



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:44 PM UTC

PDB ID : 1ZQD / pdb_00001zqd
Title : DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7) COMPLEXED WITH SEVEN BASE PAIRS OF DNA; SOAKED IN THE PRESENCE OF CACL2 (150 MILLIMOLAR)
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1996-04-12
Resolution : 3.50 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

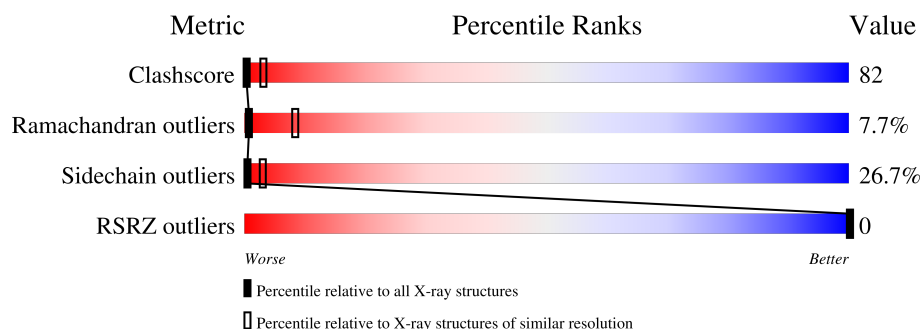
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	8	
2	P	7	
3	A	335	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3059 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*TP*AP*GP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	8	Total	C	N	O	P	0	0	0
			145	69	27	42	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	P	0	0	0
			144	69	24	44	7			

- 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	18	0	0
			2623	1657	458	499	9			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	T	13	Total	O	0	0
			13	13		
5	P	22	Total	O	0	0
			22	22		
5	A	110	Total	O	0	0
			110	110		

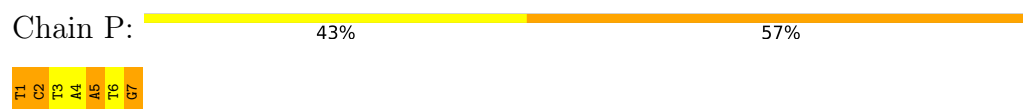
3 Residue-property plots

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 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.

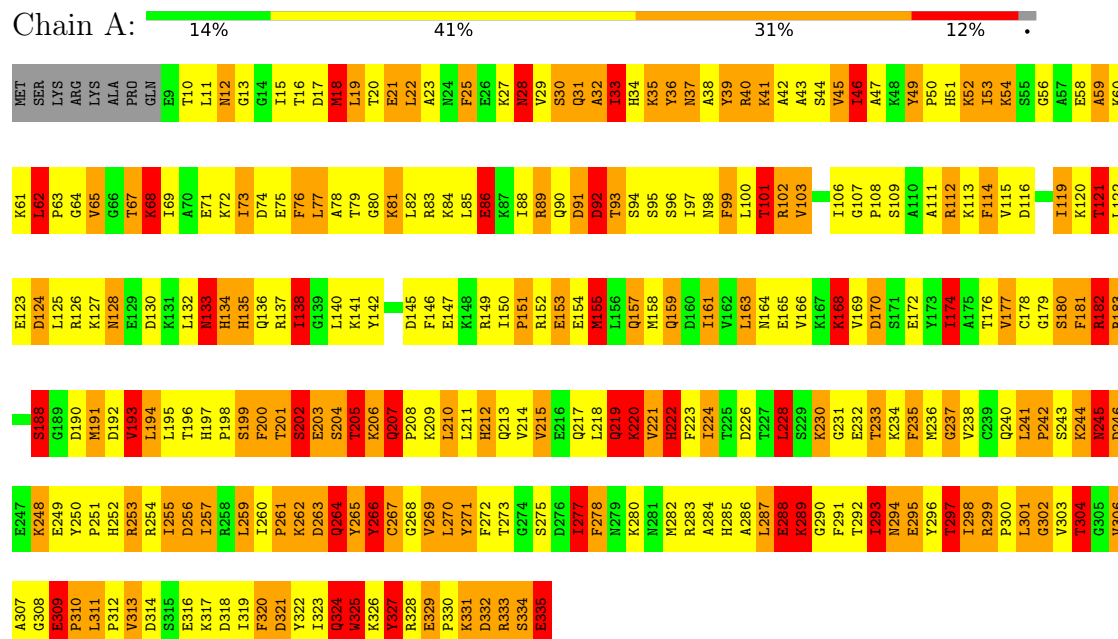
- Molecule 1: DNA (5'-D(*CP*AP*TP*TP*AP*GP*AP*A)-3')



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	178.56Å 57.83Å 47.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.50 20.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	73.0 (20.00-3.50) 73.0 (20.00-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 2.63Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.144 , (Not available) 0.141 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	5.3	Xtriage
Anisotropy	14.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 332.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3059	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.95% 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: CA

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	0.88	0/162	3.80	17/249 (6.8%)
2	P	1.18	1/160 (0.6%)	3.49	12/243 (4.9%)
3	A	1.55	11/2672 (0.4%)	2.32	166/3590 (4.6%)
All	All	1.50	12/2994 (0.4%)	2.51	195/4082 (4.8%)

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 (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	65	VAL	CA-CB	-8.43	1.44	1.54
3	A	76	PHE	CA-C	-7.02	1.43	1.52
2	P	1	DT	OP3-P	7.01	1.62	1.48
3	A	234	LYS	N-CA	-5.97	1.39	1.46
3	A	140	LEU	C-N	-5.95	1.25	1.33
3	A	91	ASP	N-CA	5.80	1.53	1.46
3	A	215	VAL	C-O	-5.75	1.17	1.24
3	A	67	THR	N-CA	-5.30	1.40	1.46
3	A	220	LYS	C-N	-5.30	1.27	1.33
3	A	103	VAL	CA-CB	-5.23	1.47	1.54
3	A	226	ASP	CA-C	-5.19	1.46	1.52
3	A	90	GLN	C-N	5.00	1.40	1.33

All (195) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	4	DT	C6-N1-C1'	-25.44	81.19	119.35
1	T	4	DT	C2-N1-C1'	24.90	156.69	119.35
2	P	1	DT	C6-N1-C1'	-20.66	88.36	119.35
2	P	1	DT	C2-N1-C1'	19.52	148.63	119.35
1	T	7	DA	C8-N9-C1'	18.18	154.32	127.05
1	T	7	DA	C4-N9-C1'	-17.92	100.18	127.05
1	T	6	DG	C8-N9-C1'	17.00	152.50	127.00
1	T	6	DG	C4-N9-C1'	-16.90	101.65	127.00
2	P	7	DG	C8-N9-C1'	16.36	151.54	127.00
2	P	5	DA	C8-N9-C1'	-15.88	103.22	127.05
2	P	5	DA	C4-N9-C1'	15.82	150.78	127.05
2	P	7	DG	C4-N9-C1'	-15.22	104.17	127.00
2	P	2	DC	C2-N1-C1'	14.40	141.30	119.70
2	P	2	DC	C6-N1-C1'	-12.63	100.75	119.70
1	T	3	DT	C6-N1-C1'	11.72	136.93	119.35
1	T	3	DT	C2-N1-C1'	-11.32	102.38	119.35
3	A	266	TYR	CA-CB-CG	-9.31	97.14	113.90
3	A	157	GLN	N-CA-CB	9.15	123.70	110.16
3	A	28	ASN	CA-CB-CG	-9.14	103.45	112.60
3	A	114	PHE	CA-CB-CG	-9.03	104.78	113.80
3	A	21	GLU	N-CA-C	-8.77	101.72	111.28
2	P	3	DT	C2-N1-C1'	8.71	132.42	119.35
3	A	278	PHE	CA-CB-CG	-8.54	105.26	113.80
3	A	138	ILE	CB-CA-C	-8.52	101.07	111.97
3	A	72	LYS	CB-CA-C	8.26	123.86	110.88
2	P	3	DT	C6-N1-C1'	-8.17	107.10	119.35
3	A	99	PHE	CA-CB-CG	-8.06	105.74	113.80
3	A	256	ASP	CA-CB-CG	8.05	120.66	112.60
2	P	3	DT	P-O5'-C5'	8.01	132.02	120.00
3	A	313	VAL	N-CA-C	7.94	119.22	108.11
3	A	190	ASP	CA-CB-CG	7.69	120.29	112.60
3	A	182	ARG	O-C-N	7.67	130.06	122.09
3	A	91	ASP	N-CA-CB	7.44	123.07	110.49
3	A	297	THR	N-CA-C	7.36	117.72	108.45
3	A	223	PHE	CA-CB-CG	-7.35	106.45	113.80
3	A	288	GLU	N-CA-C	-7.25	102.98	111.03
1	T	1	DC	C6-N1-C1'	-7.25	108.83	119.70
1	T	5	DA	C4-N9-C1'	-7.23	116.20	127.05
3	A	220	LYS	CA-C-N	-7.15	113.15	122.16
3	A	220	LYS	C-N-CA	-7.15	113.15	122.16
3	A	32	ALA	N-CA-C	7.08	125.88	110.80
3	A	46	ILE	CB-CA-C	7.07	122.89	111.29
3	A	264	GLN	N-CA-C	7.06	122.90	113.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	68	LYS	N-CA-CB	7.03	121.67	109.72
3	A	135	HIS	CA-C-N	6.95	129.91	120.38
3	A	135	HIS	C-N-CA	6.95	129.91	120.38
3	A	49	TYR	CA-C-N	6.93	127.53	120.04
3	A	49	TYR	C-N-CA	6.93	127.53	120.04
3	A	140	LEU	CA-C-O	6.89	127.73	120.42
3	A	164	ASN	N-CA-C	6.89	118.58	111.14
3	A	333	ARG	N-CA-C	-6.85	102.98	112.30
3	A	45	VAL	N-CA-CB	6.85	119.34	110.57
3	A	221	VAL	N-CA-CB	-6.85	104.68	112.21
3	A	228	LEU	N-CA-C	-6.81	103.09	111.40
3	A	40	ARG	N-CA-C	6.74	118.62	111.28
3	A	264	GLN	CB-CA-C	6.74	120.87	109.55
3	A	30	SER	CA-C-N	-6.71	112.08	122.49
3	A	30	SER	C-N-CA	-6.71	112.08	122.49
3	A	224	ILE	CA-C-N	-6.64	111.82	122.24
3	A	224	ILE	C-N-CA	-6.64	111.82	122.24
3	A	180	SER	O-C-N	6.60	128.95	122.09
1	T	1	DC	C2-N1-C1'	6.56	129.53	119.70
3	A	133	ASN	N-CA-CB	6.51	120.55	110.46
3	A	68	LYS	CA-C-N	6.50	131.31	120.64
3	A	68	LYS	C-N-CA	6.50	131.31	120.64
3	A	335	GLU	N-CA-CB	6.49	121.53	110.50
3	A	181	PHE	CB-CA-C	-6.49	99.97	110.74
3	A	12	ASN	N-CA-CB	6.47	120.38	110.61
3	A	200	PHE	CB-CA-C	-6.46	101.18	110.62
1	T	5	DA	P-O5'-C5'	-6.44	110.34	120.00
3	A	329	GLU	N-CA-C	-6.41	101.51	109.64
3	A	192	ASP	CA-CB-CG	-6.40	106.20	112.60
3	A	174	ILE	N-CA-CB	6.39	121.93	111.58
3	A	92	ASP	CB-CA-C	6.38	121.06	110.92
3	A	224	ILE	CB-CA-C	6.37	119.96	110.98
3	A	222	HIS	N-CA-CB	6.36	121.23	110.49
3	A	318	ASP	CA-CB-CG	-6.34	106.26	112.60
3	A	76	PHE	CB-CA-C	-6.31	100.31	110.79
3	A	271	TYR	N-CA-C	6.29	117.83	110.97
3	A	277	ILE	N-CA-CB	6.29	118.62	110.57
3	A	53	ILE	CB-CA-C	6.27	119.22	111.25
3	A	267	CYS	CB-CA-C	-6.27	100.26	110.79
3	A	84	LYS	N-CA-C	-6.27	103.75	111.33
3	A	18	MET	CA-C-N	6.26	128.96	120.38
3	A	18	MET	C-N-CA	6.26	128.96	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	76	PHE	O-C-N	6.26	128.75	122.12
1	T	5	DA	C8-N9-C1'	6.25	136.42	127.05
3	A	122	LEU	N-CA-C	-6.22	104.50	111.28
3	A	299	ARG	CB-CA-C	6.22	118.24	108.84
3	A	188	SER	N-CA-CB	-6.18	100.79	111.55
3	A	293	ILE	O-C-N	6.18	129.52	123.03
3	A	74	ASP	N-CA-CB	6.18	118.97	110.01
3	A	267	CYS	O-C-N	6.16	129.62	122.17
1	T	1	DC	P-O3'-C3'	6.14	129.41	120.20
3	A	170	ASP	CA-CB-CG	-6.07	106.53	112.60
3	A	35	LYS	N-CA-C	-6.05	104.68	111.28
3	A	155	MET	CA-C-N	6.03	128.85	120.29
3	A	155	MET	C-N-CA	6.03	128.85	120.29
3	A	235	PHE	CA-CB-CG	-6.03	107.77	113.80
3	A	17	ASP	CB-CA-C	6.02	122.14	110.46
3	A	86	GLU	N-CA-C	5.99	117.89	111.36
3	A	205	THR	N-CA-CB	5.99	120.61	110.49
3	A	49	TYR	O-C-N	5.93	126.24	121.38
3	A	62	LEU	N-CA-C	5.93	119.47	109.87
3	A	202	SER	N-CA-C	5.92	123.40	110.80
3	A	93	THR	N-CA-CB	-5.88	101.49	110.01
3	A	98	ASN	CB-CA-C	5.88	121.50	110.63
3	A	327	TYR	N-CA-C	-5.87	101.36	110.10
3	A	219	GLN	N-CA-C	-5.85	104.81	111.07
3	A	163	LEU	N-CA-C	-5.83	105.42	112.54
3	A	36	TYR	CA-CB-CG	-5.82	103.43	113.90
3	A	309	GLU	N-CA-C	5.80	122.63	109.81
3	A	253	ARG	N-CA-C	5.79	118.91	109.59
3	A	271	TYR	N-CA-CB	-5.78	101.47	109.91
3	A	52	LYS	CA-C-N	-5.78	115.15	122.43
3	A	52	LYS	C-N-CA	-5.78	115.15	122.43
3	A	332	ASP	N-CA-C	5.76	117.91	110.65
3	A	147	GLU	CB-CG-CD	-5.73	102.86	112.60
3	A	59	ALA	O-C-N	5.72	127.98	122.03
3	A	248	LYS	N-CA-CB	5.70	119.43	110.71
3	A	31	GLN	CA-C-N	5.69	132.40	121.54
3	A	31	GLN	C-N-CA	5.69	132.40	121.54
3	A	168	LYS	N-CA-CB	5.69	118.42	109.94
3	A	241	LEU	O-C-N	5.69	126.14	121.31
3	A	124	ASP	N-CA-C	-5.68	104.29	111.11
3	A	112	ARG	O-C-N	5.67	127.91	122.07
3	A	213	GLN	CB-CA-C	-5.67	101.74	110.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	280	LYS	N-CA-C	-5.67	104.31	111.11
3	A	325	TRP	CB-CA-C	-5.66	100.67	111.48
3	A	95	SER	N-CA-C	-5.65	105.02	111.07
3	A	37	ASN	N-CA-C	-5.65	105.11	112.23
3	A	207	GLN	N-CA-C	-5.64	97.34	109.81
3	A	99	PHE	CB-CA-C	-5.64	102.21	110.95
3	A	246	ASP	CA-CB-CG	-5.62	106.97	112.60
3	A	76	PHE	CA-CB-CG	-5.62	108.19	113.80
3	A	95	SER	CB-CA-C	-5.60	102.09	110.88
3	A	151	PRO	N-CA-CB	5.59	108.23	103.19
3	A	224	ILE	CA-CB-CG1	-5.59	100.89	110.40
3	A	67	THR	CA-CB-OG1	5.59	117.98	109.60
3	A	193	VAL	N-CA-C	5.58	116.76	108.23
3	A	221	VAL	CB-CA-C	5.55	117.78	110.84
3	A	91	ASP	N-CA-C	5.54	122.61	110.80
3	A	219	GLN	CB-CA-C	-5.51	102.23	110.88
2	P	3	DT	P-O3'-C3'	5.50	128.46	120.20
3	A	334	SER	CB-CA-C	5.48	119.88	110.79
3	A	12	ASN	CB-CA-C	5.47	119.42	110.17
3	A	92	ASP	N-CA-C	5.46	117.69	111.02
3	A	320	PHE	N-CA-CB	5.45	117.87	109.91
1	T	7	DA	P-O5'-C5'	-5.45	111.83	120.00
3	A	261	PRO	CB-CA-C	-5.44	102.58	111.56
3	A	68	LYS	N-CA-C	5.44	120.29	111.37
3	A	303	VAL	N-CA-C	5.41	118.64	111.17
3	A	241	LEU	CA-C-N	5.39	126.58	119.84
3	A	241	LEU	C-N-CA	5.39	126.58	119.84
1	T	6	DG	P-O3'-C3'	-5.38	112.13	120.20
3	A	215	VAL	N-CA-CB	5.37	116.47	110.51
3	A	116	ASP	N-CA-CB	5.36	118.59	110.28
3	A	324	GLN	N-CA-C	5.36	119.03	111.52
3	A	101	THR	CA-CB-CG2	5.35	119.60	110.50
1	T	4	DT	P-O5'-C5'	-5.35	111.98	120.00
3	A	68	LYS	O-C-N	5.31	128.62	122.20
3	A	312	PRO	CA-C-N	5.31	130.09	123.14
3	A	312	PRO	C-N-CA	5.31	130.09	123.14
3	A	130	ASP	CA-CB-CG	5.29	117.89	112.60
3	A	210	LEU	N-CA-C	-5.28	104.78	111.11
3	A	246	ASP	N-CA-C	5.28	122.03	110.80
3	A	320	PHE	CA-C-N	5.25	127.57	120.38
3	A	320	PHE	C-N-CA	5.25	127.57	120.38
3	A	242	PRO	CB-CA-C	-5.22	102.94	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	134	HIS	CA-CB-CG	5.22	119.02	113.80
3	A	114	PHE	CA-C-O	5.20	126.46	120.90
3	A	207	GLN	CA-C-N	5.20	124.82	119.05
3	A	207	GLN	C-N-CA	5.20	124.82	119.05
3	A	321	ASP	CB-CA-C	-5.18	101.88	110.68
3	A	33	ILE	CA-C-N	5.18	127.48	120.44
3	A	33	ILE	C-N-CA	5.18	127.48	120.44
3	A	212	HIS	CA-C-N	5.17	127.52	120.54
3	A	212	HIS	C-N-CA	5.17	127.52	120.54
3	A	237	GLY	CA-C-N	5.16	130.23	122.75
3	A	237	GLY	C-N-CA	5.16	130.23	122.75
3	A	221	VAL	CA-C-O	5.15	123.85	118.96
3	A	39	TYR	N-CA-C	5.14	117.28	111.11
3	A	270	LEU	CA-C-N	5.13	127.42	120.65
3	A	270	LEU	C-N-CA	5.13	127.42	120.65
3	A	271	TYR	CA-CB-CG	-5.10	104.72	113.90
3	A	302	GLY	N-CA-C	-5.09	101.12	113.18
3	A	314	ASP	N-CA-CB	5.09	117.90	110.88
3	A	86	GLU	N-CA-CB	5.08	117.68	110.16
3	A	164	ASN	N-CA-CB	5.08	117.43	110.07
3	A	293	ILE	N-CA-C	-5.08	101.03	108.85
3	A	101	THR	CB-CA-C	5.06	119.29	110.68
3	A	248	LYS	N-CA-C	5.06	116.42	107.61
3	A	67	THR	N-CA-C	-5.06	105.04	111.11
3	A	259	LEU	N-CA-CB	5.06	118.66	110.41
3	A	121	THR	N-CA-C	5.05	117.54	109.81

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	68	LYS	CA
3	A	202	SER	CA
3	A	264	GLN	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	145	0	80	11	0
2	P	144	0	81	23	0
3	A	2623	0	2641	430	0
4	A	2	0	0	0	0
5	A	110	0	0	23	0
5	P	22	0	0	2	0
5	T	13	0	0	2	0
All	All	3059	0	2802	459	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 82.

All (459) 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)
2:P:5:DA:H2''	2:P:6:DT:H5''	1.20	1.19
3:A:82:LEU:HD23	3:A:85:LEU:HB2	1.21	1.16
2:P:6:DT:H2''	2:P:7:DG:H5''	1.17	1.12
3:A:150:ILE:HG12	3:A:253:ARG:HD3	1.34	1.05
3:A:218:LEU:HB3	3:A:224:ILE:HD12	1.37	1.05
3:A:103:VAL:HB	3:A:106:ILE:HD12	1.33	1.04
3:A:62:LEU:HD12	3:A:63:PRO:HD2	1.38	1.02
3:A:270:LEU:HD22	3:A:319:ILE:HD13	1.47	0.96
3:A:97:ILE:HG23	3:A:111:ALA:HB1	1.47	0.96
3:A:245:ASN:H	3:A:245:ASN:ND2	1.66	0.93
3:A:177:VAL:HG11	3:A:191:MET:HE2	1.50	0.93
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.49	0.92
3:A:245:ASN:HD22	3:A:245:ASN:N	1.65	0.91
3:A:155:MET:HE2	3:A:188:SER:HB2	1.52	0.91
3:A:311:LEU:HB3	3:A:322:TYR:HE2	1.36	0.90
3:A:243:SER:HB3	3:A:249:GLU:HA	1.51	0.90
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.12	0.89
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.07	0.88
3:A:218:LEU:CB	3:A:224:ILE:HD12	2.04	0.88
3:A:18:MET:CE	3:A:76:PHE:HB2	2.04	0.87
3:A:201:THR:HA	3:A:261:PRO:HB3	1.55	0.86
3:A:328:ARG:HB2	3:A:333:ARG:HD3	1.56	0.84
3:A:201:THR:HA	3:A:261:PRO:CA	2.07	0.84
3:A:245:ASN:H	3:A:245:ASN:HD22	0.87	0.84
1:T:6:DG:H2''	1:T:7:DA:C8	2.12	0.83
3:A:103:VAL:CB	3:A:106:ILE:HD12	2.08	0.83
3:A:128:ASN:N	3:A:128:ASN:ND2	2.27	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.25	0.83
3:A:150:ILE:CG1	3:A:253:ARG:HD3	2.09	0.83
2:P:5:DA:C2'	2:P:6:DT:H5''	2.05	0.83
3:A:311:LEU:HB3	3:A:322:TYR:CE2	2.14	0.82
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.61	0.82
3:A:68:LYS:HB2	3:A:68:LYS:NZ	1.95	0.82
3:A:201:THR:HA	3:A:261:PRO:CB	2.08	0.82
3:A:82:LEU:CD2	3:A:85:LEU:HB2	2.07	0.82
3:A:243:SER:CB	3:A:249:GLU:HA	2.09	0.82
2:P:6:DT:H2''	2:P:7:DG:C5'	2.08	0.81
3:A:278:PHE:CE1	3:A:328:ARG:HD3	2.15	0.81
3:A:29:VAL:HG22	3:A:97:ILE:HD12	1.61	0.80
3:A:138:ILE:HD12	3:A:228:LEU:HD12	1.63	0.80
3:A:82:LEU:HD23	3:A:85:LEU:CB	2.08	0.80
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.62	0.80
3:A:180:SER:HA	3:A:183:ARG:HH21	1.44	0.80
3:A:254:ARG:NH1	3:A:255:ILE:N	2.29	0.80
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.62	0.79
3:A:323:ILE:O	3:A:324:GLN:HG2	1.82	0.79
3:A:138:ILE:HD12	3:A:228:LEU:CD1	2.13	0.78
3:A:328:ARG:HB2	3:A:333:ARG:CD	2.13	0.78
3:A:174:ILE:O	3:A:195:LEU:HD12	1.83	0.78
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.63	0.78
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.13	0.78
3:A:121:THR:HG23	3:A:124:ASP:OD1	1.83	0.78
3:A:97:ILE:HD13	3:A:112:ARG:HG2	1.64	0.78
3:A:62:LEU:CD1	3:A:63:PRO:HD2	2.13	0.77
3:A:49:TYR:CE2	3:A:51:HIS:HB2	2.19	0.77
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.68	0.76
3:A:266:TYR:O	3:A:270:LEU:HB2	1.86	0.76
3:A:165:GLU:HA	3:A:168:LYS:HG2	1.68	0.75
3:A:282:MET:HE3	5:A:555:HOH:O	1.86	0.75
3:A:300:PRO:HD2	3:A:308:GLY:O	1.87	0.74
3:A:81:LYS:NZ	3:A:86:GLU:HB2	2.02	0.74
3:A:286:ALA:HB1	3:A:293:ILE:HD11	1.70	0.74
3:A:18:MET:O	3:A:21:GLU:HB2	1.88	0.74
3:A:11:LEU:HD23	3:A:11:LEU:H	1.52	0.74
3:A:179:GLY:O	3:A:182:ARG:HB3	1.88	0.73
3:A:320:PHE:CE2	3:A:328:ARG:HG3	2.24	0.73
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.70	0.73
3:A:41:LYS:O	3:A:44:SER:HB3	1.87	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:211:LEU:O	3:A:214:VAL:HG22	1.89	0.72
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.25	0.72
2:P:5:DA:H2''	2:P:6:DT:C5'	2.12	0.72
3:A:128:ASN:N	3:A:128:ASN:HD22	1.87	0.72
3:A:177:VAL:CG1	3:A:191:MET:HE2	2.20	0.72
3:A:330:PRO:HA	3:A:333:ARG:CG	2.19	0.72
3:A:200:PHE:CE2	3:A:261:PRO:HD3	2.25	0.71
3:A:328:ARG:HB2	3:A:333:ARG:NE	2.05	0.71
3:A:306:VAL:HG22	5:A:650:HOH:O	1.90	0.71
3:A:146:PHE:HZ	3:A:238:VAL:HG22	1.54	0.71
3:A:18:MET:HE3	3:A:76:PHE:HB2	1.73	0.71
3:A:277:ILE:HD11	3:A:335:GLU:HB3	1.71	0.71
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.88	0.71
3:A:201:THR:HA	3:A:261:PRO:HA	1.71	0.70
3:A:141:LYS:HE2	3:A:142:TYR:OH	1.90	0.70
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.19	0.70
3:A:211:LEU:O	3:A:211:LEU:HD12	1.92	0.70
1:T:4:DT:H1'	5:T:527:HOH:O	1.92	0.70
3:A:92:ASP:HB3	5:A:647:HOH:O	1.91	0.70
3:A:267:CYS:HB3	5:A:592:HOH:O	1.91	0.69
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.07	0.69
3:A:208:PRO:HB3	3:A:232:GLU:HB2	1.73	0.69
3:A:285:HIS:NE2	3:A:289:LYS:HG2	2.06	0.69
3:A:328:ARG:HB2	3:A:333:ARG:HE	1.58	0.69
3:A:165:GLU:HB3	3:A:217:GLN:CG	2.23	0.69
3:A:328:ARG:O	3:A:333:ARG:NE	2.26	0.68
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.24	0.68
3:A:73:ILE:HG22	3:A:77:LEU:CD2	2.24	0.68
3:A:73:ILE:O	3:A:77:LEU:HD22	1.94	0.67
3:A:262:LYS:O	3:A:262:LYS:HG3	1.94	0.67
3:A:25:PHE:CE2	3:A:88:ILE:HG12	2.30	0.67
3:A:243:SER:HB2	5:A:636:HOH:O	1.94	0.66
3:A:240:GLN:NE2	3:A:250:TYR:O	2.28	0.66
3:A:22:LEU:HD22	3:A:85:LEU:HD13	1.76	0.66
3:A:93:THR:O	3:A:96:SER:HB2	1.96	0.66
3:A:193:VAL:HB	3:A:257:ILE:HG23	1.76	0.66
3:A:124:ASP:O	3:A:128:ASN:ND2	2.28	0.66
3:A:141:LYS:HE2	3:A:142:TYR:CZ	2.31	0.66
3:A:195:LEU:O	3:A:259:LEU:HD12	1.94	0.66
3:A:220:LYS:O	3:A:220:LYS:HG2	1.96	0.66
3:A:327:TYR:HD1	3:A:328:ARG:N	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:294:ASN:O	3:A:296:TYR:N	2.29	0.66
3:A:152:ARG:HB2	5:A:530:HOH:O	1.94	0.65
3:A:194:LEU:HD21	3:A:272:PHE:HD2	1.61	0.65
1:T:6:DG:N7	5:T:652:HOH:O	2.30	0.65
3:A:41:LYS:C	3:A:44:SER:HB3	2.21	0.65
3:A:46:ILE:HD12	3:A:46:ILE:C	2.22	0.65
3:A:159:GLN:O	3:A:163:LEU:HG	1.95	0.65
3:A:41:LYS:NZ	3:A:64:GLY:O	2.30	0.65
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.78	0.64
3:A:157:GLN:HG3	3:A:241:LEU:HD13	1.79	0.64
3:A:270:LEU:HD13	3:A:316:GLU:HG2	1.78	0.64
3:A:79:THR:O	3:A:81:LYS:N	2.30	0.64
3:A:12:ASN:ND2	5:A:642:HOH:O	2.31	0.64
3:A:278:PHE:HB2	3:A:333:ARG:O	1.98	0.64
3:A:285:HIS:NE2	5:A:583:HOH:O	2.30	0.64
3:A:81:LYS:HZ2	3:A:86:GLU:HB2	1.61	0.64
3:A:309:GLU:N	3:A:309:GLU:OE1	2.31	0.64
3:A:114:PHE:CZ	3:A:132:LEU:HD23	2.33	0.63
3:A:180:SER:CA	3:A:183:ARG:HH21	2.10	0.63
3:A:288:GLU:C	3:A:290:GLY:H	2.06	0.63
3:A:270:LEU:HD22	3:A:319:ILE:CD1	2.24	0.63
3:A:108:PRO:O	3:A:112:ARG:HG3	1.99	0.63
3:A:286:ALA:O	3:A:291:PHE:N	2.29	0.63
3:A:15:ILE:CG2	3:A:46:ILE:HD11	2.29	0.63
1:T:3:DT:H2'	1:T:4:DT:H71	1.79	0.62
3:A:36:TYR:O	3:A:40:ARG:HG2	1.99	0.62
3:A:150:ILE:HG12	3:A:253:ARG:CD	2.19	0.62
3:A:68:LYS:HB2	3:A:68:LYS:HZ3	1.64	0.62
3:A:83:ARG:O	3:A:86:GLU:N	2.32	0.62
3:A:217:GLN:NE2	3:A:217:GLN:HA	2.14	0.62
3:A:22:LEU:HD22	3:A:85:LEU:CD1	2.30	0.62
3:A:254:ARG:NH1	3:A:255:ILE:H	1.95	0.62
3:A:22:LEU:CD2	3:A:85:LEU:HD13	2.30	0.62
3:A:128:ASN:HD22	3:A:128:ASN:H	1.48	0.62
3:A:56:GLY:O	3:A:59:ALA:N	2.33	0.62
3:A:169:VAL:HG13	3:A:170:ASP:N	2.15	0.61
3:A:254:ARG:NH1	3:A:254:ARG:HB3	2.15	0.61
3:A:120:LYS:N	3:A:124:ASP:OD2	2.24	0.61
3:A:201:THR:OG1	3:A:202:SER:N	2.31	0.61
3:A:45:VAL:HG21	3:A:63:PRO:O	2.01	0.61
3:A:174:ILE:HD12	3:A:196:THR:CG2	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:135:HIS:O	3:A:138:ILE:HB	2.01	0.61
3:A:214:VAL:HG23	3:A:215:VAL:N	2.16	0.61
3:A:288:GLU:O	3:A:290:GLY:N	2.34	0.61
3:A:289:LYS:HD3	3:A:289:LYS:N	2.08	0.60
3:A:152:ARG:HA	3:A:155:MET:HB2	1.83	0.60
3:A:133:ASN:O	3:A:137:ARG:HG3	2.02	0.60
3:A:284:ALA:O	3:A:287:LEU:HB2	2.02	0.60
3:A:157:GLN:HE22	3:A:244:LYS:HZ1	1.50	0.60
3:A:200:PHE:O	3:A:261:PRO:HA	2.01	0.60
3:A:76:PHE:HD2	3:A:77:LEU:HD13	1.66	0.60
3:A:205:THR:HA	5:A:624:HOH:O	2.00	0.60
3:A:264:GLN:NE2	3:A:296:TYR:HB3	2.16	0.60
3:A:266:TYR:HB2	3:A:313:VAL:CG1	2.31	0.60
3:A:201:THR:CA	3:A:261:PRO:HB3	2.28	0.60
3:A:121:THR:H	3:A:124:ASP:CG	2.09	0.60
3:A:11:LEU:HD23	3:A:11:LEU:N	2.17	0.59
2:P:5:DA:H1'	5:A:565:HOH:O	2.00	0.59
3:A:320:PHE:HE2	3:A:328:ARG:HG3	1.67	0.59
3:A:29:VAL:HG21	3:A:94:SER:HA	1.84	0.59
3:A:244:LYS:C	3:A:246:ASP:H	2.10	0.59
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.37	0.59
1:T:1:DC:H2''	1:T:2:DA:OP2	2.02	0.59
3:A:82:LEU:HD23	3:A:85:LEU:HD22	1.84	0.59
3:A:15:ILE:HG22	3:A:19:LEU:HD22	1.85	0.58
3:A:49:TYR:CG	3:A:50:PRO:HD2	2.38	0.58
3:A:176:THR:HA	5:A:618:HOH:O	2.02	0.58
2:P:5:DA:OP2	3:A:109:SER:HB3	2.03	0.58
3:A:259:LEU:C	3:A:260:ILE:HG12	2.28	0.58
3:A:259:LEU:HD12	3:A:260:ILE:H	1.67	0.58
3:A:157:GLN:O	3:A:161:ILE:HG13	2.04	0.57
3:A:277:ILE:CG1	3:A:335:GLU:HB2	2.33	0.57
1:T:3:DT:C2'	1:T:4:DT:H71	2.34	0.57
3:A:81:LYS:HZ2	3:A:86:GLU:CB	2.17	0.57
3:A:236:MET:HG3	3:A:256:ASP:OD1	2.05	0.57
3:A:277:ILE:HG13	3:A:335:GLU:HB2	1.86	0.57
3:A:97:ILE:HG23	3:A:111:ALA:CB	2.30	0.57
2:P:1:DT:H2''	2:P:2:DC:C5'	2.34	0.57
1:T:4:DT:H2''	1:T:5:DA:C8	2.39	0.57
2:P:1:DT:H2''	2:P:2:DC:O4'	2.05	0.57
3:A:69:ILE:O	3:A:73:ILE:HG13	2.04	0.57
3:A:211:LEU:HD23	3:A:231:GLY:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:292:THR:O	3:A:298:ILE:HA	2.03	0.57
3:A:254:ARG:HH11	3:A:255:ILE:N	2.02	0.57
3:A:31:GLN:N	5:A:641:HOH:O	2.29	0.57
3:A:145:ASP:HB3	3:A:252:HIS:O	2.04	0.57
3:A:29:VAL:HG21	3:A:94:SER:CB	2.35	0.56
3:A:182:ARG:HG2	3:A:182:ARG:HH11	1.69	0.56
3:A:194:LEU:HD21	3:A:272:PHE:CD2	2.38	0.56
3:A:295:GLU:OE1	3:A:295:GLU:N	2.26	0.56
3:A:177:VAL:HG11	3:A:191:MET:CE	2.29	0.56
3:A:251:PRO:HG2	3:A:253:ARG:NH2	2.20	0.56
3:A:323:ILE:C	3:A:324:GLN:HG2	2.30	0.56
3:A:157:GLN:HE22	3:A:244:LYS:NZ	2.04	0.56
3:A:133:ASN:ND2	3:A:135:HIS:H	2.03	0.56
3:A:181:PHE:HD1	5:A:530:HOH:O	1.89	0.56
3:A:295:GLU:HA	5:A:592:HOH:O	2.05	0.56
3:A:253:ARG:NH1	5:A:503:HOH:O	2.38	0.56
3:A:151:PRO:HB2	3:A:153:GLU:HG2	1.88	0.56
3:A:218:LEU:O	3:A:221:VAL:HG22	2.06	0.56
2:P:6:DT:C2'	2:P:7:DG:H5''	2.12	0.55
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.41	0.55
3:A:249:GLU:HG3	3:A:250:TYR:N	2.21	0.55
3:A:76:PHE:HD2	3:A:77:LEU:CD1	2.20	0.55
3:A:180:SER:HA	3:A:183:ARG:NH2	2.19	0.55
3:A:52:LYS:HG2	5:A:642:HOH:O	2.07	0.55
3:A:254:ARG:HH12	3:A:255:ILE:N	2.04	0.55
3:A:311:LEU:HD13	3:A:311:LEU:N	2.22	0.55
3:A:73:ILE:HG22	3:A:77:LEU:HD22	1.88	0.55
3:A:142:TYR:CE1	3:A:252:HIS:CG	2.94	0.55
3:A:25:PHE:CD2	3:A:88:ILE:HG12	2.42	0.55
3:A:237:GLY:O	3:A:254:ARG:NH1	2.40	0.55
3:A:328:ARG:CB	3:A:333:ARG:HD3	2.32	0.54
3:A:165:GLU:CB	3:A:217:GLN:HG3	2.36	0.54
3:A:217:GLN:HA	3:A:217:GLN:HE21	1.71	0.54
3:A:49:TYR:CZ	3:A:51:HIS:HD2	2.25	0.54
2:P:1:DT:H2''	2:P:2:DC:H5'	1.89	0.54
3:A:201:THR:OG1	3:A:263:ASP:HB3	2.08	0.54
3:A:260:ILE:HG22	3:A:261:PRO:N	2.22	0.54
3:A:182:ARG:HH11	3:A:182:ARG:CG	2.19	0.54
3:A:254:ARG:HH11	3:A:254:ARG:CA	2.20	0.54
3:A:123:GLU:HG3	5:A:623:HOH:O	2.08	0.53
3:A:169:VAL:HG13	3:A:170:ASP:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:111:ALA:O	3:A:115:VAL:HG23	2.08	0.53
3:A:119:ILE:CG2	3:A:124:ASP:HB3	2.39	0.53
3:A:138:ILE:HG21	3:A:228:LEU:HD11	1.88	0.53
3:A:191:MET:HG2	3:A:255:ILE:CG1	2.36	0.53
3:A:249:GLU:HG3	3:A:250:TYR:H	1.72	0.53
3:A:200:PHE:CZ	3:A:261:PRO:HD3	2.43	0.53
3:A:49:TYR:OH	3:A:51:HIS:HD2	1.90	0.53
3:A:76:PHE:HA	3:A:81:LYS:O	2.08	0.53
3:A:196:THR:OG1	3:A:260:ILE:O	2.26	0.53
3:A:49:TYR:CZ	3:A:51:HIS:CD2	2.96	0.53
3:A:18:MET:HE2	3:A:82:LEU:HD22	1.91	0.53
3:A:278:PHE:HE1	3:A:328:ARG:HD3	1.71	0.53
3:A:34:HIS:O	3:A:38:ALA:N	2.37	0.52
3:A:266:TYR:HB2	3:A:313:VAL:HG11	1.90	0.52
3:A:278:PHE:CZ	3:A:328:ARG:HD3	2.45	0.52
3:A:151:PRO:HD2	3:A:154:GLU:OE1	2.10	0.52
3:A:285:HIS:CE1	3:A:289:LYS:HG2	2.45	0.52
3:A:211:LEU:HD12	3:A:211:LEU:C	2.34	0.52
3:A:254:ARG:HB3	3:A:254:ARG:CZ	2.40	0.52
3:A:201:THR:HB	3:A:263:ASP:H	1.75	0.52
3:A:302:GLY:N	3:A:307:ALA:HB2	2.25	0.52
3:A:182:ARG:HH12	3:A:273:THR:HG21	1.75	0.51
3:A:107:GLY:O	3:A:111:ALA:HB2	2.10	0.51
3:A:172:GLU:HG2	3:A:198:PRO:HG2	1.93	0.51
3:A:165:GLU:CD	3:A:168:LYS:HD3	2.36	0.51
3:A:165:GLU:HA	3:A:168:LYS:CG	2.39	0.51
3:A:332:ASP:OD1	3:A:332:ASP:O	2.29	0.50
3:A:180:SER:O	3:A:183:ARG:HB2	2.12	0.50
3:A:79:THR:C	3:A:81:LYS:H	2.19	0.50
3:A:200:PHE:HB2	3:A:210:LEU:CD1	2.42	0.50
3:A:265:TYR:O	3:A:268:GLY:N	2.44	0.50
3:A:275:SER:OG	3:A:334:SER:O	2.30	0.50
3:A:15:ILE:HD13	3:A:73:ILE:HD13	1.93	0.50
3:A:68:LYS:HB2	3:A:68:LYS:HZ2	1.76	0.50
3:A:114:PHE:HZ	3:A:132:LEU:HD23	1.75	0.50
3:A:29:VAL:HG21	3:A:94:SER:CA	2.41	0.50
3:A:317:LYS:NZ	3:A:321:ASP:OD1	2.39	0.50
3:A:119:ILE:HA	3:A:124:ASP:HB3	1.94	0.50
3:A:212:HIS:N	3:A:212:HIS:CD2	2.76	0.49
3:A:243:SER:OG	3:A:249:GLU:HA	2.12	0.49
2:P:6:DT:C2'	2:P:7:DG:C8	2.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:292:THR:C	3:A:293:ILE:HD13	2.38	0.49
2:P:6:DT:C4	2:P:7:DG:C6	3.00	0.49
3:A:142:TYR:CZ	3:A:252:HIS:CD2	2.99	0.49
3:A:183:ARG:HH11	3:A:275:SER:CA	2.26	0.49
3:A:271:TYR:CE1	3:A:283:ARG:NH2	2.80	0.49
3:A:316:GLU:O	3:A:320:PHE:HD1	1.94	0.49
3:A:81:LYS:HZ3	3:A:86:GLU:HB2	1.77	0.49
3:A:191:MET:HA	5:A:502:HOH:O	2.12	0.49
3:A:259:LEU:CD1	3:A:260:ILE:H	2.24	0.49
3:A:306:VAL:HG23	3:A:307:ALA:N	2.28	0.49
3:A:42:ALA:O	3:A:46:ILE:HG23	2.12	0.49
3:A:16:THR:O	3:A:20:THR:HG23	2.13	0.49
3:A:166:VAL:O	3:A:169:VAL:HG12	2.13	0.49
3:A:243:SER:OG	3:A:249:GLU:HG3	2.13	0.49
3:A:311:LEU:HD12	3:A:311:LEU:HA	1.59	0.48
3:A:31:GLN:HE21	3:A:112:ARG:NH1	2.05	0.48
3:A:43:ALA:O	3:A:47:ALA:HB2	2.12	0.48
3:A:19:LEU:CB	3:A:43:ALA:HB2	2.41	0.48
3:A:46:ILE:HD12	3:A:46:ILE:O	2.13	0.48
3:A:59:ALA:O	3:A:62:LEU:HB2	2.13	0.48
3:A:82:LEU:CD2	3:A:85:LEU:HD22	2.42	0.48
3:A:183:ARG:HH11	3:A:275:SER:CB	2.27	0.48
3:A:49:TYR:HE2	3:A:51:HIS:HB2	1.73	0.48
3:A:182:ARG:NH1	3:A:182:ARG:HG2	2.29	0.48
3:A:253:ARG:NH2	5:A:620:HOH:O	2.40	0.48
3:A:218:LEU:HD23	3:A:224:ILE:HD11	1.95	0.48
3:A:11:LEU:H	3:A:11:LEU:CD2	2.23	0.48
3:A:180:SER:CB	3:A:183:ARG:HH21	2.27	0.48
3:A:259:LEU:HD12	3:A:260:ILE:N	2.29	0.48
1:T:4:DT:O2	2:P:4:DA:H2	1.97	0.48
3:A:133:ASN:HD22	3:A:134:HIS:N	2.12	0.48
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.94	0.48
3:A:15:ILE:HG21	3:A:46:ILE:CD1	2.44	0.47
3:A:203:GLU:CD	3:A:203:GLU:H	2.22	0.47
3:A:81:LYS:HB3	3:A:82:LEU:H	1.35	0.47
3:A:121:THR:HG23	3:A:124:ASP:CG	2.39	0.47
3:A:155:MET:SD	3:A:158:MET:HE1	2.54	0.47
3:A:146:PHE:CE2	3:A:254:ARG:HD3	2.50	0.47
3:A:183:ARG:NH1	3:A:275:SER:HA	2.30	0.47
3:A:99:PHE:O	3:A:102:ARG:HG3	2.15	0.47
3:A:204:SER:O	3:A:206:LYS:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:40:ARG:O	3:A:44:SER:HB2	2.14	0.47
3:A:207:GLN:O	3:A:210:LEU:HB2	2.15	0.47
3:A:243:SER:HB3	3:A:249:GLU:HB2	1.95	0.47
3:A:49:TYR:HA	3:A:50:PRO:HD3	1.55	0.47
3:A:270:LEU:CD2	3:A:319:ILE:HD13	2.32	0.47
3:A:327:TYR:CD1	3:A:328:ARG:N	2.78	0.47
2:P:5:DA:P	3:A:109:SER:HB3	2.55	0.47
3:A:75:GLU:OE2	3:A:82:LEU:HA	2.15	0.47
3:A:180:SER:N	5:A:631:HOH:O	2.48	0.47
3:A:295:GLU:H	3:A:295:GLU:CD	2.20	0.47
1:T:6:DG:O6	2:P:2:DC:N3	2.47	0.47
3:A:121:THR:O	3:A:124:ASP:HB2	2.14	0.47
2:P:1:DT:H2'	2:P:2:DC:C6	2.51	0.46
3:A:200:PHE:C	3:A:201:THR:HG22	2.40	0.46
3:A:269:VAL:HG12	3:A:270:LEU:N	2.29	0.46
3:A:302:GLY:C	3:A:304:THR:HG23	2.40	0.46
3:A:309:GLU:HA	3:A:310:PRO:HD2	1.75	0.46
3:A:35:LYS:O	3:A:38:ALA:HB3	2.15	0.46
3:A:112:ARG:O	3:A:115:VAL:HB	2.15	0.46
3:A:174:ILE:HD12	3:A:196:THR:HG23	1.97	0.46
3:A:243:SER:CB	3:A:249:GLU:HB2	2.46	0.46
3:A:169:VAL:CG1	3:A:170:ASP:N	2.77	0.46
3:A:158:MET:HG3	3:A:241:LEU:HD21	1.98	0.46
3:A:293:ILE:HD12	3:A:298:ILE:HG13	1.94	0.46
3:A:114:PHE:CZ	3:A:132:LEU:CD2	2.98	0.46
3:A:169:VAL:CG1	3:A:170:ASP:H	2.28	0.46
3:A:196:THR:OG1	3:A:262:LYS:HA	2.16	0.46
3:A:271:TYR:CD2	3:A:272:PHE:N	2.84	0.46
2:P:4:DA:H5'	5:P:569:HOH:O	2.14	0.46
3:A:41:LYS:HD3	3:A:42:ALA:N	2.30	0.46
3:A:215:VAL:HG12	3:A:219:GLN:OE1	2.15	0.46
3:A:194:LEU:N	3:A:194:LEU:CD1	2.79	0.46
3:A:243:SER:HB3	3:A:249:GLU:CA	2.35	0.46
3:A:259:LEU:O	3:A:260:ILE:HD13	2.16	0.46
3:A:28:ASN:ND2	3:A:108:PRO:HG3	2.30	0.46
3:A:298:ILE:N	5:A:578:HOH:O	2.49	0.46
3:A:59:ALA:O	3:A:62:LEU:N	2.29	0.45
3:A:266:TYR:HB2	3:A:313:VAL:HG12	1.98	0.45
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.45	0.45
3:A:261:PRO:O	3:A:264:GLN:N	2.32	0.45
3:A:52:LYS:O	3:A:58:GLU:OE2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:297:THR:HA	5:A:578:HOH:O	2.16	0.45
3:A:235:PHE:CD1	3:A:235:PHE:C	2.95	0.45
3:A:311:LEU:N	3:A:311:LEU:CD1	2.78	0.45
1:T:1:DC:H6	1:T:1:DC:H2'	1.37	0.45
3:A:295:GLU:HG2	3:A:296:TYR:CZ	2.52	0.45
3:A:331:LYS:HG2	3:A:332:ASP:N	2.25	0.45
3:A:88:ILE:HG22	3:A:89:ARG:N	2.29	0.45
3:A:149:ARG:HD2	3:A:149:ARG:HA	1.76	0.45
3:A:193:VAL:C	3:A:194:LEU:HD12	2.42	0.45
3:A:309:GLU:O	3:A:311:LEU:HD13	2.17	0.45
3:A:254:ARG:NH1	3:A:254:ARG:CB	2.80	0.44
3:A:259:LEU:HD12	3:A:259:LEU:HA	1.54	0.44
1:T:2:DA:H2''	1:T:3:DT:OP2	2.18	0.44
3:A:182:ARG:NH1	3:A:273:THR:CG2	2.77	0.44
3:A:42:ALA:C	3:A:44:SER:H	2.22	0.44
3:A:125:LEU:HD22	3:A:132:LEU:HD21	1.98	0.44
3:A:269:VAL:HG12	3:A:316:GLU:OE2	2.18	0.44
3:A:71:GLU:O	3:A:71:GLU:HG3	2.18	0.44
3:A:28:ASN:HD22	3:A:28:ASN:HA	1.15	0.44
3:A:200:PHE:CE2	3:A:261:PRO:CD	2.98	0.44
3:A:18:MET:HG2	3:A:19:LEU:N	2.24	0.44
3:A:254:ARG:HH11	3:A:255:ILE:H	1.62	0.44
3:A:214:VAL:CG2	3:A:215:VAL:N	2.80	0.44
3:A:288:GLU:OE2	3:A:288:GLU:N	2.50	0.44
3:A:233:THR:O	3:A:259:LEU:N	2.43	0.43
3:A:79:THR:O	3:A:79:THR:OG1	2.34	0.43
3:A:289:LYS:HD3	3:A:289:LYS:HA	1.34	0.43
3:A:76:PHE:CD2	3:A:77:LEU:HD13	2.49	0.43
3:A:197:HIS:CE1	3:A:199:SER:HB3	2.52	0.43
3:A:320:PHE:HE2	3:A:328:ARG:CG	2.29	0.43
2:P:6:DT:H2''	2:P:7:DG:C8	2.53	0.43
3:A:12:ASN:HD22	3:A:12:ASN:HA	1.78	0.43
3:A:58:GLU:O	3:A:61:LYS:HG3	2.18	0.43
3:A:82:LEU:HD23	3:A:85:LEU:CD2	2.48	0.43
3:A:330:PRO:HA	3:A:333:ARG:HG2	1.99	0.43
2:P:5:DA:O5'	3:A:107:GLY:HA3	2.18	0.43
3:A:52:LYS:HD3	3:A:54:LYS:HE3	2.01	0.43
3:A:202:SER:N	3:A:263:ASP:OD1	2.34	0.43
3:A:210:LEU:HB3	3:A:259:LEU:HD21	2.00	0.43
3:A:53:ILE:O	3:A:54:LYS:HD2	2.19	0.43
3:A:289:LYS:HG3	3:A:323:ILE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:1:DT:H73	5:P:571:HOH:O	2.19	0.43
3:A:287:LEU:HB3	3:A:288:GLU:OE2	2.19	0.43
3:A:22:LEU:HD13	3:A:22:LEU:HA	1.75	0.42
3:A:183:ARG:HH11	3:A:275:SER:HA	1.84	0.42
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.48	0.42
3:A:99:PHE:CD2	3:A:99:PHE:C	2.94	0.42
3:A:38:ALA:O	3:A:41:LYS:HD3	2.20	0.42
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.72	0.42
3:A:285:HIS:NE2	3:A:289:LYS:CG	2.79	0.42
3:A:299:ARG:HG2	3:A:310:PRO:N	2.33	0.42
3:A:29:VAL:HG11	3:A:94:SER:HB2	2.01	0.42
3:A:152:ARG:NH2	3:A:181:PHE:O	2.44	0.42
3:A:326:LYS:O	3:A:326:LYS:HG3	2.19	0.42
3:A:33:ILE:O	3:A:36:TYR:HD2	2.02	0.42
3:A:200:PHE:HB2	5:A:625:HOH:O	2.20	0.42
3:A:19:LEU:O	3:A:22:LEU:HB2	2.20	0.42
3:A:108:PRO:O	3:A:111:ALA:HB3	2.20	0.42
3:A:119:ILE:HG22	3:A:124:ASP:HB3	2.01	0.42
3:A:150:ILE:CD1	3:A:253:ARG:HD3	2.50	0.42
3:A:259:LEU:CG	3:A:260:ILE:N	2.83	0.42
3:A:202:SER:OG	3:A:263:ASP:OD1	2.30	0.42
3:A:207:GLN:OE1	3:A:210:LEU:HD11	2.20	0.42
3:A:101:THR:C	3:A:103:VAL:H	2.28	0.41
3:A:294:ASN:C	3:A:296:TYR:H	2.28	0.41
3:A:158:MET:HB2	3:A:158:MET:HE3	1.64	0.41
3:A:261:PRO:C	3:A:263:ASP:N	2.79	0.41
2:P:6:DT:C5'	2:P:6:DT:H6	2.33	0.41
3:A:53:ILE:C	3:A:54:LYS:HD2	2.46	0.41
3:A:191:MET:HE3	3:A:191:MET:HB2	1.85	0.41
3:A:219:GLN:O	3:A:222:HIS:N	2.47	0.41
3:A:243:SER:HB3	3:A:249:GLU:CB	2.51	0.41
3:A:282:MET:HA	3:A:325:TRP:CH2	2.56	0.41
3:A:299:ARG:HA	3:A:300:PRO:HD3	1.87	0.41
3:A:127:LYS:C	3:A:128:ASN:ND2	2.78	0.41
3:A:200:PHE:CD2	3:A:260:ILE:C	2.99	0.41
3:A:201:THR:C	3:A:261:PRO:HB3	2.45	0.41
3:A:119:ILE:H	3:A:119:ILE:HG12	1.41	0.41
3:A:155:MET:SD	3:A:158:MET:CE	3.08	0.41
2:P:6:DT:H2'	2:P:7:DG:C8	2.56	0.41
3:A:125:LEU:HD22	3:A:132:LEU:HD11	2.03	0.41
3:A:265:TYR:HD2	3:A:266:TYR:CE1	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:278:PHE:CZ	3:A:333:ARG:HD2	2.55	0.41
3:A:327:TYR:HD1	3:A:327:TYR:C	2.28	0.41
3:A:54:LYS:HD2	3:A:54:LYS:HA	1.69	0.41
3:A:209:LYS:HA	3:A:212:HIS:HB2	2.02	0.41
3:A:327:TYR:CD1	3:A:327:TYR:C	2.97	0.41
3:A:62:LEU:HD13	3:A:62:LEU:HA	1.88	0.41
3:A:150:ILE:N	3:A:188:SER:O	2.54	0.41
3:A:212:HIS:CD2	3:A:212:HIS:H	2.38	0.41
3:A:230:LYS:HE2	3:A:230:LYS:HB3	1.96	0.41
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.44	0.41
3:A:25:PHE:CD1	3:A:25:PHE:C	2.98	0.40
3:A:125:LEU:HD23	3:A:125:LEU:HA	1.71	0.40
3:A:320:PHE:CE2	3:A:328:ARG:CG	2.97	0.40
3:A:101:THR:C	3:A:103:VAL:N	2.79	0.40
3:A:126:ARG:C	3:A:128:ASN:N	2.79	0.40
3:A:183:ARG:HH11	3:A:275:SER:HB3	1.85	0.40
3:A:244:LYS:C	3:A:246:ASP:N	2.78	0.40
3:A:127:LYS:HD2	3:A:127:LYS:N	2.36	0.40
3:A:287:LEU:HA	3:A:287:LEU:HD13	1.65	0.40
3:A:62:LEU:HB2	3:A:65:VAL:HG21	2.04	0.40
3:A:301:LEU:HA	3:A:307:ALA:HB3	2.04	0.40
3:A:311:LEU:CB	3:A:322:TYR:HE2	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	325/335 (97%)	257 (79%)	43 (13%)	25 (8%)	1 8

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	32	ALA
3	A	202	SER
3	A	205	THR
3	A	244	LYS
3	A	245	ASN
3	A	265	TYR
3	A	266	TYR
3	A	289	LYS
3	A	295	GLU
3	A	13	GLY
3	A	80	GLY
3	A	91	ASP
3	A	204	SER
3	A	206	LYS
3	A	222	HIS
3	A	28	ASN
3	A	102	ARG
3	A	304	THR
3	A	60	LYS
3	A	78	ALA
3	A	220	LYS
3	A	242	PRO
3	A	207	GLN
3	A	33	ILE
3	A	310	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
3	A	288/295 (98%)	211 (73%)	77 (27%)	0 3

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	10	THR
3	A	18	MET

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Mol	Chain	Res	Type
3	A	19	LEU
3	A	22	LEU
3	A	25	PHE
3	A	27	LYS
3	A	30	SER
3	A	37	ASN
3	A	41	LYS
3	A	46	ILE
3	A	54	LYS
3	A	62	LEU
3	A	67	THR
3	A	68	LYS
3	A	73	ILE
3	A	77	LEU
3	A	81	LYS
3	A	86	GLU
3	A	89	ARG
3	A	92	ASP
3	A	100	LEU
3	A	101	THR
3	A	113	LYS
3	A	119	ILE
3	A	121	THR
3	A	128	ASN
3	A	133	ASN
3	A	136	GLN
3	A	138	ILE
3	A	153	GLU
3	A	155	MET
3	A	159	GLN
3	A	161	ILE
3	A	168	LYS
3	A	174	ILE
3	A	177	VAL
3	A	182	ARG
3	A	183	ARG
3	A	188	SER
3	A	191	MET
3	A	193	VAL
3	A	194	LEU
3	A	199	SER
3	A	201	THR

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Mol	Chain	Res	Type
3	A	203	GLU
3	A	219	GLN
3	A	220	LYS
3	A	228	LEU
3	A	230	LYS
3	A	233	THR
3	A	245	ASN
3	A	248	LYS
3	A	255	ILE
3	A	257	ILE
3	A	262	LYS
3	A	263	ASP
3	A	264	GLN
3	A	269	VAL
3	A	277	ILE
3	A	287	LEU
3	A	288	GLU
3	A	289	LYS
3	A	293	ILE
3	A	294	ASN
3	A	297	THR
3	A	298	ILE
3	A	301	LEU
3	A	304	THR
3	A	306	VAL
3	A	309	GLU
3	A	311	LEU
3	A	324	GLN
3	A	325	TRP
3	A	327	TYR
3	A	329	GLU
3	A	331	LYS
3	A	335	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) 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	51	HIS

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Mol	Chain	Res	Type
3	A	128	ASN
3	A	133	ASN
3	A	136	GLN
3	A	157	GLN
3	A	213	GLN
3	A	217	GLN
3	A	240	GLN
3	A	245	ASN
3	A	264	GLN
3	A	279	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 ⓘ

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	8/8 (100%)	-0.54	0 100 100	24, 39, 81, 98	0
2	P	7/7 (100%)	-0.52	0 100 100	15, 24, 41, 73	0
3	A	325/335 (97%)	-0.86	0 100 100	2, 30, 80, 100	0
All	All	340/350 (97%)	-0.85	0 100 100	2, 30, 82, 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	CA	A	342	1/1	0.97	0.04	66,66,66,66	0
4	CA	A	341	1/1	0.99	0.03	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.