:153:LYS:HD3	1:B:183:VAL:CG1	2.40	0.41
1:C:36:PRO:HD2	1:C:42:ILE:HG21	2.03	0.41
1:A:48:LEU:CD2	1:A:52:LYS:HD3	2.51	0.40
1:C:59:HIS:HB3	1:C:130:TRP:CD1	2.56	0.40
1:A:36:PRO:HD2	1:A:42:ILE:HG21	2.04	0.40
1:B:50:LYS:O	1:B:54:LYS:HG2	2.22	0.40
1:B:113:LEU:O	1:B:117:ILE:HG13	2.21	0.40
1:D:177:VAL:HG21	1:D:235:LEU:CG	2.50	0.40
1:B:14:ARG:HD3	1:B:262:GLU:OE1	2.21	0.40
1:B:148:LEU:HD23	1:B:148:LEU:O	2.22	0.40
1:D:91:THR:CG2	1:D:96:ILE:HD11	2.51	0.40
1:B:87:VAL:HG21	1:B:91:THR:CB	2.52	0.40
1:C:67:ASN:OD1	1:C:305:GLY:HA2	2.21	0.40
1:C:172:LEU:O	1:C:176:VAL:HG23	2.21	0.40
1:A:61:VAL:HG22	1:A:130:TRP:CE3	2.55	0.40
1:C:146:THR:HG21	1:C:182:GLU:OE2	2.22	0.40
1:C:316:LEU:HD12	1:C:316:LEU:HA	1.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	325/327 (99%)	304 (94%)	18 (6%)	3 (1%)	17	35
1	B	325/327 (99%)	305 (94%)	18 (6%)	2 (1%)	25	47
1	C	325/327 (99%)	303 (93%)	18 (6%)	4 (1%)	13	27
1	D	325/327 (99%)	303 (93%)	19 (6%)	3 (1%)	17	35
All	All	1300/1308 (99%)	1215 (94%)	73 (6%)	12 (1%)	17	35

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	326	LEU
1	B	326	LEU
1	C	326	LEU
1	D	326	LEU
1	B	31	MET
1	D	31	MET
1	C	31	MET
1	A	31	MET
1	C	109	VAL
1	A	109	VAL
1	C	224	GLY
1	D	224	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	259/259 (100%)	238 (92%)	21 (8%)	11	23
1	B	259/259 (100%)	239 (92%)	20 (8%)	13	25
1	C	259/259 (100%)	239 (92%)	20 (8%)	13	25
1	D	259/259 (100%)	237 (92%)	22 (8%)	10	21
All	All	1036/1036 (100%)	953 (92%)	83 (8%)	12	24

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	MET
1	A	25	THR
1	A	48	LEU
1	A	98	ARG
1	A	99	LEU
1	A	113	LEU
1	A	163	ILE
1	A	180	LEU
1	A	209	LYS
1	A	210	LEU
1	A	213	LEU
1	A	223	LEU
1	A	227	THR
1	A	235	LEU
1	A	244	GLU
1	A	249	GLN
1	A	253	THR
1	A	277	VAL
1	A	310	LEU
1	A	316	LEU
1	A	326	LEU
1	B	17	MET
1	B	25	THR
1	B	48	LEU
1	B	98	ARG
1	B	99	LEU
1	B	113	LEU
1	B	163	ILE
1	B	180	LEU
1	B	209	LYS
1	B	210	LEU
1	B	223	LEU
1	B	227	THR
1	B	235	LEU
1	B	244	GLU
1	B	249	GLN
1	B	253	THR
1	B	277	VAL
1	B	310	LEU
1	B	316	LEU
1	B	326	LEU
1	C	17	MET
1	C	25	THR

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Mol	Chain	Res	Type
1	C	48	LEU
1	C	98	ARG
1	C	99	LEU
1	C	113	LEU
1	C	163	ILE
1	C	180	LEU
1	C	209	LYS
1	C	210	LEU
1	C	223	LEU
1	C	227	THR
1	C	235	LEU
1	C	244	GLU
1	C	249	GLN
1	C	253	THR
1	C	277	VAL
1	C	310	LEU
1	C	316	LEU
1	C	326	LEU
1	D	17	MET
1	D	25	THR
1	D	48	LEU
1	D	98	ARG
1	D	99	LEU
1	D	113	LEU
1	D	163	ILE
1	D	180	LEU
1	D	183	VAL
1	D	186	GLU
1	D	209	LYS
1	D	210	LEU
1	D	223	LEU
1	D	227	THR
1	D	235	LEU
1	D	244	GLU
1	D	249	GLN
1	D	253	THR
1	D	277	VAL
1	D	310	LEU
1	D	316	LEU
1	D	326	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	145	HIS
1	A	178	GLN
1	A	231	GLN
1	A	249	GLN
1	A	319	GLN
1	A	323	ASN
1	B	35	GLN
1	B	126	ASN
1	B	145	HIS
1	B	178	GLN
1	B	231	GLN
1	B	249	GLN
1	B	319	GLN
1	B	323	ASN
1	C	35	GLN
1	C	126	ASN
1	C	145	HIS
1	C	178	GLN
1	C	231	GLN
1	C	249	GLN
1	C	319	GLN
1	C	323	ASN
1	D	35	GLN
1	D	145	HIS
1	D	178	GLN
1	D	231	GLN
1	D	249	GLN
1	D	319	GLN
1	D	323	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	PLV	C	330	-	23,23,23	3.59	12 (52%)	29,32,32	3.34	11 (37%)
3	PLV	A	328	-	23,23,23	3.71	12 (52%)	29,32,32	3.30	12 (41%)
3	PLV	D	331	-	23,23,23	3.68	12 (52%)	29,32,32	3.30	11 (37%)
3	PLV	B	329	-	23,23,23	3.64	12 (52%)	29,32,32	3.29	11 (37%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLV	C	330	-	-	4/18/18/18	0/1/1/1
3	PLV	A	328	-	-	4/18/18/18	0/1/1/1
3	PLV	D	331	-	-	4/18/18/18	0/1/1/1
3	PLV	B	329	-	-	4/18/18/18	0/1/1/1

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	330	PLV	C3-C4	9.58	1.54	1.40
3	B	329	PLV	C3-C4	8.84	1.53	1.40
3	A	328	PLV	C3-C2	8.83	1.49	1.40
3	D	331	PLV	C3-C4	8.81	1.53	1.40
3	A	328	PLV	C3-C4	8.77	1.53	1.40
3	B	329	PLV	C3-C2	8.38	1.49	1.40
3	D	331	PLV	C3-C2	8.34	1.49	1.40
3	C	330	PLV	C3-C2	7.04	1.48	1.40
3	A	328	PLV	P-O4P	-6.07	1.40	1.60
3	D	331	PLV	P-O4P	-5.98	1.41	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	330	PLV	P-O4P	-5.92	1.41	1.60
3	B	329	PLV	P-O4P	-5.75	1.41	1.60
3	B	329	PLV	C4A-N	-4.87	1.32	1.46
3	A	328	PLV	C4A-N	-4.79	1.32	1.46
3	C	330	PLV	C4A-N	-4.78	1.32	1.46
3	D	331	PLV	C4A-N	-4.74	1.32	1.46
3	A	328	PLV	C5-C4	4.26	1.46	1.40
3	D	331	PLV	C2-N1	4.24	1.41	1.33
3	C	330	PLV	C2-N1	4.22	1.41	1.33
3	A	328	PLV	C2-N1	4.10	1.41	1.33
3	B	329	PLV	C2-N1	4.07	1.41	1.33
3	B	329	PLV	C5-C4	3.98	1.46	1.40
3	C	330	PLV	C5-C4	3.96	1.46	1.40
3	A	328	PLV	C6-C5	3.96	1.46	1.37
3	D	331	PLV	C6-C5	3.90	1.45	1.37
3	D	331	PLV	C5-C4	3.88	1.45	1.40
3	D	331	PLV	CA-C	3.85	1.62	1.52
3	B	329	PLV	C6-C5	3.76	1.45	1.37
3	A	328	PLV	P-O3P	-3.57	1.39	1.50
3	C	330	PLV	CA-C	3.56	1.61	1.52
3	B	329	PLV	P-O3P	-3.56	1.39	1.50
3	D	331	PLV	P-O3P	-3.54	1.39	1.50
3	C	330	PLV	C6-C5	3.50	1.45	1.37
3	B	329	PLV	CA-C	3.36	1.61	1.52
3	A	328	PLV	CA-C	3.19	1.60	1.52
3	C	330	PLV	P-O3P	-3.16	1.40	1.50
3	D	331	PLV	P-O2P	-3.04	1.43	1.54
3	A	328	PLV	C6-N1	2.95	1.40	1.34
3	D	331	PLV	C6-N1	2.95	1.40	1.34
3	B	329	PLV	P-O2P	-2.94	1.43	1.54
3	A	328	PLV	P-O2P	-2.91	1.43	1.54
3	C	330	PLV	C6-N1	2.79	1.40	1.34
3	C	330	PLV	P-O2P	-2.79	1.44	1.54
3	B	329	PLV	C6-N1	2.75	1.40	1.34
3	A	328	PLV	O-C	-2.53	1.22	1.30
3	D	331	PLV	O-C	-2.25	1.23	1.30
3	B	329	PLV	O-C	-2.21	1.23	1.30
3	C	330	PLV	O-C	-2.04	1.23	1.30

All (45) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	330	PLV	C4A-N-CA	10.91	134.60	113.92
3	A	328	PLV	C4A-N-CA	10.70	134.21	113.92
3	B	329	PLV	C4A-N-CA	10.66	134.14	113.92
3	D	331	PLV	C4A-N-CA	10.55	133.92	113.92
3	C	330	PLV	O4P-P-O3P	7.50	127.51	106.47
3	D	331	PLV	O4P-P-O3P	7.43	127.33	106.47
3	B	329	PLV	O4P-P-O3P	7.37	127.14	106.47
3	A	328	PLV	O4P-P-O3P	7.18	126.61	106.47
3	B	329	PLV	C4-C4A-N	6.61	129.97	111.78
3	A	328	PLV	C4-C4A-N	6.57	129.87	111.78
3	C	330	PLV	C4-C4A-N	6.55	129.82	111.78
3	D	331	PLV	C4-C4A-N	6.52	129.72	111.78
3	A	328	PLV	O3-C3-C2	4.11	126.45	117.49
3	C	330	PLV	C6-N1-C2	4.08	126.73	119.17
3	B	329	PLV	C6-N1-C2	4.02	126.61	119.17
3	B	329	PLV	O3-C3-C2	3.92	126.03	117.49
3	D	331	PLV	C6-N1-C2	3.91	126.41	119.17
3	A	328	PLV	C6-N1-C2	3.89	126.38	119.17
3	D	331	PLV	O3-C3-C2	3.88	125.95	117.49
3	C	330	PLV	O3-C3-C2	3.57	125.27	117.49
3	A	328	PLV	OG-CB-CA	3.43	119.04	109.39
3	D	331	PLV	OG-CB-CA	3.39	118.92	109.39
3	C	330	PLV	OG-CB-CA	3.34	118.76	109.39
3	B	329	PLV	OG-CB-CA	3.24	118.49	109.39
3	D	331	PLV	O-C-OXT	-3.12	117.01	124.09
3	A	328	PLV	O-C-OXT	-3.01	117.25	124.09
3	C	330	PLV	O-C-OXT	-2.97	117.35	124.09
3	B	329	PLV	O-C-OXT	-2.86	117.60	124.09
3	C	330	PLV	C5-C6-N1	-2.75	119.23	123.82
3	D	331	PLV	C3-C2-N1	-2.73	117.24	120.77
3	C	330	PLV	O4P-C5A-C5	2.70	114.50	109.35
3	B	329	PLV	C5-C6-N1	-2.69	119.33	123.82
3	A	328	PLV	CB-CA-N	2.68	115.42	108.58
3	B	329	PLV	O4P-C5A-C5	2.65	114.41	109.35
3	A	328	PLV	O4P-C5A-C5	2.63	114.37	109.35
3	A	328	PLV	C5-C6-N1	-2.63	119.44	123.82
3	D	331	PLV	C5-C6-N1	-2.62	119.45	123.82
3	B	329	PLV	C3-C2-N1	-2.58	117.44	120.77
3	C	330	PLV	C3-C2-N1	-2.54	117.49	120.77
3	D	331	PLV	O4P-C5A-C5	2.52	114.16	109.35
3	A	328	PLV	C3-C2-N1	-2.50	117.54	120.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	331	PLV	CB-CA-N	2.49	114.95	108.58
3	C	330	PLV	CB-CA-N	2.41	114.72	108.58
3	A	328	PLV	O-C-CA	2.10	120.38	113.40
3	B	329	PLV	CB-CA-N	2.08	113.89	108.58

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	328	PLV	C-CA-N-C4A
3	A	328	PLV	C3-C4-C4A-N
3	A	328	PLV	C5-C4-C4A-N
3	B	329	PLV	C-CA-N-C4A
3	B	329	PLV	C3-C4-C4A-N
3	B	329	PLV	C5-C4-C4A-N
3	C	330	PLV	C-CA-N-C4A
3	C	330	PLV	C3-C4-C4A-N
3	C	330	PLV	C5-C4-C4A-N
3	D	331	PLV	C-CA-N-C4A
3	D	331	PLV	C3-C4-C4A-N
3	D	331	PLV	C5-C4-C4A-N
3	A	328	PLV	CB-CA-N-C4A
3	B	329	PLV	CB-CA-N-C4A
3	C	330	PLV	CB-CA-N-C4A
3	D	331	PLV	CB-CA-N-C4A

There are no ring outliers.

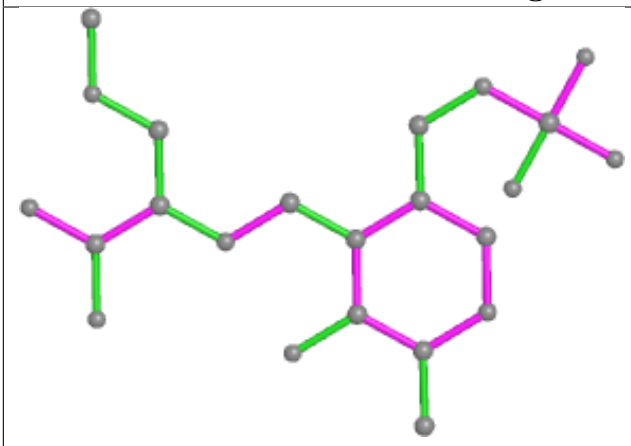
4 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	330	PLV	7	0
3	A	328	PLV	6	0
3	D	331	PLV	6	0
3	B	329	PLV	7	0

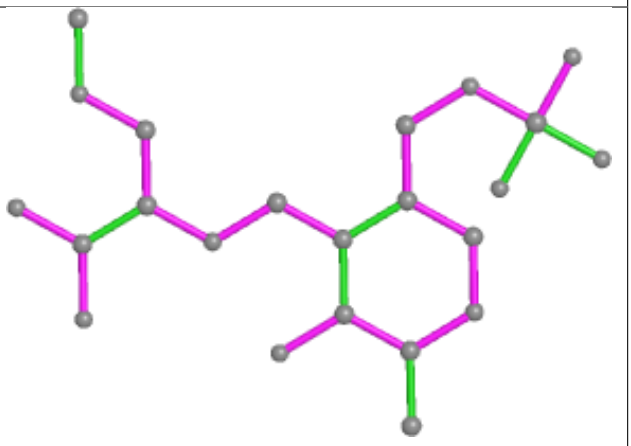
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

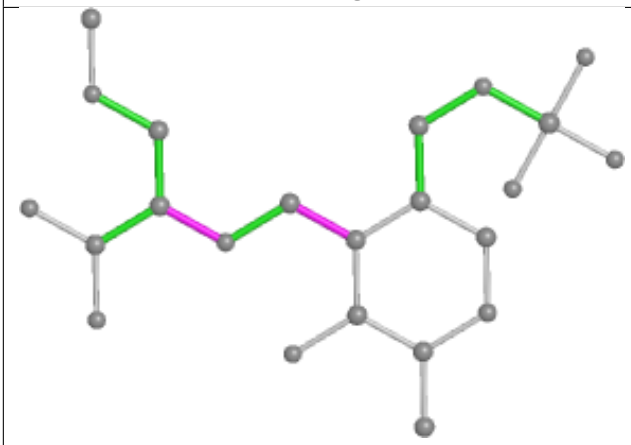
Ligand PLV C 330



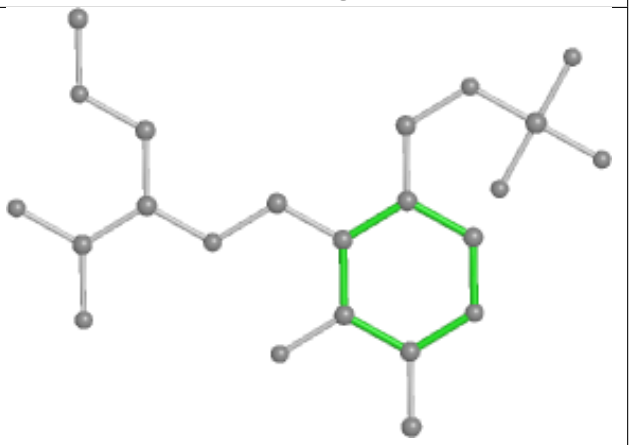
Bond lengths



Bond angles

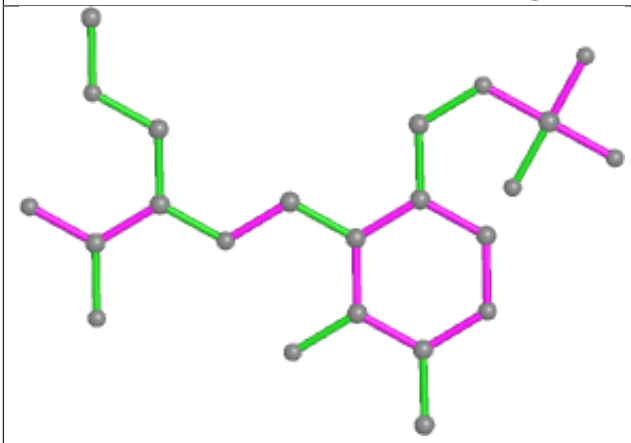


Torsions

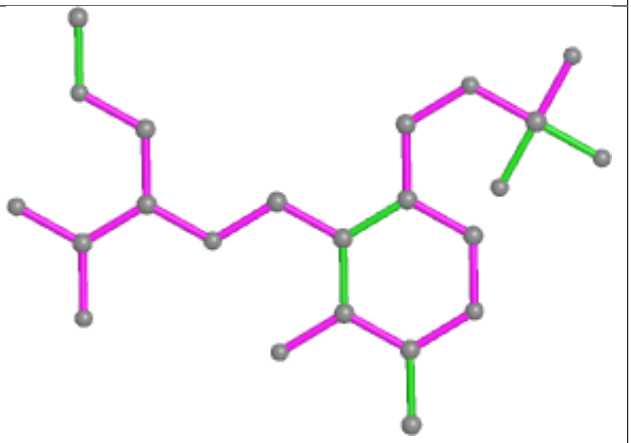


Rings

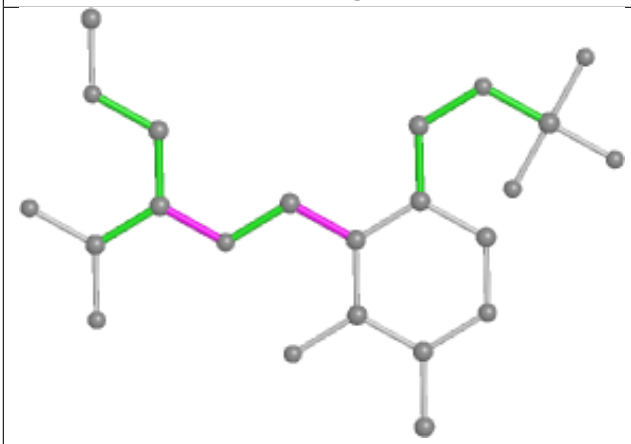
Ligand PLV A 328



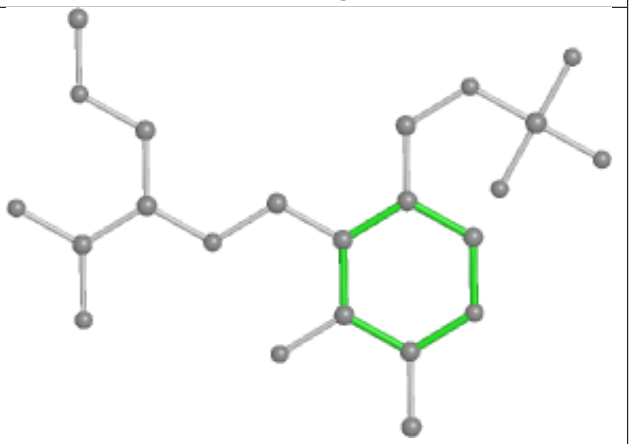
Bond lengths



Bond angles

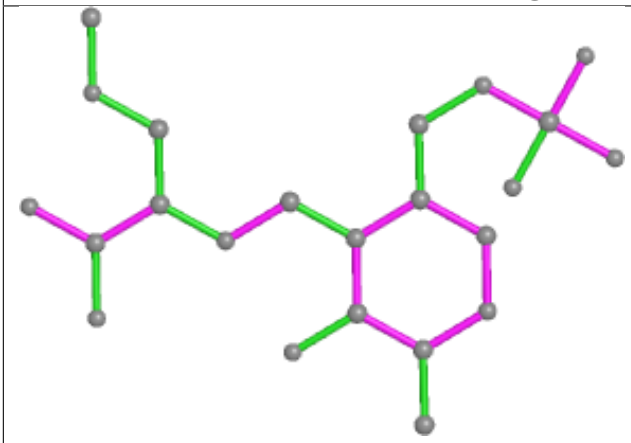


Torsions

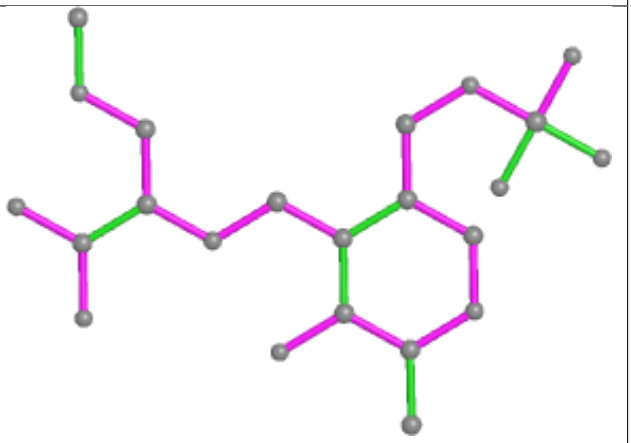


Rings

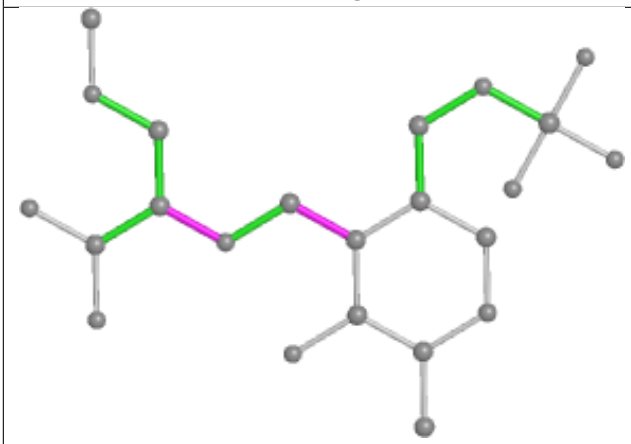
Ligand PLV D 331



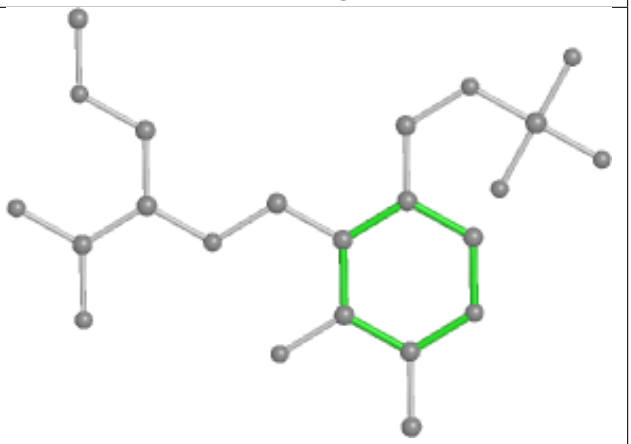
Bond lengths



Bond angles

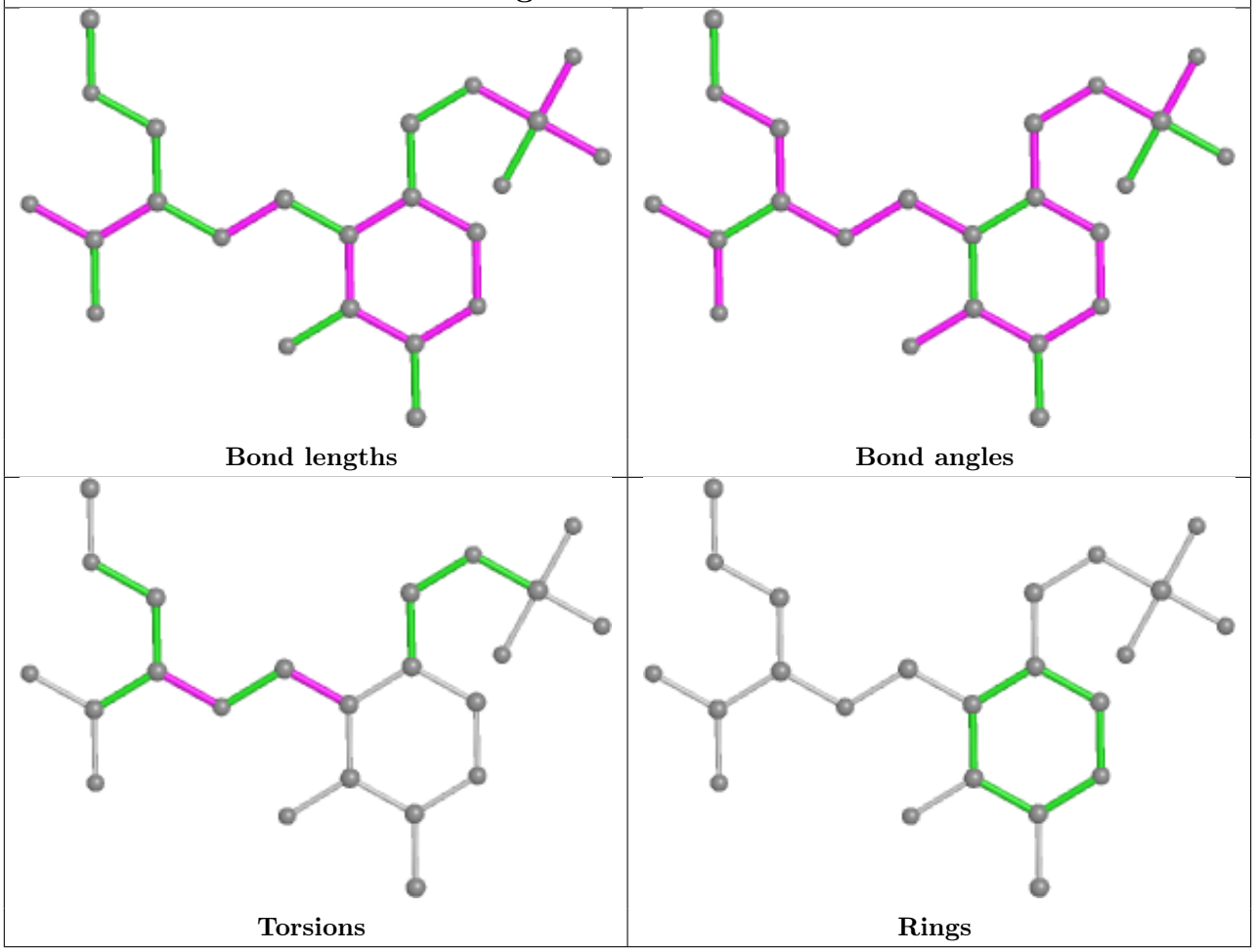


Torsions



Rings

Ligand PLV B 329



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.