



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:14 AM UTC

PDB ID : 1E8U / pdb_00001e8u
Title : Structure of the multifunctional paramyxovirus hemagglutinin-neuraminidase
Authors : Crennell, S.; Takimoto, T.; Portner, A.; Taylor, G.
Deposited on : 2000-10-01
Resolution : 2.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

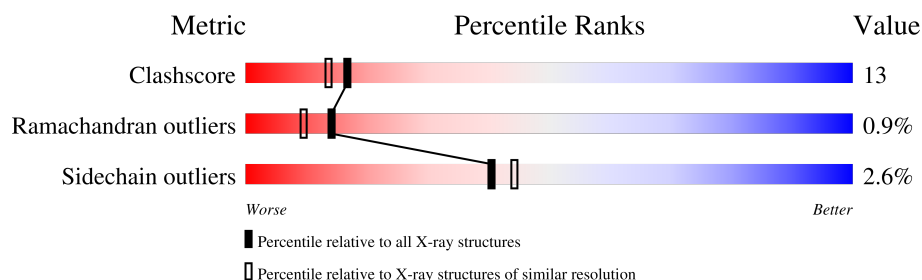
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	454	
1	B	454	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	A	1573	X	-	-	-
4	NAG	B	1575	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7401 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.

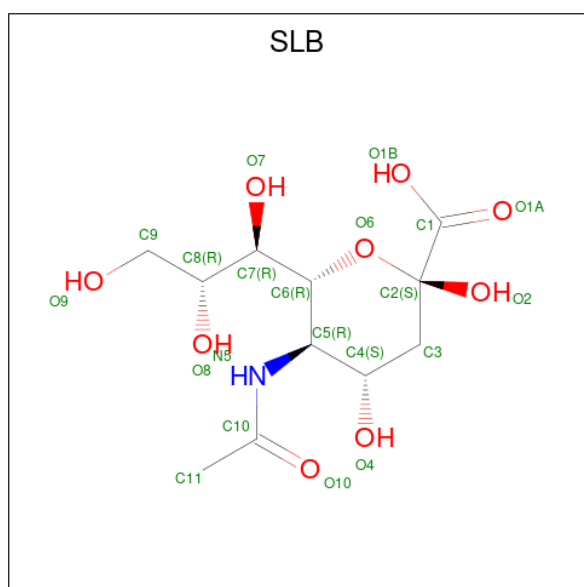
- Molecule 1 is a protein called HEMAGGLUTININ-NEURAMINIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	447	Total	C	N	O	S	0	0	1
			3446	2172	588	667	19			
1	B	450	Total	C	N	O	S	0	0	1
			3468	2185	594	670	19			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

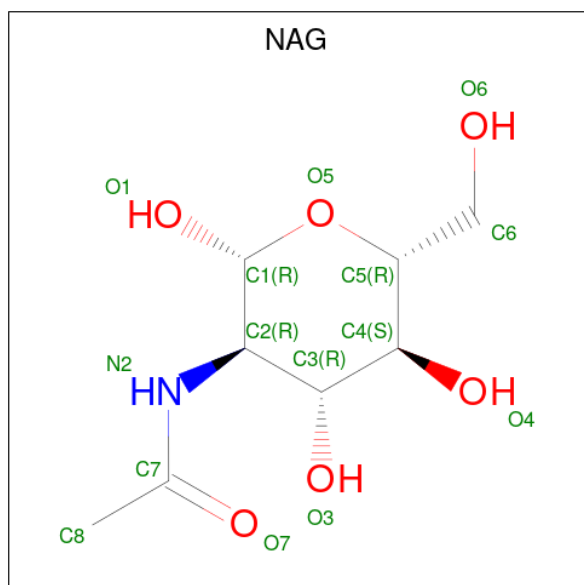
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

- Molecule 3 is N-acetyl-beta-neuraminic acid (CCD ID: SLB) (formula: C₁₁H₁₉NO₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	11	1	9		
3	B	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			15	8	1	6		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			15	8	1	6		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 5 is water.

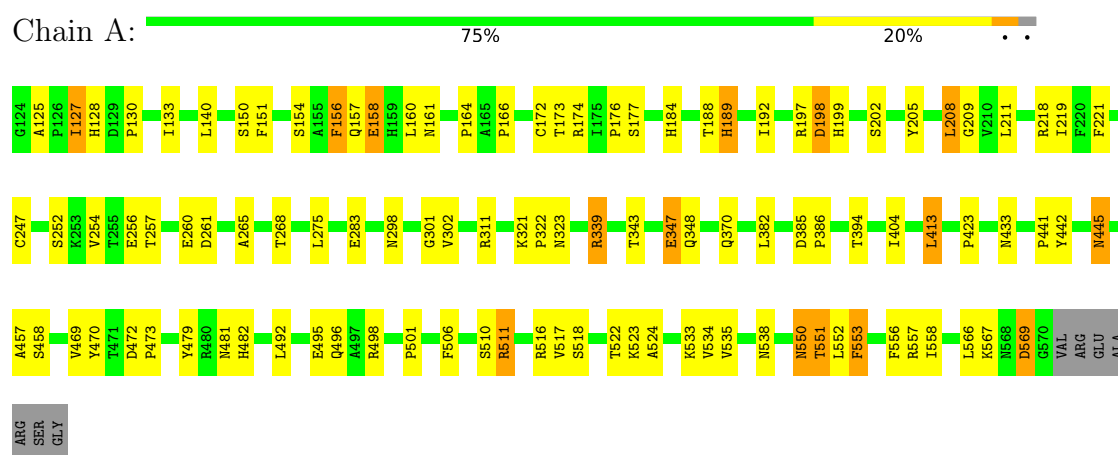
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	232	Total	O	0	0
			232	232		
5	B	138	Total	O	0	0
			138	138		

3 Residue-property plots

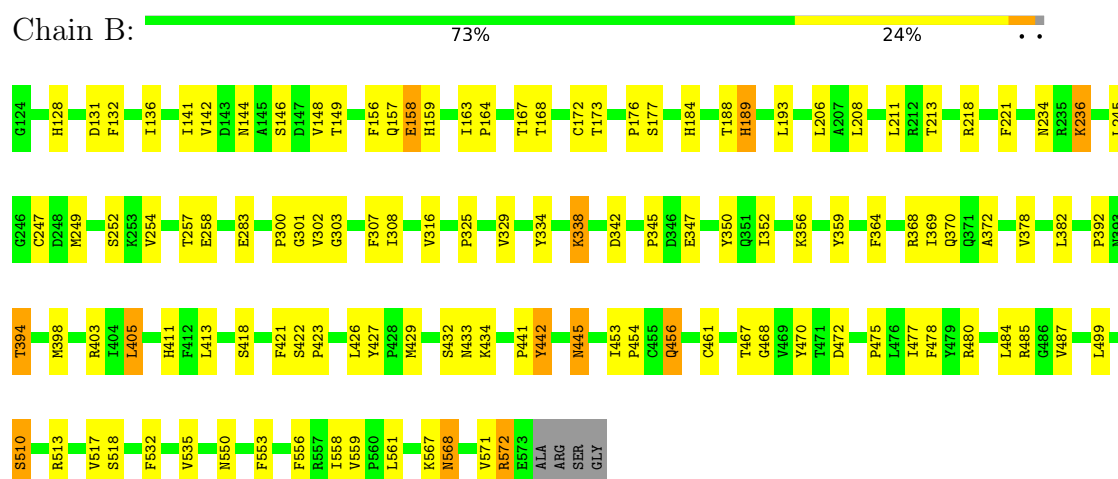
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



• Molecule 1: HEMAGGLUTININ-NEURAMINIDASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.56Å 78.49Å 199.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.00	Depositor
% Data completeness (in resolution range)	97.0 (6.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.267	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7401	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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: CA, NAG, SLB

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	0.40	1/3531 (0.0%)	0.94	13/4804 (0.3%)
1	B	0.37	1/3553 (0.0%)	0.88	10/4833 (0.2%)
All	All	0.39	2/7084 (0.0%)	0.91	23/9637 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	572	ARG	C-N	-5.78	1.25	1.33
1	A	569	ASP	C-N	-5.66	1.25	1.33

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	394	THR	N-CA-C	-8.19	103.00	113.16
1	B	394	THR	N-CA-C	-7.47	103.76	113.17
1	B	442	TYR	N-CA-C	-6.98	100.14	110.48
1	A	442	TYR	N-CA-C	-6.85	99.42	110.32
1	B	370	GLN	N-CA-C	6.34	119.80	109.59
1	A	441	PRO	N-CA-C	6.26	121.09	111.57
1	A	445	ASN	N-CA-C	6.20	119.69	111.75
1	A	370	GLN	N-CA-C	6.05	119.33	109.59
1	B	445	ASN	N-CA-C	5.86	118.42	111.33
1	A	553	PHE	N-CA-C	5.84	119.38	112.72
1	B	173	THR	N-CA-C	-5.77	99.00	108.76
1	B	472	ASP	N-CA-C	5.76	118.65	110.24
1	A	510	SER	N-CA-C	5.72	118.57	109.81
1	A	150	SER	N-CA-C	-5.66	105.87	112.89
1	A	472	ASP	N-CA-C	5.51	118.29	110.24
1	B	300	PRO	N-CA-C	-5.50	103.17	111.41
1	A	173	THR	N-CA-C	-5.49	100.45	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	252	SER	N-CA-C	-5.41	101.35	109.95
1	B	513	ARG	N-CA-C	-5.38	102.42	110.23
1	A	433	ASN	N-CA-C	5.31	117.66	111.02
1	B	510	SER	N-CA-C	5.19	117.78	110.14
1	B	252	SER	N-CA-C	-5.18	101.72	109.95
1	A	479	TYR	N-CA-C	-5.05	104.01	110.53

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	3446	0	3341	78	0
1	B	3468	0	3365	96	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	21	0	18	1	0
3	B	21	0	18	2	0
4	A	44	0	43	1	0
4	B	29	0	28	2	0
5	A	232	0	0	1	0
5	B	138	0	0	2	0
All	All	7401	0	6813	177	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 13.

All (177) 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:B:156:PHE:HE2	1:B:517:VAL:HA	1.25	1.00
1:A:511:ARG:HG2	1:A:511:ARG:HH11	1.29	0.93
1:B:128:HIS:HD2	1:B:211:LEU:H	1.19	0.87
1:B:156:PHE:CE2	1:B:517:VAL:HA	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ASP:O	1:B:535:VAL:HG22	1.83	0.79
1:A:218:ARG:NE	1:A:218:ARG:HA	2.01	0.75
1:B:338:LYS:HD3	1:B:338:LYS:H	1.51	0.74
1:B:128:HIS:CD2	1:B:211:LEU:H	2.06	0.73
1:A:197:ARG:HE	1:A:199:HIS:HB2	1.53	0.72
1:A:567:LYS:HE2	1:A:569:ASP:HB3	1.73	0.70
1:A:511:ARG:HG2	1:A:511:ARG:NH1	2.07	0.70
1:A:208:LEU:HD23	1:A:247:CYS:SG	2.31	0.69
1:B:144:ASN:OD1	1:B:480:ARG:HG3	1.92	0.69
1:A:176:PRO:HB3	1:A:558:ILE:HD13	1.74	0.69
1:B:206:LEU:HD13	1:B:249:MET:CE	2.24	0.68
1:B:338:LYS:HD3	1:B:338:LYS:N	2.08	0.68
1:B:421:PHE:CE2	1:B:423:PRO:HG2	2.29	0.67
1:A:156:PHE:CE2	1:A:517:VAL:HA	2.30	0.67
1:B:421:PHE:CZ	1:B:423:PRO:HG2	2.29	0.67
1:A:218:ARG:HE	1:A:219:ILE:H	1.40	0.67
1:A:157:GLN:O	1:A:158:GLU:HG3	1.94	0.67
1:B:206:LEU:HD13	1:B:249:MET:HE3	1.77	0.66
4:B:1574:NAG:O4	4:B:1575:NAG:H1	1.96	0.66
1:A:265:ALA:O	1:A:321:LYS:HE2	1.97	0.64
1:B:456:GLN:H	1:B:456:GLN:CD	2.05	0.64
1:B:338:LYS:H	1:B:338:LYS:CD	2.11	0.64
1:B:159:HIS:HE1	1:B:559:VAL:HG13	1.62	0.63
1:B:454:PRO:HA	1:B:456:GLN:OE1	1.98	0.63
1:B:176:PRO:HB3	1:B:558:ILE:HD13	1.81	0.62
1:A:339:ARG:HD3	1:A:423:PRO:CG	2.30	0.61
1:A:130:PRO:HA	1:A:133:ILE:HG23	1.81	0.61
1:A:192:ILE:HD13	1:A:202:SER:HB3	1.82	0.60
1:A:197:ARG:C	1:A:199:HIS:H	2.10	0.60
1:B:146:SER:HB2	1:B:567:LYS:HZ1	1.66	0.60
1:B:245:LEU:HD12	1:B:245:LEU:N	2.17	0.60
1:A:156:PHE:HE2	1:A:517:VAL:HA	1.66	0.59
1:B:316:VAL:HG23	1:B:372:ALA:HB3	1.84	0.59
1:A:218:ARG:HE	1:A:219:ILE:N	2.00	0.59
1:A:339:ARG:NH2	1:A:457:ALA:O	2.36	0.59
1:A:154:SER:HB3	1:A:566:LEU:HD11	1.86	0.58
4:A:1572:NAG:O4	4:A:1573:NAG:H4	2.03	0.58
1:A:523:LYS:HD3	5:A:2224:HOH:O	2.04	0.58
1:A:133:ILE:O	1:A:535:VAL:HG21	2.04	0.57
1:B:352:ILE:HG22	1:B:356:LYS:HZ3	1.68	0.57
1:B:236:LYS:HB2	1:B:236:LYS:NZ	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ARG:HH12	1:A:198:ASP:HA	1.71	0.56
1:B:325:PRO:O	1:B:329:VAL:HG23	2.06	0.56
1:A:339:ARG:HD2	1:A:445:ASN:OD1	2.06	0.55
1:A:172:CYS:HB2	1:A:556:PHE:O	2.06	0.55
1:B:177:SER:HB3	1:B:188:THR:HG22	1.89	0.55
1:A:127:ILE:HG22	1:A:128:HIS:O	2.08	0.54
1:A:211:LEU:HD21	1:A:221:PHE:CZ	2.43	0.53
1:A:339:ARG:HD3	1:A:423:PRO:HG2	1.90	0.53
1:A:257:THR:OG1	1:A:260:GLU:HG3	2.08	0.53
1:A:133:ILE:O	1:A:133:ILE:HG13	2.08	0.53
1:B:345:PRO:HD2	1:B:461:CYS:SG	2.49	0.53
1:B:568:ASN:HD22	1:B:568:ASN:N	2.06	0.52
1:A:469:VAL:HG11	1:A:492:LEU:HD22	1.91	0.51
1:A:501:PRO:HG3	1:A:524:ALA:HB2	1.92	0.51
1:B:167:THR:HG23	1:B:168:THR:HG23	1.92	0.51
1:B:334:TYR:OH	1:B:352:ILE:HD12	2.10	0.51
1:A:256:GLU:OE2	1:A:261:ASP:HA	2.10	0.51
1:B:423:PRO:HB3	1:B:445:ASN:HA	1.91	0.51
1:B:347:GLU:HG3	1:B:350:TYR:HB2	1.91	0.51
1:B:405:LEU:HD23	1:B:405:LEU:N	2.25	0.51
1:A:339:ARG:NH2	1:A:458:SER:HA	2.25	0.50
1:B:517:VAL:HG13	1:B:561:LEU:HD11	1.92	0.50
1:A:551:THR:OG1	1:A:552:LEU:HD22	2.12	0.50
1:B:352:ILE:CG2	1:B:356:LYS:HZ3	2.24	0.50
1:B:453:ILE:HA	1:B:456:GLN:OE1	2.11	0.50
1:B:206:LEU:HD13	1:B:249:MET:HE1	1.94	0.50
1:A:218:ARG:NE	1:A:218:ARG:CA	2.73	0.49
1:A:208:LEU:C	1:A:208:LEU:HD13	2.37	0.49
1:B:369:ILE:HB	1:B:398:MET:HG3	1.94	0.49
1:A:164:PRO:HG2	1:A:205:TYR:CZ	2.48	0.49
1:B:236:LYS:HE3	3:B:1573:SLB:H113	1.95	0.49
1:B:568:ASN:OD1	1:B:571:VAL:HG11	2.13	0.48
1:A:533:LYS:HD3	1:A:538:ASN:HD22	1.77	0.48
1:A:516:ARG:HG2	1:A:516:ARG:HH11	1.78	0.48
1:A:174:ARG:NH1	1:A:198:ASP:HA	2.29	0.48
1:B:193:LEU:HD12	1:B:193:LEU:N	2.27	0.48
1:B:257:THR:HG22	1:B:258:GLU:N	2.28	0.48
1:B:475:PRO:HA	1:B:487:VAL:HG12	1.96	0.48
1:A:404:ILE:HD13	1:A:413:LEU:HD23	1.94	0.48
1:A:157:GLN:C	1:A:158:GLU:HG3	2.38	0.47
1:B:568:ASN:O	1:B:568:ASN:ND2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:HIS:CD2	1:A:208:LEU:HD21	2.49	0.47
1:A:339:ARG:HH22	1:A:458:SER:HA	1.80	0.47
1:B:234:ASN:HB2	1:B:254:VAL:O	2.14	0.47
1:B:141:ILE:O	1:B:477:ILE:HA	2.15	0.47
1:B:568:ASN:N	1:B:568:ASN:ND2	2.62	0.47
1:B:236:LYS:HB2	1:B:236:LYS:HZ3	1.78	0.46
1:A:160:LEU:C	1:A:161:ASN:HD22	2.23	0.46
1:B:568:ASN:ND2	1:B:568:ASN:H	2.13	0.46
1:A:154:SER:HB3	1:A:566:LEU:CD1	2.45	0.46
1:A:197:ARG:HG2	1:A:199:HIS:HD2	1.81	0.46
1:A:481:ASN:O	1:A:482:HIS:HB2	2.15	0.46
1:B:303:GLY:HA3	1:B:403:ARG:HB2	1.97	0.46
1:A:125:ALA:O	1:A:127:ILE:HG13	2.15	0.46
1:A:177:SER:HB3	1:A:188:THR:HG22	1.98	0.46
1:B:211:LEU:HD21	1:B:221:PHE:CZ	2.51	0.46
1:A:218:ARG:HA	1:A:218:ARG:HE	1.79	0.46
1:B:149:THR:HG21	1:B:510:SER:HB2	1.97	0.46
1:A:130:PRO:HA	1:A:133:ILE:CG2	2.47	0.45
1:A:506:PHE:CE2	1:A:511:ARG:HD3	2.52	0.45
1:B:364:PHE:HB2	5:B:2078:HOH:O	2.16	0.45
1:A:567:LYS:CE	1:A:569:ASP:HB3	2.44	0.45
1:B:132:PHE:CE1	1:B:213:THR:HG23	2.51	0.45
1:A:166:PRO:HD3	1:A:557:ARG:HG3	1.99	0.45
1:B:453:ILE:HG23	1:B:454:PRO:HA	1.98	0.45
4:B:1574:NAG:C4	4:B:1575:NAG:H1	2.47	0.45
1:B:188:THR:OG1	1:B:249:MET:HE1	2.16	0.44
1:A:518:SER:HB3	1:A:522:THR:OG1	2.18	0.44
1:B:535:VAL:HG21	5:B:2004:HOH:O	2.15	0.44
1:A:498:ARG:NH2	3:A:1570:SLB:O1A	2.48	0.44
1:B:411:HIS:HB2	1:B:429:MET:O	2.17	0.44
1:B:142:VAL:HG23	1:B:142:VAL:O	2.17	0.44
1:B:172:CYS:HB2	1:B:556:PHE:O	2.17	0.44
1:B:188:THR:HG21	1:B:249:MET:HE2	1.99	0.44
1:B:427:TYR:CD1	1:B:441:PRO:HB3	2.53	0.44
1:A:197:ARG:O	1:A:199:HIS:N	2.50	0.44
1:B:136:ILE:HD13	1:B:532:PHE:HB2	2.00	0.44
1:B:148:VAL:HG21	1:B:485:ARG:HG2	1.99	0.44
1:A:322:PRO:O	1:A:323:ASN:HB2	2.16	0.44
1:B:571:VAL:HG23	1:B:572:ARG:N	2.33	0.43
1:A:151:PHE:CE2	1:A:567:LYS:HD2	2.53	0.43
1:B:144:ASN:HD21	1:B:480:ARG:H	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:ARG:HG2	1:A:199:HIS:CD2	2.53	0.43
1:B:316:VAL:CG2	1:B:372:ALA:HB3	2.47	0.43
1:B:347:GLU:CG	1:B:350:TYR:HB2	2.48	0.43
1:B:245:LEU:HD13	1:B:378:VAL:CG1	2.49	0.43
1:B:359:TYR:O	1:B:368:ARG:HA	2.19	0.43
1:A:552:LEU:HD22	1:A:552:LEU:N	2.33	0.43
1:B:413:LEU:C	1:B:413:LEU:HD23	2.44	0.43
1:A:254:VAL:HG12	1:A:268:THR:HG23	2.01	0.43
1:B:432:SER:O	1:B:433:ASN:HB2	2.18	0.43
1:A:301:GLY:O	1:A:302:VAL:HB	2.19	0.43
1:B:245:LEU:N	1:B:245:LEU:CD1	2.81	0.43
1:B:467:THR:HG23	1:B:468:GLY:N	2.33	0.43
1:B:329:VAL:O	1:B:329:VAL:HG12	2.19	0.42
1:B:334:TYR:CE2	1:B:356:LYS:NZ	2.86	0.42
1:B:193:LEU:N	1:B:193:LEU:CD1	2.82	0.42
1:A:189:HIS:C	1:A:189:HIS:CD2	2.98	0.42
1:B:418:SER:HA	1:B:467:THR:O	2.19	0.42
1:A:130:PRO:O	1:A:133:ILE:HG12	2.19	0.42
1:B:157:GLN:O	1:B:158:GLU:C	2.63	0.42
1:B:189:HIS:C	1:B:189:HIS:CD2	2.98	0.42
1:B:283:GLU:HA	1:B:382:LEU:HD13	2.02	0.42
1:A:550:ASN:HB3	1:A:553:PHE:HD2	1.85	0.42
1:A:385:ASP:N	1:A:386:PRO:HD3	2.34	0.42
1:B:301:GLY:O	1:B:302:VAL:HB	2.20	0.42
1:B:307:PHE:C	1:B:308:ILE:HG13	2.45	0.42
1:B:392:PRO:C	1:B:394:THR:H	2.28	0.42
1:B:550:ASN:HB3	1:B:553:PHE:HB2	2.01	0.42
1:A:156:PHE:O	1:A:157:GLN:C	2.63	0.41
1:A:208:LEU:HD13	1:A:209:GLY:N	2.35	0.41
1:A:516:ARG:HG2	1:A:516:ARG:NH1	2.34	0.41
1:B:236:LYS:HE3	3:B:1573:SLB:C11	2.50	0.41
1:B:422:SER:N	1:B:423:PRO:HD2	2.36	0.41
1:B:470:TYR:CD1	1:B:470:TYR:C	2.98	0.41
1:A:283:GLU:HA	1:A:382:LEU:HD13	2.02	0.41
1:B:338:LYS:N	1:B:338:LYS:CD	2.77	0.41
1:B:499:LEU:HD12	1:B:499:LEU:C	2.46	0.41
1:B:550:ASN:CG	1:B:553:PHE:CD1	2.99	0.41
1:A:347:GLU:CD	1:A:348:GLN:N	2.79	0.41
1:A:534:VAL:O	1:A:538:ASN:N	2.53	0.41
1:A:470:TYR:CD1	1:A:470:TYR:C	2.99	0.41
1:B:158:GLU:HG2	1:B:218:ARG:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:ILE:HA	1:B:164:PRO:HD3	1.96	0.41
1:B:208:LEU:HD13	1:B:247:CYS:SG	2.61	0.40
1:B:442:TYR:CZ	1:B:484:LEU:HB3	2.57	0.40
1:B:184:HIS:CD2	1:B:208:LEU:HD11	2.56	0.40
1:B:426:LEU:HD12	1:B:426:LEU:HA	1.87	0.40
1:B:478:PHE:CD1	1:B:478:PHE:N	2.89	0.40
1:A:197:ARG:C	1:A:199:HIS:N	2.76	0.40
1:A:197:ARG:NE	1:A:199:HIS:HB2	2.28	0.40
1:A:495:GLU:HG3	1:A:496:GLN:HG3	2.02	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	445/454 (98%)	417 (94%)	23 (5%)	5 (1%)	11	7
1	B	448/454 (99%)	415 (93%)	30 (7%)	3 (1%)	18	14
All	All	893/908 (98%)	832 (93%)	53 (6%)	8 (1%)	14	9

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	127	ILE
1	B	158	GLU
1	A	198	ASP
1	A	156	PHE
1	A	551	THR
1	B	342	ASP
1	B	518	SER
1	A	473	PRO

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	387/392 (99%)	374 (97%)	13 (3%)	32	33
1	B	389/392 (99%)	382 (98%)	7 (2%)	51	58
All	All	776/784 (99%)	756 (97%)	20 (3%)	40	44

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

Mol	Chain	Res	Type
1	A	140	LEU
1	A	158	GLU
1	A	189	HIS
1	A	208	LEU
1	A	275	LEU
1	A	298	ASN
1	A	311	ARG
1	A	339	ARG
1	A	343	THR
1	A	347	GLU
1	A	413	LEU
1	A	511	ARG
1	A	550	ASN
1	B	189	HIS
1	B	236	LYS
1	B	338	LYS
1	B	405	LEU
1	B	434	LYS
1	B	456	GLN
1	B	568	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	161	ASN
1	A	199	HIS

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Mol	Chain	Res	Type
1	A	203	HIS
1	A	233	GLN
1	A	323	ASN
1	A	341	ASN
1	A	371	GLN
1	A	415	GLN
1	A	496	GLN
1	A	538	ASN
1	B	128	HIS
1	B	157	GLN
1	B	159	HIS
1	B	263	ASN
1	B	351	GLN
1	B	371	GLN
1	B	415	GLN
1	B	500	ASN
1	B	568	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1574	1	14,14,15	0.50	0	17,19,21	0.63	0
3	SLB	B	1573	-	21,21,21	0.73	0	24,31,31	1.08	1 (4%)
4	NAG	B	1575	-	15,15,15	0.39	0	21,21,21	0.56	0
4	NAG	A	1573	-	15,15,15	0.40	0	21,21,21	0.53	0
4	NAG	A	1572	1	14,14,15	0.52	0	17,19,21	0.72	1 (5%)
4	NAG	A	1571	-	15,15,15	0.40	0	21,21,21	0.57	0
3	SLB	A	1570	-	21,21,21	0.73	0	24,31,31	0.95	1 (4%)

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
4	NAG	B	1574	1	-	1/6/23/26	0/1/1/1
3	SLB	B	1573	-	-	5/20/38/38	0/1/1/1
4	NAG	B	1575	-	1/1/6/7	2/6/26/26	0/1/1/1
4	NAG	A	1573	-	1/1/6/7	3/6/26/26	0/1/1/1
4	NAG	A	1572	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1571	-	-	0/6/26/26	0/1/1/1
3	SLB	A	1570	-	-	5/20/38/38	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1573	SLB	O1A-C1-C2	-3.39	118.19	123.85
3	A	1570	SLB	O1A-C1-C2	-3.28	118.38	123.85
4	A	1572	NAG	C2-N2-C7	-2.18	119.98	122.90

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1573	NAG	C1
4	B	1575	NAG	C1

All (18) torsion outliers are listed below:

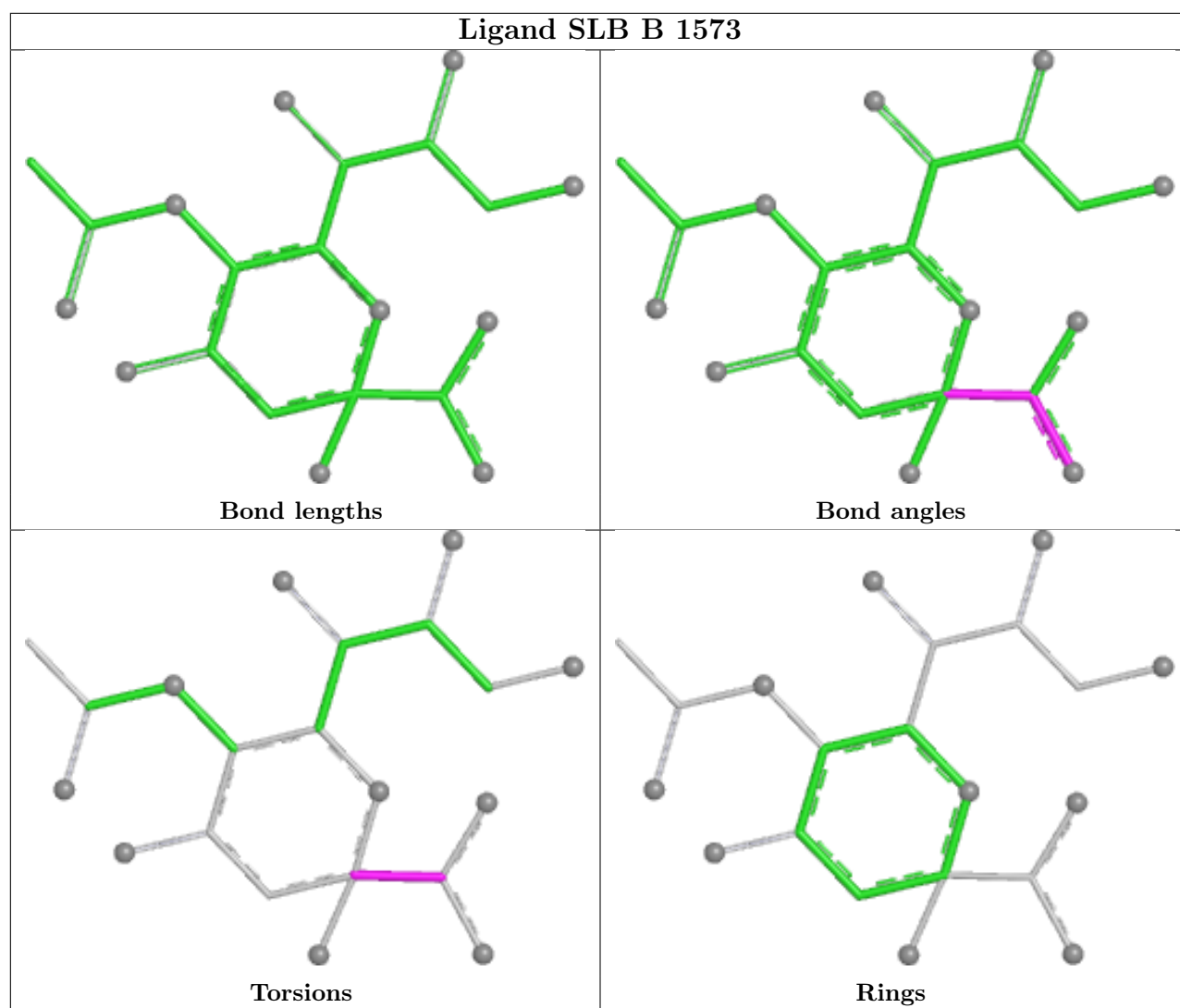
Mol	Chain	Res	Type	Atoms
3	A	1570	SLB	O1A-C1-C2-O2
3	A	1570	SLB	O1B-C1-C2-O2
3	A	1570	SLB	O1B-C1-C2-O6
3	B	1573	SLB	O1A-C1-C2-O2
3	B	1573	SLB	O1B-C1-C2-O6
4	A	1573	NAG	C4-C5-C6-O6
4	B	1574	NAG	O5-C5-C6-O6
4	B	1575	NAG	O5-C5-C6-O6
4	B	1575	NAG	C4-C5-C6-O6
4	A	1573	NAG	O5-C5-C6-O6
4	A	1572	NAG	C4-C5-C6-O6
4	A	1572	NAG	O5-C5-C6-O6
3	A	1570	SLB	O1B-C1-C2-C3
3	B	1573	SLB	O1A-C1-C2-O6
4	A	1573	NAG	C1-C2-N2-C7
3	B	1573	SLB	O1B-C1-C2-O2
3	A	1570	SLB	O1A-C1-C2-C3
3	B	1573	SLB	O1A-C1-C2-C3

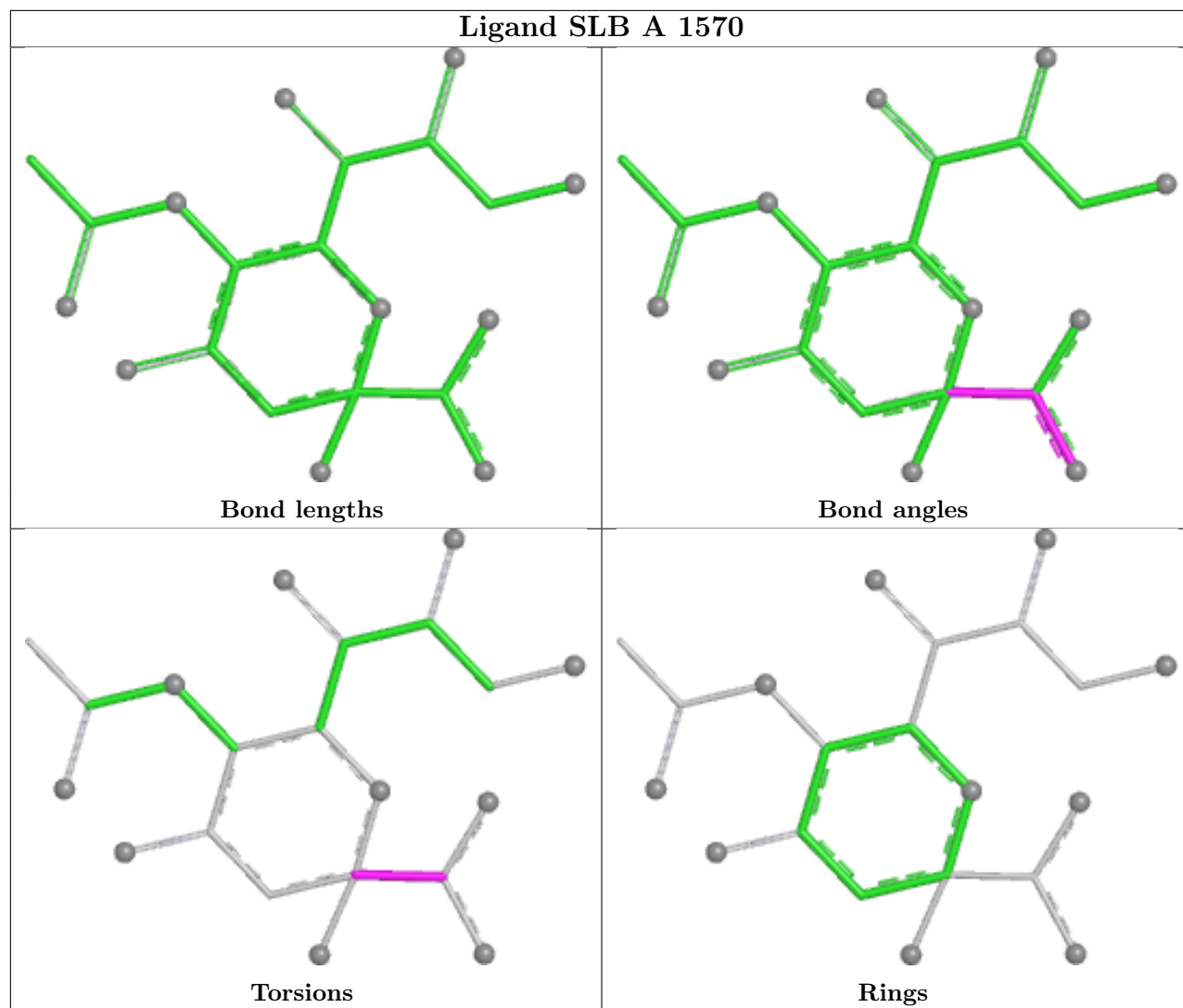
There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1574	NAG	2	0
3	B	1573	SLB	2	0
4	B	1575	NAG	2	0
4	A	1573	NAG	1	0
4	A	1572	NAG	1	0
3	A	1570	SLB	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.