



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 03:59 AM GMT

PDB ID : 3V4I
Title : Crystal structure of HIV-1 reverse transcriptase (RT) with DNA and AZTTP
Authors : Das, K.; Martinez, S.E.; Arnold, E.
Deposited on : 2011-12-15
Resolution : 2.80 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

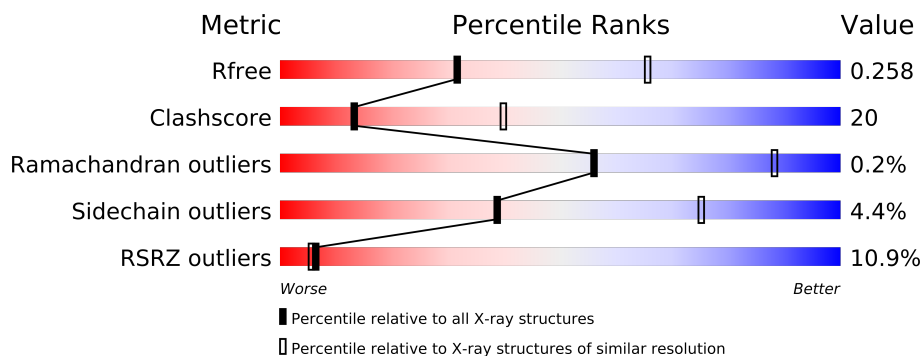
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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))
R_{free}	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	556	
1	C	556	
2	B	428	
2	D	428	
3	E	27	
3	T	27	
4	F	21	
4	P	21	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17696 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HIV-1 Reverse Transcriptase P66 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	0	0
			4511	2920	751	832	8			
1	C	555	Total	C	N	O	S	0	0	0
			4511	2920	751	832	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP P03366
A	0	VAL	-	EXPRESSION TAG	UNP P03366
A	258	CYS	GLN	ENGINEERED MUTATION	UNP P03366
A	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
A	498	ASN	ASP	ENGINEERED MUTATION	UNP P03366
C	-1	MET	-	EXPRESSION TAG	UNP P03366
C	0	VAL	-	EXPRESSION TAG	UNP P03366
C	258	CYS	GLN	ENGINEERED MUTATION	UNP P03366
C	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
C	498	ASN	ASP	ENGINEERED MUTATION	UNP P03366

- Molecule 2 is a protein called HIV-1 Reverse Transcriptase P51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			
2	D	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
D	280	SER	CYS	ENGINEERED MUTATION	UNP P03366

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	24	Total	C	N	O	P	0	0	0
			497	234	102	138	23			
3	E	24	Total	C	N	O	P	0	0	0
			497	234	102	138	23			

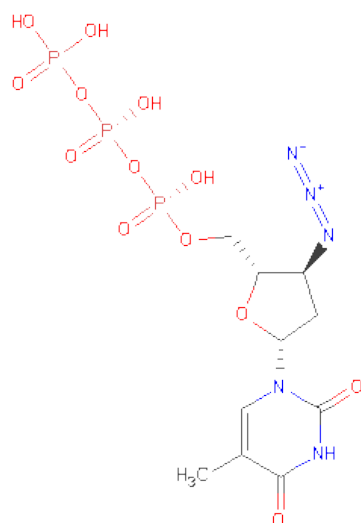
- Molecule 4 is a DNA chain called DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*(ATM))-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	P	20	Total	C	N	O	P	S	0	0	0
			408	195	72	121	19	1			
4	F	20	Total	C	N	O	P	S	0	0	0
			408	195	72	121	19	1			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		

- Molecule 6 is 3'-AZIDO-3'-DEOXYTHYMIDINE-5'-TRIPHOSPHATE (three-letter code: AZT) (formula: C₁₀H₁₆N₅O₁₃P₃).



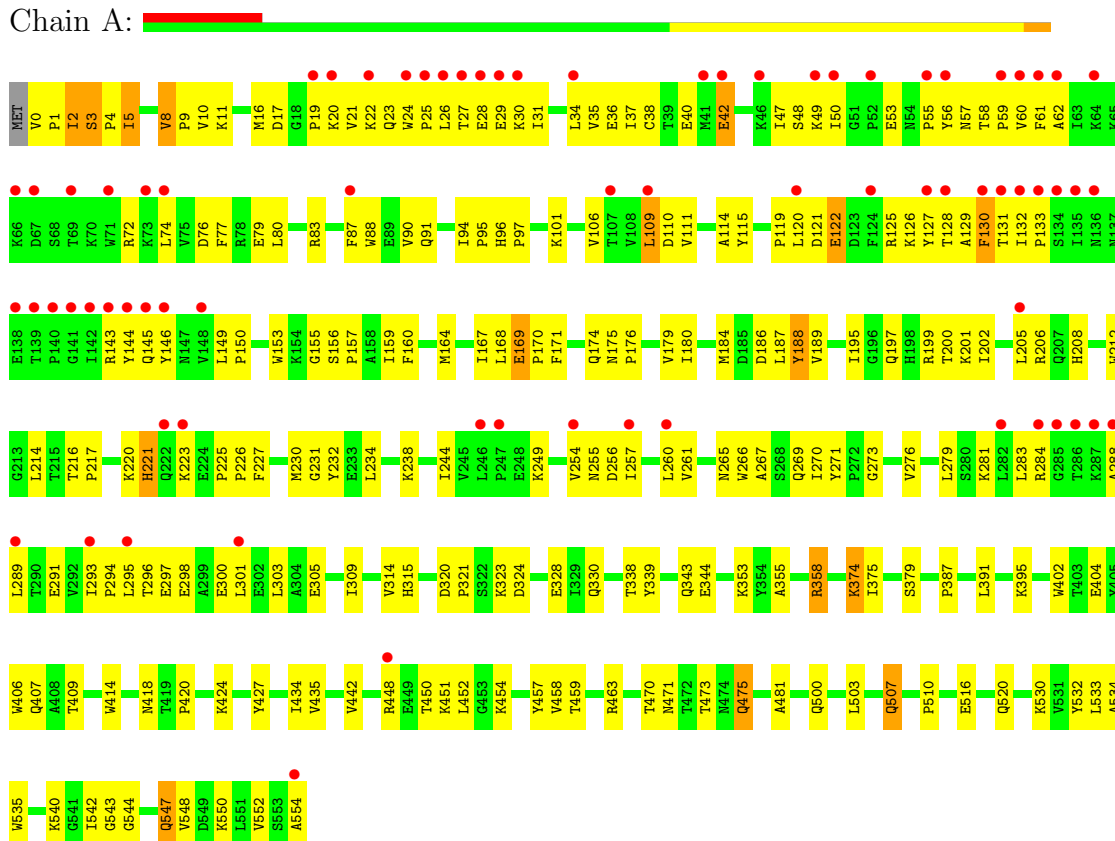
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
6	C	1	Total 31	C 10	N 5	O 13	P 3	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

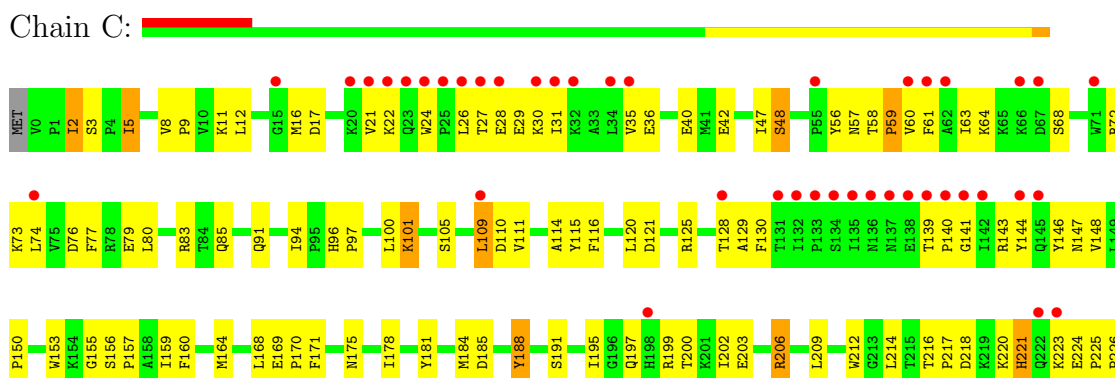
• Molecule 1: HIV-1 Reverse Transcriptase P66 subunit

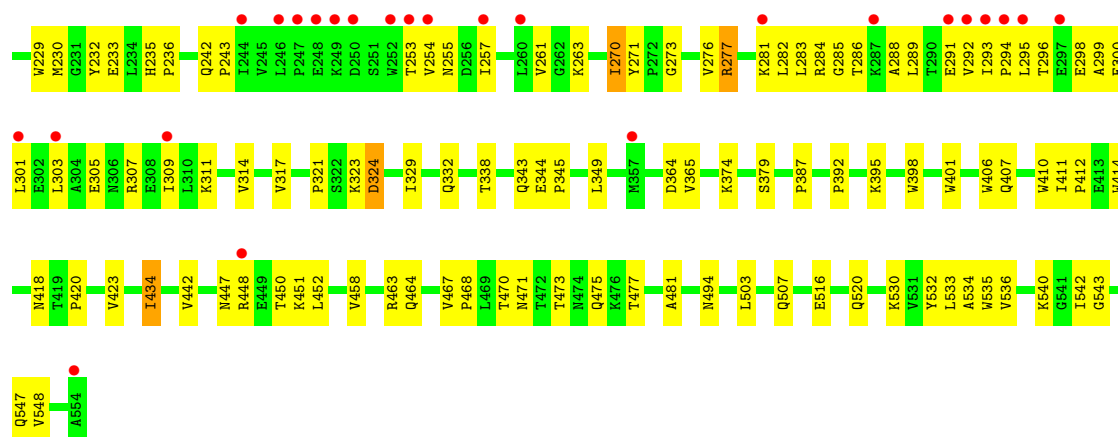
Chain A:



• Molecule 1: HIV-1 Reverse Transcriptase P66 subunit

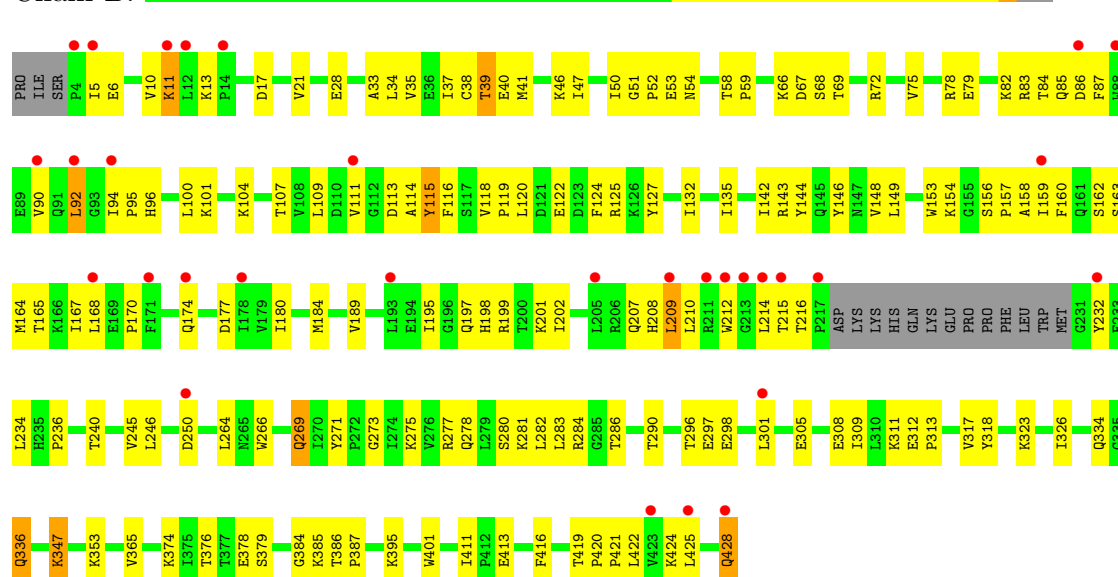
Chain C:





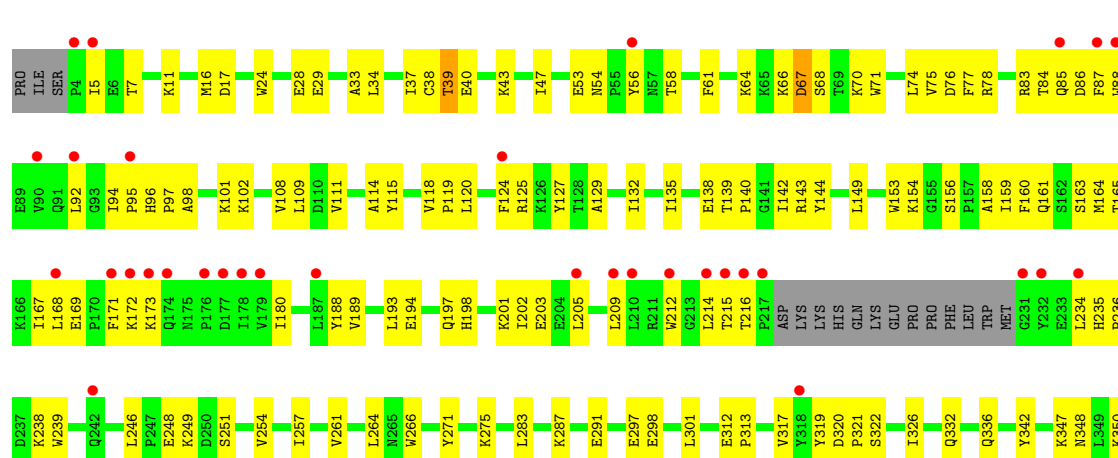
• Molecule 2: HIV-1 Reverse Transcriptase P51 subunit

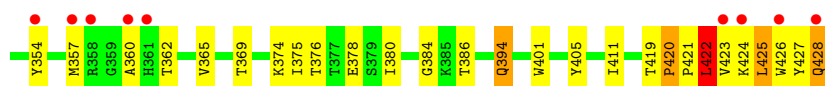
Chain B:



• Molecule 2: HIV-1 Reverse Transcriptase P51 subunit

Chain D:





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

Chain T:



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

Chain E:



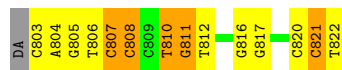
- Molecule 4: DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(M RG)P*CP*GP*CP*CP*(ATM))-3')

Chain P:



- Molecule 4: DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(M RG)P*CP*GP*CP*CP*(ATM))-3')

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.05Å 132.65Å 138.01Å 90.00° 98.12° 90.00°	Depositor
Resolution (Å)	45.54 – 2.80 45.54 – 2.80	Depositor EDS
% Data completeness (in resolution range)	92.3 (45.54-2.80) 92.3 (45.54-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.229 , 0.262 0.222 , 0.258	Depositor DCC
R_{free} test set	2208 reflections (3.02%)	DCC
Wilson B-factor (Å ²)	65.4	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 24.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 73180 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17696	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATM, MG, MRG, AZT

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	0.48	0/4629	0.63	0/6290
1	C	0.45	0/4629	0.60	0/6290
2	B	0.50	0/3497	0.62	0/4751
2	D	0.49	0/3497	0.62	1/4751 (0.0%)
3	E	0.81	0/560	1.58	10/864 (1.2%)
3	T	0.79	0/560	1.55	13/864 (1.5%)
4	F	0.80	0/400	1.55	8/612 (1.3%)
4	P	0.79	0/400	1.70	9/612 (1.5%)
All	All	0.52	0/18172	0.80	41/25034 (0.2%)

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
2	D	0	1

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	807	DC	O4'-C1'-N1	12.48	116.73	108.00
4	P	820	DC	O4'-C4'-C3'	-10.09	99.95	106.00
4	P	816	DG	O4'-C1'-N9	9.64	114.75	108.00
3	E	718	DA	O4'-C1'-N9	9.52	114.67	108.00
4	F	807	DC	O4'-C1'-N1	9.05	114.34	108.00
3	T	719	DG	O4'-C1'-N9	8.97	114.28	108.00
4	F	820	DC	O4'-C4'-C3'	-8.59	100.85	106.00
4	P	810	DT	O4'-C1'-N1	8.52	113.96	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	719	DG	O4'-C1'-N9	7.94	113.56	108.00
4	P	819	DG	O4'-C4'-C3'	-7.53	101.48	106.00
4	F	816	DG	O4'-C1'-N9	7.14	113.00	108.00
4	F	811	DG	O4'-C1'-N9	7.10	112.97	108.00
3	E	719	DG	C1'-O4'-C4'	-6.76	103.34	110.10
3	T	707	DG	O4'-C4'-C3'	-6.71	101.81	104.50
3	T	710	DG	O4'-C4'-C3'	-6.50	101.90	104.50
3	E	707	DG	O4'-C4'-C3'	-6.39	101.94	104.50
3	T	708	DG	O4'-C4'-C3'	-6.27	101.99	104.50
3	T	703	DG	O4'-C1'-N9	6.23	112.36	108.00
3	T	718	DA	O4'-C1'-N9	6.22	112.35	108.00
4	F	821	DC	O4'-C4'-C3'	-6.22	102.01	104.50
3	E	717	DC	O4'-C1'-N1	6.19	112.33	108.00
4	P	810	DT	C4'-C3'-C2'	-6.05	97.65	103.10
3	T	714	DG	C3'-C2'-C1'	-6.05	95.24	102.50
2	D	422	LEU	CA-CB-CG	6.04	129.19	115.30
4	F	808	DC	C5'-C4'-C3'	-5.91	103.46	114.10
3	T	719	DG	C3'-C2'-C1'	-5.82	95.51	102.50
3	E	711	DC	C4'-C3'-C2'	-5.74	97.93	103.10
4	F	812	DT	C6-C5-C7	-5.66	119.50	122.90
3	T	703	DG	O4'-C4'-C3'	-5.57	102.27	104.50
4	F	810	DT	P-O5'-C5'	-5.50	112.11	120.90
4	P	814	DC	O4'-C1'-C2'	-5.45	101.54	105.90
3	E	722	DA	O4'-C1'-N9	5.40	111.78	108.00
3	T	709	DC	O4'-C1'-N1	-5.31	104.28	108.00
3	E	718	DA	C3'-C2'-C1'	-5.30	96.14	102.50
3	E	709	DC	C4'-C3'-C2'	-5.24	98.38	103.10
3	T	708	DG	O4'-C1'-N9	5.22	111.65	108.00
3	E	710	DG	O4'-C4'-C3'	-5.21	102.42	104.50
4	P	818	DC	C4'-C3'-C2'	-5.12	98.49	103.10
3	T	709	DC	C4'-C3'-C2'	-5.10	98.51	103.10
4	P	810	DT	C3'-C2'-C1'	-5.10	96.38	102.50
3	T	708	DG	C4'-C3'-C2'	-5.02	98.59	103.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	420	PRO	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4511	0	4570	217	0
1	C	4511	0	4570	180	0
2	B	3400	0	3433	145	0
2	D	3400	0	3433	142	0
3	E	497	0	268	13	0
3	T	497	0	268	13	0
4	F	408	0	231	19	0
4	P	408	0	231	12	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	31	0	12	2	0
6	C	31	0	12	2	0
All	All	17696	0	17028	709	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 20.

All (709) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:115:TYR:HD2	2:D:156:SER:HB3	1.15	1.07
2:D:115:TYR:CD2	2:D:156:SER:HB3	1.91	1.05
4:F:807:DC:H2"	4:F:808:DC:H5"	1.39	1.04
2:B:266:TRP:CD1	2:B:425:LEU:HD22	1.91	1.04
1:A:5:ILE:HG22	1:A:212:TRP:HD1	1.22	1.04
1:A:358:ARG:HH11	1:A:358:ARG:HG3	1.24	1.02
1:A:34:LEU:HD21	1:A:132:ILE:HD12	1.36	1.01
2:D:419:THR:HB	2:D:421:PRO:HG3	1.41	1.00
2:B:115:TYR:HD1	2:B:156:SER:HB3	1.30	0.97
1:A:130:PHE:CE2	1:A:144:TYR:HB2	2.00	0.95
4:F:807:DC:H2"	4:F:808:DC:C5'	1.96	0.94
2:B:114:ALA:HB2	2:B:214:LEU:HD22	1.48	0.94
1:C:195:ILE:HD11	1:C:199:ARG:HH21	1.31	0.94
1:A:199:ARG:NH2	1:A:223:LYS:HB2	1.83	0.93
2:B:47:ILE:HD12	2:B:144:TYR:CD1	2.06	0.91

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:128:THR:HG21	1:C:146:TYR:HB2	1.51	0.90
1:C:303:LEU:O	1:C:307:ARG:HG3	1.70	0.89
2:D:47:ILE:HD12	2:D:144:TYR:CD1	2.09	0.87
1:A:128:THR:HG21	1:A:146:TYR:CD2	2.09	0.87
1:A:5:ILE:HG22	1:A:212:TRP:CD1	2.08	0.87
2:D:143:ARG:HH11	2:D:143:ARG:HG2	1.40	0.87
2:B:278:GLN:HE21	2:B:298:GLU:HB2	1.40	0.86
1:A:155:GLY:O	1:A:159:ILE:HG13	1.75	0.85
2:D:209:LEU:HD22	2:D:214:LEU:HD23	1.59	0.84
1:A:47:ILE:CG1	1:A:144:TYR:HB3	2.08	0.83
2:B:13:LYS:HD2	2:B:85:GLN:HB3	1.59	0.83
2:D:419:THR:O	2:D:421:PRO:HD3	1.78	0.82
1:A:320:ASP:OD2	1:A:323:LYS:HE2	1.79	0.82
1:A:128:THR:HG21	1:A:146:TYR:HD2	1.43	0.81
1:C:516:GLU:O	1:C:520:GLN:HG3	1.80	0.81
1:A:199:ARG:HH22	1:A:223:LYS:HB2	1.38	0.81
2:D:342:TYR:HB3	2:D:348:ASN:HD22	1.46	0.81
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.64	0.79
1:C:199:ARG:NH2	1:C:223:LYS:HB2	1.97	0.79
1:A:58:THR:HG22	1:A:129:ALA:O	1.81	0.79
2:B:336:GLN:HG2	2:B:353:LYS:HD2	1.65	0.79
3:E:704:DG:OP2	3:E:704:DG:N2	2.15	0.78
2:B:180:ILE:HG12	2:B:189:VAL:HG22	1.66	0.78
4:F:807:DC:C2'	4:F:808:DC:H5''	2.13	0.78
2:B:197:GLN:O	2:B:201:LYS:HG2	1.83	0.78
1:A:358:ARG:HG3	1:A:358:ARG:NH1	1.94	0.78
1:A:167:ILE:O	1:A:170:PRO:HD2	1.83	0.78
2:B:278:GLN:NE2	2:B:298:GLU:HB2	1.99	0.78
1:A:223:LYS:O	1:A:225:PRO:HD2	1.84	0.77
1:A:184:MET:HA	1:A:184:MET:HE3	1.64	0.77
1:A:434:ILE:HD13	1:A:530:LYS:HB3	1.66	0.77
4:F:806:DT:H2'	4:F:807:DC:C6	2.20	0.77
1:A:255:ASN:HB2	1:A:289:LEU:HG	1.67	0.77
2:D:428:GLN:HA	2:D:428:GLN:HE21	1.48	0.76
2:D:17:ASP:O	2:D:83:ARG:HD3	1.85	0.76
1:C:447:ASN:HB3	1:C:450:THR:HB	1.67	0.76
2:B:312:GLU:HB3	2:B:313:PRO:HD2	1.68	0.75
1:A:167:ILE:O	1:A:170:PRO:CD	2.35	0.75
1:C:296:THR:HG23	1:C:299:ALA:H	1.50	0.75
4:F:803:DC:H2'	4:F:804:DA:C8	2.22	0.75
1:A:206:ARG:NH2	1:A:216:THR:O	2.20	0.75
1:A:115:TYR:CE2	6:A:823:AZT:H2'1	2.21	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:421:PRO:HG2	2:D:423:VAL:HB	1.68	0.74
1:A:128:THR:CG2	1:A:146:TYR:HD2	2.00	0.74
2:B:120:LEU:HD23	2:B:125:ARG:HG2	1.70	0.74
1:C:184:MET:HE3	1:C:184:MET:HA	1.69	0.73
2:B:266:TRP:CD1	2:B:425:LEU:CD2	2.71	0.73
2:B:115:TYR:CD1	2:B:156:SER:HB3	2.20	0.73
1:A:516:GLU:O	1:A:520:GLN:HG3	1.88	0.73
1:C:261:VAL:HG13	1:C:276:VAL:HG11	1.71	0.72
1:A:47:ILE:HG13	1:A:144:TYR:HB3	1.69	0.72
2:D:168:LEU:HD13	2:D:172:LYS:HE3	1.72	0.72
3:E:722:DA:H2''	3:E:723:DC:H5''	1.71	0.72
4:F:804:DA:H2'	4:F:805:DG:C8	2.25	0.71
1:A:130:PHE:HE2	1:A:144:TYR:HB2	1.49	0.71
2:D:160:PHE:CD2	2:D:160:PHE:O	2.44	0.71
1:C:206:ARG:NH2	1:C:216:THR:O	2.22	0.71
1:A:175:ASN:OD1	1:A:201:LYS:NZ	2.20	0.71
1:C:458:VAL:HG23	1:C:548:VAL:HB	1.73	0.71
1:C:5:ILE:HG22	1:C:212:TRP:HD1	1.55	0.70
1:A:21:VAL:HG23	1:A:59:PRO:HD3	1.72	0.70
2:D:92:LEU:HB3	2:D:158:ALA:HB1	1.73	0.70
1:C:22:LYS:HA	1:C:57:ASN:HD22	1.54	0.70
2:D:421:PRO:HB2	2:D:423:VAL:HG23	1.73	0.70
2:D:114:ALA:HB2	2:D:214:LEU:HD13	1.73	0.70
1:A:79:GLU:OE1	1:A:83:ARG:NH2	2.23	0.70
1:A:132:ILE:HG12	1:A:144:TYR:HE2	1.54	0.70
1:C:36:GLU:O	1:C:40:GLU:HG2	1.92	0.70
2:B:195:ILE:O	2:B:199:ARG:HG3	1.91	0.70
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.27	0.70
1:C:475:GLN:N	1:C:475:GLN:OE1	2.22	0.70
1:C:253:THR:HG22	1:C:292:VAL:HA	1.74	0.69
1:C:293:ILE:HG13	1:C:294:PRO:HD2	1.74	0.69
1:A:28:GLU:HA	1:A:31:ILE:HD12	1.74	0.69
2:B:275:LYS:HD2	2:B:277:ARG:HH21	1.58	0.69
2:D:33:ALA:O	2:D:37:ILE:HG12	1.93	0.69
1:A:5:ILE:CG2	1:A:212:TRP:HD1	2.01	0.69
2:B:298:GLU:CD	2:B:298:GLU:H	1.97	0.69
1:C:398:TRP:CZ2	1:C:411:ILE:HG13	2.28	0.69
1:C:5:ILE:CG2	1:C:212:TRP:HD1	2.06	0.68
1:A:132:ILE:HG12	1:A:144:TYR:CE2	2.28	0.68
1:C:199:ARG:HH22	1:C:223:LYS:HB2	1.57	0.68
1:A:296:THR:CG2	1:A:298:GLU:HG2	2.23	0.68
2:B:167:ILE:HG23	2:B:212:TRP:CD1	2.27	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:68:SER:O	2:B:69:THR:HB	1.93	0.68
1:A:293:ILE:HG13	1:A:294:PRO:HD2	1.76	0.68
1:A:184:MET:HG2	4:P:822:ATM:H2'	1.76	0.67
1:C:406:TRP:CZ2	2:D:420:PRO:HG3	2.29	0.67
1:A:47:ILE:HG13	1:A:48:SER:H	1.59	0.67
2:B:113:ASP:HB3	2:B:214:LEU:CD1	2.24	0.67
4:F:805:DG:H4'	4:F:806:DT:OP1	1.95	0.67
1:A:458:VAL:HG23	1:A:548:VAL:HB	1.77	0.67
1:C:434:ILE:HD13	1:C:530:LYS:HB3	1.75	0.67
2:B:86:ASP:CG	2:B:87:PHE:H	1.96	0.67
2:D:312:GLU:HB3	2:D:313:PRO:HD2	1.77	0.67
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.76	0.67
1:A:120:LEU:HD12	1:A:121:ASP:H	1.59	0.67
2:D:425:LEU:HG	2:D:426:TRP:N	2.10	0.66
1:A:60:VAL:HG21	1:A:130:PHE:HD1	1.61	0.66
4:F:807:DC:H2''	4:F:808:DC:O5'	1.95	0.66
1:A:418:ASN:O	1:A:420:PRO:HD3	1.96	0.66
1:A:23:GLN:HG3	1:A:131:THR:HG22	1.78	0.66
2:D:423:VAL:HG13	2:D:426:TRP:HE1	1.61	0.66
1:C:5:ILE:HG22	1:C:212:TRP:CD1	2.31	0.66
1:C:434:ILE:HG13	1:C:494:ASN:OD1	1.96	0.66
1:A:5:ILE:HD11	1:A:119:PRO:HD2	1.78	0.65
2:D:28:GLU:HA	2:D:135:ILE:HD11	1.78	0.65
2:B:317:VAL:HG12	2:B:347:LYS:HB3	1.78	0.65
2:B:53:GLU:HG2	2:B:54:ASN:N	2.10	0.65
1:C:128:THR:CG2	1:C:146:TYR:HD2	2.09	0.65
1:C:418:ASN:O	1:C:420:PRO:HD3	1.96	0.65
1:A:284:ARG:HB2	3:T:714:DG:OP1	1.97	0.65
1:A:62:ALA:HB1	1:A:72:ARG:O	1.97	0.65
3:T:713:DC:H2''	3:T:714:DG:H5'	1.78	0.65
1:A:128:THR:CG2	1:A:146:TYR:CD2	2.78	0.65
2:B:118:VAL:HG12	2:B:119:PRO:O	1.97	0.65
2:D:374:LYS:O	2:D:378:GLU:HG3	1.97	0.65
1:C:171:PHE:CE2	1:C:175:ASN:ND2	2.65	0.65
2:D:287:LYS:NZ	2:D:291:GLU:OE2	2.26	0.64
1:C:281:LYS:O	1:C:284:ARG:HG2	1.97	0.64
2:B:5:ILE:HD13	2:B:119:PRO:HD3	1.79	0.64
1:A:324:ASP:O	1:A:343:GLN:HG2	1.98	0.64
2:D:332:GLN:HE22	2:D:424:LYS:HA	1.62	0.64
2:D:17:ASP:O	2:D:83:ARG:NH1	2.30	0.64
1:A:305:GLU:O	1:A:309:ILE:HG13	1.97	0.64
2:D:425:LEU:O	2:D:425:LEU:HD12	1.96	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:120:LEU:HD23	2:D:125:ARG:HG2	1.80	0.64
2:D:317:VAL:HG12	2:D:347:LYS:HB3	1.80	0.64
1:A:296:THR:HG22	1:A:298:GLU:HG2	1.80	0.63
1:A:97:PRO:HD3	1:A:232:TYR:CE2	2.34	0.63
1:A:169:GLU:N	1:A:170:PRO:CD	2.62	0.63
1:C:110:ASP:OD2	1:C:111:VAL:N	2.31	0.63
1:A:88:TRP:CD1	2:B:143:ARG:NH1	2.67	0.63
1:C:503:LEU:HD22	1:C:535:TRP:HB2	1.80	0.63
2:D:246:LEU:HD11	2:D:264:LEU:HD21	1.80	0.63
1:A:114:ALA:HB1	1:A:160:PHE:CE2	2.33	0.62
2:B:86:ASP:CG	2:B:87:PHE:N	2.53	0.62
2:B:318:TYR:CE1	1:C:418:ASN:OD1	2.52	0.62
1:A:23:GLN:HG3	1:A:131:THR:CG2	2.29	0.62
2:D:109:LEU:HD13	2:D:216:THR:HG21	1.81	0.62
2:D:423:VAL:O	2:D:426:TRP:HD1	1.81	0.62
2:D:53:GLU:HG2	2:D:54:ASN:N	2.13	0.62
3:T:704:DG:H5"	3:T:704:DG:N3	2.15	0.62
2:D:143:ARG:HG2	2:D:143:ARG:NH1	2.11	0.62
1:C:21:VAL:CG2	1:C:59:PRO:HD3	2.30	0.62
1:A:543:GLY:HA2	2:B:283:LEU:O	1.99	0.62
2:B:101:LYS:O	2:B:236:PRO:HB2	2.00	0.62
4:P:807:DC:H2"	4:P:808:DC:H5"	1.82	0.62
1:C:128:THR:HG21	1:C:146:TYR:CB	2.29	0.62
1:A:101:LYS:HZ3	1:A:321:PRO:HG3	1.65	0.62
2:B:297:GLU:HB2	2:B:298:GLU:OE2	2.00	0.62
1:A:115:TYR:CD2	6:A:823:AZT:H2'1	2.35	0.62
1:C:31:ILE:O	1:C:35:VAL:HG23	1.99	0.62
1:A:23:GLN:NE2	1:A:131:THR:O	2.32	0.61
1:C:254:VAL:HG21	1:C:286:THR:HG21	1.80	0.61
1:A:29:GLU:HG3	1:A:30:LYS:N	2.14	0.61
1:C:2:ILE:HD12	1:C:2:ILE:H	1.65	0.61
1:C:295:LEU:HB3	1:C:300:GLU:OE2	1.99	0.61
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.35	0.61
1:A:249:LYS:HG3	1:A:256:ASP:OD1	2.01	0.61
2:B:115:TYR:HD2	2:B:115:TYR:H	1.47	0.61
1:A:31:ILE:O	1:A:35:VAL:HG23	2.00	0.61
2:B:170:PRO:HB2	2:B:208:HIS:CE1	2.36	0.61
1:C:271:TYR:CE1	1:C:314:VAL:HG22	2.36	0.61
1:A:110:ASP:OD1	1:A:111:VAL:N	2.34	0.61
2:D:266:TRP:CZ3	2:D:425:LEU:HD21	2.36	0.60
1:A:503:LEU:HD12	1:A:533:LEU:HD13	1.83	0.60
1:C:26:LEU:H	1:C:26:LEU:HD23	1.66	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:164:MET:HE2	2:D:168:LEU:HD11	1.83	0.60
2:B:419:THR:O	2:B:419:THR:HG22	2.02	0.60
1:A:10:VAL:O	1:A:11:LYS:HG3	2.00	0.60
2:D:101:LYS:O	2:D:236:PRO:HB2	2.00	0.60
1:A:2:ILE:N	1:A:2:ILE:HD12	2.16	0.60
1:C:255:ASN:HB2	1:C:289:LEU:HG	1.83	0.60
3:E:723:DC:OP1	3:E:723:DC:H4'	2.00	0.60
2:B:318:TYR:HE1	1:C:418:ASN:OD1	1.84	0.60
1:C:209:LEU:O	1:C:214:LEU:HB2	2.01	0.60
2:D:114:ALA:HB1	2:D:160:PHE:CZ	2.36	0.60
1:C:111:VAL:HG11	1:C:214:LEU:HD22	1.84	0.60
2:B:160:PHE:CD2	2:B:160:PHE:O	2.55	0.60
1:C:450:THR:CG2	1:C:452:LEU:HB2	2.33	0.59
1:A:254:VAL:HG13	1:A:283:LEU:HD22	1.85	0.59
2:D:423:VAL:O	2:D:426:TRP:CD1	2.55	0.59
3:E:723:DC:H5''	3:E:723:DC:H6	1.67	0.59
2:B:266:TRP:NE1	2:B:425:LEU:HD22	2.17	0.59
1:A:500:GLN:HG2	2:B:422:LEU:HD13	1.85	0.59
1:A:281:LYS:O	1:A:284:ARG:HG2	2.03	0.59
1:C:503:LEU:CD1	1:C:533:LEU:HG	2.33	0.59
2:D:86:ASP:OD2	2:D:87:PHE:N	2.36	0.59
1:A:53:GLU:O	1:A:55:PRO:HD3	2.02	0.59
1:A:23:GLN:HE22	1:A:60:VAL:HB	1.68	0.59
1:C:293:ILE:CG1	1:C:294:PRO:HD2	2.33	0.59
1:C:284:ARG:HB2	3:E:714:DG:OP1	2.02	0.59
3:T:703:DG:C2	3:T:704:DG:H1'	2.38	0.58
1:A:29:GLU:HG3	1:A:30:LYS:H	1.68	0.58
1:C:536:VAL:HB	1:C:542:ILE:HD12	1.85	0.58
1:A:406:TRP:CZ2	2:B:420:PRO:HG3	2.38	0.58
1:A:169:GLU:N	1:A:170:PRO:HD3	2.19	0.58
1:C:22:LYS:HA	1:C:57:ASN:ND2	2.18	0.58
1:C:130:PHE:CE2	1:C:144:TYR:HB2	2.38	0.58
2:D:425:LEU:C	2:D:425:LEU:HD12	2.24	0.58
1:C:109:LEU:N	1:C:109:LEU:HD23	2.19	0.58
2:D:66:LYS:O	2:D:67:ASP:HB2	2.03	0.58
2:B:115:TYR:O	2:B:149:LEU:HB2	2.03	0.57
1:A:120:LEU:CD1	1:A:121:ASP:H	2.18	0.57
2:D:98:ALA:O	2:D:102:LYS:HE3	2.03	0.57
1:C:503:LEU:O	1:C:507:GLN:HB2	2.05	0.57
2:D:419:THR:HB	2:D:421:PRO:CG	2.24	0.57
1:C:543:GLY:HA3	2:D:283:LEU:O	2.05	0.57
1:A:26:LEU:HD11	1:A:30:LYS:HD2	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:164:MET:HE2	2:B:168:LEU:HD11	1.85	0.57
2:B:209:LEU:HD22	2:B:214:LEU:HB3	1.87	0.57
2:B:395:LYS:HG3	2:B:416:PHE:CE2	2.40	0.57
1:A:128:THR:O	1:A:128:THR:HG22	2.04	0.56
2:D:16:MET:HG2	2:D:83:ARG:HG2	1.87	0.56
4:P:807:DC:H2''	4:P:808:DC:C5'	2.35	0.56
4:P:815:DG:H2''	4:P:816:DG:OP2	2.05	0.56
1:A:128:THR:HG21	1:A:146:TYR:HB2	1.88	0.56
1:C:21:VAL:HG23	1:C:59:PRO:HD3	1.87	0.56
1:A:244:ILE:HD13	1:A:267:ALA:HB2	1.85	0.56
1:C:288:ALA:HB3	1:C:291:GLU:HB2	1.86	0.56
4:F:805:DG:H2''	4:F:806:DT:C5'	2.36	0.56
2:B:84:THR:HG22	2:B:87:PHE:HB3	1.88	0.56
1:A:276:VAL:O	1:A:276:VAL:HG12	2.03	0.56
1:C:398:TRP:CH2	1:C:411:ILE:HG13	2.40	0.56
1:A:184:MET:HA	1:A:184:MET:CE	2.36	0.56
1:C:203:GLU:OE2	1:C:206:ARG:HD3	2.06	0.56
2:D:87:PHE:HZ	2:D:159:ILE:HG13	1.68	0.56
1:A:260:LEU:HD23	1:A:279:LEU:HD22	1.87	0.56
1:C:448:ARG:O	1:C:451:LYS:NZ	2.38	0.56
2:B:376:THR:HG23	2:B:386:THR:HG22	1.86	0.56
2:B:124:PHE:CD1	2:B:127:TYR:HD2	2.24	0.56
2:B:114:ALA:N	2:B:214:LEU:HD13	2.21	0.56
1:C:395:LYS:HD2	1:C:414:TRP:CH2	2.41	0.56
1:C:473:THR:O	1:C:477:THR:HG23	2.05	0.56
2:D:84:THR:O	2:D:87:PHE:HB3	2.06	0.55
2:B:124:PHE:CE2	2:B:153:TRP:CZ2	2.94	0.55
2:B:17:ASP:O	2:B:83:ARG:NH1	2.38	0.55
1:A:295:LEU:HB3	1:A:300:GLU:HG2	1.88	0.55
2:D:115:TYR:O	2:D:149:LEU:HB2	2.07	0.55
4:P:806:DT:H2'	4:P:807:DC:C6	2.42	0.55
2:D:194:GLU:OE1	2:D:197:GLN:HG2	2.07	0.55
2:D:198:HIS:NE2	2:D:202:ILE:HD11	2.21	0.55
2:B:115:TYR:CD2	2:B:115:TYR:N	2.73	0.55
1:A:261:VAL:HG22	1:A:276:VAL:HG13	1.89	0.55
1:C:317:VAL:HG23	1:C:349:LEU:HD23	1.88	0.55
2:B:82:LYS:HE2	2:B:413:GLU:OE2	2.06	0.54
1:A:50:ILE:HG12	1:A:143:ARG:O	2.06	0.54
2:B:28:GLU:HA	2:B:135:ILE:HD11	1.88	0.54
2:D:421:PRO:HG2	2:D:423:VAL:CB	2.37	0.54
2:D:53:GLU:HG2	2:D:54:ASN:H	1.71	0.54
1:C:407:GLN:OE1	2:D:394:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:139:THR:HG23	1:C:140:PRO:HD2	1.90	0.54
2:B:33:ALA:O	2:B:37:ILE:HG12	2.06	0.54
2:D:332:GLN:CD	2:D:427:TYR:HB3	2.28	0.54
2:B:47:ILE:HD12	2:B:144:TYR:HD1	1.69	0.54
1:C:114:ALA:HB1	1:C:160:PHE:CE1	2.42	0.54
1:C:76:ASP:C	1:C:76:ASP:OD2	2.45	0.54
1:C:115:TYR:CD2	6:C:823:AZT:H2'1	2.43	0.54
2:B:323:LYS:O	2:B:385:LYS:NZ	2.41	0.54
1:C:79:GLU:OE1	1:C:83:ARG:NH2	2.41	0.54
2:B:157:PRO:HG3	2:B:184:MET:HA	1.89	0.54
2:D:266:TRP:HH2	2:D:426:TRP:CZ2	2.26	0.54
2:D:142:ILE:HG22	2:D:144:TYR:CE2	2.43	0.54
1:C:47:ILE:HG13	1:C:48:SER:H	1.72	0.54
1:C:395:LYS:NZ	1:C:414:TRP:O	2.41	0.54
3:E:716:DA:H2''	3:E:717:DC:OP2	2.07	0.54
2:D:115:TYR:CE2	2:D:156:SER:HB3	2.43	0.54
2:D:342:TYR:HB3	2:D:348:ASN:ND2	2.21	0.53
2:B:78:ARG:HD3	2:B:411:ILE:O	2.07	0.53
1:C:223:LYS:O	1:C:225:PRO:HD3	2.09	0.53
2:D:114:ALA:HB2	2:D:214:LEU:HD22	1.90	0.53
2:D:114:ALA:HB2	2:D:214:LEU:CD1	2.39	0.53
1:A:76:ASP:OD2	1:A:76:ASP:C	2.47	0.53
1:A:281:LYS:HG2	1:A:284:ARG:NH1	2.24	0.53
1:A:101:LYS:NZ	1:A:321:PRO:HG3	2.22	0.53
1:A:164:MET:HE2	1:A:187:LEU:HD11	1.90	0.53
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.90	0.53
1:A:358:ARG:HH11	1:A:358:ARG:CG	2.09	0.53
2:B:198:HIS:NE2	2:B:202:ILE:HD11	2.23	0.53
1:C:139:THR:HG22	1:C:141:GLY:H	1.74	0.53
2:B:109:LEU:HD22	2:B:216:THR:HG21	1.90	0.53
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.91	0.53
1:A:120:LEU:HD12	1:A:121:ASP:N	2.23	0.53
2:B:10:VAL:C	2:B:11:LYS:HD2	2.29	0.53
1:A:164:MET:CE	1:A:168:LEU:HD11	2.39	0.53
1:C:282:LEU:HD21	1:C:296:THR:CG2	2.39	0.52
1:C:532:TYR:CE2	1:C:534:ALA:HB2	2.45	0.52
4:F:805:DG:H2''	4:F:806:DT:H5''	1.91	0.52
1:A:434:ILE:HD13	1:A:530:LYS:CB	2.38	0.52
1:A:91:GLN:O	3:T:708:DG:H4'	2.09	0.52
1:A:22:LYS:HA	1:A:57:ASN:ND2	2.25	0.52
1:C:273:GLY:HA2	1:C:338:THR:HG21	1.92	0.52
1:A:208:HIS:O	1:A:212:TRP:HE3	1.93	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:202:ILE:HG21	1:C:220:LYS:NZ	2.25	0.52
2:D:171:PHE:CE2	2:D:205:LEU:HB2	2.44	0.52
1:A:72:ARG:HD3	1:A:74:LEU:HD21	1.91	0.52
1:C:114:ALA:HB1	1:C:160:PHE:CZ	2.45	0.52
1:A:132:ILE:CG1	1:A:144:TYR:HE2	2.22	0.52
1:C:169:GLU:N	1:C:170:PRO:HD2	2.24	0.52
1:A:542:ILE:HG23	2:B:283:LEU:HD13	1.92	0.52
2:B:428:GLN:HE21	2:B:428:GLN:HA	1.74	0.52
3:T:706:DA:H2'	3:T:707:DG:C8	2.45	0.52
2:D:297:GLU:O	2:D:301:LEU:HG	2.10	0.52
1:A:288:ALA:HB3	1:A:291:GLU:HB2	1.91	0.52
2:D:422:LEU:O	2:D:425:LEU:HB3	2.09	0.52
1:A:548:VAL:O	1:A:552:VAL:HG22	2.10	0.52
1:C:242:GLN:HB3	1:C:243:PRO:HD2	1.92	0.52
2:D:354:TYR:HE2	2:D:375:ILE:HG13	1.73	0.52
2:B:266:TRP:O	2:B:269:GLN:HG3	2.09	0.51
1:C:450:THR:HG21	1:C:452:LEU:HB2	1.92	0.51
3:T:713:DC:H2'	3:T:714:DG:C8	2.45	0.51
1:A:260:LEU:HD21	1:A:303:LEU:HD13	1.91	0.51
2:B:282:LEU:HD21	2:B:296:THR:HG23	1.91	0.51
2:B:50:ILE:HG13	2:B:51:GLY:N	2.25	0.51
1:A:230:MET:HE3	4:P:821:DC:H4'	1.92	0.51
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.50	0.51
2:D:257:ILE:O	2:D:261:VAL:HG23	2.10	0.51
2:B:69:THR:CG2	2:B:69:THR:O	2.58	0.51
2:B:86:ASP:OD2	2:B:87:PHE:N	2.43	0.51
2:D:354:TYR:CE2	2:D:375:ILE:HG13	2.45	0.51
3:T:720:DG:H1'	3:T:721:DG:H5'	1.91	0.51
1:C:47:ILE:HD11	1:C:130:PHE:HE2	1.75	0.51
2:B:96:HIS:CD2	2:B:384:GLY:HA3	2.45	0.51
1:A:38:CYS:SG	1:A:132:ILE:HG13	2.51	0.51
1:A:301:LEU:O	1:A:305:GLU:HG2	2.10	0.51
1:A:503:LEU:O	1:A:507:GLN:HB2	2.09	0.51
2:B:113:ASP:HB3	2:B:214:LEU:HD11	1.93	0.51
1:C:195:ILE:O	1:C:199:ARG:HG3	2.10	0.51
2:B:87:PHE:HZ	2:B:159:ILE:HG13	1.74	0.51
1:A:320:ASP:OD2	1:A:323:LYS:CE	2.54	0.51
1:A:122:GLU:OE2	1:A:125:ARG:NH1	2.44	0.51
4:P:807:DC:H1'	4:P:808:DC:H5''	1.93	0.51
2:B:214:LEU:HD12	2:B:215:THR:H	1.75	0.51
4:P:807:DC:C2'	4:P:808:DC:H5''	2.40	0.51
1:C:202:ILE:HG21	1:C:220:LYS:HZ2	1.76	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:169:GLU:HG2	2:D:173:LYS:HG2	1.93	0.51
1:C:100:LEU:HD11	1:C:229:TRP:CZ3	2.46	0.51
3:E:717:DC:H2''	3:E:718:DA:OP2	2.09	0.50
2:D:419:THR:CB	2:D:421:PRO:HG3	2.28	0.50
1:A:19:PRO:O	1:A:57:ASN:N	2.43	0.50
2:D:357:MET:O	2:D:360:ALA:HB2	2.11	0.50
1:C:254:VAL:HG13	1:C:283:LEU:HD22	1.92	0.50
1:A:24:TRP:CZ2	3:T:703:DG:N2	2.78	0.50
1:C:109:LEU:H	1:C:109:LEU:HD23	1.75	0.50
1:C:77:PHE:O	1:C:80:LEU:N	2.45	0.50
1:A:179:VAL:O	1:A:189:VAL:HA	2.11	0.50
2:D:43:LYS:NZ	2:D:43:LYS:HB2	2.27	0.50
1:C:226:PRO:HB2	1:C:233:GLU:HB3	1.93	0.50
2:B:142:ILE:HG22	2:B:144:TYR:CE2	2.46	0.50
2:D:168:LEU:O	2:D:171:PHE:N	2.43	0.50
1:C:305:GLU:O	1:C:309:ILE:HG13	2.11	0.50
2:B:84:THR:O	2:B:84:THR:HG22	2.12	0.50
3:T:716:DA:H2''	3:T:717:DC:O5'	2.09	0.50
1:A:77:PHE:O	1:A:80:LEU:N	2.43	0.50
2:B:115:TYR:HD2	2:B:115:TYR:N	2.06	0.50
2:D:161:GLN:O	2:D:165:THR:HG22	2.11	0.50
4:F:806:DT:H2''	4:F:807:DC:OP1	2.11	0.50
2:D:425:LEU:CD1	2:D:425:LEU:C	2.80	0.50
1:C:206:ARG:HG2	1:C:216:THR:OG1	2.12	0.50
2:B:53:GLU:HG2	2:B:54:ASN:H	1.74	0.50
1:A:37:ILE:HD13	1:A:40:GLU:OE2	2.11	0.50
2:B:305:GLU:O	2:B:309:ILE:HG13	2.12	0.50
2:D:235:HIS:N	2:D:236:PRO:HD3	2.27	0.50
1:C:24:TRP:CD1	1:C:59:PRO:HB3	2.47	0.50
2:B:28:GLU:HB2	2:B:135:ILE:CD1	2.42	0.50
2:B:298:GLU:N	2:B:298:GLU:CD	2.64	0.49
4:P:810:DT:H2'	4:P:810:DT:O5'	2.12	0.49
2:D:332:GLN:OE1	2:D:427:TYR:HB3	2.12	0.49
1:A:532:TYR:CE2	1:A:534:ALA:HB2	2.48	0.49
2:D:369:THR:HG21	2:D:405:TYR:HB2	1.93	0.49
2:D:193:LEU:CD1	2:D:201:LYS:HG3	2.43	0.49
1:C:406:TRP:CE2	2:D:420:PRO:HG3	2.48	0.49
2:B:41:MET:CE	2:B:47:ILE:HG12	2.43	0.49
2:D:124:PHE:CE2	2:D:153:TRP:CZ2	3.00	0.49
1:A:26:LEU:HD23	1:A:133:PRO:HG2	1.95	0.49
1:A:47:ILE:HG13	1:A:48:SER:N	2.27	0.49
2:D:96:HIS:HA	2:D:97:PRO:HD2	1.66	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:235:HIS:O	2:D:238:LYS:HB2	2.13	0.49
1:C:128:THR:O	1:C:128:THR:HG22	2.11	0.49
2:D:350:LYS:HE2	2:D:378:GLU:OE2	2.13	0.48
1:C:2:ILE:HD12	1:C:2:ILE:N	2.26	0.48
4:P:815:DG:OP2	4:P:815:DG:H2'	2.13	0.48
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.95	0.48
4:F:804:DA:H2''	4:F:805:DG:O5'	2.13	0.48
1:C:452:LEU:HD23	1:C:470:THR:HA	1.94	0.48
2:B:90:VAL:HG22	1:C:345:PRO:HG2	1.94	0.48
1:A:171:PHE:CD1	1:A:205:LEU:HD12	2.47	0.48
2:B:271:TYR:CD2	2:B:271:TYR:N	2.79	0.48
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.95	0.48
2:B:177:ASP:OD1	2:B:177:ASP:N	2.42	0.48
1:A:238:LYS:HB2	1:A:315:HIS:ND1	2.28	0.48
1:A:101:LYS:HZ2	1:A:321:PRO:HG2	1.77	0.48
1:A:195:ILE:O	1:A:199:ARG:HG3	2.14	0.48
1:C:276:VAL:O	1:C:276:VAL:CG1	2.60	0.48
3:E:721:DG:H2''	3:E:722:DA:OP2	2.14	0.48
1:A:96:HIS:CD2	1:A:97:PRO:HD2	2.49	0.48
1:C:185:ASP:OD1	6:C:823:AZT:H5'1	2.13	0.48
2:B:312:GLU:HB3	2:B:313:PRO:CD	2.41	0.48
1:A:109:LEU:HD23	1:A:109:LEU:N	2.29	0.48
2:B:286:THR:O	2:B:286:THR:HG22	2.12	0.48
1:C:282:LEU:HD21	1:C:296:THR:HG22	1.96	0.48
1:C:21:VAL:O	1:C:57:ASN:HB3	2.14	0.48
1:C:418:ASN:O	1:C:418:ASN:CG	2.52	0.48
1:A:24:TRP:HA	1:A:24:TRP:CE3	2.49	0.48
2:B:124:PHE:HE2	2:B:153:TRP:CZ2	2.31	0.48
2:D:108:VAL:HG22	2:D:188:TYR:CD1	2.48	0.48
1:C:61:PHE:HE1	1:C:74:LEU:HD12	1.78	0.48
2:B:107:THR:HA	2:B:232:TYR:O	2.12	0.48
1:A:434:ILE:CD1	1:A:530:LYS:HB3	2.40	0.48
1:A:379:SER:CB	1:A:387:PRO:HD3	2.44	0.48
1:C:442:VAL:HB	1:C:481:ALA:HB1	1.96	0.48
1:C:540:LYS:HD3	1:C:540:LYS:HA	1.67	0.48
1:C:101:LYS:NZ	1:C:321:PRO:HG2	2.28	0.48
2:B:422:LEU:H	2:B:422:LEU:CD2	2.26	0.48
1:C:155:GLY:O	1:C:159:ILE:HG13	2.13	0.48
2:D:365:VAL:HG11	2:D:401:TRP:HB2	1.96	0.47
1:A:281:LYS:HG2	1:A:284:ARG:CZ	2.44	0.47
4:F:817:MRG:H222	4:F:817:MRG:N3	2.29	0.47
1:C:121:ASP:O	1:C:125:ARG:HG3	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:307:ARG:O	1:C:311:LYS:HG3	2.13	0.47
2:D:357:MET:SD	2:D:374:LYS:HE2	2.55	0.47
1:A:150:PRO:HG2	1:A:153:TRP:HB2	1.96	0.47
1:C:181:TYR:CE2	2:D:138:GLU:HG3	2.49	0.47
2:D:118:VAL:HG12	2:D:119:PRO:O	2.15	0.47
1:C:298:GLU:HA	1:C:298:GLU:OE1	2.15	0.47
1:A:475:GLN:NE2	1:A:475:GLN:N	2.62	0.47
4:F:805:DG:H2''	4:F:806:DT:O5'	2.15	0.47
2:D:422:LEU:HD13	2:D:422:LEU:C	2.34	0.47
1:C:128:THR:HG21	1:C:146:TYR:CD2	2.49	0.47
2:B:336:GLN:CG	2:B:353:LYS:HD2	2.40	0.47
1:A:101:LYS:NZ	1:A:321:PRO:CG	2.77	0.47
1:A:2:ILE:H	1:A:2:ILE:HD12	1.79	0.47
2:D:39:THR:HG22	2:D:40:GLU:N	2.30	0.47
1:C:197:GLN:O	1:C:200:THR:HB	2.14	0.47
2:D:180:ILE:HG12	2:D:189:VAL:HG22	1.96	0.47
1:C:195:ILE:HD11	1:C:199:ARG:NH2	2.14	0.47
2:B:195:ILE:HG22	2:B:199:ARG:NE	2.30	0.47
1:A:271:TYR:CE1	1:A:314:VAL:HG22	2.50	0.47
2:B:66:LYS:O	2:B:67:ASP:HB2	2.15	0.47
1:A:56:TYR:O	1:A:129:ALA:HB3	2.15	0.47
2:D:34:LEU:HD11	2:D:61:PHE:HA	1.97	0.47
1:C:253:THR:HG22	1:C:292:VAL:CA	2.42	0.46
1:C:257:ILE:HB	1:C:283:LEU:HD21	1.98	0.46
2:B:28:GLU:CB	2:B:135:ILE:HD11	2.45	0.46
2:D:167:ILE:HD13	2:D:212:TRP:HB3	1.97	0.46
1:A:544:GLY:HA2	1:A:547:GLN:HG2	1.97	0.46
1:A:202:ILE:HG21	1:A:220:LYS:NZ	2.30	0.46
1:A:402:TRP:HB2	1:A:409:THR:HG23	1.97	0.46
2:B:5:ILE:HG22	2:B:6:GLU:N	2.30	0.46
1:A:36:GLU:O	1:A:40:GLU:HG3	2.15	0.46
1:C:91:GLN:O	3:E:708:DG:H4'	2.15	0.46
1:C:410:TRP:CH2	1:C:412:PRO:HA	2.50	0.46
1:A:42:GLU:OE1	1:A:49:LYS:HE3	2.16	0.46
2:B:308:GLU:O	2:B:311:LYS:HB2	2.16	0.46
1:A:244:ILE:CD1	1:A:267:ALA:HB2	2.46	0.46
2:B:79:GLU:OE2	2:B:83:ARG:NH2	2.42	0.46
1:C:301:LEU:O	1:C:305:GLU:HG2	2.15	0.46
2:D:266:TRP:CH2	2:D:425:LEU:HD21	2.51	0.46
1:C:285:GLY:HA2	3:E:714:DG:H5''	1.98	0.46
1:C:181:TYR:HB2	1:C:188:TYR:HB3	1.97	0.46
1:A:475:GLN:NE2	1:A:475:GLN:H	2.13	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:273:GLY:HA2	1:A:338:THR:HG21	1.96	0.46
2:B:92:LEU:HB3	2:B:158:ALA:HB1	1.98	0.46
4:F:810:DT:H2''	4:F:811:DG:C8	2.51	0.46
1:A:120:LEU:CG	1:A:121:ASP:H	2.27	0.46
2:D:84:THR:O	2:D:84:THR:HG22	2.15	0.46
1:A:58:THR:HG23	1:A:130:PHE:HB3	1.97	0.46
2:B:170:PRO:O	2:B:174:GLN:HG3	2.16	0.46
2:B:154:LYS:HG2	2:B:184:MET:SD	2.55	0.46
1:A:448:ARG:O	1:A:451:LYS:NZ	2.42	0.46
1:A:257:ILE:HB	1:A:283:LEU:HD21	1.98	0.46
1:C:97:PRO:HD3	1:C:232:TYR:CE2	2.50	0.46
2:B:41:MET:HE2	2:B:47:ILE:HG12	1.97	0.46
4:P:807:DC:C1'	4:P:808:DC:H5''	2.46	0.46
2:B:90:VAL:CG2	1:C:345:PRO:HG2	2.45	0.46
1:C:329:ILE:O	1:C:392:PRO:HD3	2.16	0.46
1:C:450:THR:HG22	1:C:452:LEU:HB2	1.98	0.45
1:A:221:HIS:HD2	1:A:227:PHE:HA	1.81	0.45
1:C:295:LEU:HD13	1:C:300:GLU:OE1	2.16	0.45
2:D:111:VAL:HG23	2:D:115:TYR:HE1	1.81	0.45
2:D:43:LYS:HB2	2:D:43:LYS:HZ3	1.82	0.45
1:A:110:ASP:OD1	1:A:111:VAL:O	2.33	0.45
2:B:281:LYS:NZ	2:B:284:ARG:HH12	2.14	0.45
2:D:422:LEU:C	2:D:424:LYS:N	2.69	0.45
2:D:319:TYR:CZ	2:D:321:PRO:HA	2.52	0.45
2:D:271:TYR:N	2:D:271:TYR:CD2	2.84	0.45
1:A:270:ILE:HD12	1:A:270:ILE:HA	1.77	0.45
1:C:8:VAL:HA	1:C:9:PRO:HD2	1.59	0.45
2:D:380:ILE:O	2:D:384:GLY:HA2	2.17	0.45
1:A:31:ILE:HD13	1:A:133:PRO:HB2	1.98	0.45
2:D:266:TRP:CE3	2:D:425:LEU:CD2	3.00	0.45
1:A:115:TYR:HB3	1:A:149:LEU:O	2.16	0.45
1:C:184:MET:HG2	4:F:822:ATM:H2'	1.98	0.45
2:D:360:ALA:C	2:D:362:THR:H	2.19	0.45
2:D:163:SER:O	2:D:167:ILE:HG13	2.16	0.45
1:C:178:ILE:CD1	1:C:191:SER:HB3	2.47	0.45
2:D:94:ILE:HG23	2:D:95:PRO:HD2	1.99	0.45
1:C:128:THR:CG2	1:C:146:TYR:CD2	2.95	0.45
1:A:16:MET:HE1	1:A:83:ARG:HG2	1.99	0.45
1:A:457:TYR:HA	1:A:548:VAL:HG21	1.99	0.45
2:B:162:SER:O	2:B:165:THR:HG22	2.17	0.45
1:A:87:PHE:HD1	2:B:52:PRO:O	2.00	0.45
1:A:115:TYR:OH	1:A:157:PRO:HG3	2.15	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:236:PRO:HA	2:D:239:TRP:CD2	2.52	0.45
1:A:500:GLN:HG2	2:B:422:LEU:CD1	2.47	0.45
1:C:17:ASP:O	1:C:83:ARG:HD2	2.16	0.45
1:C:96:HIS:CG	1:C:97:PRO:HD2	2.52	0.45
1:A:355:ALA:HB3	3:T:712:DC:OP2	2.16	0.45
1:A:395:LYS:HD2	1:A:414:TRP:CH2	2.52	0.45
2:D:266:TRP:CE3	2:D:425:LEU:HD22	2.52	0.44
1:A:3:SER:HA	1:A:4:PRO:HD3	1.91	0.44
2:B:379:SER:CB	2:B:387:PRO:HD3	2.47	0.44
1:A:145:GLN:O	1:A:145:GLN:HG3	2.16	0.44
1:A:164:MET:HE2	1:A:168:LEU:HD11	1.99	0.44
1:C:178:ILE:HD13	1:C:191:SER:HB3	1.99	0.44
2:D:74:LEU:HD12	2:D:75:VAL:N	2.32	0.44
2:B:39:THR:HG22	2:B:40:GLU:N	2.32	0.44
1:A:61:PHE:CE1	1:A:74:LEU:HB2	2.53	0.44
2:B:273:GLY:HA3	2:B:309:ILE:HD13	2.00	0.44
1:A:47:ILE:HG12	1:A:144:TYR:HB3	1.93	0.44
1:A:121:ASP:O	1:A:125:ARG:HG3	2.18	0.44
1:A:111:VAL:HG11	1:A:214:LEU:HD22	1.99	0.44
1:C:63:ILE:HG12	1:C:74:LEU:HD11	2.00	0.44
2:D:64:LYS:HE3	2:D:71:TRP:CZ2	2.53	0.44
1:A:374:LYS:HD2	1:A:374:LYS:C	2.38	0.44
1:C:276:VAL:HG12	1:C:276:VAL:O	2.18	0.44
2:B:420:PRO:HA	2:B:421:PRO:HD3	1.81	0.44
2:B:11:LYS:HD2	2:B:11:LYS:N	2.32	0.44
1:C:230:MET:HE3	4:F:821:DC:H4'	1.99	0.44
1:A:226:PRO:HA	1:A:234:LEU:O	2.17	0.44
1:A:34:LEU:CD2	1:A:132:ILE:HD12	2.27	0.44
1:A:24:TRP:HE3	1:A:25:PRO:HD2	1.83	0.44
2:D:85:GLN:HA	2:D:88:TRP:CE2	2.53	0.44
1:C:223:LYS:O	1:C:225:PRO:CD	2.66	0.44
2:B:162:SER:HA	2:B:165:THR:HG22	2.00	0.44
2:D:68:SER:C	2:D:70:LYS:H	2.20	0.44
1:A:427:TYR:OH	1:A:510:PRO:HD2	2.18	0.44
1:C:470:THR:HG22	1:C:471:ASN:HB3	2.00	0.44
1:A:454:LYS:NZ	1:A:554:ALA:C	2.71	0.44
1:A:130:PHE:N	1:A:130:PHE:CD2	2.85	0.43
1:C:16:MET:CE	1:C:83:ARG:HH11	2.30	0.43
1:A:106:VAL:O	1:A:227:PHE:CZ	2.70	0.43
1:C:94:ILE:HD12	3:E:709:DC:H1'	2.00	0.43
2:D:167:ILE:HG12	2:D:212:TRP:CE3	2.53	0.43
2:B:281:LYS:HG2	2:B:284:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:452:LEU:HD23	1:A:470:THR:HA	2.00	0.43
2:D:38:CYS:SG	2:D:132:ILE:HD11	2.58	0.43
1:A:60:VAL:HG21	1:A:130:PHE:CD1	2.47	0.43
1:C:450:THR:CG2	1:C:452:LEU:HD12	2.48	0.43
1:A:296:THR:HG22	1:A:297:GLU:N	2.33	0.43
1:A:8:VAL:O	1:A:8:VAL:HG12	2.19	0.43
2:D:203:GLU:HA	2:D:203:GLU:OE1	2.18	0.43
1:A:164:MET:CE	1:A:187:LEU:HD11	2.48	0.43
2:B:94:ILE:HG23	2:B:95:PRO:HD2	2.01	0.43
1:A:265:ASN:OD1	1:A:353:LYS:CE	2.66	0.43
1:C:235:HIS:HB3	1:C:236:PRO:CD	2.49	0.43
2:D:139:THR:HG22	2:D:140:PRO:N	2.34	0.43
4:F:804:DA:C2'	4:F:805:DG:C8	2.99	0.43
1:C:277:ARG:HD2	1:C:281:LYS:HE3	2.00	0.43
1:A:451:LYS:O	1:A:471:ASN:N	2.52	0.43
1:C:72:ARG:HG3	1:C:74:LEU:HD21	2.01	0.43
1:C:365:VAL:HG11	1:C:401:TRP:CG	2.54	0.43
1:A:344:GLU:HA	1:A:344:GLU:OE1	2.18	0.43
2:B:58:THR:CG2	2:B:75:VAL:HG12	2.48	0.43
2:B:58:THR:HG21	2:B:75:VAL:HG12	2.01	0.43
1:C:150:PRO:HG2	1:C:153:TRP:HB2	2.00	0.43
2:D:376:THR:HG23	2:D:386:THR:HG22	2.00	0.43
1:C:5:ILE:CG2	1:C:212:TRP:CD1	2.93	0.43
2:D:197:GLN:O	2:D:201:LYS:HG2	2.18	0.43
2:D:78:ARG:HD3	2:D:411:ILE:O	2.18	0.43
1:C:11:LYS:HD2	1:C:11:LYS:N	2.33	0.43
1:C:379:SER:CB	1:C:387:PRO:HD3	2.49	0.43
2:D:332:GLN:NE2	2:D:424:LYS:HA	2.32	0.43
1:A:186:ASP:C	1:A:187:LEU:HD12	2.38	0.43
1:A:126:LYS:HG3	1:A:127:TYR:N	2.34	0.43
2:B:34:LEU:HA	2:B:34:LEU:HD23	1.86	0.43
2:D:421:PRO:HG2	2:D:423:VAL:CG2	2.49	0.43
2:B:47:ILE:HG22	2:B:146:TYR:HA	2.00	0.43
2:B:47:ILE:HD12	2:B:144:TYR:CE1	2.49	0.43
1:C:47:ILE:HD11	1:C:130:PHE:CE2	2.52	0.43
1:C:27:THR:HB	1:C:30:LYS:HG3	2.00	0.43
2:B:100:LEU:O	2:B:100:LEU:HD12	2.19	0.43
2:D:275:LYS:HD3	2:D:275:LYS:HA	1.86	0.43
1:A:164:MET:HE3	1:A:168:LEU:HD11	2.01	0.42
2:B:104:LYS:HE2	2:B:104:LYS:HB3	1.80	0.42
1:C:221:HIS:N	1:C:221:HIS:ND1	2.67	0.42
1:C:56:TYR:O	1:C:143:ARG:NH2	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:61:PHE:CE1	1:C:74:LEU:HD12	2.54	0.42
2:D:320:ASP:C	2:D:320:ASP:OD1	2.57	0.42
1:C:116:PHE:O	1:C:148:VAL:HG11	2.18	0.42
2:D:115:TYR:H	2:D:115:TYR:HD1	1.65	0.42
1:A:27:THR:O	1:A:31:ILE:HG13	2.19	0.42
2:B:167:ILE:HG12	2:B:212:TRP:CD2	2.55	0.42
1:A:110:ASP:OD1	1:A:110:ASP:C	2.55	0.42
1:C:61:PHE:CE1	1:C:74:LEU:HB2	2.55	0.42
1:C:324:ASP:O	1:C:343:GLN:HG2	2.19	0.42
1:C:364:ASP:HB3	1:C:423:VAL:HG13	2.00	0.42
2:B:334:GLN:HA	2:B:334:GLN:OE1	2.19	0.42
2:D:249:LYS:HE3	2:D:249:LYS:HB3	1.78	0.42
1:C:261:VAL:CG1	1:C:276:VAL:HG11	2.47	0.42
1:A:61:PHE:HE1	1:A:74:LEU:HD12	1.83	0.42
1:C:85:GLN:NE2	2:D:53:GLU:O	2.53	0.42
2:D:24:TRP:HZ2	2:D:61:PHE:CD2	2.38	0.42
2:B:21:VAL:HB	2:B:59:PRO:HD3	2.01	0.42
2:D:58:THR:HG23	2:D:76:ASP:O	2.20	0.42
1:C:73:LYS:NZ	1:C:130:PHE:CZ	2.82	0.42
2:B:164:MET:HG3	2:B:168:LEU:CD1	2.49	0.42
2:B:281:LYS:HZ2	2:B:284:ARG:HH12	1.66	0.42
2:B:336:GLN:HE21	2:B:336:GLN:HB2	1.44	0.42
3:T:714:DG:O5'	3:T:714:DG:H2'	2.20	0.42
1:A:406:TRP:CD1	1:A:407:GLN:HG3	2.55	0.42
2:D:254:VAL:HG13	2:D:283:LEU:HD22	2.02	0.42
2:B:28:GLU:HB2	2:B:135:ILE:HD11	2.00	0.42
2:D:214:LEU:HD12	2:D:215:THR:N	2.35	0.42
1:C:332:GLN:OE1	1:C:338:THR:HG23	2.20	0.42
1:A:174:GLN:C	1:A:176:PRO:HD3	2.39	0.42
1:C:223:LYS:O	1:C:223:LYS:HG2	2.19	0.42
1:A:21:VAL:O	1:A:57:ASN:ND2	2.52	0.42
1:C:139:THR:CG2	1:C:140:PRO:HD2	2.50	0.42
2:D:88:TRP:CZ2	2:D:154:LYS:HD3	2.55	0.42
2:D:85:GLN:HG3	2:D:88:TRP:CH2	2.55	0.42
1:A:296:THR:HG21	1:A:298:GLU:HG2	1.98	0.42
2:B:317:VAL:O	2:B:317:VAL:HG23	2.20	0.42
1:A:540:LYS:HA	1:A:540:LYS:HD3	1.54	0.42
1:A:435:VAL:HA	2:B:290:THR:HG21	2.02	0.41
2:B:209:LEU:CD2	2:B:214:LEU:HD23	2.50	0.41
1:A:457:TYR:HE1	1:A:463:ARG:HG2	1.85	0.41
1:A:199:ARG:NH2	1:A:223:LYS:CB	2.70	0.41
1:A:266:TRP:O	1:A:269:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:180:ILE:HA	1:A:188:TYR:O	2.20	0.41
2:B:374:LYS:O	2:B:378:GLU:HG3	2.20	0.41
1:A:404:GLU:HA	1:A:404:GLU:OE1	2.20	0.41
2:B:163:SER:O	2:B:167:ILE:HG13	2.19	0.41
2:D:7:THR:HG22	2:D:119:PRO:HB2	2.02	0.41
3:T:711:DC:H2'	3:T:712:DC:C6	2.54	0.41
2:D:11:LYS:HA	2:D:11:LYS:HD2	1.87	0.41
1:A:266:TRP:CE3	1:A:269:GLN:NE2	2.88	0.41
1:A:339:TYR:CD2	1:A:375:ILE:HD11	2.56	0.41
2:B:207:GLN:O	2:B:210:LEU:N	2.53	0.41
1:A:276:VAL:O	1:A:276:VAL:CG1	2.68	0.41
1:A:197:GLN:O	1:A:200:THR:HB	2.20	0.41
1:A:132:ILE:HA	1:A:133:PRO:HD3	1.76	0.41
1:C:516:GLU:OE1	1:C:516:GLU:HA	2.19	0.41
1:C:12:LEU:HB3	1:C:83:ARG:O	2.20	0.41
1:C:225:PRO:HA	1:C:226:PRO:C	2.41	0.41
2:D:317:VAL:O	2:D:317:VAL:HG23	2.21	0.41
2:D:238:LYS:HA	2:D:238:LYS:HD3	1.87	0.41
3:E:717:DC:C2'	3:E:718:DA:OP2	2.68	0.41
2:D:298:GLU:H	2:D:298:GLU:CD	2.24	0.41
2:D:56:TYR:O	2:D:129:ALA:HB3	2.21	0.41
1:A:328:GLU:HG2	1:A:330:GLN:HE22	1.86	0.41
1:A:328:GLU:HG2	1:A:330:GLN:NE2	2.35	0.41
1:A:20:LYS:HA	1:A:57:ASN:H	1.86	0.41
2:B:275:LYS:HA	2:B:275:LYS:HD3	1.87	0.41
1:A:121:ASP:O	1:A:122:GLU:C	2.57	0.41
2:B:124:PHE:CD1	2:B:127:TYR:CD2	3.07	0.41
1:C:156:SER:HB2	1:C:157:PRO:HD3	2.02	0.41
2:B:301:LEU:HD23	2:B:301:LEU:HA	1.93	0.41
1:C:463:ARG:HG2	1:C:464:GLN:N	2.35	0.41
1:C:129:ALA:HA	1:C:144:TYR:O	2.20	0.41
2:D:124:PHE:CD1	2:D:127:TYR:HD2	2.39	0.41
1:A:106:VAL:O	1:A:227:PHE:CE1	2.74	0.41
1:A:8:VAL:HA	1:A:9:PRO:HD2	1.69	0.41
1:C:27:THR:CG2	1:C:29:GLU:HG2	2.51	0.41
1:C:164:MET:CE	1:C:168:LEU:HG	2.51	0.41
1:C:270:ILE:HD12	1:C:270:ILE:O	2.20	0.41
1:C:467:VAL:HA	1:C:468:PRO:HD3	1.95	0.41
2:B:111:VAL:HG23	2:B:115:TYR:HE2	1.85	0.40
1:A:265:ASN:OD1	1:A:353:LYS:HE3	2.21	0.40
1:C:323:LYS:HE2	1:C:344:GLU:OE2	2.21	0.40
2:D:423:VAL:HG13	2:D:426:TRP:NE1	2.30	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:422:LEU:N	2:B:422:LEU:HD23	2.36	0.40
1:C:64:LYS:HE2	1:C:68:SER:O	2.22	0.40
1:A:48:SER:O	1:A:144:TYR:HA	2.22	0.40
2:D:428:GLN:HA	2:D:428:GLN:NE2	2.26	0.40
1:C:42:GLU:N	1:C:47:ILE:HG22	2.37	0.40
2:B:164:MET:HG3	2:B:168:LEU:HD12	2.02	0.40
1:A:0:VAL:HA	1:A:1:PRO:HD3	1.86	0.40
1:A:94:ILE:HA	1:A:95:PRO:HD3	1.94	0.40
4:F:803:DC:H2'	4:F:804:DA:N7	2.36	0.40
2:B:266:TRP:NE1	2:B:425:LEU:CD2	2.84	0.40
2:B:47:ILE:CD1	2:B:144:TYR:CD1	2.93	0.40
2:B:122:GLU:HG3	2:B:122:GLU:O	2.21	0.40
1:C:450:THR:HG21	1:C:452:LEU:HD12	2.03	0.40
2:B:118:VAL:O	2:B:148:VAL:HB	2.21	0.40
2:D:109:LEU:HA	2:D:109:LEU:HD23	1.88	0.40
1:C:16:MET:HE1	1:C:83:ARG:HH11	1.86	0.40
1:A:231:GLY:N	4:P:821:DC:H5''	2.37	0.40
1:C:60:VAL:HG22	1:C:61:PHE:N	2.37	0.40
1:C:120:LEU:HG	1:C:121:ASP:H	1.85	0.40
2:D:75:VAL:HG11	2:D:77:PHE:CZ	2.57	0.40
1:C:94:ILE:CD1	3:E:709:DC:H1'	2.51	0.40
2:B:46:LYS:HE2	2:B:116:PHE:HB3	2.04	0.40

There are no symmetry-related clashes.

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	553/556 (100%)	524 (95%)	27 (5%)	2 (0%)	43	80
1	C	553/556 (100%)	521 (94%)	30 (5%)	2 (0%)	43	80
2	B	408/428 (95%)	387 (95%)	21 (5%)	0	100	100
2	D	408/428 (95%)	384 (94%)	24 (6%)	0	100	100
All	All	1922/1968 (98%)	1816 (94%)	102 (5%)	4 (0%)	56	88

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	GLU
1	C	217	PRO
1	A	217	PRO
1	C	59	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	495/497 (100%)	472 (95%)	23 (5%)	37	73
1	C	495/497 (100%)	473 (96%)	22 (4%)	39	75
2	B	374/390 (96%)	356 (95%)	18 (5%)	35	72
2	D	374/390 (96%)	360 (96%)	14 (4%)	45	81
All	All	1738/1774 (98%)	1661 (96%)	77 (4%)	39	75

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

Mol	Chain	Res	Type
1	A	2	ILE
1	A	3	SER
1	A	5	ILE
1	A	8	VAL
1	A	17	ASP
1	A	42	GLU
1	A	90	VAL
1	A	109	LEU
1	A	130	PHE
1	A	169	GLU
1	A	188	TYR
1	A	221	HIS
1	A	358	ARG
1	A	374	LYS
1	A	391	LEU
1	A	424	LYS
1	A	450	THR

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Mol	Chain	Res	Type
1	A	459	THR
1	A	473	THR
1	A	475	GLN
1	A	507	GLN
1	A	547	GLN
1	A	550	LYS
2	B	11	LYS
2	B	35	VAL
2	B	39	THR
2	B	72	ARG
2	B	92	LEU
2	B	115	TYR
2	B	209	LEU
2	B	234	LEU
2	B	240	THR
2	B	245	VAL
2	B	250	ASP
2	B	269	GLN
2	B	280	SER
2	B	326	ILE
2	B	336	GLN
2	B	347	LYS
2	B	424	LYS
2	B	428	GLN
1	C	2	ILE
1	C	3	SER
1	C	5	ILE
1	C	28	GLU
1	C	48	SER
1	C	58	THR
1	C	101	LYS
1	C	105	SER
1	C	109	LEU
1	C	147	ASN
1	C	188	TYR
1	C	206	ARG
1	C	218	ASP
1	C	221	HIS
1	C	224	GLU
1	C	263	LYS
1	C	270	ILE
1	C	277	ARG

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Mol	Chain	Res	Type
1	C	324	ASP
1	C	374	LYS
1	C	434	ILE
1	C	547	GLN
2	D	5	ILE
2	D	29	GLU
2	D	39	THR
2	D	67	ASP
2	D	234	LEU
2	D	248	GLU
2	D	251	SER
2	D	322	SER
2	D	326	ILE
2	D	336	GLN
2	D	394	GLN
2	D	422	LEU
2	D	425	LEU
2	D	428	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	57	ASN
1	A	407	GLN
2	B	96	HIS
2	B	278	GLN
2	B	394	GLN
1	C	222	GLN
1	C	407	GLN
1	C	509	GLN
1	C	520	GLN
2	D	161	GLN
2	D	278	GLN
2	D	336	GLN
2	D	348	ASN
2	D	394	GLN
2	D	407	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are 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
4	MRG	F	817	1,3,4	26,28,29	2.62	10 (38%)	33,39,42	2.83	6 (18%)
4	ATM	F	822	3,4	21,23,24	1.17	2 (9%)	24,32,35	2.52	7 (29%)
4	MRG	P	817	1,3,4	26,28,29	2.69	10 (38%)	33,39,42	3.29	6 (18%)
4	ATM	P	822	3,4	21,23,24	1.24	4 (19%)	24,32,35	2.28	6 (25%)

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
4	MRG	F	817	1,3,4	-	0/11/26/27	0/1/3/3
4	ATM	F	822	3,4	-	0/8/24/25	0/2/2/2
4	MRG	P	817	1,3,4	-	0/11/26/27	0/1/3/3
4	ATM	P	822	3,4	-	0/8/24/25	0/2/2/2

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	817	MRG	C4-N3	6.10	1.46	1.35
4	P	817	MRG	C2-N2	5.83	1.49	1.32
4	F	817	MRG	C2-N2	5.63	1.48	1.32
4	F	817	MRG	C4-N3	5.62	1.45	1.35
4	F	817	MRG	P-OP1	5.00	1.52	1.46
4	P	817	MRG	C2-N3	4.94	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	817	MRG	P-OP1	4.86	1.52	1.46
4	F	817	MRG	C2-N3	4.84	1.44	1.33
4	F	817	MRG	C6-C5	4.55	1.48	1.41
4	P	817	MRG	C6-C5	4.53	1.48	1.41
4	P	817	MRG	C2'-C3'	-3.12	1.44	1.52
4	F	817	MRG	C2'-C3'	-3.11	1.44	1.52
4	F	822	ATM	N5'-N4'	3.00	1.26	1.15
4	P	817	MRG	C2-N1	2.95	1.43	1.36
4	F	817	MRG	C2-N1	2.57	1.42	1.36
4	P	822	ATM	N5'-N4'	2.54	1.24	1.15
4	P	817	MRG	O4'-C4'	-2.53	1.39	1.45
4	F	817	MRG	O4'-C4'	-2.49	1.39	1.45
4	P	817	MRG	C6-N1	2.49	1.41	1.37
4	P	817	MRG	O3'-C3'	-2.47	1.37	1.43
4	P	822	ATM	C6-N1	2.43	1.40	1.34
4	F	822	ATM	C6-N1	2.39	1.40	1.34
4	F	817	MRG	O3'-C3'	-2.33	1.38	1.43
4	F	817	MRG	C6-N1	2.26	1.41	1.37
4	P	822	ATM	C4-N3	2.25	1.41	1.37
4	P	822	ATM	P-OP1	2.12	1.49	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	817	MRG	C6-C5-N7	-16.70	131.89	134.14
4	F	817	MRG	C6-C5-N7	-13.75	132.29	134.14
4	F	822	ATM	C6-N1-C2	-8.48	120.00	122.41
4	P	822	ATM	C6-N1-C2	-7.09	120.39	122.41
4	F	822	ATM	N3-C2-N1	5.99	120.97	115.97
4	P	822	ATM	N3-C2-N1	5.22	120.33	115.97
4	P	817	MRG	N3-C4-N9	3.73	132.38	126.91
4	F	817	MRG	N3-C4-N9	3.69	132.32	126.91
4	F	817	MRG	C5-C4-N3	-3.67	120.62	125.94
4	P	817	MRG	C5-C4-N3	-3.48	120.89	125.94
4	F	817	MRG	C2-N3-C4	3.25	119.41	115.03
4	F	822	ATM	N5'-N4'-N3'	3.19	179.74	172.25
4	P	817	MRG	C22-C21-N2	3.13	119.97	111.26
4	F	822	ATM	C4-N3-C2	-3.09	119.06	125.39
4	P	822	ATM	C4-N3-C2	-2.99	119.26	125.39
4	P	822	ATM	N5'-N4'-N3'	2.93	179.12	172.25
4	P	817	MRG	C2-N3-C4	2.91	118.95	115.03
4	F	817	MRG	C22-C21-N2	2.53	118.31	111.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	817	MRG	O4'-C1'-N9	2.39	112.17	107.68
4	F	822	ATM	C5'-C4'-C3'	-2.34	106.10	114.50
4	P	817	MRG	O4'-C1'-N9	2.32	112.04	107.68
4	F	822	ATM	C5-C6-N1	-2.31	119.34	121.59
4	P	822	ATM	C3'-N3'-N4'	2.21	123.43	115.95
4	F	822	ATM	C6-C5-C4	2.13	120.27	115.11
4	P	822	ATM	C6-C5-C4	2.12	120.25	115.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
6	AZT	A	823	5	32,32,32	2.50	7 (21%)	44,49,49	2.01	12 (27%)
6	AZT	C	823	5	32,32,32	2.52	7 (21%)	44,49,49	2.14	12 (27%)

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
6	AZT	A	823	5	-	0/22/37/37	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	AZT	C	823	5	-	0/22/37/37	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	823	AZT	O4-C4	8.93	1.42	1.24
6	A	823	AZT	O4-C4	8.75	1.41	1.24
6	A	823	AZT	O2-C2	7.13	1.38	1.23
6	C	823	AZT	O2-C2	7.09	1.38	1.23
6	A	823	AZT	C4-N3	4.30	1.44	1.37
6	C	823	AZT	C4-N3	4.25	1.44	1.37
6	C	823	AZT	C2-N1	4.10	1.42	1.38
6	A	823	AZT	C2-N1	3.69	1.42	1.38
6	A	823	AZT	C6-N1	3.41	1.42	1.34
6	C	823	AZT	C6-N1	3.35	1.42	1.34
6	A	823	AZT	C2-N3	3.04	1.43	1.37
6	C	823	AZT	C2-N3	2.88	1.42	1.37
6	A	823	AZT	N5'-N4'	2.70	1.25	1.15
6	C	823	AZT	N5'-N4'	2.59	1.25	1.15

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	823	AZT	C6-N1-C2	-8.19	120.08	122.41
6	A	823	AZT	C6-N1-C2	-6.28	120.62	122.41
6	C	823	AZT	O3B-PB-O3A	5.29	112.42	101.66
6	A	823	AZT	N3-C2-N1	5.14	120.26	115.97
6	C	823	AZT	N3-C2-N1	5.09	120.22	115.97
6	A	823	AZT	O3B-PB-O3A	4.00	109.80	101.66
6	A	823	AZT	PB-O3B-PG	-3.09	122.64	131.68
6	A	823	AZT	O4'-C4'-C3'	2.94	108.90	105.48
6	A	823	AZT	C4-N3-C2	-2.89	119.47	125.39
6	C	823	AZT	N5'-N4'-N3'	2.84	178.92	172.25
6	C	823	AZT	C4-N3-C2	-2.78	119.69	125.39
6	A	823	AZT	C3'-C2'-C1'	2.64	106.07	103.12
6	A	823	AZT	N5'-N4'-N3'	2.59	178.32	172.25
6	C	823	AZT	PB-O3B-PG	-2.59	124.09	131.68
6	A	823	AZT	PB-O3A-PA	-2.53	124.25	131.68
6	C	823	AZT	PB-O3A-PA	-2.27	125.04	131.68
6	C	823	AZT	O2A-PA-O1A	-2.23	99.75	112.21
6	A	823	AZT	C6-C5-C4	2.20	120.44	115.11
6	C	823	AZT	C6-C5-C4	2.16	120.34	115.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	823	AZT	O2G-PG-O3B	2.13	115.23	105.14
6	A	823	AZT	O2B-PB-O3A	2.09	115.05	105.14
6	C	823	AZT	O3A-PA-O5'	2.05	112.58	103.41
6	A	823	AZT	O2G-PG-O3B	2.04	114.81	105.14
6	C	823	AZT	O2B-PB-O1B	-2.02	100.94	112.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	A	555/556 (99%)	0.78	74 (13%) 4 3	20, 62, 118, 137	0
1	C	555/556 (99%)	0.78	67 (12%) 5 4	21, 62, 117, 137	0
2	B	412/428 (96%)	0.60	31 (7%) 14 12	21, 51, 109, 122	0
2	D	412/428 (96%)	0.62	42 (10%) 7 6	25, 54, 113, 127	0
3	E	24/27 (88%)	0.20	2 (8%) 11 10	42, 86, 136, 149	0
3	T	24/27 (88%)	0.44	3 (12%) 5 4	40, 80, 137, 146	0
4	F	20/21 (95%)	-0.31	0 100 100	42, 72, 129, 129	0
4	P	20/21 (95%)	0.01	1 (5%) 28 28	42, 69, 130, 131	0
All	All	2022/2064 (97%)	0.68	220 (10%) 6 5	20, 57, 117, 149	0

All (220) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	214	LEU	16.4
2	D	4	PRO	10.7
1	A	133	PRO	10.2
3	T	702	DT	8.4
2	B	4	PRO	8.2
2	B	212	TRP	8.0
1	C	135	ILE	7.4
1	C	134	SER	7.1
1	A	135	ILE	6.9
1	C	133	PRO	6.8
1	C	24	TRP	6.7
2	D	214	LEU	6.6
1	C	28	GLU	6.5
1	C	132	ILE	6.5
1	C	142	ILE	6.4
1	A	67	ASP	6.2

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Mol	Chain	Res	Type	RSRZ
1	C	252	TRP	6.2
2	B	5	ILE	6.0
1	A	74	LEU	5.9
1	A	73	LYS	5.9
1	C	137	ASN	5.7
1	C	34	LEU	5.6
2	B	215	THR	5.5
1	C	144	TYR	5.4
1	C	61	PHE	5.4
1	C	287	LYS	5.3
1	A	66	LYS	5.3
2	D	215	THR	5.3
2	D	423	VAL	5.2
1	C	293	ILE	5.2
2	D	92	LEU	5.2
1	C	26	LEU	5.1
2	D	178	ILE	5.1
1	C	32	LYS	5.1
2	D	358	ARG	5.1
1	A	223	LYS	4.9
1	C	247	PRO	4.9
1	A	131	THR	4.8
2	D	212	TRP	4.7
1	A	34	LEU	4.7
2	D	428	GLN	4.7
1	C	136	ASN	4.6
3	E	702	DT	4.6
1	A	140	PRO	4.5
1	A	71	TRP	4.4
1	C	25	PRO	4.4
1	A	61	PHE	4.3
1	C	138	GLU	4.3
2	D	172	LYS	4.3
1	A	60	VAL	4.3
1	C	292	VAL	4.3
2	B	209	LEU	4.3
1	C	141	GLY	4.2
1	A	22	LYS	4.1
2	D	179	VAL	4.1
1	C	246	LEU	4.1
2	B	88	TRP	4.1
1	C	222	GLN	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	134	SER	4.1
1	C	27	THR	4.1
2	D	173	LYS	4.1
1	C	22	LYS	4.0
1	C	223	LYS	4.0
1	A	62	ALA	4.0
1	C	140	PRO	4.0
2	B	90	VAL	4.0
1	A	145	GLN	4.0
1	C	60	VAL	4.0
1	A	26	LEU	3.9
2	D	232	TYR	3.9
1	A	287	LYS	3.9
1	C	31	ILE	3.8
2	D	87	PHE	3.8
1	A	282	LEU	3.8
1	C	260	LEU	3.7
1	C	294	PRO	3.7
1	A	59	PRO	3.7
1	A	132	ILE	3.6
2	B	213	GLY	3.6
1	A	52	PRO	3.6
1	A	50	ILE	3.6
1	C	67	ASP	3.6
1	C	301	LEU	3.6
1	C	131	THR	3.6
1	A	285	GLY	3.5
1	A	127	TYR	3.5
1	C	254	VAL	3.5
1	A	28	GLU	3.5
1	C	66	LYS	3.5
2	D	5	ILE	3.5
1	C	295	LEU	3.5
1	A	49	LYS	3.4
1	A	27	THR	3.4
1	A	136	ASN	3.4
2	D	354	TYR	3.4
1	A	286	THR	3.4
1	A	141	GLY	3.3
2	D	177	ASP	3.3
1	C	145	GLN	3.3
2	D	216	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	24	TRP	3.3
1	A	55	PRO	3.3
1	C	74	LEU	3.3
2	D	210	LEU	3.3
1	A	128	THR	3.2
1	A	56	TYR	3.2
2	B	211	ARG	3.2
1	A	124	PHE	3.2
1	A	130	PHE	3.2
3	T	725	DG	3.2
1	A	254	VAL	3.2
2	B	428	GLN	3.2
2	B	171	PHE	3.1
2	D	95	PRO	3.1
1	A	146	TYR	3.1
1	C	291	GLU	3.1
1	C	257	ILE	3.1
1	C	128	THR	3.1
1	A	25	PRO	3.0
1	C	109	LEU	3.0
2	D	360	ALA	3.0
1	A	30	LYS	3.0
1	A	143	ARG	3.0
1	C	139	THR	3.0
2	D	88	TRP	3.0
1	A	138	GLU	2.9
1	A	554	ALA	2.9
2	D	361	HIS	2.9
1	C	303	LEU	2.9
2	B	168	LEU	2.9
2	D	171	PHE	2.9
1	C	71	TRP	2.9
1	A	260	LEU	2.9
1	A	142	ILE	2.9
2	D	168	LEU	2.9
1	A	109	LEU	2.8
1	A	41	MET	2.8
1	C	249	LYS	2.8
2	D	242	GLN	2.8
2	B	12	LEU	2.8
2	D	56	TYR	2.8
2	D	209	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	293	ILE	2.8
2	B	301	LEU	2.8
1	C	20	LYS	2.7
1	A	288	ALA	2.7
1	A	246	LEU	2.7
1	C	448	ARG	2.7
1	C	23	GLN	2.7
1	C	30	LYS	2.7
4	P	803	DC	2.6
1	A	107	THR	2.6
1	A	144	TYR	2.6
1	C	244	ILE	2.6
2	D	217	PRO	2.6
1	A	19	PRO	2.6
2	D	174	GLN	2.6
2	D	187	LEU	2.5
2	D	176	PRO	2.5
2	D	231	GLY	2.5
2	B	174	GLN	2.5
1	A	148	VAL	2.5
1	A	295	LEU	2.4
2	D	318	TYR	2.4
1	A	284	ARG	2.4
2	B	92	LEU	2.4
2	B	425	LEU	2.4
2	B	232	TYR	2.4
2	B	94	ILE	2.4
1	A	247	PRO	2.4
2	D	234	LEU	2.4
1	A	222	GLN	2.4
2	B	217	PRO	2.4
1	C	15	GLY	2.3
1	A	87	PHE	2.3
1	C	309	ILE	2.3
2	B	178	ILE	2.3
2	B	250	ASP	2.3
1	C	357	MET	2.3
1	C	297	GLU	2.3
1	C	253	THR	2.3
2	D	90	VAL	2.3
2	B	14	PRO	2.3
1	C	55	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	42	GLU	2.2
2	B	86	ASP	2.2
2	B	111	VAL	2.2
1	C	250	ASP	2.2
1	C	248	GLU	2.2
1	C	554	ALA	2.2
2	B	11	LYS	2.2
1	C	35	VAL	2.2
1	C	281	LYS	2.2
1	C	21	VAL	2.2
2	B	205	LEU	2.2
1	A	29	GLU	2.2
1	A	139	THR	2.2
1	C	198	HIS	2.2
1	A	20	LYS	2.2
1	A	46	LYS	2.2
1	A	69	THR	2.1
1	A	448	ARG	2.1
1	A	120	LEU	2.1
2	D	426	TRP	2.1
2	D	357	MET	2.1
1	A	64	LYS	2.1
2	B	193	LEU	2.1
2	D	205	LEU	2.1
3	T	724	DT	2.1
2	D	85	GLN	2.1
1	A	289	LEU	2.1
1	A	301	LEU	2.1
1	A	205	LEU	2.1
2	D	424	LYS	2.0
1	C	62	ALA	2.0
3	E	704	DG	2.0
2	D	124	PHE	2.0
1	A	257	ILE	2.0
2	B	159	ILE	2.0
2	B	423	VAL	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	ATM	P	822	22/23	0.19	0.64	56,63,78,82	0
4	ATM	F	822	22/23	0.20	0.08	55,64,81,83	0
4	MRG	P	817	26/27	0.17	-0.19	58,74,93,106	0
4	MRG	F	817	26/27	0.13	-0.80	66,81,99,115	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	MG	C	600	1/1	0.24	0.68	82,82,82,82	0
5	MG	A	600	1/1	0.17	-0.23	87,87,87,87	0
6	AZT	A	823	31/31	0.17	-0.54	72,90,106,109	0
6	AZT	C	823	31/31	0.18	-0.75	69,85,104,111	0

6.5 Other polymers

There are no such residues in this entry.