



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:27 PM UTC

PDB ID : 1BPE / pdb_00001bpe
Title : CRYSTAL STRUCTURE OF RAT DNA POLYMERASE BETA; EVIDENCE FOR A COMMON POLYMERASE MECHANISM
Authors : Sawaya, M.R.; Pelletier, H.; Kumar, A.; Wilson, S.H.; Kraut, J.
Deposited on : 1994-04-12
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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

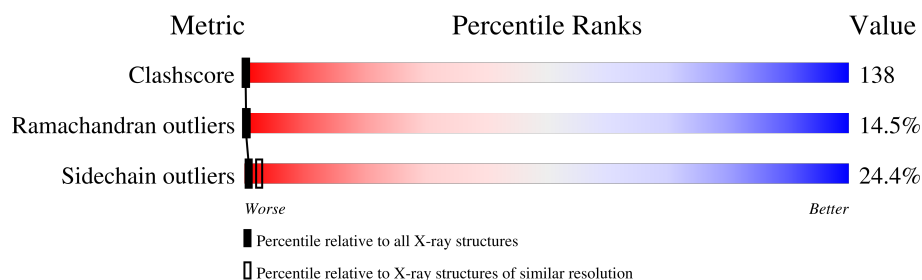
1 Overall quality at a glance

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)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	335	12% 34% 31% 8% 15%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DTP	A	338	-	-	X	-

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2158 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

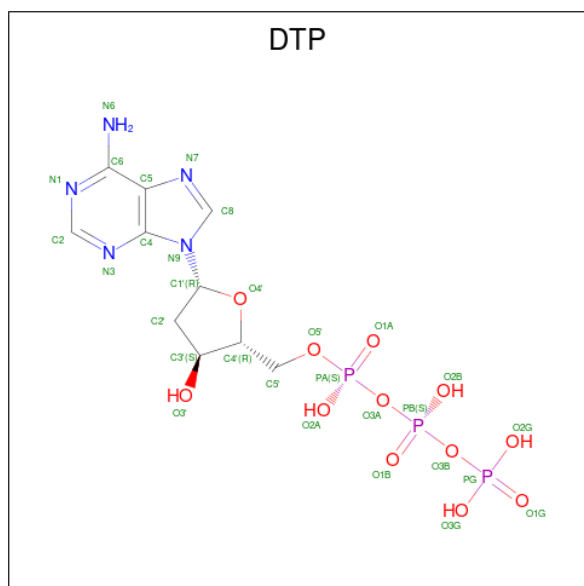
- Molecule 1 is a protein called DNA POLYMERASE BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	284	2128	1335	377	408	8	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	ARG	GLN	conflict	UNP P06766

- Molecule 2 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$)



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	30	10	5	12	3	0	0

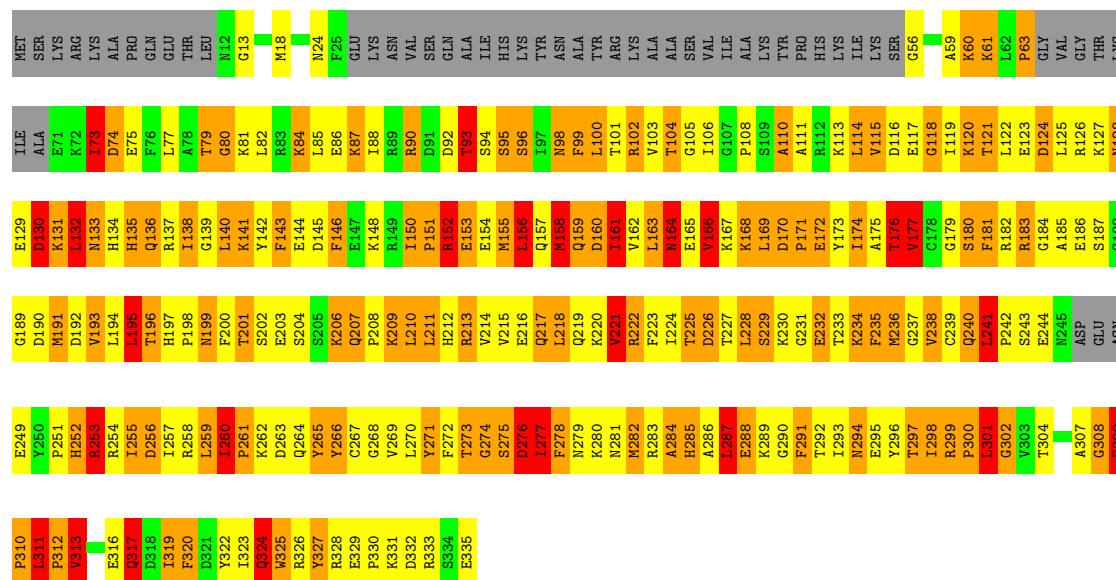
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: DNA POLYMERASE BETA

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.32Å 68.21Å 75.04Å 90.00° 91.77° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.199 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2158	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.84	26/2165 (1.2%)	2.19	97/2926 (3.3%)

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
1	A	1	1

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	87	LYS	C-N	36.52	1.77	1.33
1	A	74	ASP	N-CA	12.53	1.62	1.46
1	A	278	PHE	N-CA	-8.61	1.36	1.46
1	A	256	ASP	CA-C	-8.13	1.43	1.52
1	A	84	LYS	C-N	-7.89	1.22	1.33
1	A	261	PRO	CA-C	-7.44	1.44	1.52
1	A	161	ILE	CA-CB	-7.02	1.45	1.54
1	A	121	THR	N-CA	6.51	1.53	1.45
1	A	174	ILE	CA-C	-6.44	1.44	1.52
1	A	211	LEU	N-CA	-6.04	1.38	1.46
1	A	177	VAL	CA-CB	-5.89	1.47	1.54
1	A	176	THR	CA-C	-5.87	1.45	1.52
1	A	277	ILE	C-N	-5.73	1.26	1.33
1	A	287	LEU	N-CA	-5.70	1.38	1.46
1	A	186	GLU	N-CA	-5.61	1.38	1.46
1	A	256	ASP	N-CA	-5.56	1.39	1.46
1	A	193	VAL	CA-CB	-5.55	1.47	1.54
1	A	235	PHE	CA-C	-5.39	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	300	PRO	N-CA	-5.38	1.40	1.47
1	A	77	LEU	C-N	5.32	1.40	1.33
1	A	260	ILE	N-CA	-5.31	1.40	1.46
1	A	166	VAL	N-CA	-5.28	1.40	1.46
1	A	121	THR	CA-C	5.06	1.59	1.52
1	A	155	MET	CA-C	-5.04	1.46	1.52
1	A	297	THR	C-N	5.01	1.39	1.33
1	A	203	GLU	CA-CB	5.00	1.61	1.53

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	87	LYS	O-C-N	-11.20	106.46	122.36
1	A	180	SER	N-CA-C	10.71	122.65	110.97
1	A	297	THR	N-CA-C	9.67	122.84	108.14
1	A	73	ILE	CA-C-N	-9.11	104.13	121.54
1	A	73	ILE	C-N-CA	-9.11	104.13	121.54
1	A	278	PHE	CA-CB-CG	-8.84	104.96	113.80
1	A	121	THR	N-CA-C	8.74	123.96	110.42
1	A	310	PRO	CB-CA-C	-8.67	102.11	111.56
1	A	74	ASP	N-CA-C	8.60	129.11	110.80
1	A	238	VAL	N-CA-C	8.46	119.89	107.37
1	A	13	GLY	CA-C-N	8.04	128.90	119.98
1	A	13	GLY	C-N-CA	8.04	128.90	119.98
1	A	60	LYS	N-CA-C	-7.99	103.51	113.18
1	A	266	TYR	N-CA-C	7.99	120.70	111.11
1	A	150	ILE	C-N-CD	-7.97	92.31	125.00
1	A	169	LEU	N-CA-C	7.90	121.04	111.40
1	A	225	THR	N-CA-C	7.67	119.64	111.28
1	A	74	ASP	N-CA-CB	-7.59	97.66	110.49
1	A	243	SER	N-CA-C	7.51	121.82	109.96
1	A	146	PHE	CA-CB-CG	-7.46	106.34	113.80
1	A	150	ILE	CA-C-N	7.42	129.12	119.84
1	A	150	ILE	C-N-CA	7.42	129.12	119.84
1	A	115	VAL	N-CA-C	-7.32	103.16	110.62
1	A	241	LEU	C-N-CD	-7.28	95.14	125.00
1	A	275	SER	CB-CA-C	-7.25	96.33	110.10
1	A	63	PRO	N-CA-CB	7.22	110.94	103.00
1	A	170	ASP	C-N-CD	-7.15	95.70	125.00
1	A	18	MET	N-CA-C	-7.03	103.62	111.71
1	A	98	ASN	CA-CB-CG	-6.92	105.68	112.60
1	A	94	SER	N-CA-C	-6.89	104.85	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	124	ASP	N-CA-C	-6.82	103.77	111.07
1	A	256	ASP	CB-CA-C	-6.82	99.64	110.14
1	A	187	SER	N-CA-C	6.67	119.60	108.13
1	A	138	ILE	N-CA-C	6.46	116.60	110.53
1	A	261	PRO	CB-CA-C	-6.43	103.16	111.39
1	A	308	GLY	N-CA-C	6.42	118.80	110.45
1	A	164	ASN	CA-CB-CG	6.41	119.01	112.60
1	A	199	ASN	CA-CB-CG	6.41	119.01	112.60
1	A	221	VAL	N-CA-CB	-6.39	100.68	111.23
1	A	222	ARG	CB-CA-C	6.35	123.03	110.65
1	A	300	PRO	N-CA-C	-6.33	101.27	111.14
1	A	130	ASP	CA-CB-CG	-6.21	106.39	112.60
1	A	288	GLU	N-CA-C	-6.21	103.45	111.02
1	A	99	PHE	N-CA-C	-6.18	104.47	111.14
1	A	252	HIS	CA-CB-CG	6.15	119.95	113.80
1	A	271	TYR	N-CA-C	6.14	117.97	111.28
1	A	234	LYS	N-CA-C	6.14	117.73	108.46
1	A	156	LEU	O-C-N	6.13	128.62	122.12
1	A	301	LEU	N-CA-C	6.13	123.86	110.80
1	A	164	ASN	N-CA-C	-6.07	104.95	112.90
1	A	104	THR	N-CA-CB	6.05	118.91	110.26
1	A	302	GLY	N-CA-C	6.05	119.92	110.91
1	A	253	ARG	N-CA-C	6.05	118.98	108.76
1	A	159	GLN	N-CA-C	-6.04	101.40	111.37
1	A	300	PRO	CB-CA-C	-6.03	103.68	111.46
1	A	312	PRO	CB-CA-C	-5.99	102.18	111.22
1	A	82	LEU	N-CA-C	-5.97	104.68	111.07
1	A	186	GLU	CA-C-N	-5.96	112.45	121.86
1	A	186	GLU	C-N-CA	-5.96	112.45	121.86
1	A	153	GLU	CA-C-N	5.88	129.24	120.31
1	A	153	GLU	C-N-CA	5.88	129.24	120.31
1	A	158	MET	O-C-N	5.88	128.35	122.12
1	A	13	GLY	N-CA-C	-5.86	105.56	113.24
1	A	291	PHE	CA-CB-CG	5.85	119.65	113.80
1	A	298	ILE	N-CA-CB	5.75	117.40	110.95
1	A	96	SER	N-CA-C	-5.71	103.87	111.24
1	A	282	MET	N-CA-C	5.71	118.71	111.69
1	A	87	LYS	N-CA-C	-5.69	105.44	112.90
1	A	296	TYR	CB-CA-C	5.64	118.87	109.56
1	A	152	ARG	N-CA-CB	5.63	120.01	110.49
1	A	90	ARG	N-CA-C	-5.62	106.25	113.23
1	A	211	LEU	N-CA-C	-5.62	105.25	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	LYS	CA-C-N	-5.59	109.74	121.64
1	A	84	LYS	C-N-CA	-5.59	109.74	121.64
1	A	276	ASP	CB-CA-C	-5.58	99.32	110.42
1	A	310	PRO	N-CA-C	5.54	119.21	110.50
1	A	61	LYS	N-CA-C	-5.51	104.96	110.97
1	A	276	ASP	CA-CB-CG	5.42	118.02	112.60
1	A	260	ILE	O-C-N	5.42	127.28	121.10
1	A	196	THR	N-CA-CB	5.37	120.77	111.69
1	A	131	LYS	N-CA-C	5.31	119.50	113.19
1	A	193	VAL	N-CA-C	5.28	115.92	108.36
1	A	191	MET	N-CA-C	-5.26	103.74	110.53
1	A	195	LEU	N-CA-CB	-5.25	102.77	110.85
1	A	132	LEU	N-CA-C	5.23	116.23	108.86
1	A	93	THR	N-CA-C	-5.22	106.74	113.01
1	A	298	ILE	CB-CA-C	-5.21	104.98	111.08
1	A	24	ASN	N-CA-C	-5.21	105.50	111.07
1	A	320	PHE	N-CA-C	-5.20	106.03	112.38
1	A	80	GLY	N-CA-C	-5.18	100.90	113.18
1	A	141	LYS	CA-C-N	-5.15	114.04	122.79
1	A	141	LYS	C-N-CA	-5.15	114.04	122.79
1	A	222	ARG	N-CA-CB	5.13	121.19	113.65
1	A	193	VAL	CB-CA-C	-5.08	103.93	110.84
1	A	201	THR	N-CA-C	5.07	115.73	108.74
1	A	311	LEU	N-CA-C	-5.02	102.97	110.20
1	A	95	SER	N-CA-C	-5.01	107.17	113.28

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	222	ARG	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	73	ILE	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2128	0	1946	552	2
2	A	30	0	12	16	0
All	All	2158	0	1958	567	2

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 138.

All (567) 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:A:338:DTP:O1A	2:A:338:DTP:PA	1.10	1.49
1:A:87:LYS:C	1:A:88:ILE:N	1.77	1.41
2:A:338:DTP:PG	2:A:338:DTP:C5'	2.28	1.22
2:A:338:DTP:O2G	2:A:338:DTP:H5'2	1.37	1.17
2:A:338:DTP:PG	2:A:338:DTP:H5'2	1.84	1.17
1:A:241:LEU:HD23	1:A:242:PRO:HD2	1.27	1.13
1:A:317:GLN:H	1:A:317:GLN:NE2	1.52	1.08
1:A:309:GLU:HG3	1:A:310:PRO:HD2	1.32	1.06
1:A:122:LEU:HD13	1:A:126:ARG:HH12	1.22	1.04
2:A:338:DTP:PG	2:A:338:DTP:H5'1	1.92	1.04
1:A:100:LEU:HD23	1:A:115:VAL:HG22	1.40	1.03
1:A:259:LEU:HD12	1:A:260:ILE:H	1.22	1.00
1:A:104:THR:HB	1:A:139:GLY:HA3	1.42	1.00
1:A:289:LYS:HD2	1:A:323:ILE:HB	1.43	0.99
2:A:338:DTP:C5'	2:A:338:DTP:O1G	2.10	0.98
1:A:302:GLY:HA3	1:A:307:ALA:HB3	1.45	0.98
1:A:114:LEU:HA	1:A:117:GLU:HG2	1.46	0.98
1:A:218:LEU:HB3	1:A:224:ILE:HG13	1.45	0.97
1:A:56:GLY:HA2	1:A:59:ALA:HB3	1.42	0.97
1:A:319:ILE:HA	1:A:322:TYR:CD2	2.00	0.96
1:A:195:LEU:HD12	1:A:196:THR:H	1.31	0.93
1:A:104:THR:CB	1:A:139:GLY:HA3	1.99	0.92
1:A:106:ILE:HD12	1:A:111:ALA:HB2	1.47	0.92
1:A:158:MET:HG3	1:A:191:MET:HE1	1.51	0.92
1:A:99:PHE:HA	1:A:102:ARG:HE	1.32	0.92
1:A:319:ILE:HA	1:A:322:TYR:HD2	1.35	0.92
1:A:317:GLN:H	1:A:317:GLN:HE21	1.07	0.91
1:A:300:PRO:HD3	1:A:311:LEU:HD11	1.53	0.91
1:A:260:ILE:HG23	1:A:261:PRO:HD2	1.49	0.91
1:A:113:LYS:HG3	1:A:114:LEU:HD13	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:GLU:HG3	1:A:198:PRO:HG2	1.53	0.90
1:A:87:LYS:N	1:A:88:ILE:N	2.19	0.90
1:A:158:MET:HA	1:A:161:ILE:CD1	2.02	0.89
1:A:317:GLN:HE21	1:A:317:GLN:N	1.69	0.88
1:A:87:LYS:CA	1:A:88:ILE:N	2.36	0.88
1:A:286:ALA:HA	1:A:323:ILE:HG21	1.54	0.87
1:A:260:ILE:HG21	1:A:265:TYR:HA	1.55	0.87
1:A:289:LYS:CD	1:A:323:ILE:HB	2.05	0.87
1:A:261:PRO:HG2	1:A:264:GLN:HB2	1.56	0.86
1:A:309:GLU:HG3	1:A:310:PRO:CD	2.05	0.86
1:A:157:GLN:HB3	1:A:241:LEU:HD11	1.57	0.86
1:A:73:ILE:CB	1:A:75:GLU:H	1.88	0.85
1:A:56:GLY:CA	1:A:59:ALA:HB3	2.05	0.85
1:A:150:ILE:HG12	1:A:253:ARG:CZ	2.07	0.85
1:A:100:LEU:CD2	1:A:115:VAL:HG22	2.06	0.84
1:A:270:LEU:HD22	1:A:319:ILE:HD11	1.59	0.84
1:A:99:PHE:HB2	1:A:102:ARG:HH21	1.42	0.84
1:A:259:LEU:HD12	1:A:260:ILE:N	1.92	0.83
1:A:330:PRO:HA	1:A:333:ARG:CD	2.07	0.83
1:A:143:PHE:HA	1:A:146:PHE:HB2	1.60	0.83
2:A:338:DTP:C5'	2:A:338:DTP:O2G	2.16	0.83
1:A:161:ILE:HA	1:A:164:ASN:CG	2.04	0.82
1:A:241:LEU:HD23	1:A:242:PRO:CD	2.10	0.81
2:A:338:DTP:H5'1	2:A:338:DTP:O3B	1.75	0.81
1:A:285:HIS:HA	1:A:288:GLU:HB2	1.63	0.81
1:A:294:ASN:ND2	1:A:299:ARG:NH1	2.28	0.81
1:A:302:GLY:CA	1:A:307:ALA:HB3	2.10	0.81
1:A:234:LYS:HG3	1:A:235:PHE:N	1.94	0.81
1:A:234:LYS:NZ	1:A:258:ARG:HH22	1.78	0.81
1:A:209:LYS:HA	1:A:212:HIS:HB2	1.64	0.80
1:A:201:THR:C	1:A:261:PRO:HB3	2.05	0.80
1:A:209:LYS:CA	1:A:212:HIS:HB2	2.12	0.80
1:A:182:ARG:HH11	1:A:273:THR:HG21	1.46	0.80
1:A:150:ILE:HG12	1:A:253:ARG:NH1	1.97	0.79
1:A:173:TYR:CD1	1:A:195:LEU:HD11	2.17	0.79
1:A:207:GLN:HB3	1:A:210:LEU:HD12	1.63	0.79
1:A:139:GLY:O	1:A:143:PHE:HB2	1.82	0.79
1:A:113:LYS:HA	1:A:116:ASP:HB2	1.63	0.79
1:A:234:LYS:HZ2	1:A:258:ARG:NH2	1.80	0.79
1:A:228:LEU:HD23	1:A:237:GLY:HA2	1.65	0.79
1:A:265:TYR:O	1:A:269:VAL:HG23	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:SER:N	1:A:261:PRO:HB3	1.98	0.79
1:A:227:THR:HG23	1:A:235:PHE:HE1	1.46	0.78
1:A:319:ILE:HG12	1:A:320:PHE:N	1.97	0.78
1:A:211:LEU:HB2	1:A:259:LEU:HD23	1.65	0.78
1:A:114:LEU:HA	1:A:117:GLU:CG	2.14	0.78
1:A:270:LEU:HD12	1:A:333:ARG:HH12	1.48	0.78
1:A:155:MET:O	1:A:158:MET:HG2	1.83	0.78
1:A:157:GLN:HB3	1:A:241:LEU:CD1	2.14	0.78
1:A:122:LEU:HD13	1:A:126:ARG:NH1	2.00	0.77
1:A:110:ALA:HA	1:A:113:LYS:CE	2.14	0.77
1:A:204:SER:O	1:A:206:LYS:HG2	1.84	0.77
1:A:111:ALA:O	1:A:115:VAL:HG23	1.84	0.77
1:A:197:HIS:CG	1:A:198:PRO:HD2	2.20	0.77
1:A:231:GLY:O	1:A:232:GLU:HG2	1.85	0.77
1:A:274:GLY:HA2	1:A:279:ASN:OD1	1.84	0.77
1:A:221:VAL:CG2	1:A:223:PHE:H	1.98	0.76
1:A:234:LYS:NZ	1:A:258:ARG:NH2	2.33	0.76
1:A:241:LEU:CD2	1:A:242:PRO:HD2	2.12	0.76
1:A:330:PRO:HA	1:A:333:ARG:HD2	1.66	0.76
1:A:122:LEU:HD22	1:A:126:ARG:NH1	2.01	0.76
1:A:182:ARG:NH1	1:A:273:THR:HG21	2.01	0.75
1:A:114:LEU:CA	1:A:117:GLU:HG2	2.16	0.75
1:A:131:LYS:O	1:A:132:LEU:HD13	1.86	0.75
1:A:131:LYS:C	1:A:132:LEU:HD22	2.12	0.75
1:A:287:LEU:HA	1:A:291:PHE:H	1.49	0.75
1:A:191:MET:HB3	1:A:255:ILE:HB	1.69	0.75
1:A:277:ILE:HD13	1:A:277:ILE:H	1.50	0.75
1:A:165:GLU:OE1	1:A:168:LYS:HE3	1.87	0.75
1:A:122:LEU:HB3	1:A:126:ARG:NH1	2.01	0.75
1:A:158:MET:HA	1:A:161:ILE:HD12	1.68	0.74
1:A:104:THR:CG2	1:A:139:GLY:HA3	2.17	0.74
1:A:253:ARG:HG2	1:A:253:ARG:HH11	1.52	0.74
1:A:286:ALA:CB	1:A:323:ILE:HG21	2.18	0.74
1:A:311:LEU:HD12	1:A:311:LEU:H	1.52	0.74
1:A:134:HIS:HA	1:A:137:ARG:NH1	2.03	0.73
1:A:197:HIS:CD2	1:A:198:PRO:HD2	2.22	0.73
1:A:106:ILE:HG22	1:A:136:GLN:NE2	2.02	0.73
1:A:195:LEU:HD12	1:A:196:THR:N	2.01	0.73
1:A:286:ALA:CA	1:A:323:ILE:HG21	2.18	0.73
1:A:110:ALA:HA	1:A:113:LYS:NZ	2.03	0.73
1:A:183:ARG:HD3	1:A:333:ARG:HB2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:LEU:C	1:A:87:LYS:H	1.97	0.73
1:A:311:LEU:HB3	1:A:312:PRO:HD2	1.70	0.73
1:A:100:LEU:CD1	1:A:125:LEU:HD11	2.17	0.73
1:A:209:LYS:C	1:A:212:HIS:HB2	2.14	0.73
1:A:221:VAL:HG23	1:A:223:PHE:H	1.54	0.72
1:A:117:GLU:C	1:A:119:ILE:H	1.96	0.72
1:A:110:ALA:HA	1:A:113:LYS:HE3	1.70	0.72
1:A:145:ASP:OD2	1:A:251:PRO:HB3	1.89	0.72
1:A:261:PRO:HG2	1:A:264:GLN:CB	2.20	0.72
1:A:122:LEU:HB3	1:A:126:ARG:HH11	1.54	0.72
1:A:135:HIS:HB3	1:A:136:GLN:HG3	1.69	0.72
1:A:287:LEU:HD12	1:A:287:LEU:O	1.89	0.72
1:A:80:GLY:HA3	1:A:84:LYS:CB	2.20	0.72
1:A:294:ASN:ND2	1:A:299:ARG:HH12	1.86	0.72
2:A:338:DTP:O1A	2:A:338:DTP:O2B	2.08	0.72
1:A:158:MET:HG3	1:A:191:MET:CE	2.19	0.71
1:A:99:PHE:HD1	1:A:102:ARG:NE	1.87	0.71
1:A:260:ILE:HG23	1:A:261:PRO:CD	2.21	0.71
1:A:215:VAL:O	1:A:219:GLN:HG3	1.91	0.71
1:A:150:ILE:HD11	1:A:253:ARG:CB	2.21	0.71
1:A:110:ALA:O	1:A:114:LEU:HD22	1.90	0.71
1:A:330:PRO:HA	1:A:333:ARG:HG3	1.73	0.71
1:A:119:ILE:O	1:A:120:LYS:HG3	1.89	0.70
1:A:122:LEU:HD22	1:A:126:ARG:CZ	2.21	0.70
1:A:270:LEU:HD22	1:A:319:ILE:CD1	2.21	0.70
1:A:113:LYS:O	1:A:117:GLU:N	2.25	0.70
1:A:132:LEU:HD22	1:A:132:LEU:N	2.07	0.69
1:A:228:LEU:CD2	1:A:237:GLY:HA2	2.22	0.69
1:A:294:ASN:N	1:A:294:ASN:HD22	1.88	0.69
1:A:326:ARG:O	1:A:328:ARG:N	2.25	0.69
1:A:330:PRO:HA	1:A:333:ARG:CG	2.23	0.69
1:A:110:ALA:C	1:A:114:LEU:HD22	2.16	0.69
1:A:105:GLY:HA3	1:A:136:GLN:HG2	1.75	0.69
1:A:169:LEU:HD11	1:A:217:GLN:HG2	1.75	0.69
1:A:284:ALA:O	1:A:288:GLU:N	2.26	0.69
1:A:134:HIS:O	1:A:138:ILE:HG12	1.93	0.69
1:A:142:TYR:O	1:A:144:GLU:N	2.26	0.68
1:A:281:ASN:O	1:A:284:ALA:HB3	1.94	0.68
1:A:300:PRO:O	1:A:308:GLY:HA2	1.94	0.68
1:A:275:SER:HG	1:A:277:ILE:HG12	1.58	0.67
1:A:106:ILE:HB	1:A:110:ALA:CB	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:MET:HE3	1:A:223:PHE:HZ	1.59	0.67
1:A:172:GLU:HG3	1:A:198:PRO:CG	2.23	0.67
1:A:152:ARG:NH2	1:A:184:GLY:HA2	2.09	0.67
1:A:316:GLU:OE1	1:A:333:ARG:NH2	2.27	0.67
1:A:260:ILE:CG2	1:A:265:TYR:HA	2.24	0.67
1:A:227:THR:HG23	1:A:235:PHE:CE1	2.30	0.67
1:A:138:ILE:C	1:A:140:LEU:H	2.03	0.67
1:A:150:ILE:HG22	1:A:151:PRO:N	2.11	0.66
1:A:236:MET:HE3	1:A:254:ARG:NH2	2.09	0.66
1:A:100:LEU:O	1:A:106:ILE:HD11	1.94	0.66
1:A:204:SER:HG	1:A:207:GLN:HE21	1.43	0.66
1:A:328:ARG:NH1	1:A:332:ASP:O	2.28	0.66
1:A:217:GLN:O	1:A:221:VAL:HG13	1.94	0.66
1:A:254:ARG:NH1	1:A:255:ILE:O	2.29	0.66
1:A:254:ARG:NH1	1:A:256:ASP:OD1	2.27	0.66
1:A:100:LEU:HD11	1:A:125:LEU:HD11	1.75	0.66
1:A:183:ARG:NH1	1:A:273:THR:O	2.27	0.66
1:A:297:THR:O	1:A:299:ARG:NH1	2.29	0.66
1:A:106:ILE:HB	1:A:110:ALA:HB3	1.76	0.66
1:A:211:LEU:HD23	1:A:232:GLU:O	1.96	0.66
1:A:162:VAL:HG12	1:A:163:LEU:N	2.11	0.66
1:A:217:GLN:O	1:A:220:LYS:N	2.29	0.65
1:A:277:ILE:HG12	1:A:278:PHE:N	2.10	0.65
1:A:151:PRO:HG2	1:A:154:GLU:CD	2.21	0.65
1:A:287:LEU:HD11	1:A:301:LEU:HD22	1.78	0.65
1:A:209:LYS:O	1:A:213:ARG:N	2.29	0.65
1:A:229:SER:OG	1:A:230:LYS:N	2.28	0.65
1:A:311:LEU:HD12	1:A:311:LEU:N	2.11	0.65
1:A:130:ASP:OD1	1:A:130:ASP:N	2.29	0.65
1:A:183:ARG:CD	1:A:333:ARG:HB2	2.26	0.65
1:A:330:PRO:CA	1:A:333:ARG:HG3	2.27	0.65
1:A:93:THR:O	1:A:96:SER:HB2	1.97	0.64
1:A:143:PHE:O	1:A:146:PHE:HB2	1.98	0.64
1:A:253:ARG:HH11	1:A:253:ARG:CG	2.10	0.64
1:A:261:PRO:CG	1:A:264:GLN:HB2	2.28	0.64
1:A:152:ARG:NH2	1:A:181:PHE:O	2.29	0.64
1:A:276:ASP:O	1:A:279:ASN:N	2.29	0.64
1:A:143:PHE:CA	1:A:146:PHE:HB2	2.27	0.64
1:A:166:VAL:O	1:A:169:LEU:N	2.30	0.64
1:A:183:ARG:O	1:A:331:LYS:HA	1.97	0.64
1:A:119:ILE:HA	1:A:124:ASP:OD2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:ASP:O	1:A:280:LYS:N	2.31	0.64
1:A:286:ALA:HA	1:A:323:ILE:CG2	2.24	0.64
1:A:193:VAL:C	1:A:194:LEU:HD12	2.23	0.64
1:A:73:ILE:CB	1:A:75:GLU:N	2.59	0.63
1:A:286:ALA:O	1:A:291:PHE:N	2.31	0.63
1:A:106:ILE:CD1	1:A:111:ALA:HB2	2.24	0.63
1:A:161:ILE:HA	1:A:164:ASN:OD1	1.99	0.63
1:A:298:ILE:HG12	1:A:311:LEU:HD13	1.80	0.63
1:A:236:MET:HA	1:A:256:ASP:HA	1.79	0.63
1:A:98:ASN:O	1:A:101:THR:HG22	1.99	0.62
1:A:331:LYS:NZ	1:A:332:ASP:OD2	2.31	0.62
2:A:338:DTP:H5'1	2:A:338:DTP:O1G	1.90	0.62
2:A:338:DTP:O1G	2:A:338:DTP:C4'	2.47	0.62
1:A:105:GLY:HA3	1:A:136:GLN:CG	2.30	0.62
1:A:123:GLU:HA	1:A:126:ARG:HB2	1.81	0.62
1:A:173:TYR:O	1:A:174:ILE:HG13	1.98	0.62
1:A:104:THR:CG2	1:A:136:GLN:HA	2.30	0.62
1:A:261:PRO:HB2	1:A:263:ASP:OD1	1.99	0.62
1:A:150:ILE:HD11	1:A:253:ARG:CG	2.30	0.61
1:A:260:ILE:HG22	1:A:261:PRO:O	2.01	0.61
1:A:270:LEU:CD2	1:A:319:ILE:HD11	2.29	0.61
1:A:267:CYS:SG	1:A:297:THR:HA	2.40	0.61
1:A:122:LEU:CD1	1:A:126:ARG:HH12	2.07	0.61
1:A:113:LYS:O	1:A:117:GLU:HG2	2.00	0.61
1:A:238:VAL:HG12	1:A:252:HIS:HB3	1.82	0.61
1:A:143:PHE:C	1:A:146:PHE:HB2	2.26	0.60
1:A:183:ARG:HD2	1:A:330:PRO:O	2.01	0.60
1:A:312:PRO:O	1:A:313:VAL:HG23	2.02	0.60
1:A:278:PHE:CZ	1:A:328:ARG:HD3	2.36	0.60
1:A:298:ILE:HG23	1:A:311:LEU:HD13	1.83	0.60
1:A:104:THR:HG22	1:A:136:GLN:HA	1.83	0.60
1:A:145:ASP:CG	1:A:251:PRO:HB3	2.26	0.60
1:A:234:LYS:HD2	1:A:236:MET:SD	2.42	0.60
1:A:270:LEU:HD12	1:A:333:ARG:NH1	2.17	0.60
1:A:87:LYS:C	1:A:88:ILE:CA	2.72	0.59
1:A:227:THR:CG2	1:A:235:PHE:HE1	2.13	0.59
1:A:311:LEU:H	1:A:311:LEU:CD1	2.15	0.59
1:A:182:ARG:HH11	1:A:273:THR:CG2	2.13	0.59
1:A:191:MET:HG3	1:A:192:ASP:H	1.68	0.59
1:A:270:LEU:HD21	1:A:282:MET:CE	2.32	0.59
1:A:300:PRO:HD3	1:A:311:LEU:CD1	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LEU:HA	1:A:166:VAL:HG13	1.84	0.59
1:A:155:MET:O	1:A:159:GLN:N	2.28	0.59
1:A:113:LYS:HG3	1:A:114:LEU:CD1	2.31	0.58
1:A:218:LEU:HB3	1:A:224:ILE:CG1	2.27	0.58
1:A:309:GLU:CG	1:A:310:PRO:HD2	2.21	0.58
1:A:206:LYS:C	1:A:207:GLN:HG2	2.27	0.58
1:A:207:GLN:C	1:A:209:LYS:HD2	2.28	0.58
1:A:289:LYS:NZ	1:A:323:ILE:O	2.36	0.58
1:A:92:ASP:O	1:A:95:SER:HB3	2.03	0.58
1:A:299:ARG:HG3	1:A:299:ARG:HH11	1.67	0.58
1:A:105:GLY:CA	1:A:136:GLN:HG2	2.33	0.58
1:A:134:HIS:ND1	1:A:137:ARG:NH2	2.51	0.58
1:A:316:GLU:CD	1:A:333:ARG:HH22	2.12	0.58
1:A:106:ILE:N	1:A:136:GLN:HG2	2.19	0.58
1:A:116:ASP:C	1:A:118:GLY:H	2.11	0.57
1:A:197:HIS:CE1	1:A:199:ASN:HB2	2.40	0.57
1:A:180:SER:O	1:A:183:ARG:N	2.38	0.57
1:A:218:LEU:O	1:A:221:VAL:HG22	2.04	0.57
1:A:284:ALA:O	1:A:287:LEU:N	2.38	0.57
1:A:254:ARG:HH22	1:A:256:ASP:CG	2.13	0.56
1:A:156:LEU:HA	1:A:159:GLN:CB	2.35	0.56
1:A:218:LEU:HB2	1:A:224:ILE:HD12	1.87	0.56
1:A:278:PHE:HZ	1:A:328:ARG:HD3	1.69	0.56
1:A:285:HIS:O	1:A:289:LYS:HG3	2.06	0.56
1:A:99:PHE:CB	1:A:102:ARG:HH21	2.17	0.56
1:A:138:ILE:N	1:A:138:ILE:HD13	2.20	0.56
1:A:197:HIS:CE1	1:A:199:ASN:H	2.23	0.56
1:A:288:GLU:C	1:A:290:GLY:H	2.11	0.56
1:A:329:GLU:HB3	1:A:330:PRO:HD2	1.86	0.56
1:A:60:LYS:HA	1:A:63:PRO:CB	2.36	0.56
1:A:114:LEU:HD21	1:A:132:LEU:CD1	2.36	0.56
1:A:292:THR:HB	1:A:301:LEU:HD11	1.86	0.56
1:A:302:GLY:HA3	1:A:307:ALA:CB	2.29	0.56
1:A:317:GLN:HG3	1:A:327:TYR:CG	2.40	0.56
2:A:338:DTP:O1G	2:A:338:DTP:H4'	2.06	0.56
1:A:110:ALA:HA	1:A:113:LYS:HZ1	1.71	0.55
1:A:110:ALA:O	1:A:113:LYS:HG2	2.07	0.55
1:A:156:LEU:O	1:A:160:ASP:N	2.39	0.55
1:A:133:ASN:C	1:A:133:ASN:HD22	2.14	0.55
1:A:218:LEU:H	1:A:218:LEU:HD22	1.71	0.55
1:A:260:ILE:CG2	1:A:261:PRO:HD2	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:MET:N	1:A:254:ARG:O	2.35	0.55
1:A:234:LYS:HZ3	1:A:258:ARG:HH22	1.54	0.55
1:A:216:GLU:O	1:A:219:GLN:HB2	2.06	0.55
1:A:113:LYS:CA	1:A:116:ASP:HB2	2.36	0.54
1:A:234:LYS:HZ3	1:A:258:ARG:HH12	1.54	0.54
1:A:275:SER:OG	1:A:278:PHE:N	2.30	0.54
2:A:338:DTP:O1A	2:A:338:DTP:PB	2.63	0.54
1:A:114:LEU:C	1:A:117:GLU:H	2.16	0.54
1:A:138:ILE:O	1:A:142:TYR:N	2.40	0.54
1:A:166:VAL:HG22	1:A:167:LYS:N	2.22	0.54
1:A:172:GLU:HB3	1:A:197:HIS:CD2	2.42	0.54
1:A:288:GLU:OE1	1:A:288:GLU:HA	2.08	0.54
1:A:85:LEU:C	1:A:87:LYS:N	2.63	0.53
1:A:278:PHE:HE2	1:A:328:ARG:NH1	2.06	0.53
1:A:172:GLU:HB3	1:A:197:HIS:NE2	2.22	0.53
1:A:172:GLU:CG	1:A:198:PRO:HG2	2.34	0.53
1:A:197:HIS:ND1	1:A:199:ASN:N	2.51	0.53
1:A:253:ARG:NH1	1:A:253:ARG:HG2	2.22	0.53
1:A:286:ALA:O	1:A:291:PHE:HB2	2.09	0.53
1:A:135:HIS:O	1:A:138:ILE:HG12	2.09	0.53
1:A:158:MET:HG2	1:A:159:GLN:H	1.73	0.53
1:A:158:MET:HG2	1:A:159:GLN:N	2.23	0.53
1:A:268:GLY:HA2	1:A:295:GLU:O	2.09	0.53
1:A:285:HIS:ND1	1:A:325:TRP:CE2	2.77	0.53
1:A:113:LYS:CG	1:A:114:LEU:HD13	2.31	0.53
1:A:204:SER:OG	1:A:207:GLN:NE2	2.34	0.53
1:A:232:GLU:HG3	1:A:233:THR:HG23	1.89	0.53
1:A:150:ILE:CG2	1:A:151:PRO:HD2	2.39	0.53
1:A:270:LEU:HD21	1:A:282:MET:HE1	1.91	0.53
1:A:99:PHE:HD1	1:A:102:ARG:CZ	2.22	0.53
1:A:90:ARG:O	1:A:93:THR:HG22	2.08	0.53
1:A:209:LYS:O	1:A:212:HIS:HB2	2.09	0.52
1:A:157:GLN:O	1:A:160:ASP:HB2	2.08	0.52
1:A:317:GLN:H	1:A:317:GLN:CD	2.11	0.52
1:A:158:MET:HA	1:A:161:ILE:HD11	1.91	0.52
1:A:197:HIS:HE1	1:A:199:ASN:CG	2.17	0.52
1:A:285:HIS:ND1	1:A:289:LYS:NZ	2.57	0.52
1:A:117:GLU:O	1:A:119:ILE:N	2.42	0.52
1:A:232:GLU:HG2	1:A:233:THR:H	1.75	0.52
1:A:287:LEU:HD11	1:A:301:LEU:CD2	2.39	0.52
1:A:261:PRO:HG3	1:A:264:GLN:OE1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LEU:O	1:A:215:VAL:HG23	2.10	0.51
1:A:142:TYR:HB2	1:A:146:PHE:CE2	2.45	0.51
1:A:277:ILE:HD13	1:A:277:ILE:N	2.22	0.51
1:A:329:GLU:CB	1:A:330:PRO:HD2	2.40	0.51
1:A:142:TYR:HB3	1:A:146:PHE:CE1	2.46	0.51
1:A:204:SER:OG	1:A:206:LYS:HE3	2.10	0.51
1:A:207:GLN:O	1:A:210:LEU:HB2	2.10	0.51
1:A:317:GLN:HG3	1:A:327:TYR:CD2	2.45	0.51
1:A:142:TYR:CE1	1:A:252:HIS:CD2	2.98	0.51
1:A:234:LYS:HD2	1:A:236:MET:CG	2.41	0.51
1:A:260:ILE:HD12	1:A:261:PRO:HD2	1.92	0.51
1:A:110:ALA:CA	1:A:113:LYS:HE3	2.38	0.51
1:A:221:VAL:HG22	1:A:223:PHE:H	1.74	0.51
1:A:142:TYR:CB	1:A:146:PHE:CZ	2.93	0.51
1:A:190:ASP:OD1	1:A:190:ASP:O	2.29	0.51
1:A:298:ILE:HD13	1:A:322:TYR:CD2	2.45	0.51
1:A:157:GLN:O	1:A:161:ILE:HG13	2.10	0.51
1:A:159:GLN:O	1:A:163:LEU:HG	2.11	0.51
1:A:114:LEU:HD21	1:A:132:LEU:HD11	1.91	0.51
1:A:122:LEU:O	1:A:126:ARG:HG3	2.11	0.51
1:A:106:ILE:HD12	1:A:111:ALA:CB	2.31	0.51
1:A:156:LEU:O	1:A:160:ASP:OD2	2.28	0.51
1:A:260:ILE:HG21	1:A:265:TYR:CA	2.34	0.51
1:A:286:ALA:HB2	1:A:323:ILE:HD13	1.93	0.51
1:A:261:PRO:HG2	1:A:264:GLN:H	1.75	0.50
1:A:124:ASP:O	1:A:128:ASN:ND2	2.44	0.50
1:A:99:PHE:HA	1:A:102:ARG:NE	2.13	0.50
1:A:253:ARG:O	1:A:255:ILE:HG22	2.12	0.50
1:A:275:SER:OG	1:A:277:ILE:HG12	2.10	0.50
1:A:144:GLU:N	1:A:144:GLU:OE1	2.45	0.50
1:A:170:ASP:OD2	1:A:172:GLU:N	2.44	0.50
1:A:174:ILE:HD12	1:A:262:LYS:HE3	1.93	0.50
1:A:141:LYS:NZ	1:A:142:TYR:CE1	2.80	0.50
1:A:204:SER:OG	1:A:206:LYS:HG3	2.12	0.50
1:A:207:GLN:CB	1:A:210:LEU:HD12	2.39	0.50
1:A:236:MET:HE3	1:A:254:ARG:HH22	1.75	0.50
1:A:279:ASN:O	1:A:283:ARG:HG2	2.11	0.50
1:A:116:ASP:O	1:A:118:GLY:N	2.41	0.49
1:A:142:TYR:HB2	1:A:146:PHE:CZ	2.47	0.49
1:A:158:MET:CG	1:A:191:MET:HE1	2.34	0.49
1:A:100:LEU:HB3	1:A:111:ALA:HB1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:PHE:O	1:A:102:ARG:HB2	2.11	0.49
1:A:191:MET:HG3	1:A:192:ASP:N	2.27	0.49
1:A:122:LEU:HD21	1:A:144:GLU:OE2	2.12	0.49
1:A:174:ILE:HD12	1:A:262:LYS:HZ2	1.78	0.49
1:A:173:TYR:OH	1:A:210:LEU:O	2.29	0.49
1:A:174:ILE:HD12	1:A:262:LYS:NZ	2.27	0.49
1:A:323:ILE:O	1:A:324:GLN:O	2.31	0.49
1:A:138:ILE:HG22	1:A:142:TYR:HD2	1.77	0.49
1:A:143:PHE:HA	1:A:146:PHE:CB	2.39	0.49
1:A:168:LYS:HB3	1:A:168:LYS:NZ	2.28	0.49
1:A:193:VAL:O	1:A:194:LEU:HD12	2.13	0.49
1:A:221:VAL:HG23	1:A:223:PHE:N	2.24	0.48
1:A:116:ASP:C	1:A:118:GLY:N	2.71	0.48
1:A:169:LEU:HD21	1:A:217:GLN:OE1	2.13	0.48
1:A:285:HIS:ND1	1:A:325:TRP:CZ2	2.81	0.48
1:A:297:THR:OG1	1:A:298:ILE:N	2.45	0.48
1:A:154:GLU:O	1:A:157:GLN:HB2	2.13	0.48
1:A:294:ASN:ND2	1:A:297:THR:H	2.11	0.48
1:A:298:ILE:CD1	1:A:322:TYR:CD2	2.96	0.48
1:A:98:ASN:O	1:A:102:ARG:HG3	2.14	0.48
1:A:151:PRO:C	1:A:153:GLU:H	2.21	0.48
1:A:152:ARG:NH2	1:A:184:GLY:CA	2.77	0.48
1:A:217:GLN:O	1:A:219:GLN:N	2.46	0.48
1:A:217:GLN:HE21	1:A:217:GLN:HA	1.78	0.48
1:A:100:LEU:HG	1:A:125:LEU:HD11	1.95	0.48
1:A:156:LEU:CD1	1:A:181:PHE:HE2	2.27	0.48
1:A:177:VAL:O	1:A:177:VAL:HG13	2.14	0.48
1:A:114:LEU:CD2	1:A:132:LEU:HD11	2.43	0.48
1:A:202:SER:HB3	1:A:264:GLN:HG3	1.95	0.48
1:A:100:LEU:CG	1:A:125:LEU:HD11	2.43	0.48
1:A:278:PHE:C	1:A:280:LYS:H	2.22	0.48
1:A:261:PRO:C	1:A:263:ASP:H	2.21	0.48
1:A:95:SER:O	1:A:99:PHE:HB3	2.14	0.47
1:A:158:MET:HE3	1:A:223:PHE:CZ	2.45	0.47
1:A:202:SER:OG	1:A:263:ASP:OD2	2.29	0.47
1:A:209:LYS:HA	1:A:212:HIS:CB	2.41	0.47
1:A:279:ASN:O	1:A:283:ARG:HD3	2.14	0.47
1:A:293:ILE:HA	1:A:297:THR:O	2.14	0.47
1:A:317:GLN:NE2	1:A:317:GLN:N	2.33	0.47
1:A:99:PHE:CA	1:A:102:ARG:HE	2.17	0.47
1:A:285:HIS:ND1	1:A:289:LYS:CE	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:HIS:CE1	1:A:325:TRP:HE1	2.33	0.47
1:A:133:ASN:HD21	1:A:135:HIS:HB3	1.78	0.47
1:A:113:LYS:HZ2	1:A:114:LEU:HD13	1.79	0.47
1:A:265:TYR:HD2	1:A:266:TYR:CE1	2.32	0.47
1:A:196:THR:HA	1:A:259:LEU:HD11	1.97	0.47
2:A:338:DTP:O5'	2:A:338:DTP:H8	2.15	0.47
1:A:144:GLU:O	1:A:148:LYS:HE3	2.15	0.47
1:A:165:GLU:O	1:A:169:LEU:HG	2.14	0.47
1:A:197:HIS:CE1	1:A:199:ASN:CB	2.98	0.47
1:A:229:SER:O	1:A:230:LYS:HB2	2.15	0.47
1:A:101:THR:O	1:A:103:VAL:O	2.32	0.47
1:A:261:PRO:C	1:A:263:ASP:N	2.72	0.47
1:A:285:HIS:CG	1:A:289:LYS:HE3	2.50	0.47
1:A:311:LEU:HB3	1:A:312:PRO:CD	2.44	0.47
1:A:104:THR:O	1:A:136:GLN:HG2	2.15	0.46
1:A:232:GLU:CG	1:A:233:THR:N	2.77	0.46
1:A:207:GLN:HB3	1:A:210:LEU:CD1	2.39	0.46
1:A:236:MET:CE	1:A:254:ARG:NH2	2.78	0.46
1:A:146:PHE:N	1:A:146:PHE:CD1	2.79	0.46
1:A:328:ARG:NH2	1:A:335:GLU:OXT	2.48	0.46
1:A:115:VAL:O	1:A:119:ILE:O	2.33	0.46
1:A:200:PHE:CD1	1:A:201:THR:N	2.83	0.46
1:A:276:ASP:HB2	1:A:277:ILE:HD13	1.98	0.46
1:A:207:GLN:N	1:A:208:PRO:CD	2.79	0.46
1:A:127:LYS:O	1:A:129:GLU:HG3	2.16	0.46
1:A:157:GLN:HB3	1:A:241:LEU:HD13	1.96	0.46
1:A:275:SER:HG	1:A:278:PHE:H	1.59	0.46
1:A:191:MET:CG	1:A:192:ASP:N	2.79	0.46
1:A:284:ALA:O	1:A:287:LEU:HB3	2.15	0.46
1:A:316:GLU:O	1:A:319:ILE:HG23	2.15	0.46
1:A:179:GLY:HA2	1:A:272:PHE:O	2.15	0.46
1:A:317:GLN:CG	1:A:327:TYR:CD2	2.99	0.46
1:A:181:PHE:CD1	1:A:181:PHE:C	2.94	0.46
1:A:174:ILE:HD12	1:A:262:LYS:CE	2.47	0.45
1:A:174:ILE:CD1	1:A:262:LYS:NZ	2.79	0.45
1:A:150:ILE:CG2	1:A:151:PRO:N	2.78	0.45
1:A:308:GLY:O	1:A:309:GLU:HB2	2.17	0.45
1:A:104:THR:HB	1:A:139:GLY:CA	2.29	0.45
1:A:298:ILE:HG23	1:A:298:ILE:O	2.16	0.45
1:A:99:PHE:CD1	1:A:102:ARG:CZ	3.00	0.45
1:A:99:PHE:CD1	1:A:102:ARG:NH2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:TYR:HB2	1:A:313:VAL:CG1	2.46	0.45
1:A:190:ASP:HA	1:A:254:ARG:O	2.17	0.45
1:A:289:LYS:HD3	1:A:323:ILE:O	2.16	0.45
1:A:100:LEU:HD12	1:A:100:LEU:HA	1.65	0.45
1:A:151:PRO:HG2	1:A:154:GLU:OE2	2.17	0.45
1:A:156:LEU:HD13	1:A:181:PHE:CE2	2.52	0.45
1:A:113:LYS:NZ	1:A:114:LEU:HD13	2.32	0.45
1:A:270:LEU:HD21	1:A:282:MET:HE2	1.99	0.45
1:A:277:ILE:O	1:A:281:ASN:OD1	2.34	0.45
1:A:215:VAL:HG13	1:A:235:PHE:CE2	2.52	0.44
1:A:111:ALA:C	1:A:115:VAL:HG23	2.41	0.44
1:A:156:LEU:HA	1:A:156:LEU:HD13	1.63	0.44
1:A:234:LYS:HZ3	1:A:258:ARG:NH1	2.14	0.44
1:A:275:SER:O	1:A:279:ASN:OD1	2.35	0.44
1:A:311:LEU:N	1:A:311:LEU:CD1	2.77	0.44
1:A:151:PRO:HG2	1:A:154:GLU:OE1	2.17	0.44
1:A:136:GLN:HG3	1:A:136:GLN:H	1.48	0.44
1:A:234:LYS:NZ	1:A:258:ARG:CZ	2.81	0.44
1:A:271:TYR:CD2	1:A:295:GLU:HA	2.53	0.44
1:A:105:GLY:C	1:A:136:GLN:HG2	2.43	0.44
1:A:154:GLU:HA	1:A:157:GLN:HB2	1.99	0.44
1:A:271:TYR:CE2	1:A:295:GLU:HB3	2.52	0.44
1:A:106:ILE:HB	1:A:110:ALA:HB1	1.98	0.44
1:A:114:LEU:HA	1:A:114:LEU:HD12	1.69	0.44
1:A:254:ARG:HH12	1:A:255:ILE:C	2.26	0.44
1:A:114:LEU:CD1	1:A:114:LEU:N	2.80	0.44
1:A:211:LEU:HB2	1:A:259:LEU:CD2	2.44	0.44
1:A:329:GLU:O	1:A:333:ARG:HG3	2.18	0.44
1:A:180:SER:OG	2:A:338:DTP:O1B	2.33	0.43
1:A:236:MET:HA	1:A:256:ASP:OD1	2.17	0.43
1:A:170:ASP:CG	1:A:171:PRO:N	2.75	0.43
1:A:202:SER:HB2	1:A:264:GLN:NE2	2.33	0.43
1:A:150:ILE:HD11	1:A:253:ARG:HB2	1.96	0.43
1:A:158:MET:HA	1:A:161:ILE:CG1	2.47	0.43
1:A:113:LYS:NZ	1:A:114:LEU:CD1	2.81	0.43
1:A:119:ILE:C	1:A:120:LYS:HG3	2.42	0.43
1:A:150:ILE:HG23	1:A:151:PRO:HD2	1.99	0.43
1:A:177:VAL:H	1:A:177:VAL:HG12	1.53	0.43
1:A:191:MET:O	1:A:192:ASP:HB2	2.18	0.43
1:A:331:LYS:CG	1:A:332:ASP:N	2.81	0.43
1:A:158:MET:HB2	1:A:223:PHE:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:GLU:O	1:A:198:PRO:HD3	2.18	0.43
1:A:196:THR:HA	1:A:259:LEU:CD1	2.48	0.43
1:A:285:HIS:CE1	1:A:325:TRP:NE1	2.86	0.43
1:A:311:LEU:CB	1:A:312:PRO:HD2	2.42	0.43
1:A:98:ASN:HA	1:A:101:THR:HG22	2.00	0.43
1:A:176:THR:N	1:A:194:LEU:O	2.51	0.43
1:A:270:LEU:CD1	1:A:333:ARG:NH1	2.81	0.43
2:A:338:DTP:H5'2	2:A:338:DTP:O1G	1.89	0.43
1:A:221:VAL:CG2	1:A:223:PHE:HB2	2.49	0.43
1:A:285:HIS:CA	1:A:288:GLU:HB2	2.41	0.43
1:A:100:LEU:HB3	1:A:111:ALA:CB	2.49	0.42
1:A:260:ILE:CG2	1:A:265:TYR:CA	2.94	0.42
1:A:270:LEU:HD12	1:A:270:LEU:HA	1.64	0.42
1:A:127:LYS:C	1:A:129:GLU:H	2.25	0.42
1:A:133:ASN:ND2	1:A:135:HIS:HB3	2.33	0.42
1:A:160:ASP:O	1:A:164:ASN:HB3	2.19	0.42
1:A:259:LEU:O	1:A:260:ILE:HD13	2.19	0.42
1:A:115:VAL:HG13	1:A:120:LYS:HA	2.00	0.42
1:A:166:VAL:CG2	1:A:167:LYS:N	2.82	0.42
1:A:218:LEU:HD22	1:A:218:LEU:N	2.34	0.42
1:A:218:LEU:HD13	1:A:218:LEU:HA	1.87	0.42
1:A:224:ILE:HD13	1:A:235:PHE:HE2	1.84	0.42
1:A:241:LEU:HA	1:A:242:PRO:HD2	1.76	0.42
1:A:221:VAL:HG13	1:A:221:VAL:H	1.14	0.42
1:A:99:PHE:CD1	1:A:102:ARG:NE	2.77	0.42
1:A:104:THR:HG22	1:A:139:GLY:HA3	1.96	0.42
1:A:231:GLY:C	1:A:232:GLU:HG2	2.43	0.42
1:A:319:ILE:O	1:A:322:TYR:HB2	2.18	0.42
1:A:150:ILE:HD11	1:A:253:ARG:HG2	1.99	0.42
1:A:163:LEU:CA	1:A:166:VAL:HG13	2.50	0.42
1:A:268:GLY:O	1:A:271:TYR:HB3	2.20	0.42
1:A:96:SER:OG	1:A:120:LYS:HG2	2.20	0.41
1:A:100:LEU:HD23	1:A:115:VAL:CG2	2.30	0.41
1:A:221:VAL:CG2	1:A:223:PHE:CB	2.97	0.41
1:A:115:VAL:HA	1:A:119:ILE:O	2.20	0.41
1:A:170:ASP:CG	1:A:172:GLU:H	2.28	0.41
1:A:240:GLN:HG2	1:A:241:LEU:O	2.21	0.41
1:A:263:ASP:C	1:A:265:TYR:N	2.77	0.41
1:A:287:LEU:CD1	1:A:301:LEU:HD22	2.46	0.41
1:A:104:THR:OG1	1:A:105:GLY:N	2.52	0.41
1:A:111:ALA:HA	1:A:114:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:ARG:HA	1:A:155:MET:HB2	2.01	0.41
1:A:164:ASN:O	1:A:168:LYS:HG3	2.20	0.41
1:A:173:TYR:CD1	1:A:195:LEU:CD1	2.99	0.41
1:A:260:ILE:CG2	1:A:265:TYR:N	2.83	0.41
1:A:218:LEU:O	1:A:223:PHE:HB3	2.20	0.41
1:A:101:THR:C	1:A:103:VAL:N	2.77	0.41
1:A:102:ARG:HB3	1:A:143:PHE:CE1	2.54	0.41
1:A:156:LEU:HD13	1:A:181:PHE:HE2	1.84	0.41
1:A:158:MET:CG	1:A:159:GLN:N	2.83	0.41
1:A:289:LYS:HG3	1:A:289:LYS:H	1.51	0.41
1:A:135:HIS:HB3	1:A:136:GLN:H	1.19	0.41
1:A:138:ILE:O	1:A:141:LYS:N	2.54	0.41
1:A:294:ASN:HD21	1:A:299:ARG:NH1	2.13	0.41
1:A:85:LEU:O	1:A:87:LYS:N	2.53	0.41
1:A:175:ALA:HA	1:A:194:LEU:O	2.21	0.41
1:A:220:LYS:C	1:A:222:ARG:H	2.29	0.41
1:A:277:ILE:H	1:A:277:ILE:CD1	2.27	0.41
1:A:103:VAL:CG1	1:A:104:THR:N	2.82	0.41
1:A:157:GLN:HA	1:A:160:ASP:OD2	2.21	0.41
1:A:217:GLN:C	1:A:219:GLN:N	2.77	0.41
1:A:103:VAL:HG12	1:A:104:THR:N	2.36	0.41
1:A:114:LEU:HD13	1:A:114:LEU:N	2.35	0.41
1:A:144:GLU:C	1:A:146:PHE:N	2.78	0.41
1:A:166:VAL:O	1:A:169:LEU:HB2	2.21	0.41
1:A:292:THR:HG22	1:A:301:LEU:HD12	2.02	0.41
1:A:113:LYS:CG	1:A:114:LEU:N	2.83	0.41
1:A:133:ASN:ND2	1:A:135:HIS:CB	2.84	0.41
1:A:150:ILE:HD13	1:A:253:ARG:HD3	2.03	0.41
1:A:291:PHE:HD2	1:A:323:ILE:HG22	1.86	0.41
1:A:292:THR:CB	1:A:301:LEU:HD11	2.51	0.41
1:A:330:PRO:O	1:A:333:ARG:HG3	2.21	0.41
1:A:140:LEU:HG	1:A:141:LYS:N	2.23	0.40
1:A:163:LEU:HA	1:A:166:VAL:CG1	2.51	0.40
1:A:223:PHE:O	1:A:225:THR:N	2.54	0.40
1:A:234:LYS:HZ3	1:A:258:ARG:NH2	2.14	0.40
1:A:261:PRO:HB2	1:A:263:ASP:H	1.86	0.40
1:A:59:ALA:C	1:A:61:LYS:N	2.78	0.40
1:A:235:PHE:O	1:A:257:ILE:N	2.55	0.40
1:A:156:LEU:CD1	1:A:181:PHE:CE2	3.04	0.40
1:A:217:GLN:C	1:A:219:GLN:H	2.29	0.40
1:A:218:LEU:CB	1:A:224:ILE:CD1	2.99	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ASP:O	1:A:95:SER:N	2.45	0.40
1:A:122:LEU:CD2	1:A:126:ARG:NH1	2.79	0.40
1:A:180:SER:C	1:A:182:ARG:N	2.79	0.40
1:A:239:CYS:HB2	1:A:240:GLN:H	1.73	0.40

All (2) 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)
1:A:227:THR:N	1:A:335:GLU:OE2[2_656]	2.06	0.14
1:A:226:ASP:CA	1:A:335:GLU:OE2[2_656]	2.11	0.09

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	276/335 (82%)	183 (66%)	53 (19%)	40 (14%)	0 0

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	ASP
1	A	79	THR
1	A	81	LYS
1	A	86	GLU
1	A	128	ASN
1	A	135	HIS
1	A	143	PHE
1	A	185	ALA
1	A	244	GLU
1	A	304	THR
1	A	309	GLU

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Mol	Chain	Res	Type
1	A	324	GLN
1	A	73	ILE
1	A	110	ALA
1	A	118	GLY
1	A	120	LYS
1	A	130	ASP
1	A	136	GLN
1	A	218	LEU
1	A	240	GLN
1	A	274	GLY
1	A	301	LEU
1	A	327	TYR
1	A	151	PRO
1	A	160	ASP
1	A	189	GLY
1	A	232	GLU
1	A	284	ALA
1	A	102	ARG
1	A	152	ARG
1	A	276	ASP
1	A	317	GLN
1	A	171	PRO
1	A	161	ILE
1	A	183	ARG
1	A	207	GLN
1	A	228	LEU
1	A	265	TYR
1	A	108	PRO
1	A	313	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	205/296 (69%)	155 (76%)	50 (24%)	1 2

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	THR
1	A	93	THR
1	A	100	LEU
1	A	114	LEU
1	A	121	THR
1	A	132	LEU
1	A	133	ASN
1	A	140	LEU
1	A	156	LEU
1	A	158	MET
1	A	161	ILE
1	A	163	LEU
1	A	164	ASN
1	A	166	VAL
1	A	168	LYS
1	A	172	GLU
1	A	176	THR
1	A	177	VAL
1	A	181	PHE
1	A	195	LEU
1	A	206	LYS
1	A	209	LYS
1	A	210	LEU
1	A	213	ARG
1	A	214	VAL
1	A	217	GLN
1	A	221	VAL
1	A	226	ASP
1	A	229	SER
1	A	236	MET
1	A	241	LEU
1	A	249	GLU
1	A	253	ARG
1	A	255	ILE
1	A	259	LEU
1	A	260	ILE
1	A	273	THR
1	A	276	ASP
1	A	277	ILE
1	A	285	HIS
1	A	287	LEU
1	A	294	ASN

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Mol	Chain	Res	Type
1	A	299	ARG
1	A	309	GLU
1	A	311	LEU
1	A	313	VAL
1	A	317	GLN
1	A	319	ILE
1	A	324	GLN
1	A	325	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	ASN
1	A	133	ASN
1	A	135	HIS
1	A	136	GLN
1	A	157	GLN
1	A	199	ASN
1	A	207	GLN
1	A	217	GLN
1	A	294	ASN
1	A	317	GLN

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](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DTP	A	338	-	31,32,32	7.48	11 (35%)	46,50,50	1.41	5 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DTP	A	338	-	-	10/22/34/34	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	338	DTP	PB-O3A	-35.15	1.21	1.59
2	A	338	DTP	PA-O1A	-11.68	1.10	1.50
2	A	338	DTP	PG-O2G	-8.56	1.23	1.54
2	A	338	DTP	PB-O3B	-8.39	1.50	1.59
2	A	338	DTP	PG-O3G	-6.94	1.29	1.54
2	A	338	DTP	PG-O1G	-6.69	1.29	1.50
2	A	338	DTP	PB-O1B	5.91	1.71	1.50
2	A	338	DTP	PA-O3A	-5.70	1.53	1.59
2	A	338	DTP	C3'-C4'	4.33	1.64	1.53
2	A	338	DTP	PA-O5'	-3.50	1.45	1.59
2	A	338	DTP	O3'-C3'	3.12	1.49	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	338	DTP	O2B-PB-O3B	-4.84	94.20	107.27
2	A	338	DTP	O3G-PG-O2G	4.18	123.47	107.80
2	A	338	DTP	O3A-PA-O1A	3.82	122.21	110.70
2	A	338	DTP	O2A-PA-O3A	2.39	113.72	107.27
2	A	338	DTP	O2B-PB-O1B	-2.07	102.81	112.44

There are no chirality outliers.

All (10) torsion outliers are listed below:

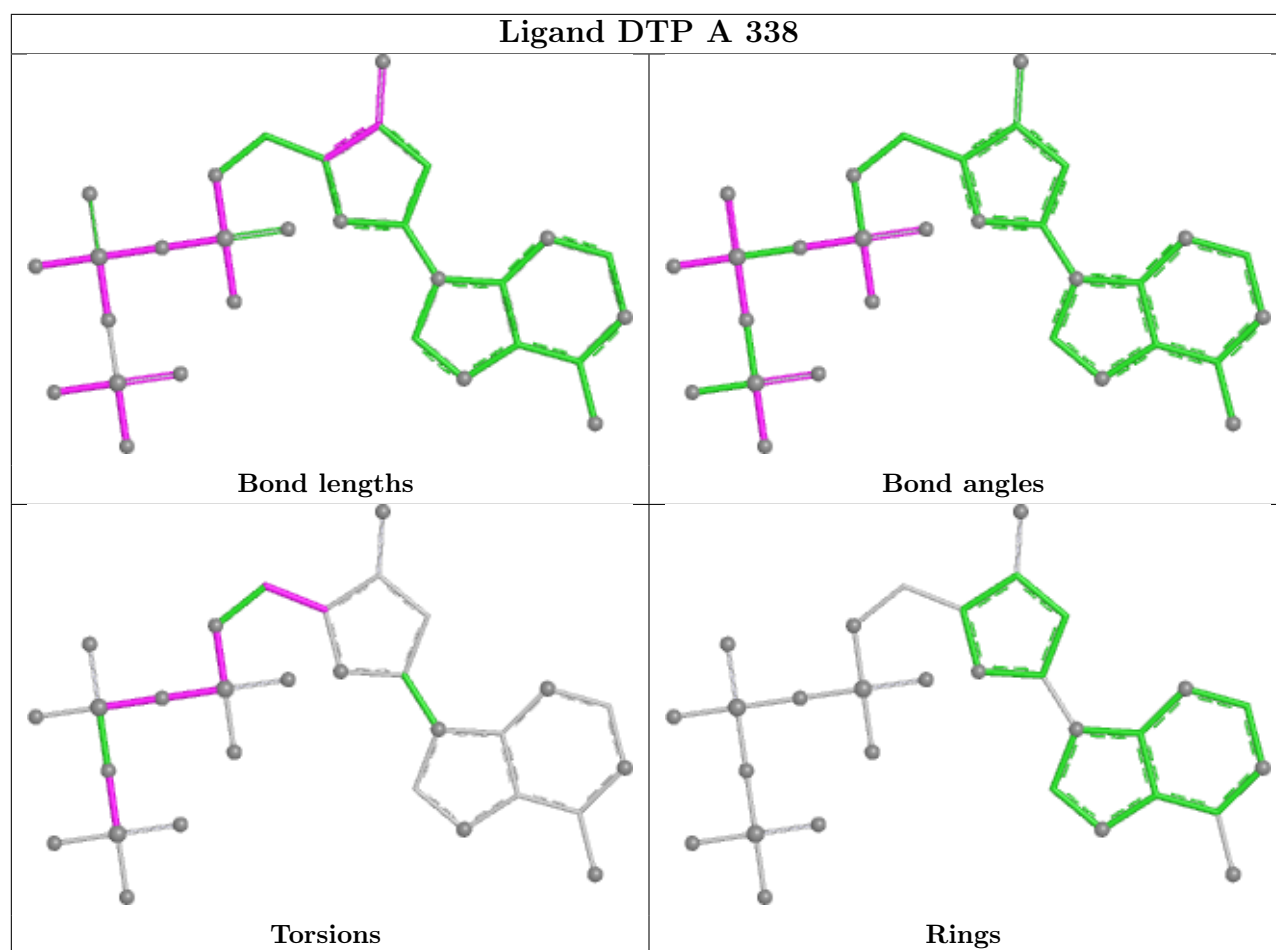
Mol	Chain	Res	Type	Atoms
2	A	338	DTP	PB-O3B-PG-O2G
2	A	338	DTP	PB-O3B-PG-O3G
2	A	338	DTP	O4'-C4'-C5'-O5'
2	A	338	DTP	C3'-C4'-C5'-O5'
2	A	338	DTP	C5'-O5'-PA-O1A
2	A	338	DTP	PA-O3A-PB-O2B
2	A	338	DTP	PB-O3A-PA-O1A
2	A	338	DTP	PB-O3B-PG-O1G
2	A	338	DTP	PB-O3A-PA-O2A
2	A	338	DTP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	338	DTP	16	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	87:LYS	C	88:ILE	N	1.77

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.