



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:12 AM UTC

PDB ID : 2J68 / pdb_00002j68
Title : Bacterial dynamin-like protein BDLP, GDP bound
Authors : Low, H.H.; Lowe, J.
Deposited on : 2006-09-26
Resolution : 3.10 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

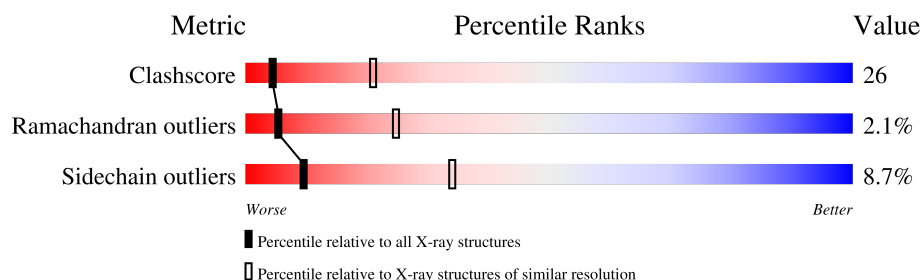
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)

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	A	695	

2 Entry composition [i](#)

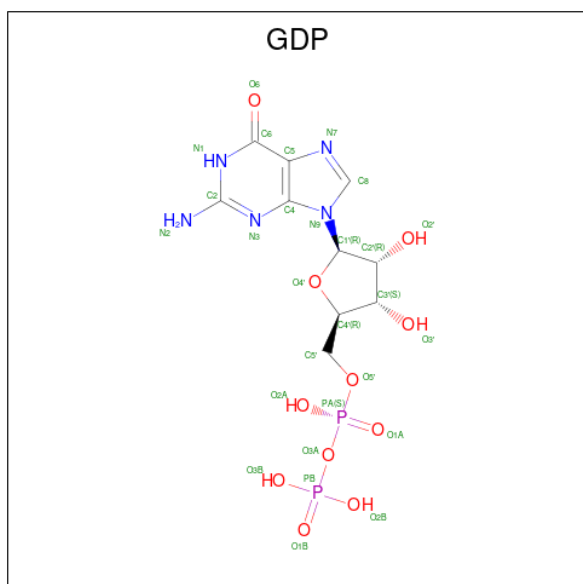
There are 2 unique types of molecules in this entry. The entry contains 5457 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BACTERIAL DYNAMIN-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	680	5429	3423	952	1043	11	0	0	0

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

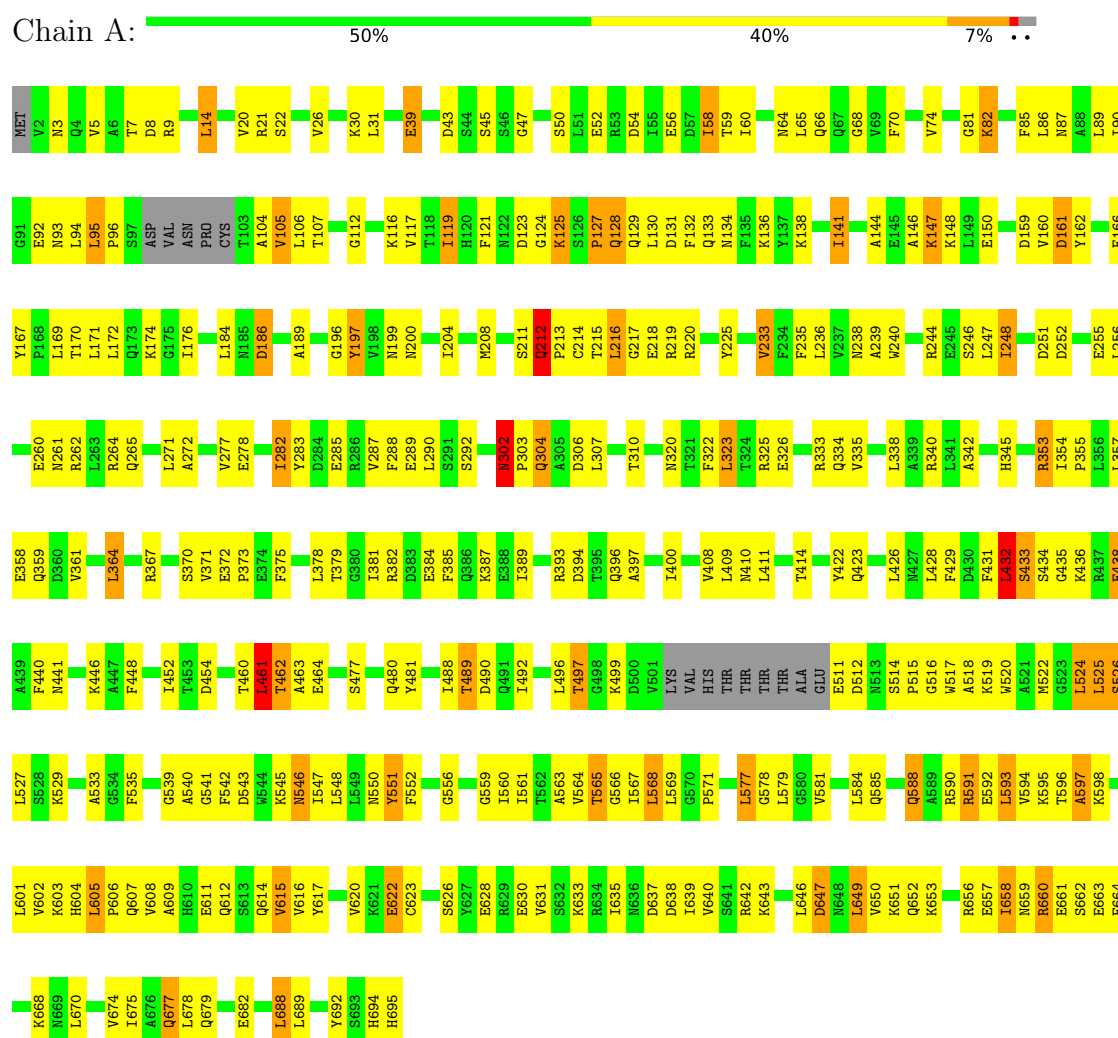


3 Residue-property plots

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: BACTERIAL DYNAMIN-LIKE PROTEIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	77.59Å 154.95Å 247.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10	Depositor
% Data completeness (in resolution range)	99.5 (50.00-3.10)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.223 , 0.269	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5457	wwPDB-VP
Average B, all atoms (Å ²)	69.0	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: GDP

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	0/5513	0.96	26/7440 (0.3%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	LEU	N-CA-C	-7.87	102.79	111.36
1	A	546	ASN	N-CA-C	-7.11	104.42	113.23
1	A	615	VAL	N-CA-C	-6.99	104.17	111.58
1	A	591	ARG	N-CA-C	-6.70	105.09	113.20
1	A	588	GLN	N-CA-C	-6.54	104.95	113.12
1	A	248	ILE	N-CA-C	-6.45	103.59	110.36
1	A	524	LEU	N-CA-C	-6.11	105.99	113.50
1	A	285	GLU	N-CA-C	-5.92	104.53	113.89
1	A	461	LEU	N-CA-C	-5.87	104.80	111.14
1	A	212	GLN	CA-C-N	5.83	126.75	119.98
1	A	212	GLN	C-N-CA	5.83	126.75	119.98
1	A	147	LYS	N-CA-C	-5.77	105.73	112.89
1	A	609	ALA	N-CA-C	-5.69	104.77	110.97
1	A	186	ASP	N-CA-C	5.58	118.29	111.82
1	A	422	TYR	N-CA-C	-5.57	102.24	110.48
1	A	95	LEU	CA-C-N	5.46	126.67	119.84
1	A	95	LEU	C-N-CA	5.46	126.67	119.84
1	A	288	PHE	N-CA-C	5.34	117.10	108.34
1	A	660	ARG	N-CA-C	5.34	117.79	111.33
1	A	626	SER	N-CA-C	-5.32	105.40	111.14
1	A	304	GLN	N-CA-C	-5.28	107.01	112.93
1	A	668	LYS	N-CA-C	-5.17	105.64	111.28
1	A	640	VAL	N-CA-C	5.09	116.43	110.62
1	A	353	ARG	N-CA-C	5.08	117.59	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	323	LEU	N-CA-C	5.06	116.49	110.97
1	A	551	TYR	N-CA-C	-5.05	107.07	113.43

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	5429	0	5434	288	0
2	A	28	0	12	0	0
All	All	5457	0	5446	288	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 26.

All (288) 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:A:104:ALA:HB2	1:A:141:ILE:HD12	1.30	1.09
1:A:128:GLN:HG2	1:A:129:GLN:H	1.22	1.02
1:A:585:GLN:H	1:A:588:GLN:NE2	1.72	0.86
1:A:215:THR:HB	1:A:218:GLU:HG3	1.57	0.85
1:A:375:PHE:HD2	1:A:643:LYS:HE2	1.40	0.84
1:A:334:GLN:HE21	1:A:525:LEU:HA	1.43	0.83
1:A:94:LEU:HD22	1:A:95:LEU:HD12	1.59	0.82
1:A:409:LEU:HD21	1:A:606:PRO:HA	1.62	0.81
1:A:334:GLN:HE22	1:A:539:GLY:H	1.28	0.81
1:A:90:ILE:HD12	1:A:169:LEU:HD13	1.64	0.80
1:A:520:TRP:HH2	1:A:527:LEU:HG	1.47	0.79
1:A:302:ASN:ND2	1:A:304:GLN:H	1.80	0.79
1:A:123:ASP:OD2	1:A:125:LYS:HE3	1.83	0.79
1:A:367:ARG:O	1:A:370:SER:HB3	1.83	0.78
1:A:277:VAL:HG22	1:A:282:ILE:HD12	1.65	0.77
1:A:564:VAL:HG13	1:A:601:LEU:HD11	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:GLN:O	1:A:611:GLU:HG3	1.84	0.76
1:A:375:PHE:CD2	1:A:643:LYS:HE2	2.21	0.75
1:A:436:LYS:HA	1:A:436:LYS:HE2	1.68	0.75
1:A:129:GLN:C	1:A:130:LEU:HD12	2.13	0.74
1:A:199:ASN:HD21	1:A:546:ASN:HD22	1.32	0.74
1:A:31:LEU:HD11	1:A:674:VAL:HG13	1.68	0.74
1:A:652:GLN:HE22	1:A:656:ARG:NH2	1.84	0.74
1:A:167:TYR:CD2	1:A:169:LEU:HG	2.24	0.73
1:A:393:ARG:HG3	1:A:394:ASP:N	2.02	0.72
1:A:105:VAL:O	1:A:107:THR:HG23	1.90	0.72
1:A:585:GLN:H	1:A:588:GLN:HE21	1.39	0.70
1:A:128:GLN:HG2	1:A:129:GLN:N	2.03	0.70
1:A:647:ASP:O	1:A:651:LYS:HG2	1.91	0.70
1:A:578:GLY:O	1:A:584:LEU:HB2	1.90	0.70
1:A:21:ARG:HG3	1:A:65:LEU:CD2	2.22	0.69
1:A:167:TYR:HD2	1:A:169:LEU:HG	1.55	0.69
1:A:307:LEU:O	1:A:310:THR:HG23	1.92	0.68
1:A:652:GLN:OE1	1:A:656:ARG:HD2	1.93	0.68
1:A:87:ASN:HB3	1:A:92:GLU:O	1.94	0.67
1:A:131:ASP:OD2	1:A:133:GLN:HB2	1.94	0.67
1:A:65:LEU:HD11	1:A:335:VAL:HG21	1.76	0.67
1:A:128:GLN:CG	1:A:129:GLN:H	1.99	0.67
1:A:96:PRO:HB3	1:A:136:LYS:HE3	1.77	0.66
1:A:563:ALA:O	1:A:567:ILE:HG12	1.96	0.65
1:A:141:ILE:HD13	1:A:141:ILE:H	1.62	0.65
1:A:436:LYS:C	1:A:438:GLU:H	2.04	0.65
1:A:260:GLU:O	1:A:264:ARG:HG3	1.98	0.64
1:A:21:ARG:HG3	1:A:65:LEU:HD22	1.78	0.64
1:A:497:THR:HG23	1:A:499:LYS:H	1.61	0.63
1:A:70:PHE:HD2	1:A:323:LEU:HD22	1.63	0.63
1:A:302:ASN:ND2	1:A:302:ASN:C	2.55	0.63
1:A:236:LEU:HD22	1:A:290:LEU:HD11	1.80	0.63
1:A:372:GLU:N	1:A:373:PRO:HD2	2.14	0.63
1:A:375:PHE:CE1	1:A:492:ILE:HD13	2.34	0.63
1:A:543:ASP:OD2	1:A:545:LYS:HG2	1.99	0.63
1:A:551:TYR:HD1	1:A:552:PHE:HD1	1.44	0.62
1:A:568:LEU:HD11	1:A:601:LEU:HD21	1.83	0.61
1:A:633:LYS:O	1:A:637:ASP:HB2	2.00	0.61
1:A:333:ARG:HH12	1:A:511:GLU:HB3	1.64	0.61
1:A:595:LYS:HD3	1:A:595:LYS:C	2.25	0.61
1:A:675:ILE:O	1:A:679:GLN:HG3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:678:LEU:HD13	1:A:682:GLU:HG3	1.83	0.61
1:A:432:LEU:HD13	1:A:432:LEU:N	2.17	0.60
1:A:199:ASN:HB2	1:A:547:ILE:HD11	1.83	0.60
1:A:605:LEU:HA	1:A:608:VAL:HG22	1.83	0.59
1:A:85:PHE:CZ	1:A:236:LEU:HD13	2.37	0.59
1:A:9:ARG:CZ	1:A:9:ARG:HB3	2.32	0.59
1:A:220:ARG:NH1	1:A:454:ASP:OD1	2.35	0.59
1:A:9:ARG:HH22	1:A:320:ASN:HD22	1.51	0.58
1:A:514:SER:HB2	1:A:515:PRO:HD2	1.84	0.58
1:A:529:LYS:HG3	1:A:540:ALA:HB2	1.84	0.58
1:A:215:THR:HG22	1:A:216:LEU:N	2.18	0.58
1:A:359:GLN:HE21	1:A:367:ARG:CZ	2.16	0.58
1:A:364:LEU:HD13	1:A:650:VAL:HG22	1.84	0.58
1:A:93:ASN:C	1:A:93:ASN:HD22	2.12	0.58
1:A:612:GLN:C	1:A:614:GLN:H	2.12	0.58
1:A:560:ILE:O	1:A:564:VAL:HG23	2.03	0.58
1:A:141:ILE:HD13	1:A:141:ILE:N	2.18	0.58
1:A:302:ASN:HD21	1:A:304:GLN:H	1.50	0.58
1:A:556:GLY:O	1:A:560:ILE:HG12	2.04	0.58
1:A:517:TRP:CG	1:A:635:ILE:HG12	2.39	0.57
1:A:381:ILE:HG23	1:A:481:TYR:HD2	1.69	0.57
1:A:302:ASN:C	1:A:302:ASN:HD22	2.12	0.57
1:A:515:PRO:HG2	1:A:518:ALA:HB2	1.87	0.57
1:A:134:ASN:OD1	1:A:138:LYS:HE3	2.05	0.57
1:A:384:GLU:HB3	1:A:481:TYR:HE2	1.70	0.57
1:A:364:LEU:HD11	1:A:649:LEU:HD13	1.86	0.56
1:A:378:LEU:HB3	1:A:639:ILE:HD11	1.88	0.56
1:A:497:THR:HG23	1:A:499:LYS:N	2.21	0.56
1:A:90:ILE:HD12	1:A:169:LEU:CD1	2.33	0.56
1:A:282:ILE:HD13	1:A:282:ILE:H	1.71	0.55
1:A:551:TYR:HD1	1:A:552:PHE:CD1	2.22	0.55
1:A:359:GLN:HE21	1:A:367:ARG:NH2	2.03	0.55
1:A:112:GLY:HA3	1:A:166:GLU:HB3	1.87	0.55
1:A:389:ILE:HG21	1:A:628:GLU:HB2	1.89	0.55
1:A:591:ARG:HG2	1:A:591:ARG:HH21	1.71	0.55
1:A:375:PHE:CE2	1:A:643:LYS:HG3	2.41	0.55
1:A:657:GLU:O	1:A:657:GLU:HG3	2.05	0.55
1:A:397:ALA:O	1:A:617:TYR:CD1	2.60	0.55
1:A:216:LEU:HA	1:A:219:ARG:NH2	2.23	0.54
1:A:565:THR:HG22	1:A:566:GLY:N	2.21	0.54
1:A:431:PHE:HB3	1:A:432:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:LEU:HD22	1:A:688:LEU:O	2.07	0.54
1:A:215:THR:HG22	1:A:217:GLY:H	1.73	0.54
1:A:31:LEU:CD1	1:A:674:VAL:HG13	2.38	0.53
1:A:39:GLU:OE1	1:A:39:GLU:HA	2.08	0.53
1:A:238:ASN:ND2	1:A:239:ALA:H	2.05	0.53
1:A:334:GLN:NE2	1:A:539:GLY:H	2.01	0.53
1:A:525:LEU:O	1:A:526:SER:HB3	2.08	0.53
1:A:186:ASP:OD1	1:A:220:ARG:NH2	2.40	0.53
1:A:379:THR:HG23	1:A:382:ARG:HH11	1.73	0.53
1:A:148:LYS:C	1:A:150:GLU:H	2.17	0.53
1:A:520:TRP:CH2	1:A:527:LEU:HG	2.35	0.53
1:A:694:HIS:C	1:A:695:HIS:ND1	2.67	0.53
1:A:141:ILE:HG12	1:A:146:ALA:HB2	1.91	0.52
1:A:264:ARG:HD3	1:A:289:GLU:OE1	2.09	0.52
1:A:385:PHE:HE2	1:A:631:VAL:HG11	1.74	0.52
1:A:256:LEU:O	1:A:260:GLU:HG3	2.09	0.51
1:A:233:VAL:HG22	1:A:235:PHE:CZ	2.45	0.51
1:A:571:PRO:HB3	1:A:596:THR:HG21	1.92	0.51
1:A:204:ILE:HB	1:A:233:VAL:HB	1.93	0.51
1:A:568:LEU:C	1:A:571:PRO:HD2	2.35	0.51
1:A:30:LYS:HD2	1:A:677:GLN:OE1	2.09	0.51
1:A:252:ASP:C	1:A:252:ASP:OD2	2.54	0.51
1:A:590:ARG:HD2	1:A:590:ARG:N	2.26	0.51
1:A:283:TYR:CE1	1:A:287:VAL:HG21	2.46	0.51
1:A:605:LEU:N	1:A:606:PRO:HD2	2.26	0.51
1:A:238:ASN:HD21	1:A:292:SER:H	1.59	0.51
1:A:432:LEU:N	1:A:432:LEU:CD1	2.73	0.51
1:A:282:ILE:HD13	1:A:282:ILE:N	2.25	0.50
1:A:577:LEU:O	1:A:581:VAL:HG22	2.11	0.50
1:A:658:ILE:HD13	1:A:658:ILE:O	2.11	0.50
1:A:74:VAL:HG21	1:A:86:LEU:HD21	1.93	0.50
1:A:371:VAL:C	1:A:373:PRO:HD2	2.37	0.50
1:A:663:GLU:OE1	1:A:663:GLU:HA	2.10	0.50
1:A:353:ARG:O	1:A:354:ILE:C	2.55	0.50
1:A:477:SER:O	1:A:480:GLN:HG2	2.12	0.50
1:A:520:TRP:CZ3	1:A:526:SER:HA	2.47	0.49
1:A:652:GLN:NE2	1:A:656:ARG:NH2	2.55	0.49
1:A:529:LYS:HB3	1:A:542:PHE:CD1	2.47	0.49
1:A:552:PHE:HD2	1:A:615:VAL:HG12	1.77	0.49
1:A:436:LYS:C	1:A:438:GLU:N	2.70	0.49
1:A:515:PRO:HG2	1:A:518:ALA:CB	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:ILE:HD11	1:A:160:VAL:HG22	1.93	0.49
1:A:132:PHE:HE1	1:A:136:LYS:HD2	1.75	0.49
1:A:302:ASN:HD21	1:A:304:GLN:HB2	1.76	0.49
1:A:359:GLN:NE2	1:A:367:ARG:NH2	2.61	0.49
1:A:361:VAL:HG22	1:A:653:LYS:HB3	1.94	0.49
1:A:480:GLN:HG3	1:A:481:TYR:N	2.28	0.49
1:A:215:THR:CB	1:A:218:GLU:HG3	2.37	0.49
1:A:21:ARG:HG3	1:A:65:LEU:HD23	1.95	0.49
1:A:22:SER:O	1:A:26:VAL:HG23	2.12	0.49
1:A:358:GLU:OE2	1:A:660:ARG:HD2	2.12	0.49
1:A:105:VAL:O	1:A:106:LEU:C	2.56	0.49
1:A:244:ARG:HB3	1:A:256:LEU:HD13	1.95	0.48
1:A:518:ALA:HB1	1:A:522:MET:HE2	1.94	0.48
1:A:393:ARG:CG	1:A:394:ASP:N	2.73	0.48
1:A:9:ARG:HB3	1:A:9:ARG:NH2	2.28	0.48
1:A:598:LYS:O	1:A:602:VAL:HG23	2.13	0.48
1:A:400:ILE:HD12	1:A:620:VAL:HG11	1.95	0.48
1:A:551:TYR:CD1	1:A:552:PHE:CD1	3.02	0.48
1:A:591:ARG:HG2	1:A:591:ARG:NH2	2.29	0.48
1:A:302:ASN:ND2	1:A:304:GLN:N	2.55	0.48
1:A:563:ALA:C	1:A:565:THR:N	2.71	0.48
1:A:196:GLY:HA3	1:A:200:ASN:HD22	1.78	0.48
1:A:378:LEU:HB3	1:A:639:ILE:CD1	2.44	0.48
1:A:460:THR:OG1	1:A:550:ASN:ND2	2.47	0.47
1:A:552:PHE:CD2	1:A:615:VAL:HG12	2.49	0.47
1:A:604:HIS:C	1:A:606:PRO:HD2	2.40	0.47
1:A:302:ASN:HD22	1:A:303:PRO:N	2.13	0.47
1:A:563:ALA:C	1:A:565:THR:H	2.23	0.47
1:A:43:ASP:O	1:A:656:ARG:CZ	2.63	0.47
1:A:14:LEU:HB3	1:A:174:LYS:HB3	1.97	0.47
1:A:70:PHE:CD2	1:A:323:LEU:HD22	2.47	0.47
1:A:322:PHE:O	1:A:326:GLU:HB2	2.15	0.46
1:A:579:LEU:HD12	1:A:584:LEU:O	2.15	0.46
1:A:496:LEU:HD11	1:A:646:LEU:HD11	1.97	0.46
1:A:60:ILE:HG22	1:A:64:ASN:ND2	2.31	0.46
1:A:123:ASP:OD1	1:A:125:LYS:HG3	2.15	0.46
1:A:338:LEU:HD13	1:A:525:LEU:HD11	1.97	0.46
1:A:568:LEU:HD11	1:A:601:LEU:CD2	2.44	0.46
1:A:448:PHE:O	1:A:452:ILE:HG13	2.16	0.46
1:A:577:LEU:C	1:A:579:LEU:H	2.23	0.46
1:A:104:ALA:O	1:A:105:VAL:HB	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:514:SER:OG	1:A:522:MET:HE1	2.15	0.46
1:A:525:LEU:CD2	1:A:526:SER:H	2.29	0.46
1:A:128:GLN:CG	1:A:129:GLN:N	2.68	0.46
1:A:597:ALA:O	1:A:598:LYS:C	2.59	0.46
1:A:54:ASP:OD1	1:A:345:HIS:HD2	1.98	0.45
1:A:129:GLN:O	1:A:130:LEU:HD12	2.15	0.45
1:A:215:THR:HG22	1:A:216:LEU:H	1.82	0.45
1:A:240:TRP:HZ2	1:A:260:GLU:HB3	1.81	0.45
1:A:333:ARG:NH1	1:A:511:GLU:HB3	2.31	0.45
1:A:577:LEU:O	1:A:577:LEU:HD22	2.16	0.45
1:A:334:GLN:HE21	1:A:525:LEU:CA	2.23	0.45
1:A:604:HIS:O	1:A:605:LEU:C	2.59	0.45
1:A:144:ALA:C	1:A:146:ALA:H	2.24	0.45
1:A:212:GLN:N	1:A:213:PRO:HD3	2.31	0.45
1:A:354:ILE:HB	1:A:355:PRO:CD	2.46	0.45
1:A:141:ILE:N	1:A:141:ILE:CD1	2.79	0.45
1:A:410:ASN:O	1:A:410:ASN:ND2	2.49	0.45
1:A:240:TRP:NE1	1:A:260:GLU:OE1	2.50	0.45
1:A:432:LEU:O	1:A:433:SER:C	2.59	0.45
1:A:638:ASP:O	1:A:642:ARG:HG3	2.17	0.45
1:A:233:VAL:HG22	1:A:235:PHE:CE1	2.52	0.45
1:A:612:GLN:C	1:A:614:GLN:N	2.73	0.45
1:A:411:LEU:HD23	1:A:411:LEU:HA	1.85	0.44
1:A:605:LEU:HA	1:A:608:VAL:CG2	2.48	0.44
1:A:70:PHE:HB2	1:A:176:ILE:HD13	1.98	0.44
1:A:116:LYS:HG3	1:A:129:GLN:HE22	1.82	0.44
1:A:408:VAL:HG11	1:A:560:ILE:CD1	2.47	0.44
1:A:659:ASN:HD22	1:A:662:SER:CB	2.31	0.44
1:A:20:VAL:HG21	1:A:688:LEU:HG	2.00	0.44
1:A:147:LYS:O	1:A:150:GLU:HB3	2.17	0.44
1:A:208:MET:HE2	1:A:218:GLU:OE1	2.18	0.44
1:A:372:GLU:N	1:A:373:PRO:CD	2.80	0.44
1:A:541:GLY:O	1:A:542:PHE:C	2.60	0.44
1:A:106:LEU:HD21	1:A:197:TYR:CE1	2.53	0.44
1:A:357:LEU:O	1:A:660:ARG:HD3	2.18	0.44
1:A:594:VAL:O	1:A:595:LYS:C	2.61	0.44
1:A:121:PHE:HD1	1:A:159:ASP:O	2.01	0.44
1:A:409:LEU:HD21	1:A:606:PRO:CA	2.41	0.44
1:A:66:GLN:C	1:A:68:GLY:H	2.26	0.44
1:A:124:GLY:O	1:A:125:LYS:C	2.60	0.44
1:A:325:ARG:HG2	1:A:692:TYR:CE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:GLN:HE22	1:A:656:ARG:HH22	1.64	0.43
1:A:199:ASN:O	1:A:542:PHE:HB3	2.19	0.43
1:A:578:GLY:HA3	1:A:584:LEU:HD12	2.00	0.43
1:A:592:GLU:O	1:A:593:LEU:C	2.61	0.43
1:A:5:VAL:HG12	1:A:306:ASP:HA	1.99	0.43
1:A:105:VAL:HG21	1:A:160:VAL:HG11	2.01	0.43
1:A:9:ARG:NH2	1:A:9:ARG:CB	2.81	0.43
1:A:45:SER:C	1:A:47:GLY:H	2.27	0.43
1:A:464:GLU:OE1	1:A:546:ASN:OD1	2.37	0.43
1:A:169:LEU:HB2	1:A:172:LEU:HG	2.01	0.43
1:A:196:GLY:CA	1:A:200:ASN:HD22	2.32	0.43
1:A:517:TRP:CD2	1:A:635:ILE:HG12	2.54	0.43
1:A:601:LEU:C	1:A:603:LYS:H	2.26	0.43
1:A:85:PHE:CE1	1:A:236:LEU:HD13	2.54	0.43
1:A:569:LEU:HD23	1:A:569:LEU:HA	1.87	0.43
1:A:340:ARG:NE	1:A:682:GLU:OE1	2.48	0.43
1:A:200:ASN:HA	1:A:542:PHE:CD1	2.53	0.42
1:A:462:THR:HG22	1:A:463:ALA:N	2.33	0.42
1:A:647:ASP:HB3	1:A:651:LYS:HE2	2.02	0.42
1:A:379:THR:CG2	1:A:382:ARG:HH11	2.32	0.42
1:A:385:PHE:CE2	1:A:389:ILE:HD11	2.54	0.42
1:A:559:GLY:O	1:A:563:ALA:N	2.51	0.42
1:A:104:ALA:HB2	1:A:141:ILE:CD1	2.22	0.42
1:A:213:PRO:O	1:A:214:CYS:C	2.63	0.42
1:A:5:VAL:O	1:A:8:ASP:HB2	2.20	0.42
1:A:429:PHE:O	1:A:433:SER:HB2	2.20	0.42
1:A:52:GLU:O	1:A:56:GLU:HG3	2.19	0.42
1:A:189:ALA:HB1	1:A:225:TYR:CZ	2.55	0.42
1:A:247:LEU:O	1:A:248:ILE:C	2.63	0.42
1:A:525:LEU:HD22	1:A:526:SER:H	1.83	0.42
1:A:516:GLY:O	1:A:519:LYS:N	2.51	0.42
1:A:603:LYS:HE3	1:A:604:HIS:NE2	2.34	0.42
1:A:689:LEU:HD23	1:A:689:LEU:HA	1.86	0.42
1:A:94:LEU:C	1:A:94:LEU:HD23	2.45	0.42
1:A:278:GLU:OE1	1:A:278:GLU:HA	2.20	0.42
1:A:548:LEU:HD13	1:A:548:LEU:C	2.44	0.42
1:A:277:VAL:O	1:A:277:VAL:HG23	2.20	0.42
1:A:488:ILE:O	1:A:492:ILE:HG13	2.20	0.42
1:A:518:ALA:O	1:A:522:MET:HE3	2.20	0.41
1:A:85:PHE:CZ	1:A:236:LEU:CD1	3.03	0.41
1:A:271:LEU:O	1:A:272:ALA:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:PHE:CE2	1:A:631:VAL:HG11	2.54	0.41
1:A:161:ASP:O	1:A:162:TYR:HB3	2.20	0.41
1:A:39:GLU:OE2	1:A:50:SER:N	2.54	0.41
1:A:244:ARG:C	1:A:246:SER:H	2.27	0.41
1:A:92:GLU:HG3	1:A:169:LEU:HD21	2.02	0.41
1:A:408:VAL:HG11	1:A:560:ILE:HD12	2.02	0.41
1:A:489:THR:HG22	1:A:490:ASP:N	2.36	0.41
1:A:622:GLU:O	1:A:623:CYS:C	2.63	0.41
1:A:387:LYS:HB3	1:A:387:LYS:HE2	1.87	0.41
1:A:460:THR:HG21	1:A:550:ASN:HA	2.01	0.41
1:A:141:ILE:CG1	1:A:146:ALA:HB2	2.50	0.41
1:A:397:ALA:O	1:A:617:TYR:HD1	2.03	0.41
1:A:81:GLY:O	1:A:82:LYS:C	2.63	0.41
1:A:240:TRP:CZ2	1:A:260:GLU:HB3	2.56	0.41
1:A:262:ARG:O	1:A:265:GLN:HG2	2.21	0.41
1:A:358:GLU:CD	1:A:660:ARG:HD2	2.45	0.41
1:A:561:ILE:C	1:A:563:ALA:N	2.77	0.41
1:A:58:ILE:HD11	1:A:342:ALA:CB	2.51	0.41
1:A:461:LEU:HA	1:A:461:LEU:HD23	1.85	0.40
1:A:533:ALA:HB3	1:A:535:PHE:CD1	2.56	0.40
1:A:664:PHE:CD1	1:A:664:PHE:C	2.99	0.40
1:A:440:PHE:CD1	1:A:440:PHE:C	2.99	0.40
1:A:601:LEU:C	1:A:603:LYS:N	2.75	0.40
1:A:261:ASN:HD22	1:A:264:ARG:HE	1.68	0.40
1:A:247:LEU:HB3	1:A:255:GLU:CD	2.46	0.40
1:A:441:ASN:HD22	1:A:441:ASN:HA	1.63	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	674/695 (97%)	575 (85%)	85 (13%)	14 (2%)	5	25

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	197	TYR
1	A	125	LYS
1	A	433	SER
1	A	434	SER
1	A	597	ALA
1	A	127	PRO
1	A	435	GLY
1	A	526	SER
1	A	432	LEU
1	A	3	ASN
1	A	105	VAL
1	A	117	VAL
1	A	302	ASN

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	587/601 (98%)	536 (91%)	51 (9%)	9	34

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	14	LEU
1	A	39	GLU
1	A	58	ILE
1	A	59	THR
1	A	82	LYS
1	A	89	LEU

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Mol	Chain	Res	Type
1	A	119	ILE
1	A	127	PRO
1	A	141	ILE
1	A	161	ASP
1	A	170	THR
1	A	171	LEU
1	A	184	LEU
1	A	211	SER
1	A	212	GLN
1	A	233	VAL
1	A	251	ASP
1	A	282	ILE
1	A	302	ASN
1	A	364	LEU
1	A	396	GLN
1	A	414	THR
1	A	423	GLN
1	A	426	LEU
1	A	428	LEU
1	A	432	LEU
1	A	438	GLU
1	A	446	LYS
1	A	461	LEU
1	A	462	THR
1	A	489	THR
1	A	497	THR
1	A	512	ASP
1	A	524	LEU
1	A	525	LEU
1	A	565	THR
1	A	568	LEU
1	A	577	LEU
1	A	593	LEU
1	A	605	LEU
1	A	616	VAL
1	A	622	GLU
1	A	630	GLU
1	A	647	ASP
1	A	649	LEU
1	A	658	ILE
1	A	661	GLU
1	A	670	LEU

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Mol	Chain	Res	Type
1	A	677	GLN
1	A	688	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	12	GLN
1	A	19	GLN
1	A	67	GLN
1	A	93	ASN
1	A	122	ASN
1	A	128	GLN
1	A	151	GLN
1	A	199	ASN
1	A	238	ASN
1	A	261	ASN
1	A	294	GLN
1	A	302	ASN
1	A	320	ASN
1	A	334	GLN
1	A	345	HIS
1	A	359	GLN
1	A	386	GLN
1	A	396	GLN
1	A	410	ASN
1	A	423	GLN
1	A	441	ASN
1	A	486	ASN
1	A	546	ASN
1	A	550	ASN
1	A	588	GLN
1	A	607	GLN
1	A	618	ASN
1	A	659	ASN
1	A	671	GLN
1	A	687	ASN

5.3.3 RNA ⓘ

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](#)

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$
2	GDP	A	999	-	29,30,30	1.01	1 (3%)	45,47,47	1.79	12 (26%)

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
2	GDP	A	999	-	-	0/16/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	999	GDP	PA-O3A	2.92	1.62	1.59

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	999	GDP	C2-N3-C4	5.42	121.63	112.30
2	A	999	GDP	C5-C4-N3	-4.85	120.68	128.39
2	A	999	GDP	N9-C4-N3	3.61	133.18	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	999	GDP	O4'-C4'-C3'	3.01	111.12	105.15
2	A	999	GDP	C6-C5-N7	2.64	135.09	130.29
2	A	999	GDP	C8-N7-C5	2.62	108.93	104.26
2	A	999	GDP	PA-O5'-C5'	-2.34	107.92	121.35
2	A	999	GDP	C2-N1-C6	-2.31	120.92	125.11
2	A	999	GDP	C5'-C4'-C3'	-2.19	107.34	115.21
2	A	999	GDP	C4-C5-N7	-2.14	107.28	110.67
2	A	999	GDP	O6-C6-C5	-2.08	121.04	126.53
2	A	999	GDP	C3'-C2'-C1'	2.05	105.34	101.46

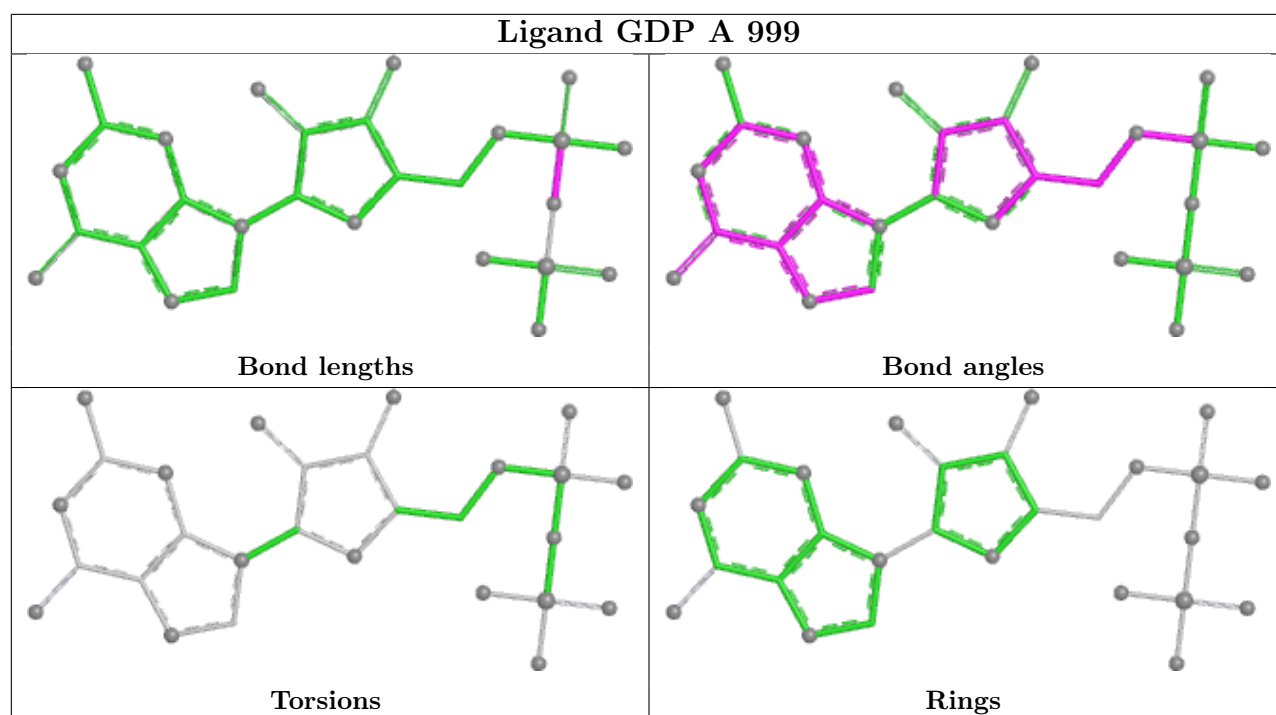
There are no chirality outliers.

There are no torsion outliers.

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

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.