



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:46 AM UTC

PDB ID : 2V0Z / pdb_00002v0z
Title : Crystal Structure of Renin with Inhibitor 10 (Aliskiren)
Authors : Rahuel, J.; Rasetti, V.; Maibaum, J.; Rueger, H.; Goschke, R.; Cohen, N.C.;
Stutz, S.; Cumin, F.; Fuhrer, W.; Wood, J.M.; Grutter, M.G.
Deposited on : 2007-05-21
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

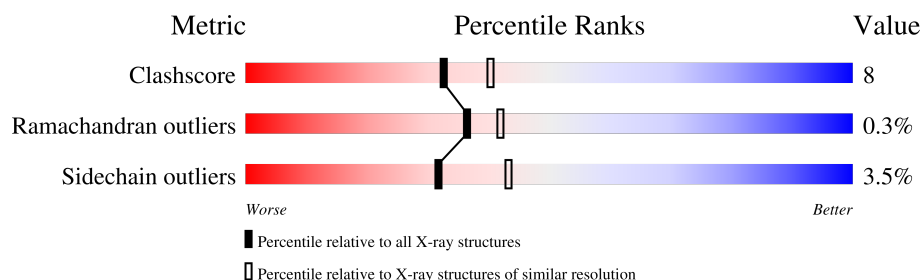
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	340	
1	O	340	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	C	1327	X	-	-	-
2	NAG	O	1328	X	-	-	-

2 Entry composition [i](#)

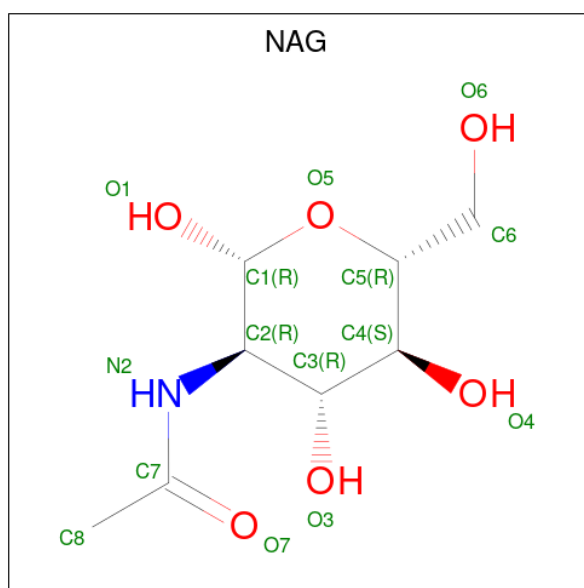
There are 4 unique types of molecules in this entry. The entry contains 5981 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 RENIN.

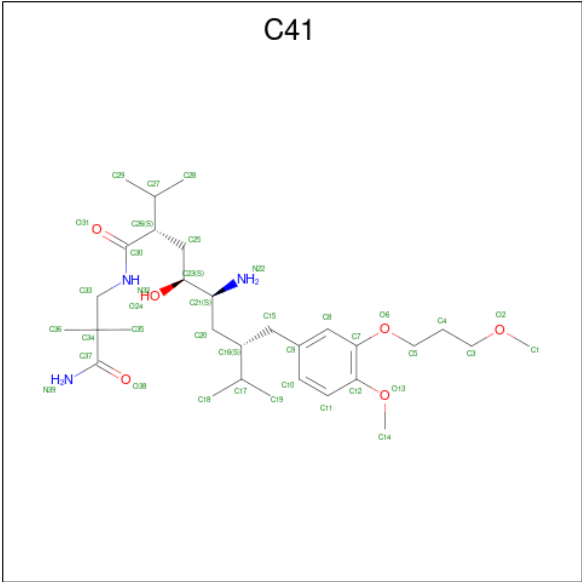
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	339	Total	C	N	O	S	0	0	1
			2597	1659	421	503	14			
1	O	337	Total	C	N	O	S	0	0	1
			2593	1657	420	502	14			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	O	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ALISKIREN (CCD ID: C41) (formula: $C_{30}H_{53}N_3O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			39	30	3	6		
3	O	1	Total	C	N	O	0	0
			39	30	3	6		

- Molecule 4 is water.

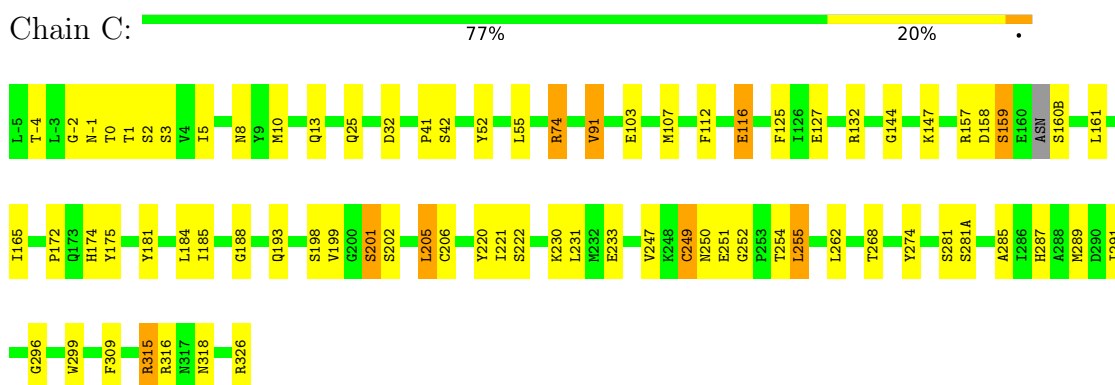
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	352	Total	O	0	0
			352	352		
4	O	333	Total	O	0	0
			333	333		

3 Residue-property plots

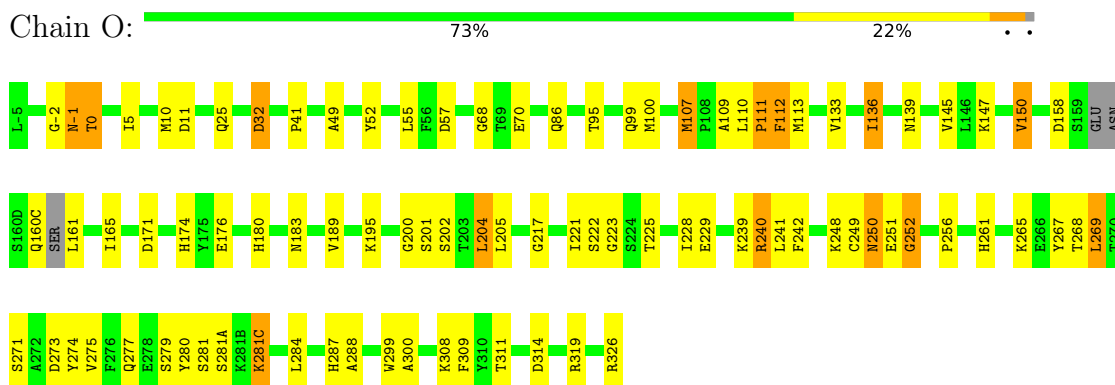
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: RENIN



• Molecule 1: RENIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	141.60 Å 141.60 Å 141.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.20	Depositor
% Data completeness (in resolution range)	97.0 (40.00-2.20)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.205 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5981	wwPDB-VP
Average B, all atoms (Å ²)	37.0	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: NAG, C41

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	C	0.61	1/2656 (0.0%)	1.05	21/3601 (0.6%)
1	O	0.57	1/2650 (0.0%)	1.03	23/3590 (0.6%)
All	All	0.59	2/5306 (0.0%)	1.04	44/7191 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	159	SER	C-N	-5.56	1.25	1.33
1	O	158	ASP	C-N	-5.04	1.26	1.33

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	201	SER	N-CA-C	9.03	120.82	110.97
1	O	221	ILE	N-CA-C	-8.12	96.75	108.36
1	C	112	PHE	N-CA-C	7.71	121.78	112.38
1	O	112	PHE	N-CA-C	7.28	121.27	112.38
1	C	221	ILE	N-CA-C	-6.96	98.55	108.58
1	O	174	HIS	N-CA-C	6.51	121.28	112.88
1	C	25	GLN	N-CA-C	-6.31	98.24	108.52
1	C	107	MET	CA-C-N	6.30	126.25	119.76
1	C	107	MET	C-N-CA	6.30	126.25	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	32	ASP	N-CA-C	6.29	118.95	108.20
1	O	280	TYR	N-CA-C	-6.20	105.56	112.57
1	C	157	ARG	N-CA-C	-6.04	104.03	112.25
1	C	202	SER	N-CA-C	6.00	118.53	109.41
1	O	68	GLY	N-CA-C	5.95	121.77	114.69
1	C	299	TRP	N-CA-C	-5.90	102.59	110.55
1	O	180	HIS	N-CA-C	-5.78	99.58	109.24
1	O	171	ASP	CA-C-N	5.75	125.42	119.56
1	O	171	ASP	C-N-CA	5.75	125.42	119.56
1	O	299	TRP	N-CA-C	-5.69	102.09	110.52
1	O	241	LEU	N-CA-C	-5.62	105.53	112.72
1	O	268	THR	N-CA-C	5.59	118.07	109.07
1	C	181	TYR	N-CA-C	5.57	118.81	109.95
1	C	1	THR	N-CA-C	-5.55	99.62	109.06
1	C	32	ASP	N-CA-C	5.55	117.69	108.20
1	O	309	PHE	N-CA-C	5.48	117.34	108.41
1	C	249	CYS	N-CA-C	5.42	117.89	111.33
1	C	268	THR	N-CA-C	5.41	118.05	109.24
1	O	107	MET	CA-C-N	5.39	125.31	119.76
1	O	107	MET	C-N-CA	5.39	125.31	119.76
1	O	311	THR	N-CA-C	5.38	118.17	109.40
1	O	281(C)	LYS	N-CA-C	5.33	117.29	109.24
1	C	309	PHE	N-CA-C	5.31	117.31	108.02
1	C	116	GLU	N-CA-C	-5.30	105.55	112.23
1	C	0	THR	N-CA-C	5.29	118.73	110.32
1	O	223	GLY	N-CA-C	-5.21	103.50	111.10
1	C	91	VAL	CB-CA-C	-5.15	104.60	110.73
1	O	52	TYR	N-CA-C	5.14	119.65	113.17
1	C	52	TYR	N-CA-C	5.13	119.53	113.16
1	C	10	MET	N-CA-C	5.10	118.63	111.90
1	O	-2	GLY	N-CA-C	-5.08	105.23	112.55
1	O	136	ILE	N-CA-C	5.04	115.75	110.62
1	C	233	GLU	N-CA-C	-5.03	105.71	111.14
1	O	252	GLY	CA-C-N	5.02	124.74	119.82
1	O	252	GLY	C-N-CA	5.02	124.74	119.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	267	TYR	Sidechain

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	C	2597	0	2527	36	0
1	O	2593	0	2529	47	0
2	C	14	0	13	0	0
2	O	14	0	13	0	0
3	C	39	0	53	0	0
3	O	39	0	53	0	0
4	C	352	0	0	5	0
4	O	333	0	0	5	0
All	All	5981	0	5188	83	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 8.

All (83) 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:C:13:GLN:HE22	1:C:116:GLU:H	1.10	0.93
1:O:99:GLN:NE2	1:O:139:ASN:HD22	1.89	0.70
1:O:49:ALA:HB3	1:O:107:MET:HG3	1.74	0.69
1:O:95:THR:HG22	4:O:2124:HOH:O	1.93	0.68
1:O:49:ALA:HB1	1:O:107:MET:HE2	1.77	0.66
1:O:-1:ASN:HA	1:O:147:LYS:HG2	1.76	0.66
1:O:25:GLN:HE22	1:O:57:ASP:H	1.45	0.65
1:O:99:GLN:HE22	1:O:139:ASN:HD22	1.46	0.62
1:O:99:GLN:NE2	1:O:136:ILE:HA	2.14	0.62
1:O:107:MET:HE3	1:O:112:PHE:HB3	1.82	0.61
1:C:13:GLN:NE2	1:C:116:GLU:H	1.90	0.59
1:O:281:SER:HB3	1:O:281(C):LYS:HG3	1.84	0.59
1:O:183:ASN:HD22	1:O:319:ARG:HB3	1.66	0.59
1:O:202:SER:HB2	1:O:204:LEU:HD23	1.85	0.58
1:C:201:SER:HB2	4:C:2242:HOH:O	2.01	0.58
1:O:250:ASN:H	1:O:250:ASN:HD22	1.50	0.58
1:O:225:THR:O	1:O:229:GLU:HG3	2.04	0.58
1:O:176:GLU:HG3	1:O:326:ARG:HD3	1.86	0.57
1:O:5:ILE:HG23	1:O:161:LEU:CD1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:THR:HA	4:O:2137:HOH:O	2.05	0.56
1:C:255:LEU:HB3	1:C:274:TYR:OH	2.05	0.56
1:O:240:ARG:HD2	4:O:2250:HOH:O	2.06	0.56
1:C:251:GLU:O	1:C:254:THR:HB	2.06	0.55
1:O:0:THR:HB	1:O:145:VAL:O	2.07	0.54
1:C:172:PRO:HA	1:C:175:TYR:CE1	2.42	0.54
1:C:172:PRO:HD3	4:C:2218:HOH:O	2.09	0.52
1:O:-1:ASN:HD22	1:O:-1:ASN:H	1.56	0.52
1:C:42:SER:HB2	1:C:103:GLU:HB3	1.92	0.52
1:O:204:LEU:HD12	1:O:205:LEU:HG	1.91	0.51
1:O:99:GLN:HE22	1:O:136:ILE:HA	1.75	0.51
1:C:-1:ASN:HA	1:C:147:LYS:HD2	1.92	0.51
1:C:132:ARG:HG2	4:C:2179:HOH:O	2.10	0.51
1:C:252:GLY:HA2	1:C:255:LEU:HD22	1.93	0.50
1:O:150:VAL:HG22	1:O:314:ASP:HA	1.92	0.50
1:C:205:LEU:HD13	1:C:230:LYS:HD3	1.94	0.50
1:O:275:VAL:HG22	1:O:284:LEU:HD22	1.94	0.50
1:O:269:LEU:HD22	1:O:308:LYS:HG2	1.93	0.49
1:C:-2:GLY:O	1:C:147:LYS:HD2	2.12	0.48
1:O:195:LYS:HG3	4:O:2268:HOH:O	2.11	0.48
1:O:107:MET:CE	1:O:112:PHE:HB3	2.43	0.48
1:O:249:CYS:HB3	1:O:279:SER:O	2.13	0.48
1:C:-4:THR:O	1:C:144:GLY:HA2	2.13	0.47
1:C:-1:ASN:HA	1:C:147:LYS:CD	2.45	0.47
1:C:159:SER:O	1:C:160(B):SER:N	2.47	0.47
1:C:206:CYS:SG	1:C:206:CYS:O	2.72	0.47
1:O:271:SER:HA	1:O:274:TYR:CE2	2.49	0.47
1:O:100:MET:HB3	1:O:133:VAL:CG1	2.45	0.46
1:O:222:SER:OG	1:O:300:ALA:HB3	2.15	0.46
1:O:109:ALA:O	1:O:113:MET:HB2	2.14	0.46
1:C:5:ILE:HG23	1:C:161:LEU:HD12	1.97	0.46
1:C:41:PRO:HB2	1:C:55:LEU:HD23	1.96	0.46
1:C:291:ILE:O	1:C:296:GLY:HA3	2.16	0.46
1:O:252:GLY:HA3	1:O:277:GLN:OE1	2.15	0.46
1:O:222:SER:HA	1:O:287:HIS:O	2.15	0.45
1:O:-1:ASN:HD22	1:O:-1:ASN:N	2.14	0.45
1:C:220:TYR:HB3	1:C:285:ALA:O	2.17	0.44
1:C:74:ARG:NH1	4:C:2135:HOH:O	2.51	0.44
1:O:10:MET:O	1:O:11:ASP:HB2	2.18	0.44
1:O:160(C):GLN:N	4:O:2174:HOH:O	2.50	0.44
1:C:222:SER:HA	1:C:287:HIS:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:261:HIS:HD2	1:O:265:LYS:O	2.02	0.43
1:C:125:PHE:HB3	1:C:127:GLU:OE1	2.19	0.42
1:C:250:ASN:OD1	1:C:281(A):SER:HA	2.19	0.42
1:C:199:VAL:HG21	1:C:231:LEU:HD12	2.02	0.42
1:C:184:LEU:HG	1:C:318:ASN:C	2.44	0.42
1:O:248:LYS:HB2	1:O:251:GLU:HG2	2.02	0.42
1:C:125:PHE:CG	1:C:188:GLY:HA2	2.54	0.42
1:C:289:MET:HG3	4:C:2139:HOH:O	2.19	0.42
1:O:41:PRO:HB2	1:O:55:LEU:HD23	2.01	0.42
1:O:228:ILE:HG13	1:O:288:ALA:HA	2.02	0.42
1:O:32:ASP:OD1	1:O:217:GLY:HA3	2.19	0.42
1:O:269:LEU:HB3	1:O:273:ASP:HB2	2.01	0.42
1:C:174:HIS:C	1:C:326:ARG:HG2	2.44	0.42
1:C:185:ILE:HD13	1:C:193:GLN:HB2	2.01	0.41
1:O:239:LYS:HE2	1:O:242:PHE:O	2.20	0.41
1:C:249:CYS:HB2	1:C:281:SER:O	2.19	0.41
1:C:8:ASN:HB3	1:C:158:ASP:HB3	2.01	0.41
1:O:250:ASN:ND2	1:O:281(A):SER:HA	2.36	0.41
1:O:86:GLN:HE21	1:O:100:MET:HE2	1.86	0.40
1:O:110:LEU:HA	1:O:111:PRO:HA	1.78	0.40
1:C:315:ARG:HB3	1:C:315:ARG:HH11	1.86	0.40
1:O:200:GLY:CA	1:O:256:PRO:HB2	2.51	0.40
1:C:3:SER:HA	1:C:165:ILE:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	C	335/340 (98%)	327 (98%)	8 (2%)	0	100	100
1	O	331/340 (97%)	321 (97%)	8 (2%)	2 (1%)	21	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	666/680 (98%)	648 (97%)	16 (2%)	2 (0%)	36	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	240	ARG
1	O	201	SER

5.3.2 Protein sidechains ⓘ

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	C	285/290 (98%)	275 (96%)	10 (4%)	32	43
1	O	286/290 (99%)	276 (96%)	10 (4%)	32	43
All	All	571/580 (98%)	551 (96%)	20 (4%)	32	43

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2	SER
1	C	74	ARG
1	C	91	VAL
1	C	198	SER
1	C	205	LEU
1	C	247	VAL
1	C	255	LEU
1	C	262	LEU
1	C	315	ARG
1	C	316	ARG
1	O	-1	ASN
1	O	0	THR
1	O	70	GLU
1	O	111	PRO
1	O	150	VAL
1	O	165	ILE

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Mol	Chain	Res	Type
1	O	189	VAL
1	O	204	LEU
1	O	250	ASN
1	O	269	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	13	GLN
1	C	143	GLN
1	C	191	GLN
1	C	318	ASN
1	O	-1	ASN
1	O	25	GLN
1	O	86	GLN
1	O	99	GLN
1	O	183	ASN
1	O	191	GLN
1	O	250	ASN
1	O	261	HIS
1	O	318	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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	C41	O	1327	-	38,39,39	1.07	3 (7%)	42,53,53	0.66	0
2	NAG	O	1328	1	14,14,15	1.79	2 (14%)	17,19,21	3.03	9 (52%)
2	NAG	C	1327	1	14,14,15	2.14	5 (35%)	17,19,21	3.28	8 (47%)
3	C41	C	1328	-	38,39,39	1.21	2 (5%)	42,53,53	0.78	1 (2%)

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	C41	O	1327	-	-	3/48/48/48	0/1/1/1
2	NAG	O	1328	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	C	1327	1	1/1/5/7	0/6/23/26	0/1/1/1
3	C41	C	1328	-	-	1/48/48/48	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	1328	NAG	C1-C2	5.21	1.59	1.52
2	C	1327	NAG	O5-C5	4.99	1.53	1.43
3	C	1328	C41	C34-C37	-4.66	1.42	1.53
3	C	1328	C41	O13-C12	3.55	1.42	1.37
3	O	1327	C41	C34-C37	-3.53	1.45	1.53
2	O	1328	NAG	C3-C2	3.19	1.59	1.52
2	C	1327	NAG	C1-C2	3.12	1.56	1.52
2	C	1327	NAG	O5-C1	3.10	1.48	1.43
3	O	1327	C41	O13-C12	3.07	1.42	1.37
2	C	1327	NAG	C3-C2	2.80	1.58	1.52
2	C	1327	NAG	C6-C5	2.57	1.60	1.51
3	O	1327	C41	O6-C7	2.33	1.42	1.37

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1327	NAG	C1-O5-C5	9.22	124.54	112.19
2	O	1328	NAG	C3-C4-C5	-7.57	96.50	110.23
2	C	1327	NAG	C3-C4-C5	-6.06	99.25	110.23
2	O	1328	NAG	C1-O5-C5	4.96	118.84	112.19
2	O	1328	NAG	O4-C4-C5	4.21	119.70	109.32
2	O	1328	NAG	O5-C1-C2	-4.13	104.90	111.29
2	C	1327	NAG	O4-C4-C3	3.73	119.16	110.38
2	C	1327	NAG	C1-C2-N2	3.45	115.87	110.43
2	C	1327	NAG	O4-C4-C5	3.13	117.02	109.32
2	C	1327	NAG	O7-C7-C8	-3.09	116.55	122.05
2	O	1328	NAG	O3-C3-C2	2.59	114.77	109.40
2	O	1328	NAG	O5-C5-C6	2.54	112.61	107.66
3	C	1328	C41	C20-C16-C15	-2.43	108.35	111.45
2	O	1328	NAG	C1-C2-N2	2.43	114.26	110.43
2	O	1328	NAG	O5-C5-C4	-2.38	105.03	110.83
2	C	1327	NAG	C8-C7-N2	2.25	119.85	116.12
2	C	1327	NAG	C4-C3-C2	-2.08	107.98	111.02
2	O	1328	NAG	C8-C7-N2	-2.05	112.72	116.12

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1327	NAG	C1
2	O	1328	NAG	C1

All (4) torsion outliers are listed below:

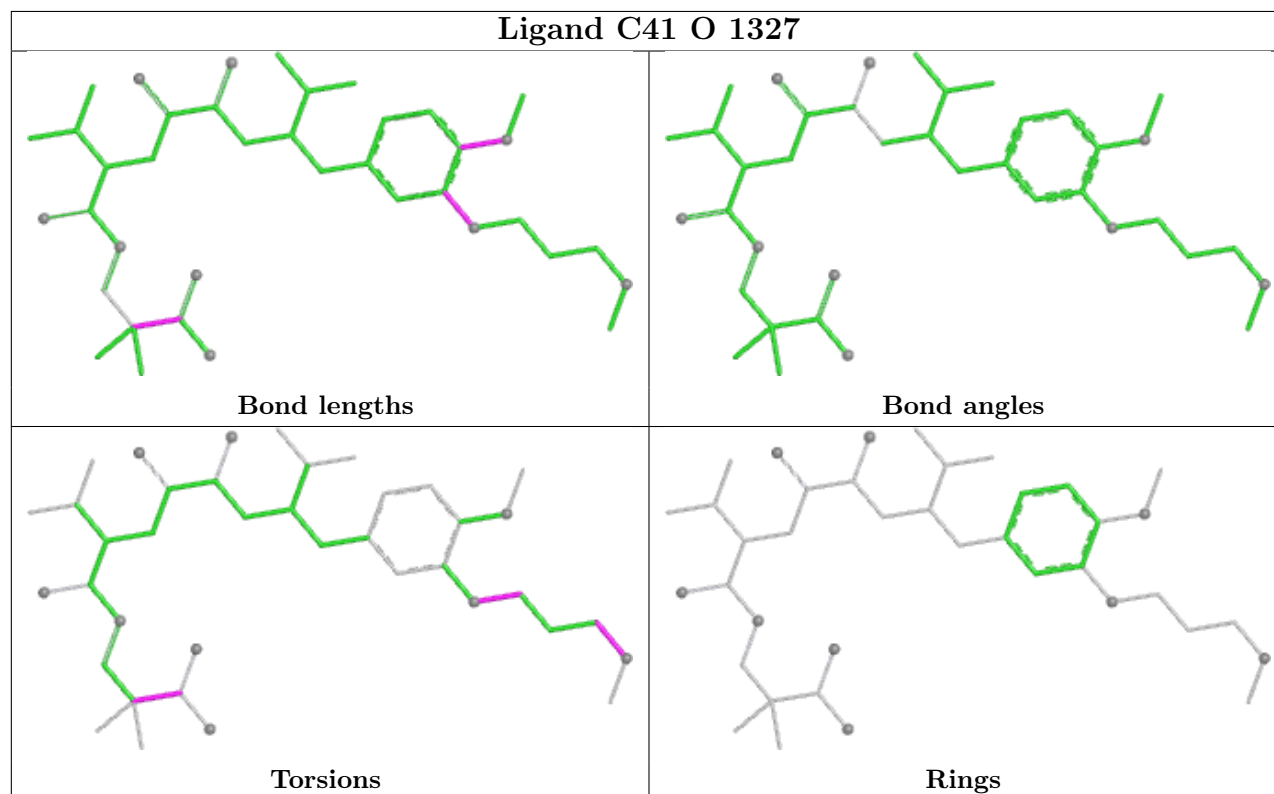
Mol	Chain	Res	Type	Atoms
3	O	1327	C41	C36-C34-C37-O38
3	C	1328	C41	C4-C3-O2-C1
3	O	1327	C41	C4-C3-O2-C1
3	O	1327	C41	C4-C5-O6-C7

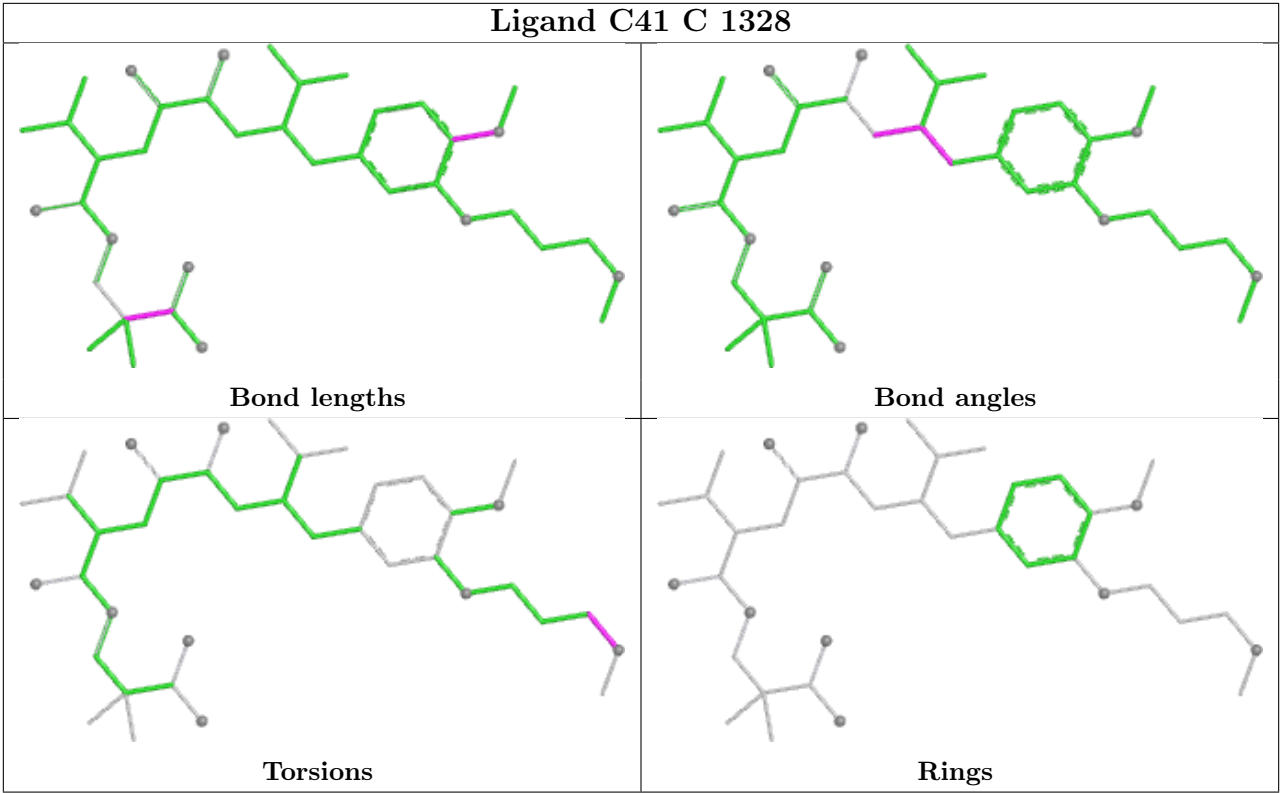
There are no ring outliers.

No monomer is involved in short contacts.

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 than 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.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	O	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	O	160(D):SER	C	160(C):GLN	N	4.86

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.