



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:55 PM UTC

PDB ID : 1ZQF / pdb_00001zqf
Title : DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7) COMPLEXED WITH SEVEN BASE PAIRS OF DNA; SOAKED IN THE PRESENCE OF CSCL (150 MILLIMOLAR)
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1996-04-12
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

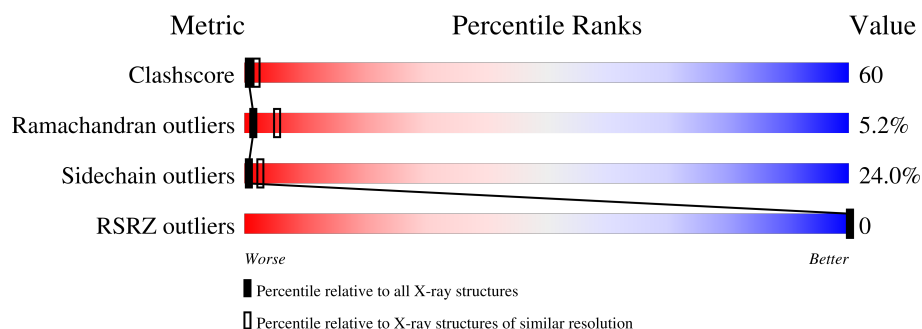
1 Overall quality at a glance

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	8	25% 12% 62%
2	P	7	14% 86%
3	A	335	20% 44% 29% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3056 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 CESIUM ION (CCD ID: CS) (formula: Cs).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	T	14	Total	O	0	0
			14	14		
5	P	22	Total	O	0	0
			22	22		
5	A	106	Total	O	0	0
			106	106		

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.

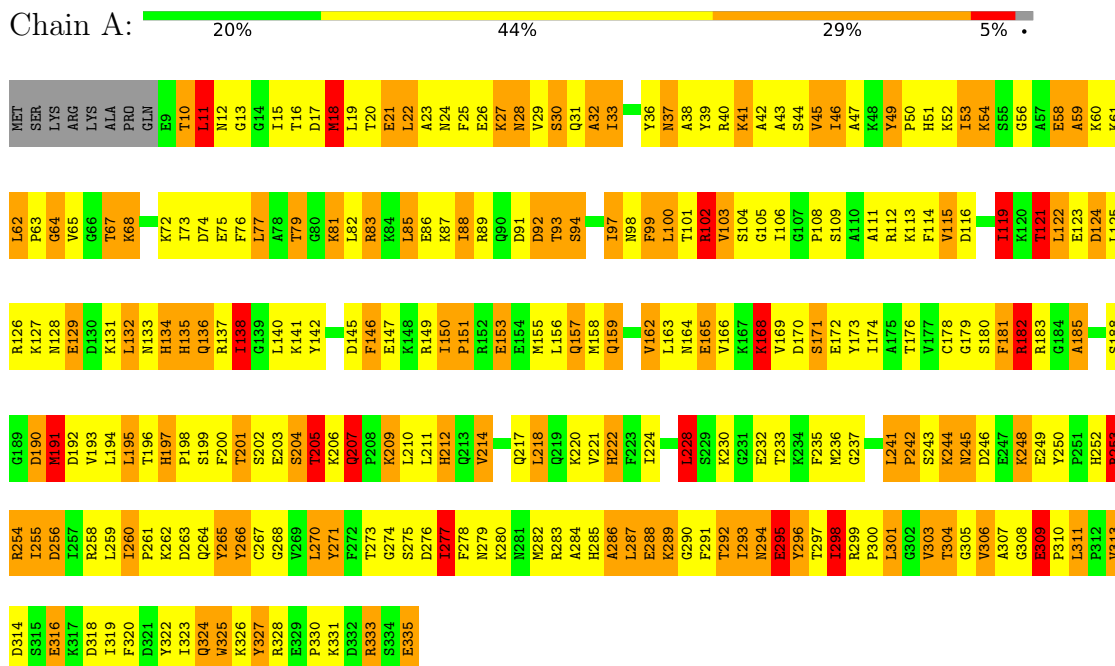
- Molecule 1: DNA (5'-D(*CP*AP*TP*TP*AP*GP*AP*A)-3')



- 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	178.89Å 57.77Å 48.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-2.90) 89.7 (20.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.63Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.183 , (Not available) (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.454	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 183.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3056	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.75% 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: CS

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	0.91	0/162	3.76	16/249 (6.4%)
2	P	1.28	1/160 (0.6%)	4.09	19/243 (7.8%)
3	A	1.50	18/2672 (0.7%)	2.12	112/3590 (3.1%)
All	All	1.47	19/2994 (0.6%)	2.41	147/4082 (3.6%)

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	2	0

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	1	DT	OP3-P	7.00	1.62	1.48
3	A	150	ILE	CA-CB	6.77	1.61	1.53
3	A	138	ILE	CA-CB	-6.50	1.46	1.54
3	A	132	LEU	C-O	-6.20	1.16	1.23
3	A	224	ILE	CA-CB	-6.13	1.46	1.54
3	A	30	SER	C-N	-5.88	1.26	1.33
3	A	254	ARG	C-O	-5.83	1.17	1.23
3	A	103	VAL	C-O	-5.77	1.18	1.24
3	A	51	HIS	CA-C	-5.77	1.45	1.52
3	A	115	VAL	CA-C	-5.55	1.46	1.52
3	A	176	THR	CA-C	-5.52	1.45	1.52
3	A	65	VAL	C-N	-5.31	1.27	1.33
3	A	296	TYR	C-N	-5.23	1.28	1.33
3	A	58	GLU	CD-OE1	5.18	1.35	1.25
3	A	271	TYR	N-CA	-5.16	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	165	GLU	N-CA	-5.15	1.40	1.46
3	A	242	PRO	N-CA	-5.14	1.40	1.47
3	A	270	LEU	C-N	-5.06	1.27	1.33
3	A	104	SER	C-O	-5.01	1.18	1.24

All (147) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	4	DT	C6-N1-C1'	-23.53	84.05	119.35
1	T	4	DT	C2-N1-C1'	22.58	153.23	119.35
2	P	1	DT	C6-N1-C1'	-22.11	86.19	119.35
1	T	6	DG	C8-N9-C1'	21.65	159.47	127.00
1	T	6	DG	C4-N9-C1'	-21.33	95.01	127.00
2	P	1	DT	C2-N1-C1'	21.04	150.90	119.35
2	P	5	DA	C4-N9-C1'	17.80	153.75	127.05
2	P	7	DG	C8-N9-C1'	17.60	153.40	127.00
2	P	7	DG	C4-N9-C1'	-17.42	100.87	127.00
2	P	5	DA	C8-N9-C1'	-17.23	101.21	127.05
1	T	7	DA	C4-N9-C1'	-15.67	103.54	127.05
1	T	7	DA	C8-N9-C1'	15.64	150.51	127.05
2	P	3	DT	C6-N1-C1'	-15.00	96.84	119.35
2	P	3	DT	C2-N1-C1'	14.40	140.96	119.35
2	P	2	DC	C2-N1-C1'	13.68	140.23	119.70
2	P	6	DT	C6-N1-C1'	-13.40	99.25	119.35
2	P	6	DT	C2-N1-C1'	13.26	139.23	119.35
3	A	99	PHE	CA-CB-CG	-12.26	101.54	113.80
1	T	5	DA	C4-N9-C1'	-11.79	109.36	127.05
2	P	2	DC	C6-N1-C1'	-11.71	102.13	119.70
1	T	5	DA	C8-N9-C1'	11.42	144.18	127.05
3	A	212	HIS	CA-CB-CG	-11.25	102.55	113.80
3	A	222	HIS	CA-CB-CG	-11.03	102.77	113.80
3	A	146	PHE	CA-CB-CG	-9.97	103.83	113.80
3	A	49	TYR	CA-C-N	9.94	131.15	120.12
3	A	49	TYR	C-N-CA	9.94	131.15	120.12
3	A	157	GLN	N-CA-CB	9.27	123.45	110.01
3	A	318	ASP	CA-CB-CG	-8.77	103.83	112.60
3	A	253	ARG	N-CA-C	8.63	122.97	108.90
3	A	168	LYS	N-CA-CB	8.49	124.16	109.72
3	A	303	VAL	N-CA-C	8.47	120.27	110.62
3	A	134	HIS	CA-CB-CG	8.46	122.26	113.80
3	A	30	SER	CA-C-N	-8.43	109.44	122.60
3	A	30	SER	C-N-CA	-8.43	109.44	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	49	TYR	O-C-N	8.43	128.65	121.31
3	A	17	ASP	CB-CA-C	7.97	123.49	110.90
3	A	333	ARG	N-CA-C	-7.91	103.19	112.92
3	A	228	LEU	N-CA-C	-7.87	101.52	112.45
3	A	256	ASP	CA-CB-CG	7.81	120.41	112.60
3	A	97	ILE	CB-CA-C	-7.77	101.65	112.14
3	A	124	ASP	CA-CB-CG	7.67	120.28	112.60
3	A	121	THR	N-CA-C	7.38	121.39	110.46
3	A	151	PRO	N-CA-CB	7.29	109.80	103.31
1	T	2	DA	C4-N9-C1'	-7.27	116.14	127.05
3	A	157	GLN	CB-CA-C	7.25	122.27	110.88
3	A	64	GLY	CA-C-N	-7.16	113.53	122.48
3	A	64	GLY	C-N-CA	-7.16	113.53	122.48
3	A	205	THR	CA-C-O	7.11	130.67	120.51
3	A	224	ILE	CA-CB-CG1	-6.99	98.51	110.40
3	A	309	GLU	CA-C-N	6.95	128.53	119.84
3	A	309	GLU	C-N-CA	6.95	128.53	119.84
2	P	3	DT	N1-C1'-C2'	6.91	123.86	113.50
3	A	20	THR	N-CA-CB	6.88	120.35	110.16
2	P	2	DC	P-O5'-C5'	-6.81	109.79	120.00
3	A	197	HIS	CB-CA-C	6.78	119.15	109.92
3	A	83	ARG	N-CA-CB	6.71	119.70	109.91
3	A	253	ARG	CD-NE-CZ	6.60	133.64	124.40
2	P	3	DT	O4'-C1'-N1	6.49	118.13	108.40
1	T	2	DA	C8-N9-C1'	6.43	136.70	127.05
1	T	5	DA	P-O5'-C5'	-6.39	110.42	120.00
3	A	266	TYR	CA-CB-CG	-6.35	102.46	113.90
3	A	277	ILE	N-CA-CB	6.30	118.64	110.57
3	A	17	ASP	N-CA-CB	6.28	119.18	110.07
3	A	65	VAL	CA-C-N	-6.27	116.17	122.69
3	A	65	VAL	C-N-CA	-6.27	116.17	122.69
3	A	12	ASN	CB-CA-C	6.23	120.49	110.09
2	P	3	DT	O5'-C5'-C4'	-6.22	101.47	110.80
3	A	292	THR	CB-CA-C	6.22	119.72	110.14
3	A	65	VAL	N-CA-C	6.18	116.60	107.15
3	A	252	HIS	CA-CB-CG	-6.14	107.66	113.80
3	A	190	ASP	CA-C-N	-6.13	111.58	122.74
3	A	190	ASP	C-N-CA	-6.13	111.58	122.74
3	A	68	LYS	N-CA-CB	6.13	118.85	109.91
3	A	313	VAL	N-CA-C	6.04	116.56	107.80
3	A	288	GLU	N-CA-C	-6.04	104.61	111.14
3	A	135	HIS	CA-CB-CG	-6.03	107.77	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	209	LYS	O-C-N	6.02	128.35	122.09
1	T	1	DC	P-O3'-C3'	5.99	129.18	120.20
1	T	1	DC	C6-N1-C1'	-5.98	110.73	119.70
2	P	4	DA	P-O5'-C5'	5.95	128.93	120.00
3	A	64	GLY	N-CA-C	-5.92	107.59	115.40
3	A	193	VAL	N-CA-C	5.90	117.07	108.58
3	A	11	LEU	N-CA-C	-5.88	104.82	112.23
3	A	28	ASN	CA-CB-CG	-5.88	106.72	112.60
3	A	119	ILE	N-CA-CB	-5.85	104.99	111.66
3	A	41	LYS	N-CA-C	-5.84	104.99	111.36
3	A	195	LEU	N-CA-C	5.84	119.06	109.72
3	A	181	PHE	CB-CA-C	-5.83	100.93	110.85
3	A	191	MET	CB-CA-C	5.80	119.37	109.80
1	T	4	DT	N1-C1'-C2'	5.75	122.12	113.50
3	A	162	VAL	N-CA-C	5.69	117.10	110.62
3	A	205	THR	CA-CB-CG2	5.68	120.17	110.50
3	A	98	ASN	CB-CA-C	5.63	120.13	110.79
3	A	286	ALA	CA-C-N	5.61	127.74	120.44
3	A	286	ALA	C-N-CA	5.61	127.74	120.44
3	A	98	ASN	CA-C-N	5.61	128.25	120.63
3	A	98	ASN	C-N-CA	5.61	128.25	120.63
3	A	260	ILE	CB-CA-C	-5.60	101.16	111.36
3	A	40	ARG	N-CA-C	5.60	118.58	111.69
3	A	98	ASN	O-C-N	5.57	128.02	122.12
3	A	98	ASN	N-CA-CB	5.56	118.29	110.12
3	A	27	LYS	N-CA-CB	-5.55	101.96	110.01
3	A	182	ARG	O-C-N	5.54	127.99	122.12
3	A	164	ASN	CA-CB-CG	-5.52	107.08	112.60
1	T	1	DC	C2-N1-C1'	5.50	127.95	119.70
3	A	59	ALA	O-C-N	5.48	127.93	122.12
3	A	192	ASP	CA-C-N	-5.44	115.35	122.37
3	A	192	ASP	C-N-CA	-5.44	115.35	122.37
3	A	88	ILE	CB-CA-C	-5.43	104.81	112.14
3	A	116	ASP	CB-CA-C	5.42	119.90	110.68
3	A	67	THR	CA-CB-OG1	5.42	117.73	109.60
2	P	3	DT	P-O5'-C5'	5.41	128.12	120.00
3	A	292	THR	N-CA-CB	5.41	119.60	110.77
3	A	271	TYR	CA-CB-CG	-5.40	104.17	113.90
3	A	168	LYS	CB-CA-C	5.39	119.80	110.84
3	A	53	ILE	CB-CA-C	5.38	120.09	111.69
3	A	316	GLU	CA-C-N	5.38	127.75	120.65
3	A	316	GLU	C-N-CA	5.38	127.75	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	18	MET	CA-C-N	5.38	127.49	120.28
3	A	18	MET	C-N-CA	5.38	127.49	120.28
2	P	5	DA	C2'-C3'-O3'	5.35	119.53	111.50
3	A	147	GLU	CA-C-N	5.33	128.28	120.71
3	A	147	GLU	C-N-CA	5.33	128.28	120.71
3	A	74	ASP	N-CA-CB	5.31	117.67	109.91
3	A	24	ASN	CA-CB-CG	-5.30	107.30	112.60
3	A	267	CYS	N-CA-C	-5.30	105.50	111.28
3	A	102	ARG	CA-CB-CG	-5.29	103.51	114.10
3	A	116	ASP	CA-CB-CG	-5.27	107.33	112.60
3	A	92	ASP	CB-CA-C	5.24	119.59	110.68
3	A	298	ILE	N-CA-CB	5.24	119.88	111.23
3	A	21	GLU	N-CA-C	-5.23	105.00	111.33
3	A	212	HIS	O-C-N	5.22	127.52	122.09
3	A	277	ILE	N-CA-C	5.17	115.39	110.53
1	T	5	DA	O4'-C1'-N9	-5.17	100.64	108.40
3	A	129	GLU	CB-CG-CD	-5.17	103.82	112.60
3	A	241	LEU	O-C-N	5.16	126.89	121.42
3	A	270	LEU	CA-C-O	5.15	126.73	121.07
3	A	92	ASP	CA-CB-CG	5.12	117.72	112.60
3	A	105	GLY	CA-C-N	5.11	128.76	122.37
3	A	105	GLY	C-N-CA	5.11	128.76	122.37
3	A	207	GLN	CA-C-N	5.11	126.22	119.84
3	A	207	GLN	C-N-CA	5.11	126.22	119.84
3	A	252	HIS	CA-C-O	-5.10	114.94	120.81
3	A	94	SER	CA-CB-OG	-5.07	100.97	111.10
3	A	67	THR	CB-CA-C	5.05	119.17	110.79
3	A	12	ASN	N-CA-C	5.02	119.50	113.17
3	A	132	LEU	N-CA-C	5.01	117.97	109.76

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	157	GLN	CA
3	A	168	LYS	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	5	0
2	P	144	0	81	20	0
3	A	2623	0	2641	314	0
4	A	2	0	0	0	0
5	A	106	0	0	16	0
5	P	22	0	0	3	0
5	T	14	0	0	1	0
All	All	3056	0	2802	337	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 60.

All (337) 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''	1.31	1.10
2:P:6:DT:H2''	2:P:7:DG:H5''	1.39	1.04
3:A:201:THR:HA	3:A:261:PRO:HB3	1.39	1.02
3:A:245:ASN:HD22	3:A:245:ASN:N	1.53	1.00
3:A:245:ASN:H	3:A:245:ASN:ND2	1.59	0.98
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.60	0.97
3:A:243:SER:HB3	3:A:249:GLU:HA	1.46	0.97
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.43	0.96
3:A:182:ARG:HG2	3:A:182:ARG:HH11	1.31	0.93
3:A:270:LEU:HD21	3:A:282:MET:HE1	1.52	0.91
2:P:5:DA:H2''	2:P:6:DT:C5'	2.00	0.90
3:A:73:ILE:HG22	3:A:77:LEU:HD22	1.49	0.90
3:A:11:LEU:HD23	3:A:11:LEU:H	1.37	0.89
3:A:201:THR:HA	3:A:261:PRO:CB	2.02	0.88
3:A:155:MET:HA	3:A:158:MET:HE3	1.53	0.88
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.57	0.86
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.57	0.86
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.25	0.85
1:T:6:DG:H2''	1:T:7:DA:C8	2.13	0.84
2:P:1:DT:H2''	2:P:2:DC:H5'	1.62	0.81
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.23	0.79
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.63	0.79
3:A:330:PRO:HA	3:A:333:ARG:CG	2.12	0.79
3:A:300:PRO:HD3	3:A:311:LEU:HD22	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.66	0.77
3:A:138:ILE:HD12	3:A:228:LEU:CD1	2.14	0.77
3:A:165:GLU:HA	3:A:168:LYS:HG2	1.68	0.76
3:A:169:VAL:HG13	3:A:170:ASP:H	1.50	0.76
3:A:121:THR:HG23	3:A:124:ASP:OD1	1.86	0.75
2:P:1:DT:H72	5:P:571:HOH:O	1.87	0.75
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.16	0.75
3:A:289:LYS:HD3	3:A:289:LYS:N	2.01	0.74
2:P:5:DA:C2'	2:P:6:DT:H5''	2.14	0.73
3:A:111:ALA:O	3:A:115:VAL:HG23	1.88	0.73
3:A:41:LYS:HD3	3:A:42:ALA:H	1.51	0.73
3:A:129:GLU:HG2	3:A:137:ARG:HD3	1.72	0.71
3:A:243:SER:CB	3:A:249:GLU:HA	2.20	0.71
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.55	0.70
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.20	0.70
3:A:271:TYR:HB2	5:A:592:HOH:O	1.92	0.70
3:A:172:GLU:HB3	3:A:197:HIS:NE2	2.07	0.69
3:A:243:SER:OG	3:A:249:GLU:HG3	1.93	0.69
2:P:6:DT:C2'	2:P:7:DG:H5''	2.21	0.69
3:A:292:THR:O	3:A:298:ILE:HA	1.92	0.69
3:A:162:VAL:O	3:A:166:VAL:HG23	1.93	0.68
3:A:82:LEU:HD23	3:A:85:LEU:HB2	1.74	0.68
3:A:201:THR:CA	3:A:261:PRO:HB3	2.21	0.68
3:A:277:ILE:HG13	3:A:335:GLU:HB2	1.77	0.67
3:A:285:HIS:NE2	3:A:289:LYS:HG2	2.09	0.67
3:A:323:ILE:C	3:A:324:GLN:HG2	2.18	0.67
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.76	0.66
3:A:150:ILE:HG12	3:A:253:ARG:HG2	1.78	0.66
3:A:294:ASN:O	3:A:296:TYR:N	2.27	0.66
2:P:1:DT:H2''	2:P:2:DC:C5'	2.25	0.66
3:A:15:ILE:HB	3:A:46:ILE:HD11	1.76	0.66
3:A:41:LYS:HD3	3:A:42:ALA:N	2.11	0.66
3:A:41:LYS:O	3:A:45:VAL:HG13	1.96	0.66
3:A:286:ALA:HB2	3:A:323:ILE:HG21	1.77	0.66
3:A:31:GLN:HE21	3:A:112:ARG:NH1	1.92	0.65
3:A:277:ILE:CG1	3:A:335:GLU:HB2	2.25	0.65
3:A:211:LEU:HD12	3:A:211:LEU:O	1.97	0.65
3:A:58:GLU:O	3:A:61:LYS:HG3	1.96	0.65
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.77	0.65
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.31	0.65
3:A:277:ILE:HD11	3:A:335:GLU:HB3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:6:DG:N7	5:T:652:HOH:O	2.29	0.65
3:A:255:ILE:HG12	3:A:256:ASP:N	2.11	0.65
3:A:200:PHE:O	3:A:262:LYS:N	2.30	0.65
3:A:103:VAL:CG1	3:A:106:ILE:HG13	2.26	0.65
3:A:278:PHE:HB2	3:A:333:ARG:O	1.97	0.65
3:A:18:MET:CE	3:A:76:PHE:HB2	2.27	0.65
3:A:159:GLN:O	3:A:163:LEU:HG	1.96	0.64
3:A:11:LEU:HD23	3:A:11:LEU:N	2.11	0.64
3:A:254:ARG:NH2	5:A:657:HOH:O	2.31	0.64
3:A:295:GLU:N	3:A:295:GLU:OE1	2.30	0.64
3:A:169:VAL:HG13	3:A:170:ASP:N	2.13	0.64
3:A:270:LEU:HD21	3:A:282:MET:CE	2.26	0.63
1:T:1:DC:H2''	1:T:2:DA:OP2	1.96	0.63
3:A:328:ARG:O	3:A:333:ARG:NE	2.28	0.63
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.33	0.63
3:A:155:MET:CA	3:A:158:MET:HE3	2.28	0.63
3:A:180:SER:HB3	3:A:183:ARG:NH2	2.12	0.63
3:A:207:GLN:HB3	3:A:210:LEU:CD1	2.28	0.63
3:A:16:THR:HG21	3:A:47:ALA:HB2	1.81	0.63
2:P:5:DA:H2'	2:P:6:DT:H71	1.81	0.62
3:A:59:ALA:O	3:A:62:LEU:HB2	1.99	0.62
3:A:270:LEU:HD23	3:A:319:ILE:HD13	1.80	0.62
3:A:11:LEU:H	3:A:11:LEU:CD2	2.10	0.62
3:A:157:GLN:HE22	3:A:244:LYS:NZ	1.98	0.62
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.29	0.61
3:A:73:ILE:HG22	3:A:77:LEU:CD2	2.29	0.61
3:A:270:LEU:CD2	3:A:319:ILE:HD13	2.31	0.61
3:A:140:LEU:HD12	3:A:140:LEU:O	2.00	0.61
3:A:75:GLU:O	3:A:79:THR:HG23	2.01	0.61
3:A:83:ARG:O	3:A:86:GLU:N	2.34	0.61
3:A:323:ILE:O	3:A:324:GLN:HG2	2.00	0.60
3:A:326:LYS:O	3:A:328:ARG:HG2	2.00	0.60
3:A:217:GLN:NE2	3:A:217:GLN:HA	2.16	0.60
3:A:248:LYS:O	3:A:248:LYS:HG2	2.00	0.60
3:A:26:GLU:HB3	3:A:32:ALA:HB3	1.84	0.60
3:A:108:PRO:O	3:A:112:ARG:HG3	2.01	0.60
3:A:158:MET:HB3	3:A:191:MET:HE3	1.83	0.60
3:A:295:GLU:HA	5:A:592:HOH:O	2.01	0.60
3:A:18:MET:HE2	3:A:82:LEU:HD22	1.82	0.60
3:A:150:ILE:CG2	3:A:158:MET:HE1	2.32	0.60
3:A:19:LEU:HD23	3:A:43:ALA:CA	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:31:GLN:NE2	3:A:112:ARG:NH1	2.42	0.60
3:A:330:PRO:HA	3:A:333:ARG:HG2	1.82	0.60
2:P:6:DT:H2''	2:P:7:DG:C8	2.36	0.59
3:A:180:SER:CB	3:A:183:ARG:HH21	2.15	0.59
3:A:327:TYR:HD1	3:A:328:ARG:N	2.01	0.59
3:A:241:LEU:HB2	3:A:250:TYR:CD2	2.36	0.59
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.27	0.59
3:A:182:ARG:HG2	3:A:182:ARG:NH1	2.05	0.59
3:A:29:VAL:HG21	3:A:94:SER:CB	2.33	0.59
3:A:188:SER:HB3	5:A:522:HOH:O	2.03	0.59
3:A:299:ARG:HG2	3:A:310:PRO:N	2.18	0.59
3:A:15:ILE:CG2	3:A:46:ILE:HD11	2.34	0.58
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.36	0.58
2:P:1:DT:H2'	2:P:2:DC:C6	2.39	0.57
3:A:270:LEU:HD12	5:A:584:HOH:O	2.04	0.57
3:A:242:PRO:HB2	5:A:589:HOH:O	2.03	0.57
3:A:287:LEU:HB3	3:A:288:GLU:OE2	2.04	0.57
3:A:294:ASN:HB2	3:A:295:GLU:OE1	2.04	0.57
3:A:180:SER:CA	3:A:183:ARG:HH21	2.18	0.57
3:A:31:GLN:N	5:A:641:HOH:O	2.27	0.56
3:A:73:ILE:O	3:A:77:LEU:HD13	2.06	0.56
3:A:138:ILE:HD12	3:A:228:LEU:HD12	1.85	0.56
3:A:245:ASN:HD22	3:A:245:ASN:H	0.75	0.56
3:A:83:ARG:O	3:A:87:LYS:N	2.36	0.56
3:A:326:LYS:O	3:A:326:LYS:HG3	2.04	0.56
3:A:99:PHE:O	3:A:102:ARG:HG3	2.06	0.56
3:A:127:LYS:HB2	3:A:128:ASN:ND2	2.21	0.56
3:A:183:ARG:HD3	3:A:273:THR:O	2.05	0.56
1:T:5:DA:H2''	1:T:6:DG:O5'	2.05	0.56
3:A:181:PHE:HD1	5:A:530:HOH:O	1.88	0.55
3:A:205:THR:HA	5:A:624:HOH:O	2.05	0.55
3:A:282:MET:HB2	3:A:325:TRP:CZ3	2.41	0.55
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.40	0.55
3:A:114:PHE:CZ	3:A:132:LEU:HD23	2.41	0.55
2:P:1:DT:C2'	2:P:2:DC:H5'	2.36	0.54
3:A:11:LEU:HA	3:A:52:LYS:NZ	2.21	0.54
3:A:277:ILE:HD11	3:A:335:GLU:CB	2.37	0.54
3:A:291:PHE:HD2	3:A:323:ILE:HG22	1.72	0.54
3:A:174:ILE:O	3:A:195:LEU:HD12	2.07	0.54
3:A:18:MET:O	3:A:21:GLU:HB2	2.07	0.54
3:A:180:SER:HB2	3:A:185:ALA:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:182:ARG:HG2	3:A:273:THR:HG23	1.89	0.54
3:A:294:ASN:ND2	5:A:593:HOH:O	2.37	0.54
3:A:300:PRO:HD3	3:A:311:LEU:CD2	2.36	0.54
3:A:319:ILE:O	3:A:322:TYR:HB2	2.08	0.53
3:A:29:VAL:HG21	3:A:94:SER:OG	2.09	0.53
3:A:182:ARG:HG2	3:A:273:THR:CG2	2.38	0.53
3:A:254:ARG:HB3	3:A:254:ARG:NH1	2.23	0.53
3:A:204:SER:O	3:A:206:LYS:N	2.42	0.53
3:A:15:ILE:HG21	3:A:46:ILE:CD1	2.39	0.53
2:P:6:DT:H5'	5:P:567:HOH:O	2.09	0.53
3:A:19:LEU:HD23	3:A:43:ALA:HA	1.88	0.52
3:A:150:ILE:CD1	3:A:190:ASP:HA	2.39	0.52
3:A:316:GLU:O	3:A:320:PHE:HD2	1.93	0.52
3:A:81:LYS:NZ	3:A:86:GLU:HB2	2.25	0.52
3:A:38:ALA:O	3:A:41:LYS:HD3	2.10	0.51
3:A:270:LEU:CD2	3:A:319:ILE:HG21	2.40	0.51
3:A:200:PHE:C	3:A:201:THR:HG22	2.35	0.51
3:A:103:VAL:HG11	3:A:106:ILE:HG13	1.92	0.51
3:A:15:ILE:CB	3:A:46:ILE:HD11	2.41	0.51
3:A:196:THR:OG1	3:A:262:LYS:HA	2.11	0.51
3:A:60:LYS:HE3	5:A:665:HOH:O	2.11	0.51
3:A:209:LYS:HA	3:A:212:HIS:HB2	1.92	0.51
3:A:254:ARG:NH1	3:A:255:ILE:N	2.59	0.51
3:A:288:GLU:C	3:A:290:GLY:H	2.19	0.51
3:A:236:MET:HG3	3:A:256:ASP:OD1	2.11	0.51
3:A:265:TYR:O	3:A:268:GLY:N	2.44	0.51
3:A:282:MET:HE3	5:A:555:HOH:O	2.10	0.51
3:A:103:VAL:HG12	3:A:106:ILE:HG13	1.92	0.50
3:A:271:TYR:CE1	3:A:283:ARG:NH2	2.80	0.50
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.42	0.50
3:A:121:THR:HG23	3:A:124:ASP:CG	2.36	0.50
3:A:76:PHE:O	3:A:79:THR:O	2.29	0.49
3:A:253:ARG:NH1	5:A:503:HOH:O	2.41	0.49
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.94	0.49
3:A:264:GLN:NE2	3:A:296:TYR:HB3	2.27	0.49
3:A:122:LEU:HD23	3:A:126:ARG:CZ	2.41	0.49
3:A:211:LEU:HD12	3:A:211:LEU:C	2.37	0.49
3:A:207:GLN:HB3	3:A:210:LEU:HG	1.95	0.49
3:A:165:GLU:HB3	3:A:217:GLN:CG	2.38	0.49
3:A:271:TYR:CD1	3:A:283:ARG:NH2	2.81	0.49
3:A:141:LYS:HE2	3:A:142:TYR:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:11:LEU:HA	3:A:52:LYS:HZ1	1.78	0.48
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.43	0.48
3:A:286:ALA:O	3:A:291:PHE:N	2.42	0.48
3:A:31:GLN:HE21	3:A:112:ARG:HH22	1.61	0.48
3:A:214:VAL:O	3:A:218:LEU:HD13	2.14	0.48
3:A:119:ILE:HG21	3:A:125:LEU:HD23	1.95	0.48
3:A:259:LEU:O	3:A:260:ILE:HD13	2.13	0.48
3:A:270:LEU:HD22	3:A:319:ILE:CD1	2.43	0.48
3:A:149:ARG:NH2	3:A:188:SER:HA	2.28	0.48
3:A:157:GLN:HE22	3:A:244:LYS:HZ1	1.60	0.48
3:A:99:PHE:HD2	3:A:100:LEU:HD13	1.79	0.48
3:A:134:HIS:O	3:A:137:ARG:HB2	2.14	0.48
3:A:309:GLU:HA	3:A:310:PRO:HD2	1.51	0.48
3:A:27:LYS:HG3	3:A:28:ASN:ND2	2.29	0.48
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.30	0.47
2:P:5:DA:C2'	2:P:6:DT:H71	2.44	0.47
3:A:159:GLN:HG3	3:A:163:LEU:HD11	1.95	0.47
3:A:220:LYS:O	3:A:220:LYS:HG2	2.14	0.47
2:P:6:DT:C2'	2:P:7:DG:C8	2.97	0.47
3:A:99:PHE:C	3:A:99:PHE:CD2	2.92	0.47
3:A:180:SER:HA	3:A:183:ARG:HE	1.79	0.47
3:A:228:LEU:HD12	3:A:228:LEU:HA	1.79	0.47
3:A:254:ARG:CA	3:A:254:ARG:HH11	2.27	0.47
3:A:270:LEU:HD23	3:A:319:ILE:HG21	1.96	0.47
3:A:286:ALA:HB1	3:A:291:PHE:HB2	1.96	0.47
3:A:276:ASP:O	3:A:280:LYS:HG3	2.15	0.47
3:A:133:ASN:ND2	3:A:135:HIS:H	2.12	0.47
3:A:212:HIS:N	3:A:212:HIS:CD2	2.79	0.47
3:A:182:ARG:HH11	3:A:273:THR:CG2	2.28	0.46
3:A:217:GLN:HA	3:A:217:GLN:HE21	1.79	0.46
2:P:6:DT:H5'	2:P:6:DT:H6	1.80	0.46
3:A:209:LYS:O	3:A:212:HIS:N	2.49	0.46
3:A:241:LEU:CB	3:A:250:TYR:CD2	2.98	0.46
3:A:93:THR:HG22	3:A:94:SER:N	2.28	0.46
3:A:180:SER:HA	3:A:183:ARG:HH21	1.80	0.46
3:A:200:PHE:CD2	3:A:261:PRO:HA	2.51	0.46
3:A:53:ILE:HG21	3:A:59:ALA:HB2	1.97	0.46
3:A:77:LEU:N	3:A:77:LEU:CD1	2.78	0.46
3:A:327:TYR:HD1	3:A:327:TYR:C	2.23	0.46
3:A:59:ALA:O	3:A:62:LEU:N	2.43	0.46
3:A:282:MET:HB2	3:A:325:TRP:HZ3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:183:ARG:NH1	3:A:275:SER:HB3	2.31	0.46
3:A:170:ASP:OD1	3:A:171:SER:N	2.49	0.46
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.64	0.46
3:A:284:ALA:O	3:A:287:LEU:HB2	2.16	0.45
3:A:327:TYR:HE1	3:A:333:ARG:HH21	1.64	0.45
3:A:133:ASN:OD1	3:A:136:GLN:HG3	2.15	0.45
3:A:327:TYR:C	3:A:327:TYR:CD1	2.94	0.45
3:A:33:ILE:O	3:A:36:TYR:HD2	2.00	0.45
3:A:207:GLN:HB3	3:A:210:LEU:HD12	1.98	0.45
3:A:303:VAL:O	3:A:305:GLY:N	2.49	0.45
3:A:306:VAL:HG22	5:A:650:HOH:O	2.16	0.45
3:A:36:TYR:CD2	3:A:37:ASN:N	2.85	0.45
3:A:298:ILE:N	5:A:578:HOH:O	2.49	0.45
1:T:7:DA:H61	2:P:1:DT:H3	1.65	0.45
3:A:60:LYS:HG3	3:A:60:LYS:O	2.17	0.45
3:A:150:ILE:HD11	3:A:190:ASP:HA	1.97	0.45
3:A:179:GLY:O	3:A:182:ARG:HB3	2.17	0.45
3:A:156:LEU:HD23	3:A:156:LEU:HA	1.83	0.45
3:A:245:ASN:N	3:A:245:ASN:ND2	2.30	0.45
3:A:286:ALA:HA	3:A:323:ILE:HG21	1.98	0.45
3:A:82:LEU:CD2	3:A:85:LEU:HD22	2.47	0.45
3:A:271:TYR:CD2	3:A:271:TYR:C	2.94	0.45
3:A:309:GLU:N	3:A:309:GLU:OE1	2.50	0.45
3:A:287:LEU:HD13	3:A:287:LEU:HA	1.45	0.44
3:A:303:VAL:C	3:A:305:GLY:H	2.25	0.44
3:A:250:TYR:HB3	5:A:577:HOH:O	2.17	0.44
3:A:100:LEU:HD21	3:A:119:ILE:O	2.18	0.44
3:A:121:THR:OG1	3:A:122:LEU:N	2.46	0.44
3:A:170:ASP:HB3	3:A:173:TYR:CD2	2.53	0.44
3:A:254:ARG:HB3	3:A:254:ARG:CZ	2.47	0.44
3:A:308:GLY:O	3:A:309:GLU:HB2	2.18	0.44
3:A:266:TYR:HB2	3:A:313:VAL:HG11	1.99	0.44
3:A:286:ALA:HB1	3:A:293:ILE:HD11	1.98	0.44
3:A:146:PHE:CE2	3:A:254:ARG:HD3	2.53	0.43
3:A:158:MET:HB3	3:A:191:MET:CE	2.48	0.43
3:A:254:ARG:HH11	3:A:255:ILE:N	2.16	0.43
3:A:330:PRO:CA	3:A:333:ARG:HG2	2.46	0.43
3:A:259:LEU:HD12	3:A:259:LEU:HA	1.45	0.43
3:A:306:VAL:HG23	3:A:307:ALA:N	2.32	0.43
3:A:200:PHE:O	3:A:261:PRO:HA	2.18	0.43
3:A:122:LEU:CD2	3:A:126:ARG:CZ	2.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:183:ARG:HH11	3:A:275:SER:HB3	1.83	0.43
3:A:194:LEU:CD1	3:A:258:ARG:HD3	2.48	0.43
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.53	0.43
3:A:207:GLN:HB3	3:A:210:LEU:CG	2.48	0.43
3:A:100:LEU:HD12	3:A:100:LEU:HA	1.49	0.43
3:A:123:GLU:O	3:A:127:LYS:HG2	2.18	0.43
3:A:285:HIS:NE2	3:A:289:LYS:CG	2.79	0.43
3:A:286:ALA:CA	3:A:323:ILE:HG21	2.49	0.43
3:A:15:ILE:HG21	3:A:46:ILE:HD11	2.01	0.42
3:A:18:MET:HE2	3:A:82:LEU:HD13	2.00	0.42
3:A:124:ASP:O	3:A:128:ASN:ND2	2.50	0.42
3:A:182:ARG:HB3	3:A:273:THR:HG23	2.00	0.42
3:A:22:LEU:HD13	3:A:22:LEU:HA	1.70	0.42
3:A:138:ILE:O	3:A:141:LYS:HB3	2.20	0.42
3:A:244:LYS:C	3:A:246:ASP:H	2.27	0.42
3:A:293:ILE:CD1	3:A:298:ILE:CD1	2.97	0.42
3:A:151:PRO:HB2	3:A:153:GLU:HG2	2.01	0.42
3:A:182:ARG:HH11	3:A:273:THR:HG21	1.84	0.42
3:A:303:VAL:C	3:A:305:GLY:N	2.77	0.42
3:A:320:PHE:CE1	3:A:328:ARG:HG3	2.54	0.42
3:A:235:PHE:CZ	3:A:237:GLY:HA3	2.55	0.42
3:A:260:ILE:HG22	3:A:261:PRO:O	2.18	0.42
3:A:46:ILE:HD13	3:A:53:ILE:HD12	2.02	0.42
3:A:264:GLN:HE21	3:A:297:THR:HG23	1.85	0.42
3:A:133:ASN:HD21	3:A:135:HIS:CB	2.33	0.42
3:A:133:ASN:HD21	3:A:135:HIS:HB3	1.84	0.42
3:A:198:PRO:C	3:A:200:PHE:H	2.28	0.42
3:A:25:PHE:CD1	3:A:25:PHE:C	2.98	0.42
3:A:31:GLN:HE21	3:A:112:ARG:NH2	2.17	0.42
3:A:39:TYR:OH	3:A:72:LYS:HE3	2.19	0.42
3:A:29:VAL:O	3:A:29:VAL:HG12	2.20	0.41
3:A:232:GLU:O	3:A:233:THR:HG23	2.20	0.41
3:A:73:ILE:CG2	3:A:77:LEU:HD22	2.36	0.41
3:A:81:LYS:NZ	3:A:86:GLU:CB	2.83	0.41
3:A:301:LEU:HD12	3:A:301:LEU:HA	1.52	0.41
3:A:29:VAL:HG21	3:A:94:SER:HB2	2.03	0.41
3:A:207:GLN:O	3:A:210:LEU:HB2	2.20	0.41
2:P:6:DT:C5'	2:P:6:DT:H6	2.34	0.41
3:A:54:LYS:HD2	3:A:54:LYS:HA	1.81	0.41
3:A:207:GLN:OE1	3:A:210:LEU:HD11	2.21	0.41
3:A:18:MET:HE3	3:A:76:PHE:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:82:LEU:HD23	3:A:85:LEU:HD22	2.02	0.41
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.34	0.41
3:A:81:LYS:HZ2	3:A:86:GLU:HB2	1.84	0.41
3:A:260:ILE:CG2	3:A:261:PRO:CD	2.98	0.41
3:A:289:LYS:HD3	3:A:289:LYS:HA	1.43	0.41
2:P:3:DT:H73	5:P:525:HOH:O	2.20	0.41
3:A:274:GLY:HA3	3:A:275:SER:HA	1.78	0.41
2:P:5:DA:P	3:A:109:SER:HB3	2.60	0.41
3:A:270:LEU:HD22	3:A:319:ILE:HD12	2.03	0.41
3:A:25:PHE:CE2	3:A:88:ILE:HG12	2.56	0.41
3:A:37:ASN:HD22	3:A:37:ASN:HA	1.63	0.41
3:A:56:GLY:O	3:A:59:ALA:N	2.54	0.41
3:A:125:LEU:HD23	3:A:125:LEU:HA	1.84	0.41
3:A:129:GLU:HG2	3:A:137:ARG:CD	2.46	0.41
3:A:241:LEU:HB2	3:A:250:TYR:CG	2.55	0.41
3:A:288:GLU:C	3:A:290:GLY:N	2.79	0.41
3:A:255:ILE:CG1	3:A:256:ASP:N	2.82	0.41
3:A:15:ILE:CD1	3:A:73:ILE:HG23	2.51	0.40
3:A:207:GLN:OE1	3:A:210:LEU:HD21	2.20	0.40
3:A:201:THR:HA	3:A:261:PRO:CA	2.49	0.40
3:A:62:LEU:HD12	3:A:63:PRO:HD2	2.02	0.40
3:A:133:ASN:ND2	3:A:133:ASN:C	2.79	0.40
3:A:195:LEU:HD12	3:A:195:LEU:HA	1.55	0.40
3:A:327:TYR:CD1	3:A:328:ARG:N	2.86	0.40
3:A:126:ARG:C	3:A:128:ASN:N	2.78	0.40
3:A:244:LYS:H	3:A:244:LYS:HG2	1.66	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%)	263 (81%)	45 (14%)	17 (5%)	1 5

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	32	ALA
3	A	202	SER
3	A	204	SER
3	A	205	THR
3	A	244	LYS
3	A	295	GLU
3	A	309	GLU
3	A	13	GLY
3	A	185	ALA
3	A	304	THR
3	A	91	ASP
3	A	265	TYR
3	A	289	LYS
3	A	10	THR
3	A	207	GLN
3	A	222	HIS
3	A	298	ILE

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	10	THR
3	A	11	LEU
3	A	18	MET
3	A	22	LEU

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Mol	Chain	Res	Type
3	A	30	SER
3	A	33	ILE
3	A	37	ASN
3	A	44	SER
3	A	45	VAL
3	A	46	ILE
3	A	54	LYS
3	A	62	LEU
3	A	67	THR
3	A	68	LYS
3	A	77	LEU
3	A	79	THR
3	A	81	LYS
3	A	85	LEU
3	A	89	ARG
3	A	92	ASP
3	A	93	THR
3	A	97	ILE
3	A	100	LEU
3	A	101	THR
3	A	102	ARG
3	A	113	LYS
3	A	119	ILE
3	A	121	THR
3	A	122	LEU
3	A	131	LYS
3	A	136	GLN
3	A	138	ILE
3	A	145	ASP
3	A	153	GLU
3	A	159	GLN
3	A	168	LYS
3	A	171	SER
3	A	182	ARG
3	A	191	MET
3	A	199	SER
3	A	201	THR
3	A	203	GLU
3	A	214	VAL
3	A	218	LEU
3	A	221	VAL
3	A	228	LEU

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Mol	Chain	Res	Type
3	A	230	LYS
3	A	245	ASN
3	A	248	LYS
3	A	253	ARG
3	A	255	ILE
3	A	263	ASP
3	A	277	ILE
3	A	279	ASN
3	A	287	LEU
3	A	293	ILE
3	A	294	ASN
3	A	295	GLU
3	A	301	LEU
3	A	304	THR
3	A	306	VAL
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	324	GLN
3	A	325	TRP
3	A	327	TYR
3	A	331	LYS
3	A	335	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) 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
3	A	128	ASN
3	A	133	ASN
3	A	134	HIS
3	A	157	GLN
3	A	212	HIS
3	A	217	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 [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	8/8 (100%)	-0.19	0 100 100	16, 39, 98, 99	0
2	P	7/7 (100%)	-0.55	0 100 100	15, 20, 48, 76	0
3	A	325/335 (97%)	-0.65	0 100 100	2, 32, 84, 100	0
All	All	340/350 (97%)	-0.64	0 100 100	2, 32, 84, 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	CS	A	341	1/1	0.99	0.06	41,41,41,41	0
4	CS	A	342	1/1	0.99	0.05	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.