



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 04:08 AM GMT

PDB ID : 1R1L  
Title : Structure of dimeric antithrombin complexed with a P14-P9 reactive loop peptide and an exogenous tripeptide (formyl-norleucine-LF)  
Authors : Zhou, A.; Huntington, J.A.; Lomas, D.A.; Stein, P.E.; Carrell, R.W.  
Deposited on : 2003-09-24  
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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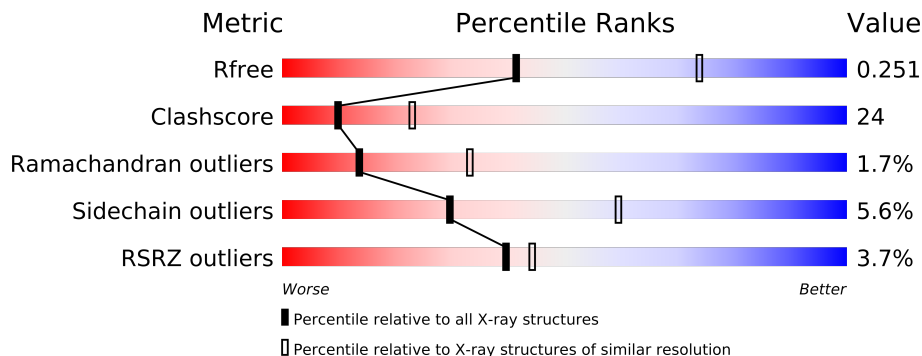
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 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))
$R_{free}$	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	I	432	
1	L	432	
2	C	7	
3	D	3	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	NAG	I	942	-	X
4	NAG	I	961	-	X
4	NAG	L	801	-	X
4	NAG	L	841	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6898 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Antithrombin-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	409	Total	C	N	O	S	0	0	0
			3270	2085	550	617	18			
1	I	416	Total	C	N	O	S	0	0	0
			3328	2121	562	627	18			

- Molecule 2 is a protein called Antithrombin P14-P9 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			40	22	6	12			

- Molecule 3 is a protein called EXOGENOUS TRIPEPTIDE formyl-(NLE)LF.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	3	Total	C	N	O	0	0	0
			28	21	3	4			

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	L	1	Total	C	N	O	0	0
			15	8	1	6		
4	L	1	Total	C	N	O	0	0
			15	8	1	6		
4	I	1	Total	C	N	O	0	0
			15	8	1	6		
4	I	1	Total	C	N	O	0	0
			15	8	1	6		
4	I	1	Total	C	N	O	0	0
			15	8	1	6		
4	I	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 5 is FORMYL GROUP (three-letter code: FOR) (formula: CH<sub>2</sub>O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			2	1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $\text{C}_3\text{H}_8\text{O}_3$ ).



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

- Molecule 7 is water.

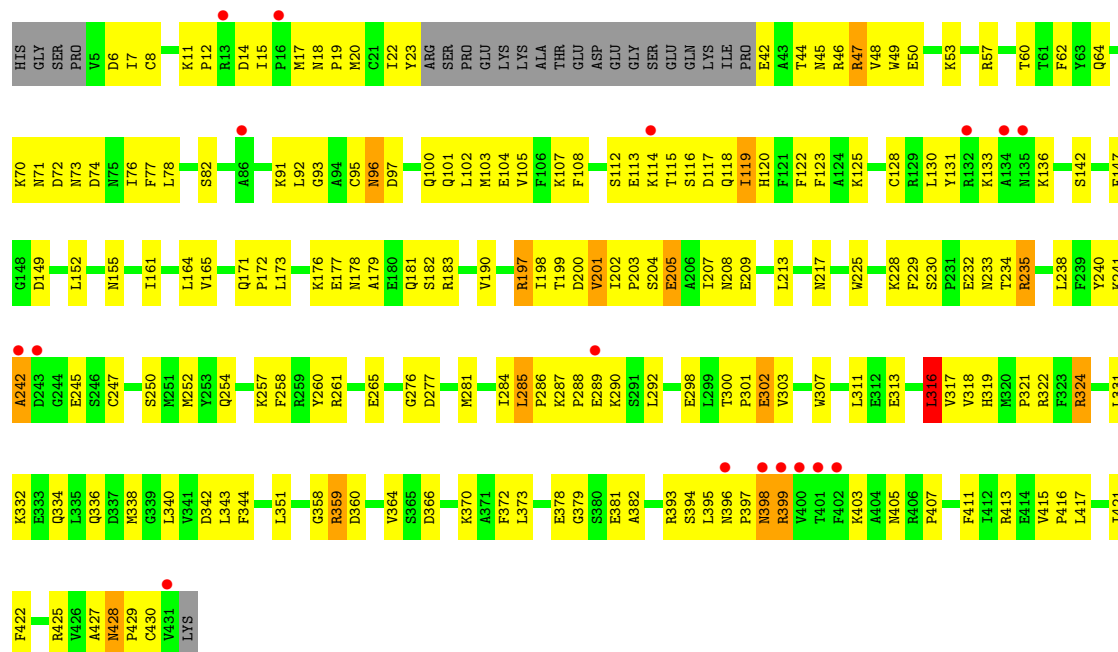
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total 1	O 1	0	0
7	I	76	Total 76	O 76	0	0
7	L	42	Total 42	O 42	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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.

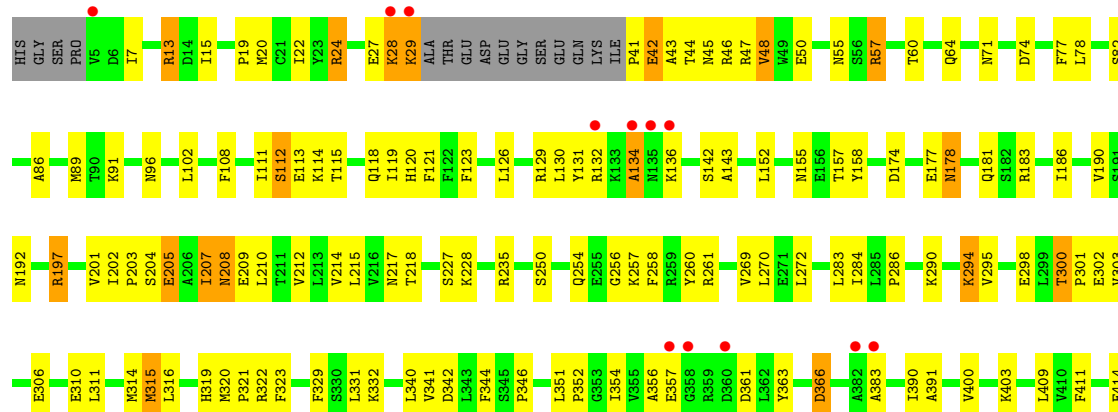
- Molecule 1: Antithrombin-III

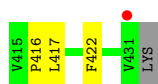
Chain L:



- Molecule 1: Antithrombin-III

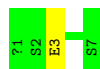
Chain I: 





- Molecule 2: Antithrombin P14-P9 peptide

Chain C:



- Molecule 3: EXOGENOUS TRIPEPTIDE formyl-(NLE)LF

Chain D:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.17Å 100.42Å 87.20Å 90.00° 104.29° 90.00°	Depositor
Resolution (Å)	24.99 – 2.70 24.99 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (24.99-2.70) 99.6 (24.99-2.70)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 2.72Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.204 , 0.249 0.203 , 0.251	Depositor DCC
$R_{free}$ test set	1602 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.7	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 31687 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6898	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NLE, FOR, ACE, NAG

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	I	0.37	0/3394	0.61	0/4580
1	L	0.37	0/3334	0.61	1/4501 (0.0%)
2	C	0.46	0/37	0.46	0/48
3	D	0.75	0/20	0.84	0/24
All	All	0.38	0/6785	0.61	1/9153 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	316	LEU	CA-CB-CG	5.94	128.97	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	3328	0	3335	145	0
1	L	3270	0	3270	176	0
2	C	40	0	34	1	0
3	D	28	0	30	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	75	0	75	18	0
4	L	30	0	30	9	0
5	D	2	0	0	0	0
6	C	6	0	8	1	0
7	D	1	0	0	0	0
7	I	76	0	0	3	0
7	L	42	0	0	1	0
All	All	6898	0	6782	325	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 24.

All (325) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:155:ASN:HD21	4:L:841:NAG:H1	1.14	1.13
1:L:155:ASN:HD21	4:L:841:NAG:C1	1.60	1.12
1:I:96:ASN:HD21	4:I:901:NAG:C1	1.62	1.11
1:L:155:ASN:ND2	4:L:841:NAG:H1	1.69	1.05
1:I:57:ARG:HB3	1:I:57:ARG:HH11	1.21	1.03
1:L:7:ILE:HD11	1:L:164:LEU:HG	1.33	1.02
1:I:96:ASN:HD21	4:I:901:NAG:H1	1.19	1.02
1:I:96:ASN:ND2	4:I:901:NAG:H1	1.74	1.02
1:I:227:SER:HB3	1:I:254:GLN:HE22	1.28	0.97
1:I:208:ASN:ND2	1:I:210:LEU:H	1.67	0.92
1:I:316:LEU:HB3	1:I:400:VAL:HG13	1.52	0.91
1:I:319:HIS:HB2	1:I:403:LYS:HA	1.54	0.89
4:I:941:NAG:H61	4:I:942:NAG:H81	1.54	0.88
1:I:91:LYS:NZ	1:I:120:HIS:NE2	2.22	0.88
1:I:19:PRO:HG3	1:I:22:ILE:HD11	1.56	0.87
1:L:428:ASN:HD21	1:L:430:CYS:HB2	1.41	0.85
1:I:57:ARG:HB3	1:I:57:ARG:NH1	1.92	0.83
1:I:178:ASN:HD22	1:I:178:ASN:N	1.74	0.82
1:L:17:MET:SD	1:L:161:ILE:HD11	2.21	0.80
1:L:287:LYS:HG2	1:L:290:LYS:HB2	1.63	0.79
1:L:91:LYS:NZ	1:L:120:HIS:NE2	2.31	0.79
1:L:332:LYS:O	1:L:336:GLN:HG3	1.84	0.77
1:I:208:ASN:HD22	1:I:210:LEU:H	1.32	0.77
1:L:18:ASN:ND2	4:L:841:NAG:H62	2.00	0.76
1:L:42:GLU:HB3	1:L:45:ASN:HD22	1.51	0.76
1:L:183:ARG:HD2	1:L:203:PRO:O	1.87	0.74
1:I:300:THR:CG2	1:I:302:GLU:HG2	2.19	0.73
1:L:46:ARG:O	1:L:50:GLU:HG3	1.89	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:208:ASN:HD22	1:I:208:ASN:C	1.92	0.72
1:I:7:ILE:HG13	1:I:15:ILE:CD1	2.20	0.71
1:L:102:LEU:HD23	1:L:340:LEU:HD21	1.72	0.71
1:L:71:ASN:HB3	1:L:74:ASP:OD2	1.91	0.70
1:L:230:SER:HB2	1:L:233:ASN:HD22	1.54	0.70
1:I:209:GLU:CD	1:I:209:GLU:H	1.95	0.70
1:L:209:GLU:CD	1:L:209:GLU:H	1.95	0.69
1:I:46:ARG:O	1:I:50:GLU:HG3	1.93	0.69
1:L:49:TRP:CH2	1:L:53:LYS:HD2	2.27	0.68
1:I:41:PRO:O	1:I:42:GLU:HB3	1.94	0.68
1:L:96:ASN:N	1:L:96:ASN:HD22	1.90	0.68
1:L:155:ASN:ND2	4:L:841:NAG:C1	2.39	0.67
1:I:91:LYS:HZ1	1:I:120:HIS:CE1	2.12	0.67
1:L:176:LYS:HE3	1:L:359:ARG:HH22	1.58	0.67
1:I:300:THR:HG21	1:I:302:GLU:HG2	1.76	0.66
1:L:77:PHE:CE2	1:L:373:LEU:HB2	2.32	0.65
1:I:82:SER:HA	1:I:217:ASN:ND2	2.12	0.65
1:L:300:THR:HB	1:L:303:VAL:HG23	1.79	0.65
1:L:108:PHE:HB3	1:L:119:ILE:HG13	1.78	0.64
1:L:254:GLN:NE2	1:L:258:PHE:HZ	1.95	0.64
4:L:841:NAG:H82	4:L:841:NAG:O1	1.98	0.64
1:L:96:ASN:ND2	4:L:801:NAG:O1	2.30	0.64
1:I:177:GLU:C	1:I:178:ASN:HD22	2.01	0.64
1:I:96:ASN:ND2	4:I:901:NAG:C1	2.41	0.64
1:L:428:ASN:ND2	1:L:430:CYS:HB2	2.13	0.64
1:L:427:ALA:O	1:L:429:PRO:HD3	1.98	0.63
1:L:398:ASN:N	1:L:398:ASN:HD22	1.95	0.63
1:I:155:ASN:ND2	4:I:941:NAG:O1	2.31	0.63
1:I:208:ASN:ND2	1:I:210:LEU:N	2.45	0.63
1:I:28:LYS:HE3	1:I:29:LYS:HE3	1.79	0.63
1:L:91:LYS:CE	1:L:103:MET:HE3	2.28	0.63
1:I:178:ASN:N	1:I:178:ASN:ND2	2.47	0.63
1:L:70:LYS:HD2	1:L:76:ILE:HG12	1.81	0.62
1:I:111:ILE:HG22	1:I:114:LYS:HG3	1.81	0.62
1:I:414:GLU:OE1	1:I:416:PRO:HG2	1.98	0.62
1:I:192:ASN:ND2	4:I:961:NAG:O5	2.32	0.62
1:L:285:LEU:N	1:L:285:LEU:HD23	2.14	0.62
1:I:152:LEU:CD1	1:I:212:VAL:HB	2.29	0.62
1:I:294:LYS:O	1:I:298:GLU:HG3	2.00	0.62
1:I:306:GLU:O	1:I:310:GLU:HG3	1.98	0.62
1:I:192:ASN:HD21	4:I:961:NAG:C5	2.13	0.62
1:L:230:SER:HB3	1:L:232:GLU:OE2	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:201:VAL:HG23	1:I:202:ILE:HG13	1.82	0.61
1:L:60:THR:O	1:L:64:GLN:HG3	2.00	0.61
1:L:324:ARG:HA	1:L:373:LEU:O	2.01	0.61
1:L:287:LYS:HG2	1:L:290:LYS:CB	2.30	0.61
1:I:28:LYS:HB3	1:I:112:SER:OG	2.00	0.61
1:L:178:ASN:HB3	1:L:181:GLN:HB2	1.81	0.60
1:L:230:SER:HB2	1:L:233:ASN:ND2	2.16	0.60
1:L:407:PRO:HB3	1:L:427:ALA:HB2	1.82	0.60
1:I:183:ARG:NE	1:I:204:SER:HA	2.17	0.60
1:I:356:ALA:HB1	4:I:941:NAG:H81	1.83	0.60
3:D:12:PHE:N	3:D:12:PHE:CD1	2.69	0.60
1:L:91:LYS:HE2	1:L:103:MET:HE3	1.82	0.60
1:L:116:SER:O	1:L:119:ILE:HG22	2.00	0.60
1:I:300:THR:HG22	1:I:303:VAL:H	1.66	0.60
1:I:332:LYS:HB2	7:I:1038:HOH:O	2.02	0.60
4:I:961:NAG:O4	4:I:962:NAG:N2	2.35	0.60
1:L:284:ILE:HD13	1:L:307:TRP:CZ3	2.36	0.60
1:I:227:SER:HB3	1:I:254:GLN:NE2	2.08	0.60
1:I:7:ILE:HG13	1:I:15:ILE:HD13	1.84	0.60
1:I:283:LEU:HD11	1:I:320:MET:CE	2.32	0.59
1:L:18:ASN:N	1:L:19:PRO:HD3	2.18	0.59
1:I:341:VAL:HG23	1:I:342:ASP:N	2.17	0.59
1:L:208:ASN:HD22	1:L:393:ARG:NH1	1.99	0.59
1:I:152:LEU:HD11	1:I:212:VAL:HB	1.84	0.59
1:L:44:THR:O	1:L:48:VAL:HG23	2.02	0.59
1:I:108:PHE:HB3	1:I:119:ILE:HG12	1.84	0.59
1:I:208:ASN:HD22	1:I:210:LEU:N	1.99	0.59
1:I:294:LYS:HA	1:I:294:LYS:HE3	1.84	0.59
1:L:316:LEU:HD23	1:L:318:VAL:HG23	1.83	0.59
1:L:415:VAL:HB	1:L:416:PRO:HD3	1.84	0.59
1:L:265:GLU:OE2	1:L:290:LYS:HE2	2.02	0.59
1:L:332:LYS:NZ	1:L:394:SER:OG	2.33	0.58
1:I:192:ASN:HD21	4:I:961:NAG:H61	1.69	0.58
1:L:428:ASN:HD22	1:L:428:ASN:C	2.07	0.58
1:I:174:ASP:OD2	1:I:177:GLU:HB2	2.04	0.58
1:I:366:ASP:HB2	3:D:11:LEU:HD11	1.85	0.58
1:L:398:ASN:N	1:L:398:ASN:ND2	2.52	0.57
1:I:286:PRO:HB3	1:I:295:VAL:HG21	1.86	0.57
1:I:202:ILE:HG21	1:I:207:ILE:CD1	2.34	0.57
1:I:102:LEU:HD23	1:I:340:LEU:HD11	1.86	0.57
1:L:300:THR:CG2	1:L:302:GLU:HG2	2.34	0.57
1:L:260:TYR:CG	1:L:261:ARG:N	2.72	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:23:TYR:CE2	1:L:100:GLN:HG3	2.40	0.57
1:I:269:VAL:HG12	1:I:311:LEU:HD21	1.86	0.57
1:I:186:ILE:HD13	1:I:214:VAL:HG11	1.86	0.56
1:I:250:SER:O	1:I:321:PRO:HA	2.05	0.56
1:L:96:ASN:N	1:L:96:ASN:ND2	2.54	0.56
1:I:346:PRO:HG3	1:I:363:TYR:CZ	2.40	0.56
1:I:129:ARG:HB3	1:I:417:LEU:HD11	1.86	0.56
1:I:290:LYS:HE3	1:I:294:LYS:HG2	1.87	0.56
1:I:19:PRO:CG	1:I:22:ILE:HD11	2.33	0.56
1:L:234:THR:C	1:L:235:ARG:HD2	2.25	0.56
1:I:130:LEU:HD23	1:I:414:GLU:HG3	1.88	0.55
1:L:230:SER:HB3	1:L:232:GLU:HG2	1.87	0.55
1:L:62:PHE:HZ	1:L:331:LEU:HD22	1.72	0.55
1:L:7:ILE:CD1	1:L:165:VAL:HA	2.37	0.55
1:L:225:TRP:CD1	1:L:379:GLY:HA2	2.42	0.55
1:I:341:VAL:HG23	1:I:342:ASP:H	1.71	0.55
1:I:257:LYS:HG3	1:I:315:MET:HE2	1.87	0.54
1:L:398:ASN:O	1:L:399:ARG:HB3	2.08	0.54
1:I:202:ILE:HD13	1:I:207:ILE:HD11	1.88	0.54
1:I:300:THR:HG23	1:I:302:GLU:OE2	2.07	0.54
1:I:24:ARG:HD2	1:I:115:THR:HG22	1.89	0.54
1:L:47:ARG:HG2	1:L:122:PHE:CE2	2.43	0.54
1:L:19:PRO:HG2	1:L:117:ASP:HB2	1.89	0.54
1:I:41:PRO:O	1:I:42:GLU:CB	2.56	0.54
1:I:203:PRO:HB2	1:I:205:GLU:OE2	2.08	0.53
1:L:300:THR:HG22	1:L:302:GLU:HG2	1.90	0.53
1:L:62:PHE:CZ	1:L:331:LEU:HD22	2.44	0.53
1:L:47:ARG:HG2	1:L:122:PHE:CZ	2.42	0.53
1:I:132:ARG:CD	1:I:136:LYS:HE3	2.39	0.53
1:L:7:ILE:HD12	1:L:165:VAL:HA	1.91	0.53
1:L:265:GLU:O	1:L:287:LYS:HD2	2.08	0.53
1:L:261:ARG:HB3	1:L:311:LEU:HD23	1.91	0.53
1:L:77:PHE:CZ	1:L:373:LEU:HB2	2.43	0.53
1:I:82:SER:HA	1:I:217:ASN:HD21	1.74	0.53
1:L:49:TRP:CZ3	1:L:53:LYS:HD2	2.44	0.53
1:L:15:ILE:HG23	1:L:164:LEU:HD21	1.90	0.52
1:I:42:GLU:O	1:I:44:THR:N	2.42	0.52
1:L:316:LEU:CD2	1:L:318:VAL:HG23	2.40	0.52
1:L:203:PRO:HB2	1:L:395:LEU:HD12	1.91	0.52
1:I:15:ILE:HD12	1:I:121:PHE:HE1	1.74	0.52
1:L:321:PRO:HD3	1:I:391:ALA:O	2.09	0.52
1:L:95:CYS:SG	1:L:96:ASN:ND2	2.83	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:47:ARG:NH1	1:I:50:GLU:OE1	2.40	0.52
1:I:190:VAL:HG11	1:I:201:VAL:HG11	1.91	0.52
1:L:257:LYS:HB3	1:L:257:LYS:NZ	2.25	0.52
1:I:192:ASN:ND2	4:I:961:NAG:H61	2.24	0.52
1:L:298:GLU:O	1:L:303:VAL:HG21	2.10	0.51
1:I:192:ASN:HD21	4:I:961:NAG:C6	2.24	0.51
1:I:257:LYS:HG3	1:I:315:MET:CE	2.41	0.51
1:L:133:LYS:O	1:L:136:LYS:HG3	2.11	0.51
1:I:356:ALA:CB	4:I:941:NAG:H81	2.41	0.51
1:I:300:THR:HG23	1:I:301:PRO:HD2	1.93	0.51
1:L:300:THR:HG22	1:L:302:GLU:H	1.76	0.50
1:I:290:LYS:HE3	1:I:294:LYS:CG	2.42	0.50
1:I:201:VAL:HG23	1:I:202:ILE:N	2.26	0.50
1:L:22:ILE:HG22	1:L:23:TYR:N	2.27	0.50
1:L:113:GLU:OE1	1:L:118:GLN:HG3	2.11	0.50
1:L:172:PRO:O	1:L:173:LEU:HD12	2.12	0.50
1:I:158:TYR:CE2	1:I:354:ILE:HG23	2.47	0.50
1:L:428:ASN:HD22	1:L:430:CYS:H	1.60	0.49
1:I:60:THR:O	1:I:64:GLN:HG3	2.12	0.49
1:L:183:ARG:NH1	1:L:202:ILE:O	2.45	0.49
1:I:283:LEU:HD11	1:I:320:MET:HE1	1.95	0.49
1:L:276:GLY:O	1:L:277:ASP:HB2	2.12	0.49
1:L:11:LYS:HB3	1:L:12:PRO:HD2	1.94	0.49
1:L:82:SER:HA	1:L:217:ASN:ND2	2.27	0.49
1:L:91:LYS:CD	1:L:103:MET:HE3	2.43	0.49
1:L:205:GLU:HB2	1:L:395:LEU:HD21	1.94	0.49
1:L:93:GLY:O	1:L:351:LEU:HA	2.12	0.49
1:I:186:ILE:HG21	1:I:202:ILE:CD1	2.42	0.48
1:I:183:ARG:CZ	1:I:204:SER:HA	2.43	0.48
1:I:208:ASN:ND2	1:I:208:ASN:C	2.64	0.48
1:I:134:ALA:O	1:I:136:LYS:N	2.42	0.48
1:L:18:ASN:HD22	4:L:841:NAG:H62	1.73	0.48
1:I:131:TYR:CE2	1:I:142:SER:HB2	2.48	0.48
1:L:22:ILE:CG2	1:L:23:TYR:N	2.76	0.48
1:I:132:ARG:HD3	1:I:136:LYS:HE3	1.96	0.48
1:L:190:VAL:HG11	1:L:201:VAL:HG21	1.95	0.48
1:L:284:ILE:C	1:L:285:LEU:HD23	2.34	0.48
1:L:319:HIS:HB2	1:I:390:ILE:HA	1.95	0.48
1:L:101:GLN:O	1:L:105:VAL:HG23	2.14	0.48
1:I:414:GLU:CD	1:I:416:PRO:HG2	2.34	0.47
1:I:45:ASN:HB3	1:I:48:VAL:HG13	1.96	0.47
1:L:343:LEU:HD11	1:L:364:VAL:HG23	1.97	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:332:LYS:HG3	1:L:344:PHE:CD2	2.49	0.47
1:L:238:LEU:HD23	1:L:240:TYR:OH	2.14	0.47
1:I:178:ASN:HB3	1:I:181:GLN:HB3	1.97	0.47
1:I:208:ASN:HD22	1:I:209:GLU:N	2.13	0.47
1:L:147:PHE:O	1:L:213:LEU:HD12	2.15	0.47
1:L:152:LEU:HD22	1:L:358:GLY:HA3	1.96	0.47
1:I:284:ILE:HB	1:I:409:LEU:HB2	1.95	0.47
1:L:228:LYS:HE2	1:L:378:GLU:O	2.14	0.47
1:I:208:ASN:HD21	1:I:210:LEU:HB2	1.80	0.47
4:I:941:NAG:O4	4:I:942:NAG:O7	2.33	0.47
1:I:302:GLU:CD	1:I:302:GLU:H	2.18	0.47
1:I:346:PRO:HG3	1:I:363:TYR:CE1	2.50	0.47
1:L:47:ARG:HG2	1:L:122:PHE:CE1	2.50	0.47
1:L:235:ARG:HH11	1:L:235:ARG:HG2	1.78	0.47
1:I:115:THR:OG1	1:I:118:GLN:NE2	2.48	0.47
1:I:89:MET:HB3	1:I:215:LEU:HD11	1.97	0.47
1:L:173:LEU:HD23	1:L:182:SER:HB3	1.97	0.47
1:L:372:PHE:CD1	1:L:372:PHE:C	2.87	0.47
1:I:20:MET:CE	1:I:352:PRO:HB2	2.46	0.46
1:I:332:LYS:HB3	7:I:999:HOH:O	2.14	0.46
1:L:57:ARG:HH11	1:L:57:ARG:HG3	1.80	0.46
1:L:317:VAL:HG21	1:I:228:LYS:HG3	1.95	0.46
1:L:17:MET:CE	1:L:161:ILE:HD11	2.46	0.46
1:I:126:LEU:HD12	1:I:417:LEU:HD13	1.96	0.46
1:L:131:TYR:CZ	1:L:142:SER:HB2	2.51	0.46
1:I:15:ILE:HD12	1:I:121:PHE:CE1	2.51	0.46
1:I:7:ILE:HG13	1:I:15:ILE:HD11	1.96	0.46
1:L:18:ASN:N	1:L:19:PRO:CD	2.78	0.46
1:I:111:ILE:O	1:I:114:LYS:HB2	2.16	0.46
1:L:413:ARG:HH11	1:L:413:ARG:HG2	1.80	0.46
1:I:340:LEU:HD23	1:I:344:PHE:HE1	1.80	0.46
1:L:407:PRO:HB2	1:L:425:ARG:HG2	1.98	0.46
1:L:284:ILE:HD13	1:L:307:TRP:HZ3	1.78	0.46
1:I:86:ALA:HB2	6:C:200:GOL:H11	1.98	0.46
1:L:183:ARG:CZ	1:L:204:SER:HA	2.45	0.45
1:L:372:PHE:O	1:L:382:ALA:HA	2.16	0.45
1:I:322:ARG:O	1:I:323:PHE:HB3	2.16	0.45
1:L:6:ASP:OD1	1:L:8:CYS:HB2	2.16	0.45
1:L:428:ASN:ND2	1:L:430:CYS:H	2.14	0.45
1:L:91:LYS:HE3	1:L:120:HIS:CE1	2.52	0.45
1:L:97:ASP:HB2	1:L:342:ASP:OD2	2.17	0.45
1:I:260:TYR:CG	1:I:261:ARG:N	2.84	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:I:942:NAG:O1	4:I:942:NAG:H82	2.17	0.45
1:I:152:LEU:HD12	1:I:212:VAL:HB	1.97	0.45
1:L:47:ARG:HG2	1:L:122:PHE:CD2	2.52	0.45
1:I:270:LEU:HD21	1:I:272:LEU:HD21	1.98	0.45
1:L:91:LYS:HD2	1:L:103:MET:HE3	1.99	0.45
1:L:286:PRO:HD3	1:L:292:LEU:HD13	1.99	0.45
1:I:314:MET:SD	1:I:400:VAL:HG11	2.57	0.45
1:L:343:LEU:CD1	1:L:364:VAL:HG23	2.47	0.45
1:I:13:ARG:HH11	1:I:13:ARG:CB	2.30	0.44
1:L:20:MET:HE2	4:L:841:NAG:H2	1.99	0.44
1:I:155:ASN:ND2	4:I:941:NAG:O5	2.50	0.44
1:L:235:ARG:HD2	1:L:235:ARG:N	2.32	0.44
1:I:186:ILE:HG21	1:I:202:ILE:HD12	1.98	0.44
1:L:190:VAL:HG11	1:L:201:VAL:CG2	2.48	0.44
1:L:260:TYR:O	1:L:261:ARG:HB2	2.18	0.44
1:L:198:ILE:HG22	1:L:201:VAL:HG22	2.00	0.44
1:L:131:TYR:CE2	1:L:142:SER:HB2	2.51	0.44
1:L:147:PHE:C	1:L:213:LEU:HD12	2.38	0.44
1:L:287:LYS:CG	1:L:290:LYS:HB2	2.41	0.44
1:I:340:LEU:HD23	1:I:344:PHE:CE1	2.53	0.44
1:L:149:ASP:HA	1:L:173:LEU:O	2.18	0.44
1:L:288:PRO:O	1:L:289:GLU:CB	2.66	0.44
1:I:143:ALA:HB3	1:I:218:THR:OG1	2.17	0.44
1:L:17:MET:C	1:L:19:PRO:HD3	2.38	0.44
1:I:197:ARG:NH1	2:C:3:GLU:OE1	2.45	0.44
1:L:197:ARG:NH1	1:L:381:GLU:OE2	2.51	0.44
1:L:201:VAL:HG23	7:L:857:HOH:O	2.17	0.43
1:I:77:PHE:CZ	1:I:422:PHE:HB3	2.53	0.43
1:L:203:PRO:HB2	1:L:395:LEU:CD1	2.48	0.43
1:L:261:ARG:HB2	1:L:311:LEU:HA	2.00	0.43
1:I:13:ARG:HB3	1:I:13:ARG:NH1	2.33	0.43
1:L:91:LYS:HD2	1:L:103:MET:CE	2.48	0.43
1:L:399:ARG:HG3	1:L:399:ARG:HH11	1.84	0.43
1:L:300:THR:HG21	1:L:302:GLU:HG2	2.01	0.43
1:L:228:LYS:HD3	1:L:378:GLU:HA	2.00	0.43
1:I:20:MET:HE2	1:I:352:PRO:HB2	2.00	0.43
1:L:15:ILE:HG23	1:L:164:LEU:CD2	2.48	0.43
1:L:407:PRO:HB3	1:L:427:ALA:CB	2.46	0.43
1:I:71:ASN:HB3	1:I:74:ASP:OD2	2.19	0.43
1:I:47:ARG:HD3	1:I:47:ARG:HA	1.87	0.43
1:L:113:GLU:HB3	1:L:114:LYS:H	1.64	0.43
1:I:131:TYR:CZ	1:I:142:SER:HB2	2.54	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:241:LYS:O	1:L:242:ALA:C	2.56	0.43
1:L:229:PHE:CD2	1:L:254:GLN:HB2	2.53	0.42
1:L:171:GLN:HA	1:L:172:PRO:HD3	1.83	0.42
1:I:256:GLY:HA2	1:I:315:MET:CE	2.50	0.42
1:I:351:LEU:N	1:I:352:PRO:CD	2.82	0.42
1:L:125:LYS:O	1:L:128:CYS:HB2	2.19	0.42
1:L:334:GLN:O	1:L:338:MET:HG3	2.19	0.42
1:L:115:THR:HB	1:L:117:ASP:OD2	2.19	0.42
1:I:155:ASN:OD1	1:I:157:THR:N	2.51	0.42
1:L:119:ILE:HD13	1:L:119:ILE:C	2.39	0.42
1:L:197:ARG:HD2	1:L:197:ARG:HA	1.76	0.42
4:I:941:NAG:O4	4:I:942:NAG:C7	2.68	0.42
1:L:42:GLU:CD	1:L:42:GLU:N	2.73	0.42
1:L:198:ILE:CG2	1:L:201:VAL:HG22	2.49	0.42
1:L:104:GLU:O	1:L:107:LYS:HD2	2.19	0.42
1:I:27:GLU:O	1:I:28:LYS:O	2.38	0.42
1:I:130:LEU:CD2	1:I:414:GLU:HG3	2.48	0.42
1:I:346:PRO:HA	1:I:363:TYR:CD2	2.54	0.42
1:I:132:ARG:HD2	1:I:136:LYS:HG3	2.02	0.42
1:L:71:ASN:O	1:L:73:ASN:N	2.52	0.41
1:I:411:PHE:N	1:I:411:PHE:CD1	2.88	0.41
1:I:55:ASN:HA	7:I:963:HOH:O	2.19	0.41
1:I:414:GLU:OE2	1:I:416:PRO:HG2	2.19	0.41
1:L:11:LYS:HB2	1:L:14:ASP:OD2	2.20	0.41
1:L:421:ILE:HG22	1:L:422:PHE:CD1	2.55	0.41
1:L:396:ASN:OD1	1:L:397:PRO:HD2	2.20	0.41
1:L:92:LEU:HD13	1:L:161:ILE:HG23	2.01	0.41
1:L:202:ILE:HA	1:L:203:PRO:HD3	1.89	0.41
1:L:19:PRO:HG2	1:L:117:ASP:CB	2.50	0.41
1:L:179:ALA:HB1	1:L:207:ILE:O	2.20	0.41
1:L:281:MET:HA	1:L:411:PHE:O	2.21	0.41
1:I:254:GLN:NE2	1:I:258:PHE:HZ	2.19	0.41
1:L:340:LEU:HB3	1:L:344:PHE:HE1	1.86	0.41
1:I:269:VAL:CG1	1:I:311:LEU:HD21	2.49	0.41
1:L:130:LEU:HG	1:L:417:LEU:HD13	2.02	0.41
1:L:200:ASP:HB3	1:L:370:LYS:NZ	2.36	0.41
1:L:252:MET:CG	1:L:322:ARG:HG3	2.51	0.41
1:I:300:THR:HG22	1:I:302:GLU:N	2.36	0.40
1:L:241:LYS:HE3	1:L:247:CYS:SG	2.61	0.40
1:I:329:PHE:HE1	1:I:331:LEU:HD23	1.85	0.40
1:L:119:ILE:O	1:L:119:ILE:HD13	2.22	0.40
1:I:152:LEU:HD11	1:I:212:VAL:CG1	2.51	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:257:LYS:NZ	1:L:313:GLU:HB3	2.36	0.40
1:L:250:SER:HB2	1:L:322:ARG:HB2	2.03	0.40
1:L:300:THR:HG23	1:L:301:PRO:HD2	2.04	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	I	412/432 (95%)	381 (92%)	22 (5%)	9 (2%)	10	25
1	L	405/432 (94%)	364 (90%)	36 (9%)	5 (1%)	19	45
2	C	5/7 (71%)	5 (100%)	0	0	100	100
3	D	1/3 (33%)	1 (100%)	0	0	100	100
All	All	823/874 (94%)	751 (91%)	58 (7%)	14 (2%)	14	33

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	28	LYS
1	I	42	GLU
1	I	43	ALA
1	L	112	SER
1	L	242	ALA
1	I	112	SER
1	L	72	ASP
1	L	403	LYS
1	I	383	ALA
1	I	113	GLU
1	I	134	ALA
1	L	399	ARG
1	I	207	ILE
1	I	357	GLU

### 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	I	370/383 (97%)	353 (95%)	17 (5%)	37	70
1	L	363/383 (95%)	341 (94%)	22 (6%)	26	54
2	C	3/3 (100%)	3 (100%)	0	100	100
3	D	2/2 (100%)	0	2 (100%)	0	0
All	All	738/771 (96%)	697 (94%)	41 (6%)	30	59

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	47	ARG
1	L	78	LEU
1	L	96	ASN
1	L	119	ILE
1	L	123	PHE
1	L	177	GLU
1	L	197	ARG
1	L	199	THR
1	L	201	VAL
1	L	205	GLU
1	L	235	ARG
1	L	245	GLU
1	L	285	LEU
1	L	302	GLU
1	L	316	LEU
1	L	324	ARG
1	L	359	ARG
1	L	360	ASP
1	L	366	ASP
1	L	398	ASN
1	L	405	ASN
1	L	428	ASN
1	I	13	ARG
1	I	24	ARG
1	I	29	LYS
1	I	48	VAL

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Mol	Chain	Res	Type
1	I	57	ARG
1	I	78	LEU
1	I	123	PHE
1	I	178	ASN
1	I	197	ARG
1	I	205	GLU
1	I	208	ASN
1	I	235	ARG
1	I	294	LYS
1	I	300	THR
1	I	315	MET
1	I	361	ASP
1	I	366	ASP
3	D	11	LEU
3	D	12	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	18	ASN
1	L	96	ASN
1	L	135	ASN
1	L	155	ASN
1	L	217	ASN
1	L	233	ASN
1	L	254	GLN
1	L	398	ASN
1	L	405	ASN
1	L	428	ASN
1	I	96	ASN
1	I	118	GLN
1	I	127	ASN
1	I	178	ASN
1	I	187	ASN
1	I	192	ASN
1	I	208	ASN
1	I	217	ASN
1	I	254	GLN
1	I	319	HIS
1	I	336	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	NLE	D	10	3,5	7,7,8	7.44	2 (28%)	5,7,9	1.69	1 (20%)

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	NLE	D	10	3,5	-	0/4/6/8	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	10	NLE	O-C	19.48	1.24	1.11
3	D	10	NLE	CA-C	2.39	1.52	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	10	NLE	C-CA-N	-3.69	110.15	113.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

9 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	$\# Z  > 2$
6	GOL	C	200	-	5,5,5	0.80	0	5,5,5	0.56	0
5	FOR	D	9	3	1,1,1	0.13	0	0,0,0	0.00	-
4	NAG	I	901	-	15,15,15	0.39	0	21,21,21	0.65	0
4	NAG	I	941	-	15,15,15	0.37	0	21,21,21	0.54	0
4	NAG	I	942	-	15,15,15	0.48	0	21,21,21	0.51	0
4	NAG	I	961	-	15,15,15	0.48	0	21,21,21	0.66	0
4	NAG	I	962	-	15,15,15	0.37	0	21,21,21	0.53	0
4	NAG	L	801	-	15,15,15	0.49	0	21,21,21	0.50	0
4	NAG	L	841	-	15,15,15	0.41	0	21,21,21	0.64	0

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
6	GOL	C	200	-	-	0/4/4/4	0/0/0/0
5	FOR	D	9	3	-	0/0/0/0	0/0/0/0
4	NAG	I	901	-	1/1/6/7	1/6/26/26	0/1/1/1
4	NAG	I	941	-	-	0/6/26/26	0/1/1/1
4	NAG	I	942	-	1/1/6/7	0/6/26/26	0/1/1/1
4	NAG	I	961	-	-	0/6/26/26	0/1/1/1
4	NAG	I	962	-	1/1/6/7	0/6/26/26	0/1/1/1
4	NAG	L	801	-	-	0/6/26/26	0/1/1/1
4	NAG	L	841	-	1/1/6/7	0/6/26/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	L	841	NAG	C1
4	I	962	NAG	C1
4	I	901	NAG	C1
4	I	942	NAG	C1

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	901	NAG	O7-C7-N2-C2

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	I	416/432 (96%)	-0.27	13 (3%) 47 52	14, 36, 88, 196	0
1	L	409/432 (94%)	-0.02	17 (4%) 35 39	18, 43, 114, 191	0
2	C	7/7 (100%)	-0.75	0 100 100	19, 28, 32, 36	0
3	D	3/3 (100%)	0.12	0 100 100	27, 27, 35, 43	0
All	All	835/874 (95%)	-0.15	30 (3%) 39 46	14, 39, 104, 196	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	431	VAL	6.8
1	L	134	ALA	5.6
1	I	357	GLU	5.5
1	L	135	ASN	4.9
1	I	358	GLY	4.7
1	L	398	ASN	4.4
1	L	401	THR	4.3
1	I	134	ALA	4.3
1	I	383	ALA	4.0
1	I	135	ASN	3.9
1	L	402	PHE	3.8
1	I	132	ARG	3.6
1	I	28	LYS	3.6
1	L	399	ARG	3.3
1	I	360	ASP	3.1
1	L	242	ALA	2.9
1	I	382	ALA	2.9
1	L	114	LYS	2.8
1	L	243	ASP	2.7
1	L	132	ARG	2.6
1	I	136	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	L	16	PRO	2.5
1	L	13	ARG	2.4
1	L	396	ASN	2.4
1	L	289	GLU	2.4
1	I	5	VAL	2.3
1	I	431	VAL	2.3
1	L	400	VAL	2.3
1	L	86	ALA	2.1
1	I	29	LYS	2.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NLE	D	10	8/9	0.21	0.37	23,25,29,30	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	I	961	15/15	0.31	23.00	88,88,88,88	0
4	NAG	L	801	15/15	0.37	7.66	48,103,112,121	0
4	NAG	I	942	15/15	0.50	6.13	143,143,143,143	0
4	NAG	L	841	15/15	0.24	2.09	44,75,85,94	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	I	901	15/15	0.23	1.77	66,66,66,66	0
6	GOL	C	200	6/6	0.22	0.90	45,45,45,45	0
5	FOR	D	9	2/2	0.20	0.62	33,33,33,33	0
4	NAG	I	941	15/15	0.20	0.01	54,54,54,54	0
4	NAG	I	962	15/15	0.41	-	109,109,109,109	0

## 6.5 Other polymers

There are no such residues in this entry.