



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:43 PM UTC

PDB ID : 9ICM / pdb_00009icm
Title : DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7) COMPLEXED WITH SIX BASE PAIRS OF DOUBLE STRANDED DNA (NO 5'-PHOSPHATE)
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1995-12-16
Resolution : 2.90 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
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

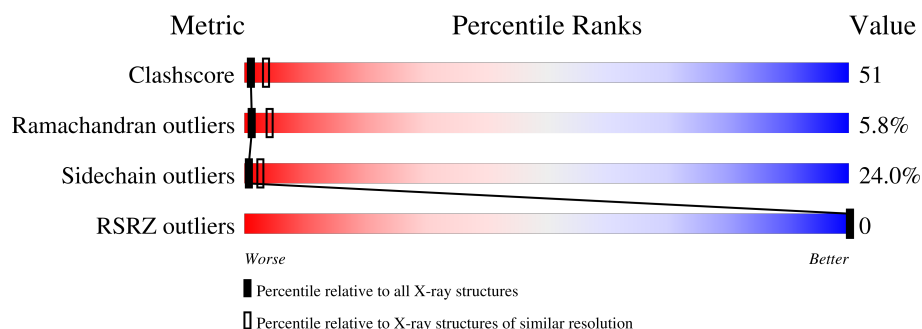
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	T	7	
2	P	6	
3	A	335	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3027 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 DNA chain called DNA (5'-D(*CP*AP*TP*CP*TP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	7	Total	C	N	O	P	0	0	0
			122	58	20	38	6			

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*AP*GP*AP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	6	Total	C	N	O	P	0	0	0
			126	59	25	36	6			

- Molecule 3 is a protein called PROTEIN (DNA POLYMERASE BETA (E.C.2.7.7.7)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	327	Total	C	N	O	S	26	0	0
			2623	1657	458	499	9			

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Na	0	0
			2	2		

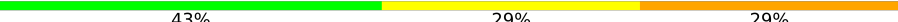
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	T	18	Total	O	0	0
			18	18		
5	P	18	Total	O	0	0
			18	18		
5	A	118	Total	O	0	0
			118	118		

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 (5'-D(*CP*AP*TP*CP*TP*GP*T)-3')

Chain T: 



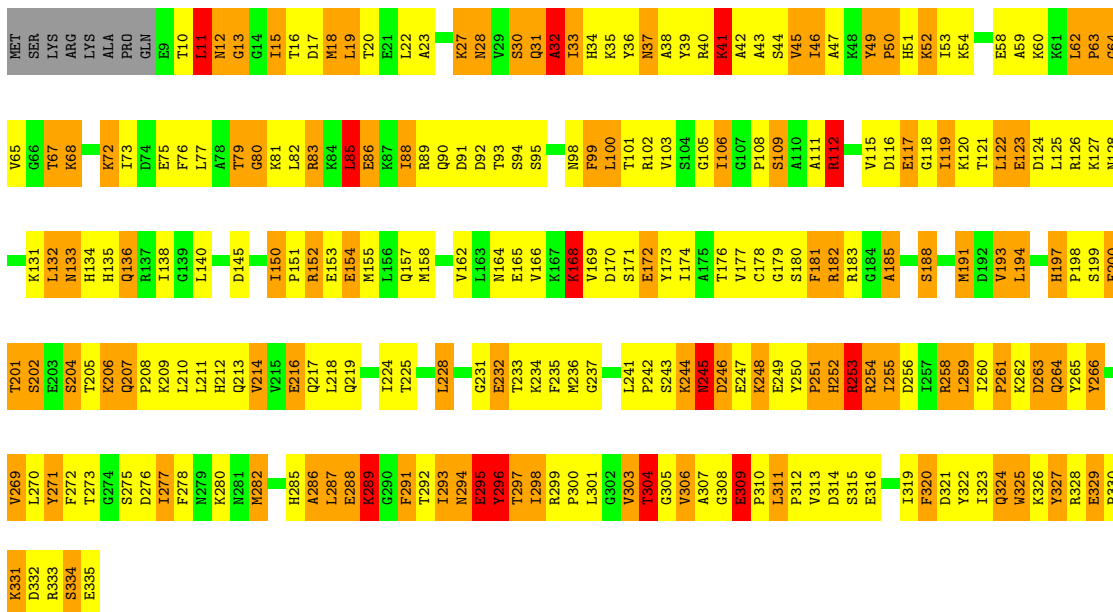
- Molecule 2: DNA (5'-D(*CP*AP*GP*AP*TP*G)-3')

Chain P: 



- Molecule 3: PROTEIN (DNA POLYMERASE BETA (E.C.2.7.7.7))

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	178.70Å 57.87Å 48.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	89.0 (20.00-2.90) 88.8 (20.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.57Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.155 , (Not available) 0.151 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 218.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3027	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.11% 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 i

5.1 Standard geometry i

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

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	T	1.01	0/135	2.23	6/207 (2.9%)
2	P	1.61	3/141 (2.1%)	2.08	3/214 (1.4%)
3	A	1.56	14/2672 (0.5%)	2.08	101/3590 (2.8%)
All	All	1.54	17/2948 (0.6%)	2.09	110/4011 (2.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	3	0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	1	DC	OP3-P	9.92	1.68	1.48
2	P	1	DC	P-O5'	6.12	1.72	1.60
3	A	254	ARG	C-N	-6.11	1.26	1.33
3	A	106	ILE	CA-C	-5.98	1.45	1.52
3	A	15	ILE	CA-C	-5.88	1.46	1.52
3	A	224	ILE	CA-CB	-5.78	1.47	1.54
3	A	106	ILE	C-O	-5.64	1.18	1.24
3	A	232	GLU	CA-C	-5.55	1.44	1.52
2	P	5	DT	C1'-N1	5.50	1.66	1.49
3	A	83	ARG	NE-CZ	5.35	1.39	1.33
3	A	94	SER	N-CA	-5.29	1.40	1.46
3	A	116	ASP	CA-C	-5.20	1.45	1.52
3	A	109	SER	CA-C	-5.11	1.46	1.52
3	A	58	GLU	CA-C	-5.10	1.46	1.52
3	A	15	ILE	CA-CB	-5.05	1.49	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	51	HIS	CA-C	-5.05	1.46	1.52
3	A	269	VAL	N-CA	-5.01	1.40	1.46

All (110) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	4	DT	C6-N1-C1'	-15.38	96.28	119.35
1	T	4	DT	C2-N1-C1'	15.18	142.11	119.35
2	P	5	DT	C2-N1-C1'	14.28	140.77	119.35
3	A	49	TYR	CA-C-N	13.72	133.26	119.82
3	A	49	TYR	C-N-CA	13.72	133.26	119.82
2	P	5	DT	C6-N1-C1'	-13.25	99.47	119.35
3	A	272	PHE	CA-CB-CG	-12.06	101.74	113.80
3	A	152	ARG	N-CA-CB	9.71	124.63	110.06
3	A	49	TYR	O-C-N	8.71	128.26	121.47
3	A	291	PHE	N-CA-C	8.68	122.07	109.14
3	A	98	ASN	CA-CB-CG	-8.43	104.17	112.60
3	A	86	GLU	N-CA-CB	8.17	121.85	110.01
3	A	83	ARG	N-CA-CB	7.80	121.56	109.94
3	A	86	GLU	CB-CA-C	7.50	122.65	110.88
3	A	34	HIS	CA-CB-CG	-7.49	106.31	113.80
3	A	30	SER	CA-C-N	-7.31	111.16	122.49
3	A	30	SER	C-N-CA	-7.31	111.16	122.49
3	A	32	ALA	N-CA-C	7.27	126.28	110.80
3	A	138	ILE	CB-CA-C	-7.22	102.64	111.88
3	A	214	VAL	N-CA-CB	7.07	119.62	110.57
3	A	168	LYS	N-CA-CB	7.01	120.39	109.94
1	T	2	DC	C2-N1-C1'	6.87	130.01	119.70
3	A	65	VAL	N-CA-C	6.84	116.57	106.85
3	A	291	PHE	CA-CB-CG	-6.75	107.05	113.80
3	A	52	LYS	N-CA-CB	6.58	120.67	110.21
3	A	253	ARG	CD-NE-CZ	6.51	133.52	124.40
3	A	117	GLU	N-CA-C	-6.51	104.97	113.17
3	A	92	ASP	N-CA-CB	6.35	120.00	110.22
3	A	309	GLU	CA-C-N	6.35	127.77	119.84
3	A	309	GLU	C-N-CA	6.35	127.77	119.84
3	A	296	TYR	CB-CA-C	-6.31	98.77	109.38
3	A	286	ALA	CA-C-N	6.25	128.66	120.28
3	A	286	ALA	C-N-CA	6.25	128.66	120.28
3	A	49	TYR	CA-C-O	6.23	125.01	119.59
3	A	99	PHE	CA-CB-CG	-6.19	107.61	113.80
3	A	271	TYR	CA-CB-CG	-6.16	102.81	113.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	123	GLU	CB-CA-C	6.16	120.63	110.90
3	A	40	ARG	N-CA-C	6.15	118.06	111.36
3	A	50	PRO	CA-C-N	-6.08	109.93	121.54
3	A	50	PRO	C-N-CA	-6.08	109.93	121.54
3	A	90	GLN	O-C-N	6.05	129.32	122.19
3	A	213	GLN	CB-CA-C	-6.00	100.83	110.79
1	T	2	DC	C6-N1-C1'	-6.00	110.71	119.70
1	T	4	DT	N1-C1'-C2'	5.97	122.45	113.50
3	A	41	LYS	N-CA-CB	5.96	119.52	110.28
3	A	116	ASP	CA-C-N	-5.95	112.72	122.54
3	A	116	ASP	C-N-CA	-5.95	112.72	122.54
3	A	30	SER	N-CA-C	-5.89	100.59	109.79
3	A	313	VAL	N-CA-CB	-5.88	103.29	111.41
3	A	109	SER	O-C-N	5.88	128.13	122.07
3	A	304	THR	N-CA-CB	-5.86	100.58	110.49
3	A	15	ILE	N-CA-CB	5.86	116.77	110.62
3	A	264	GLN	O-C-N	5.84	128.77	122.05
3	A	12	ASN	CA-C-N	5.84	126.59	119.99
3	A	12	ASN	C-N-CA	5.84	126.59	119.99
3	A	252	HIS	CA-CB-CG	-5.82	107.98	113.80
3	A	105	GLY	CA-C-N	-5.80	115.48	122.90
3	A	105	GLY	C-N-CA	-5.80	115.48	122.90
3	A	225	THR	N-CA-C	5.79	120.47	113.41
3	A	320	PHE	O-C-N	5.78	128.10	122.09
3	A	102	ARG	CD-NE-CZ	-5.76	116.33	124.40
3	A	28	ASN	CA-CB-CG	-5.75	106.85	112.60
3	A	245	ASN	CB-CA-C	5.73	121.15	111.41
3	A	261	PRO	CB-CA-C	-5.70	104.10	111.46
3	A	50	PRO	CB-CA-C	-5.69	103.32	111.62
3	A	246	ASP	N-CA-C	5.66	122.86	110.80
3	A	181	PHE	CA-C-N	5.58	128.80	120.31
3	A	181	PHE	C-N-CA	5.58	128.80	120.31
3	A	250	TYR	N-CA-C	5.57	117.98	110.29
3	A	15	ILE	CA-CB-CG2	-5.54	101.09	110.50
3	A	327	TYR	N-CA-CB	5.53	118.25	109.51
3	A	108	PRO	CB-CA-C	-5.50	104.30	112.55
3	A	286	ALA	O-C-N	5.50	127.81	122.09
3	A	64	GLY	N-CA-C	-5.49	108.08	115.21
3	A	28	ASN	N-CA-C	5.48	118.43	111.69
3	A	313	VAL	N-CA-C	5.46	115.76	108.11
3	A	88	ILE	N-CA-C	5.45	116.83	110.62
3	A	216	GLU	N-CA-CB	-5.44	101.84	109.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	112	ARG	N-CA-CB	5.42	117.87	110.01
3	A	251	PRO	CB-CA-C	-5.42	104.30	111.23
3	A	154	GLU	N-CA-CB	5.35	118.49	110.19
3	A	201	THR	N-CA-C	5.32	116.37	108.60
3	A	211	LEU	CA-C-N	5.30	127.64	120.38
3	A	211	LEU	C-N-CA	5.30	127.64	120.38
3	A	246	ASP	N-CA-CB	5.30	119.44	110.49
3	A	197	HIS	CA-C-N	5.29	124.48	118.97
3	A	197	HIS	C-N-CA	5.29	124.48	118.97
3	A	88	ILE	CB-CA-C	-5.27	105.14	112.04
3	A	231	GLY	CA-C-N	-5.25	112.88	122.38
3	A	231	GLY	C-N-CA	-5.25	112.88	122.38
3	A	329	GLU	N-CA-C	-5.24	102.86	110.08
3	A	49	TYR	N-CA-C	5.22	117.12	109.71
3	A	176	THR	CA-C-N	-5.20	116.25	122.90
3	A	176	THR	C-N-CA	-5.20	116.25	122.90
1	T	7	DG	N9-C1'-C2'	-5.20	105.71	113.50
3	A	85	LEU	N-CA-C	-5.18	105.63	111.28
3	A	207	GLN	CA-C-N	5.17	124.79	119.05
3	A	207	GLN	C-N-CA	5.17	124.79	119.05
3	A	63	PRO	CB-CA-C	-5.14	104.38	111.21
3	A	11	LEU	N-CA-CB	5.12	117.84	110.20
3	A	297	THR	CB-CA-C	-5.11	101.15	111.17
3	A	13	GLY	N-CA-C	5.09	118.81	112.64
3	A	31	GLN	CA-C-N	5.08	131.25	121.54
3	A	31	GLN	C-N-CA	5.08	131.25	121.54
3	A	200	PHE	N-CA-C	5.08	116.33	107.49
3	A	266	TYR	CA-CB-CG	-5.06	104.78	113.90
3	A	193	VAL	N-CA-C	5.06	116.25	108.71
3	A	40	ARG	N-CA-CB	5.05	117.64	110.16
3	A	301	LEU	N-CA-C	5.04	116.48	108.67
2	P	2	DA	C5'-C4'-O4'	-5.04	101.84	109.40

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	86	GLU	CA
3	A	152	ARG	CA
3	A	246	ASP	CA

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	T	122	0	69	4	0
2	P	126	0	68	11	0
3	A	2623	0	2641	269	1
4	A	2	0	0	0	0
5	A	118	0	0	9	0
5	P	18	0	0	2	0
5	T	18	0	0	4	0
All	All	3027	0	2778	282	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 51.

All (282) 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)
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.25	1.11
3:A:31:GLN:HE21	3:A:112:ARG:NH1	1.56	1.04
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.55	1.04
3:A:150:ILE:HD13	3:A:253:ARG:HG2	1.42	0.98
3:A:31:GLN:HE21	3:A:112:ARG:HH12	0.95	0.94
2:P:1:DC:H2''	2:P:2:DA:H5''	1.47	0.93
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.53	0.90
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.52	0.89
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.03	0.88
3:A:182:ARG:HG2	3:A:182:ARG:HH11	1.39	0.88
3:A:277:ILE:HG13	3:A:335:GLU:HB3	1.54	0.88
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.57	0.87
3:A:245:ASN:N	3:A:245:ASN:HD22	1.73	0.86
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.05	0.86
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.11	0.86
3:A:245:ASN:HD22	3:A:245:ASN:H	1.21	0.85
3:A:286:ALA:HA	3:A:323:ILE:HG21	1.58	0.85
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.06	0.84
3:A:41:LYS:HE2	3:A:64:GLY:HA2	1.58	0.84
3:A:23:ALA:HB2	3:A:39:TYR:HB2	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:15:ILE:HD11	3:A:77:LEU:HD11	1.62	0.81
3:A:270:LEU:HD21	3:A:282:MET:HE2	1.63	0.80
3:A:212:HIS:HB3	5:A:541:HOH:O	1.81	0.79
3:A:289:LYS:HD2	3:A:324:GLN:OE1	1.83	0.79
3:A:285:HIS:CE1	3:A:289:LYS:HE3	2.19	0.78
3:A:119:ILE:HG23	3:A:124:ASP:HB3	1.64	0.77
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.66	0.77
3:A:133:ASN:H	3:A:136:GLN:HE21	1.34	0.76
3:A:270:LEU:HD21	3:A:282:MET:CE	2.16	0.76
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.15	0.75
3:A:255:ILE:HG12	3:A:256:ASP:N	2.02	0.75
3:A:194:LEU:CD1	3:A:258:ARG:HD3	2.18	0.74
3:A:277:ILE:HG13	3:A:335:GLU:CB	2.17	0.74
3:A:150:ILE:HG21	3:A:158:MET:CE	2.18	0.74
3:A:151:PRO:HG2	3:A:154:GLU:HG3	1.69	0.73
3:A:194:LEU:HD11	3:A:258:ARG:HD3	1.69	0.73
3:A:201:THR:HA	3:A:261:PRO:HB3	1.70	0.73
3:A:18:MET:HE1	3:A:76:PHE:CB	2.19	0.72
3:A:330:PRO:HA	3:A:333:ARG:CG	2.20	0.72
3:A:11:LEU:HD23	3:A:11:LEU:H	1.53	0.71
3:A:242:PRO:HG2	5:A:589:HOH:O	1.90	0.71
3:A:12:ASN:HD21	3:A:53:ILE:H	1.37	0.71
3:A:49:TYR:CG	3:A:50:PRO:HD2	2.25	0.71
3:A:68:LYS:HB2	3:A:68:LYS:NZ	2.06	0.71
3:A:41:LYS:HD3	3:A:42:ALA:N	2.06	0.71
3:A:172:GLU:HG2	3:A:198:PRO:HG2	1.71	0.71
3:A:111:ALA:O	3:A:115:VAL:HG23	1.91	0.71
3:A:201:THR:HA	3:A:261:PRO:CB	2.20	0.70
3:A:292:THR:O	3:A:298:ILE:HA	1.91	0.70
3:A:15:ILE:HG21	3:A:46:ILE:HD13	1.73	0.69
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.27	0.69
2:P:1:DC:C2'	2:P:2:DA:H5''	2.23	0.69
3:A:42:ALA:O	3:A:46:ILE:HG23	1.93	0.69
3:A:200:PHE:CD2	3:A:261:PRO:HA	2.29	0.68
3:A:264:GLN:HA	5:A:536:HOH:O	1.92	0.68
3:A:197:HIS:ND1	3:A:198:PRO:HD2	2.08	0.68
3:A:119:ILE:CG2	3:A:124:ASP:HB3	2.24	0.68
3:A:170:ASP:HB3	3:A:173:TYR:CD2	2.29	0.68
3:A:286:ALA:HB1	3:A:293:ILE:HD11	1.76	0.67
3:A:261:PRO:HG2	3:A:264:GLN:CG	2.24	0.67
3:A:18:MET:CE	3:A:76:PHE:HB2	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:31:GLN:N	5:A:641:HOH:O	2.28	0.65
3:A:41:LYS:O	3:A:45:VAL:HG13	1.96	0.65
3:A:278:PHE:HB2	3:A:333:ARG:O	1.96	0.65
2:P:2:DA:C8	2:P:2:DA:H5'	2.31	0.65
3:A:155:MET:HE3	3:A:188:SER:OG	1.97	0.65
3:A:27:LYS:HB3	3:A:36:TYR:CD1	2.32	0.65
3:A:276:ASP:O	3:A:280:LYS:HG3	1.98	0.64
3:A:59:ALA:O	3:A:62:LEU:HB2	1.97	0.64
3:A:75:GLU:O	3:A:79:THR:HG23	1.96	0.64
3:A:315:SER:OG	3:A:316:GLU:N	2.29	0.64
1:T:7:DG:N3	5:T:634:HOH:O	2.31	0.63
3:A:62:LEU:HD12	3:A:63:PRO:HD2	1.79	0.63
3:A:79:THR:O	3:A:81:LYS:N	2.32	0.62
2:P:5:DT:H2''	2:P:6:DG:H5'	1.80	0.62
3:A:244:LYS:HB2	3:A:245:ASN:HD22	1.65	0.61
3:A:244:LYS:CB	3:A:245:ASN:HD22	2.13	0.61
3:A:271:TYR:HB2	5:A:592:HOH:O	2.01	0.61
3:A:261:PRO:HG2	3:A:264:GLN:HG2	1.83	0.61
3:A:12:ASN:ND2	3:A:53:ILE:H	1.98	0.60
3:A:157:GLN:NE2	3:A:244:LYS:NZ	2.49	0.60
3:A:245:ASN:N	3:A:245:ASN:ND2	2.46	0.60
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.17	0.60
3:A:286:ALA:O	3:A:291:PHE:HB2	2.02	0.60
3:A:103:VAL:HB	3:A:106:ILE:HD12	1.83	0.60
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.28	0.59
5:T:664:HOH:O	3:A:133:ASN:HB2	2.02	0.59
3:A:155:MET:CE	3:A:188:SER:HB2	2.32	0.59
3:A:166:VAL:O	3:A:169:VAL:HG12	2.02	0.59
3:A:133:ASN:H	3:A:136:GLN:NE2	2.00	0.59
3:A:243:SER:HB3	3:A:249:GLU:HA	1.85	0.58
3:A:306:VAL:HG23	3:A:307:ALA:N	2.17	0.58
3:A:248:LYS:O	3:A:248:LYS:HG2	2.03	0.58
3:A:154:GLU:HB3	3:A:241:LEU:HD11	1.84	0.58
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.34	0.58
3:A:299:ARG:HB3	3:A:300:PRO:HD2	1.86	0.58
3:A:44:SER:O	3:A:47:ALA:HB3	2.03	0.57
3:A:157:GLN:HE22	3:A:244:LYS:NZ	2.02	0.57
3:A:179:GLY:O	3:A:182:ARG:HB3	2.05	0.57
3:A:31:GLN:NE2	3:A:112:ARG:NH1	2.31	0.56
3:A:85:LEU:O	3:A:89:ARG:HG3	2.04	0.56
3:A:182:ARG:HH11	3:A:182:ARG:CG	2.16	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:237:GLY:O	3:A:254:ARG:NH1	2.38	0.56
3:A:82:LEU:CD2	3:A:85:LEU:HD22	2.35	0.56
3:A:326:LYS:HE3	3:A:328:ARG:HG2	1.87	0.56
3:A:326:LYS:HG3	3:A:326:LYS:O	2.04	0.56
3:A:122:LEU:O	3:A:126:ARG:HG3	2.06	0.55
3:A:191:MET:CG	3:A:255:ILE:HG13	2.32	0.55
3:A:15:ILE:HD11	3:A:77:LEU:CD1	2.34	0.55
3:A:72:LYS:HG2	3:A:82:LEU:HD11	1.88	0.55
1:T:3:DA:H2''	5:T:573:HOH:O	2.07	0.55
3:A:303:VAL:C	3:A:305:GLY:H	2.15	0.55
3:A:325:TRP:HD1	5:A:583:HOH:O	1.90	0.55
3:A:259:LEU:O	3:A:260:ILE:HD13	2.06	0.55
3:A:295:GLU:HG2	3:A:296:TYR:CE1	2.41	0.55
3:A:321:ASP:O	3:A:324:GLN:N	2.37	0.55
3:A:121:THR:O	3:A:124:ASP:HB2	2.07	0.55
3:A:182:ARG:HG2	3:A:273:THR:HG23	1.87	0.54
3:A:261:PRO:HB2	3:A:263:ASP:OD1	2.07	0.54
2:P:3:DG:N3	5:P:511:HOH:O	2.33	0.54
3:A:210:LEU:HB2	3:A:259:LEU:HD21	1.89	0.54
3:A:35:LYS:O	3:A:38:ALA:HB3	2.07	0.54
3:A:18:MET:HE2	3:A:82:LEU:HD13	1.90	0.54
3:A:182:ARG:HG2	3:A:273:THR:CG2	2.38	0.54
3:A:12:ASN:HA	5:A:642:HOH:O	2.07	0.53
3:A:162:VAL:O	3:A:166:VAL:HG23	2.08	0.53
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.47	0.53
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.90	0.53
3:A:133:ASN:HD21	3:A:135:HIS:HB3	1.72	0.53
3:A:243:SER:CB	3:A:249:GLU:HA	2.37	0.53
3:A:326:LYS:HE2	3:A:328:ARG:HE	1.73	0.53
3:A:120:LYS:N	3:A:124:ASP:OD2	2.30	0.53
3:A:217:GLN:NE2	3:A:217:GLN:HA	2.24	0.53
3:A:331:LYS:HD2	3:A:332:ASP:N	2.24	0.52
3:A:259:LEU:HD12	3:A:260:ILE:H	1.75	0.52
3:A:182:ARG:HH11	3:A:273:THR:HG21	1.75	0.52
3:A:82:LEU:HD23	3:A:85:LEU:HD22	1.92	0.52
3:A:201:THR:OG1	3:A:202:SER:N	2.41	0.51
1:T:2:DC:H2''	1:T:3:DA:C8	2.45	0.51
3:A:208:PRO:O	3:A:212:HIS:HD2	1.94	0.51
3:A:259:LEU:HD12	3:A:260:ILE:N	2.25	0.51
3:A:327:TYR:CD1	3:A:328:ARG:N	2.79	0.51
3:A:332:ASP:C	3:A:334:SER:H	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:27:LYS:HG3	3:A:28:ASN:N	2.26	0.51
3:A:152:ARG:NH2	3:A:181:PHE:O	2.41	0.50
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.26	0.50
3:A:32:ALA:HB1	3:A:35:LYS:HB2	1.93	0.50
3:A:79:THR:C	3:A:81:LYS:H	2.18	0.50
3:A:294:ASN:HB2	3:A:295:GLU:OE2	2.12	0.50
3:A:33:ILE:O	3:A:37:ASN:HB2	2.11	0.50
3:A:183:ARG:HD3	3:A:273:THR:O	2.12	0.50
3:A:261:PRO:HG2	3:A:264:GLN:HG3	1.93	0.50
5:T:617:HOH:O	3:A:234:LYS:HD3	2.12	0.50
2:P:2:DA:H5'	2:P:2:DA:H8	1.77	0.50
3:A:262:LYS:O	3:A:262:LYS:HG3	2.06	0.49
3:A:308:GLY:O	3:A:309:GLU:HB2	2.12	0.49
3:A:288:GLU:OE1	3:A:288:GLU:HA	1.91	0.49
3:A:157:GLN:NE2	3:A:244:LYS:HZ1	2.09	0.49
3:A:205:THR:O	3:A:206:LYS:O	2.31	0.49
3:A:275:SER:OG	3:A:334:SER:O	2.29	0.49
3:A:322:TYR:C	3:A:324:GLN:H	2.21	0.49
3:A:150:ILE:O	3:A:188:SER:N	2.46	0.49
3:A:286:ALA:CA	3:A:323:ILE:HG21	2.38	0.48
3:A:309:GLU:OE1	3:A:309:GLU:HA	2.12	0.48
3:A:155:MET:HA	3:A:158:MET:HE3	1.94	0.48
3:A:197:HIS:CE1	3:A:198:PRO:HD2	2.48	0.48
3:A:200:PHE:O	3:A:262:LYS:N	2.38	0.48
3:A:319:ILE:O	3:A:322:TYR:HB2	2.13	0.48
3:A:210:LEU:CB	3:A:259:LEU:HD21	2.43	0.48
3:A:155:MET:SD	3:A:158:MET:HE3	2.54	0.48
3:A:204:SER:O	3:A:204:SER:OG	2.29	0.48
3:A:182:ARG:HG2	3:A:182:ARG:NH1	2.17	0.48
3:A:23:ALA:O	3:A:36:TYR:HD1	1.97	0.48
3:A:170:ASP:HB3	3:A:173:TYR:CE2	2.49	0.48
3:A:15:ILE:CG2	3:A:46:ILE:HD13	2.43	0.47
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.94	0.47
3:A:123:GLU:HG2	3:A:126:ARG:HH11	1.79	0.47
3:A:251:PRO:HG2	3:A:253:ARG:CZ	2.44	0.47
3:A:312:PRO:O	3:A:322:TYR:OH	2.28	0.47
3:A:327:TYR:HD1	3:A:328:ARG:N	2.11	0.47
3:A:68:LYS:HB2	3:A:68:LYS:HZ1	1.75	0.47
3:A:200:PHE:CE2	3:A:261:PRO:N	2.83	0.47
3:A:174:ILE:HG22	3:A:265:TYR:CE2	2.49	0.47
3:A:200:PHE:O	3:A:261:PRO:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:306:VAL:CG2	3:A:307:ALA:N	2.78	0.47
3:A:296:TYR:HB2	3:A:297:THR:HG23	1.95	0.47
3:A:244:LYS:HB3	3:A:245:ASN:ND2	2.30	0.47
3:A:253:ARG:NH1	5:A:503:HOH:O	2.47	0.46
3:A:134:HIS:HD2	5:A:515:HOH:O	1.98	0.46
3:A:169:VAL:HG13	3:A:170:ASP:N	2.30	0.46
3:A:311:LEU:HD12	3:A:311:LEU:HA	1.77	0.46
3:A:127:LYS:HD2	3:A:127:LYS:HA	1.71	0.46
3:A:264:GLN:HE21	3:A:264:GLN:HB3	1.57	0.46
3:A:197:HIS:CE1	3:A:199:SER:HB3	2.50	0.46
3:A:23:ALA:CB	3:A:39:TYR:HB2	2.35	0.46
3:A:235:PHE:CZ	3:A:237:GLY:HA3	2.50	0.46
3:A:157:GLN:NE2	3:A:244:LYS:HZ3	2.13	0.46
3:A:255:ILE:HG23	3:A:255:ILE:O	2.14	0.46
3:A:27:LYS:CB	3:A:36:TYR:CD1	2.99	0.46
3:A:118:GLY:HA2	3:A:120:LYS:HE3	1.98	0.46
3:A:155:MET:HE3	3:A:188:SER:CB	2.45	0.46
3:A:244:LYS:CB	3:A:245:ASN:ND2	2.79	0.46
3:A:150:ILE:N	3:A:188:SER:O	2.35	0.46
2:P:4:DA:H5"	5:P:614:HOH:O	2.16	0.45
3:A:294:ASN:C	3:A:294:ASN:HD22	2.23	0.45
3:A:300:PRO:HD3	3:A:311:LEU:HD22	1.98	0.45
2:P:5:DT:P	3:A:109:SER:HB3	2.57	0.45
3:A:287:LEU:HD13	3:A:287:LEU:HA	1.56	0.45
3:A:289:LYS:HD3	3:A:289:LYS:HA	1.41	0.45
3:A:298:ILE:O	3:A:311:LEU:HB2	2.16	0.45
3:A:323:ILE:C	3:A:324:GLN:HG2	2.42	0.45
3:A:68:LYS:NZ	3:A:68:LYS:CB	2.79	0.45
3:A:198:PRO:C	3:A:200:PHE:H	2.24	0.45
3:A:60:LYS:HE2	3:A:67:THR:HB	1.98	0.45
3:A:133:ASN:C	3:A:133:ASN:HD22	2.25	0.44
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.67	0.44
3:A:316:GLU:CD	3:A:333:ARG:HH22	2.24	0.44
3:A:80:GLY:O	3:A:81:LYS:HG2	2.17	0.44
3:A:295:GLU:CD	3:A:295:GLU:H	2.25	0.44
3:A:81:LYS:NZ	3:A:86:GLU:OE1	2.40	0.44
3:A:132:LEU:HB3	3:A:136:GLN:HB3	1.99	0.44
3:A:197:HIS:ND1	3:A:199:SER:HB3	2.32	0.44
3:A:232:GLU:C	3:A:233:THR:HG23	2.42	0.44
3:A:99:PHE:HD2	3:A:100:LEU:HD12	1.83	0.44
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:125:LEU:HD23	3:A:125:LEU:HA	1.79	0.43
3:A:198:PRO:O	3:A:200:PHE:N	2.51	0.43
3:A:289:LYS:HG3	3:A:323:ILE:O	2.18	0.43
3:A:135:HIS:CD2	3:A:135:HIS:C	2.96	0.43
3:A:309:GLU:HA	3:A:310:PRO:HD2	1.80	0.43
3:A:88:ILE:HD13	3:A:88:ILE:HG21	1.80	0.43
3:A:154:GLU:O	3:A:158:MET:HG3	2.19	0.43
3:A:178:CYS:SG	3:A:194:LEU:CD2	3.07	0.43
3:A:16:THR:O	3:A:20:THR:HG23	2.18	0.43
3:A:124:ASP:O	3:A:128:ASN:ND2	2.51	0.43
3:A:180:SER:HB2	3:A:185:ALA:CB	2.48	0.43
3:A:266:TYR:HA	3:A:269:VAL:HB	2.00	0.43
3:A:182:ARG:HH11	3:A:273:THR:CG2	2.30	0.43
2:P:5:DT:C2'	2:P:6:DG:H5'	2.48	0.43
3:A:133:ASN:ND2	3:A:136:GLN:H	2.17	0.43
3:A:270:LEU:HD21	3:A:282:MET:HE1	1.95	0.43
3:A:152:ARG:HA	3:A:155:MET:HB2	2.00	0.43
3:A:28:ASN:N	3:A:28:ASN:HD22	2.08	0.42
3:A:36:TYR:CD2	3:A:37:ASN:N	2.87	0.42
3:A:13:GLY:O	3:A:17:ASP:N	2.49	0.42
3:A:121:THR:HG23	3:A:124:ASP:OD2	2.19	0.42
3:A:79:THR:C	3:A:81:LYS:N	2.78	0.42
3:A:331:LYS:O	3:A:331:LYS:HG2	2.17	0.42
3:A:15:ILE:CG2	3:A:46:ILE:CD1	2.97	0.42
3:A:260:ILE:HG23	3:A:260:ILE:HD12	1.73	0.42
3:A:82:LEU:HD22	3:A:85:LEU:HD22	2.01	0.42
3:A:273:THR:O	3:A:273:THR:HG22	2.19	0.42
3:A:76:PHE:O	3:A:79:THR:O	2.38	0.41
3:A:194:LEU:HD12	3:A:194:LEU:HA	1.46	0.41
3:A:197:HIS:CG	3:A:198:PRO:CD	2.99	0.41
3:A:209:LYS:HD3	3:A:209:LYS:HA	1.69	0.41
3:A:235:PHE:CD1	3:A:235:PHE:C	2.98	0.41
3:A:197:HIS:HA	3:A:198:PRO:HD3	1.92	0.41
3:A:150:ILE:HD13	3:A:253:ARG:CG	2.31	0.41
3:A:37:ASN:HD22	3:A:37:ASN:HA	1.70	0.41
3:A:73:ILE:HD13	3:A:73:ILE:HG21	1.77	0.41
3:A:165:GLU:OE1	3:A:168:LYS:NZ	2.52	0.41
3:A:316:GLU:O	3:A:320:PHE:HD2	2.03	0.41
3:A:177:VAL:HG22	3:A:193:VAL:HG22	2.02	0.41
3:A:327:TYR:CD1	3:A:327:TYR:C	2.97	0.41
2:P:2:DA:H5'	2:P:2:DA:H2'	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:133:ASN:C	3:A:133:ASN:ND2	2.78	0.41
3:A:164:ASN:O	3:A:168:LYS:HG2	2.21	0.41
3:A:294:ASN:C	3:A:294:ASN:ND2	2.77	0.41
3:A:18:MET:HG3	3:A:82:LEU:HD22	2.03	0.41
3:A:41:LYS:HD3	3:A:42:ALA:H	1.83	0.41
3:A:155:MET:CE	3:A:188:SER:CB	2.98	0.41
3:A:150:ILE:HD11	3:A:253:ARG:HG2	1.97	0.40
3:A:157:GLN:HE22	3:A:244:LYS:HZ3	1.69	0.40
1:T:3:DA:N1	2:P:5:DT:C4	2.89	0.40
3:A:31:GLN:HG3	3:A:112:ARG:HH22	1.87	0.40
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.97	0.40
3:A:212:HIS:O	3:A:216:GLU:HB2	2.20	0.40
3:A:294:ASN:O	3:A:296:TYR:N	2.54	0.40
3:A:322:TYR:C	3:A:324:GLN:N	2.79	0.40
3:A:145:ASP:HB3	3:A:252:HIS:O	2.22	0.40
3:A:228:LEU:HB2	3:A:236:MET:O	2.21	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)
3:A:83:ARG:NH1	3:A:117:GLU:CB[3_558]	1.63	0.57

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
3	A	325/335 (97%)	282 (87%)	24 (7%)	19 (6%)	1 4

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	32	ALA
3	A	185	ALA
3	A	206	LYS
3	A	244	LYS
3	A	247	GLU
3	A	295	GLU
3	A	309	GLU
3	A	80	GLY
3	A	202	SER
3	A	334	SER
3	A	91	ASP
3	A	204	SER
3	A	207	GLN
3	A	246	ASP
3	A	289	LYS
3	A	10	THR
3	A	263	ASP
3	A	304	THR
3	A	324	GLN

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
3	A	288/295 (98%)	219 (76%)	69 (24%)	1 2

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	11	LEU
3	A	18	MET
3	A	19	LEU
3	A	22	LEU
3	A	27	LYS
3	A	30	SER
3	A	33	ILE
3	A	37	ASN

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Mol	Chain	Res	Type
3	A	41	LYS
3	A	45	VAL
3	A	46	ILE
3	A	52	LYS
3	A	54	LYS
3	A	62	LEU
3	A	67	THR
3	A	68	LYS
3	A	72	LYS
3	A	79	THR
3	A	85	LEU
3	A	93	THR
3	A	95	SER
3	A	100	LEU
3	A	101	THR
3	A	112	ARG
3	A	119	ILE
3	A	122	LEU
3	A	131	LYS
3	A	132	LEU
3	A	133	ASN
3	A	136	GLN
3	A	140	LEU
3	A	150	ILE
3	A	153	GLU
3	A	168	LYS
3	A	171	SER
3	A	172	GLU
3	A	182	ARG
3	A	188	SER
3	A	191	MET
3	A	194	LEU
3	A	214	VAL
3	A	218	LEU
3	A	219	GLN
3	A	228	LEU
3	A	245	ASN
3	A	248	LYS
3	A	253	ARG
3	A	255	ILE
3	A	258	ARG
3	A	259	LEU

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Mol	Chain	Res	Type
3	A	277	ILE
3	A	282	MET
3	A	287	LEU
3	A	288	GLU
3	A	289	LYS
3	A	293	ILE
3	A	294	ASN
3	A	295	GLU
3	A	296	TYR
3	A	298	ILE
3	A	303	VAL
3	A	304	THR
3	A	306	VAL
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	325	TRP
3	A	329	GLU
3	A	331	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	12	ASN
3	A	28	ASN
3	A	31	GLN
3	A	37	ASN
3	A	90	GLN
3	A	98	ASN
3	A	133	ASN
3	A	134	HIS
3	A	136	GLN
3	A	157	GLN
3	A	164	ASN
3	A	212	HIS
3	A	213	GLN
3	A	217	GLN
3	A	245	ASN
3	A	264	GLN
3	A	279	ASN
3	A	294	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 2 ligands modelled in this entry, 2 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	T	7/7 (100%)	-1.21	0 100 100	21, 35, 63, 100	0
2	P	6/6 (100%)	-1.35	0 100 100	22, 29, 33, 35	0
3	A	324/335 (96%)	-1.01	0 100 100	9, 36, 83, 100	0
All	All	337/348 (96%)	-1.02	0 100 100	9, 35, 83, 100	0

There are no RSRZ outliers to report.

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
4	NA	A	341	1/1	0.98	0.03	26,26,26,26	0
4	NA	A	342	1/1	1.00	0.06	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.