



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:41 PM UTC

PDB ID : 4OAV / pdb_00004oav
Title : Complete human RNase L in complex with 2-5A (5'-ppp heptamer), AMPPCP and RNA substrate.
Authors : Han, Y.; Donovan, J.; Rath, S.; Whitney, G.; Chitrakar, A.; Korennykh, A.
Deposited on : 2014-01-06
Resolution : 2.10 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

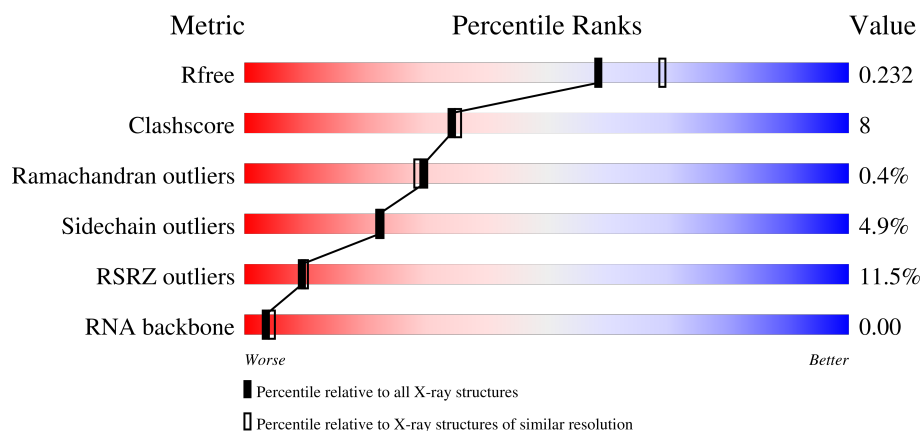
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)
RNA backbone	3983	1006 (2.42-1.78)

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	B	699	11% 79% 15% • •
1	D	699	11% 79% 15% • •
2	A	7	71% 29%
2	C	7	29% 43% 29%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11963 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 PROTEIN (RNase L).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	673	Total	C	N	O	S	0	0	0
			5372	3397	943	1010	22			
1	D	674	Total	C	N	O	S	0	0	0
			5379	3400	945	1012	22			

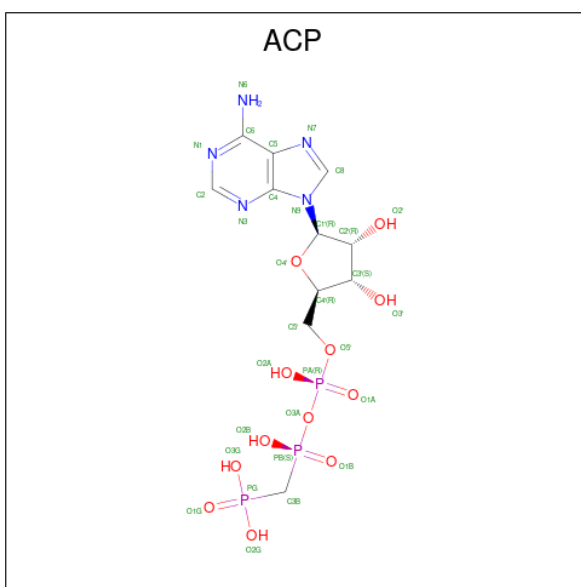
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	672	ASN	HIS	engineered mutation	UNP Q05823
D	672	ASN	HIS	engineered mutation	UNP Q05823

- Molecule 2 is a RNA chain called RNA (5'-R(P*(PO4)P*(PO4)P*AP*AP*AP*AP*(PO4))-2').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	7	Total	C	N	O	P	0	0	0
			101	40	20	34	7			
2	C	7	Total	C	N	O	P	0	0	0
			101	40	20	34	7			

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).

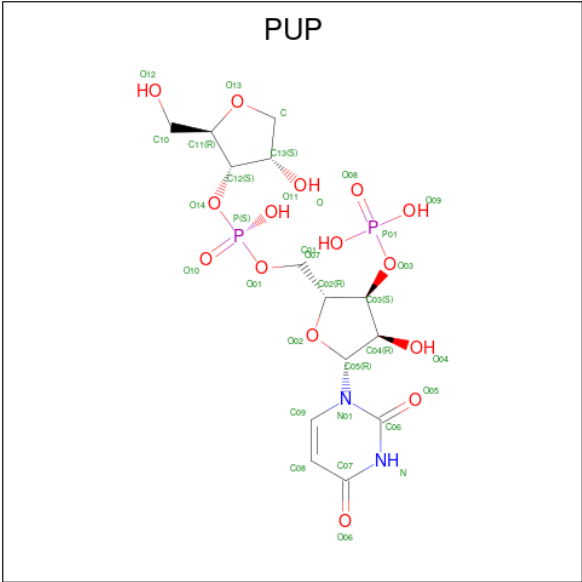


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total 31	C 11	N 5	O 12	P 3	0	0
3	D	1	Total 31	C 11	N 5	O 12	P 3	0	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Mg 2 2	0	0
4	D	2	Total Mg 2 2	0	0

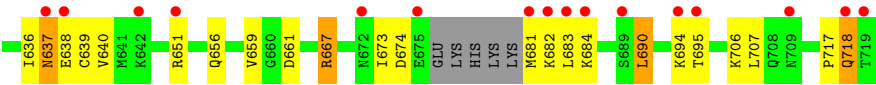
- Molecule 5 is (2R,3S,4R,5R)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-4-hydroxy-2-([[(S)-hydroxy{[(2R,3S,4S)-4-hydroxy-2-(hydroxymethyl)tetrahydrofuran-3-yl]oxy}phosphoryl]oxy}methyl)tetrahydrofuran-3-yl dihydrogen phosphate (CCD ID: PUP) (formula: C₁₄H₂₂N₂O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	N	O	P	0	0
			33	14	2	15	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	433	Total	O	0	0
			433	433		
6	A	15	Total	O	0	0
			15	15		
6	D	446	Total	O	0	0
			446	446		
6	C	17	Total	O	0	0
			17	17		



● Molecule 2: RNA (5'-R(P*(PO4)P*(PO4)P*AP*AP*AP*AP*(PO4))-2')



● Molecule 2: RNA (5'-R(P*(PO4)P*(PO4)P*AP*AP*AP*AP*(PO4))-2')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.61Å 160.70Å 230.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.62 – 2.10 46.62 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.62-2.10) 100.0 (46.62-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.198 , 0.229 0.201 , 0.232	Depositor DCC
R_{free} test set	6407 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.6	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	0.95	EDS
Total number of atoms	11963	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.34 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.8155e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: PUP, PO4, MG, ACP

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	B	0.33	0/5469	0.70	3/7362 (0.0%)
1	D	0.33	0/5476	0.74	7/7373 (0.1%)
2	A	2.43	9/96 (9.4%)	2.04	4/140 (2.9%)
2	C	2.42	8/96 (8.3%)	2.02	3/140 (2.1%)
All	All	0.46	17/11137 (0.2%)	0.77	17/15015 (0.1%)

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	B	0	1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	6	A	C6-N6	7.23	1.48	1.33
2	C	6	A	C6-N6	7.15	1.48	1.33
2	C	5	A	C6-N6	6.84	1.47	1.33
2	A	5	A	C6-N6	6.81	1.47	1.33
2	C	3	A	C3'-C2'	-6.61	1.42	1.52
2	A	3	A	C3'-C2'	-6.31	1.43	1.52
2	A	3	A	C6-N6	6.23	1.46	1.33
2	A	5	A	C3'-C2'	-6.07	1.43	1.52
2	C	3	A	C6-N6	6.00	1.46	1.33
2	A	4	A	C3'-C2'	-5.99	1.43	1.52
2	A	4	A	C4'-C3'	-5.94	1.43	1.52
2	C	5	A	C3'-C2'	-5.84	1.44	1.52
2	C	4	A	C3'-C2'	-5.84	1.44	1.52
2	C	4	A	C4'-C3'	-5.67	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	6	A	C3'-C2'	-5.66	1.44	1.52
2	A	6	A	C3'-C2'	-5.24	1.45	1.52
2	A	6	A	C4'-C3'	-5.11	1.45	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	626	SER	N-CA-C	-7.25	101.56	111.56
1	D	496	LYS	N-CA-C	7.22	122.14	113.12
1	D	509	LYS	N-CA-C	7.12	125.96	110.80
1	D	637	ASN	N-CA-C	6.76	122.46	111.37
1	B	625	HIS	N-CA-C	6.60	120.21	109.59
1	D	343	TRP	N-CA-C	-6.14	101.39	110.48
1	B	496	LYS	N-CA-C	5.87	120.48	112.68
1	D	509	LYS	CA-C-N	5.86	132.25	121.70
1	D	509	LYS	C-N-CA	5.86	132.25	121.70
2	A	6	A	C4'-C3'-C2'	5.83	108.43	102.60
2	A	4	A	OP1-P-OP2	-5.73	102.41	119.60
2	C	3	A	OP1-P-OP2	-5.62	102.73	119.60
2	A	3	A	OP1-P-OP2	-5.57	102.90	119.60
2	C	4	A	OP1-P-OP2	-5.55	102.94	119.60
1	D	718	GLN	N-CA-C	5.49	117.34	111.36
2	A	5	A	OP1-P-OP2	-5.28	103.76	119.60
2	C	6	A	C5'-C4'-C3'	-5.10	108.34	116.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	624	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5372	0	5377	79	0
1	D	5379	0	5381	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	101	0	44	8	0
2	C	101	0	44	4	0
3	B	31	0	14	1	0
3	D	31	0	14	1	0
4	B	2	0	0	0	0
4	D	2	0	0	0	0
5	D	33	0	19	3	0
6	A	15	0	0	3	0
6	B	433	0	0	21	0
6	C	17	0	0	1	0
6	D	446	0	0	18	0
All	All	11963	0	10893	167	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 8.

All (167) 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:B:309:ARG:NH1	1:B:327:GLU:OE2	1.91	1.03
2:A:6:A:OP2	6:A:111:HOH:O	1.85	0.94
1:D:261:GLN:OE1	6:D:1138:HOH:O	1.86	0.94
1:D:532:VAL:O	6:D:1249:HOH:O	1.87	0.92
1:B:248:GLU:OE1	6:B:1170:HOH:O	1.87	0.91
1:D:606:LYS:NZ	6:D:1475:HOH:O	2.04	0.90
1:D:639:CYS:HB3	1:D:684:LYS:HZ1	1.41	0.83
1:D:237:GLU:OE2	6:D:1505:HOH:O	1.97	0.83
1:B:411:SER:OG	6:B:988:HOH:O	2.01	0.76
2:A:7:PO4:O4	6:A:108:HOH:O	2.05	0.74
1:B:232:VAL:HG11	1:B:261:GLN:HG3	1.68	0.74
1:B:624:GLU:OE2	1:B:706:LYS:NZ	2.21	0.74
1:D:639:CYS:HB3	1:D:684:LYS:NZ	2.02	0.73
1:D:674:ASP:OD2	6:D:1507:HOH:O	2.06	0.73
1:D:282:GLU:OE2	6:D:1440:HOH:O	2.04	0.73
1:B:595:THR:HG21	1:B:717:PRO:HD3	1.69	0.72
1:D:624:GLU:OE2	1:D:706:LYS:NZ	2.21	0.71
1:B:160:ASP:OD2	6:B:1227:HOH:O	2.06	0.71
1:D:203:ARG:NH1	1:D:237:GLU:OE1	2.21	0.71
5:D:1004:PUP:O06	6:D:1128:HOH:O	2.09	0.70
1:D:301:CYS:O	6:D:1235:HOH:O	2.09	0.69
1:D:588:THR:OG1	6:D:1380:HOH:O	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:72:GLU:OE2	6:D:1203:HOH:O	2.10	0.69
1:B:357:MET:SD	6:B:995:HOH:O	2.51	0.69
1:B:578:SER:OG	6:B:998:HOH:O	2.10	0.69
2:C:1:PO4:O3	6:C:105:HOH:O	2.11	0.69
1:B:203:ARG:NH2	2:C:1:PO4:O3	2.26	0.68
2:A:1:PO4:O3	6:A:106:HOH:O	2.12	0.68
1:B:519:ARG:NH1	6:B:1323:HOH:O	2.24	0.67
1:B:474:GLU:OE2	6:B:1239:HOH:O	2.12	0.66
1:D:411:SER:OG	6:D:1155:HOH:O	2.15	0.65
1:D:214:ASP:OD2	1:D:216:SER:OG	2.15	0.64
2:A:1:PO4:O3	1:D:203:ARG:NH2	2.31	0.63
1:D:374:THR:HB	1:D:378:GLY:HA2	1.80	0.63
1:D:595:THR:HG21	1:D:717:PRO:HD3	1.81	0.63
1:B:237:GLU:O	6:B:1035:HOH:O	2.16	0.62
1:D:607:THR:O	1:D:609:LYS:N	2.31	0.62
1:B:680:LYS:NZ	6:B:1206:HOH:O	2.21	0.62
1:B:642:LYS:NZ	6:B:1196:HOH:O	2.24	0.61
1:D:480:GLY:O	1:D:510:TRP:N	2.34	0.60
1:B:344:GLY:HA2	1:B:347:LEU:HB2	1.83	0.60
1:B:259:LEU:HD13	1:B:295:ARG:HG3	1.84	0.59
1:B:669:LEU:HD21	1:B:685:ILE:HD13	1.85	0.59
1:B:625:HIS:HB2	1:B:627:LYS:HG2	1.84	0.59
1:D:556:ASP:OD1	1:D:559:THR:HG23	2.03	0.59
1:D:232:VAL:HG11	1:D:261:GLN:HG3	1.85	0.58
1:D:673:ILE:HG23	1:D:682:LYS:HG2	1.86	0.58
1:D:591:SER:O	1:D:595:THR:HG23	2.03	0.58
1:D:690:LEU:HD22	1:D:694:LYS:HG3	1.84	0.58
1:B:609:LYS:HB3	1:B:612:SER:HB2	1.84	0.58
1:B:496:LYS:HB2	1:B:498:ALA:H	1.68	0.57
2:A:6:A:O3'	1:D:55:GLU:OE2	2.22	0.57
1:B:591:SER:O	1:B:595:THR:HG23	2.05	0.57
1:B:559:THR:HG22	1:B:585:PHE:CE1	2.40	0.56
1:D:496:LYS:N	1:D:497:LYS:HA	2.20	0.56
1:B:496:LYS:N	1:B:497:LYS:HA	2.21	0.56
1:B:377:GLY:O	1:D:163:ARG:NH1	2.38	0.56
1:B:607:THR:O	1:B:609:LYS:N	2.38	0.56
1:D:640:VAL:HG13	1:D:681:MET:HE1	1.88	0.56
1:B:559:THR:HG22	1:B:585:PHE:HE1	1.72	0.56
1:D:45:LEU:HD11	1:D:78:LEU:HD23	1.87	0.55
1:D:36:GLU:HB3	1:D:71:ARG:NH1	2.22	0.55
1:D:659:VAL:HG23	6:D:1256:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:636:ILE:HG22	1:D:637:ASN:H	1.70	0.55
1:B:355:ARG:HD2	1:B:364:PHE:HB2	1.87	0.55
1:B:673:ILE:HG12	1:B:682:LYS:HG2	1.89	0.55
1:B:556:ASP:OD1	1:B:559:THR:HG23	2.07	0.54
1:B:90:LYS:HG3	6:B:1223:HOH:O	2.06	0.54
1:D:36:GLU:OE2	1:D:71:ARG:HD3	2.08	0.54
1:B:214:ASP:N	1:B:214:ASP:OD1	2.39	0.54
1:B:301:CYS:O	6:B:950:HOH:O	2.18	0.53
1:D:559:THR:HG22	1:D:585:PHE:CE1	2.43	0.53
1:B:510:TRP:HZ3	1:B:516:GLU:HB2	1.73	0.53
1:B:54:GLN:HG2	1:B:61:THR:HG22	1.89	0.53
1:D:54:GLN:HG2	1:D:61:THR:HG22	1.89	0.53
1:D:529:LEU:HD12	1:D:550:VAL:HG13	1.90	0.53
1:D:496:LYS:H	1:D:497:LYS:HA	1.74	0.53
1:D:601:ASN:OD1	1:D:667:ARG:NH1	2.39	0.52
1:B:496:LYS:H	1:B:497:LYS:HA	1.74	0.52
1:B:457:GLU:OE2	1:B:462:ARG:NH2	2.42	0.52
1:B:34:GLN:HE22	2:C:6:A:H2	1.57	0.52
1:D:718:GLN:NE2	6:D:1443:HOH:O	2.41	0.51
1:B:158:LYS:NZ	6:B:909:HOH:O	2.42	0.51
1:B:161:GLN:HG3	1:B:166:LYS:HD3	1.92	0.51
1:D:656:GLN:HG2	1:D:661:ASP:OD2	2.10	0.51
1:B:617:LEU:HD11	1:B:710:THR:HG21	1.93	0.50
1:D:355:ARG:HD2	1:D:364:PHE:HB2	1.94	0.50
1:D:559:THR:HG22	1:D:585:PHE:HE1	1.74	0.50
1:D:419:THR:H	1:D:435:THR:CG2	2.25	0.50
1:D:637:ASN:OD1	1:D:684:LYS:NZ	2.37	0.50
1:B:518:LYS:O	1:B:522:GLU:HG2	2.13	0.49
1:D:355:ARG:HB2	1:D:362:LYS:HE3	1.95	0.49
1:B:574:ARG:NH1	6:B:1165:HOH:O	2.34	0.49
1:D:259:LEU:HD12	1:D:291:LEU:HD13	1.95	0.49
1:D:371:ILE:HD11	1:D:381:LEU:HD13	1.93	0.49
1:B:419:THR:HG23	1:B:435:THR:OG1	2.13	0.49
1:B:659:VAL:HG23	6:B:1242:HOH:O	2.12	0.48
1:D:518:LYS:O	1:D:522:GLU:HG2	2.14	0.48
1:B:223:HIS:HE1	6:B:1264:HOH:O	1.97	0.48
1:D:510:TRP:HD1	6:D:1142:HOH:O	1.96	0.48
1:B:608:ARG:NH2	1:B:654:PHE:O	2.45	0.47
1:B:493:ILE:CG2	1:B:497:LYS:HB3	2.44	0.47
1:D:496:LYS:HB2	1:D:498:ALA:H	1.79	0.47
1:D:396:GLU:O	6:D:1171:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:GLU:OE2	2:C:3:A:N1	2.47	0.47
1:D:482:THR:HG21	1:D:484:GLN:HE21	1.79	0.47
1:D:475:LEU:HD22	1:D:481:TYR:HB2	1.97	0.47
1:D:622:PRO:HA	1:D:623:SER:HA	1.49	0.47
1:D:651:ARG:NH1	5:D:1004:PUP:H11	2.29	0.47
3:D:1001:ACP:H8	3:D:1001:ACP:O5'	2.15	0.47
1:B:691:TYR:O	1:B:695:THR:HG23	2.15	0.46
1:D:612:SER:OG	1:D:615:LEU:HB2	2.15	0.46
1:B:398:SER:O	1:B:402:GLN:HG2	2.16	0.46
1:B:326:LYS:H	1:B:326:LYS:HG3	1.45	0.46
1:D:419:THR:H	1:D:435:THR:HG23	1.80	0.46
1:B:427:ARG:NH1	2:A:1:PO4:O4	2.50	0.45
1:B:58:GLY:N	6:B:1223:HOH:O	2.33	0.45
3:B:801:ACP:H8	3:B:801:ACP:O5'	2.15	0.45
1:B:355:ARG:HB2	1:B:362:LYS:HE3	1.98	0.45
1:D:460:PHE:O	1:D:464:VAL:HG12	2.17	0.45
1:B:473:GLN:OE1	1:B:578:SER:OG	2.25	0.45
1:B:510:TRP:CZ3	1:B:517:VAL:HG23	2.52	0.45
1:D:259:LEU:HD22	1:D:295:ARG:HG2	1.99	0.45
1:B:622:PRO:HA	1:B:623:SER:HA	1.55	0.45
1:D:620:PRO:HB2	1:D:621:GLY:H	1.65	0.44
1:D:441:LEU:HD21	1:D:531:VAL:HG22	1.99	0.44
1:D:609:LYS:HB3	1:D:612:SER:HB3	1.97	0.44
1:B:309:ARG:NE	6:B:1009:HOH:O	2.40	0.44
1:D:445:LEU:HD13	1:D:535:GLY:HA3	2.00	0.44
1:B:584:PRO:HA	1:B:587:TRP:CG	2.53	0.44
1:D:178:LYS:HA	1:D:178:LYS:HD3	1.85	0.43
1:B:374:THR:HB	1:B:378:GLY:HA2	2.00	0.43
1:B:481:TYR:CZ	1:B:509:LYS:HD3	2.54	0.43
1:B:669:LEU:O	1:B:673:ILE:HB	2.19	0.43
1:D:482:THR:HB	6:D:1142:HOH:O	2.17	0.43
1:B:57:GLU:HG2	1:D:353:ILE:CG2	2.49	0.43
1:D:337:LYS:HD2	1:D:338:PRO:HD2	2.00	0.43
1:D:651:ARG:HH12	5:D:1004:PUP:H11	1.82	0.43
1:B:36:GLU:OE1	1:B:69:MET:HE3	2.18	0.43
1:D:541:ASP:O	1:D:545:GLN:HG2	2.19	0.43
1:B:81:HIS:HE1	6:B:954:HOH:O	2.02	0.42
1:B:616:ARG:O	1:B:619:GLN:HG2	2.19	0.42
1:D:446:ASP:CG	6:D:1486:HOH:O	2.62	0.42
1:B:203:ARG:HG2	1:B:207:ILE:HG21	2.01	0.42
1:B:309:ARG:NH2	6:B:1009:HOH:O	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:584:PRO:HA	1:B:587:TRP:CD2	2.55	0.42
1:D:441:LEU:O	1:D:445:LEU:HG	2.20	0.42
1:B:243:LEU:HB2	1:B:264:ILE:HD11	2.02	0.42
1:B:357:MET:SD	1:B:362:LYS:HB2	2.60	0.42
2:A:2:PO4:O1	2:A:3:A:H5''	2.20	0.42
1:D:482:THR:HG21	1:D:484:GLN:NE2	2.35	0.42
1:D:683:LEU:HD23	1:D:683:LEU:HA	1.92	0.42
2:A:3:A:N1	1:D:131:GLU:OE2	2.53	0.42
1:B:360:LYS:HB3	1:B:384:TYR:O	2.19	0.41
1:B:617:LEU:O	1:B:706:LYS:HG3	2.20	0.41
1:D:482:THR:HG22	1:D:484:GLN:HG2	2.02	0.41
1:B:36:GLU:OE1	1:D:314:HIS:HE1	2.04	0.41
1:D:160:ASP:OD1	1:D:163:ARG:NH2	2.54	0.41
1:B:158:LYS:NZ	6:B:1107:HOH:O	2.52	0.41
1:D:584:PRO:HA	1:D:587:TRP:CG	2.56	0.41
1:D:595:THR:CG2	1:D:717:PRO:HD3	2.49	0.41
1:B:371:ILE:HD11	1:B:381:LEU:HD13	2.01	0.41
1:D:543:LYS:HE2	1:D:543:LYS:HB3	1.86	0.41
1:B:606:LYS:HA	1:B:664:LYS:HD3	2.03	0.41
1:B:615:LEU:HD12	1:B:615:LEU:HA	1.84	0.40
1:D:595:THR:HG22	6:D:1496:HOH:O	2.20	0.40
1:D:370:LYS:NZ	1:D:373:ASP:OD1	2.40	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	B	665/699 (95%)	638 (96%)	25 (4%)	2 (0%)	36	36
1	D	666/699 (95%)	638 (96%)	25 (4%)	3 (0%)	24	22
All	All	1331/1398 (95%)	1276 (96%)	50 (4%)	5 (0%)	30	28

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	608	ARG
1	D	608	ARG
1	D	620	PRO
1	D	238	ARG
1	B	237	GLU

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	B	585/607 (96%)	555 (95%)	30 (5%)	21	21
1	D	586/607 (96%)	559 (95%)	27 (5%)	24	25
All	All	1171/1214 (96%)	1114 (95%)	57 (5%)	22	22

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	27	HIS
1	B	161	GLN
1	B	162	GLU
1	B	184	LEU
1	B	214	ASP
1	B	237	GLU
1	B	263	HIS
1	B	291	LEU
1	B	326	LYS
1	B	363	PHE
1	B	374	THR
1	B	381	LEU
1	B	405	VAL
1	B	417	LEU
1	B	419	THR
1	B	434	VAL
1	B	463	ASN
1	B	475	LEU

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Mol	Chain	Res	Type
1	B	486	LEU
1	B	501	LEU
1	B	524	LEU
1	B	552	GLN
1	B	576	CYS
1	B	615	LEU
1	B	640	VAL
1	B	667	ARG
1	B	673	ILE
1	B	695	THR
1	B	707	LEU
1	B	710	THR
1	D	164	LEU
1	D	184	LEU
1	D	237	GLU
1	D	286	LYS
1	D	291	LEU
1	D	363	PHE
1	D	374	THR
1	D	381	LEU
1	D	405	VAL
1	D	417	LEU
1	D	419	THR
1	D	435	THR
1	D	455	ASN
1	D	475	LEU
1	D	482	THR
1	D	486	LEU
1	D	494	ASP
1	D	501	LEU
1	D	524	LEU
1	D	529	LEU
1	D	553	LEU
1	D	615	LEU
1	D	638	GLU
1	D	667	ARG
1	D	690	LEU
1	D	695	THR
1	D	707	LEU

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

Mol	Chain	Res	Type
1	B	34	GLN
1	B	261	GLN
1	B	263	HIS
1	B	429	HIS
1	B	545	GLN
1	B	568	HIS
1	D	314	HIS
1	D	351	HIS
1	D	455	ASN
1	D	515	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	0/7	-	-
2	C	0/7	-	-
All	All	0/14	-	-

There are no RNA backbone outliers to report.

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 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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
3	ACP	D	1001	4	31,33,33	1.67	8 (25%)	47,52,52	2.07	15 (31%)
5	PUP	D	1004	-	35,35,35	2.37	10 (28%)	51,53,53	1.63	9 (17%)
3	ACP	B	801	4	31,33,33	1.65	7 (22%)	47,52,52	2.10	15 (31%)

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
3	ACP	D	1001	4	-	0/19/38/38	0/3/3/3
5	PUP	D	1004	-	-	4/22/51/51	0/3/3/3
3	ACP	B	801	4	-	0/19/38/38	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	1004	PUP	O06-C07	8.56	1.41	1.24
5	D	1004	PUP	C13-C12	-5.19	1.44	1.53
5	D	1004	PUP	C04-C03	-5.12	1.41	1.53
3	D	1001	ACP	C6-N6	3.96	1.44	1.34
3	B	801	ACP	C6-N6	3.86	1.44	1.34
3	D	1001	ACP	C2'-C3'	-3.73	1.43	1.53
3	B	801	ACP	C2'-C3'	-3.70	1.43	1.53
5	D	1004	PUP	C-C13	-3.49	1.46	1.51
5	D	1004	PUP	C09-C08	3.11	1.42	1.35
5	D	1004	PUP	O13-C11	-2.78	1.39	1.44
3	B	801	ACP	PB-O2B	-2.68	1.49	1.56
3	D	1001	ACP	C3'-C4'	-2.65	1.46	1.53
5	D	1004	PUP	C12-C11	-2.65	1.46	1.52
3	B	801	ACP	C3'-C4'	-2.58	1.46	1.53
3	D	1001	ACP	PB-O2B	-2.55	1.50	1.56
5	D	1004	PUP	O02-C02	-2.54	1.39	1.45
5	D	1004	PUP	O-C13	-2.28	1.38	1.43
3	D	1001	ACP	PA-O3A	-2.27	1.57	1.59
3	B	801	ACP	PG-O2G	-2.24	1.50	1.55
3	B	801	ACP	C4-N3	2.23	1.38	1.34
5	D	1004	PUP	C04-C05	-2.18	1.46	1.53
3	D	1001	ACP	PG-O2G	-2.10	1.50	1.55
3	D	1001	ACP	O4'-C4'	-2.09	1.40	1.45
3	B	801	ACP	O4'-C4'	-2.02	1.40	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1001	ACP	C4-N3	2.01	1.38	1.34

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	ACP	C5-C4-N3	-5.76	118.78	126.72
5	D	1004	PUP	N-C06-N01	5.59	122.17	114.89
3	D	1001	ACP	C5-C4-N3	-5.58	119.03	126.72
3	B	801	ACP	N3-C2-N1	-5.07	120.91	128.58
3	D	1001	ACP	N3-C2-N1	-4.98	121.04	128.58
5	D	1004	PUP	C07-N-C06	-4.82	120.62	126.61
3	B	801	ACP	N3-C4-N9	4.23	134.36	127.17
3	B	801	ACP	C2-N3-C4	4.01	121.63	111.83
3	D	1001	ACP	N3-C4-N9	4.01	133.99	127.17
3	D	1001	ACP	C2-N3-C4	3.85	121.24	111.83
3	B	801	ACP	N9-C8-N7	-3.61	108.81	113.94
3	D	1001	ACP	N9-C8-N7	-3.60	108.82	113.94
5	D	1004	PUP	C08-C07-N	3.30	119.42	114.80
3	D	1001	ACP	O3G-PG-C3B	3.29	114.38	106.40
3	B	801	ACP	C5-N7-C8	3.28	108.60	103.45
3	D	1001	ACP	C5-N7-C8	3.23	108.53	103.45
5	D	1004	PUP	C-C13-C12	3.15	104.74	101.78
3	B	801	ACP	C4-C5-N7	-3.09	107.05	110.58
3	D	1001	ACP	C4-C5-N7	-3.07	107.07	110.58
3	D	1001	ACP	O3G-PG-O1G	-3.00	104.62	112.39
3	B	801	ACP	O3G-PG-C3B	2.99	113.65	106.40
5	D	1004	PUP	O06-C07-C08	-2.96	120.06	125.16
5	D	1004	PUP	O02-C05-N01	2.95	115.03	108.36
5	D	1004	PUP	O01-C01-C02	2.91	118.91	108.99
3	B	801	ACP	O2G-PG-C3B	2.80	113.20	106.40
3	B	801	ACP	C4-N9-C8	2.80	108.68	105.74
3	B	801	ACP	O3G-PG-O1G	-2.73	105.33	112.39
3	D	1001	ACP	C4-N9-C8	2.72	108.59	105.74
3	B	801	ACP	O2G-PG-O1G	-2.66	105.51	112.39
3	D	1001	ACP	O2G-PG-O1G	-2.58	105.71	112.39
3	D	1001	ACP	PB-O3A-PA	-2.56	124.02	132.37
3	D	1001	ACP	O2G-PG-C3B	2.52	112.51	106.40
5	D	1004	PUP	O05-C06-N01	-2.22	119.90	122.80
5	D	1004	PUP	C05-N01-C06	2.20	121.55	117.59
3	B	801	ACP	O2B-PB-O1B	-2.20	102.80	109.95
3	B	801	ACP	PB-O3A-PA	-2.18	125.25	132.37
3	B	801	ACP	O2A-PA-O1A	-2.18	102.30	112.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1001	ACP	O2B-PB-O1B	-2.03	103.35	109.95
3	D	1001	ACP	O2A-PA-O1A	-2.01	103.11	112.44

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1004	PUP	C01-O01-P-O11
5	D	1004	PUP	C01-O01-P-O14
5	D	1004	PUP	O01-C01-C02-O02
5	D	1004	PUP	O01-C01-C02-C03

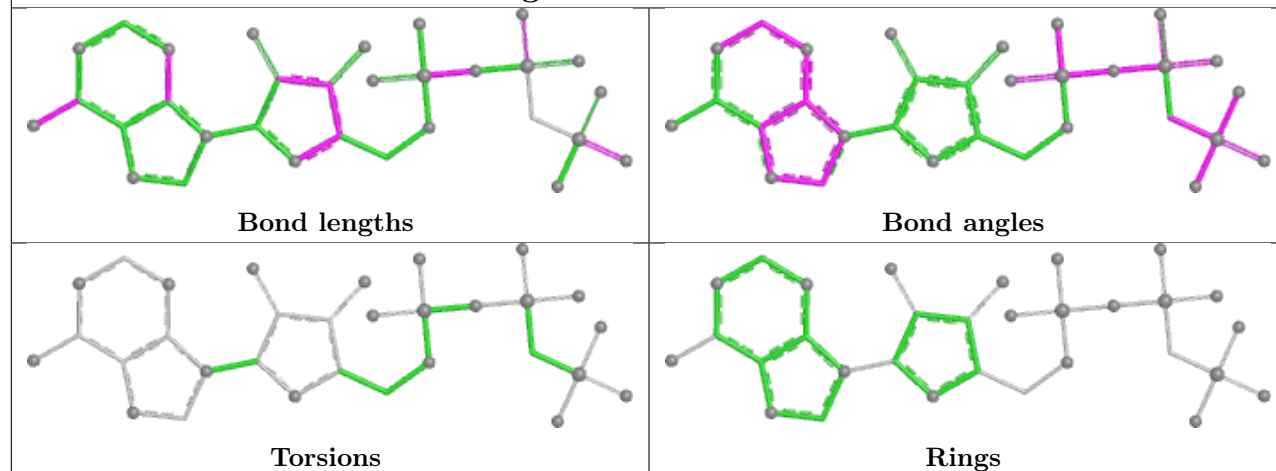
There are no ring outliers.

3 monomers are involved in 5 short contacts:

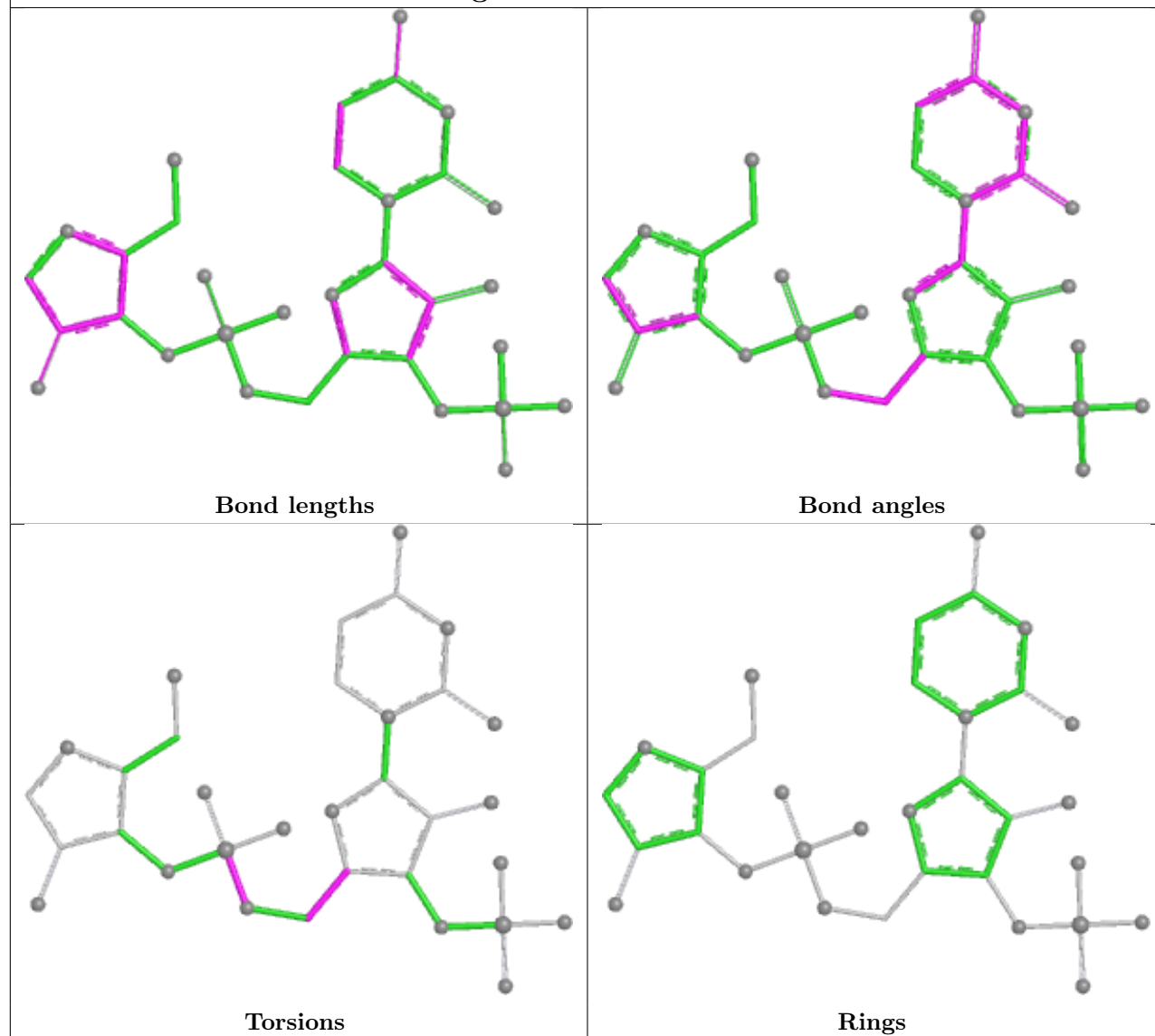
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1001	ACP	1	0
5	D	1004	PUP	3	0
3	B	801	ACP	1	0

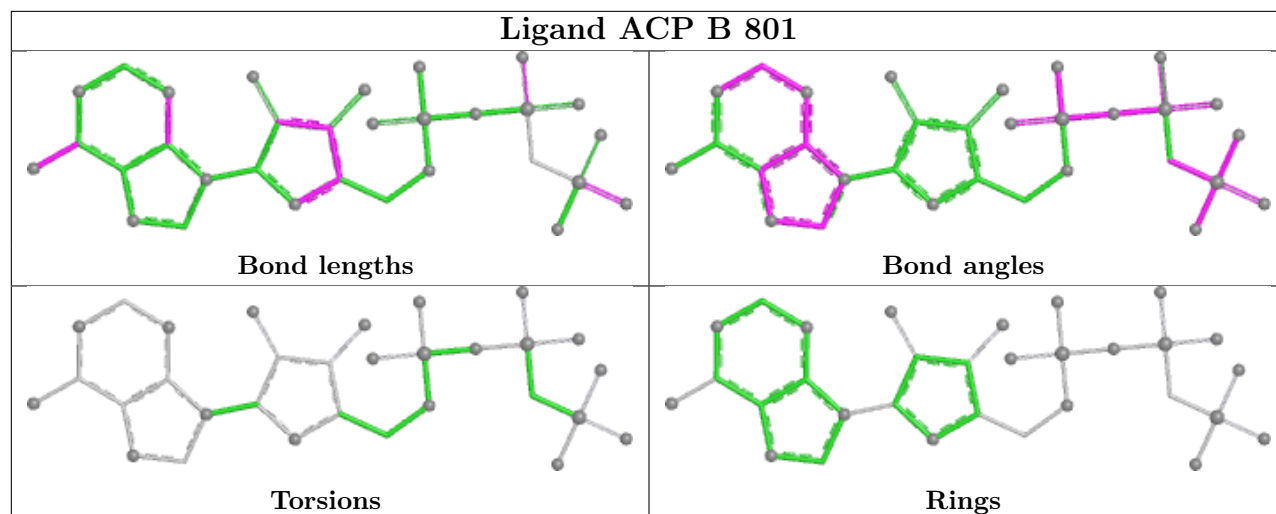
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand ACP D 1001



Ligand PUP D 1004





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	B	673/699 (96%)	0.66	77 (11%)	10	10	33, 53, 92, 136	0
1	D	674/699 (96%)	0.68	79 (11%)	9	9	34, 54, 89, 130	0
2	A	4/7 (57%)	0.13	0	100	100	43, 45, 45, 102	0
2	C	4/7 (57%)	-0.02	0	100	100	40, 41, 44, 97	0
All	All	1355/1412 (95%)	0.67	156 (11%)	9	10	33, 54, 92, 136	0

All (156) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	509	LYS	6.6
1	D	607	THR	6.5
1	D	447	VAL	6.4
1	B	510	TRP	5.7
1	D	719	THR	5.1
1	D	301	CYS	4.7
1	B	447	VAL	4.7
1	D	510	TRP	4.6
1	B	622	PRO	4.6
1	B	685	ILE	4.6
1	D	237	GLU	4.4
1	D	455	ASN	4.3
1	D	445	LEU	4.3
1	B	647	PHE	4.2
1	D	216	SER	4.1
1	B	344	GLY	4.1
1	D	327	GLU	4.1
1	D	623	SER	3.9
1	B	27	HIS	3.9
1	B	214	ASP	3.9
1	B	695	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	414	ASN	3.9
1	B	672	ASN	3.9
1	B	494	ASP	3.8
1	D	675	GLU	3.8
1	B	497	LYS	3.8
1	D	494	ASP	3.8
1	D	397	GLY	3.7
1	B	623	SER	3.7
1	D	211	LEU	3.6
1	D	214	ASP	3.5
1	D	27	HIS	3.5
1	B	674	ASP	3.5
1	D	573	VAL	3.5
1	B	673	ILE	3.4
1	B	626	SER	3.4
1	B	496	LYS	3.4
1	B	680	LYS	3.4
1	B	669	LEU	3.4
1	D	683	LEU	3.4
1	B	397	GLY	3.3
1	B	625	HIS	3.3
1	B	681	MET	3.3
1	D	603	SER	3.3
1	B	572	HIS	3.3
1	B	215	ASP	3.2
1	D	303	ASP	3.2
1	D	295	ARG	3.2
1	D	638	GLU	3.2
1	D	35	ASN	3.1
1	D	571	GLU	3.1
1	B	478	SER	3.1
1	D	622	PRO	3.1
1	D	637	ASN	3.1
1	B	263	HIS	3.1
1	B	621	GLY	3.0
1	D	215	ASP	3.0
1	B	426	HIS	3.0
1	D	496	LYS	3.0
1	B	571	GLU	2.9
1	D	610	SER	2.9
1	D	642	LYS	2.9
1	B	477	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	326	LYS	2.9
1	B	314	HIS	2.8
1	B	686	GLY	2.8
1	B	710	THR	2.8
1	B	211	LEU	2.8
1	D	511	ALA	2.7
1	B	603	SER	2.7
1	D	339	GLN	2.7
1	B	216	SER	2.7
1	B	327	GLU	2.6
1	B	374	THR	2.6
1	D	212	SER	2.6
1	D	495	SER	2.6
1	B	684	LYS	2.6
1	B	24	GLU	2.6
1	B	463	ASN	2.6
1	D	497	LYS	2.6
1	D	689	SER	2.6
1	D	694	LYS	2.6
1	D	28	LEU	2.6
1	D	575	ASP	2.6
1	D	414	ASN	2.6
1	B	642	LYS	2.6
1	D	682	LYS	2.6
1	B	615	LEU	2.6
1	D	213	SER	2.6
1	D	718	GLN	2.5
1	B	670	GLY	2.5
1	D	124	TYR	2.5
1	D	621	GLY	2.5
1	D	238	ARG	2.5
1	D	572	HIS	2.5
1	D	595	THR	2.5
1	B	636	ILE	2.5
1	B	26	ASN	2.5
1	D	651	ARG	2.5
1	D	548	GLU	2.4
1	D	630	ASP	2.4
1	B	628	SER	2.4
1	D	681	MET	2.4
1	B	511	ALA	2.4
1	D	474	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	468	ILE	2.4
1	B	640	VAL	2.4
1	B	607	THR	2.4
1	D	426	HIS	2.4
1	D	417	LEU	2.4
1	D	26	ASN	2.4
1	D	31	LYS	2.4
1	B	124	TYR	2.3
1	B	425	SER	2.3
1	D	625	HIS	2.3
1	B	624	GLU	2.3
1	B	237	GLU	2.3
1	D	46	GLU	2.3
1	B	650	LYS	2.3
1	B	683	LEU	2.3
1	D	262	GLU	2.2
1	D	406	SER	2.2
1	B	688	PRO	2.2
1	D	620	PRO	2.2
1	B	608	ARG	2.2
1	D	574	ARG	2.2
1	D	337	LYS	2.2
1	B	160	ASP	2.2
1	B	541	ASP	2.2
1	D	344	GLY	2.2
1	B	417	LEU	2.2
1	B	643	LYS	2.2
1	D	672	ASN	2.2
1	D	541	ASP	2.2
1	D	611	GLU	2.2
1	B	509	LYS	2.2
1	B	620	PRO	2.1
1	D	482	THR	2.2
1	B	573	VAL	2.1
1	B	652	GLY	2.1
1	D	570	GLY	2.1
1	D	709	ASN	2.1
1	B	456	GLU	2.1
1	B	337	LYS	2.1
1	D	695	THR	2.1
1	D	614	ILE	2.1
1	B	57	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	489	GLN	2.1
1	B	655	TYR	2.1
1	D	263	HIS	2.1
1	D	684	LYS	2.1
1	B	336	TRP	2.1
1	B	238	ARG	2.0
1	B	262	GLU	2.0
1	D	341	SER	2.0
1	B	616	ARG	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 [i](#)

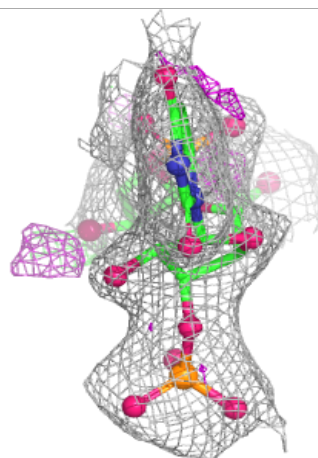
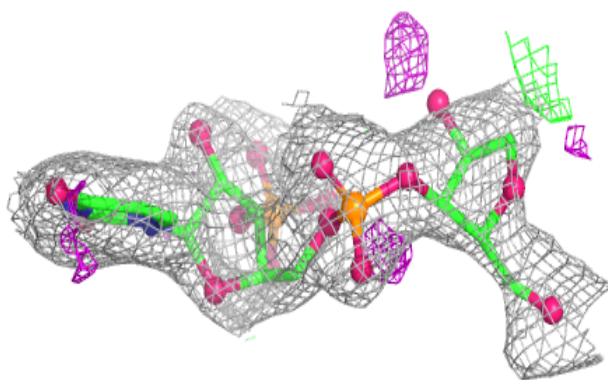
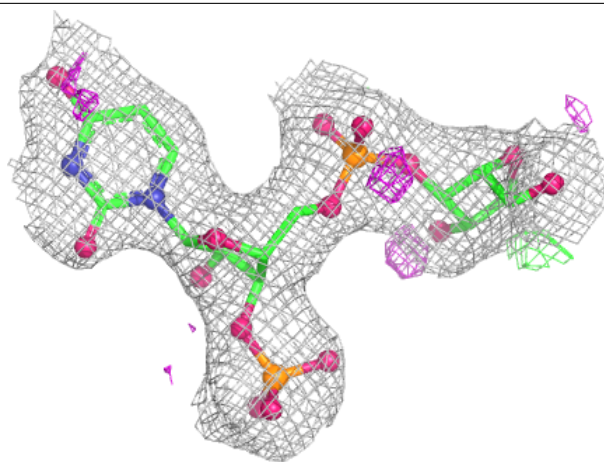
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PUP	D	1004	33/33	0.86	0.14	58,87,103,107	0
3	ACP	B	801	31/31	0.97	0.07	41,46,57,68	0
3	ACP	D	1001	31/31	0.98	0.07	40,47,65,77	0
4	MG	D	1002	1/1	0.99	0.03	47,47,47,47	0
4	MG	D	1003	1/1	0.99	0.04	48,48,48,48	0
4	MG	B	803	1/1	0.99	0.04	48,48,48,48	0
4	MG	B	802	1/1	1.00	0.04	49,49,49,49	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.

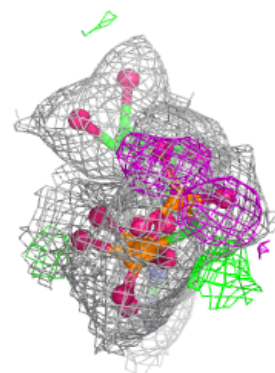
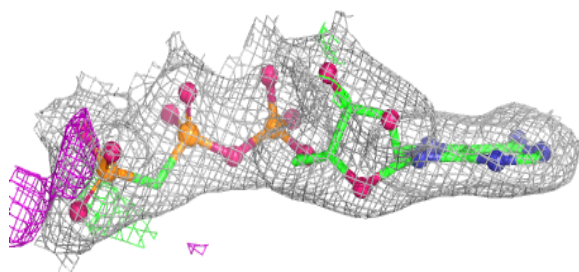
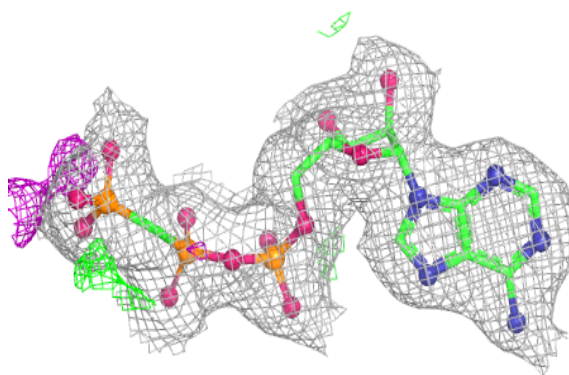
Electron density around PUP D 1004:

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

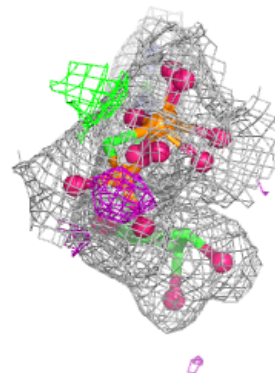
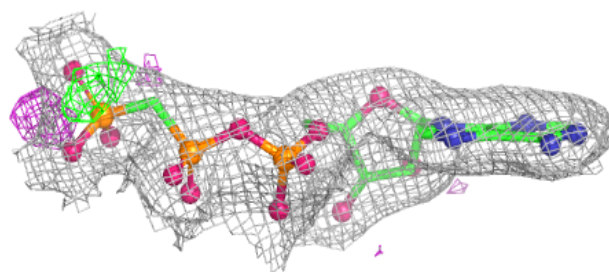
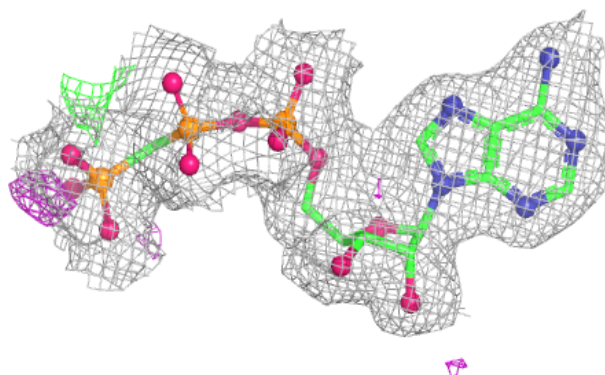


Electron density around ACP B 801:

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

**Electron density around ACP D 1001:**

$2mF_o-DF_c$ (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.