



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:51 PM UTC

PDB ID : 4PQU / pdb_00004pqu
Title : Crystal structure of HIV-1 Reverse Transcriptase in complex with RNA/DNA and dATP
Authors : Das, K.; Bandwar, R.P.; Arnold, E.
Deposited on : 2014-03-04
Resolution : 2.51 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)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

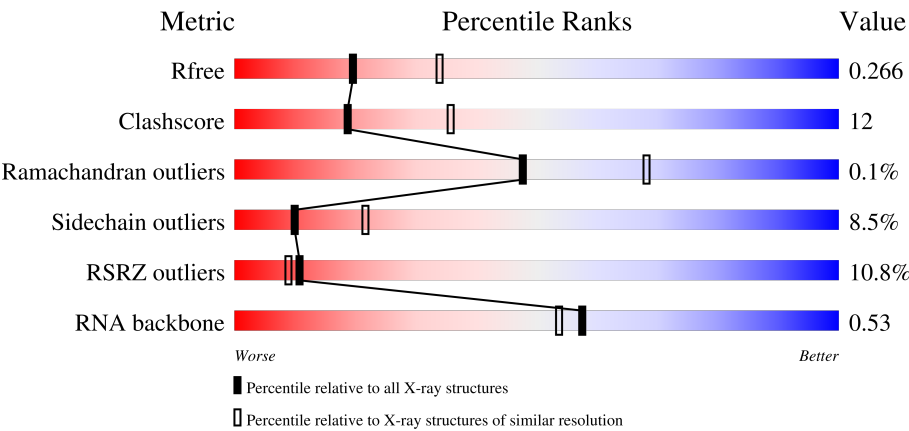
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)
RNA backbone	3983	1003 (2.78-2.22)

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

Mol	Chain	Length	Quality of chain
1	A	556	7% 69% 26% • •
1	C	556	22% 63% 31% • •
2	B	428	2% 70% 24% • •
2	D	428	7% 68% 25% • •

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Mol	Chain	Length	Quality of chain
3	E	27	15% 63% 11% • 22%
3	T	27	7% 48% 26% • 22%
4	F	21	19% 33% 52% 14%
4	P	21	10% 33% 52% 14%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 17849 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 HIV-1 Reverse Transcriptase, p66 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	0	0
			4432	2872	736	816	8			
1	C	545	Total	C	N	O	S	0	0	0
			4432	2872	736	816	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	413	Total	C	N	O	S	0	0	0
			3406	2215	564	621	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

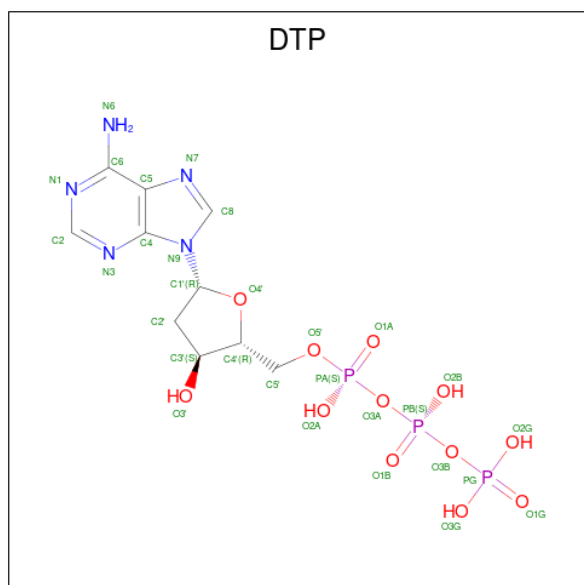
- Molecule 3 is a RNA chain called 5'-R(*AP*UP*GP*GP*UP*CP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*UP*GP*UP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	21	Total	C	N	O	P	0	0	0
			452	202	88	142	20			
3	E	21	Total	C	N	O	P	0	0	0
			452	202	88	142	20			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	P	18	Total	C	N	O	P	0	0	0
			363	173	64	109	17			
4	F	18	Total	C	N	O	P	0	0	0
			363	173	64	109	17			

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

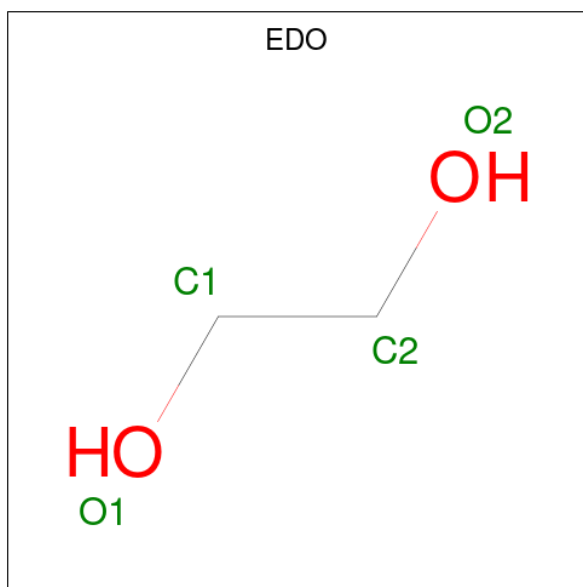


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
5	C	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

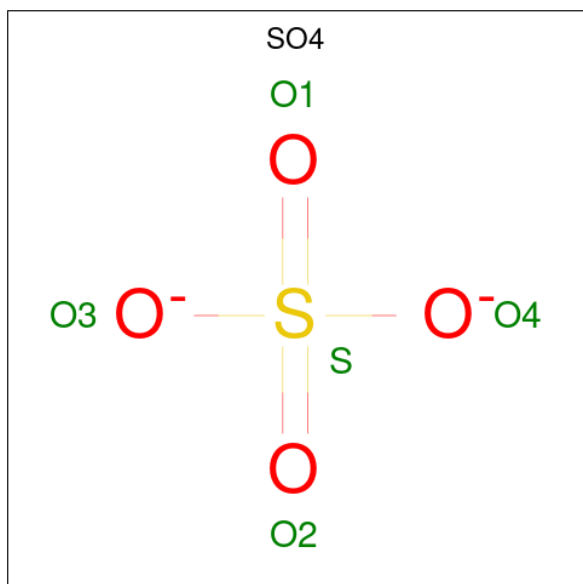
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Mg	0	0
			2	2		
6	C	2	Total	Mg	0	0
			2	2		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



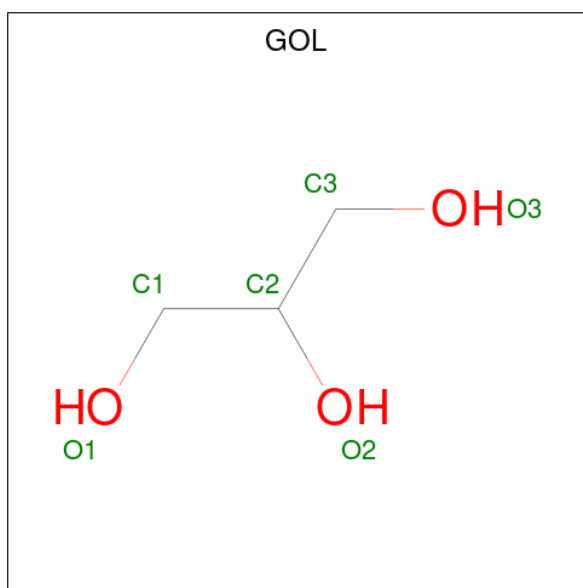
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total O S 5 4 1	0	0
8	A	1	Total O S 5 4 1	0	0
8	A	1	Total O S 5 4 1	0	0
8	B	1	Total O S 5 4 1	0	0
8	B	1	Total O S 5 4 1	0	0
8	C	1	Total O S 5 4 1	0	0
8	D	1	Total O S 5 4 1	0	0
8	D	1	Total O S 5 4 1	0	0

- Molecule 9 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C O 6 3 3	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	131	Total O 131 131	0	0

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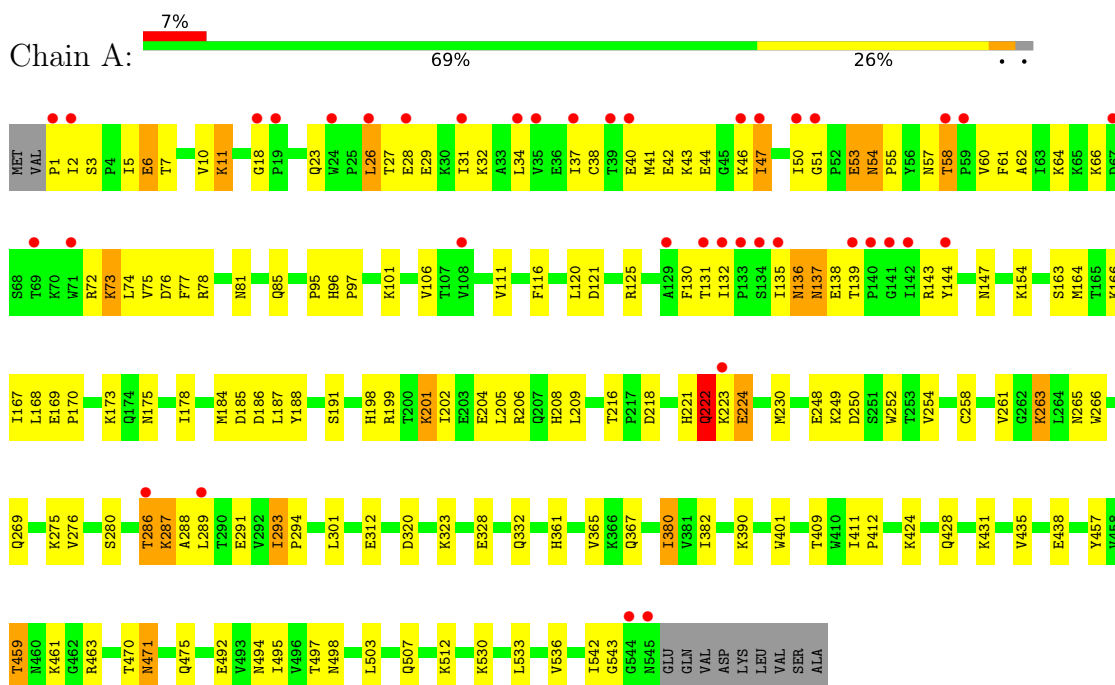
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	139	Total 139	O 139	0	0
10	C	80	Total 80	O 80	0	0
10	D	76	Total 76	O 76	0	0
10	T	3	Total 3	O 3	0	0
10	P	4	Total 4	O 4	0	0
10	E	1	Total 1	O 1	0	0
10	F	1	Total 1	O 1	0	0

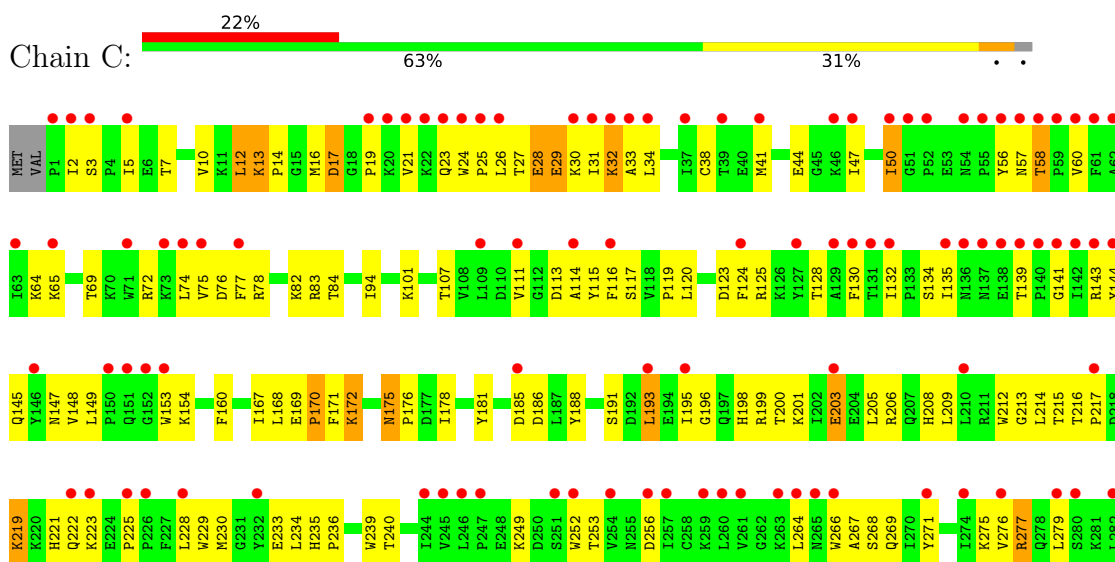
3 Residue-property plots

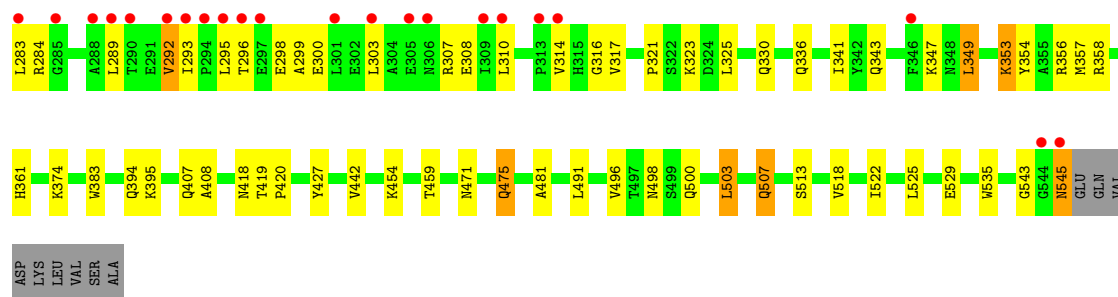
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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

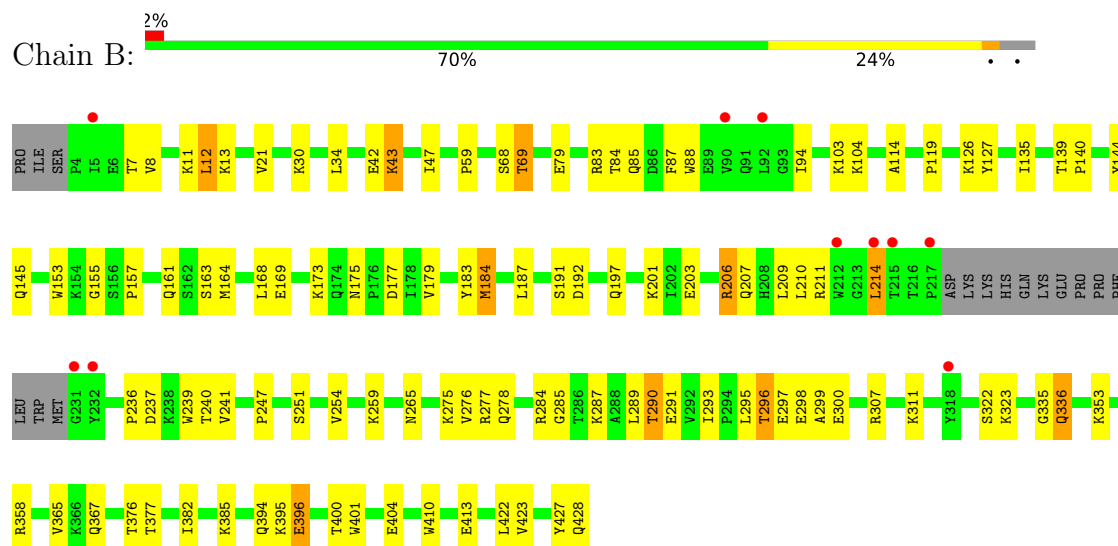


- Molecule 1: HIV-1 Reverse Transcriptase, p66 subunit

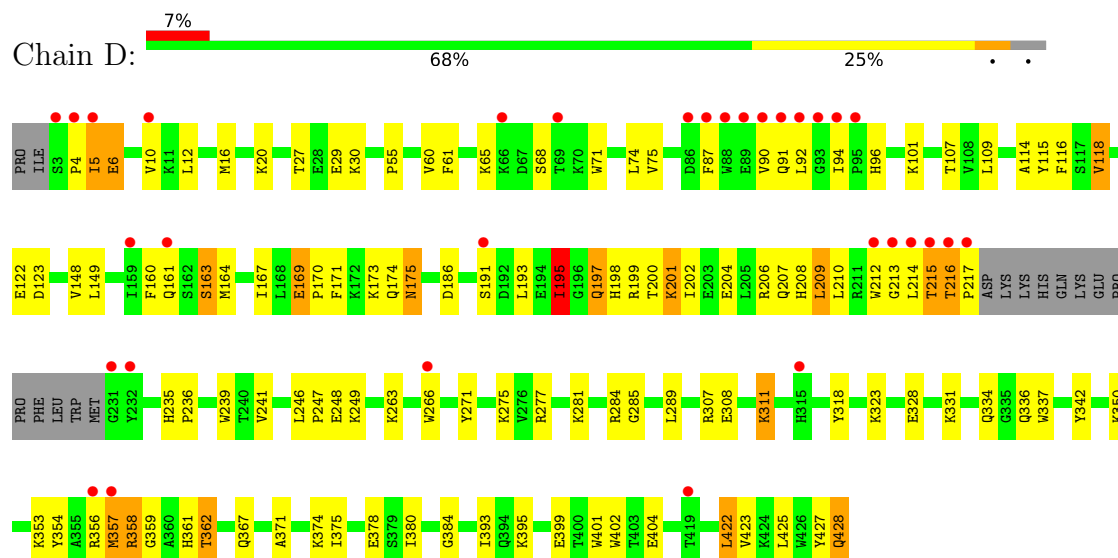




• Molecule 2: HIV-1 Reverse Transcriptase, p51 subunit



• Molecule 2: HIV-1 Reverse Transcriptase, p51 subunit



• Molecule 3: 5'-R(*AP*UP*GP*GP*UP*CP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*A
P*GP*GP*GP*AP*CP*UP*GP*UP*G)-3'

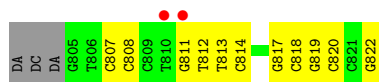




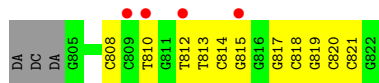
● Molecule 3: 5'-R(*AP*UP*GP*GP*UP*CP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*A
P*GP*GP*GP*AP*CP*UP*GP*UP*G)-3'



● Molecule 4: 5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*GP*CP*G
P*CP*CP*G)-3'



● Molecule 4: 5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*GP*CP*G
P*CP*CP*G)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.44Å 128.29Å 130.68Å 90.00° 101.76° 90.00°	Depositor
Resolution (Å)	40.47 – 2.51 40.47 – 2.51	Depositor EDS
% Data completeness (in resolution range)	98.1 (40.47-2.51) 98.0 (40.47-2.51)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.202 , 0.266 0.206 , 0.266	Depositor DCC
R_{free} test set	2923 reflections (2.96%)	wwPDB-VP
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17849	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GOL, DTP, EDO, SO4

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	0.68	1/4550 (0.0%)	0.96	15/6183 (0.2%)
1	C	0.60	3/4550 (0.1%)	0.95	11/6183 (0.2%)
2	B	0.69	0/3497	0.93	3/4751 (0.1%)
2	D	0.66	0/3503	1.01	16/4760 (0.3%)
3	E	0.30	0/506	0.43	0/789
3	T	0.37	0/506	0.53	0/789
4	F	0.40	0/405	0.53	0/623
4	P	0.50	0/405	0.56	0/623
All	All	0.64	4/17922 (0.0%)	0.92	45/24701 (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
1	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	176	PRO	N-CD	5.22	1.55	1.47
1	C	169	GLU	C-N	5.21	1.41	1.34
1	A	169	GLU	C-N	5.11	1.41	1.34
1	C	170	PRO	N-CD	5.06	1.54	1.47

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	271	TYR	CA-C-N	-10.34	106.91	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	271	TYR	C-N-CA	-10.34	106.91	119.84
2	D	215	THR	N-CA-C	9.86	125.60	112.88
1	C	219	LYS	N-CA-C	-9.47	101.92	112.72
1	A	312	GLU	CA-C-N	7.46	127.39	119.85
1	A	312	GLU	C-N-CA	7.46	127.39	119.85
1	A	3	SER	CA-C-N	7.37	128.62	120.45
1	A	3	SER	C-N-CA	7.37	128.62	120.45
1	A	382	ILE	N-CA-C	7.25	118.04	110.72
2	B	382	ILE	N-CA-C	7.01	117.80	110.72
1	A	54	ASN	CA-C-N	6.62	126.21	119.19
1	A	54	ASN	C-N-CA	6.62	126.21	119.19
2	D	195	ILE	N-CA-C	6.58	116.74	110.42
2	D	118	VAL	CA-C-N	6.56	128.04	119.84
2	D	118	VAL	C-N-CA	6.56	128.04	119.84
2	D	212	TRP	N-CA-C	-6.55	103.98	112.23
1	A	144	TYR	N-CA-C	6.02	117.35	108.86
2	D	401	TRP	N-CA-C	5.99	122.59	113.61
1	A	175	ASN	CA-C-N	5.99	126.14	119.32
1	A	175	ASN	C-N-CA	5.99	126.14	119.32
1	A	222	GLN	N-CA-C	-5.92	102.69	110.33
2	D	213	GLY	N-CA-C	5.82	126.97	113.18
1	C	222	GLN	N-CA-C	-5.80	102.70	110.24
2	D	235	HIS	CA-C-N	5.75	125.43	119.05
2	D	235	HIS	C-N-CA	5.75	125.43	119.05
1	A	471	ASN	N-CA-C	5.71	119.12	111.24
1	C	94	ILE	CA-C-N	-5.65	114.78	120.21
1	C	94	ILE	C-N-CA	-5.65	114.78	120.21
2	D	96	HIS	CA-C-N	5.57	126.80	119.84
2	D	96	HIS	C-N-CA	5.57	126.80	119.84
1	C	169	GLU	CA-C-N	-5.45	113.00	119.05
1	C	169	GLU	C-N-CA	-5.45	113.00	119.05
1	A	312	GLU	N-CA-C	-5.34	101.80	109.48
1	A	169	GLU	CA-C-N	-5.28	113.19	119.05
1	A	169	GLU	C-N-CA	-5.28	113.19	119.05
1	C	13	LYS	CA-C-N	5.26	126.41	119.84
1	C	13	LYS	C-N-CA	5.26	126.41	119.84
1	C	349	LEU	N-CA-C	-5.19	105.71	111.36
1	C	175	ASN	CA-C-N	-5.11	113.38	119.05
1	C	175	ASN	C-N-CA	-5.11	113.38	119.05
2	D	118	VAL	N-CA-C	5.09	118.70	107.92
2	D	186	ASP	N-CA-C	5.08	117.67	109.40
2	B	293	ILE	CA-C-N	5.04	124.95	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	293	ILE	C-N-CA	5.04	124.95	119.76
2	D	402	TRP	N-CA-C	5.03	116.77	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	218	ASP	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	4432	0	4488	101	0
1	C	4432	0	4488	135	0
2	B	3400	0	3433	72	0
2	D	3406	0	3437	85	0
3	E	452	0	232	2	0
3	T	452	0	232	4	0
4	F	363	0	202	15	0
4	P	363	0	202	12	0
5	A	30	0	12	1	0
5	C	30	0	12	2	0
6	A	2	0	0	0	0
6	C	2	0	0	0	0
7	A	4	0	6	1	0
8	A	15	0	0	2	0
8	B	10	0	0	1	0
8	C	5	0	0	0	0
8	D	10	0	0	1	0
9	B	6	0	8	2	0
10	A	131	0	0	6	0
10	B	139	0	0	7	0
10	C	80	0	0	1	0
10	D	76	0	0	3	0
10	E	1	0	0	0	0
10	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	P	4	0	0	1	0
10	T	3	0	0	0	0
All	All	17849	0	16752	402	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (402) 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)
1:C:32:LYS:HD3	1:C:33:ALA:N	1.75	1.01
1:C:168:LEU:HB3	1:C:172:LYS:HE2	1.45	0.96
1:A:459:THR:HG22	1:A:461:LYS:H	1.33	0.94
1:C:175:ASN:HB3	1:C:178:ILE:HD13	1.49	0.92
2:D:191:SER:HG	2:D:198:HIS:HD1	1.22	0.87
1:C:32:LYS:HD3	1:C:32:LYS:C	2.00	0.86
1:A:47:ILE:HD11	1:A:130:PHE:HZ	1.44	0.82
2:B:114:ALA:HB2	2:B:214:LEU:HD13	1.61	0.82
2:B:139:THR:HG22	2:B:140:PRO:O	1.81	0.80
2:D:5:ILE:O	2:D:5:ILE:CG1	2.30	0.80
1:C:3:SER:HB3	1:C:5:ILE:HG23	1.64	0.79
1:A:258:CYS:SG	10:P:903:HOH:O	2.39	0.79
1:C:491:LEU:HB3	1:C:529:GLU:HG3	1.66	0.78
1:C:125:ARG:HH11	1:C:147:ASN:HD22	1.29	0.77
1:C:498:ASN:HD21	1:C:545:ASN:HB3	1.50	0.76
1:C:111:VAL:HB	1:C:185:ASP:HB2	1.69	0.74
1:C:31:ILE:HG23	1:C:34:LEU:HD23	1.70	0.74
1:C:475:GLN:HG3	4:F:808:DC:H5'	1.69	0.73
2:D:263:LYS:NZ	2:D:428:GLN:OE1	2.21	0.73
2:B:276:VAL:H	2:B:277:ARG:HH11	1.35	0.72
1:A:320:ASP:OD2	1:A:323:LYS:NZ	2.20	0.72
2:B:335:GLY:HA2	2:B:367:GLN:HE22	1.54	0.71
2:D:175:ASN:N	2:D:175:ASN:HD22	1.88	0.71
2:D:353:LYS:NZ	10:D:622:HOH:O	2.21	0.71
1:A:47:ILE:HD11	1:A:130:PHE:CZ	2.26	0.70
1:C:195:ILE:HG12	1:C:199:ARG:HH21	1.54	0.70
4:P:807:DC:H2''	4:P:808:DC:H5'	1.72	0.70
1:C:31:ILE:HA	1:C:34:LEU:HB3	1.73	0.70
2:B:307:ARG:NH1	10:B:638:HOH:O	2.21	0.70
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.74	0.69
2:B:47:ILE:HD12	2:B:144:TYR:CD2	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:5:ILE:O	2:D:5:ILE:HG13	1.92	0.69
4:F:814:DC:H2'	4:F:815:DG:C8	2.27	0.69
2:B:394:GLN:HE21	2:B:396:GLU:H	1.40	0.69
2:D:114:ALA:HB2	2:D:214:LEU:HD21	1.74	0.68
1:C:3:SER:HB2	1:C:119:PRO:HD3	1.75	0.68
1:C:503:LEU:CD2	1:C:535:TRP:HB2	2.22	0.68
2:B:247:PRO:O	2:B:307:ARG:NH2	2.26	0.67
1:C:107:THR:HG1	1:C:198:HIS:HE2	1.41	0.67
1:A:222:GLN:O	1:A:224:GLU:N	2.26	0.67
1:C:289:LEU:HD21	4:F:817:DG:H4'	1.77	0.67
1:A:41:MET:HB3	1:A:46:LYS:HB2	1.77	0.67
2:B:13:LYS:HD3	2:B:85:GLN:HB3	1.76	0.66
1:A:34:LEU:HD22	1:A:73:LYS:HG2	1.78	0.66
2:D:175:ASN:N	2:D:175:ASN:ND2	2.43	0.66
3:T:708:G:H2'	3:T:709:C:C6	2.30	0.66
1:C:279:LEU:HD23	1:C:299:ALA:HB1	1.78	0.66
1:C:503:LEU:HD23	1:C:535:TRP:HB2	1.76	0.65
1:C:353:LYS:HD3	1:C:353:LYS:H	1.61	0.65
1:A:27:THR:HG22	1:A:29:GLU:H	1.62	0.64
2:B:30:LYS:NZ	2:B:404:GLU:OE1	2.30	0.64
1:A:254:VAL:HG11	1:A:286:THR:HG21	1.78	0.64
2:B:276:VAL:H	2:B:277:ARG:NH1	1.95	0.63
1:A:131:THR:HG22	1:A:143:ARG:HB3	1.80	0.63
1:C:5:ILE:HG22	1:C:212:TRP:HE3	1.62	0.63
2:D:4:PRO:CD	2:D:5:ILE:H	2.10	0.63
1:C:32:LYS:CD	1:C:33:ALA:N	2.57	0.63
1:A:459:THR:CG2	1:A:461:LYS:H	2.09	0.63
2:B:336:GLN:HG2	2:B:427:TYR:CE1	2.34	0.62
1:A:457:TYR:HE1	1:A:463:ARG:HG2	1.64	0.62
1:C:233:GLU:OE2	1:C:235:HIS:NE2	2.29	0.62
1:A:503:LEU:HD23	2:B:422:LEU:HD22	1.81	0.61
1:C:32:LYS:HD3	1:C:33:ALA:CA	2.29	0.61
1:C:5:ILE:HG22	1:C:212:TRP:CE3	2.35	0.61
1:A:6:GLU:H	1:A:6:GLU:CD	2.09	0.61
4:F:814:DC:H2'	4:F:815:DG:H8	1.66	0.61
1:A:459:THR:HG22	1:A:461:LYS:N	2.12	0.61
4:F:813:DT:H2'	4:F:814:DC:C6	2.36	0.60
1:A:95:PRO:HD2	1:A:230:MET:HE2	1.83	0.60
1:A:41:MET:HG2	1:A:46:LYS:HD2	1.84	0.60
1:A:72:ARG:NH2	5:A:601:DTP:O3A	2.35	0.60
2:D:361:HIS:O	2:D:367:GLN:NE2	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:296:THR:HG22	2:B:299:ALA:H	1.67	0.60
1:C:253:THR:HA	1:C:292:VAL:HA	1.84	0.60
4:F:819:DG:H2'	4:F:820:DC:C6	2.38	0.59
2:D:277:ARG:NE	8:D:501:SO4:O1	2.31	0.59
2:B:84:THR:HG22	2:B:87:PHE:HB3	1.84	0.59
2:D:4:PRO:HG2	2:D:5:ILE:HG23	1.83	0.59
2:B:84:THR:HG21	2:B:153:TRP:HZ2	1.68	0.59
2:B:79:GLU:HG3	2:B:83:ARG:HE	1.68	0.58
1:C:217:PRO:O	1:C:219:LYS:N	2.32	0.58
2:D:167:ILE:O	2:D:208:HIS:NE2	2.35	0.58
2:D:263:LYS:HE3	2:D:425:LEU:HA	1.85	0.58
2:B:336:GLN:OE1	2:B:353:LYS:NZ	2.27	0.58
1:C:206:ARG:NH2	1:C:216:THR:O	2.30	0.58
2:B:164:MET:HE2	2:B:168:LEU:HG	1.86	0.58
2:B:183:TYR:CE2	2:B:184:MET:HG3	2.38	0.58
2:D:174:GLN:HB3	2:D:175:ASN:ND2	2.19	0.58
1:A:536:VAL:HB	1:A:542:ILE:HD13	1.85	0.57
1:A:323:LYS:NZ	10:A:819:HOH:O	2.37	0.57
1:A:163:SER:HA	1:A:166:LYS:HE3	1.86	0.57
1:A:60:VAL:HG12	1:A:75:VAL:HG22	1.85	0.57
1:C:78:ARG:HD2	3:E:705:U:H5''	1.87	0.57
1:C:252:TRP:HZ3	1:C:295:LEU:HB2	1.69	0.57
2:D:30:LYS:NZ	2:D:404:GLU:OE2	2.35	0.57
4:F:817:DG:H2'	4:F:818:DC:C6	2.40	0.57
2:D:4:PRO:HD2	2:D:5:ILE:H	1.69	0.57
1:C:10:VAL:HG11	1:C:153:TRP:HZ2	1.70	0.57
1:A:76:ASP:OD2	1:A:78:ARG:NH2	2.39	0.56
1:A:380:ILE:HD13	9:B:502:GOL:H11	1.85	0.56
1:A:293:ILE:HD12	1:A:294:PRO:HD2	1.87	0.56
1:A:428:GLN:N	8:A:607:SO4:O1	2.34	0.56
1:C:171:PHE:CE2	1:C:205:LEU:HB2	2.40	0.56
1:C:217:PRO:C	1:C:219:LYS:H	2.13	0.56
2:D:248:GLU:OE1	2:D:307:ARG:NH2	2.35	0.56
1:A:249:LYS:HB2	1:A:252:TRP:CE2	2.41	0.56
1:A:289:LEU:HD21	4:P:817:DG:H4'	1.87	0.56
2:B:209:LEU:HD22	2:B:214:LEU:HD23	1.88	0.56
2:B:296:THR:CG2	2:B:299:ALA:H	2.19	0.56
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.40	0.56
1:C:17:ASP:OD2	1:C:56:TYR:OH	2.24	0.56
1:C:34:LEU:HD21	1:C:132:ILE:HB	1.88	0.56
2:B:358:ARG:HD2	10:B:667:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:300:GLU:OE2	1:C:307:ARG:NH2	2.39	0.55
2:B:68:SER:O	2:B:69:THR:HB	2.06	0.55
1:C:271:TYR:CE1	1:C:314:VAL:HB	2.42	0.55
2:D:92:LEU:O	2:D:161:GLN:NE2	2.39	0.55
1:A:438:GLU:OE2	1:A:459:THR:HG21	2.06	0.55
1:A:26:LEU:HD12	1:A:31:ILE:HG13	1.89	0.55
1:A:106:VAL:HG21	8:A:605:SO4:O1	2.06	0.55
2:B:322:SER:HB3	1:C:418:ASN:HD21	1.71	0.54
1:A:34:LEU:HD21	1:A:62:ALA:HB2	1.90	0.54
1:C:139:THR:HG22	1:C:141:GLY:H	1.71	0.54
1:A:34:LEU:HA	1:A:37:ILE:HD12	1.90	0.54
2:B:84:THR:HG21	2:B:153:TRP:CZ2	2.42	0.54
1:C:171:PHE:CD1	1:C:171:PHE:C	2.85	0.54
2:D:247:PRO:HG2	2:D:428:GLN:HG2	1.89	0.54
1:A:57:ASN:OD1	1:A:131:THR:HG23	2.08	0.54
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.90	0.54
2:B:164:MET:HA	2:B:164:MET:HE3	1.90	0.53
1:A:135:ILE:HB	1:A:138:GLU:HB2	1.90	0.53
1:C:170:PRO:HG2	1:C:208:HIS:CE1	2.44	0.53
1:C:72:ARG:NH2	5:C:601:DTP:O2A	2.41	0.53
2:D:263:LYS:HA	2:D:423:VAL:HG11	1.90	0.53
2:B:42:GLU:OE1	2:B:43:LYS:NZ	2.41	0.53
1:A:201:LYS:HE3	1:A:204:GLU:OE2	2.09	0.53
1:C:543:GLY:HA2	2:D:285:GLY:O	2.09	0.53
1:C:289:LEU:CD2	4:F:817:DG:H4'	2.37	0.53
1:C:125:ARG:NH1	1:C:147:ASN:HD22	2.02	0.53
2:B:135:ILE:HD12	10:B:732:HOH:O	2.09	0.53
2:B:284:ARG:NH2	10:B:693:HOH:O	2.41	0.53
2:D:170:PRO:HB2	2:D:208:HIS:HE1	1.73	0.53
1:A:263:LYS:NZ	4:P:820:DC:OP1	2.43	0.52
2:D:206:ARG:NH2	2:D:217:PRO:HB3	2.23	0.52
2:D:107:THR:HG21	2:D:202:ILE:HD13	1.91	0.52
2:B:94:ILE:HG12	2:B:161:GLN:CD	2.34	0.52
2:B:206:ARG:NH1	10:B:694:HOH:O	2.42	0.52
2:D:169:GLU:OE2	2:D:169:GLU:HA	2.02	0.52
1:C:107:THR:OG1	1:C:198:HIS:NE2	2.29	0.52
1:C:221:HIS:CD2	1:C:228:LEU:H	2.27	0.52
1:C:16:MET:HB3	1:C:83:ARG:HD3	1.92	0.52
3:T:714:G:H2'	3:T:715:A:C8	2.45	0.52
2:B:11:LYS:NZ	10:B:652:HOH:O	2.42	0.52
2:D:160:PHE:HE2	2:D:164:MET:HE2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:819:DG:H2'	4:P:820:DC:C6	2.45	0.51
1:A:287:LYS:HD2	1:A:288:ALA:H	1.76	0.51
1:C:395:LYS:NZ	10:C:744:HOH:O	2.43	0.51
2:B:157:PRO:HG3	2:B:184:MET:HA	1.92	0.51
1:C:229:TRP:CE2	1:C:230:MET:HG2	2.45	0.51
1:C:181:TYR:HB2	1:C:188:TYR:HB3	1.93	0.51
2:D:209:LEU:HD12	2:D:214:LEU:HD12	1.93	0.51
1:A:266:TRP:CE2	4:P:820:DC:H4'	2.46	0.51
4:P:812:DT:H2'	4:P:812:DT:O2	2.11	0.51
2:D:167:ILE:HD11	2:D:209:LEU:HA	1.93	0.51
1:A:106:VAL:H	1:A:223:LYS:HG2	1.76	0.50
1:C:296:THR:HG22	1:C:298:GLU:H	1.75	0.50
1:C:503:LEU:O	1:C:507:GLN:HB2	2.11	0.50
2:B:295:LEU:HB3	2:B:300:GLU:HG2	1.93	0.50
1:C:58:THR:HG21	1:C:77:PHE:CE1	2.46	0.50
2:D:193:LEU:HD23	2:D:198:HIS:HA	1.94	0.50
1:C:26:LEU:HD11	1:C:60:VAL:HG23	1.94	0.50
2:D:116:PHE:C	2:D:148:VAL:HG11	2.36	0.50
2:B:423:VAL:N	8:B:503:SO4:O3	2.34	0.49
1:C:72:ARG:HD3	1:C:74:LEU:HD21	1.93	0.49
1:C:120:LEU:HD11	1:C:124:PHE:HD2	1.77	0.49
1:A:42:GLU:HA	1:A:47:ILE:HG22	1.93	0.49
1:A:494:ASN:HB3	2:B:289:LEU:HD12	1.93	0.49
2:D:191:SER:OG	2:D:198:HIS:ND1	2.31	0.49
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.94	0.49
1:C:500:GLN:HG2	1:C:535:TRP:NE1	2.26	0.49
2:D:395:LYS:NZ	4:F:812:DT:OP1	2.43	0.49
2:D:61:PHE:CZ	2:D:74:LEU:HD23	2.48	0.49
1:A:206:ARG:NH2	1:A:216:THR:O	2.46	0.49
1:C:29:GLU:HG3	1:C:30:LYS:HD2	1.95	0.49
1:C:343:GLN:HG3	1:C:349:LEU:HD11	1.93	0.49
1:C:84:THR:HB	1:C:154:LYS:HE2	1.94	0.48
2:D:215:THR:O	2:D:217:PRO:HD3	2.12	0.48
1:A:85:GLN:O	1:A:154:LYS:NZ	2.45	0.48
1:C:10:VAL:HG21	1:C:153:TRP:HH2	1.76	0.48
1:C:113:ASP:HB3	1:C:116:PHE:HB2	1.95	0.48
1:C:408:ALA:O	2:D:393:ILE:HG13	2.13	0.48
2:D:114:ALA:CB	2:D:214:LEU:HD21	2.40	0.48
1:C:266:TRP:CE2	4:F:820:DC:H4'	2.49	0.48
2:B:103:LYS:HE3	2:B:179:VAL:HG23	1.96	0.48
1:C:168:LEU:HB3	1:C:172:LYS:CE	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:361:HIS:CE1	1:C:513:SER:HG	2.24	0.48
4:P:818:DC:H2''	4:P:819:DG:H5'	1.96	0.48
1:C:101:LYS:HD3	1:C:321:PRO:HG3	1.96	0.48
1:C:5:ILE:HG21	1:C:167:ILE:HD11	1.95	0.48
2:D:171:PHE:HE1	2:D:204:GLU:HB3	1.79	0.48
4:F:810:DT:H5''	4:F:810:DT:H6	1.78	0.48
2:D:116:PHE:O	2:D:148:VAL:HG11	2.14	0.48
1:A:275:LYS:HG3	10:A:775:HOH:O	2.13	0.48
2:B:278:GLN:HG3	2:B:298:GLU:HB3	1.96	0.48
2:D:4:PRO:CD	2:D:5:ILE:N	2.77	0.48
1:A:457:TYR:CE1	1:A:463:ARG:HG2	2.48	0.48
2:B:7:THR:HG22	2:B:119:PRO:HB2	1.95	0.48
1:C:196:GLY:O	1:C:199:ARG:HG2	2.13	0.48
2:D:239:TRP:CZ3	2:D:378:GLU:HG3	2.49	0.47
2:D:247:PRO:CG	2:D:428:GLN:HG2	2.43	0.47
2:D:164:MET:HA	2:D:167:ILE:HG22	1.95	0.47
1:A:249:LYS:HB2	1:A:252:TRP:CD2	2.49	0.47
1:C:64:LYS:HE3	1:C:69:THR:HA	1.97	0.47
2:B:277:ARG:H	2:B:277:ARG:HD2	1.80	0.47
1:C:116:PHE:O	1:C:148:VAL:HG11	2.14	0.47
1:C:65:LYS:NZ	5:C:601:DTP:O3G	2.45	0.47
1:A:266:TRP:O	1:A:269:GLN:HG2	2.14	0.47
1:A:164:MET:HE2	1:A:168:LEU:HG	1.96	0.47
1:A:475:GLN:CD	4:P:808:DC:H5''	2.39	0.47
1:A:495:ILE:HB	1:A:533:LEU:HD23	1.96	0.47
1:C:84:THR:HG21	1:C:153:TRP:HE1	1.79	0.47
4:P:819:DG:H2'	4:P:820:DC:H6	1.80	0.47
2:B:85:GLN:HA	2:B:88:TRP:NE1	2.30	0.47
1:C:134:SER:OG	1:C:139:THR:HB	2.15	0.47
1:C:215:THR:C	1:C:217:PRO:HD3	2.40	0.47
1:C:277:ARG:HB2	1:C:336:GLN:OE1	2.15	0.46
1:C:323:LYS:HB2	1:C:343:GLN:NE2	2.30	0.46
2:D:275:LYS:HD2	10:D:637:HOH:O	2.14	0.46
2:D:308:GLU:HA	2:D:311:LYS:HD3	1.96	0.46
2:D:357:MET:C	2:D:359:GLY:H	2.23	0.46
2:B:84:THR:O	2:B:87:PHE:HB3	2.15	0.46
2:B:203:GLU:OE2	2:B:207:GLN:NE2	2.48	0.46
1:C:518:VAL:O	1:C:522:ILE:HG13	2.15	0.46
1:A:202:ILE:O	1:A:206:ARG:HG3	2.16	0.46
1:A:288:ALA:HB3	1:A:291:GLU:HB2	1.97	0.46
2:D:239:TRP:CH2	2:D:378:GLU:HA	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:THR:HG21	10:A:711:HOH:O	2.15	0.46
1:A:46:LYS:HD3	1:A:116:PHE:HB3	1.97	0.46
1:A:492:GLU:HG2	1:A:530:LYS:HB2	1.98	0.46
10:A:821:HOH:O	2:B:259:LYS:HG3	2.15	0.46
2:B:297:GLU:H	2:B:297:GLU:CD	2.23	0.46
1:C:115:TYR:HB3	1:C:149:LEU:O	2.15	0.46
1:A:58:THR:HG21	1:A:77:PHE:CE1	2.51	0.46
1:A:184:MET:HG2	4:P:822:DG:H2''	1.98	0.46
2:D:29:GLU:HG3	2:D:71:TRP:CZ2	2.51	0.46
1:A:10:VAL:C	1:A:11:LYS:HD2	2.41	0.46
2:B:206:ARG:HE	2:B:206:ARG:HB3	1.40	0.46
1:C:209:LEU:HD22	1:C:214:LEU:HD12	1.98	0.46
1:C:271:TYR:HE1	1:C:314:VAL:HB	1.80	0.46
2:D:5:ILE:O	2:D:5:ILE:HG12	2.13	0.46
2:D:311:LYS:HB2	2:D:311:LYS:HE2	1.37	0.46
1:A:66:LYS:HD2	1:A:66:LYS:HA	1.77	0.45
2:B:8:VAL:HG23	10:B:682:HOH:O	2.16	0.45
1:C:10:VAL:HG11	1:C:153:TRP:CZ2	2.51	0.45
1:C:60:VAL:HG12	1:C:75:VAL:HG22	1.98	0.45
1:C:330:GLN:HG2	1:C:419:THR:HG21	1.98	0.45
1:C:38:CYS:HB3	1:C:144:TYR:HE2	1.81	0.45
3:E:703:G:C5	3:E:704:G:C8	3.05	0.45
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.98	0.45
2:D:336:GLN:NE2	2:D:353:LYS:HD2	2.31	0.45
1:C:12:LEU:HD13	1:C:124:PHE:HE1	1.82	0.45
1:C:23:GLN:NE2	1:C:26:LEU:HG	2.31	0.45
1:C:229:TRP:CE3	1:C:234:LEU:HD21	2.51	0.45
1:C:442:VAL:HB	1:C:481:ALA:HB1	1.98	0.45
2:D:20:LYS:HD3	2:D:55:PRO:O	2.17	0.45
1:C:496:VAL:HG21	2:D:289:LEU:HD21	1.98	0.45
1:A:167:ILE:O	1:A:170:PRO:HD2	2.17	0.45
2:B:104:LYS:HB3	2:B:192:ASP:HA	1.99	0.45
1:C:3:SER:OG	1:C:117:SER:O	2.30	0.45
1:C:230:MET:HE3	4:F:821:DC:H4'	1.98	0.45
1:C:239:TRP:CE2	1:C:316:GLY:HA3	2.52	0.45
1:C:12:LEU:HD12	1:C:84:THR:HA	1.98	0.45
1:C:264:LEU:O	1:C:268:SER:N	2.48	0.45
1:A:58:THR:HG21	1:A:77:PHE:HE1	1.81	0.45
1:C:225:PRO:HB3	1:C:236:PRO:HD3	1.97	0.45
2:B:323:LYS:O	2:B:385:LYS:NZ	2.50	0.45
1:C:223:LYS:HE2	1:C:223:LYS:HB2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:65:LYS:HA	2:D:65:LYS:HD3	1.74	0.45
1:A:81:ASN:O	1:A:154:LYS:HE3	2.17	0.44
2:B:254:VAL:HG21	2:B:287:LYS:HB2	2.00	0.44
1:A:409:THR:OG1	7:A:604:EDO:H21	2.17	0.44
3:T:708:G:H2'	3:T:709:C:H6	1.76	0.44
1:A:61:PHE:CE1	1:A:74:LEU:HB2	2.52	0.44
2:B:287:LYS:HD3	2:B:291:GLU:OE2	2.17	0.44
1:C:475:GLN:CG	4:F:808:DC:H5'	2.44	0.44
2:D:87:PHE:HA	2:D:90:VAL:HG12	1.99	0.44
2:D:115:TYR:HB3	2:D:149:LEU:HB3	1.99	0.44
1:A:222:GLN:HE21	1:A:222:GLN:HB3	1.53	0.44
2:D:199:ARG:O	2:D:202:ILE:HG13	2.18	0.44
1:A:276:VAL:HG12	1:A:276:VAL:O	2.17	0.44
1:C:76:ASP:OD1	1:C:78:ARG:HD3	2.17	0.44
1:C:125:ARG:HD3	1:C:147:ASN:HA	1.98	0.44
1:A:50:ILE:HD12	1:A:54:ASN:HB3	1.99	0.44
1:C:78:ARG:O	1:C:82:LYS:HG3	2.17	0.44
1:C:283:LEU:HA	1:C:283:LEU:HD23	1.77	0.44
1:A:38:CYS:O	1:A:42:GLU:HB2	2.18	0.44
1:A:367:GLN:OE1	1:A:512:LYS:HE3	2.18	0.44
2:B:296:THR:HG22	2:B:299:ALA:CB	2.48	0.44
1:C:267:ALA:C	1:C:269:GLN:H	2.26	0.44
1:C:356:ARG:NE	1:C:358:ARG:HE	2.16	0.44
2:D:101:LYS:O	2:D:236:PRO:HB2	2.17	0.44
2:D:163:SER:O	2:D:167:ILE:HG22	2.18	0.44
1:C:58:THR:HG21	1:C:77:PHE:HE1	1.82	0.43
1:A:28:GLU:O	1:A:32:LYS:HG3	2.18	0.43
2:D:353:LYS:HE2	2:D:427:TYR:HE1	1.83	0.43
2:D:201:LYS:NZ	2:D:204:GLU:OE1	2.51	0.43
4:F:813:DT:H2'	4:F:814:DC:H6	1.82	0.43
1:A:136:ASN:ND2	1:A:137:ASN:OD1	2.51	0.43
2:B:12:LEU:HD11	2:B:127:TYR:CE1	2.53	0.43
2:B:400:THR:O	9:B:502:GOL:H12	2.18	0.43
1:C:114:ALA:HB1	1:C:160:PHE:CZ	2.54	0.43
2:D:199:ARG:HA	2:D:202:ILE:HG12	2.00	0.43
1:A:507:GLN:NE2	10:A:822:HOH:O	2.42	0.43
1:C:325:LEU:HD21	1:C:383:TRP:CD2	2.53	0.43
2:B:422:LEU:HD23	2:B:422:LEU:HA	1.66	0.43
1:C:41:MET:HA	1:C:44:GLU:HG3	2.01	0.43
1:C:354:TYR:HE1	1:C:374:LYS:HZ1	1.66	0.43
1:C:475:GLN:HG3	4:F:808:DC:C5'	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:503:LEU:HD21	1:C:535:TRP:HB2	1.97	0.43
1:A:34:LEU:HD22	1:A:73:LYS:CG	2.47	0.43
2:D:350:LYS:NZ	2:D:378:GLU:OE2	2.47	0.43
1:C:209:LEU:HB3	1:C:214:LEU:HB2	1.99	0.43
1:A:28:GLU:H	1:A:28:GLU:CD	2.26	0.42
2:B:169:GLU:O	2:B:173:LYS:HG2	2.19	0.42
2:B:395:LYS:HE3	4:P:811:DG:O3'	2.19	0.42
1:C:47:ILE:HD11	1:C:130:PHE:HZ	1.84	0.42
1:A:186:ASP:O	1:A:187:LEU:HD23	2.19	0.42
1:A:5:ILE:HD13	1:A:163:SER:HB3	2.02	0.42
2:D:266:TRP:CD1	2:D:425:LEU:HD22	2.54	0.42
1:A:120:LEU:HD12	1:A:121:ASP:H	1.83	0.42
1:A:365:VAL:HG11	1:A:401:TRP:CG	2.55	0.42
2:D:29:GLU:HG3	2:D:71:TRP:CH2	2.55	0.42
2:D:65:LYS:HB2	2:D:68:SER:OG	2.19	0.42
2:D:318:TYR:HA	10:D:666:HOH:O	2.19	0.42
2:B:126:LYS:HA	2:B:145:GLN:OE1	2.19	0.42
2:B:184:MET:HB3	2:B:184:MET:HE2	1.80	0.42
2:D:6:GLU:H	2:D:6:GLU:HG2	1.46	0.42
1:A:497:THR:HG21	1:A:503:LEU:HD13	2.02	0.42
2:B:69:THR:O	2:B:69:THR:CG2	2.67	0.42
1:C:24:TRP:HB3	1:C:25:PRO:HD2	2.02	0.42
2:D:174:GLN:C	2:D:175:ASN:ND2	2.77	0.42
1:C:117:SER:HB3	1:C:213:GLY:O	2.19	0.42
2:D:195:ILE:O	2:D:199:ARG:HG3	2.19	0.42
1:A:40:GLU:O	1:A:44:GLU:HG3	2.19	0.42
1:A:198:HIS:O	1:A:202:ILE:HG12	2.20	0.42
1:A:435:VAL:HG13	2:B:290:THR:HG21	2.01	0.42
1:C:2:ILE:HG12	1:C:3:SER:H	1.85	0.42
1:C:498:ASN:HD21	1:C:545:ASN:CB	2.28	0.42
2:D:118:VAL:HB	2:D:149:LEU:HD22	2.02	0.42
3:T:720:G:H2'	3:T:721:G:C8	2.55	0.42
1:A:47:ILE:HG21	1:A:47:ILE:HD13	1.82	0.41
1:A:543:GLY:HA2	2:B:285:GLY:O	2.20	0.41
1:C:191:SER:HB2	1:C:193:LEU:HB2	2.02	0.41
1:C:427:TYR:CE2	1:C:525:LEU:HD13	2.55	0.41
1:C:199:ARG:O	1:C:203:GLU:HG2	2.20	0.41
1:A:54:ASN:HA	1:A:55:PRO:HD2	1.91	0.41
1:A:170:PRO:HG2	1:A:208:HIS:CE1	2.55	0.41
1:C:29:GLU:O	1:C:32:LYS:HB3	2.20	0.41
1:C:125:ARG:HA	1:C:128:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:197:GLN:O	2:D:201:LYS:HG2	2.20	0.41
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.55	0.41
2:B:365:VAL:HG11	2:B:401:TRP:HB2	2.02	0.41
1:C:19:PRO:O	1:C:57:ASN:N	2.53	0.41
1:A:1:PRO:HB2	1:A:2:ILE:H	1.58	0.41
1:A:205:LEU:O	1:A:209:LEU:HG	2.20	0.41
2:B:153:TRP:CH2	2:B:155:GLY:HA3	2.55	0.41
1:C:500:GLN:OE1	2:D:422:LEU:HD11	2.21	0.41
1:A:76:ASP:OD1	1:A:78:ARG:NE	2.51	0.41
2:B:34:LEU:HD23	2:B:34:LEU:HA	1.89	0.41
1:C:418:ASN:O	1:C:420:PRO:HD3	2.21	0.41
1:C:325:LEU:HD21	1:C:383:TRP:CE3	2.55	0.41
2:D:60:VAL:HG12	2:D:75:VAL:HG22	2.02	0.41
2:D:328:GLU:HG3	2:D:342:TYR:HE1	1.85	0.41
1:A:166:LYS:NZ	10:A:750:HOH:O	2.53	0.41
1:A:328:GLU:OE1	1:A:390:LYS:HE2	2.21	0.41
1:C:13:LYS:HA	1:C:14:PRO:HD2	1.74	0.41
1:C:249:LYS:HE2	1:C:249:LYS:HB2	1.84	0.41
1:C:353:LYS:HD3	1:C:353:LYS:N	2.31	0.41
2:D:114:ALA:CA	2:D:214:LEU:HD21	2.50	0.41
4:P:813:DT:H2''	4:P:814:DC:O4'	2.21	0.41
1:A:287:LYS:H	1:A:287:LYS:HG3	1.69	0.41
2:D:334:GLN:HE21	2:D:334:GLN:HB3	1.60	0.41
2:D:354:TYR:HD2	2:D:374:LYS:HD2	1.86	0.41
2:B:103:LYS:HD2	2:B:191:SER:HA	2.02	0.40
2:B:376:THR:HG21	2:B:410:TRP:CZ3	2.56	0.40
2:D:174:GLN:HB3	2:D:175:ASN:HD22	1.86	0.40
1:C:50:ILE:HD11	1:C:143:ARG:HG2	2.03	0.40
2:D:356:ARG:C	2:D:358:ARG:H	2.28	0.40
2:D:380:ILE:O	2:D:384:GLY:N	2.52	0.40
2:B:275:LYS:HA	2:B:275:LYS:HD3	1.96	0.40
2:D:331:LYS:HB2	2:D:337:TRP:CZ3	2.57	0.40
1:A:411:ILE:HG23	1:A:412:PRO:HD2	2.04	0.40
2:B:236:PRO:HA	2:B:239:TRP:CE2	2.57	0.40
1:C:271:TYR:CD2	1:C:310:LEU:HD23	2.57	0.40
2:D:216:THR:HA	2:D:217:PRO:HD3	1.68	0.40
2:D:371:ALA:O	2:D:375:ILE:HG13	2.21	0.40
2:D:422:LEU:H	2:D:422:LEU:HG	1.69	0.40
1:A:51:GLY:HA3	1:A:53:GLU:OE2	2.21	0.40
1:A:136:ASN:OD1	1:A:136:ASN:N	2.53	0.40
1:C:28:GLU:H	1:C:28:GLU:HG2	1.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:SER:CB	1:C:139:THR:HB	2.51	0.40
1:C:300:GLU:HA	1:C:303:LEU:HB3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	543/556 (98%)	505 (93%)	37 (7%)	1 (0%)	43	63
1	C	543/556 (98%)	489 (90%)	54 (10%)	0	100	100
2	B	408/428 (95%)	386 (95%)	22 (5%)	0	100	100
2	D	409/428 (96%)	379 (93%)	29 (7%)	1 (0%)	43	63
All	All	1903/1968 (97%)	1759 (92%)	142 (8%)	2 (0%)	48	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	362	THR
1	A	18	GLY

5.3.2 Protein sidechains [i](#)

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	486/497 (98%)	444 (91%)	42 (9%)	10	21
1	C	486/497 (98%)	444 (91%)	42 (9%)	10	21
2	B	374/390 (96%)	347 (93%)	27 (7%)	13	28
2	D	375/390 (96%)	339 (90%)	36 (10%)	8	17
All	All	1721/1774 (97%)	1574 (92%)	147 (8%)	10	22

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLU
1	A	11	LYS
1	A	23	GLN
1	A	26	LEU
1	A	43	LYS
1	A	47	ILE
1	A	53	GLU
1	A	58	THR
1	A	64	LYS
1	A	73	LYS
1	A	101	LYS
1	A	132	ILE
1	A	136	ASN
1	A	137	ASN
1	A	139	THR
1	A	173	LYS
1	A	178	ILE
1	A	188	TYR
1	A	191	SER
1	A	199	ARG
1	A	201	LYS
1	A	221	HIS
1	A	222	GLN
1	A	224	GLU
1	A	248	GLU
1	A	250	ASP
1	A	263	LYS
1	A	265	ASN
1	A	280	SER
1	A	286	THR
1	A	287	LYS
1	A	293	ILE
1	A	301	LEU

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Mol	Chain	Res	Type
1	A	332	GLN
1	A	361	HIS
1	A	380	ILE
1	A	424	LYS
1	A	431	LYS
1	A	459	THR
1	A	470	THR
1	A	471	ASN
1	A	498	ASN
2	B	12	LEU
2	B	43	LYS
2	B	69	THR
2	B	163	SER
2	B	175	ASN
2	B	177	ASP
2	B	184	MET
2	B	187	LEU
2	B	197	GLN
2	B	201	LYS
2	B	206	ARG
2	B	210	LEU
2	B	211	ARG
2	B	214	LEU
2	B	237	ASP
2	B	240	THR
2	B	241	VAL
2	B	251	SER
2	B	265	ASN
2	B	290	THR
2	B	296	THR
2	B	311	LYS
2	B	336	GLN
2	B	377	THR
2	B	396	GLU
2	B	413	GLU
2	B	428	GLN
1	C	7	THR
1	C	12	LEU
1	C	17	ASP
1	C	21	VAL
1	C	27	THR
1	C	28	GLU

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Mol	Chain	Res	Type
1	C	29	GLU
1	C	32	LYS
1	C	50	ILE
1	C	58	THR
1	C	123	ASP
1	C	135	ILE
1	C	145	GLN
1	C	172	LYS
1	C	186	ASP
1	C	193	LEU
1	C	200	THR
1	C	201	LYS
1	C	203	GLU
1	C	240	THR
1	C	256	ASP
1	C	275	LYS
1	C	276	VAL
1	C	277	ARG
1	C	284	ARG
1	C	292	VAL
1	C	293	ILE
1	C	308	GLU
1	C	317	VAL
1	C	341	ILE
1	C	347	LYS
1	C	353	LYS
1	C	357	MET
1	C	394	GLN
1	C	407	GLN
1	C	454	LYS
1	C	459	THR
1	C	471	ASN
1	C	475	GLN
1	C	503	LEU
1	C	507	GLN
1	C	545	ASN
2	D	5	ILE
2	D	6	GLU
2	D	10	VAL
2	D	12	LEU
2	D	16	MET
2	D	27	THR

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Mol	Chain	Res	Type
2	D	91	GLN
2	D	94	ILE
2	D	109	LEU
2	D	122	GLU
2	D	123	ASP
2	D	163	SER
2	D	169	GLU
2	D	173	LYS
2	D	175	ASN
2	D	195	ILE
2	D	197	GLN
2	D	200	THR
2	D	201	LYS
2	D	207	GLN
2	D	209	LEU
2	D	210	LEU
2	D	216	THR
2	D	241	VAL
2	D	246	LEU
2	D	249	LYS
2	D	281	LYS
2	D	284	ARG
2	D	311	LYS
2	D	323	LYS
2	D	357	MET
2	D	358	ARG
2	D	362	THR
2	D	399	GLU
2	D	422	LEU
2	D	428	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	197	GLN
1	A	222	GLN
1	A	278	GLN
1	A	332	GLN
1	A	471	ASN
1	A	487	GLN
1	A	545	ASN

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Mol	Chain	Res	Type
2	B	96	HIS
2	B	147	ASN
2	B	151	GLN
2	B	348	ASN
2	B	367	GLN
2	B	394	GLN
1	C	147	ASN
1	C	208	HIS
1	C	306	ASN
1	C	367	GLN
1	C	373	GLN
1	C	418	ASN
1	C	428	GLN
1	C	464	GLN
1	C	480	GLN
1	C	487	GLN
1	C	498	ASN
1	C	507	GLN
2	D	91	GLN
2	D	197	GLN
2	D	334	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	E	20/27 (74%)	2 (10%)	0
3	T	20/27 (74%)	3 (15%)	0
All	All	40/54 (74%)	5 (12%)	0

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	T	704	G
3	T	721	G
3	T	723	C
3	E	704	G
3	E	722	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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$
8	SO4	A	605	-	4,4,4	0.22	0	6,6,6	0.57	0
8	SO4	B	501	-	4,4,4	0.30	0	6,6,6	0.81	0
8	SO4	A	606	-	4,4,4	0.37	0	6,6,6	0.21	0
8	SO4	C	604	-	4,4,4	0.35	0	6,6,6	0.26	0
8	SO4	D	502	-	4,4,4	0.36	0	6,6,6	0.55	0
7	EDO	A	604	-	3,3,3	0.80	0	2,2,2	0.27	0
9	GOL	B	502	-	5,5,5	0.63	0	5,5,5	0.65	0
8	SO4	D	501	-	4,4,4	0.26	0	6,6,6	0.26	0
8	SO4	A	607	-	4,4,4	0.38	0	6,6,6	0.50	0
8	SO4	B	503	-	4,4,4	0.35	0	6,6,6	0.37	0
5	DTP	A	601	6	31,32,32	2.07	9 (29%)	46,50,50	2.02	9 (19%)
5	DTP	C	601	6	31,32,32	2.08	8 (25%)	46,50,50	2.10	10 (21%)

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
9	GOL	B	502	-	-	0/4/4/4	-
5	DTP	A	601	6	-	6/22/34/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	DTP	C	601	6	-	6/22/34/34	0/3/3/3
7	EDO	A	604	-	-	1/1/1/1	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	601	DTP	C6-N6	4.91	1.46	1.34
5	A	601	DTP	C6-N6	4.88	1.46	1.34
5	C	601	DTP	PB-O3A	-4.80	1.54	1.59
5	C	601	DTP	O4'-C4'	4.26	1.54	1.45
5	A	601	DTP	C5'-C4'	-4.13	1.39	1.51
5	A	601	DTP	O4'-C4'	4.11	1.54	1.45
5	C	601	DTP	C5'-C4'	-3.91	1.39	1.51
5	A	601	DTP	PB-O3A	-3.66	1.55	1.59
5	A	601	DTP	PA-O3A	3.16	1.62	1.59
5	C	601	DTP	O3'-C3'	-2.79	1.37	1.43
5	A	601	DTP	O3'-C3'	-2.63	1.37	1.43
5	C	601	DTP	PA-O3A	2.62	1.62	1.59
5	C	601	DTP	PA-O1A	2.44	1.59	1.50
5	A	601	DTP	C3'-C4'	-2.39	1.46	1.53
5	A	601	DTP	PA-O1A	2.29	1.58	1.50
5	A	601	DTP	C5-N7	-2.24	1.35	1.39
5	C	601	DTP	C8-N7	2.18	1.35	1.31

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	601	DTP	N3-C2-N1	-5.78	119.83	128.58
5	A	601	DTP	N3-C2-N1	-5.44	120.34	128.58
5	A	601	DTP	C5-C4-N3	-4.96	119.89	126.72
5	C	601	DTP	N9-C8-N7	-4.93	106.94	113.94
5	A	601	DTP	N9-C8-N7	-4.76	107.18	113.94
5	C	601	DTP	C4-N9-C8	4.69	110.66	105.74
5	C	601	DTP	C5-C4-N3	-4.43	120.62	126.72
5	A	601	DTP	C4-N9-C8	3.96	109.90	105.74
5	C	601	DTP	O4'-C1'-N9	3.93	115.02	107.96
5	A	601	DTP	N3-C4-N9	3.85	133.72	127.17
5	C	601	DTP	C2-N3-C4	3.82	121.16	111.83
5	A	601	DTP	C5-N7-C8	3.77	109.38	103.45
5	A	601	DTP	C2-N3-C4	3.61	120.65	111.83
5	C	601	DTP	C5-N7-C8	3.59	109.10	103.45
5	C	601	DTP	N3-C4-N9	3.46	133.04	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	601	DTP	C4-C5-N7	-3.17	106.96	110.58
5	A	601	DTP	C4-C5-N7	-2.99	107.16	110.58
5	A	601	DTP	O2B-PB-O3A	2.48	113.96	107.27
5	C	601	DTP	C2'-C1'-N9	-2.29	109.24	114.63

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	DTP	PB-O3B-PG-O3G
5	C	601	DTP	PB-O3B-PG-O2G
5	C	601	DTP	C5'-O5'-PA-O1A
5	C	601	DTP	O4'-C4'-C5'-O5'
5	A	601	DTP	O4'-C4'-C5'-O5'
7	A	604	EDO	O1-C1-C2-O2
5	A	601	DTP	PA-O3A-PB-O2B
5	C	601	DTP	PA-O3A-PB-O2B
5	A	601	DTP	PB-O3B-PG-O1G
5	C	601	DTP	PB-O3B-PG-O1G
5	A	601	DTP	PB-O3B-PG-O2G
5	A	601	DTP	PA-O3A-PB-O1B
5	C	601	DTP	C3'-C4'-C5'-O5'

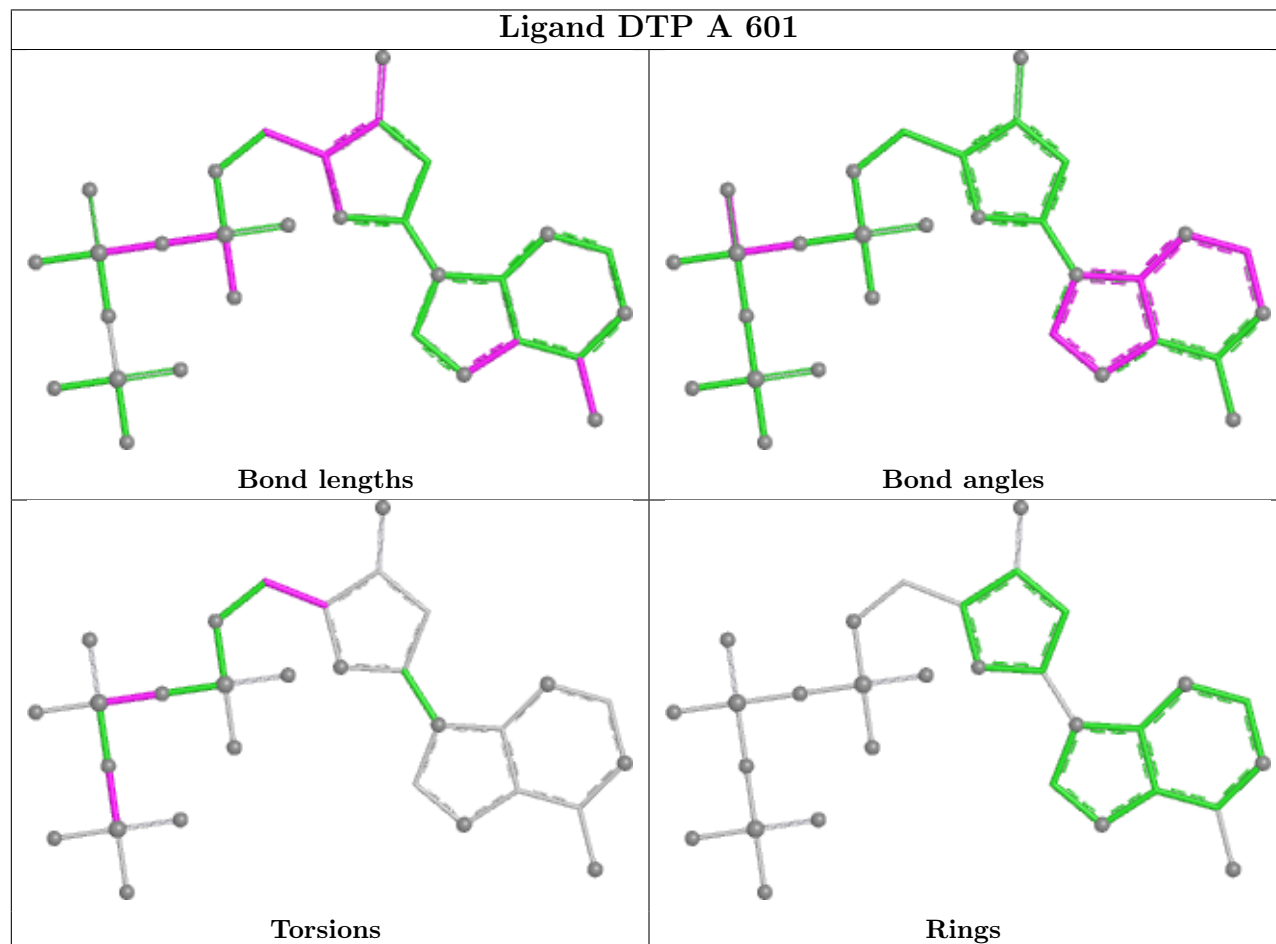
There are no ring outliers.

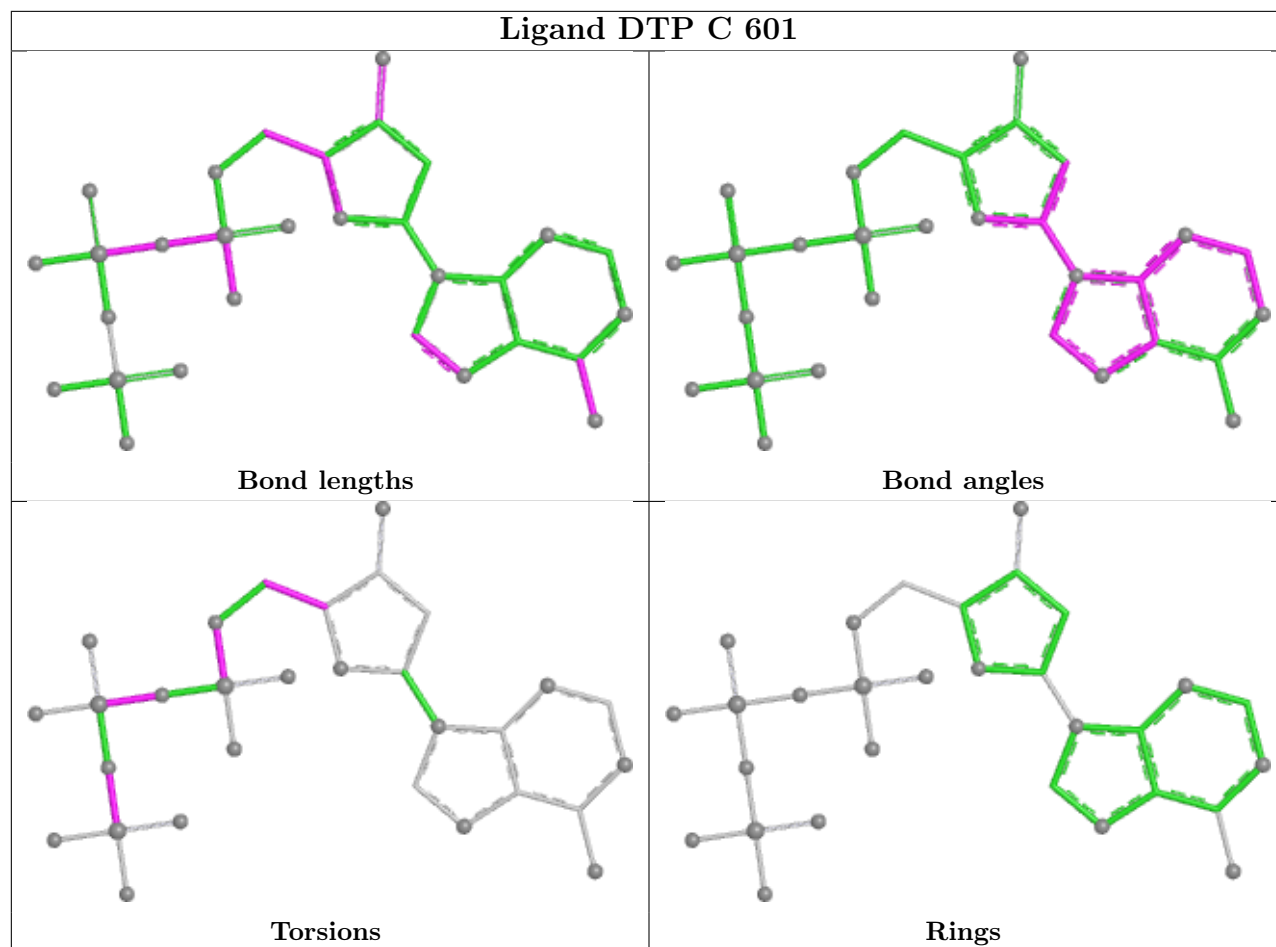
8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	605	SO4	1	0
7	A	604	EDO	1	0
9	B	502	GOL	2	0
8	D	501	SO4	1	0
8	A	607	SO4	1	0
8	B	503	SO4	1	0
5	A	601	DTP	1	0
5	C	601	DTP	2	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](#)

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	545/556 (98%)	0.25	39 (7%) 21 19	14, 40, 95, 132	0
1	C	545/556 (98%)	0.95	122 (22%) 2 2	19, 64, 140, 157	0
2	B	412/428 (96%)	-0.10	10 (2%) 59 55	15, 36, 71, 84	0
2	D	413/428 (96%)	0.34	32 (7%) 19 17	18, 45, 88, 119	0
3	E	21/27 (77%)	1.23	4 (19%) 3 2	56, 92, 122, 154	0
3	T	21/27 (77%)	0.51	2 (9%) 14 12	35, 83, 95, 128	0
4	F	18/21 (85%)	1.52	4 (22%) 2 2	59, 89, 122, 124	0
4	P	18/21 (85%)	0.85	2 (11%) 10 8	34, 81, 107, 109	0
All	All	1993/2064 (96%)	0.42	215 (10%) 11 9	14, 45, 121, 157	0

All (215) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	142	ILE	6.2
2	D	214	LEU	6.1
2	D	231	GLY	5.8
1	C	247	PRO	5.6
2	D	217	PRO	5.0
1	C	293	ILE	4.9
2	D	88	TRP	4.9
1	C	136	ASN	4.9
1	C	55	PRO	4.4
1	C	24	TRP	4.4
2	D	232	TYR	4.3
1	A	135	ILE	4.3
1	C	295	LEU	4.3
1	A	133	PRO	4.3
1	A	134	SER	4.3
2	D	215	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	C	1	PRO	4.1
2	D	216	THR	4.1
1	C	58	THR	4.1
1	C	75	VAL	4.0
1	C	34	LEU	4.0
2	D	357	MET	4.0
1	A	24	TRP	3.9
1	A	545	ASN	3.9
1	C	135	ILE	3.9
1	C	139	THR	3.8
1	C	244	ILE	3.8
1	C	282	LEU	3.7
1	C	131	THR	3.7
2	D	92	LEU	3.7
1	C	2	ILE	3.7
1	C	37	ILE	3.7
1	A	140	PRO	3.7
1	C	21	VAL	3.7
1	A	144	TYR	3.7
1	C	252	TRP	3.6
1	A	139	THR	3.6
2	B	231	GLY	3.6
1	C	60	VAL	3.6
1	C	140	PRO	3.6
1	C	217	PRO	3.6
1	C	130	PHE	3.6
1	C	74	LEU	3.5
1	C	59	PRO	3.5
1	C	257	ILE	3.5
1	C	289	LEU	3.5
2	D	86	ASP	3.4
2	D	69	THR	3.4
1	A	69	THR	3.4
1	A	50	ILE	3.4
1	C	31	ILE	3.4
1	C	346	PHE	3.4
2	D	213	GLY	3.3
1	C	41	MET	3.3
1	C	260	LEU	3.3
1	C	146	TYR	3.3
1	C	46	LYS	3.3
1	C	292	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	245	VAL	3.2
2	D	90	VAL	3.2
1	C	226	PRO	3.2
1	C	296	THR	3.2
1	C	52	PRO	3.2
1	C	294	PRO	3.2
2	B	232	TYR	3.2
1	C	33	ALA	3.1
2	D	356	ARG	3.1
2	D	94	ILE	3.1
4	F	810	DT	3.1
2	D	95	PRO	3.1
4	F	809	DC	3.1
1	C	132	ILE	3.1
2	D	66	LYS	3.1
3	E	703	G	3.1
1	A	289	LEU	3.1
1	C	306	ASN	3.1
1	A	544	GLY	3.1
1	C	51	GLY	3.1
1	C	26	LEU	3.0
1	C	279	LEU	3.0
1	A	37	ILE	3.0
1	C	39	THR	3.0
1	C	223	LYS	3.0
1	C	63	ILE	3.0
2	D	212	TRP	3.0
1	A	67	ASP	3.0
1	C	251	SER	3.0
1	C	141	GLY	3.0
2	D	91	GLN	3.0
1	C	271	TYR	2.9
1	A	35	VAL	2.9
1	C	254	VAL	2.9
1	C	290	THR	2.9
1	C	129	ALA	2.9
1	C	288	ALA	2.9
1	A	19	PRO	2.9
1	C	65	LYS	2.9
1	A	31	ILE	2.9
1	C	309	ILE	2.9
1	C	54	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	214	LEU	2.8
1	A	51	GLY	2.8
1	A	141	GLY	2.8
1	C	545	ASN	2.8
3	T	703	G	2.8
2	D	87	PHE	2.8
1	C	116	PHE	2.8
1	C	71	TRP	2.7
2	D	10	VAL	2.7
1	C	124	PHE	2.7
1	A	132	ILE	2.7
1	A	40	GLU	2.7
2	D	4	PRO	2.7
1	C	144	TYR	2.7
1	C	261	VAL	2.7
4	F	812	DT	2.7
1	A	58	THR	2.7
1	A	71	TRP	2.7
1	C	57	ASN	2.6
1	C	143	ARG	2.6
1	C	303	LEU	2.6
2	D	266	TRP	2.6
1	C	246	LEU	2.6
2	D	3	SER	2.6
1	C	25	PRO	2.6
1	A	47	ILE	2.6
1	C	297	GLU	2.6
1	C	114	ALA	2.6
1	C	544	GLY	2.6
1	A	1	PRO	2.5
1	A	59	PRO	2.5
3	E	704	G	2.5
1	C	61	PHE	2.5
1	C	73	LYS	2.5
1	C	283	LEU	2.5
1	C	32	LYS	2.5
1	C	313	PRO	2.4
1	C	153	TRP	2.4
2	D	191	SER	2.4
1	A	28	GLU	2.4
2	D	315	HIS	2.4
1	C	276	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	131	THR	2.4
1	C	203	GLU	2.4
1	A	142	ILE	2.4
1	C	47	ILE	2.4
1	C	274	ILE	2.4
1	C	193	LEU	2.4
2	B	92	LEU	2.4
1	C	138	GLU	2.4
2	B	217	PRO	2.3
1	C	152	GLY	2.3
1	C	50	ILE	2.3
1	C	195	ILE	2.3
1	C	19	PRO	2.3
2	B	215	THR	2.3
1	C	30	LYS	2.3
1	C	56	TYR	2.3
1	C	137	ASN	2.3
1	A	39	THR	2.3
1	A	34	LEU	2.3
2	B	5	ILE	2.3
1	C	111	VAL	2.3
1	C	265	ASN	2.3
4	F	815	DG	2.3
1	A	2	ILE	2.3
1	C	20	LYS	2.3
1	C	225	PRO	2.3
1	C	151	GLN	2.2
1	C	285	GLY	2.2
1	C	310	LEU	2.2
2	D	159	ILE	2.2
4	P	810	DT	2.2
2	D	93	GLY	2.2
1	C	264	LEU	2.2
3	E	717	C	2.2
1	A	46	LYS	2.2
1	C	23	GLN	2.2
1	C	259	LYS	2.2
1	A	26	LEU	2.2
1	C	210	LEU	2.2
1	C	3	SER	2.2
1	C	222	GLN	2.2
2	D	89	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	256	ASP	2.1
1	A	286	THR	2.1
2	D	5	ILE	2.1
3	T	704	G	2.1
1	C	280	SER	2.1
1	C	263	LYS	2.1
1	C	150	PRO	2.1
1	C	62	ALA	2.1
2	B	212	TRP	2.1
1	A	18	GLY	2.1
1	C	305	GLU	2.1
3	E	723	C	2.1
2	D	161	GLN	2.1
1	C	109	LEU	2.1
1	C	22	LYS	2.1
1	C	232	TYR	2.1
1	A	108	VAL	2.0
2	B	90	VAL	2.0
1	A	129	ALA	2.0
1	C	228	LEU	2.0
1	C	301	LEU	2.0
1	C	5	ILE	2.0
1	C	185	ASP	2.0
4	P	811	DG	2.0
1	C	77	PHE	2.0
1	C	314	VAL	2.0
1	A	223	LYS	2.0
2	D	419	THR	2.0
1	C	266	TRP	2.0
1	C	127	TYR	2.0
2	B	318	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

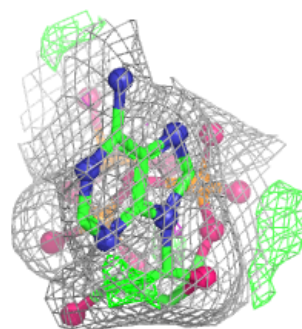
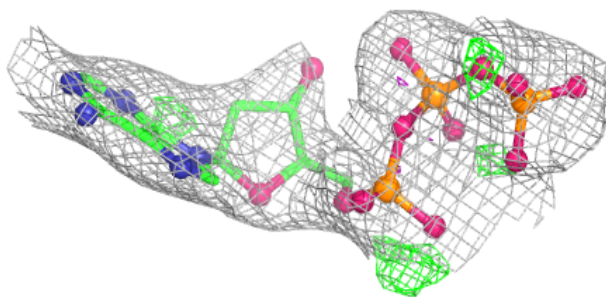
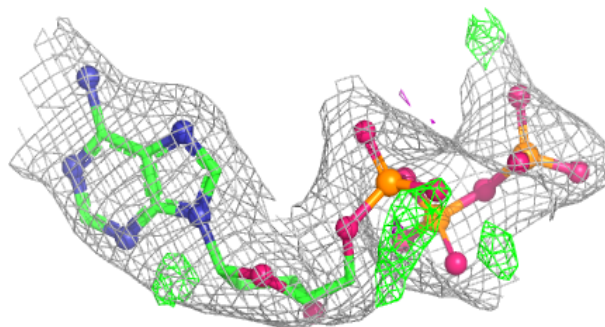
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	GOL	B	502	6/6	0.81	0.13	36,36,43,47	0
8	SO4	D	502	5/5	0.83	0.20	58,67,72,86	0
6	MG	C	603	1/1	0.84	0.12	63,63,63,63	0
5	DTP	C	601	30/30	0.87	0.13	63,71,85,88	0
8	SO4	A	606	5/5	0.89	0.14	53,58,66,77	0
8	SO4	A	607	5/5	0.90	0.23	45,46,60,70	0
8	SO4	B	503	5/5	0.92	0.14	54,54,65,77	0
8	SO4	C	604	5/5	0.92	0.20	51,63,69,83	0
5	DTP	A	601	30/30	0.94	0.08	33,43,53,55	0
6	MG	A	603	1/1	0.95	0.06	35,35,35,35	0
8	SO4	D	501	5/5	0.95	0.07	49,57,63,68	0
7	EDO	A	604	4/4	0.95	0.08	21,22,23,24	0
8	SO4	A	605	5/5	0.95	0.14	37,39,51,57	0
8	SO4	B	501	5/5	0.96	0.14	32,37,46,54	0
6	MG	C	602	1/1	0.96	0.09	59,59,59,59	0
6	MG	A	602	1/1	0.98	0.06	30,30,30,30	0

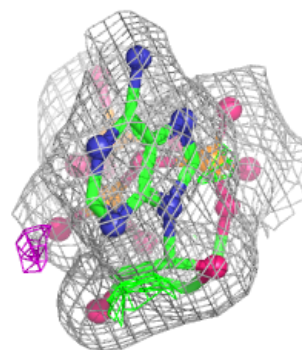
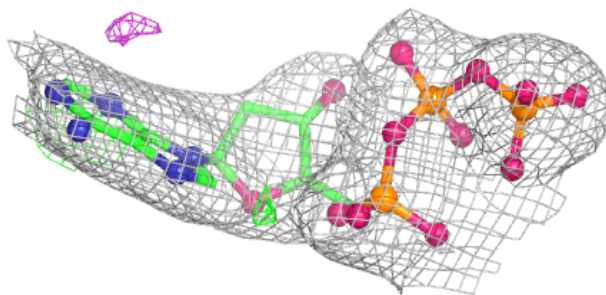
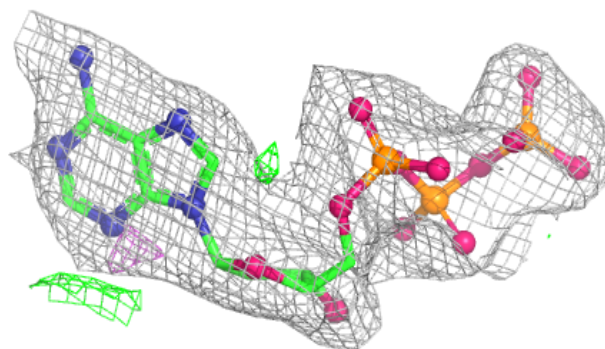
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around DTP C 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around DTP A 601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.