



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:37 AM UTC

PDB ID : 6HMF / pdb_00006hmf
Title : D-family DNA polymerase - DP1 subunit (3'-5' proof-reading exonuclease)
H451 proof-reading deficient variant
Authors : Raia, P.; Delarue, M.; Sauguet, L.
Deposited on : 2018-09-12
Resolution : 2.60 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
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

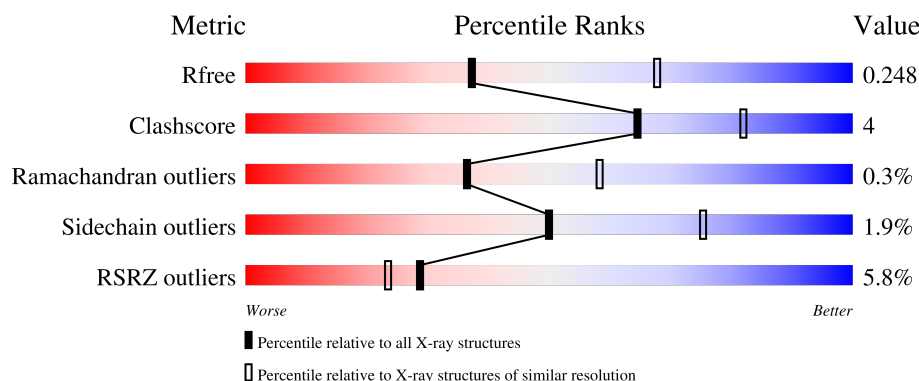
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	475	 6% 79% 12% • 7%
1	B	475	 4% 83% 9% • 7%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7128 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 DNA polymerase II small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	440	Total	C	N	O	S	0	0	0
			3512	2291	575	639	7			
1	B	442	Total	C	N	O	S	0	1	0
			3530	2304	577	642	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	451	ALA	HIS	engineered mutation	UNP Q9V2F3
B	451	ALA	HIS	engineered mutation	UNP Q9V2F3

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

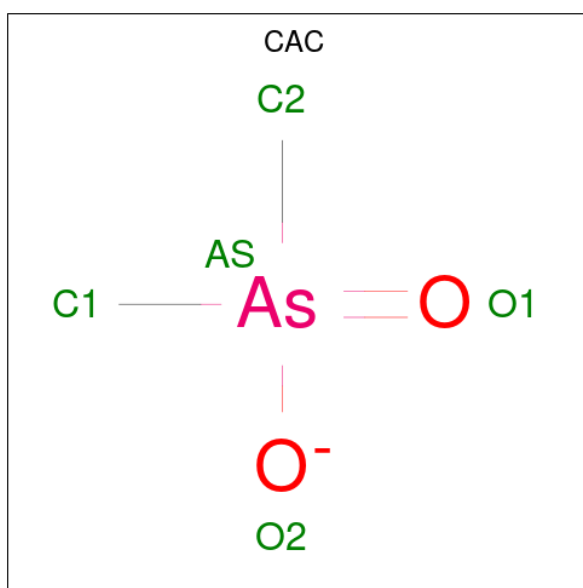
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is CACODYLATE ION (CCD ID: CAC) (formula: C₂H₆AsO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	As	C	O	0	0
			5	1	2	2		
5	B	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	Ca 1	0	0

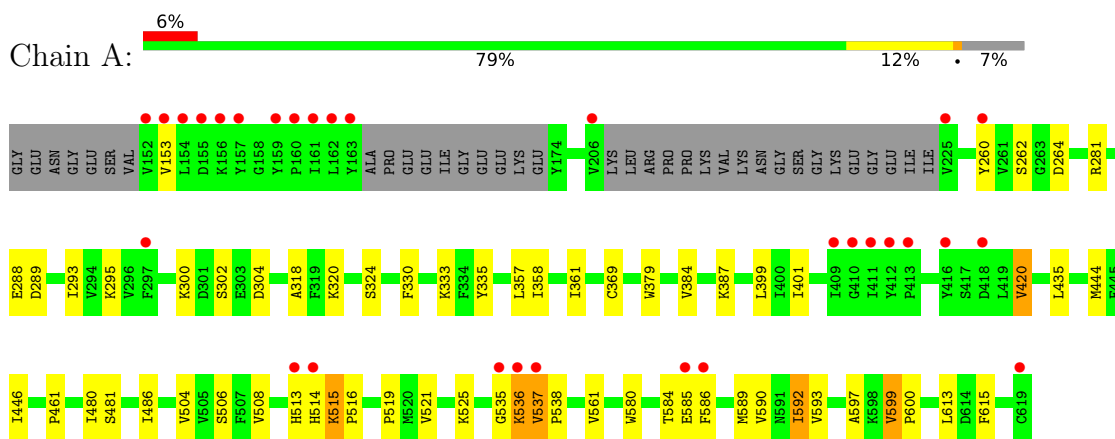
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	33	Total 33	O 33	0	0
7	B	30	Total 30	O 30	0	0

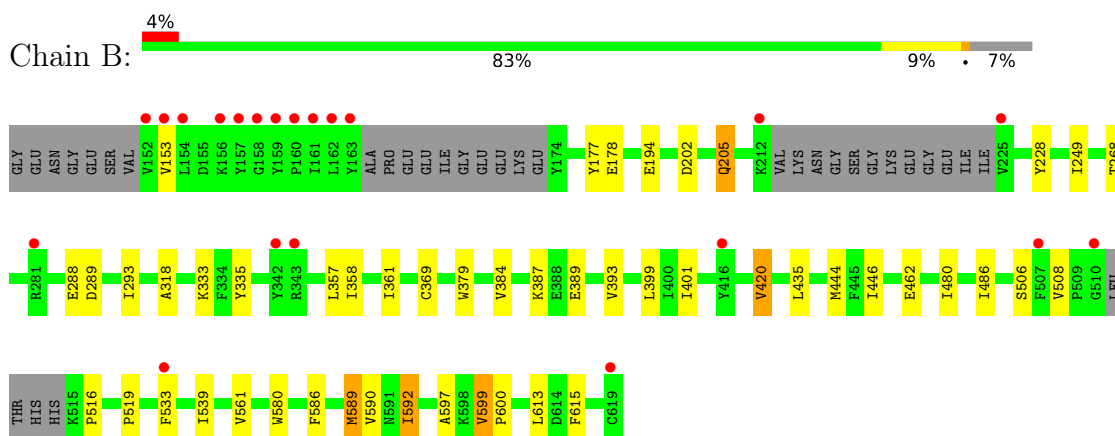
3 Residue-property plots [i](#)

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: DNA polymerase II small subunit



- Molecule 1: DNA polymerase II small subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.75Å 91.24Å 143.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.19 – 2.60 47.19 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.19-2.60) 99.9 (47.19-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.61Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.227 , 0.255 0.227 , 0.248	Depositor DCC
R_{free} test set	1653 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	73.2	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7128	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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: CA, ZN, FE, ACT, CAC

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	0.80	1/3599 (0.0%)	1.26	13/4890 (0.3%)
1	B	0.76	1/3619 (0.0%)	1.22	10/4915 (0.2%)
All	All	0.78	2/7218 (0.0%)	1.24	23/9805 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	589	MET	SD-CE	-7.24	1.61	1.79
1	A	536	LYS	C-N	6.47	1.40	1.33

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	260	TYR	N-CA-C	-7.98	102.60	113.30
1	B	289	ASP	CA-CB-CG	7.36	119.96	112.60
1	A	302	SER	N-CA-C	-7.35	98.08	109.76
1	A	599	VAL	N-CA-C	7.23	114.70	107.55
1	A	289	ASP	CA-CB-CG	6.99	119.59	112.60
1	B	599	VAL	N-CA-C	6.92	114.40	107.55
1	B	369	CYS	CA-C-N	6.36	129.12	120.54
1	B	369	CYS	C-N-CA	6.36	129.12	120.54
1	A	369	CYS	CA-C-N	6.07	128.74	120.54
1	A	369	CYS	C-N-CA	6.07	128.74	120.54
1	A	536	LYS	N-CA-C	-5.80	105.91	112.87
1	A	420	VAL	N-CA-C	-5.76	105.47	111.58
1	A	536	LYS	CA-C-N	5.61	132.50	122.13
1	A	536	LYS	C-N-CA	5.61	132.50	122.13
1	B	508	VAL	N-CA-C	5.32	112.81	107.55
1	A	508	VAL	N-CA-C	5.30	112.79	107.55
1	A	584	THR	CA-C-N	5.26	127.64	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	584	THR	C-N-CA	5.26	127.64	120.54
1	B	177	TYR	CA-C-N	5.10	127.63	120.28
1	B	177	TYR	C-N-CA	5.10	127.63	120.28
1	B	178	GLU	CA-C-N	5.04	129.25	120.68
1	B	178	GLU	C-N-CA	5.04	129.25	120.68
1	B	420	VAL	N-CA-C	-5.01	105.54	111.00

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	3512	0	3546	34	0
1	B	3530	0	3572	21	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	B	1	0	0	0	0
7	A	33	0	0	0	0
7	B	30	0	0	0	0
All	All	7128	0	7124	55	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 4.

All (55) 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:228:TYR:CE2	1:B:533:PHE:HE1	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:HIS:C	1:A:515:LYS:H	2.14	0.56
1:B:318:ALA:HB3	1:B:335:TYR:HB2	1.88	0.56
1:A:318:ALA:HB3	1:A:335:TYR:HB2	1.88	0.56
1:A:597:ALA:HB1	1:A:615:PHE:HB2	1.88	0.56
1:A:357:LEU:O	1:A:600:PRO:HD2	2.06	0.55
1:B:357:LEU:O	1:B:600:PRO:HD2	2.06	0.55
1:B:597:ALA:HB1	1:B:615:PHE:HB2	1.87	0.55
1:A:401:ILE:HD12	1:A:446:ILE:HG12	1.90	0.55
1:A:304:ASP:OD2	1:A:333:LYS:HG3	2.08	0.54
1:B:288:GLU:HG3	1:B:293:ILE:HG12	1.90	0.53
1:B:401:ILE:HD12	1:B:446:ILE:HG12	1.90	0.52
1:A:513:HIS:HE1	1:A:593:VAL:H	1.58	0.51
1:A:461:PRO:O	1:A:481:SER:HB3	2.11	0.51
1:A:262:SER:HB2	1:A:264:ASP:OD1	2.12	0.50
1:A:585:GLU:HG2	1:A:589:MET:HE2	1.94	0.49
1:A:435:LEU:HB3	1:A:444:MET:HE1	1.94	0.49
1:A:513:HIS:O	1:A:514:HIS:HB2	2.12	0.49
1:A:288:GLU:HG3	1:A:293:ILE:HG12	1.94	0.49
1:A:586:PHE:HA	1:A:589:MET:HE3	1.93	0.49
1:B:586:PHE:HA	1:B:589:MET:HE3	1.95	0.49
1:A:537:VAL:O	1:A:537:VAL:HG13	2.14	0.48
1:B:435:LEU:HB3	1:B:444:MET:HE1	1.94	0.48
1:B:361:ILE:HA	1:B:580:TRP:HB2	1.96	0.48
1:B:379:TRP:CD1	1:B:384:VAL:HG12	2.49	0.47
1:B:599:VAL:HB	1:B:613:LEU:HB2	1.96	0.47
1:A:361:ILE:HA	1:A:580:TRP:HB2	1.96	0.47
1:A:516:PRO:HB3	1:A:561:VAL:HG21	1.98	0.46
1:A:324:SER:HB2	1:A:330:PHE:CE1	2.50	0.46
1:A:599:VAL:HB	1:A:613:LEU:HB2	1.97	0.46
1:A:590:VAL:HG23	1:A:592:ILE:HD13	1.99	0.45
1:A:521:VAL:HG12	1:A:525:LYS:HE2	1.98	0.45
1:B:516:PRO:C	1:B:519:PRO:HD2	2.41	0.45
1:A:514:HIS:O	1:A:515:LYS:HG2	2.16	0.45
1:A:480:ILE:HD13	1:A:486:ILE:HD11	1.98	0.45
1:A:516:PRO:C	1:A:519:PRO:HD2	2.42	0.45
1:A:535:GLY:C	1:A:537:VAL:N	2.75	0.45
1:B:358:ILE:HG12	1:B:399:LEU:HD11	1.98	0.44
1:A:379:TRP:CD1	1:A:384:VAL:HG12	2.52	0.44
1:A:399:LEU:HD23	1:A:444:MET:HG2	1.99	0.44
1:B:399:LEU:HD23	1:B:444:MET:HG2	1.99	0.44
1:B:480:ILE:HD13	1:B:486:ILE:HD11	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:516:PRO:HB3	1:B:561:VAL:HG21	2.00	0.43
1:A:320:LYS:HB3	1:A:333:LYS:HB3	2.00	0.43
1:A:358:ILE:HG12	1:A:399:LEU:HD11	1.99	0.43
1:A:444:MET:HE2	1:A:446:ILE:HD11	2.01	0.43
1:B:444:MET:HE2	1:B:446:ILE:HD11	2.00	0.43
1:A:536:LYS:O	1:A:538:PRO:HD3	2.19	0.42
1:B:590:VAL:HG23	1:B:592:ILE:HD13	2.01	0.42
1:A:281:ARG:C	1:A:300:LYS:HG3	2.44	0.42
1:B:249:ILE:HG23	1:B:268:THR:HG21	2.02	0.42
1:A:324:SER:HB2	1:A:330:PHE:HE1	1.85	0.41
1:A:504:VAL:HG11	1:A:519:PRO:HA	2.03	0.40
1:B:202:ASP:O	1:B:205:GLN:HB2	2.21	0.40
1:B:389:GLU:O	1:B:393:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	434/475 (91%)	415 (96%)	18 (4%)	1 (0%)	43	66
1	B	435/475 (92%)	421 (97%)	12 (3%)	2 (0%)	24	46
All	All	869/950 (92%)	836 (96%)	30 (4%)	3 (0%)	36	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	537	VAL
1	B	205	GLN
1	B	462	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	A	385/415 (93%)	378 (98%)	7 (2%)	51	76
1	B	387/415 (93%)	379 (98%)	8 (2%)	47	73
All	All	772/830 (93%)	757 (98%)	15 (2%)	50	75

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	VAL
1	A	295	LYS
1	A	387	LYS
1	A	420	VAL
1	A	506	SER
1	A	515	LYS
1	A	592	ILE
1	B	153	VAL
1	B	194	GLU
1	B	333	LYS
1	B	387	LYS
1	B	420	VAL
1	B	506	SER
1	B	539	ILE
1	B	592	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	513	HIS
1	B	205	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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	$\# Z > 2$
5	CAC	B	705	3,2	2,4,4	3.35	2 (100%)	4,6,6	1.61	1 (25%)
4	ACT	B	704	-	3,3,3	1.08	0	3,3,3	1.14	0
4	ACT	A	703	-	3,3,3	1.22	0	3,3,3	1.07	0
5	CAC	A	704	2	2,4,4	3.24	2 (100%)	4,6,6	1.65	1 (25%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	705	CAC	AS-C2	3.42	1.98	1.90
5	A	704	CAC	AS-C2	3.31	1.98	1.90
5	B	705	CAC	AS-C1	3.29	1.98	1.90
5	A	704	CAC	AS-C1	3.16	1.97	1.90

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	705	CAC	O1-AS-C1	-2.48	108.41	111.50
5	A	704	CAC	O1-AS-C1	-2.32	108.61	111.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	440/475 (92%)	0.35	30 (6%)	23 19	58, 78, 124, 159	0
1	B	442/475 (93%)	0.30	21 (4%)	35 30	50, 79, 127, 162	1 (0%)
All	All	882/950 (92%)	0.33	51 (5%)	29 23	50, 78, 126, 162	1 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	413	PRO	5.5
1	A	537	VAL	5.3
1	A	513	HIS	4.7
1	A	157	TYR	4.3
1	B	160	PRO	4.2
1	B	153	VAL	4.0
1	A	152	VAL	4.0
1	A	225	VAL	3.9
1	B	510	GLY	3.9
1	A	154	LEU	3.8
1	A	159	TYR	3.7
1	B	157	TYR	3.6
1	A	412	TYR	3.6
1	A	160	PRO	3.6
1	B	161	ILE	3.4
1	A	411	ILE	3.3
1	A	619	CYS	3.2
1	B	154	LEU	3.2
1	A	162	LEU	3.2
1	B	342	TYR	3.1
1	B	281	ARG	3.1
1	A	206	VAL	3.1
1	B	507	PHE	3.0
1	B	416	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	585	GLU	2.9
1	A	155	ASP	2.8
1	A	514	HIS	2.8
1	A	156	LYS	2.7
1	A	586	PHE	2.7
1	B	158	GLY	2.6
1	A	153	VAL	2.6
1	A	536	LYS	2.6
1	A	416	TYR	2.5
1	A	163	TYR	2.5
1	A	409	ILE	2.4
1	B	533	PHE	2.4
1	A	535	GLY	2.4
1	B	156	LYS	2.4
1	B	152	VAL	2.4
1	A	260	TYR	2.3
1	A	418	ASP	2.3
1	A	410	GLY	2.2
1	B	225	VAL	2.2
1	B	159	TYR	2.2
1	B	162	LEU	2.2
1	B	343	ARG	2.1
1	B	619	CYS	2.1
1	B	163	TYR	2.1
1	A	161	ILE	2.1
1	B	212	LYS	2.1
1	A	297	PHE	2.0

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

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

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(Å ²)	Q<0.9
6	CA	B	703	1/1	0.76	0.20	137,137,137,137	0
5	CAC	B	705	5/5	0.89	0.18	135,135,136,136	0
5	CAC	A	704	5/5	0.89	0.18	137,137,138,140	0
4	ACT	A	703	4/4	0.95	0.10	69,69,70,71	0
4	ACT	B	704	4/4	0.98	0.07	61,62,62,63	0
2	FE	B	701	1/1	0.99	0.04	72,72,72,72	0
3	ZN	A	702	1/1	0.99	0.04	74,74,74,74	0
3	ZN	B	702	1/1	0.99	0.03	79,79,79,79	0
2	FE	A	701	1/1	0.99	0.03	65,65,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.