



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:23 AM UTC

PDB ID : 7ICS / pdb_00007ics
Title : DNA POLYMERASE BETA (E.C.2.7.7.7)/DNA COMPLEX, SOAKED IN THE PRESENCE OF ZNCL2
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1996-04-19
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
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

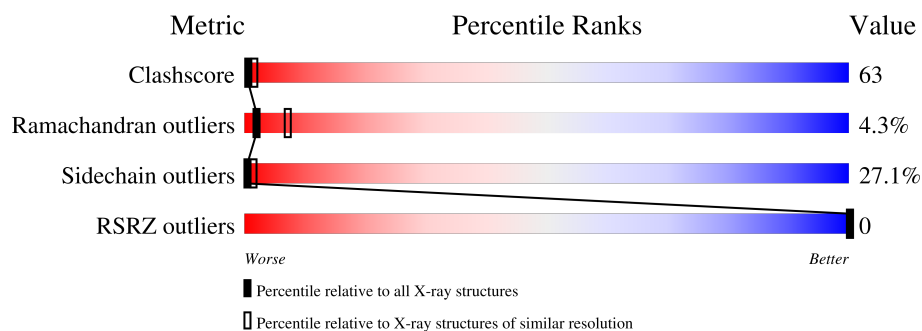
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	T	7	29% 14% 57%
2	P	6	17% 83%
3	A	335	19% 44% 28% 7% •

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3023 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		

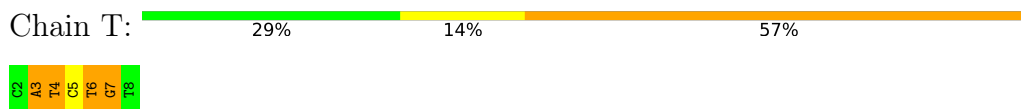
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	T	13	Total	O	0	0
			13	13		
5	P	22	Total	O	0	0
			22	22		
5	A	115	Total	O	0	0
			115	115		

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.

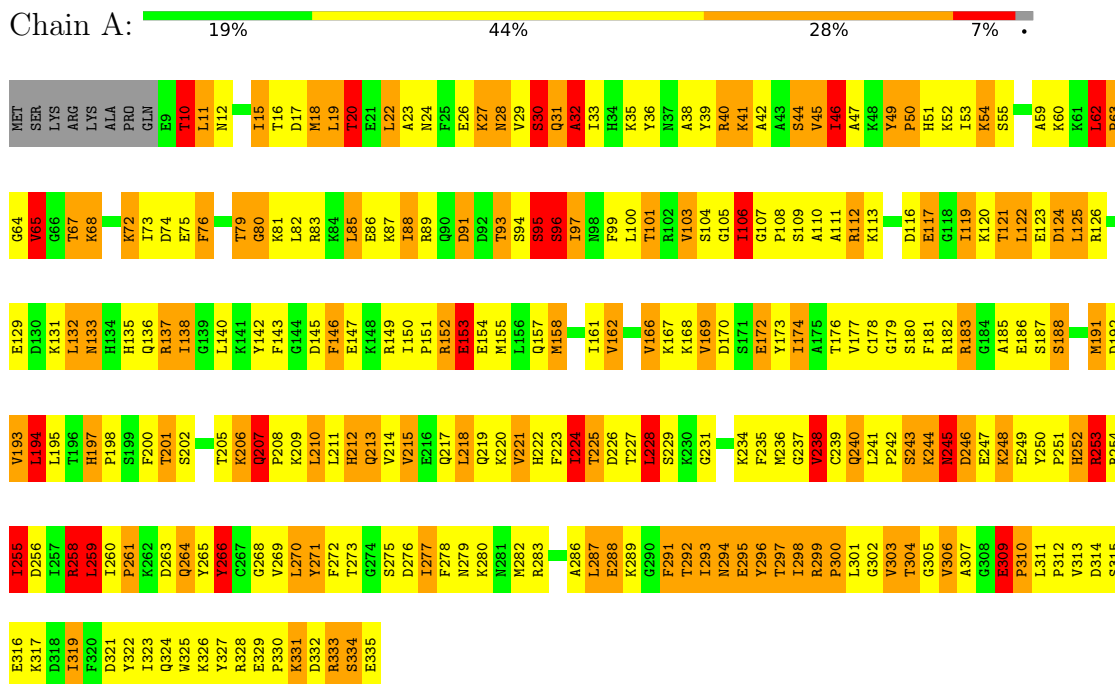
- Molecule 1: DNA (5'-D(*CP*AP*TP*CP*TP*GP*T)-3')



- Molecule 2: DNA (5'-D(*CP*AP*GP*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	178.51Å 57.73Å 48.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	83.0 (20.00-2.80) 82.4 (20.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	4.40	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.82Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.196 , (Not available) 0.186 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 155.7	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	0.93	EDS
Total number of atoms	3023	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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:
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	0.94	0/135	2.45	8/207 (3.9%)
2	P	1.21	1/141 (0.7%)	2.90	15/214 (7.0%)
3	A	1.60	15/2672 (0.6%)	2.11	114/3590 (3.2%)
All	All	1.56	16/2948 (0.5%)	2.18	137/4011 (3.4%)

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 (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	106	ILE	CA-C	-9.80	1.39	1.52
3	A	107	GLY	CA-C	-7.12	1.41	1.51
2	P	1	DC	OP3-P	6.88	1.62	1.48
3	A	252	HIS	CE1-NE2	6.25	1.38	1.32
3	A	215	VAL	CA-C	-6.14	1.44	1.52
3	A	252	HIS	CG-ND1	6.08	1.45	1.38
3	A	259	LEU	CA-C	-5.74	1.45	1.52
3	A	95	SER	CA-C	-5.66	1.44	1.52
3	A	215	VAL	C-N	-5.57	1.26	1.33
3	A	176	THR	CA-C	-5.48	1.45	1.52
3	A	62	LEU	N-CA	-5.34	1.38	1.45
3	A	226	ASP	CA-C	-5.29	1.46	1.52
3	A	103	VAL	CA-C	-5.26	1.46	1.52
3	A	255	ILE	CA-CB	-5.21	1.47	1.54
3	A	224	ILE	CA-CB	-5.19	1.48	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	227	THR	CA-CB	5.13	1.60	1.53

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	5	DT	C2-N1-C1'	19.33	148.34	119.35
2	P	5	DT	C6-N1-C1'	-18.07	92.25	119.35
1	T	4	DT	C2-N1-C1'	14.03	140.40	119.35
1	T	4	DT	C6-N1-C1'	-13.86	98.55	119.35
3	A	49	TYR	CA-C-N	12.51	132.08	119.82
3	A	49	TYR	C-N-CA	12.51	132.08	119.82
1	T	3	DA	C4-N9-C1'	10.18	142.32	127.05
1	T	3	DA	C8-N9-C1'	-9.91	112.19	127.05
3	A	96	SER	CB-CA-C	9.31	125.62	110.90
1	T	4	DT	P-O3'-C3'	9.25	134.07	120.20
3	A	272	PHE	CA-CB-CG	-8.95	104.85	113.80
3	A	40	ARG	N-CA-C	8.65	120.71	111.28
2	P	4	DA	C4-N9-C1'	-8.35	114.52	127.05
3	A	30	SER	CA-C-N	-8.07	109.74	122.73
3	A	30	SER	C-N-CA	-8.07	109.74	122.73
3	A	238	VAL	N-CA-C	8.03	120.05	107.28
2	P	4	DA	C8-N9-C1'	7.65	138.52	127.05
3	A	96	SER	N-CA-CB	7.50	120.95	110.07
3	A	86	GLU	N-CA-CB	7.47	120.84	110.01
2	P	3	DG	C8-N9-C1'	-7.44	115.84	127.00
3	A	197	HIS	CA-C-N	7.43	127.45	119.28
3	A	197	HIS	C-N-CA	7.43	127.45	119.28
3	A	297	THR	N-CA-C	7.36	117.73	108.45
3	A	24	ASN	CA-CB-CG	-7.27	105.33	112.60
3	A	253	ARG	N-CA-C	7.20	121.27	109.24
3	A	46	ILE	N-CA-CB	7.04	123.51	110.77
3	A	152	ARG	N-CA-CB	7.01	121.21	110.14
3	A	227	THR	N-CA-C	6.92	119.80	108.52
3	A	299	ARG	CA-C-N	6.90	127.28	119.83
3	A	299	ARG	C-N-CA	6.90	127.28	119.83
3	A	30	SER	N-CA-C	-6.90	101.93	110.41
3	A	197	HIS	O-C-N	6.89	127.21	121.83
3	A	99	PHE	N-CA-C	6.85	118.64	111.03
3	A	74	ASP	N-CA-CB	6.84	120.22	109.82
3	A	241	LEU	O-C-N	6.83	129.18	121.32
3	A	86	GLU	CB-CA-C	6.82	121.58	110.88
3	A	117	GLU	N-CA-C	-6.78	105.01	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	222	HIS	CA-CB-CG	-6.74	107.06	113.80
3	A	297	THR	CB-CA-C	-6.72	97.64	113.02
1	T	6	DT	C6-N1-C1'	-6.70	109.31	119.35
3	A	319	ILE	N-CA-CB	6.68	118.36	110.55
3	A	193	VAL	N-CA-CB	-6.66	103.00	110.99
1	T	7	DG	C5'-C4'-C3'	-6.65	104.92	114.90
3	A	107	GLY	O-C-N	6.64	128.41	121.77
3	A	296	TYR	N-CA-C	6.63	122.04	113.88
2	P	3	DG	O4'-C1'-N9	6.60	118.31	108.40
3	A	240	GLN	N-CA-C	6.59	118.80	107.93
3	A	65	VAL	N-CA-C	6.58	117.61	107.99
3	A	333	ARG	N-CA-C	-6.54	105.17	113.02
3	A	261	PRO	CB-CA-C	-6.48	104.50	111.56
3	A	106	ILE	N-CA-CB	6.48	120.06	111.64
3	A	62	LEU	CA-C-N	6.39	126.89	119.99
3	A	62	LEU	C-N-CA	6.39	126.89	119.99
3	A	181	PHE	CB-CA-C	-6.37	100.89	110.88
2	P	5	DT	O3'-P-O5'	6.29	113.44	104.00
2	P	2	DA	C5'-C4'-O4'	-6.25	100.03	109.40
3	A	192	ASP	CA-C-N	-6.21	115.10	122.93
3	A	192	ASP	C-N-CA	-6.21	115.10	122.93
3	A	153	GLU	N-CA-CB	6.20	119.77	110.22
3	A	179	GLY	CA-C-N	6.20	131.07	120.72
3	A	179	GLY	C-N-CA	6.20	131.07	120.72
3	A	138	ILE	O-C-N	6.16	128.28	121.94
3	A	194	LEU	N-CA-CB	6.16	120.20	110.23
3	A	193	VAL	N-CA-C	6.14	117.13	108.36
2	P	4	DA	P-O3'-C3'	6.00	129.21	120.20
3	A	20	THR	N-CA-CB	5.95	118.70	110.07
3	A	181	PHE	N-CA-C	-5.94	104.71	111.07
3	A	181	PHE	CA-CB-CG	-5.91	107.89	113.80
2	P	5	DT	C4'-C3'-O3'	-5.87	101.20	110.00
3	A	300	PRO	CA-C-N	-5.86	113.93	122.19
3	A	300	PRO	C-N-CA	-5.86	113.93	122.19
3	A	63	PRO	N-CA-C	-5.83	101.35	111.32
3	A	124	ASP	N-CA-C	-5.81	104.14	111.11
3	A	246	ASP	N-CA-CB	5.80	120.29	110.49
3	A	174	ILE	CB-CA-C	5.78	117.00	110.41
3	A	310	PRO	N-CA-CB	5.77	107.10	103.23
3	A	146	PHE	N-CA-CB	5.77	118.60	110.12
3	A	131	LYS	CB-CA-C	5.75	121.40	109.95
3	A	302	GLY	N-CA-C	-5.74	104.33	112.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	142	TYR	N-CA-C	5.74	119.59	112.59
2	P	3	DG	P-O5'-C5'	5.73	128.59	120.00
3	A	20	THR	CB-CA-C	5.72	119.94	110.90
3	A	300	PRO	CB-CA-C	-5.68	104.48	111.64
3	A	291	PHE	N-CA-C	5.67	117.79	109.24
3	A	86	GLU	N-CA-C	5.65	117.11	111.07
2	P	4	DA	P-O5'-C5'	-5.61	111.59	120.00
3	A	91	ASP	CA-CB-CG	-5.59	107.01	112.60
3	A	228	LEU	N-CA-C	-5.59	104.58	111.40
3	A	137	ARG	CA-C-O	5.55	126.65	120.82
3	A	50	PRO	CA-C-N	-5.54	112.35	123.09
3	A	50	PRO	C-N-CA	-5.54	112.35	123.09
3	A	88	ILE	CA-CB-CG2	5.53	119.89	110.50
3	A	245	ASN	CB-CA-C	5.51	118.80	111.14
3	A	266	TYR	N-CA-C	5.50	122.52	110.80
3	A	28	ASN	N-CA-C	5.49	120.43	111.37
3	A	162	VAL	N-CA-CB	5.48	116.60	110.62
3	A	125	LEU	N-CA-C	5.48	116.93	111.07
3	A	49	TYR	O-C-N	5.47	127.61	121.32
3	A	271	TYR	N-CA-CB	-5.47	101.80	109.94
3	A	32	ALA	N-CA-C	5.46	122.42	110.80
3	A	62	LEU	O-C-N	5.45	128.56	121.64
3	A	161	ILE	CB-CA-C	-5.45	104.91	111.88
3	A	146	PHE	CA-CB-CG	-5.44	108.36	113.80
3	A	207	GLN	CA-C-N	5.43	124.77	118.85
3	A	207	GLN	C-N-CA	5.43	124.77	118.85
3	A	15	ILE	CB-CA-C	-5.40	104.85	112.14
3	A	253	ARG	CD-NE-CZ	5.38	131.93	124.40
3	A	258	ARG	N-CA-C	5.36	117.35	108.13
3	A	116	ASP	N-CA-C	-5.36	106.58	113.01
3	A	31	GLN	N-CA-C	-5.35	106.62	112.72
3	A	76	PHE	CA-CB-CG	-5.33	108.47	113.80
3	A	292	THR	N-CA-CB	5.33	120.65	111.00
2	P	3	DG	C4-N9-C1'	5.32	134.98	127.00
3	A	261	PRO	N-CA-C	-5.30	102.18	110.50
3	A	129	GLU	N-CA-C	-5.29	105.51	111.28
3	A	240	GLN	N-CA-CB	5.28	119.03	110.32
2	P	1	DC	C2-N1-C1'	5.24	127.56	119.70
3	A	312	PRO	N-CA-CB	5.22	106.73	103.23
2	P	1	DC	C6-N1-C1'	-5.21	111.89	119.70
3	A	166	VAL	N-CA-C	-5.21	105.31	110.62
1	T	6	DT	P-O3'-C3'	5.18	127.96	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	51	HIS	N-CA-C	5.17	117.71	109.65
3	A	243	SER	N-CA-CB	-5.16	102.16	109.85
3	A	243	SER	CB-CA-C	5.15	118.14	109.89
3	A	215	VAL	N-CA-CB	5.15	116.91	110.47
3	A	138	ILE	CA-C-N	5.13	125.78	120.03
3	A	138	ILE	C-N-CA	5.13	125.78	120.03
3	A	258	ARG	N-CA-CB	5.13	119.06	110.59
3	A	88	ILE	CA-CB-CG1	5.12	119.11	110.40
3	A	271	TYR	N-CA-C	5.11	117.25	111.11
3	A	186	GLU	N-CA-C	5.11	118.78	112.54
3	A	225	THR	N-CA-C	5.10	120.50	113.97
3	A	304	THR	CA-C-O	5.10	125.53	119.10
3	A	270	LEU	CA-C-N	5.02	127.31	120.54
3	A	270	LEU	C-N-CA	5.02	127.31	120.54
3	A	246	ASP	N-CA-C	5.01	121.47	110.80
3	A	50	PRO	CB-CA-C	-5.00	104.31	111.62

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	86	GLU	CA
3	A	96	SER	CA
3	A	246	ASP	CA

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	10	0
2	P	126	0	68	14	0
3	A	2623	0	2641	331	1
4	A	2	0	0	0	0
5	A	115	0	0	22	0
5	P	22	0	0	4	0
5	T	13	0	0	4	0
All	All	3023	0	2778	350	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 63.

All (350) 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:119:ILE:HG22	3:A:124:ASP:HB3	1.27	1.13
3:A:300:PRO:HD3	3:A:311:LEU:HD13	1.27	1.08
3:A:152:ARG:HA	3:A:155:MET:HB2	1.37	1.04
3:A:286:ALA:HB1	3:A:293:ILE:HD11	1.35	1.03
3:A:133:ASN:ND2	3:A:136:GLN:H	1.56	1.03
3:A:210:LEU:HB3	3:A:259:LEU:HD21	1.41	1.01
2:P:1:DC:H2''	2:P:2:DA:H5''	1.45	0.94
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.03	0.93
3:A:12:ASN:HD21	3:A:53:ILE:H	1.18	0.89
3:A:119:ILE:CG2	3:A:124:ASP:HB3	2.02	0.89
3:A:11:LEU:HD23	3:A:11:LEU:H	1.40	0.87
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.10	0.85
3:A:194:LEU:HD11	3:A:258:ARG:HD3	1.57	0.85
3:A:133:ASN:HD21	3:A:136:GLN:H	1.20	0.84
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.56	0.84
3:A:60:LYS:HA	3:A:65:VAL:HG22	1.60	0.83
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.60	0.82
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.60	0.82
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.25	0.82
3:A:157:GLN:HE22	3:A:244:LYS:NZ	1.79	0.81
3:A:15:ILE:HG21	3:A:46:ILE:HD13	1.63	0.81
3:A:183:ARG:HH11	3:A:275:SER:HA	1.44	0.81
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.11	0.80
3:A:293:ILE:HG23	3:A:298:ILE:HG13	1.61	0.80
3:A:293:ILE:HD12	3:A:298:ILE:HG13	1.64	0.79
3:A:166:VAL:O	3:A:169:VAL:HG12	1.83	0.78
3:A:264:GLN:NE2	3:A:296:TYR:HB3	1.99	0.78
3:A:215:VAL:O	3:A:219:GLN:HG3	1.84	0.78
3:A:147:GLU:HG3	5:A:514:HOH:O	1.84	0.78
3:A:294:ASN:HB2	3:A:295:GLU:OE2	1.83	0.78
3:A:183:ARG:O	3:A:331:LYS:HA	1.84	0.77
3:A:276:ASP:O	3:A:280:LYS:HG3	1.85	0.77
3:A:194:LEU:HD12	3:A:258:ARG:HG2	1.67	0.76
3:A:277:ILE:HG13	3:A:335:GLU:HB3	1.67	0.76
3:A:121:THR:O	3:A:124:ASP:HB2	1.86	0.76
3:A:242:PRO:HG2	5:A:589:HOH:O	1.86	0.76
3:A:23:ALA:HB2	3:A:39:TYR:HB2	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.17	0.75
3:A:183:ARG:NH1	3:A:275:SER:HA	2.02	0.75
3:A:177:VAL:HG22	3:A:193:VAL:HG22	1.69	0.75
3:A:12:ASN:HB3	3:A:46:ILE:HD12	1.69	0.74
3:A:286:ALA:HA	3:A:323:ILE:HG21	1.69	0.74
3:A:150:ILE:HG21	3:A:158:MET:CE	2.17	0.73
2:P:1:DC:C2'	2:P:2:DA:H5''	2.16	0.73
2:P:5:DT:H1'	5:P:565:HOH:O	1.87	0.73
3:A:15:ILE:O	3:A:19:LEU:HD22	1.88	0.73
3:A:68:LYS:O	3:A:72:LYS:HE3	1.87	0.73
3:A:250:TYR:HB3	3:A:251:PRO:HD2	1.69	0.73
3:A:245:ASN:H	3:A:245:ASN:HD22	1.33	0.73
3:A:60:LYS:HA	3:A:65:VAL:CG2	2.19	0.72
3:A:27:LYS:HB3	3:A:36:TYR:CD1	2.24	0.72
3:A:44:SER:O	3:A:47:ALA:HB3	1.88	0.72
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.20	0.72
3:A:68:LYS:HB2	3:A:68:LYS:NZ	2.04	0.72
3:A:85:LEU:O	3:A:89:ARG:HG3	1.91	0.70
3:A:157:GLN:HE22	3:A:244:LYS:HZ3	1.40	0.70
3:A:287:LEU:HD22	3:A:291:PHE:O	1.91	0.70
3:A:80:GLY:O	3:A:81:LYS:HG2	1.91	0.70
3:A:229:SER:HB3	5:A:513:HOH:O	1.91	0.70
2:P:3:DG:H1'	5:P:511:HOH:O	1.90	0.70
3:A:210:LEU:CB	3:A:259:LEU:HD21	2.21	0.70
3:A:197:HIS:ND1	3:A:198:PRO:HD2	2.06	0.69
3:A:243:SER:OG	3:A:249:GLU:HG3	1.92	0.69
3:A:292:THR:C	3:A:293:ILE:HD13	2.16	0.69
3:A:194:LEU:CD1	3:A:258:ARG:HD3	2.22	0.69
3:A:300:PRO:CD	3:A:311:LEU:HD13	2.14	0.69
3:A:29:VAL:HG12	3:A:30:SER:N	2.07	0.68
3:A:49:TYR:CG	3:A:50:PRO:HD2	2.28	0.68
3:A:297:THR:HG22	5:A:626:HOH:O	1.91	0.68
3:A:288:GLU:OE1	3:A:288:GLU:HA	1.89	0.68
3:A:217:GLN:NE2	3:A:217:GLN:HA	2.07	0.68
3:A:12:ASN:HB3	3:A:46:ILE:CD1	2.23	0.68
3:A:300:PRO:HD2	3:A:309:GLU:O	1.94	0.68
3:A:138:ILE:HG21	3:A:228:LEU:HD11	1.77	0.67
3:A:237:GLY:O	3:A:254:ARG:NH1	2.27	0.67
3:A:30:SER:HA	5:A:558:HOH:O	1.93	0.67
3:A:96:SER:CB	3:A:120:LYS:HB3	2.25	0.66
3:A:79:THR:O	3:A:81:LYS:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.11	0.66
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.78	0.66
3:A:155:MET:HE3	3:A:188:SER:HB2	1.77	0.66
2:P:2:DA:C8	2:P:2:DA:H5'	2.31	0.65
3:A:133:ASN:C	3:A:133:ASN:HD22	2.04	0.65
3:A:59:ALA:O	3:A:62:LEU:HB2	1.96	0.65
3:A:151:PRO:HD2	3:A:154:GLU:OE1	1.95	0.65
3:A:251:PRO:HG2	3:A:253:ARG:CZ	2.26	0.65
3:A:277:ILE:HG13	3:A:335:GLU:CB	2.26	0.65
3:A:306:VAL:HG23	3:A:307:ALA:N	2.10	0.65
3:A:214:VAL:HG23	3:A:215:VAL:N	2.11	0.65
3:A:145:ASP:OD2	3:A:252:HIS:HB2	1.98	0.64
3:A:87:LYS:NZ	5:A:646:HOH:O	2.29	0.64
3:A:210:LEU:HB3	3:A:259:LEU:CD2	2.24	0.64
3:A:245:ASN:H	3:A:245:ASN:ND2	1.95	0.64
3:A:255:ILE:HG12	3:A:256:ASP:N	2.13	0.64
3:A:27:LYS:HG3	3:A:28:ASN:N	2.12	0.63
3:A:240:GLN:HG3	5:A:577:HOH:O	1.97	0.63
3:A:152:ARG:CA	3:A:155:MET:HB2	2.21	0.63
3:A:172:GLU:HG3	3:A:198:PRO:HG3	1.81	0.63
3:A:201:THR:HA	3:A:261:PRO:CB	2.28	0.63
3:A:150:ILE:HD11	3:A:253:ARG:HB3	1.80	0.63
3:A:259:LEU:HD12	3:A:260:ILE:H	1.63	0.63
3:A:121:THR:HG23	3:A:124:ASP:OD2	1.98	0.62
3:A:183:ARG:HH11	3:A:275:SER:CA	2.11	0.62
3:A:270:LEU:HD21	3:A:282:MET:CE	2.29	0.62
3:A:270:LEU:HA	3:A:316:GLU:OE2	1.99	0.62
3:A:68:LYS:HB2	3:A:68:LYS:HZ1	1.63	0.62
3:A:315:SER:OG	3:A:316:GLU:N	2.29	0.62
3:A:12:ASN:ND2	3:A:53:ILE:H	1.95	0.61
2:P:4:DA:H5'	5:P:511:HOH:O	2.00	0.61
3:A:12:ASN:HA	5:A:642:HOH:O	1.99	0.61
1:T:5:DC:H2''	1:T:6:DT:H5'	1.82	0.61
1:T:3:DA:H2''	5:T:573:HOH:O	2.01	0.61
3:A:178:CYS:SG	3:A:194:LEU:HD23	2.40	0.61
3:A:264:GLN:HA	5:A:536:HOH:O	2.01	0.61
3:A:228:LEU:HB2	3:A:236:MET:O	2.00	0.61
3:A:243:SER:HB3	3:A:249:GLU:HA	1.82	0.61
3:A:35:LYS:O	3:A:38:ALA:HB3	2.01	0.60
3:A:279:ASN:HA	5:A:555:HOH:O	2.00	0.60
1:T:3:DA:H1'	5:T:617:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:270:LEU:HD22	3:A:319:ILE:HD12	1.83	0.60
3:A:18:MET:HE1	3:A:76:PHE:CB	2.31	0.60
3:A:326:LYS:HE2	3:A:328:ARG:HE	1.66	0.60
3:A:79:THR:C	3:A:81:LYS:H	2.10	0.60
3:A:103:VAL:HG12	3:A:104:SER:N	2.16	0.60
3:A:300:PRO:HD3	3:A:311:LEU:CD1	2.17	0.59
3:A:119:ILE:HG22	3:A:124:ASP:CB	2.17	0.59
3:A:265:TYR:O	3:A:269:VAL:HG23	2.01	0.59
3:A:289:LYS:HD2	3:A:324:GLN:OE1	2.02	0.59
3:A:16:THR:O	3:A:20:THR:HG23	2.01	0.59
3:A:26:GLU:HG3	3:A:35:LYS:HB3	1.85	0.59
3:A:41:LYS:NZ	3:A:64:GLY:O	2.29	0.59
3:A:278:PHE:HB2	3:A:333:ARG:O	2.03	0.59
3:A:250:TYR:HB3	3:A:251:PRO:CD	2.30	0.59
3:A:270:LEU:HD21	3:A:282:MET:HE2	1.83	0.59
1:T:4:DT:H1'	1:T:5:DC:H5'	1.85	0.59
3:A:11:LEU:HD23	3:A:11:LEU:N	2.15	0.59
3:A:217:GLN:O	3:A:220:LYS:HB3	2.02	0.59
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.67	0.59
3:A:18:MET:CE	3:A:76:PHE:HB2	2.33	0.58
3:A:200:PHE:CD2	3:A:261:PRO:HA	2.37	0.58
3:A:23:ALA:O	3:A:36:TYR:HD1	1.87	0.58
3:A:245:ASN:ND2	3:A:245:ASN:N	2.52	0.58
3:A:217:GLN:HA	3:A:217:GLN:HE21	1.69	0.57
3:A:155:MET:HA	3:A:158:MET:CE	2.34	0.57
3:A:194:LEU:CD1	3:A:258:ARG:HG2	2.34	0.57
2:P:1:DC:H2''	2:P:2:DA:C5'	2.27	0.57
3:A:207:GLN:O	3:A:210:LEU:HB2	2.05	0.57
3:A:41:LYS:HE2	3:A:64:GLY:HA2	1.87	0.57
3:A:270:LEU:HD13	3:A:316:GLU:OE2	2.04	0.57
3:A:212:HIS:H	3:A:212:HIS:CD2	2.23	0.56
3:A:26:GLU:HA	3:A:30:SER:OG	2.05	0.56
3:A:62:LEU:HD12	3:A:63:PRO:HD2	1.87	0.56
3:A:155:MET:HE3	3:A:188:SER:CB	2.35	0.56
3:A:106:ILE:HG12	3:A:136:GLN:HG2	1.88	0.56
3:A:135:HIS:O	3:A:138:ILE:HB	2.06	0.56
3:A:223:PHE:O	3:A:239:CYS:HA	2.05	0.56
3:A:26:GLU:HA	3:A:26:GLU:OE1	2.05	0.56
3:A:298:ILE:N	5:A:578:HOH:O	2.33	0.56
3:A:31:GLN:N	5:A:641:HOH:O	2.31	0.56
3:A:235:PHE:CZ	3:A:237:GLY:HA3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:259:LEU:O	3:A:260:ILE:HD13	2.06	0.55
3:A:157:GLN:NE2	3:A:244:LYS:NZ	2.51	0.55
3:A:157:GLN:NE2	3:A:244:LYS:HZ3	2.02	0.55
3:A:133:ASN:ND2	3:A:136:GLN:N	2.41	0.55
3:A:155:MET:HA	3:A:158:MET:HE3	1.89	0.55
3:A:200:PHE:HB2	3:A:210:LEU:HD11	1.89	0.55
3:A:167:LYS:O	3:A:167:LYS:HG2	2.04	0.54
3:A:270:LEU:CD2	3:A:319:ILE:HD12	2.38	0.54
3:A:286:ALA:O	3:A:291:PHE:HB2	2.08	0.54
3:A:180:SER:HA	3:A:183:ARG:HB2	1.90	0.54
3:A:123:GLU:HG3	5:A:623:HOH:O	2.07	0.54
3:A:151:PRO:HD2	3:A:253:ARG:HH21	1.73	0.54
3:A:248:LYS:O	3:A:248:LYS:HG2	2.08	0.53
3:A:265:TYR:CD2	3:A:269:VAL:HG21	2.42	0.53
3:A:207:GLN:OE1	3:A:210:LEU:HG	2.09	0.53
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.38	0.53
3:A:41:LYS:O	3:A:44:SER:HB3	2.08	0.53
3:A:331:LYS:HD2	3:A:332:ASP:N	2.24	0.53
3:A:321:ASP:O	3:A:324:GLN:N	2.41	0.52
3:A:12:ASN:HD21	3:A:53:ILE:N	1.98	0.52
3:A:294:ASN:N	3:A:294:ASN:HD22	2.06	0.52
3:A:133:ASN:O	3:A:137:ARG:HG3	2.10	0.52
3:A:299:ARG:HG2	3:A:309:GLU:C	2.34	0.52
3:A:292:THR:O	3:A:298:ILE:HA	2.10	0.52
3:A:15:ILE:CG2	3:A:46:ILE:HD13	2.36	0.52
3:A:166:VAL:HG12	3:A:173:TYR:CB	2.40	0.52
3:A:177:VAL:O	3:A:182:ARG:HD2	2.10	0.52
3:A:214:VAL:HG23	3:A:215:VAL:H	1.73	0.52
3:A:12:ASN:HA	5:A:553:HOH:O	2.09	0.52
3:A:150:ILE:HA	3:A:253:ARG:NH2	2.24	0.51
3:A:218:LEU:O	3:A:221:VAL:HG22	2.10	0.51
3:A:32:ALA:HB1	3:A:35:LYS:HB2	1.92	0.51
3:A:182:ARG:HH11	3:A:273:THR:HG21	1.75	0.51
3:A:12:ASN:CB	3:A:46:ILE:HD12	2.39	0.51
3:A:120:LYS:N	3:A:124:ASP:OD2	2.29	0.50
3:A:331:LYS:HD2	3:A:332:ASP:H	1.75	0.50
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.44	0.50
3:A:211:LEU:O	3:A:214:VAL:HG22	2.10	0.50
3:A:259:LEU:HD12	3:A:260:ILE:N	2.26	0.50
3:A:298:ILE:HG21	3:A:322:TYR:HD2	1.77	0.50
3:A:11:LEU:H	3:A:11:LEU:CD2	2.16	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:172:GLU:CG	3:A:198:PRO:HG3	2.42	0.50
3:A:275:SER:OG	3:A:277:ILE:HG12	2.12	0.50
3:A:279:ASN:O	3:A:283:ARG:N	2.39	0.50
3:A:317:LYS:NZ	3:A:327:TYR:HB2	2.27	0.50
3:A:157:GLN:HE22	3:A:244:LYS:HZ1	1.55	0.49
3:A:313:VAL:HG13	3:A:315:SER:O	2.12	0.49
3:A:122:LEU:HD21	3:A:140:LEU:CD1	2.42	0.49
3:A:201:THR:HA	3:A:261:PRO:HB3	1.93	0.49
3:A:122:LEU:HD23	3:A:122:LEU:O	2.13	0.49
3:A:133:ASN:HD22	3:A:136:GLN:H	1.52	0.49
3:A:319:ILE:O	3:A:322:TYR:HB2	2.12	0.49
3:A:106:ILE:HG23	3:A:110:ALA:HB3	1.94	0.49
3:A:327:TYR:CD1	3:A:328:ARG:N	2.81	0.49
3:A:205:THR:HG23	3:A:205:THR:O	2.12	0.49
3:A:259:LEU:C	3:A:260:ILE:HG12	2.38	0.48
3:A:41:LYS:HG2	3:A:42:ALA:N	2.27	0.48
3:A:17:ASP:N	3:A:17:ASP:OD1	2.47	0.48
3:A:298:ILE:HG21	3:A:322:TYR:CD2	2.48	0.48
3:A:82:LEU:HB3	3:A:85:LEU:HB2	1.96	0.48
3:A:75:GLU:O	3:A:79:THR:HG23	2.13	0.48
3:A:152:ARG:HA	3:A:155:MET:CB	2.26	0.48
3:A:182:ARG:HH11	3:A:273:THR:CG2	2.27	0.48
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.94	0.48
3:A:149:ARG:O	3:A:253:ARG:NH2	2.47	0.48
3:A:326:LYS:HG3	3:A:326:LYS:O	2.14	0.47
3:A:29:VAL:HG21	3:A:94:SER:HB2	1.96	0.47
2:P:2:DA:C8	2:P:2:DA:C5'	2.97	0.47
3:A:54:LYS:O	3:A:55:SER:HB3	2.15	0.47
3:A:155:MET:SD	3:A:158:MET:HE3	2.54	0.47
3:A:169:VAL:CG1	3:A:173:TYR:CE2	2.97	0.47
3:A:306:VAL:CG2	3:A:307:ALA:N	2.78	0.47
3:A:265:TYR:O	3:A:268:GLY:N	2.48	0.47
3:A:331:LYS:CD	3:A:332:ASP:N	2.78	0.47
3:A:60:LYS:CE	3:A:67:THR:HG22	2.43	0.46
2:P:6:DG:OP1	3:A:105:GLY:N	2.31	0.46
3:A:32:ALA:O	3:A:36:TYR:HB3	2.16	0.46
3:A:178:CYS:SG	3:A:194:LEU:CD2	3.04	0.46
3:A:200:PHE:HD2	3:A:260:ILE:O	1.99	0.46
3:A:208:PRO:O	3:A:212:HIS:HD2	1.98	0.46
3:A:122:LEU:HD21	3:A:140:LEU:HD12	1.97	0.46
3:A:150:ILE:O	3:A:188:SER:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:169:VAL:CG1	3:A:170:ASP:N	2.79	0.46
3:A:254:ARG:HH11	3:A:254:ARG:HA	1.81	0.46
2:P:5:DT:P	3:A:109:SER:HB3	2.56	0.46
3:A:23:ALA:CB	3:A:39:TYR:HB2	2.41	0.46
3:A:38:ALA:O	3:A:41:LYS:HD3	2.15	0.46
3:A:264:GLN:HE21	3:A:264:GLN:HB3	1.34	0.46
3:A:169:VAL:O	3:A:170:ASP:HB2	2.15	0.45
1:T:5:DC:H1'	5:T:564:HOH:O	2.16	0.45
3:A:122:LEU:HD22	3:A:126:ARG:CZ	2.45	0.45
3:A:224:ILE:CD1	3:A:235:PHE:CZ	3.00	0.45
3:A:266:TYR:CD1	3:A:266:TYR:N	2.80	0.45
3:A:40:ARG:HE	3:A:40:ARG:HB2	1.51	0.45
3:A:209:LYS:O	3:A:213:GLN:HB2	2.15	0.45
3:A:11:LEU:N	3:A:11:LEU:CD2	2.78	0.45
3:A:182:ARG:NH1	3:A:273:THR:CG2	2.79	0.45
3:A:286:ALA:CA	3:A:323:ILE:HG21	2.44	0.45
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.52	0.45
3:A:41:LYS:O	3:A:45:VAL:HG13	2.17	0.45
3:A:217:GLN:HE21	3:A:217:GLN:CA	2.29	0.45
3:A:244:LYS:HB2	3:A:245:ASN:ND2	2.31	0.45
3:A:49:TYR:HA	3:A:50:PRO:HD3	1.40	0.45
3:A:146:PHE:HD1	3:A:146:PHE:HA	1.58	0.45
3:A:153:GLU:O	3:A:157:GLN:HG3	2.17	0.45
3:A:244:LYS:HB2	3:A:245:ASN:H	1.54	0.45
3:A:26:GLU:O	3:A:30:SER:O	2.35	0.44
3:A:138:ILE:HD12	3:A:138:ILE:HG23	1.57	0.44
3:A:97:ILE:HG23	3:A:111:ALA:HB1	1.99	0.44
3:A:103:VAL:HG22	3:A:143:PHE:CD2	2.53	0.44
3:A:195:LEU:O	3:A:260:ILE:N	2.51	0.44
3:A:218:LEU:HD12	3:A:218:LEU:HA	1.65	0.44
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.48	0.44
3:A:60:LYS:C	3:A:62:LEU:N	2.75	0.44
3:A:270:LEU:HD12	5:A:584:HOH:O	2.16	0.44
3:A:218:LEU:N	3:A:218:LEU:HD13	2.31	0.44
3:A:200:PHE:CE2	3:A:261:PRO:N	2.85	0.44
3:A:223:PHE:CZ	3:A:239:CYS:HB2	2.53	0.44
3:A:297:THR:CG2	3:A:310:PRO:HB3	2.47	0.44
3:A:301:LEU:HD12	3:A:301:LEU:HA	1.67	0.43
3:A:200:PHE:CE2	3:A:260:ILE:C	2.96	0.43
3:A:138:ILE:HA	3:A:138:ILE:HD13	1.52	0.43
3:A:103:VAL:CG1	3:A:104:SER:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:158:MET:O	3:A:162:VAL:HG23	2.18	0.43
3:A:31:GLN:O	3:A:31:GLN:HG2	2.17	0.43
3:A:200:PHE:HD1	5:A:625:HOH:O	2.00	0.43
3:A:294:ASN:HD22	3:A:294:ASN:H	1.67	0.43
3:A:295:GLU:CD	3:A:295:GLU:H	2.25	0.43
2:P:2:DA:H5'	2:P:2:DA:H2'	1.40	0.43
3:A:166:VAL:HG12	3:A:173:TYR:HB2	2.00	0.43
3:A:270:LEU:HD21	3:A:282:MET:HE1	2.01	0.43
3:A:151:PRO:CD	3:A:253:ARG:HH21	2.31	0.43
3:A:155:MET:HE3	3:A:188:SER:OG	2.19	0.43
3:A:280:LYS:O	3:A:283:ARG:N	2.52	0.42
3:A:39:TYR:O	3:A:42:ALA:HB3	2.19	0.42
1:T:6:DT:H6	1:T:6:DT:H2'	1.31	0.42
3:A:132:LEU:HB2	3:A:137:ARG:HG2	2.00	0.42
3:A:27:LYS:CB	3:A:36:TYR:CD1	2.99	0.42
3:A:205:THR:O	3:A:206:LYS:O	2.37	0.42
5:T:617:HOH:O	3:A:234:LYS:HD3	2.18	0.42
3:A:10:THR:O	3:A:10:THR:HG23	2.19	0.42
3:A:15:ILE:HD12	5:A:642:HOH:O	2.19	0.42
2:P:2:DA:N6	5:P:598:HOH:O	2.53	0.42
3:A:169:VAL:CG1	3:A:173:TYR:CD2	3.02	0.42
3:A:271:TYR:CD2	3:A:271:TYR:C	2.98	0.42
1:T:5:DC:C2'	1:T:6:DT:H5'	2.48	0.42
3:A:255:ILE:O	3:A:255:ILE:HG23	2.19	0.42
3:A:194:LEU:HD11	3:A:258:ARG:CD	2.40	0.42
3:A:88:ILE:HD13	3:A:88:ILE:HG21	1.72	0.42
3:A:297:THR:HG21	3:A:310:PRO:HB3	2.02	0.42
3:A:322:TYR:C	3:A:324:GLN:H	2.26	0.42
3:A:322:TYR:HD1	3:A:322:TYR:HA	1.64	0.42
3:A:150:ILE:HG12	3:A:253:ARG:CZ	2.50	0.41
3:A:30:SER:HA	5:A:641:HOH:O	2.19	0.41
3:A:172:GLU:HB2	5:A:551:HOH:O	2.21	0.41
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.49	0.41
3:A:200:PHE:HA	5:A:625:HOH:O	2.20	0.41
3:A:317:LYS:HB3	5:A:501:HOH:O	2.20	0.41
3:A:326:LYS:HE2	3:A:328:ARG:NE	2.34	0.41
3:A:12:ASN:O	3:A:46:ILE:HD11	2.21	0.41
3:A:18:MET:HG2	3:A:22:LEU:HD23	2.03	0.41
3:A:149:ARG:NH2	3:A:188:SER:HA	2.36	0.41
3:A:150:ILE:O	3:A:187:SER:HA	2.19	0.41
3:A:73:ILE:HD13	3:A:73:ILE:HG21	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:125:LEU:HD23	3:A:132:LEU:HD21	2.03	0.41
3:A:62:LEU:HD12	3:A:62:LEU:HA	1.68	0.41
3:A:275:SER:OG	3:A:334:SER:O	2.29	0.41
3:A:93:THR:C	3:A:95:SER:N	2.78	0.41
3:A:200:PHE:CD2	3:A:260:ILE:C	2.99	0.41
1:T:4:DT:OP1	3:A:231:GLY:HA3	2.21	0.41
3:A:108:PRO:O	3:A:112:ARG:HG3	2.21	0.41
3:A:108:PRO:O	3:A:111:ALA:HB3	2.21	0.41
3:A:12:ASN:ND2	5:A:642:HOH:O	2.29	0.41
3:A:214:VAL:CG2	3:A:215:VAL:N	2.79	0.41
3:A:303:VAL:C	3:A:305:GLY:H	2.27	0.41
3:A:155:MET:HA	3:A:158:MET:HE2	2.03	0.40
3:A:260:ILE:HG23	3:A:261:PRO:HD2	2.03	0.40
3:A:26:GLU:HA	3:A:30:SER:HG	1.86	0.40
3:A:166:VAL:CG1	3:A:173:TYR:CB	2.99	0.40
3:A:261:PRO:HG2	3:A:264:GLN:HG3	2.04	0.40
3:A:297:THR:HB	3:A:298:ILE:H	1.73	0.40
1:T:3:DA:H2	2:P:5:DT:H3	1.59	0.40
3:A:15:ILE:CG2	3:A:46:ILE:CD1	2.99	0.40
3:A:62:LEU:HB3	3:A:65:VAL:CG1	2.51	0.40
1:T:7:DG:N2	2:P:2:DA:C2	2.90	0.40
3:A:97:ILE:O	3:A:101:THR:HB	2.21	0.40
3:A:136:GLN:HE21	3:A:136:GLN:HB2	1.40	0.40
3:A:200:PHE:O	3:A:261:PRO:HA	2.22	0.40
3:A:212:HIS:H	3:A:212:HIS:HD2	1.68	0.40
3:A:225:THR:N	3:A:238:VAL:O	2.31	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:O[3_558]	1.64	0.56

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%)	266 (82%)	45 (14%)	14 (4%)	2 7

All (14) 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	246	ASP
3	A	247	GLU
3	A	334	SER
3	A	10	THR
3	A	80	GLY
3	A	202	SER
3	A	91	ASP
3	A	309	GLU
3	A	207	GLN
3	A	263	ASP

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%)	210 (73%)	78 (27%)	0 1

All (78) 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	19	LEU
3	A	20	THR

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Mol	Chain	Res	Type
3	A	22	LEU
3	A	27	LYS
3	A	30	SER
3	A	33	ILE
3	A	41	LYS
3	A	44	SER
3	A	45	VAL
3	A	46	ILE
3	A	52	LYS
3	A	54	LYS
3	A	62	LEU
3	A	65	VAL
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	96	SER
3	A	97	ILE
3	A	100	LEU
3	A	101	THR
3	A	106	ILE
3	A	112	ARG
3	A	113	LYS
3	A	119	ILE
3	A	121	THR
3	A	122	LEU
3	A	132	LEU
3	A	133	ASN
3	A	153	GLU
3	A	158	MET
3	A	168	LYS
3	A	169	VAL
3	A	172	GLU
3	A	174	ILE
3	A	183	ARG
3	A	188	SER
3	A	191	MET
3	A	194	LEU
3	A	201	THR

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Mol	Chain	Res	Type
3	A	210	LEU
3	A	212	HIS
3	A	213	GLN
3	A	218	LEU
3	A	221	VAL
3	A	224	ILE
3	A	228	LEU
3	A	238	VAL
3	A	245	ASN
3	A	248	LYS
3	A	253	ARG
3	A	255	ILE
3	A	258	ARG
3	A	259	LEU
3	A	264	GLN
3	A	266	TYR
3	A	277	ILE
3	A	287	LEU
3	A	288	GLU
3	A	293	ILE
3	A	294	ASN
3	A	295	GLU
3	A	298	ILE
3	A	303	VAL
3	A	304	THR
3	A	306	VAL
3	A	309	GLU
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 (17) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	12	ASN
3	A	28	ASN
3	A	31	GLN
3	A	90	GLN
3	A	128	ASN
3	A	133	ASN
3	A	136	GLN

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Mol	Chain	Res	Type
3	A	157	GLN
3	A	212	HIS
3	A	213	GLN
3	A	217	GLN
3	A	222	HIS
3	A	245	ASN
3	A	264	GLN
3	A	279	ASN
3	A	285	HIS
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 ⓘ

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%)	-0.89	0 100 100	23, 33, 64, 100	0
2	P	6/6 (100%)	-0.91	0 100 100	21, 30, 39, 44	0
3	A	324/335 (96%)	-0.42	0 100 100	1, 37, 84, 100	0
All	All	337/348 (96%)	-0.44	0 100 100	1, 37, 85, 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	342	1/1	0.98	0.06	52,52,52,52	0
4	NA	A	341	1/1	0.99	0.04	8,8,8,8	0

6.5 Other polymers [i](#)

There are no such residues in this entry.