



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:08 PM UTC

PDB ID : 3DLE / pdb_00003dle
Title : Crystal structure of hiv-1 reverse transcriptase in complex with GF128590.
Authors : Ren, J.; Chamberlain, P.P.; Stammers, D.K.
Deposited on : 2008-06-27
Resolution : 2.50 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) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

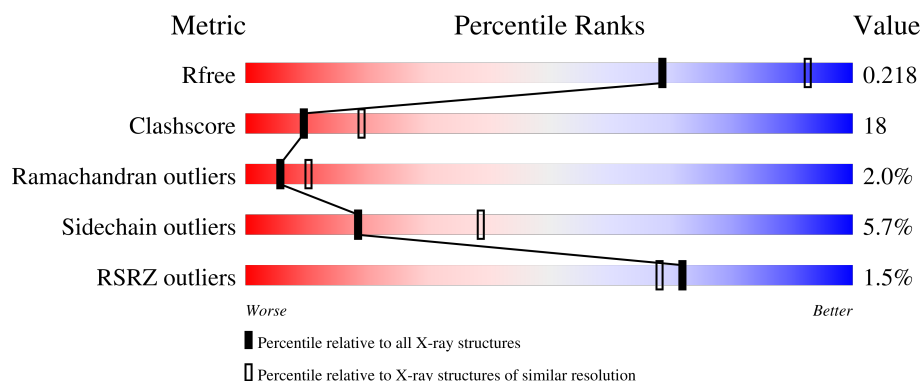
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	560	% 54% 37% . .
2	B	440	% 55% 33% . 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7865 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.

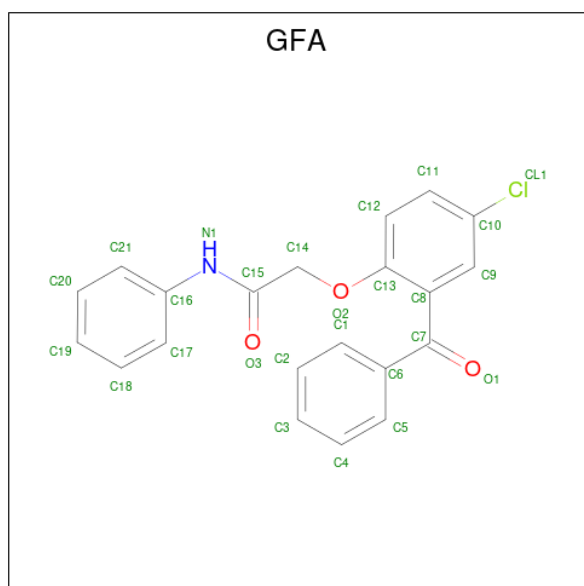
- Molecule 1 is a protein called Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	S	0	0	0
			4377	2834	727	808	8			

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	403	Total	C	N	O	S	0	0	0
			3333	2165	555	606	7			

- Molecule 3 is 2-[4-chloro-2-(phenylcarbonyl)phenoxy]-N-phenylacetamide (CCD ID: GFA) (formula: C₂₁H₁₆ClNO₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			26	21	1	1	3		

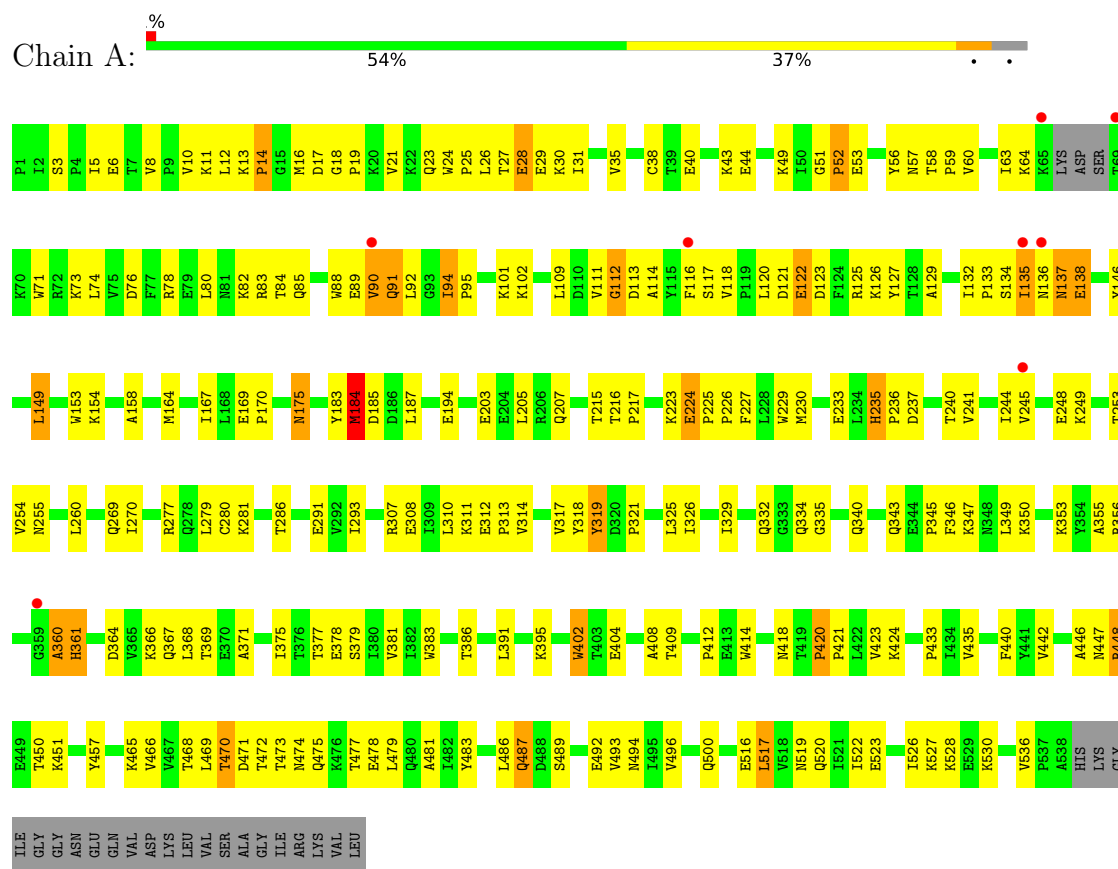
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	74	Total 74	O 74	0	0
4	B	55	Total 55	O 55	0	0

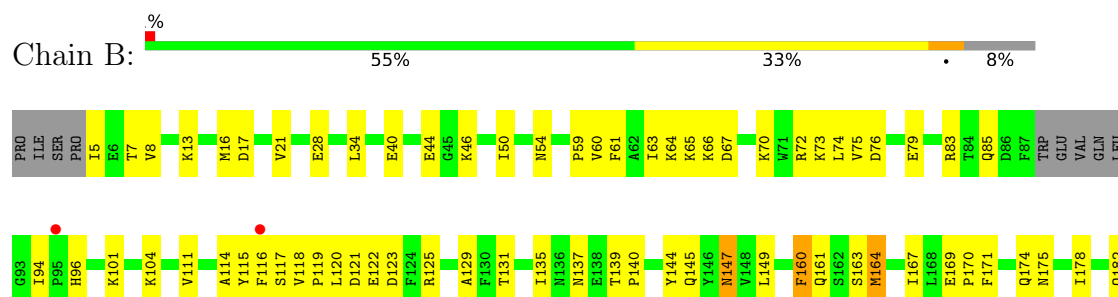
3 Residue-property plots

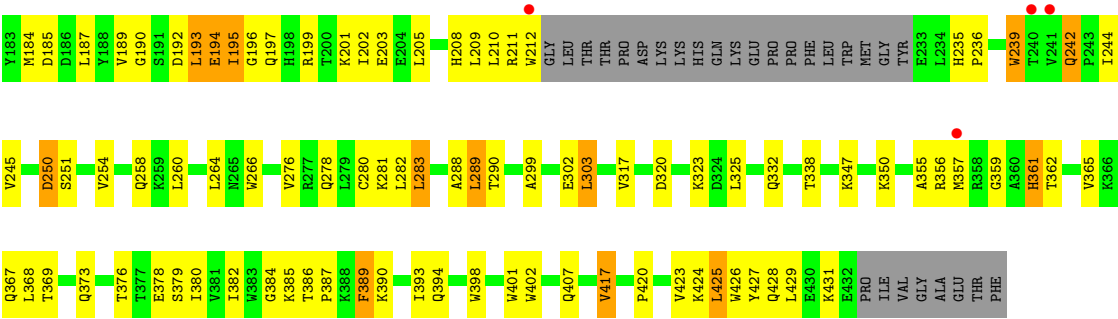
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 ($RSRZ > 2$). 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: Reverse transcriptase/ribonuclease H



• Molecule 2: p51 RT





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	137.89Å 110.25Å 72.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.79 – 2.50 25.79 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.2 (25.79-2.50) 96.2 (25.79-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.214 , 0.296 0.213 , 0.218	Depositor DCC
R_{free} test set	1863 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.346	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 65.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7865	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.49	0/4484	0.99	17/6095 (0.3%)
2	B	0.48	0/3424	0.98	20/4647 (0.4%)
All	All	0.48	0/7908	0.99	37/10742 (0.3%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	ASN	N-CA-C	-9.14	100.41	113.21
1	A	224	GLU	CA-C-N	7.73	125.31	119.66
1	A	224	GLU	C-N-CA	7.73	125.31	119.66
2	B	54	ASN	CA-C-N	7.60	128.25	120.04
2	B	54	ASN	C-N-CA	7.60	128.25	120.04
2	B	382	ILE	N-CA-C	7.60	117.67	110.53
1	A	51	GLY	CA-C-N	7.41	129.11	119.84
1	A	51	GLY	C-N-CA	7.41	129.11	119.84
2	B	402	TRP	N-CA-C	7.18	120.01	111.33
1	A	175	ASN	CA-C-N	7.08	127.68	120.04
1	A	175	ASN	C-N-CA	7.08	127.68	120.04
2	B	235	HIS	CA-C-N	6.40	126.15	119.05
2	B	235	HIS	C-N-CA	6.40	126.15	119.05
2	B	401	TRP	N-CA-C	6.28	122.53	114.56
2	B	184	MET	CB-CA-C	-6.15	109.47	116.54
1	A	494	ASN	N-CA-C	-6.12	98.92	108.90
2	B	428	GLN	N-CA-C	-6.09	104.76	111.82
2	B	160	PHE	N-CA-C	-5.99	106.22	112.93
1	A	184	MET	CB-CA-C	-5.96	109.71	116.63
2	B	147	ASN	N-CA-C	-5.94	106.67	114.04
2	B	417	VAL	N-CA-C	5.90	117.41	108.80
2	B	250	ASP	N-CA-C	-5.64	104.82	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	242	GLN	N-CA-C	5.58	116.73	109.64
1	A	235	HIS	CA-C-N	5.52	125.62	119.32
1	A	235	HIS	C-N-CA	5.52	125.62	119.32
1	A	368	LEU	N-CA-C	-5.42	105.27	111.07
2	B	96	HIS	CA-C-N	5.41	126.61	119.84
2	B	96	HIS	C-N-CA	5.41	126.61	119.84
1	A	326	ILE	N-CA-C	5.36	116.20	108.48
2	B	17	ASP	N-CA-C	-5.35	101.84	110.14
1	A	245	VAL	N-CA-C	5.18	116.43	108.71
2	B	389	PHE	N-CA-C	5.18	118.56	110.32
1	A	355	ALA	N-CA-C	5.15	117.17	110.43
1	A	319	TYR	N-CA-C	5.08	117.89	109.46
2	B	131	THR	N-CA-C	5.08	117.34	108.76
1	A	49	LYS	N-CA-C	-5.07	102.36	109.96
2	B	123	ASP	N-CA-C	5.02	118.66	112.54

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	4377	0	4424	160	0
2	B	3333	0	3369	127	0
3	A	26	0	16	0	0
4	A	74	0	0	3	0
4	B	55	0	0	1	0
All	All	7865	0	7809	277	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 18.

All (277) 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)
2:B:195:ILE:HD11	2:B:199:ARG:HE	1.14	1.07
1:A:469:LEU:HD12	1:A:477:THR:HG22	1.57	0.86
2:B:195:ILE:HD11	2:B:199:ARG:NE	1.94	0.82
2:B:175:ASN:HD21	2:B:201:LYS:HZ2	1.28	0.79
1:A:448:ARG:HG3	1:A:448:ARG:HH11	1.49	0.78
2:B:195:ILE:HG23	2:B:196:GLY:H	1.45	0.78
2:B:67:ASP:HB3	2:B:70:LYS:HD3	1.65	0.78
2:B:195:ILE:CD1	2:B:199:ARG:HE	1.96	0.78
2:B:115:TYR:HB3	2:B:149:LEU:HB2	1.65	0.77
2:B:70:LYS:HD2	2:B:70:LYS:H	1.50	0.77
2:B:161:GLN:HE21	2:B:161:GLN:HA	1.48	0.76
2:B:175:ASN:HD21	2:B:201:LYS:NZ	1.82	0.76
2:B:61:PHE:CE1	2:B:74:LEU:HD23	2.21	0.75
2:B:111:VAL:HG11	2:B:187:LEU:HD22	1.68	0.75
2:B:332:GLN:NE2	2:B:424:LYS:HE2	2.02	0.74
2:B:356:ARG:HB2	2:B:367:GLN:HG2	1.70	0.74
1:A:377:THR:O	1:A:381:VAL:HG23	1.89	0.73
2:B:125:ARG:HE	2:B:147:ASN:HA	1.54	0.72
2:B:79:GLU:O	2:B:83:ARG:HG3	1.89	0.72
2:B:254:VAL:O	2:B:258:GLN:HG3	1.90	0.72
2:B:163:SER:O	2:B:167:ILE:HG23	1.89	0.71
1:A:17:ASP:O	1:A:83:ARG:HD3	1.89	0.71
1:A:248:GLU:HG2	1:A:307:ARG:CZ	2.21	0.71
2:B:420:PRO:HB2	2:B:423:VAL:HG23	1.74	0.70
1:A:31:ILE:O	1:A:35:VAL:HG23	1.92	0.70
2:B:60:VAL:HG23	2:B:75:VAL:HG22	1.73	0.69
1:A:448:ARG:HG3	1:A:448:ARG:NH1	2.02	0.69
1:A:317:VAL:HG21	1:A:347:LYS:HB3	1.74	0.69
2:B:161:GLN:HA	2:B:161:GLN:NE2	2.07	0.68
1:A:89:GLU:C	1:A:91:GLN:H	2.01	0.68
1:A:85:GLN:O	1:A:154:LYS:HE3	1.93	0.68
1:A:112:GLY:C	1:A:114:ALA:H	2.02	0.68
1:A:335:GLY:HA2	1:A:367:GLN:OE1	1.94	0.67
1:A:277:ARG:O	1:A:281:LYS:HG3	1.94	0.67
2:B:70:LYS:HD2	2:B:70:LYS:N	2.09	0.67
1:A:516:GLU:O	1:A:520:GLN:HG3	1.95	0.67
2:B:208:HIS:O	2:B:211:ARG:HG2	1.96	0.66
2:B:365:VAL:O	2:B:369:THR:HG23	1.95	0.66
1:A:248:GLU:HG2	1:A:307:ARG:NH2	2.11	0.66
2:B:278:GLN:HB2	2:B:302:GLU:OE2	1.95	0.65
2:B:59:PRO:HG2	2:B:76:ASP:HB3	1.79	0.65
2:B:195:ILE:HG23	2:B:196:GLY:N	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:137:ASN:C	2:B:139:THR:H	2.05	0.64
1:A:329:ILE:HD12	1:A:391:LEU:CD2	2.28	0.64
1:A:420:PRO:HA	1:A:421:PRO:C	2.22	0.64
1:A:118:VAL:HB	1:A:149:LEU:HD22	1.79	0.64
2:B:175:ASN:ND2	2:B:201:LYS:NZ	2.45	0.64
1:A:312:GLU:HG2	1:A:313:PRO:HD2	1.80	0.63
2:B:239:TRP:CH2	2:B:378:GLU:HG2	2.34	0.63
2:B:320:ASP:OD2	2:B:323:LYS:HE3	1.99	0.63
1:A:418:ASN:O	1:A:420:PRO:HD3	1.98	0.62
2:B:260:LEU:HD21	2:B:303:LEU:HD21	1.82	0.62
1:A:73:LYS:HG2	1:A:74:LEU:N	2.13	0.62
2:B:245:VAL:CG2	2:B:431:LYS:HB2	2.29	0.62
1:A:13:LYS:HB3	1:A:14:PRO:HD2	1.81	0.62
1:A:90:VAL:HG12	1:A:158:ALA:HB2	1.81	0.61
1:A:114:ALA:HA	1:A:117:SER:OG	2.00	0.61
1:A:116:PHE:HE1	1:A:146:TYR:HE1	1.48	0.61
1:A:254:VAL:HG23	1:A:293:ILE:HD11	1.81	0.61
2:B:169:GLU:HB3	2:B:170:PRO:HD3	1.83	0.61
2:B:139:THR:HG22	2:B:140:PRO:O	2.01	0.60
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.36	0.60
2:B:359:GLY:HA2	2:B:361:HIS:CE1	2.37	0.60
1:A:203:GLU:O	1:A:207:GLN:HB2	2.01	0.60
1:A:293:ILE:N	1:A:293:ILE:HD12	2.17	0.59
2:B:104:LYS:HD2	2:B:192:ASP:O	2.02	0.59
2:B:65:LYS:HG3	2:B:66:LYS:H	1.66	0.59
1:A:3:SER:HB3	1:A:5:ILE:HG13	1.83	0.59
1:A:225:PRO:HA	1:A:226:PRO:C	2.28	0.59
1:A:317:VAL:HG12	1:A:318:TYR:N	2.19	0.58
1:A:408:ALA:HB3	2:B:393:ILE:HB	1.86	0.58
1:A:89:GLU:HA	4:A:1006:HOH:O	2.03	0.58
2:B:70:LYS:H	2:B:70:LYS:CD	2.17	0.58
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.04	0.58
2:B:369:THR:HG22	2:B:398:TRP:CH2	2.39	0.57
1:A:12:LEU:HD11	1:A:127:TYR:CE1	2.39	0.57
1:A:402:TRP:CD1	1:A:402:TRP:C	2.82	0.57
2:B:245:VAL:HG23	2:B:431:LYS:HB2	1.87	0.57
1:A:483:TYR:O	1:A:487:GLN:HG2	2.03	0.57
1:A:492:GLU:HA	1:A:530:LYS:O	2.04	0.56
1:A:122:GLU:H	1:A:122:GLU:CD	2.13	0.56
1:A:335:GLY:HA3	1:A:356:ARG:HD2	1.88	0.56
1:A:254:VAL:HG22	1:A:286:THR:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:114:ALA:HB1	2:B:160:PHE:CZ	2.40	0.56
1:A:76:ASP:OD2	1:A:78:ARG:HG3	2.05	0.56
2:B:239:TRP:CZ2	2:B:378:GLU:HG2	2.40	0.55
2:B:101:LYS:O	2:B:236:PRO:HB2	2.07	0.55
1:A:522:ILE:O	1:A:526:ILE:HG13	2.07	0.55
2:B:356:ARG:CB	2:B:367:GLN:HG2	2.36	0.55
1:A:78:ARG:O	1:A:82:LYS:HG3	2.07	0.55
1:A:38:CYS:SG	1:A:132:ILE:HD11	2.47	0.55
1:A:57:ASN:HA	1:A:129:ALA:O	2.07	0.55
1:A:59:PRO:HG2	1:A:76:ASP:HB3	1.88	0.54
1:A:356:ARG:HG2	1:A:356:ARG:HH11	1.72	0.54
2:B:13:LYS:HB2	2:B:16:MET:HG3	1.89	0.54
1:A:164:MET:HE3	1:A:187:LEU:CG	2.38	0.54
1:A:366:LYS:NZ	2:B:394:GLN:NE2	2.56	0.54
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.89	0.54
1:A:134:SER:O	1:A:135:ILE:C	2.50	0.53
2:B:65:LYS:HA	2:B:407:GLN:HG2	1.90	0.53
1:A:13:LYS:HB3	1:A:14:PRO:CD	2.39	0.53
2:B:426:TRP:O	2:B:429:LEU:HB2	2.09	0.53
1:A:254:VAL:CG2	1:A:293:ILE:HD11	2.38	0.53
1:A:371:ALA:O	1:A:375:ILE:HG13	2.08	0.53
2:B:63:ILE:C	2:B:64:LYS:HG3	2.33	0.53
1:A:317:VAL:HG12	1:A:318:TYR:H	1.73	0.53
2:B:129:ALA:HA	2:B:144:TYR:O	2.09	0.52
1:A:94:ILE:H	1:A:94:ILE:CD1	2.22	0.52
1:A:89:GLU:C	1:A:91:GLN:N	2.68	0.52
1:A:442:VAL:HG12	1:A:457:TYR:HB3	1.90	0.52
2:B:211:ARG:HG3	2:B:212:TRP:CD1	2.45	0.52
1:A:63:ILE:HD12	1:A:63:ILE:O	2.10	0.52
1:A:248:GLU:O	1:A:249:LYS:HG3	2.09	0.52
2:B:194:GLU:HG3	2:B:197:GLN:H	1.74	0.52
2:B:28:GLU:HG3	2:B:135:ILE:HD11	1.92	0.52
2:B:65:LYS:HE2	2:B:72:ARG:HD2	1.91	0.52
1:A:345:PRO:O	1:A:346:PHE:HB2	2.09	0.52
1:A:112:GLY:C	1:A:114:ALA:N	2.66	0.52
1:A:244:ILE:HG23	1:A:310:LEU:HD13	1.92	0.51
1:A:95:PRO:HB2	1:A:229:TRP:HH2	1.75	0.51
1:A:314:VAL:HG23	1:A:314:VAL:O	2.10	0.51
2:B:317:VAL:HG22	2:B:347:LYS:HB3	1.92	0.51
1:A:479:LEU:HB2	1:A:517:LEU:HD13	1.93	0.51
1:A:88:TRP:HA	1:A:88:TRP:CE3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:390:LYS:HD2	2:B:417:VAL:HG11	1.93	0.51
1:A:241:VAL:HG21	1:A:270:ILE:HG21	1.93	0.50
1:A:307:ARG:O	1:A:311:LYS:HG3	2.10	0.50
1:A:94:ILE:N	1:A:94:ILE:HD13	2.26	0.50
1:A:447:ASN:HA	1:A:448:ARG:NH2	2.27	0.50
1:A:402:TRP:CZ2	2:B:362:THR:HA	2.46	0.50
2:B:245:VAL:HG21	2:B:431:LYS:HB2	1.94	0.50
2:B:376:THR:O	2:B:380:ILE:HG13	2.11	0.50
1:A:225:PRO:HG3	1:A:227:PHE:CZ	2.46	0.49
2:B:266:TRP:HZ3	2:B:426:TRP:CD1	2.30	0.49
1:A:94:ILE:HG22	1:A:230:MET:HE1	1.95	0.49
1:A:312:GLU:CG	1:A:313:PRO:HD2	2.42	0.49
1:A:440:PHE:CE1	1:A:489:SER:HB3	2.47	0.49
1:A:84:THR:HG21	1:A:153:TRP:CZ2	2.48	0.49
1:A:244:ILE:HG23	1:A:244:ILE:O	2.11	0.49
1:A:448:ARG:HH11	1:A:448:ARG:CG	2.19	0.49
1:A:475:GLN:HA	1:A:478:GLU:OE1	2.12	0.49
2:B:13:LYS:HB2	2:B:16:MET:CG	2.43	0.49
1:A:88:TRP:O	1:A:89:GLU:C	2.54	0.49
1:A:95:PRO:HG3	2:B:137:ASN:HB2	1.94	0.49
1:A:30:LYS:HE2	1:A:71:TRP:CH2	2.48	0.48
2:B:356:ARG:HB2	2:B:367:GLN:CG	2.42	0.48
2:B:94:ILE:HG21	2:B:182:GLN:O	2.14	0.48
1:A:343:GLN:HG3	1:A:349:LEU:HD11	1.95	0.48
2:B:369:THR:O	2:B:373:GLN:HG3	2.13	0.48
1:A:112:GLY:O	1:A:114:ALA:N	2.46	0.48
1:A:164:MET:HE3	1:A:187:LEU:HG	1.96	0.48
2:B:125:ARG:NE	2:B:147:ASN:HA	2.24	0.48
2:B:276:VAL:HA	2:B:302:GLU:OE1	2.14	0.48
1:A:63:ILE:HD12	1:A:63:ILE:C	2.38	0.48
1:A:102:LYS:HE3	1:A:236:PRO:O	2.13	0.48
2:B:276:VAL:CA	2:B:302:GLU:OE1	2.62	0.48
2:B:242:GLN:HA	2:B:242:GLN:OE1	2.13	0.48
1:A:5:ILE:HD11	1:A:167:ILE:HD11	1.96	0.47
2:B:376:THR:CG2	2:B:386:THR:HG22	2.45	0.47
1:A:126:LYS:HE2	1:A:127:TYR:CZ	2.50	0.47
1:A:457:TYR:CD1	1:A:457:TYR:C	2.92	0.47
2:B:137:ASN:C	2:B:139:THR:N	2.72	0.47
1:A:23:GLN:OE1	1:A:60:VAL:HG12	2.15	0.47
1:A:260:LEU:HD23	1:A:279:LEU:HD22	1.97	0.47
1:A:334:GLN:O	1:A:356:ARG:HD3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1117:HOH:O	2:B:288:ALA:HB1	2.14	0.47
2:B:50:ILE:CG2	2:B:145:GLN:HG2	2.44	0.47
2:B:350:LYS:HE3	2:B:378:GLU:OE1	2.15	0.47
2:B:34:LEU:CD2	2:B:73:LYS:HG3	2.45	0.47
2:B:423:VAL:O	2:B:427:TYR:HD2	1.98	0.47
2:B:28:GLU:CG	2:B:135:ILE:HD11	2.45	0.46
1:A:28:GLU:HG3	1:A:29:GLU:N	2.30	0.46
1:A:90:VAL:HG23	1:A:90:VAL:O	2.14	0.46
1:A:319:TYR:CE2	1:A:343:GLN:NE2	2.83	0.46
1:A:446:ALA:HB2	1:A:477:THR:HG21	1.98	0.46
2:B:61:PHE:CZ	2:B:74:LEU:HD23	2.51	0.46
2:B:122:GLU:HA	2:B:125:ARG:NH1	2.31	0.46
2:B:380:ILE:O	2:B:384:GLY:N	2.45	0.46
1:A:472:THR:OG1	1:A:473:THR:N	2.48	0.46
1:A:38:CYS:SG	1:A:73:LYS:NZ	2.74	0.46
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.96	0.46
1:A:94:ILE:HG12	1:A:94:ILE:O	2.15	0.46
2:B:387:PRO:HG2	2:B:389:PHE:CE1	2.51	0.46
1:A:27:THR:O	1:A:31:ILE:HG13	2.16	0.46
2:B:67:ASP:CB	2:B:70:LYS:HD3	2.42	0.46
1:A:350:LYS:HE2	1:A:378:GLU:OE2	2.16	0.46
1:A:440:PHE:CZ	1:A:489:SER:HB3	2.50	0.46
2:B:111:VAL:HG22	2:B:185:ASP:O	2.15	0.46
2:B:379:SER:CB	2:B:387:PRO:HD3	2.46	0.46
1:A:3:SER:CB	1:A:5:ILE:HG13	2.46	0.45
1:A:18:GLY:HA3	1:A:56:TYR:CD1	2.51	0.45
1:A:329:ILE:HD12	1:A:391:LEU:HD22	1.98	0.45
2:B:61:PHE:HE1	2:B:74:LEU:HD23	1.77	0.45
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.98	0.45
2:B:423:VAL:HG21	4:B:1088:HOH:O	2.15	0.45
1:A:40:GLU:O	1:A:44:GLU:HG3	2.16	0.45
1:A:215:THR:HG22	1:A:216:THR:N	2.31	0.45
2:B:282:LEU:HD11	2:B:299:ALA:CB	2.46	0.45
1:A:183:TYR:CD1	1:A:184:MET:HB2	2.52	0.45
1:A:253:THR:HA	1:A:291:GLU:O	2.16	0.45
1:A:360:ALA:O	1:A:361:HIS:HB3	2.15	0.45
1:A:101:LYS:HD3	1:A:321:PRO:CG	2.46	0.45
1:A:519:ASN:O	1:A:523:GLU:HG2	2.17	0.45
2:B:376:THR:HG23	2:B:386:THR:HG22	1.98	0.45
1:A:135:ILE:HG22	1:A:136:ASN:N	2.32	0.45
2:B:325:LEU:HD12	2:B:385:LYS:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:GLU:C	1:A:249:LYS:HG3	2.42	0.45
1:A:418:ASN:C	1:A:420:PRO:HD3	2.42	0.45
1:A:435:VAL:HG22	2:B:290:THR:HG21	1.98	0.45
1:A:94:ILE:CD1	1:A:94:ILE:N	2.80	0.44
1:A:122:GLU:HA	1:A:125:ARG:CD	2.47	0.44
1:A:517:LEU:HA	1:A:520:GLN:OE1	2.18	0.44
2:B:202:ILE:O	2:B:205:LEU:N	2.50	0.44
1:A:164:MET:HE3	1:A:187:LEU:HD11	2.00	0.44
1:A:8:VAL:O	1:A:121:ASP:HB2	2.17	0.44
1:A:137:ASN:O	1:A:138:GLU:O	2.35	0.44
2:B:195:ILE:CG2	2:B:196:GLY:H	2.24	0.44
2:B:425:LEU:O	2:B:429:LEU:HD13	2.18	0.44
2:B:28:GLU:CB	2:B:135:ILE:HD11	2.47	0.44
2:B:170:PRO:O	2:B:174:GLN:HG3	2.17	0.44
2:B:193:LEU:HD13	2:B:197:GLN:NE2	2.33	0.44
2:B:171:PHE:CD2	2:B:205:LEU:HD12	2.52	0.44
1:A:447:ASN:O	1:A:451:LYS:N	2.47	0.43
2:B:115:TYR:C	2:B:117:SER:H	2.25	0.43
2:B:281:LYS:C	2:B:283:LEU:H	2.26	0.43
2:B:355:ALA:O	2:B:357:MET:HE2	2.17	0.43
1:A:58:THR:CG2	1:A:59:PRO:HD2	2.48	0.43
1:A:402:TRP:CH2	2:B:362:THR:HA	2.52	0.43
1:A:319:TYR:HE2	1:A:343:GLN:NE2	2.17	0.43
1:A:366:LYS:HZ1	2:B:394:GLN:NE2	2.16	0.43
1:A:183:TYR:CD1	1:A:183:TYR:C	2.96	0.43
2:B:244:ILE:HG13	2:B:426:TRP:CZ2	2.54	0.43
2:B:46:LYS:HE3	2:B:116:PHE:CD1	2.54	0.43
1:A:470:THR:O	1:A:471:ASP:HB3	2.19	0.42
1:A:325:LEU:HD12	1:A:325:LEU:HA	1.82	0.42
1:A:379:SER:HA	1:A:383:TRP:CE3	2.54	0.42
2:B:209:LEU:C	2:B:211:ARG:H	2.27	0.42
1:A:364:ASP:HB3	1:A:423:VAL:HG13	2.00	0.42
2:B:266:TRP:CZ3	2:B:426:TRP:CG	3.08	0.42
1:A:448:ARG:CZ	1:A:448:ARG:H	2.32	0.42
1:A:225:PRO:HG3	1:A:227:PHE:CE2	2.54	0.42
1:A:486:LEU:O	1:A:528:LYS:NZ	2.42	0.42
1:A:536:VAL:HG12	2:B:258:GLN:HB3	2.01	0.42
1:A:233:GLU:HB2	1:A:240:THR:OG1	2.20	0.42
2:B:7:THR:HG22	2:B:119:PRO:HG2	2.01	0.42
2:B:160:PHE:CE1	2:B:164:MET:HG2	2.55	0.42
1:A:120:LEU:O	1:A:121:ASP:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:HIS:N	1:A:235:HIS:CD2	2.87	0.41
2:B:332:GLN:HG3	2:B:338:THR:HG23	2.02	0.41
1:A:64:LYS:HE3	1:A:64:LYS:HB2	1.90	0.41
1:A:94:ILE:CG2	1:A:230:MET:HE1	2.50	0.41
2:B:369:THR:HG22	2:B:398:TRP:CZ3	2.55	0.41
2:B:178:ILE:HG23	2:B:190:GLY:O	2.18	0.41
1:A:332:GLN:HE22	1:A:353:LYS:NZ	2.18	0.41
2:B:355:ALA:O	2:B:356:ARG:C	2.63	0.41
1:A:31:ILE:HG12	1:A:133:PRO:HG2	2.02	0.41
2:B:5:ILE:HG23	2:B:119:PRO:CD	2.51	0.41
1:A:111:VAL:HG22	1:A:185:ASP:O	2.20	0.41
1:A:223:LYS:C	1:A:224:GLU:HG2	2.45	0.41
1:A:169:GLU:N	1:A:170:PRO:CD	2.84	0.41
1:A:496:VAL:CG2	2:B:289:LEU:HD11	2.51	0.41
2:B:40:GLU:O	2:B:44:GLU:HG3	2.21	0.41
2:B:118:VAL:HB	2:B:149:LEU:HG	2.02	0.41
2:B:194:GLU:O	2:B:195:ILE:C	2.63	0.41
1:A:26:LEU:HD12	1:A:133:PRO:HG3	2.03	0.41
2:B:120:LEU:O	2:B:121:ASP:C	2.63	0.41
1:A:433:PRO:HB3	2:B:289:LEU:HD23	2.02	0.41
2:B:264:LEU:HD23	2:B:264:LEU:HA	1.91	0.41
2:B:356:ARG:O	2:B:356:ARG:HG3	2.21	0.40
1:A:10:VAL:HG12	1:A:11:LYS:N	2.36	0.40
1:A:5:ILE:CD1	1:A:167:ILE:HD11	2.50	0.40
1:A:92:LEU:HD12	1:A:92:LEU:HA	1.91	0.40
1:A:465:LYS:CG	1:A:466:VAL:N	2.83	0.40
2:B:303:LEU:HD23	2:B:303:LEU:HA	1.89	0.40
1:A:217:PRO:HD2	4:A:1010:HOH:O	2.22	0.40
2:B:161:GLN:NE2	2:B:161:GLN:CA	2.75	0.40
1:A:24:TRP:CD1	1:A:25:PRO:HD2	2.57	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	A	530/560 (95%)	481 (91%)	35 (7%)	14 (3%)	4	7
2	B	397/440 (90%)	372 (94%)	20 (5%)	5 (1%)	9	18
All	All	927/1000 (93%)	853 (92%)	55 (6%)	19 (2%)	6	10

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	GLU
1	A	135	ILE
1	A	138	GLU
1	A	360	ALA
2	B	193	LEU
1	A	90	VAL
1	A	113	ASP
2	B	85	GLN
2	B	239	TRP
1	A	16	MET
1	A	52	PRO
1	A	91	GLN
1	A	361	HIS
1	A	14	PRO
2	B	195	ILE
2	B	210	LEU
1	A	412	PRO
1	A	420	PRO
1	A	112	GLY

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	A	479/499 (96%)	445 (93%)	34 (7%)	13	29
2	B	367/400 (92%)	353 (96%)	14 (4%)	29	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	846/899 (94%)	798 (94%)	48 (6%)	18	39

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLU
1	A	21	VAL
1	A	28	GLU
1	A	43	LYS
1	A	52	PRO
1	A	94	ILE
1	A	109	LEU
1	A	122	GLU
1	A	123	ASP
1	A	149	LEU
1	A	175	ASN
1	A	184	MET
1	A	194	GLU
1	A	205	LEU
1	A	237	ASP
1	A	255	ASN
1	A	269	GLN
1	A	308	GLU
1	A	340	GLN
1	A	369	THR
1	A	386	THR
1	A	402	TRP
1	A	404	GLU
1	A	409	THR
1	A	424	LYS
1	A	448	ARG
1	A	468	THR
1	A	470	THR
1	A	474	ASN
1	A	487	GLN
1	A	493	VAL
1	A	500	GLN
1	A	517	LEU
1	A	527	LYS
2	B	8	VAL
2	B	164	MET
2	B	189	VAL

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Mol	Chain	Res	Type
2	B	194	GLU
2	B	203	GLU
2	B	250	ASP
2	B	251	SER
2	B	280	CYS
2	B	283	LEU
2	B	289	LEU
2	B	303	LEU
2	B	361	HIS
2	B	368	LEU
2	B	425	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	161	GLN
1	A	174	GLN
1	A	175	ASN
1	A	197	GLN
1	A	242	GLN
1	A	255	ASN
1	A	278	GLN
1	A	330	GLN
1	A	332	GLN
1	A	334	GLN
1	A	336	GLN
1	A	340	GLN
1	A	363	ASN
1	A	373	GLN
1	A	474	ASN
1	A	500	GLN
1	A	524	GLN
2	B	147	ASN
2	B	151	GLN
2	B	161	GLN
2	B	175	ASN
2	B	182	GLN
2	B	197	GLN
2	B	235	HIS
2	B	255	ASN
2	B	278	GLN
2	B	332	GLN

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Mol	Chain	Res	Type
2	B	334	GLN
2	B	361	HIS
2	B	373	GLN
2	B	394	GLN
2	B	428	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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	$\# Z > 2$
1	CSD	A	280	1	4,7,8	0.99	0	1,8,10	2.03	1 (100%)

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
1	CSD	A	280	1	-	1/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	280	CSD	OD1-SG-CB	2.03	109.34	105.60

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	280	CSD	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	GFA	A	999	-	28,28,28	1.30	5 (17%)	37,37,37	0.87	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	GFA	A	999	-	-	4/17/17/17	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	999	GFA	O2-C13	2.71	1.42	1.37
3	A	999	GFA	C1-C6	2.30	1.42	1.39
3	A	999	GFA	C15-N1	2.25	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	999	GFA	C10-CL1	-2.23	1.69	1.74
3	A	999	GFA	C9-C8	2.22	1.43	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	999	GFA	C14-O2-C13	2.01	121.79	117.60

There are no chirality outliers.

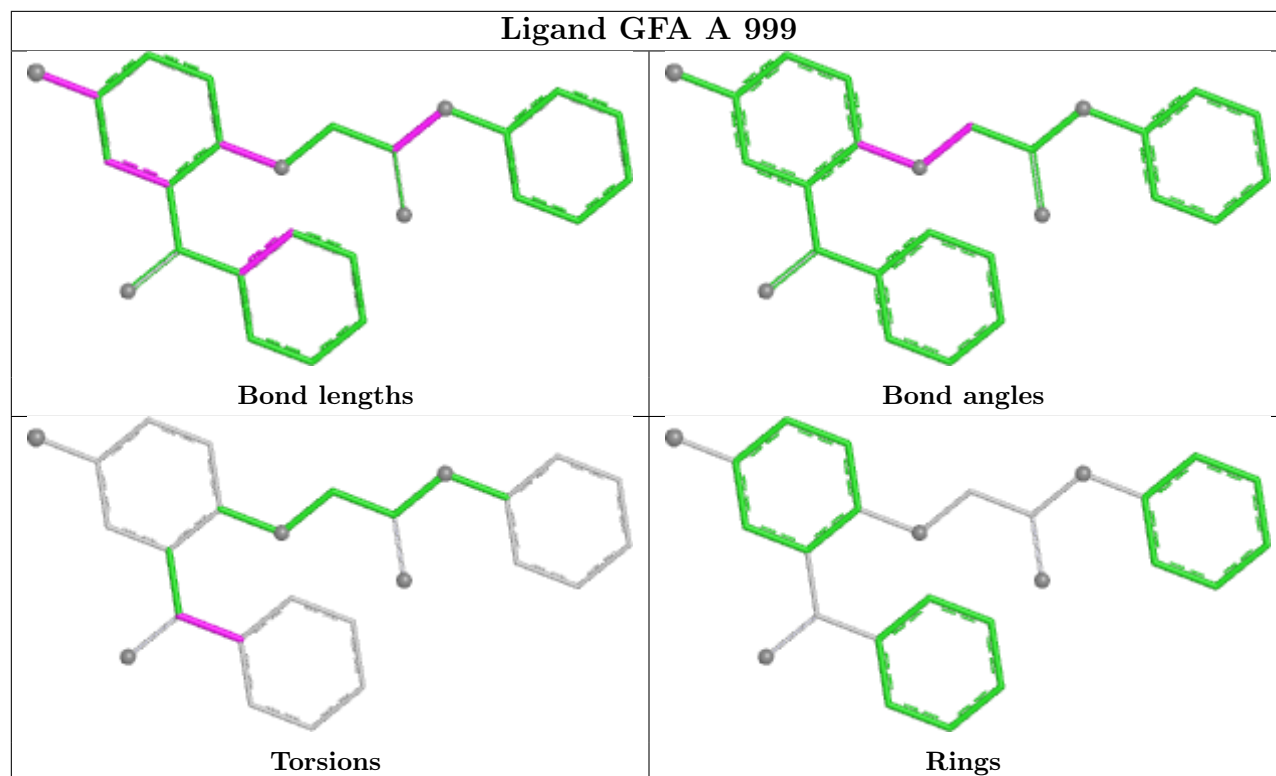
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	999	GFA	C5-C6-C7-O1
3	A	999	GFA	C1-C6-C7-O1
3	A	999	GFA	C5-C6-C7-C8
3	A	999	GFA	C1-C6-C7-C8

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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	534/560 (95%)	-0.04	8 (1%) 72 68	25, 53, 95, 134	0
2	B	403/440 (91%)	-0.14	6 (1%) 72 68	25, 50, 90, 131	0
All	All	937/1000 (93%)	-0.08	14 (1%) 72 68	25, 52, 93, 134	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90	VAL	3.7
1	A	136	ASN	2.9
2	B	241	VAL	2.8
1	A	245	VAL	2.7
2	B	116	PHE	2.6
2	B	212	TRP	2.6
1	A	69	THR	2.5
1	A	359	GLY	2.3
1	A	135	ILE	2.3
2	B	95	PRO	2.3
2	B	357	MET	2.1
1	A	65	LYS	2.1
2	B	240	THR	2.0
1	A	116	PHE	2.0

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

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. The B-factors column lists the minimum, median, 95th 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	CSD	A	280	8/9	0.94	0.08	50,54,67,72	0

6.3 Carbohydrates [i](#)

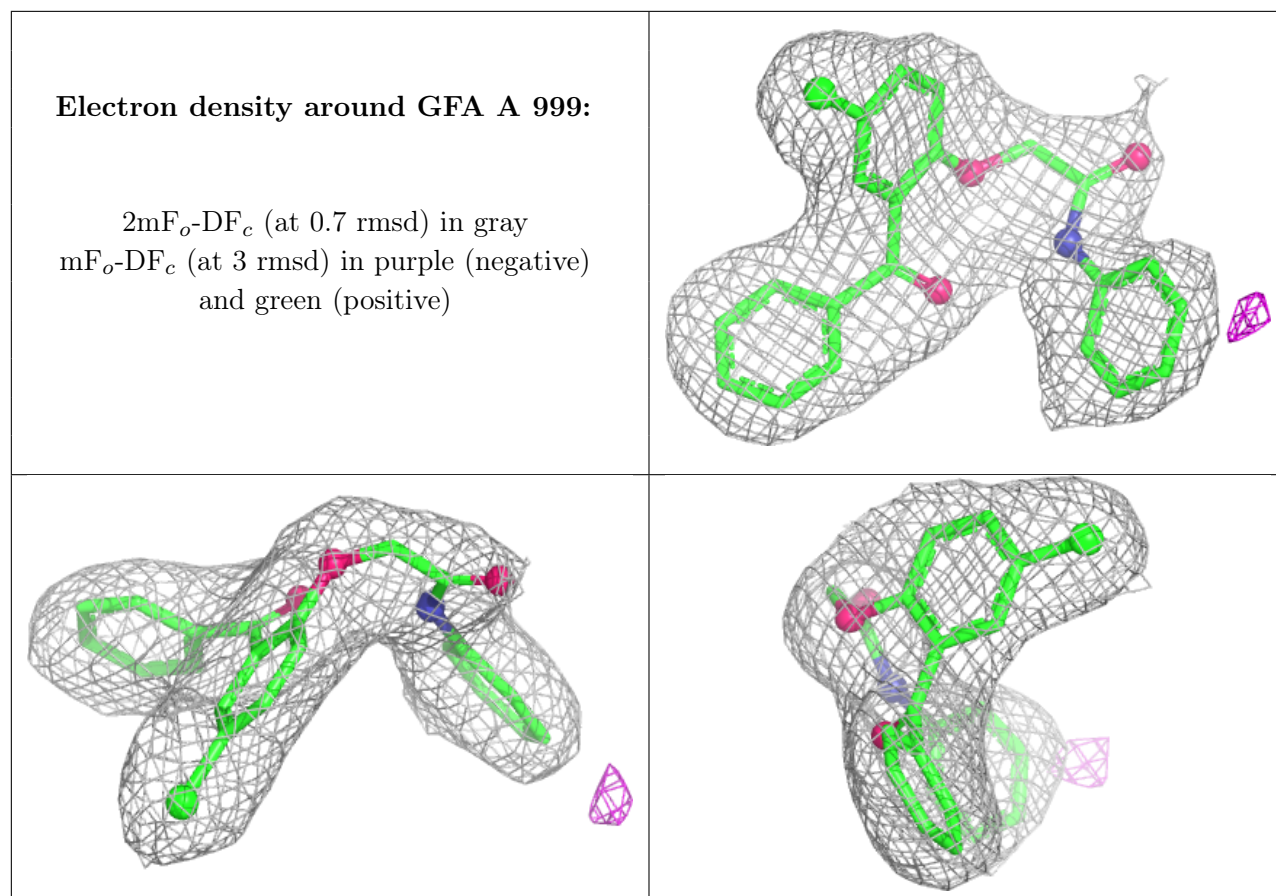
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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. The B-factors column lists the minimum, median, 95th 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GFA	A	999	26/26	0.96	0.07	27,35,44,51	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.