



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:06 AM UTC

PDB ID : 1M6S / pdb_00001m6s
Title : Crystal Structure Of Threonine Aldolase
Authors : Burley, S.K.; Kielkopf, C.L.
Deposited on : 2002-07-17
Resolution : 1.80 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

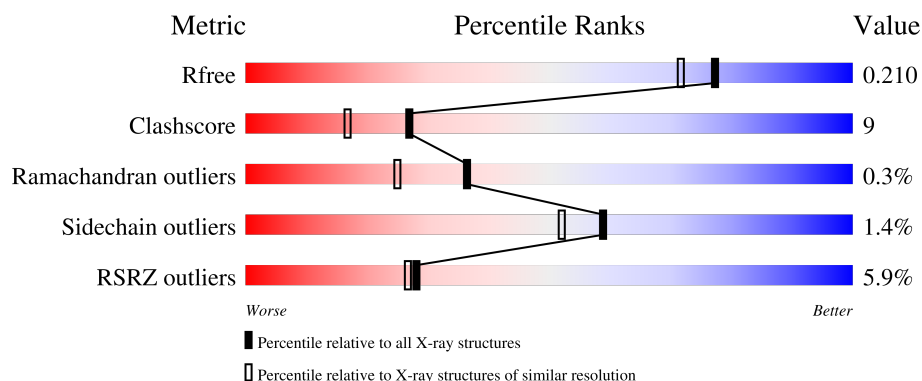
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	347	4% 83% 14% ..
1	B	347	5% 82% 15% ..
1	C	347	6% 84% 13% ..
1	D	347	8% 82% 16% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11566 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 L-allo-threonine aldolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	P	S	0	0	0
			2569	1606	456	490	1	16			
1	B	343	Total	C	N	O	P	S	0	0	0
			2590	1619	463	491	1	16			
1	C	343	Total	C	N	O	P	S	0	1	0
			2572	1611	464	480	1	16			
1	D	344	Total	C	N	O	P	S	0	0	0
			2568	1609	456	485	1	17			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	cloning artifact	UNP Q9X266
A	-2	PRO	-	cloning artifact	UNP Q9X266
A	-1	HIS	-	cloning artifact	UNP Q9X266
A	0	MET	-	cloning artifact	UNP Q9X266
A	199	LLP	LYS	modified residue	UNP Q9X266
B	-3	GLY	-	cloning artifact	UNP Q9X266
B	-2	PRO	-	cloning artifact	UNP Q9X266
B	-1	HIS	-	cloning artifact	UNP Q9X266
B	0	MET	-	cloning artifact	UNP Q9X266
B	199	LLP	LYS	modified residue	UNP Q9X266
C	-3	GLY	-	cloning artifact	UNP Q9X266
C	-2	PRO	-	cloning artifact	UNP Q9X266
C	-1	HIS	-	cloning artifact	UNP Q9X266
C	0	MET	-	cloning artifact	UNP Q9X266
C	199	LLP	LYS	modified residue	UNP Q9X266
D	-3	GLY	-	cloning artifact	UNP Q9X266
D	-2	PRO	-	cloning artifact	UNP Q9X266
D	-1	HIS	-	cloning artifact	UNP Q9X266
D	0	MET	-	cloning artifact	UNP Q9X266
D	199	LLP	LYS	modified residue	UNP Q9X266

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

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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Cl 2	0	0
3	B	1	Total 1	Cl 1	0	0
3	C	2	Total 2	Cl 2	0	0
3	D	1	Total 1	Cl 1	0	0

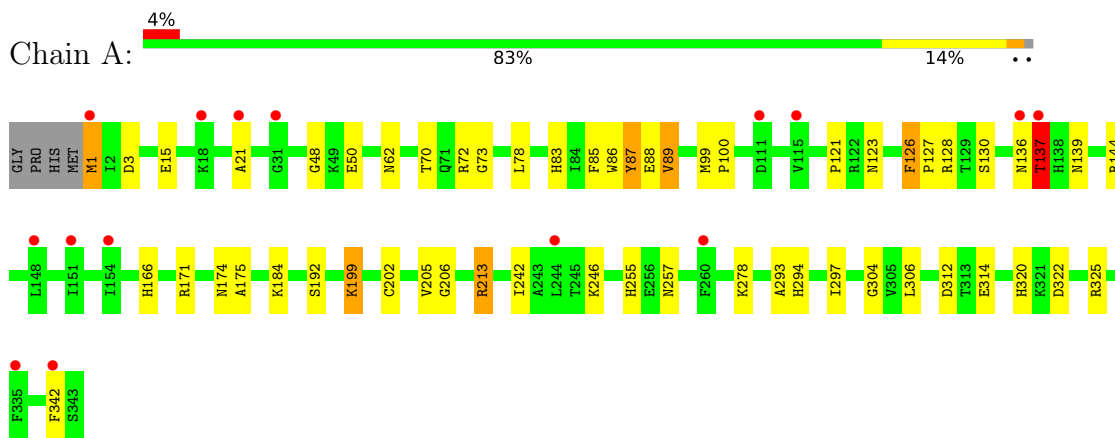
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	327	Total 327	O 327	0	0
4	B	319	Total 319	O 319	0	0
4	C	312	Total 312	O 312	0	0
4	D	297	Total 297	O 297	0	0

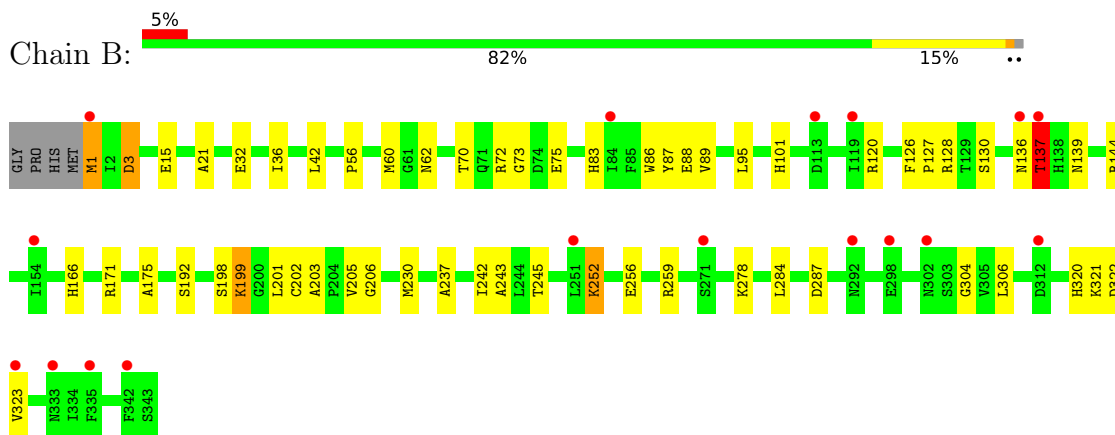
3 Residue-property plots [i](#)

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.

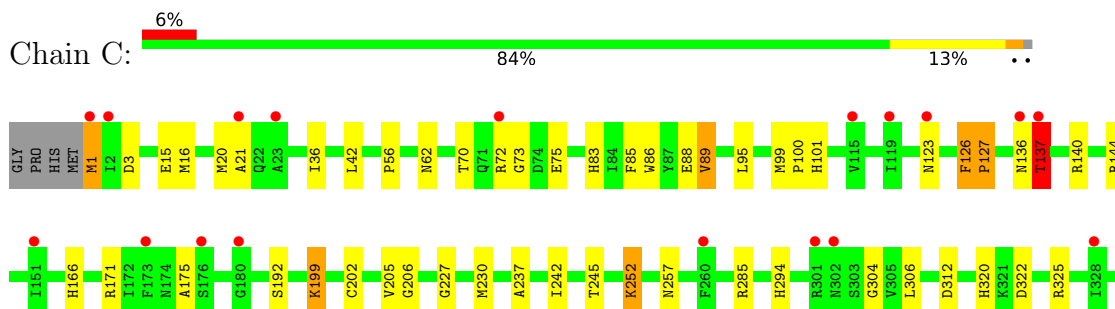
- Molecule 1: L-allo-threonine aldolase



- Molecule 1: L-allo-threonine aldolase

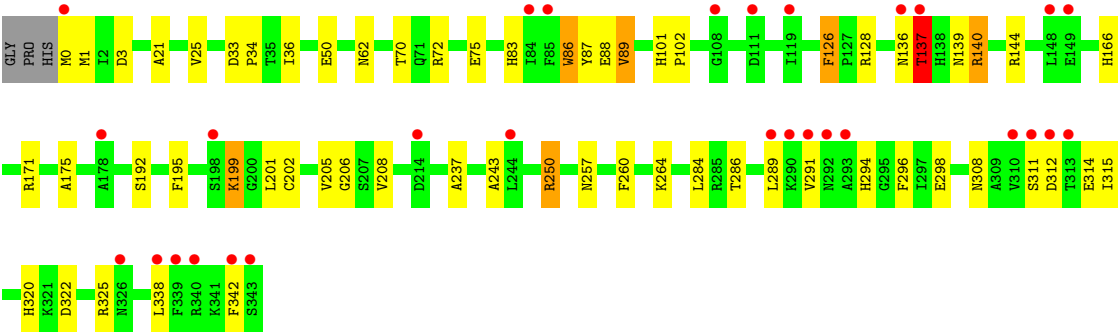
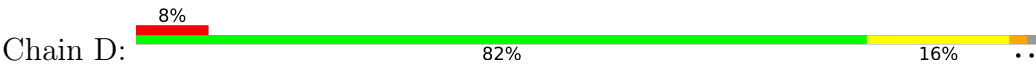


- Molecule 1: L-allo-threonine aldolase





● Molecule 1: L-allo-threonine aldolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.89Å 100.60Å 149.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 20.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.80) 98.4 (20.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.87 (at 1.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.200 , 0.213 0.199 , 0.210	Depositor DCC
R_{free} test set	6294 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	16.1	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.55 , 85.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.006 for k,h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11566	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.14% 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, CL, LLP

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	0.36	0/2585	1.00	14/3504 (0.4%)
1	B	0.37	0/2606	1.01	14/3527 (0.4%)
1	C	0.38	0/2588	1.00	13/3505 (0.4%)
1	D	0.38	0/2584	1.02	14/3501 (0.4%)
All	All	0.37	0/10363	1.01	55/14037 (0.4%)

There are no bond length outliers.

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	137	THR	N-CA-C	-13.48	82.09	110.80
1	D	137	THR	N-CA-C	-13.20	82.68	110.80
1	A	137	THR	N-CA-C	-13.16	82.77	110.80
1	C	137	THR	N-CA-C	-12.98	83.16	110.80
1	A	206	GLY	N-CA-C	12.70	126.51	112.29
1	B	206	GLY	N-CA-C	12.09	125.83	112.29
1	D	206	GLY	N-CA-C	11.91	125.63	112.29
1	C	206	GLY	N-CA-C	11.76	125.46	112.29
1	A	126	PHE	N-CA-C	7.80	120.53	110.39
1	D	136	ASN	CA-C-N	7.31	135.51	121.54
1	D	136	ASN	C-N-CA	7.31	135.51	121.54
1	C	136	ASN	CA-C-N	7.07	135.04	121.54
1	C	136	ASN	C-N-CA	7.07	135.04	121.54
1	A	137	THR	N-CA-CB	7.03	122.37	110.49
1	B	136	ASN	CA-C-N	7.00	134.91	121.54
1	B	136	ASN	C-N-CA	7.00	134.91	121.54
1	B	126	PHE	N-CA-C	6.99	119.48	110.39
1	D	137	THR	N-CA-CB	6.93	122.21	110.49
1	B	137	THR	N-CA-CB	6.93	122.20	110.49
1	C	202	CYS	N-CA-C	6.88	123.12	113.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	137	THR	N-CA-CB	6.75	121.89	110.49
1	C	126	PHE	N-CA-C	6.63	120.33	110.32
1	A	202	CYS	N-CA-C	6.60	122.74	113.56
1	D	202	CYS	N-CA-C	6.58	122.71	113.56
1	B	202	CYS	N-CA-C	6.55	122.67	113.56
1	A	136	ASN	CA-C-N	6.47	133.89	121.54
1	A	136	ASN	C-N-CA	6.47	133.89	121.54
1	D	126	PHE	N-CA-C	6.38	119.12	110.31
1	A	136	ASN	N-CA-C	6.38	118.92	108.52
1	D	139	ASN	N-CA-C	6.20	117.72	110.97
1	B	86	TRP	N-CA-C	6.09	120.91	112.45
1	B	136	ASN	N-CA-C	5.99	118.60	107.99
1	C	136	ASN	N-CA-C	5.97	118.40	108.20
1	B	70	THR	N-CA-C	5.93	118.42	109.41
1	C	70	THR	N-CA-C	5.90	118.84	109.81
1	A	342	PHE	N-CA-C	5.88	121.17	113.30
1	A	87	TYR	N-CA-C	5.74	119.88	112.41
1	D	205	VAL	N-CA-C	5.71	115.89	108.35
1	D	136	ASN	N-CA-C	5.70	117.81	108.52
1	D	70	THR	N-CA-C	5.67	118.49	109.81
1	D	86	TRP	N-CA-C	5.64	120.28	112.45
1	D	25	VAL	N-CA-C	5.51	116.79	108.96
1	A	86	TRP	N-CA-C	5.51	120.11	112.45
1	B	139	ASN	N-CA-C	5.47	116.93	110.97
1	B	205	VAL	N-CA-C	5.44	115.54	108.35
1	A	70	THR	N-CA-C	5.44	118.13	109.81
1	A	205	VAL	N-CA-C	5.36	115.43	108.35
1	C	205	VAL	N-CA-C	5.29	115.33	108.35
1	C	86	TRP	N-CA-C	5.25	119.75	112.45
1	C	127	PRO	N-CA-C	-5.24	103.89	111.22
1	A	139	ASN	N-CA-C	5.20	116.80	111.03
1	B	3	ASP	N-CA-C	5.17	116.73	108.41
1	B	32	GLU	N-CA-C	5.14	119.50	112.88
1	C	140	ARG	N-CA-C	5.12	117.52	111.33
1	D	87	TYR	N-CA-C	5.04	118.74	112.59

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	2569	0	2508	50	0
1	B	2590	0	2552	49	0
1	C	2572	0	2531	50	0
1	D	2568	0	2514	54	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	327	0	0	4	1
4	B	319	0	0	7	1
4	C	312	0	0	4	0
4	D	297	0	0	9	0
All	All	11566	0	10105	187	1

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 9.

All (187) 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:99:MET:HE3	1:C:100:PRO:HG3	1.36	1.08
1:A:100:PRO:HG3	1:C:99:MET:HE3	1.31	1.05
1:D:250:ARG:HH11	1:D:250:ARG:HG3	1.24	1.01
1:C:285:ARG:NH1	4:C:1614:HOH:O	2.01	0.92
1:A:174:ASN:HD22	1:A:255:HIS:HE1	1.18	0.91
1:D:0:MET:HG3	1:D:1:MET:H	1.41	0.85
1:C:15:GLU:HG2	1:C:242:ILE:HD13	1.60	0.84
1:D:250:ARG:HH11	1:D:250:ARG:CG	1.91	0.84
1:A:1:MET:HE2	1:A:306:LEU:HG	1.61	0.82
1:B:72:ARG:NH1	4:B:1588:HOH:O	2.12	0.79
1:D:250:ARG:O	1:D:250:ARG:NH1	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:LYS:NZ	1:C:252:LYS:HB2	1.99	0.77
1:B:1:MET:HE3	1:B:304:GLY:C	2.10	0.75
1:C:72[B]:ARG:NH1	4:C:1493:HOH:O	2.20	0.74
1:A:100:PRO:HG3	1:C:99:MET:CE	2.14	0.73
1:C:83:HIS:HE1	4:C:1505:HOH:O	1.69	0.73
1:A:137:THR:HA	1:A:144:ARG:O	1.88	0.72
1:A:99:MET:CE	1:C:100:PRO:HG3	2.17	0.72
1:B:42:LEU:HD21	1:B:245:THR:CG2	2.20	0.71
1:B:252:LYS:HE3	1:B:256:GLU:OE2	1.91	0.71
1:B:21:ALA:HB2	1:C:21:ALA:HB2	1.72	0.69
1:C:1:MET:HE2	1:C:306:LEU:HG	1.73	0.69
1:B:252:LYS:HB2	1:B:252:LYS:NZ	2.05	0.69
1:A:320:HIS:HD2	1:A:322:ASP:H	1.40	0.68
1:D:0:MET:HG3	1:D:1:MET:N	2.09	0.68
1:B:73:GLY:O	1:B:127:PRO:HB3	1.93	0.67
1:C:42:LEU:HD21	1:C:245:THR:CG2	2.24	0.67
1:C:75:GLU:OE2	1:C:101:HIS:HD2	1.78	0.67
1:B:320:HIS:HD2	1:B:322:ASP:H	1.43	0.67
1:D:320:HIS:HD2	1:D:322:ASP:H	1.42	0.66
1:C:257:ASN:ND2	1:C:325:ARG:HE	1.94	0.65
1:A:294:HIS:HD2	4:A:1546:HOH:O	1.81	0.64
1:A:85:PHE:CD1	1:C:99:MET:HE1	2.34	0.63
1:D:137:THR:HA	1:D:144:ARG:O	1.98	0.62
1:A:62:ASN:ND2	1:A:166:HIS:HE1	1.96	0.62
1:B:128:ARG:NH1	1:B:130:SER:HB3	2.15	0.62
1:B:62:ASN:ND2	1:B:166:HIS:HE1	1.98	0.62
1:C:36:ILE:HD13	1:C:237:ALA:HB2	1.81	0.62
1:B:137:THR:HA	1:B:144:ARG:O	2.00	0.61
1:D:257:ASN:ND2	1:D:325:ARG:HE	1.97	0.61
1:C:73:GLY:O	1:C:127:PRO:HB3	2.01	0.61
1:A:99:MET:HE3	1:C:100:PRO:CG	2.21	0.61
1:A:72:ARG:NH1	4:A:1385:HOH:O	2.32	0.60
1:C:137:THR:OG1	1:C:171:ARG:HB2	2.01	0.60
1:B:128:ARG:HH11	1:B:130:SER:HB3	1.66	0.60
1:C:1:MET:HE3	1:C:304:GLY:C	2.27	0.60
1:D:250:ARG:CG	1:D:250:ARG:NH1	2.61	0.60
1:A:100:PRO:CG	1:C:99:MET:HE3	2.21	0.60
1:B:15:GLU:HG2	1:B:242:ILE:HD13	1.84	0.59
1:A:21:ALA:HB2	1:D:21:ALA:HB2	1.85	0.59
1:C:294:HIS:HE1	1:C:312:ASP:OD1	1.86	0.59
1:C:137:THR:CG2	1:C:175:ALA:HB2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:ASN:ND2	1:C:166:HIS:HE1	2.01	0.58
1:A:257:ASN:ND2	1:A:325:ARG:HE	2.02	0.58
1:B:252:LYS:HB2	1:B:252:LYS:HZ2	1.68	0.58
1:D:72:ARG:NH1	4:D:1383:HOH:O	2.30	0.58
1:D:308:ASN:ND2	4:D:1544:HOH:O	2.37	0.57
1:B:137:THR:OG1	1:B:171:ARG:HB2	2.04	0.57
1:B:62:ASN:HD22	1:B:166:HIS:HE1	1.53	0.56
1:D:291:VAL:HG11	1:D:342:PHE:CD1	2.40	0.56
1:C:166:HIS:HD2	1:C:192:SER:OG	1.88	0.56
1:D:101:HIS:HE1	4:D:1477:HOH:O	1.88	0.56
1:D:294:HIS:HD2	4:D:1463:HOH:O	1.88	0.56
1:A:1:MET:HE3	1:A:304:GLY:C	2.31	0.56
1:D:137:THR:OG1	1:D:171:ARG:HB2	2.06	0.55
1:A:314:GLU:OE2	4:A:1610:HOH:O	2.17	0.55
1:C:137:THR:HA	1:C:144:ARG:O	2.06	0.54
1:A:174:ASN:HD22	1:A:255:HIS:CE1	2.11	0.54
1:B:36:ILE:HD13	1:B:237:ALA:HB2	1.90	0.54
1:D:250:ARG:HG3	1:D:250:ARG:NH1	2.05	0.54
1:D:250:ARG:NH1	1:D:250:ARG:C	2.64	0.54
1:B:95:LEU:HD22	1:C:95:LEU:HD22	1.90	0.54
1:C:252:LYS:HB2	1:C:252:LYS:HZ2	1.73	0.54
1:D:83:HIS:HD2	1:D:88:GLU:OE2	1.90	0.54
1:C:320:HIS:HD2	1:C:322:ASP:H	1.56	0.53
1:B:83:HIS:HE1	4:B:1529:HOH:O	1.90	0.53
1:C:62:ASN:HD22	1:C:166:HIS:HE1	1.56	0.53
1:A:73:GLY:O	1:A:127:PRO:HB3	2.09	0.53
1:A:137:THR:HG23	1:A:175:ALA:HB2	1.89	0.53
1:A:62:ASN:HD22	1:A:166:HIS:HE1	1.55	0.53
1:B:166:HIS:HD2	1:B:192:SER:OG	1.91	0.53
1:A:294:HIS:HE1	1:A:312:ASP:OD1	1.93	0.52
1:A:166:HIS:HD2	1:A:192:SER:OG	1.93	0.52
1:D:291:VAL:HG11	1:D:342:PHE:CE1	2.45	0.52
1:B:83:HIS:HD2	1:B:88:GLU:OE2	1.92	0.52
1:D:260:PHE:CZ	1:D:264:LYS:HE3	2.45	0.51
1:D:291:VAL:CG1	1:D:342:PHE:CD1	2.94	0.51
1:D:294:HIS:HE1	1:D:312:ASP:OD1	1.94	0.51
1:A:50:GLU:HB3	1:A:213:ARG:HG3	1.93	0.51
1:B:56:PRO:HG3	1:B:230:MET:HE2	1.93	0.51
1:A:21:ALA:HB2	1:D:21:ALA:CB	2.42	0.50
1:C:72[A]:ARG:HG2	1:C:72[A]:ARG:HH11	1.76	0.50
1:D:320:HIS:CD2	1:D:322:ASP:H	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:THR:CG2	1:B:175:ALA:HB2	2.41	0.50
1:D:201:LEU:HB3	1:D:243:ALA:HB1	1.92	0.50
1:D:62:ASN:OD1	1:D:166:HIS:HE1	1.94	0.50
1:A:48:GLY:HA3	1:A:184:LYS:HE3	1.94	0.50
1:D:250:ARG:HH11	1:D:250:ARG:C	2.20	0.50
1:C:88:GLU:C	1:C:89:VAL:HG23	2.36	0.49
1:D:140:ARG:O	1:D:140:ARG:HD2	2.12	0.49
1:C:137:THR:HG23	1:C:175:ALA:HB2	1.95	0.49
1:D:50:GLU:HG3	4:D:1331:HOH:O	2.13	0.49
1:A:87:TYR:CD1	1:C:126:PHE:HE1	2.30	0.49
1:A:137:THR:OG1	1:A:171:ARG:HB2	2.12	0.49
1:D:137:THR:CG2	1:D:175:ALA:HB2	2.43	0.49
1:A:1:MET:HE2	1:A:306:LEU:CG	2.40	0.48
1:D:3:ASP:O	1:D:320:HIS:HE1	1.96	0.48
1:A:137:THR:CG2	1:A:175:ALA:HB2	2.43	0.48
1:A:320:HIS:CD2	1:A:322:ASP:H	2.27	0.48
1:D:298:GLU:HG2	4:D:1541:HOH:O	2.12	0.48
1:A:83:HIS:HD2	1:A:88:GLU:OE2	1.97	0.48
1:D:0:MET:N	4:D:1401:HOH:O	2.38	0.48
1:B:120:ARG:HH22	1:D:86:TRP:HA	1.78	0.48
1:D:166:HIS:HD2	1:D:192:SER:OG	1.96	0.47
1:A:128:ARG:HH11	1:A:130:SER:HB3	1.79	0.47
1:C:171:ARG:NH1	1:C:199:LLP:O3	2.48	0.47
1:A:3:ASP:O	1:A:320:HIS:HE1	1.97	0.47
1:D:36:ILE:HD13	1:D:237:ALA:HB2	1.96	0.47
1:B:201:LEU:HB3	1:B:243:ALA:HB1	1.96	0.47
1:B:323:VAL:HG23	1:B:323:VAL:O	2.15	0.46
1:A:278:LYS:HG3	4:A:1391:HOH:O	2.15	0.46
1:B:278:LYS:HE3	4:B:1477:HOH:O	2.15	0.46
1:C:83:HIS:HD2	1:C:88:GLU:OE2	1.98	0.46
1:C:252:LYS:HB2	1:C:252:LYS:HZ3	1.79	0.46
1:A:121:PRO:HG2	1:A:126:PHE:CE2	2.50	0.46
1:B:1:MET:HE3	1:B:304:GLY:CA	2.45	0.46
1:A:257:ASN:HD22	1:A:325:ARG:HH21	1.63	0.46
1:B:1:MET:HE2	1:B:306:LEU:HG	1.97	0.46
1:C:72[A]:ARG:HG2	1:C:72[A]:ARG:NH1	2.32	0.45
1:D:296:PHE:HD2	1:D:315:ILE:CD1	2.30	0.45
1:C:257:ASN:HD22	1:C:325:ARG:HE	1.61	0.45
1:C:3:ASP:O	1:C:320:HIS:HE1	2.00	0.45
1:D:128:ARG:NH1	4:D:1429:HOH:O	2.48	0.45
1:D:171:ARG:NH1	1:D:199:LLP:O3	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:284:LEU:HD23	1:D:284:LEU:C	2.42	0.45
1:A:171:ARG:NH1	1:A:199:LLP:O3	2.49	0.45
1:B:1:MET:HE3	1:B:304:GLY:HA2	1.98	0.45
1:B:128:ARG:NH1	1:B:130:SER:CB	2.79	0.45
1:C:1:MET:HE3	1:C:1:MET:HB3	1.76	0.45
1:C:294:HIS:HD2	4:C:1422:HOH:O	1.99	0.45
1:B:1:MET:HE2	1:B:306:LEU:CD2	2.48	0.44
1:B:284:LEU:C	1:B:284:LEU:HD23	2.43	0.44
1:C:252:LYS:NZ	1:C:252:LYS:CB	2.74	0.44
1:A:123:ASN:HB3	1:A:126:PHE:CD2	2.53	0.44
1:B:1:MET:CA	4:B:1507:HOH:O	2.65	0.44
1:B:320:HIS:CD2	1:B:322:ASP:H	2.28	0.44
1:D:291:VAL:HG13	1:D:342:PHE:HD1	1.82	0.44
1:D:102:PRO:HD2	4:D:1512:HOH:O	2.16	0.44
1:D:257:ASN:HD22	1:D:325:ARG:HE	1.63	0.44
1:B:171:ARG:NH1	1:B:199:LLP:O3	2.51	0.44
1:C:137:THR:HG22	1:C:175:ALA:HB2	1.98	0.43
1:A:88:GLU:C	1:A:89:VAL:HG23	2.43	0.43
1:B:62:ASN:HD22	1:B:166:HIS:CE1	2.35	0.43
1:A:15:GLU:HG2	1:A:242:ILE:HD13	2.01	0.43
1:D:311:SER:OG	1:D:314:GLU:N	2.51	0.43
1:A:62:ASN:HD22	1:A:166:HIS:CE1	2.37	0.43
1:A:128:ARG:NH1	1:A:130:SER:CB	2.81	0.43
1:C:56:PRO:HG3	1:C:230:MET:HE2	1.99	0.43
1:A:126:PHE:HA	1:A:127:PRO:HD3	1.93	0.42
1:A:128:ARG:NH1	1:A:130:SER:HB3	2.34	0.42
1:B:320:HIS:H	1:B:323:VAL:CG2	2.32	0.42
1:D:338:LEU:O	1:D:342:PHE:HD2	2.02	0.42
1:B:75:GLU:OE1	1:B:101:HIS:HD2	2.01	0.42
1:B:259:ARG:HG3	4:B:1452:HOH:O	2.19	0.42
1:B:198:SER:HA	1:B:203:ALA:O	2.20	0.42
1:A:99:MET:HE1	1:C:85:PHE:CD2	2.54	0.42
1:C:126:PHE:HA	1:C:127:PRO:HD3	1.94	0.42
1:B:287:ASP:CB	4:B:1616:HOH:O	2.67	0.42
1:C:16:MET:O	1:C:20:MET:HG3	2.20	0.42
1:D:75:GLU:OE2	1:D:101:HIS:HD2	2.02	0.42
1:A:137:THR:CA	1:A:144:ARG:O	2.62	0.41
1:A:293:ALA:O	1:A:297:ILE:HG12	2.20	0.41
1:B:3:ASP:O	1:B:320:HIS:HE1	2.04	0.41
1:B:42:LEU:HD21	1:B:245:THR:HG22	2.01	0.41
1:B:83:HIS:CD2	1:B:88:GLU:HG3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:257:ASN:HD22	1:D:257:ASN:HA	1.69	0.41
1:B:1:MET:HA	4:B:1507:HOH:O	2.20	0.41
1:B:137:THR:HG22	1:B:175:ALA:HB2	2.03	0.41
1:D:286:THR:HG22	1:D:289:LEU:HD12	2.03	0.41
1:D:291:VAL:CG1	1:D:342:PHE:HD1	2.32	0.41
1:A:1:MET:HE3	1:A:1:MET:HB3	1.67	0.41
1:B:87:TYR:CD1	1:D:126:PHE:HE1	2.38	0.41
1:D:195:PHE:CE1	1:D:208:VAL:HB	2.56	0.41
1:C:123:ASN:HB3	1:C:126:PHE:CD2	2.56	0.40
1:D:88:GLU:C	1:D:89:VAL:HG23	2.46	0.40
1:B:60:MET:HB2	1:C:227:GLY:HA3	2.03	0.40
1:D:33:ASP:HA	1:D:34:PRO:HD3	1.92	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1563:HOH:O	4:B:1587:HOH:O[1_455]	2.17	0.03

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	340/347 (98%)	335 (98%)	4 (1%)	1 (0%)	36	25
1	B	340/347 (98%)	333 (98%)	6 (2%)	1 (0%)	36	25
1	C	341/347 (98%)	335 (98%)	5 (2%)	1 (0%)	36	25
1	D	341/347 (98%)	334 (98%)	6 (2%)	1 (0%)	36	25
All	All	1362/1388 (98%)	1337 (98%)	21 (2%)	4 (0%)	36	25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	137	THR
1	C	137	THR
1	D	137	THR
1	A	137	THR

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	262/283 (93%)	257 (98%)	5 (2%)	50	41
1	B	266/283 (94%)	262 (98%)	4 (2%)	57	49
1	C	260/283 (92%)	257 (99%)	3 (1%)	63	57
1	D	260/283 (92%)	257 (99%)	3 (1%)	63	57
All	All	1048/1132 (93%)	1033 (99%)	15 (1%)	59	52

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

Mol	Chain	Res	Type
1	A	1	MET
1	A	78	LEU
1	A	89	VAL
1	A	213	ARG
1	A	246	LYS
1	B	1	MET
1	B	89	VAL
1	B	252	LYS
1	B	321	LYS
1	C	1	MET
1	C	89	VAL
1	C	252	LYS
1	D	89	VAL
1	D	140	ARG
1	D	250	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	63	GLN
1	A	83	HIS
1	A	161	HIS
1	A	164	ASN
1	A	166	HIS
1	A	174	ASN
1	A	255	HIS
1	A	257	ASN
1	A	294	HIS
1	A	320	HIS
1	B	62	ASN
1	B	63	GLN
1	B	71	GLN
1	B	83	HIS
1	B	101	HIS
1	B	161	HIS
1	B	166	HIS
1	B	174	ASN
1	B	320	HIS
1	C	62	ASN
1	C	71	GLN
1	C	83	HIS
1	C	101	HIS
1	C	166	HIS
1	C	174	ASN
1	C	257	ASN
1	C	294	HIS
1	C	308	ASN
1	C	320	HIS
1	C	326	ASN
1	D	63	GLN
1	D	71	GLN
1	D	83	HIS
1	D	101	HIS
1	D	107	ASN
1	D	125	HIS
1	D	164	ASN
1	D	166	HIS
1	D	257	ASN
1	D	294	HIS
1	D	308	ASN
1	D	320	HIS

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Mol	Chain	Res	Type
1	D	333	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	LLP	B	199	1	23,24,25	3.28	7 (30%)	25,32,34	2.62	11 (44%)
1	LLP	C	199	1	23,24,25	3.22	7 (30%)	25,32,34	2.60	12 (48%)
1	LLP	A	199	1	23,24,25	3.26	7 (30%)	25,32,34	2.60	11 (44%)
1	LLP	D	199	1	23,24,25	3.30	7 (30%)	25,32,34	2.60	10 (40%)

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	LLP	B	199	1	-	7/16/17/19	0/1/1/1
1	LLP	C	199	1	-	7/16/17/19	0/1/1/1
1	LLP	A	199	1	-	7/16/17/19	0/1/1/1
1	LLP	D	199	1	-	8/16/17/19	0/1/1/1

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	199	LLP	C4-C5	11.31	1.57	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	199	LLP	C4-C5	11.20	1.57	1.42
1	A	199	LLP	C4-C5	11.07	1.57	1.42
1	C	199	LLP	C4-C5	10.98	1.57	1.42
1	D	199	LLP	C3-C2	7.46	1.48	1.41
1	A	199	LLP	C3-C2	7.41	1.48	1.41
1	B	199	LLP	C3-C2	7.39	1.48	1.41
1	C	199	LLP	C3-C2	7.11	1.48	1.41
1	B	199	LLP	C2-N1	4.37	1.41	1.33
1	A	199	LLP	C2-N1	4.33	1.41	1.33
1	C	199	LLP	C2-N1	4.30	1.41	1.33
1	D	199	LLP	C2-N1	4.26	1.41	1.33
1	C	199	LLP	C4'-NZ	3.53	1.39	1.27
1	B	199	LLP	C6-N1	3.47	1.41	1.34
1	A	199	LLP	C6-N1	3.45	1.41	1.34
1	C	199	LLP	C6-N1	3.45	1.41	1.34
1	D	199	LLP	C6-N1	3.40	1.41	1.34
1	B	199	LLP	C4'-NZ	3.28	1.38	1.27
1	D	199	LLP	C4'-NZ	3.27	1.38	1.27
1	A	199	LLP	C4'-NZ	3.21	1.37	1.27
1	D	199	LLP	C5'-C5	2.24	1.56	1.50
1	C	199	LLP	P-OP3	-2.22	1.46	1.54
1	A	199	LLP	C5'-C5	2.17	1.56	1.50
1	B	199	LLP	P-OP3	-2.15	1.46	1.54
1	D	199	LLP	P-OP3	-2.14	1.46	1.54
1	A	199	LLP	P-OP3	-2.12	1.46	1.54
1	C	199	LLP	C5'-C5	2.08	1.56	1.50
1	B	199	LLP	C5'-C5	2.03	1.56	1.50

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	199	LLP	C2'-C2-C3	6.64	128.56	120.80
1	A	199	LLP	C2'-C2-C3	6.62	128.54	120.80
1	D	199	LLP	C2'-C2-C3	6.57	128.49	120.80
1	C	199	LLP	C2'-C2-C3	6.52	128.43	120.80
1	B	199	LLP	CE-NZ-C4'	4.31	132.54	118.72
1	D	199	LLP	CE-NZ-C4'	4.29	132.47	118.72
1	D	199	LLP	C6-N1-C2	4.29	126.98	119.20
1	A	199	LLP	CE-NZ-C4'	4.29	132.44	118.72
1	A	199	LLP	C6-N1-C2	4.27	126.95	119.20
1	B	199	LLP	C6-N1-C2	4.27	126.94	119.20
1	C	199	LLP	CE-NZ-C4'	4.21	132.22	118.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	199	LLP	C6-N1-C2	4.20	126.81	119.20
1	B	199	LLP	C3-C2-N1	-3.86	116.09	120.96
1	A	199	LLP	C3-C2-N1	-3.86	116.09	120.96
1	D	199	LLP	C3-C2-N1	-3.85	116.10	120.96
1	C	199	LLP	C3-C2-N1	-3.81	116.16	120.96
1	B	199	LLP	OP4-C5'-C5	3.73	116.35	109.36
1	D	199	LLP	OP4-C5'-C5	3.73	116.34	109.36
1	A	199	LLP	OP4-C5'-C5	3.69	116.28	109.36
1	B	199	LLP	C5-C4-C4'	3.64	127.08	121.47
1	C	199	LLP	C5-C4-C4'	3.63	127.08	121.47
1	C	199	LLP	OP4-C5'-C5	3.56	116.03	109.36
1	D	199	LLP	C5-C4-C4'	3.50	126.88	121.47
1	D	199	LLP	C4-C4'-NZ	-3.48	107.99	124.04
1	A	199	LLP	C5-C4-C4'	3.38	126.68	121.47
1	C	199	LLP	C4-C4'-NZ	-3.33	108.65	124.04
1	A	199	LLP	C4-C4'-NZ	-3.32	108.73	124.04
1	B	199	LLP	C4-C4'-NZ	-3.31	108.77	124.04
1	C	199	LLP	C3-C4-C4'	-2.98	115.02	120.40
1	B	199	LLP	C3-C4-C4'	-2.97	115.03	120.40
1	C	199	LLP	C5-C6-N1	-2.97	118.99	123.83
1	D	199	LLP	C5-C6-N1	-2.95	119.03	123.83
1	B	199	LLP	C5-C6-N1	-2.94	119.04	123.83
1	A	199	LLP	C5-C6-N1	-2.93	119.06	123.83
1	D	199	LLP	C3-C4-C4'	-2.89	115.17	120.40
1	A	199	LLP	C3-C4-C4'	-2.78	115.39	120.40
1	A	199	LLP	O3-C3-C4	2.32	125.68	119.44
1	C	199	LLP	O3-C3-C4	2.29	125.61	119.44
1	B	199	LLP	O3-C3-C4	2.28	125.59	119.44
1	C	199	LLP	O3-C3-C2	-2.19	113.05	117.58
1	A	199	LLP	O3-C3-C2	-2.17	113.08	117.58
1	D	199	LLP	O3-C3-C4	2.15	125.24	119.44
1	C	199	LLP	C4-C3-C2	2.12	121.34	120.14
1	B	199	LLP	O3-C3-C2	-2.11	113.21	117.58

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	199	LLP	C4-C5-C5'-OP4
1	A	199	LLP	C6-C5-C5'-OP4
1	A	199	LLP	O-C-CA-CB
1	B	199	LLP	C4-C5-C5'-OP4

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Mol	Chain	Res	Type	Atoms
1	B	199	LLP	C6-C5-C5'-OP4
1	B	199	LLP	O-C-CA-CB
1	C	199	LLP	C4-C5-C5'-OP4
1	C	199	LLP	C6-C5-C5'-OP4
1	C	199	LLP	O-C-CA-CB
1	D	199	LLP	C4-C5-C5'-OP4
1	D	199	LLP	C6-C5-C5'-OP4
1	D	199	LLP	O-C-CA-CB
1	B	199	LLP	CG-CD-CE-NZ
1	D	199	LLP	C3-C4-C4'-NZ
1	A	199	LLP	C3-C4-C4'-NZ
1	B	199	LLP	C3-C4-C4'-NZ
1	C	199	LLP	C3-C4-C4'-NZ
1	A	199	LLP	CG-CD-CE-NZ
1	C	199	LLP	CG-CD-CE-NZ
1	D	199	LLP	CG-CD-CE-NZ
1	D	199	LLP	CD-CE-NZ-C4'
1	D	199	LLP	C5-C4-C4'-NZ
1	A	199	LLP	CD-CE-NZ-C4'
1	C	199	LLP	CD-CE-NZ-C4'
1	B	199	LLP	CD-CE-NZ-C4'
1	D	199	LLP	C5'-OP4-P-OP2
1	A	199	LLP	C5-C4-C4'-NZ
1	B	199	LLP	C5-C4-C4'-NZ
1	C	199	LLP	C5-C4-C4'-NZ

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	199	LLP	1	0
1	C	199	LLP	1	0
1	A	199	LLP	1	0
1	D	199	LLP	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	342/347 (98%)	0.52	15 (4%) 39 38	10, 16, 25, 31	0
1	B	342/347 (98%)	0.47	17 (4%) 34 33	9, 15, 26, 32	0
1	C	342/347 (98%)	0.59	20 (5%) 29 27	7, 17, 27, 34	1 (0%)
1	D	343/347 (98%)	0.59	29 (8%) 16 14	10, 15, 30, 37	0
All	All	1369/1388 (98%)	0.54	81 (5%) 28 27	7, 16, 27, 37	1 (0%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	137	THR	9.5
1	D	137	THR	8.8
1	C	137	THR	8.3
1	A	137	THR	8.2
1	C	1	MET	4.5
1	D	311	SER	4.2
1	B	1	MET	3.9
1	D	343	SER	3.9
1	D	293	ALA	3.8
1	B	302	ASN	3.8
1	A	21	ALA	3.7
1	D	291	VAL	3.5
1	D	0	MET	3.5
1	B	136	ASN	3.4
1	C	136	ASN	3.4
1	C	21	ALA	3.4
1	D	339	PHE	3.3
1	A	1	MET	3.2
1	C	176	SER	3.1
1	D	149	GLU	3.1
1	D	340	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	84	ILE	3.0
1	D	119	ILE	3.0
1	C	328	ILE	2.9
1	C	302	ASN	2.9
1	C	333	ASN	2.9
1	D	136	ASN	2.9
1	A	115	VAL	2.9
1	A	151	ILE	2.8
1	D	342	PHE	2.8
1	D	111	ASP	2.8
1	D	244	LEU	2.7
1	B	335	PHE	2.6
1	D	312	ASP	2.6
1	B	323	VAL	2.6
1	C	260	PHE	2.6
1	B	113	ASP	2.6
1	C	151	ILE	2.6
1	C	119	ILE	2.5
1	A	136	ASN	2.5
1	D	292	ASN	2.5
1	C	301	ARG	2.5
1	C	342	PHE	2.5
1	B	342	PHE	2.4
1	B	333	ASN	2.4
1	D	108	GLY	2.4
1	D	214	ASP	2.3
1	D	289	LEU	2.3
1	D	178	ALA	2.3
1	B	312	ASP	2.3
1	A	31	GLY	2.2
1	C	23	ALA	2.2
1	D	198	SER	2.2
1	D	326	ASN	2.2
1	A	244	LEU	2.2
1	C	123	ASN	2.2
1	B	271	SER	2.2
1	D	85	PHE	2.2
1	B	154	ILE	2.2
1	D	84	ILE	2.2
1	C	115	VAL	2.2
1	D	313	THR	2.2
1	D	148	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	338	LEU	2.2
1	A	342	PHE	2.1
1	B	119	ILE	2.1
1	A	148	LEU	2.1
1	A	335	PHE	2.1
1	A	154	ILE	2.1
1	C	2	ILE	2.1
1	C	180	GLY	2.1
1	B	298	GLU	2.1
1	B	251	LEU	2.1
1	A	18	LYS	2.0
1	A	260	PHE	2.0
1	D	290	LYS	2.0
1	A	111	ASP	2.0
1	C	72[A]	ARG	2.0
1	C	173	PHE	2.0
1	B	292	ASN	2.0
1	D	310	VAL	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(Å ²)	Q<0.9
1	LLP	A	199	24/25	0.88	0.13	11,19,21,21	0
1	LLP	B	199	24/25	0.91	0.10	11,18,21,21	0
1	LLP	D	199	24/25	0.91	0.10	13,18,22,24	0
1	LLP	C	199	24/25	0.92	0.10	11,19,22,23	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	CL	A	1311	1/1	0.98	0.04	24,24,24,24	0
3	CL	B	1308	1/1	0.98	0.06	23,23,23,23	0
3	CL	C	1307	1/1	0.98	0.06	19,19,19,19	0
3	CL	C	1309	1/1	0.98	0.05	21,21,21,21	0
3	CL	D	1310	1/1	0.98	0.05	25,25,25,25	0
3	CL	A	1306	1/1	0.99	0.05	17,17,17,17	0
2	CA	A	1301	1/1	0.99	0.06	15,15,15,15	0
2	CA	A	1302	1/1	0.99	0.10	15,15,15,15	0
2	CA	B	1304	1/1	0.99	0.08	19,19,19,19	0
2	CA	C	1300	1/1	0.99	0.07	16,16,16,16	0
2	CA	D	1305	1/1	0.99	0.07	13,13,13,13	0
2	CA	B	1303	1/1	1.00	0.08	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.