



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:25 PM UTC

PDB ID : 3UM5 / pdb_00003um5
Title : Double mutant (A16V+S108T) Plasmodium falciparum dihydrofolate reductase-thymidylate synthase (PfDHFR-TS-T9/94) complexed with pyrimethamine, NADPH, and dUMP
Authors : Vanichtanankul, J.; Kamchonwongpaisan, S.; Chitnumsub, P.; Yuthavong, Y.
Deposited on : 2011-11-12
Resolution : 2.40 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

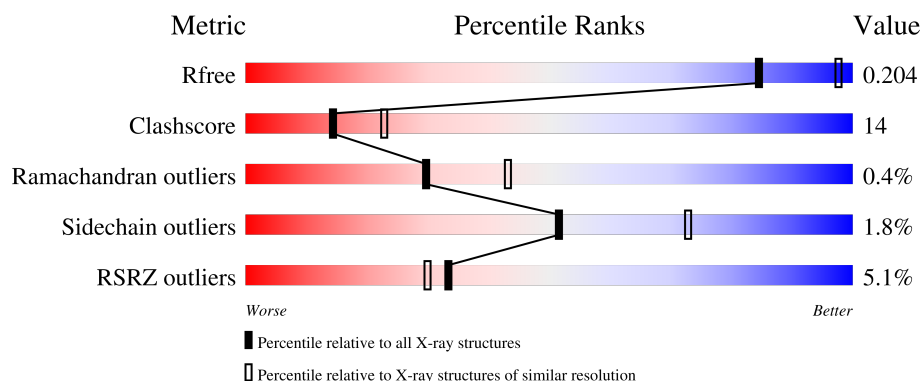
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

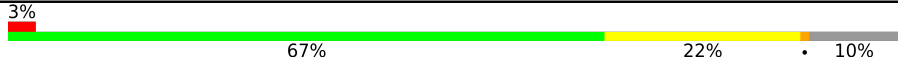
The reported resolution of this entry is 2.40 Å.

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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	608	
1	B	608	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CP6	A	609	-	X	-	-
2	CP6	B	709	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 10007 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.

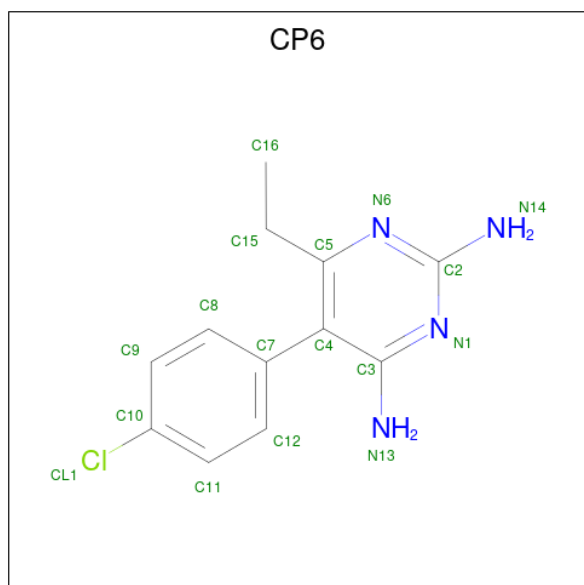
- Molecule 1 is a protein called Bifunctional dihydrofolate reductase-thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	546	Total	C	N	O	S	0	0	0
			4539	2930	749	832	28			
1	B	544	Total	C	N	O	S	0	0	0
			4517	2916	746	829	26			

There are 4 discrepancies between the modelled and reference sequences:

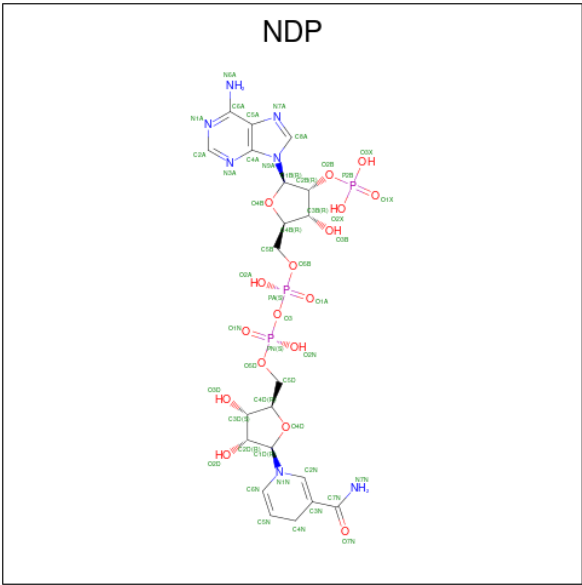
Chain	Residue	Modelled	Actual	Comment	Reference
A	16	VAL	ALA	engineered mutation	UNP A7UD81
A	108	THR	SER	engineered mutation	UNP A7UD81
B	16	VAL	ALA	engineered mutation	UNP A7UD81
B	108	THR	SER	engineered mutation	UNP A7UD81

- Molecule 2 is 5-(4-CHLORO-PHENYL)-6-ETHYL-PYRIMIDINE-2,4-DIAMINE (CCD ID: CP6) (formula: C₁₂H₁₃ClN₄).



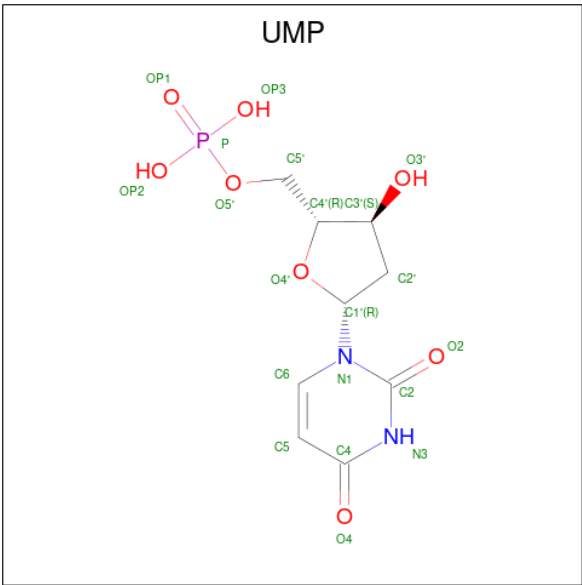
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	0	0
			17	12	1	4		
2	B	1	Total	C	Cl	N	0	0
			17	12	1	4		

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

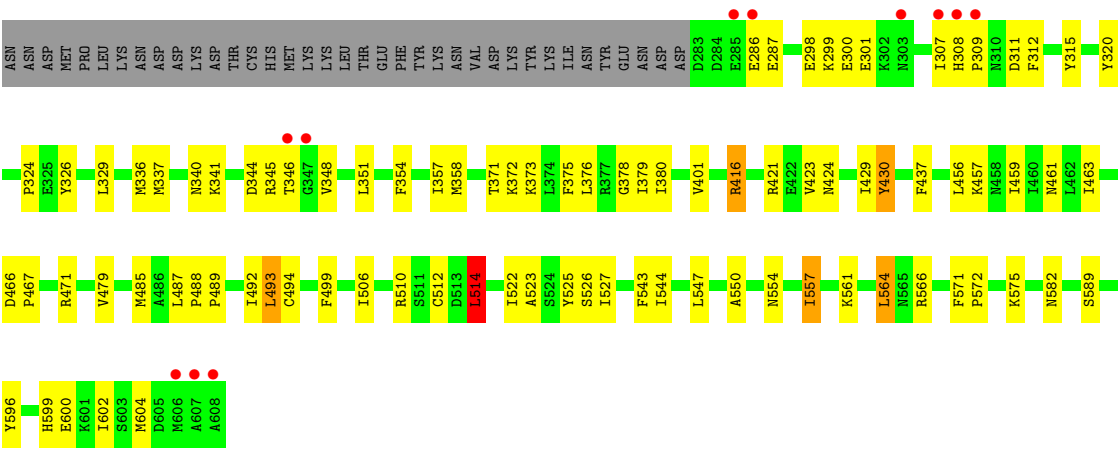
- Molecule 4 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (CCD ID: UMP) (formula: C₉H₁₃N₂O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
4	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	417	Total	O	0	0
			417	417		
5	B	364	Total	O	0	0
			364	364		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.53Å 155.12Å 165.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.28 – 2.40 28.28 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.6 (28.28-2.40) 98.6 (28.28-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.39Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.202 , 0.254 0.201 , 0.204	Depositor DCC
R_{free} test set	2840 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.423	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10007	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: CP6, UMP, NDP

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	0.38	0/4644	0.91	14/6267 (0.2%)
1	B	0.37	0/4622	0.89	12/6241 (0.2%)
All	All	0.38	0/9266	0.90	26/12508 (0.2%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	401	VAL	N-CA-C	-7.23	96.67	107.37
1	B	466	ASP	CA-C-N	7.01	127.31	119.32
1	B	466	ASP	C-N-CA	7.01	127.31	119.32
1	B	138	GLU	N-CA-C	-6.91	104.74	113.72
1	A	351	LEU	N-CA-C	-6.84	97.75	108.90
1	A	492	ILE	N-CA-C	6.57	116.73	110.42
1	A	163	ILE	N-CA-C	-6.16	99.70	108.58
1	B	599	HIS	N-CA-C	-6.14	102.27	110.55
1	A	48	TRP	N-CA-C	-6.00	101.12	110.42
1	B	514	LEU	N-CA-C	5.81	117.61	111.28
1	A	212	ASP	N-CA-C	-5.76	102.93	110.53
1	A	327	GLN	N-CA-C	-5.63	105.22	111.36
1	B	526	SER	N-CA-C	-5.50	105.20	111.14
1	B	557	ILE	N-CA-C	5.50	115.94	110.23
1	A	517	GLY	N-CA-C	5.49	119.13	112.49
1	B	543	PHE	N-CA-C	-5.47	99.60	108.52
1	A	567	ILE	CA-C-N	5.38	125.37	119.89
1	A	567	ILE	C-N-CA	5.38	125.37	119.89
1	B	351	LEU	N-CA-C	-5.27	99.82	108.41
1	B	416	ARG	N-CA-C	-5.25	106.65	113.16
1	A	466	ASP	CA-C-N	5.24	125.55	119.47
1	A	466	ASP	C-N-CA	5.24	125.55	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	302	LYS	N-CA-C	5.16	116.90	111.28
1	A	120	SER	N-CA-C	5.14	117.49	110.24
1	A	391	THR	N-CA-C	-5.09	106.19	114.09
1	B	493	LEU	N-CA-C	5.03	116.48	108.79

There are no chirality outliers.

There are no planarity outliers.

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	4539	0	4496	115	0
1	B	4517	0	4465	160	0
2	A	17	0	13	1	0
2	B	17	0	13	0	0
3	A	48	0	26	5	0
3	B	48	0	26	2	0
4	A	20	0	11	0	0
4	B	20	0	11	0	0
5	A	417	0	0	10	0
5	B	364	0	0	13	0
All	All	10007	0	9061	258	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 14.

All (258) 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:114:LYS:HE3	1:B:114:LYS:H	1.17	1.06
1:A:319:LYS:HG2	1:B:286:GLU:HG3	1.46	0.97
1:B:457:LYS:HE3	1:B:461:ASN:HD21	1.31	0.95
1:A:376:LEU:HD22	1:A:379:ILE:HD11	1.49	0.93
1:A:41:GLY:HA2	1:A:47:PRO:HD3	1.56	0.86
1:A:301:GLU:HB2	1:A:304:LYS:HB2	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:GLU:HG2	1:B:22:SER:H	1.42	0.81
1:B:118:PRO:HB2	1:B:124:ASN:ND2	1.96	0.81
1:B:41:GLY:HA2	1:B:47:PRO:HD3	1.63	0.80
1:B:336:MET:HE3	1:B:557:ILE:HG23	1.67	0.76
1:B:98:LEU:HD23	1:B:98:LEU:H	1.51	0.75
1:B:171:GLN:HE21	1:B:175:GLU:HG3	1.52	0.74
1:B:114:LYS:H	1:B:114:LYS:CE	1.99	0.73
1:A:308:HIS:HB3	1:A:310:ASN:ND2	2.02	0.73
1:B:118:PRO:HB2	1:B:124:ASN:HD21	1.53	0.73
1:B:575:LYS:HG2	5:B:1707:HOH:O	1.89	0.71
1:A:582:ASN:HB2	1:A:585:ASP:OD2	1.92	0.69
1:B:114:LYS:HA	1:B:117:LYS:HG2	1.75	0.68
1:A:324:PRO:HG2	1:A:571:PHE:CE2	2.29	0.68
1:A:127:LEU:HD23	1:A:143:ILE:HG13	1.77	0.67
1:B:147:GLU:HA	1:B:150:ILE:HG12	1.76	0.66
1:A:112:ILE:O	1:A:117:LYS:HE3	1.95	0.66
1:B:147:GLU:CD	1:B:147:GLU:H	2.02	0.66
1:A:376:LEU:HD22	1:A:379:ILE:CD1	2.25	0.65
1:B:12:TYR:CE1	1:B:180:LYS:HD3	2.31	0.65
1:A:27:LYS:N	1:A:27:LYS:HD2	2.11	0.65
1:B:127:LEU:HD23	1:B:143:ILE:HG13	1.77	0.65
1:B:376:LEU:HD22	1:B:379:ILE:HD11	1.77	0.65
1:B:197:PHE:HE1	1:B:200:ILE:HD11	1.62	0.64
1:B:201:ASN:HB3	1:B:204:GLU:HG2	1.79	0.64
1:B:114:LYS:HE3	1:B:114:LYS:N	2.02	0.63
1:A:324:PRO:HG2	1:A:571:PHE:HE2	1.64	0.63
1:B:29:ASN:HB2	1:B:32:PHE:CE1	2.34	0.63
1:B:493:LEU:HD12	1:B:493:LEU:C	2.24	0.63
1:B:23:LYS:NZ	1:B:23:LYS:HB3	2.13	0.62
1:B:21:GLU:HG2	1:B:22:SER:N	2.15	0.61
1:B:227:LYS:NZ	1:B:227:LYS:HB3	2.16	0.61
1:A:26:GLY:C	1:A:27:LYS:HD2	2.26	0.60
1:A:411:GLU:HB2	5:A:1538:HOH:O	2.01	0.60
1:A:491:HIS:HD2	1:A:509:GLN:HG3	1.66	0.60
1:A:290:PHE:HB2	1:B:320:TYR:OH	2.01	0.59
1:B:131:LEU:HG	1:B:136:PHE:HE1	1.67	0.59
1:A:487:LEU:HD12	1:A:487:LEU:O	2.02	0.59
1:B:299:LYS:HG3	1:B:300:GLU:CD	2.28	0.58
1:A:78:CYS:HB3	1:A:83:LYS:O	2.02	0.58
1:B:309:PRO:HA	1:B:312:PHE:HD2	1.68	0.58
1:B:378:GLY:HA3	5:B:1034:HOH:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:PRO:HG2	1:B:116:PHE:HD2	1.68	0.58
1:B:197:PHE:CE1	1:B:200:ILE:HD11	2.39	0.58
1:B:67:GLU:HG2	1:B:98:LEU:HD21	1.85	0.57
1:B:201:ASN:HD21	1:B:203:ASN:HB2	1.69	0.57
1:B:23:LYS:HB3	1:B:23:LYS:HZ2	1.68	0.57
1:A:304:LYS:NZ	1:A:309:PRO:HG3	2.19	0.57
1:B:506:ILE:HG12	1:B:544:ILE:HB	1.85	0.57
1:B:10:ASP:OD2	1:B:73:LEU:HD22	2.03	0.57
1:B:299:LYS:HG3	1:B:300:GLU:OE2	2.04	0.56
1:B:77:ARG:O	1:B:81:LEU:HG	2.04	0.56
1:A:299:LYS:HG3	1:A:299:LYS:O	2.04	0.56
1:A:402:ARG:HG2	1:A:402:ARG:HH11	1.71	0.56
1:A:23:LYS:HD2	1:A:30:GLU:OE1	2.06	0.56
1:A:109:TRP:O	1:A:117:LYS:HE2	2.06	0.56
1:A:23:LYS:HB2	1:A:23:LYS:NZ	2.21	0.56
1:B:512:CYS:SG	1:B:547:LEU:HD22	2.45	0.55
1:A:305:ASN:N	1:A:305:ASN:HD22	2.04	0.55
1:B:523:ALA:O	1:B:527:ILE:HG13	2.06	0.55
1:B:26:GLY:O	1:B:27:LYS:HB2	2.07	0.55
1:B:179:ILE:HB	1:B:205:TYR:OH	2.07	0.55
1:B:67:GLU:HA	1:B:98:LEU:HD21	1.89	0.54
1:A:506:ILE:HG12	1:A:544:ILE:HB	1.89	0.54
1:B:4:GLN:HG3	1:B:7:ASP:OD2	2.08	0.54
1:A:210:VAL:HB	5:A:1119:HOH:O	2.07	0.54
1:B:589:SER:HB3	5:B:1571:HOH:O	2.08	0.54
1:B:336:MET:HE1	1:B:561:LYS:HG3	1.90	0.54
1:B:457:LYS:HD2	5:B:1539:HOH:O	2.07	0.54
1:B:102:VAL:HG23	1:B:102:VAL:O	2.08	0.53
1:B:324:PRO:HB2	1:B:571:PHE:HE2	1.73	0.53
1:B:604:MET:HE3	5:B:1231:HOH:O	2.07	0.53
1:A:296:ASN:C	1:A:298:GLU:H	2.16	0.53
1:A:319:LYS:HG2	1:B:286:GLU:CG	2.31	0.53
1:A:354:PHE:CE2	1:B:506:ILE:HG13	2.43	0.53
1:B:308:HIS:HB2	1:B:311:ASP:OD2	2.09	0.53
1:A:447:ASN:OD1	1:A:449:GLU:HG2	2.09	0.52
1:A:202:GLU:HG2	5:A:1410:HOH:O	2.07	0.52
1:A:307:ILE:HD12	1:A:336:MET:O	2.10	0.52
1:B:329:LEU:HD22	1:B:564:LEU:HD12	1.90	0.52
1:A:66:ASN:ND2	1:A:69:LYS:HE3	2.25	0.52
1:A:301:GLU:OE1	1:A:337:MET:HB3	2.10	0.52
1:B:171:GLN:HE21	1:B:175:GLU:CG	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:LYS:HE3	1:B:461:ASN:ND2	2.11	0.52
1:B:128:SER:HB2	3:B:710:NDP:O3X	2.09	0.52
1:B:214:TYR:O	1:B:220:THR:HA	2.09	0.52
1:B:227:LYS:HB3	1:B:227:LYS:HZ2	1.73	0.52
1:B:572:PRO:HB3	1:B:596:TYR:HA	1.92	0.52
1:A:397:LEU:HD21	1:A:405:GLU:HB2	1.92	0.51
1:B:29:ASN:HD22	1:B:32:PHE:HE1	1.57	0.51
1:A:83:LYS:O	1:A:84:GLU:HG3	2.10	0.51
1:A:284:ASP:HB3	1:B:69:LYS:HE2	1.93	0.51
1:A:304:LYS:HZ2	1:A:309:PRO:HG3	1.75	0.51
1:A:309:PRO:HA	1:A:312:PHE:HD2	1.74	0.51
1:B:376:LEU:O	1:B:380:ILE:HG13	2.11	0.51
1:B:600:GLU:HG3	5:B:1140:HOH:O	2.10	0.51
1:B:67:GLU:HG2	1:B:98:LEU:CD2	2.41	0.51
1:B:22:SER:HB2	1:B:25:GLU:O	2.10	0.50
1:B:346:THR:C	1:B:348:VAL:H	2.18	0.50
1:B:423:VAL:O	1:B:424:ASN:HB2	2.10	0.50
1:A:41:GLY:N	1:A:195:VAL:HG23	2.26	0.49
1:A:335:ILE:HD12	1:A:514:LEU:CD1	2.41	0.49
1:B:141:TYR:CD1	1:B:141:TYR:N	2.79	0.49
1:B:186:ARG:HB2	1:B:222:ASP:OD1	2.12	0.49
1:B:373:LYS:HE2	1:B:375:PHE:CE1	2.48	0.49
1:A:41:GLY:H	1:A:195:VAL:HG23	1.77	0.49
1:B:312:PHE:HB3	1:B:315:TYR:HB3	1.94	0.49
1:B:70:TYR:CG	1:B:98:LEU:HD13	2.47	0.49
1:B:227:LYS:C	1:B:227:LYS:HD2	2.38	0.49
1:A:20:VAL:HG21	1:A:38:ARG:HH11	1.77	0.49
1:A:165:GLY:HA3	3:A:610:NDP:C5N	2.43	0.49
1:B:287:GLU:HB3	5:B:1562:HOH:O	2.13	0.49
1:B:307:ILE:HG21	1:B:336:MET:HE2	1.95	0.49
1:A:513:ASP:OD2	1:A:516:LEU:HB2	2.12	0.48
1:A:165:GLY:HA3	3:A:610:NDP:H5N	1.96	0.48
1:A:572:PRO:HB3	1:A:596:TYR:HA	1.94	0.48
1:B:28:LYS:NZ	1:B:28:LYS:HB3	2.28	0.48
1:B:301:GLU:HB3	1:B:337:MET:O	2.13	0.48
1:A:144:ASN:C	1:A:144:ASN:HD22	2.20	0.48
1:B:113:PRO:CG	1:B:116:PHE:HD2	2.26	0.48
1:A:340:ASN:HB3	1:B:499:PHE:CE1	2.48	0.48
1:A:428:PRO:O	1:A:485:MET:HE2	2.13	0.48
1:A:493:LEU:CD2	1:B:492:ILE:HG21	2.43	0.48
1:A:284:ASP:HB3	1:B:69:LYS:CE	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:LYS:HG3	1:A:337:MET:HE1	1.94	0.48
1:A:221:LEU:N	1:A:221:LEU:HD23	2.28	0.48
1:B:201:ASN:HD22	1:B:204:GLU:HG2	1.79	0.48
1:A:106:ARG:HB2	1:A:128:SER:HB2	1.95	0.47
1:A:301:GLU:OE1	1:A:337:MET:HE3	2.14	0.47
1:A:376:LEU:O	1:A:380:ILE:HG13	2.14	0.47
1:B:182:ILE:HB	1:B:226:TYR:HB2	1.95	0.47
1:B:357:ILE:HG23	1:B:357:ILE:O	2.14	0.47
1:A:27:LYS:C	1:A:29:ASN:H	2.22	0.47
1:A:506:ILE:HG13	1:B:354:PHE:CE2	2.49	0.47
1:B:114:LYS:HA	1:B:117:LYS:CG	2.43	0.47
1:B:358:MET:HE1	1:B:522:ILE:HD11	1.97	0.47
1:B:73:LEU:HA	1:B:76:LYS:HE3	1.97	0.47
1:B:582:ASN:HB2	5:B:1524:HOH:O	2.15	0.47
1:B:57:TYR:O	1:B:61:VAL:HG23	2.14	0.47
1:B:101:VAL:HG22	1:B:123:ILE:HB	1.97	0.47
1:A:109:TRP:CE3	1:A:126:ILE:HD11	2.50	0.47
1:A:493:LEU:C	1:A:493:LEU:HD12	2.40	0.47
1:A:499:PHE:CE1	1:B:340:ASN:HB3	2.50	0.47
1:B:554:ASN:HB2	5:B:1151:HOH:O	2.15	0.47
1:A:23:LYS:HB2	1:A:23:LYS:HZ2	1.79	0.46
1:A:335:ILE:HD12	1:A:514:LEU:HD11	1.96	0.46
1:A:400:ASN:OD1	1:A:402:ARG:NH2	2.48	0.46
1:B:81:LEU:O	1:B:82:ASN:HB3	2.14	0.46
1:B:85:THR:HG23	1:B:85:THR:O	2.14	0.46
1:B:153:LEU:C	1:B:155:LYS:H	2.24	0.46
1:A:332:ILE:CG2	1:A:336:MET:HE3	2.45	0.46
1:A:100:ASN:OD1	1:A:159:TYR:HB3	2.16	0.46
1:A:375:PHE:N	1:A:375:PHE:CD1	2.84	0.46
1:B:171:GLN:NE2	1:B:175:GLU:HG3	2.26	0.46
1:A:2:MET:N	1:A:2:MET:HE2	2.31	0.46
1:A:7:ASP:OD1	1:A:180:LYS:HE3	2.15	0.46
1:A:305:ASN:N	1:A:305:ASN:ND2	2.63	0.46
1:A:345:ARG:HG2	1:A:345:ARG:HH11	1.80	0.46
1:B:98:LEU:H	1:B:98:LEU:CD2	2.25	0.45
1:B:137:ASP:HB2	1:B:140:VAL:HG23	1.97	0.45
1:A:499:PHE:CZ	1:B:340:ASN:HB3	2.51	0.45
1:B:127:LEU:O	3:B:710:NDP:H1B	2.15	0.45
1:A:200:ILE:HG13	5:A:1211:HOH:O	2.16	0.45
1:B:131:LEU:HG	1:B:136:PHE:CE1	2.49	0.45
1:A:470:ARG:HH12	1:B:344:ASP:CB	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:TYR:CE2	1:A:160:LYS:HD3	2.52	0.45
1:A:58:PHE:CZ	2:A:609:CP6:H12	2.52	0.45
1:A:567:ILE:HA	1:A:568:PRO:HD3	1.84	0.45
1:A:377:ARG:NH1	5:A:1726:HOH:O	2.49	0.45
1:A:586:PHE:HB2	5:A:1059:HOH:O	2.17	0.45
1:A:510:ARG:HG3	1:A:511:SER:N	2.32	0.44
1:A:492:ILE:HG21	1:B:493:LEU:CD2	2.47	0.44
1:A:488:PRO:HG3	1:B:471:ARG:HD3	1.99	0.44
1:B:376:LEU:HD22	1:B:379:ILE:CD1	2.46	0.44
1:A:214:TYR:O	1:A:220:THR:HA	2.18	0.44
1:A:437:PHE:CD1	1:B:479:VAL:HB	2.52	0.44
1:B:201:ASN:HB3	1:B:204:GLU:CG	2.47	0.44
1:B:74:LYS:C	1:B:76:LYS:H	2.26	0.44
1:A:349:GLY:C	1:A:554:ASN:ND2	2.76	0.44
1:A:492:ILE:HD11	1:A:510:ARG:HD3	1.98	0.44
1:B:459:ILE:O	1:B:463:ILE:HG13	2.18	0.44
1:B:83:LYS:HG2	1:B:84:GLU:N	2.33	0.44
1:B:566:ARG:NH1	1:B:602:ILE:HD11	2.33	0.44
1:B:227:LYS:HD2	1:B:228:LYS:O	2.17	0.43
1:A:127:LEU:O	3:A:610:NDP:H1B	2.18	0.43
1:B:416:ARG:NH2	1:B:488:PRO:HD3	2.33	0.43
1:A:342:GLN:HG2	5:A:1129:HOH:O	2.18	0.43
1:B:467:PRO:HD2	5:B:1587:HOH:O	2.18	0.43
1:B:73:LEU:O	1:B:77:ARG:HG3	2.18	0.43
1:A:127:LEU:CD2	1:A:143:ILE:HG13	2.47	0.43
1:B:98:LEU:HD23	1:B:98:LEU:N	2.27	0.43
1:B:312:PHE:CE1	1:B:564:LEU:HD23	2.53	0.43
1:B:14:ILE:HD13	1:B:58:PHE:HD1	1.84	0.43
1:B:78:CYS:SG	1:B:85:THR:HG22	2.58	0.43
1:B:171:GLN:NE2	1:B:175:GLU:CG	2.80	0.43
1:A:304:LYS:HG3	1:A:337:MET:CE	2.49	0.43
1:A:331:ILE:HG22	1:A:514:LEU:HD11	2.01	0.43
1:A:459:ILE:HG13	1:A:460:ILE:N	2.34	0.43
1:B:201:ASN:ND2	1:B:203:ASN:HB2	2.32	0.43
1:B:326:TYR:HA	1:B:329:LEU:HB2	1.99	0.43
1:B:456:LEU:O	1:B:459:ILE:HG13	2.19	0.43
1:A:172:GLU:OE2	3:A:610:NDP:N7A	2.51	0.42
1:A:402:ARG:HG2	1:A:402:ARG:NH1	2.33	0.42
5:A:1515:HOH:O	1:B:345:ARG:HD2	2.19	0.42
1:A:208:ILE:HD13	1:A:227:LYS:HB2	2.01	0.42
1:B:147:GLU:CD	1:B:147:GLU:N	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:LYS:NZ	5:A:1520:HOH:O	2.52	0.42
1:B:429:ILE:O	1:B:430:TYR:C	2.62	0.42
1:A:479:VAL:HB	1:B:437:PHE:CD1	2.54	0.42
1:B:494:CYS:SG	1:B:525:TYR:CE2	3.12	0.42
1:A:350:VAL:HG12	1:A:553:TYR:HA	2.01	0.42
1:B:66:ASN:C	1:B:66:ASN:HD22	2.26	0.42
1:B:485:MET:SD	1:B:489:PRO:HD3	2.59	0.42
1:A:514:LEU:CD2	1:A:518:VAL:HG21	2.50	0.42
1:B:371:THR:O	1:B:372:LYS:HB3	2.19	0.42
1:B:493:LEU:HD12	1:B:493:LEU:O	2.20	0.42
1:A:382:GLU:O	1:A:385:TRP:HB3	2.20	0.41
1:B:341:LYS:HE3	5:B:1752:HOH:O	2.20	0.41
1:B:298:GLU:OE1	1:B:298:GLU:HA	2.20	0.41
1:B:307:ILE:CG2	1:B:336:MET:HE2	2.50	0.41
1:A:332:ILE:HG22	1:A:336:MET:HE3	2.02	0.41
1:A:480:LYS:HD3	5:A:1115:HOH:O	2.19	0.41
1:B:42:ASN:HA	1:B:194:ASP:OD2	2.20	0.41
1:B:4:GLN:O	1:B:8:VAL:HG23	2.21	0.41
1:B:69:LYS:C	1:B:71:GLU:H	2.29	0.41
1:B:104:MET:HA	1:B:165:GLY:O	2.20	0.41
1:A:423:VAL:O	1:A:424:ASN:HB2	2.20	0.41
1:A:444:MET:HE3	1:A:445:TYR:CZ	2.56	0.41
1:A:514:LEU:HD23	1:A:518:VAL:HG21	2.03	0.41
1:B:133:LYS:HD3	1:B:133:LYS:N	2.35	0.41
1:B:97:LYS:HG3	1:B:97:LYS:O	2.21	0.41
1:A:8:VAL:HA	1:A:76:LYS:HD3	2.03	0.41
1:A:27:LYS:C	1:A:29:ASN:N	2.79	0.41
1:B:21:GLU:CG	1:B:22:SER:H	2.23	0.41
1:B:151:VAL:O	1:B:152:LEU:C	2.64	0.41
1:A:23:LYS:NZ	1:A:23:LYS:CB	2.84	0.41
1:A:40:LEU:O	3:A:610:NDP:H2N	2.20	0.41
1:A:309:PRO:HA	1:A:312:PHE:CD2	2.54	0.41
1:A:470:ARG:HH12	1:B:344:ASP:HB2	1.86	0.41
1:A:575:LYS:HD3	1:A:575:LYS:HA	1.79	0.41
1:B:66:ASN:OD1	1:B:69:LYS:HG3	2.20	0.41
1:B:69:LYS:HD2	1:B:159:TYR:OH	2.21	0.41
1:B:17:CYS:HB2	1:B:184:PHE:CZ	2.55	0.41
1:B:62:THR:O	1:B:122:ARG:HG2	2.21	0.41
1:B:69:LYS:C	1:B:71:GLU:N	2.79	0.41
1:B:132:LYS:HB3	1:B:134:GLU:CD	2.46	0.41
1:B:492:ILE:HD11	1:B:510:ARG:HD3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:421:ARG:NH2	5:B:1498:HOH:O	2.51	0.40
1:A:377:ARG:NH2	1:A:399:LYS:O	2.53	0.40
1:B:152:LEU:HD11	1:B:156:LEU:HD11	2.04	0.40
1:B:493:LEU:C	1:B:493:LEU:CD1	2.94	0.40
1:B:50:CYS:HA	5:B:1623:HOH:O	2.20	0.40
1:B:514:LEU:HD11	1:B:550:ALA:HB1	2.04	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	540/608 (89%)	508 (94%)	30 (6%)	2 (0%)	30	43
1	B	538/608 (88%)	490 (91%)	46 (9%)	2 (0%)	30	43
All	All	1078/1216 (89%)	998 (93%)	76 (7%)	4 (0%)	30	43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	430	TYR
1	A	21	GLU
1	A	430	TYR
1	B	152	LEU

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	510/571 (89%)	502 (98%)	8 (2%)	55	76
1	B	507/571 (89%)	497 (98%)	10 (2%)	48	70
All	All	1017/1142 (89%)	999 (98%)	18 (2%)	51	73

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LYS
1	A	50	CYS
1	A	144	ASN
1	A	177	LYS
1	A	310	ASN
1	A	353	LYS
1	A	375	PHE
1	A	512	CYS
1	B	23	LYS
1	B	28	LYS
1	B	114	LYS
1	B	141	TYR
1	B	147	GLU
1	B	189	SER
1	B	227	LYS
1	B	487	LEU
1	B	514	LEU
1	B	564	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	99	GLN
1	A	144	ASN
1	A	231	ASN
1	A	296	ASN
1	A	305	ASN
1	A	310	ASN
1	A	394	ASN
1	A	407	ASN
1	A	424	ASN

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Mol	Chain	Res	Type
1	A	534	GLN
1	A	554	ASN
1	A	582	ASN
1	A	594	GLN
1	B	29	ASN
1	B	42	ASN
1	B	99	GLN
1	B	124	ASN
1	B	157	ASN
1	B	171	GLN
1	B	201	ASN
1	B	203	ASN
1	B	296	ASN
1	B	316	ASN
1	B	338	ASN
1	B	342	GLN
1	B	394	ASN
1	B	424	ASN
1	B	461	ASN
1	B	534	GLN
1	B	554	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands 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	UMP	A	611	-	21,21,21	1.81	7 (33%)	30,31,31	1.93	11 (36%)
2	CP6	A	609	-	18,18,18	3.69	15 (83%)	25,25,25	2.20	9 (36%)
2	CP6	B	709	-	18,18,18	4.00	14 (77%)	25,25,25	2.14	9 (36%)
4	UMP	B	711	-	21,21,21	1.77	6 (28%)	30,31,31	1.97	12 (40%)
3	NDP	A	610	-	51,52,52	1.37	7 (13%)	71,80,80	1.82	14 (19%)
3	NDP	B	710	-	51,52,52	1.43	9 (17%)	71,80,80	1.64	12 (16%)

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	UMP	A	611	-	-	0/10/22/22	0/2/2/2
2	CP6	A	609	-	-	0/6/6/6	0/2/2/2
2	CP6	B	709	-	-	0/6/6/6	0/2/2/2
4	UMP	B	711	-	-	1/10/22/22	0/2/2/2
3	NDP	A	610	-	-	4/34/77/77	0/5/5/5
3	NDP	B	710	-	-	4/34/77/77	0/5/5/5

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	709	CP6	C4-C5	7.21	1.56	1.40
2	A	609	CP6	C4-C5	6.51	1.54	1.40
2	B	709	CP6	C9-C10	6.40	1.49	1.38
2	A	609	CP6	C9-C10	6.07	1.49	1.38
2	A	609	CP6	C12-C7	5.77	1.50	1.39
2	B	709	CP6	C12-C7	5.72	1.50	1.39
2	B	709	CP6	C4-C3	5.20	1.53	1.43
3	B	710	NDP	C6N-N1N	5.11	1.49	1.37
2	B	709	CP6	C12-C11	4.90	1.46	1.38
3	A	610	NDP	C6N-N1N	4.65	1.48	1.37
2	B	709	CP6	C3-N1	4.47	1.41	1.35
2	B	709	CP6	C9-C8	4.32	1.45	1.38
2	A	609	CP6	C10-CL1	-4.25	1.64	1.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	609	CP6	C4-C3	4.22	1.51	1.43
4	B	711	UMP	O4'-C1'	4.13	1.51	1.42
2	A	609	CP6	C12-C11	4.13	1.45	1.38
4	A	611	UMP	O4'-C1'	3.71	1.50	1.42
2	A	609	CP6	C2-N6	3.69	1.41	1.35
3	A	610	NDP	C8A-N7A	3.57	1.38	1.31
3	B	710	NDP	C8A-N7A	3.52	1.38	1.31
4	A	611	UMP	C2-N1	3.50	1.43	1.38
2	A	609	CP6	C3-N1	3.47	1.39	1.35
2	B	709	CP6	C2-N1	3.33	1.41	1.35
2	B	709	CP6	C2-N6	3.32	1.41	1.35
2	B	709	CP6	C2-N14	3.19	1.40	1.33
2	B	709	CP6	C10-CL1	-3.17	1.67	1.74
2	A	609	CP6	C2-N14	3.17	1.40	1.33
2	B	709	CP6	C8-C7	3.15	1.45	1.39
2	B	709	CP6	C11-C10	2.92	1.43	1.38
2	A	609	CP6	C9-C8	2.89	1.43	1.38
2	B	709	CP6	C5-N6	2.88	1.39	1.34
4	B	711	UMP	C2-N1	2.81	1.42	1.38
2	A	609	CP6	C4-C7	-2.79	1.45	1.50
2	A	609	CP6	C11-C10	2.79	1.43	1.38
2	A	609	CP6	C8-C7	2.75	1.44	1.39
4	A	611	UMP	P-OP3	-2.73	1.44	1.54
3	B	710	NDP	C4A-N3A	2.70	1.39	1.34
3	B	710	NDP	C7N-C3N	2.62	1.54	1.48
4	A	611	UMP	C4-N3	2.58	1.43	1.38
3	A	610	NDP	C5A-N7A	-2.54	1.34	1.39
2	A	609	CP6	C5-N6	2.54	1.38	1.34
4	B	711	UMP	P-OP3	-2.54	1.45	1.54
3	A	610	NDP	C7N-C3N	2.52	1.54	1.48
4	B	711	UMP	C4-N3	2.41	1.42	1.38
2	A	609	CP6	C2-N1	2.39	1.39	1.35
3	A	610	NDP	C4A-N3A	2.36	1.38	1.34
3	B	710	NDP	C5A-N7A	-2.32	1.34	1.39
4	A	611	UMP	C6-C5	2.32	1.40	1.35
4	A	611	UMP	P-OP1	-2.27	1.43	1.50
3	B	710	NDP	C5D-C4D	2.22	1.58	1.51
3	A	610	NDP	C5D-C4D	2.20	1.58	1.51
4	A	611	UMP	P-OP2	-2.18	1.46	1.54
3	B	710	NDP	O4D-C1D	2.08	1.46	1.42
3	B	710	NDP	PA-O2A	-2.07	1.45	1.55
3	B	710	NDP	C1D-N1N	2.05	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	711	UMP	C6-C5	2.03	1.39	1.35
3	A	610	NDP	PA-O2A	-2.03	1.46	1.55
4	B	711	UMP	P-OP2	-2.01	1.47	1.54

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	710	NDP	N3A-C2A-N1A	-6.12	119.32	128.58
3	A	610	NDP	N3A-C2A-N1A	-5.97	119.55	128.58
3	A	610	NDP	C1D-N1N-C2N	-5.12	112.71	121.14
2	B	709	CP6	C2-N6-C5	5.00	119.91	116.26
2	B	709	CP6	C3-C4-C5	-4.72	112.57	115.97
3	B	710	NDP	C5A-C4A-N3A	-4.53	120.48	126.72
4	B	711	UMP	O4'-C1'-N1	4.49	115.83	107.86
4	A	611	UMP	C1'-N1-C6	-4.26	113.16	121.53
4	B	711	UMP	C1'-N1-C6	-4.26	113.16	121.53
4	A	611	UMP	O4'-C1'-N1	4.24	115.39	107.86
3	A	610	NDP	O2B-C2B-C3B	-4.19	96.65	111.68
3	A	610	NDP	C5A-C4A-N3A	-4.08	121.10	126.72
2	A	609	CP6	C2-N6-C5	3.94	119.13	116.26
2	A	609	CP6	C3-C4-C5	-3.92	113.14	115.97
2	A	609	CP6	C15-C5-C4	-3.88	119.89	122.47
2	A	609	CP6	C7-C4-C3	3.88	125.31	120.33
3	B	710	NDP	O4B-C1B-C2B	-3.60	100.40	106.59
2	A	609	CP6	C9-C10-CL1	-3.53	114.15	119.36
2	A	609	CP6	C11-C10-CL1	3.43	124.42	119.36
2	B	709	CP6	C11-C10-CL1	3.29	124.22	119.36
3	B	710	NDP	C2A-N3A-C4A	3.16	119.55	111.83
3	B	710	NDP	C1D-N1N-C2N	-3.12	116.00	121.14
3	B	710	NDP	O2B-C2B-C3B	-3.11	100.52	111.68
3	A	610	NDP	C6N-N1N-C2N	3.10	122.64	119.32
4	B	711	UMP	O4'-C1'-C2'	-3.03	100.58	106.25
4	B	711	UMP	C2'-C1'-N1	2.99	121.28	113.81
3	A	610	NDP	C2A-N3A-C4A	2.99	119.12	111.83
2	B	709	CP6	C15-C5-C4	-2.96	120.50	122.47
3	B	710	NDP	C2A-N1A-C6A	2.95	123.58	118.73
4	A	611	UMP	C1'-N1-C2	2.94	123.40	117.66
4	A	611	UMP	O4'-C1'-C2'	-2.91	100.80	106.25
2	A	609	CP6	C2-N1-C3	2.90	120.76	117.28
3	A	610	NDP	C3N-C2N-N1N	-2.87	118.99	123.20
4	A	611	UMP	C4'-O4'-C1'	2.86	116.30	109.51
4	B	711	UMP	C4'-O4'-C1'	2.85	116.29	109.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	709	CP6	C7-C4-C3	2.84	123.97	120.33
4	B	711	UMP	C1'-N1-C2	2.83	123.19	117.66
3	A	610	NDP	C1B-N9A-C8A	2.83	133.37	127.09
3	A	610	NDP	N9A-C8A-N7A	-2.78	109.99	113.94
3	A	610	NDP	C2A-N1A-C6A	2.76	123.27	118.73
3	A	610	NDP	C4A-N9A-C1B	-2.76	120.18	126.63
4	B	711	UMP	O4'-C4'-C3'	-2.74	99.40	105.65
2	B	709	CP6	C9-C10-CL1	-2.70	115.38	119.36
3	A	610	NDP	O4B-C1B-C2B	-2.67	101.99	106.59
4	A	611	UMP	C2'-C1'-N1	2.63	120.38	113.81
3	B	710	NDP	C5A-C4A-N9A	2.62	108.66	105.81
4	A	611	UMP	O4'-C4'-C3'	-2.52	99.89	105.65
4	A	611	UMP	C2'-C3'-C4'	2.50	107.86	102.80
3	B	710	NDP	C3N-C2N-N1N	-2.43	119.63	123.20
2	B	709	CP6	C2-N1-C3	2.42	120.19	117.28
3	A	610	NDP	C5A-C4A-N9A	2.39	108.42	105.81
4	A	611	UMP	O2-C2-N1	2.37	125.89	122.80
4	B	711	UMP	C2'-C3'-C4'	2.35	107.56	102.80
3	A	610	NDP	P2B-O2B-C2B	-2.34	117.17	123.43
3	B	710	NDP	C1B-N9A-C8A	2.27	132.13	127.09
4	B	711	UMP	O4-C4-N3	2.27	122.56	119.27
4	A	611	UMP	O4-C4-N3	2.24	122.52	119.27
4	B	711	UMP	C6-N1-C2	2.18	123.65	121.00
3	B	710	NDP	N3A-C4A-N9A	2.17	130.85	127.17
3	B	710	NDP	C2B-C1B-N9A	2.15	117.29	113.75
4	B	711	UMP	O2-C2-N1	2.14	125.58	122.80
2	A	609	CP6	N13-C3-N1	2.13	119.90	117.03
2	B	709	CP6	N13-C3-N1	2.12	119.88	117.03
2	A	609	CP6	C4-C3-N1	-2.09	121.34	122.55
4	B	711	UMP	O4-C4-C5	-2.08	121.58	125.16
2	B	709	CP6	C16-C15-C5	2.07	120.17	114.59
4	A	611	UMP	C6-N1-C2	2.01	123.45	121.00

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	610	NDP	O4D-C1D-N1N-C2N
3	A	610	NDP	C2N-C3N-C7N-N7N
3	B	710	NDP	O4D-C1D-N1N-C2N
3	B	710	NDP	C2N-C3N-C7N-N7N
3	A	610	NDP	C2D-C1D-N1N-C2N

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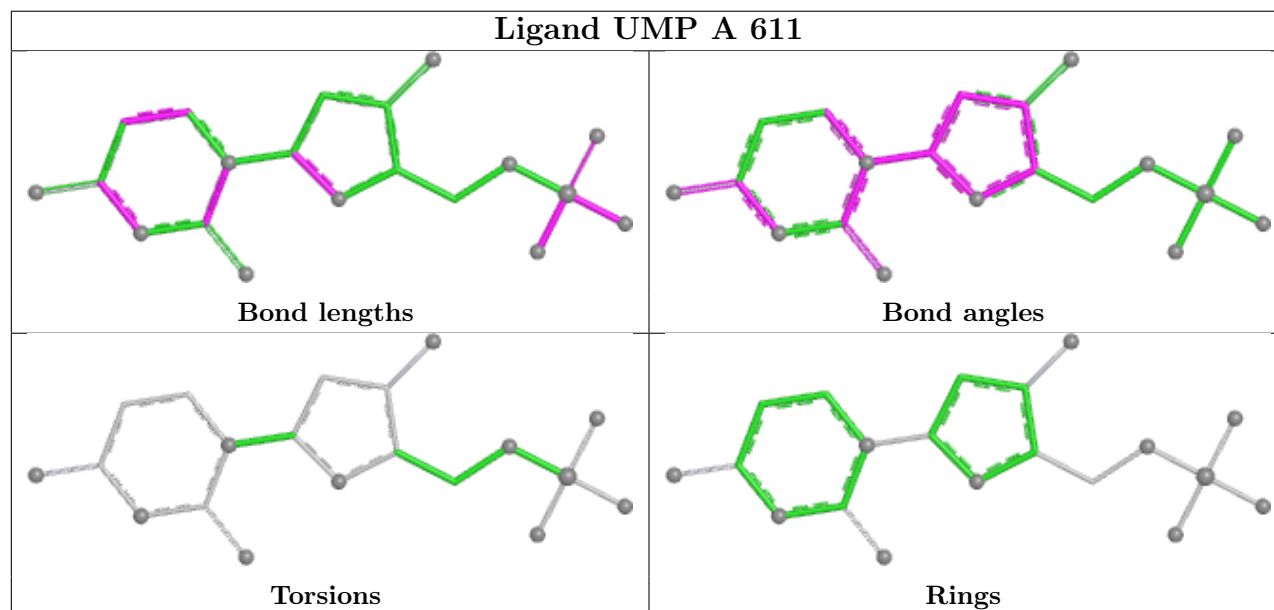
Mol	Chain	Res	Type	Atoms
3	B	710	NDP	C2D-C1D-N1N-C2N
4	B	711	UMP	O4'-C4'-C5'-O5'
3	A	610	NDP	O4D-C1D-N1N-C6N
3	B	710	NDP	C2B-O2B-P2B-O1X

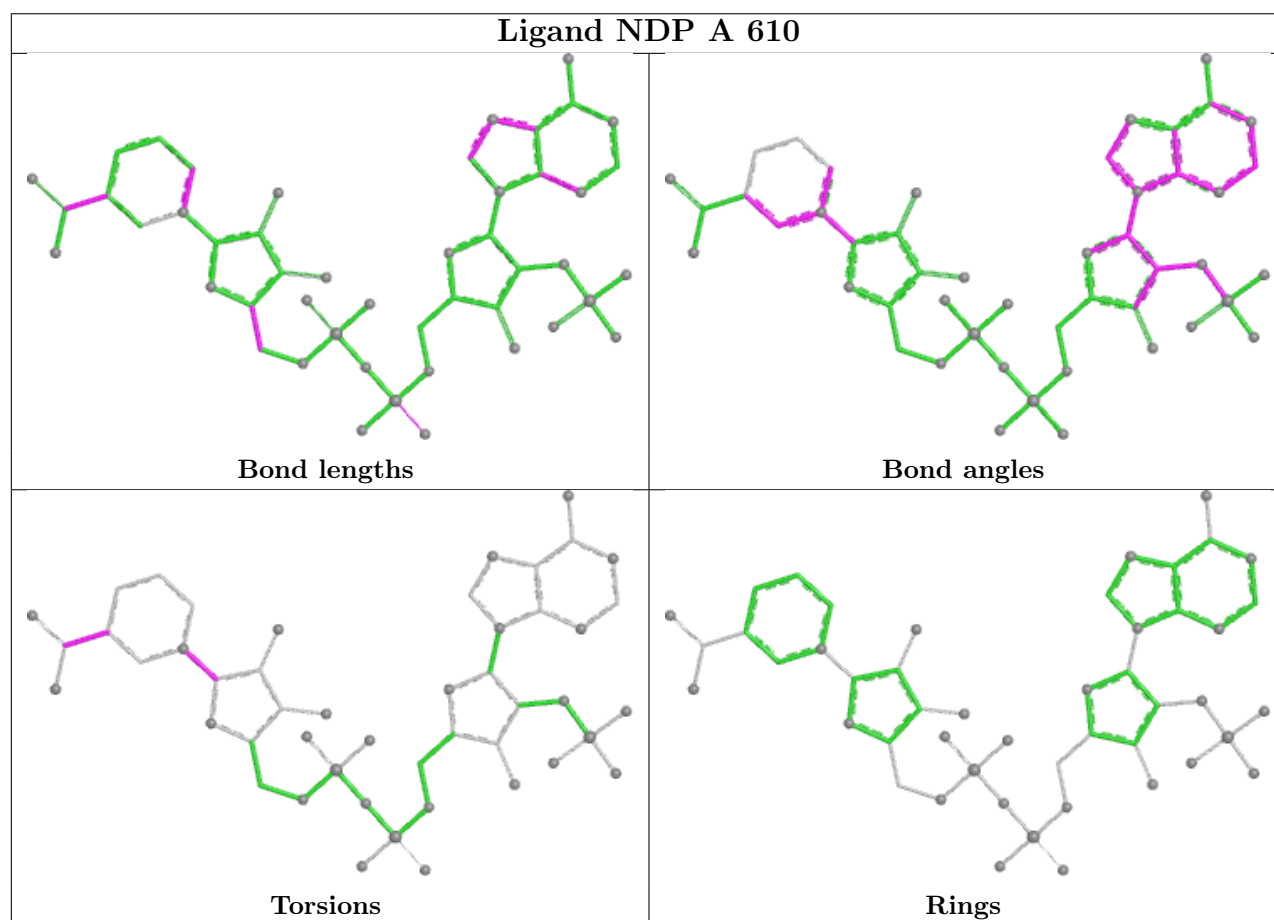
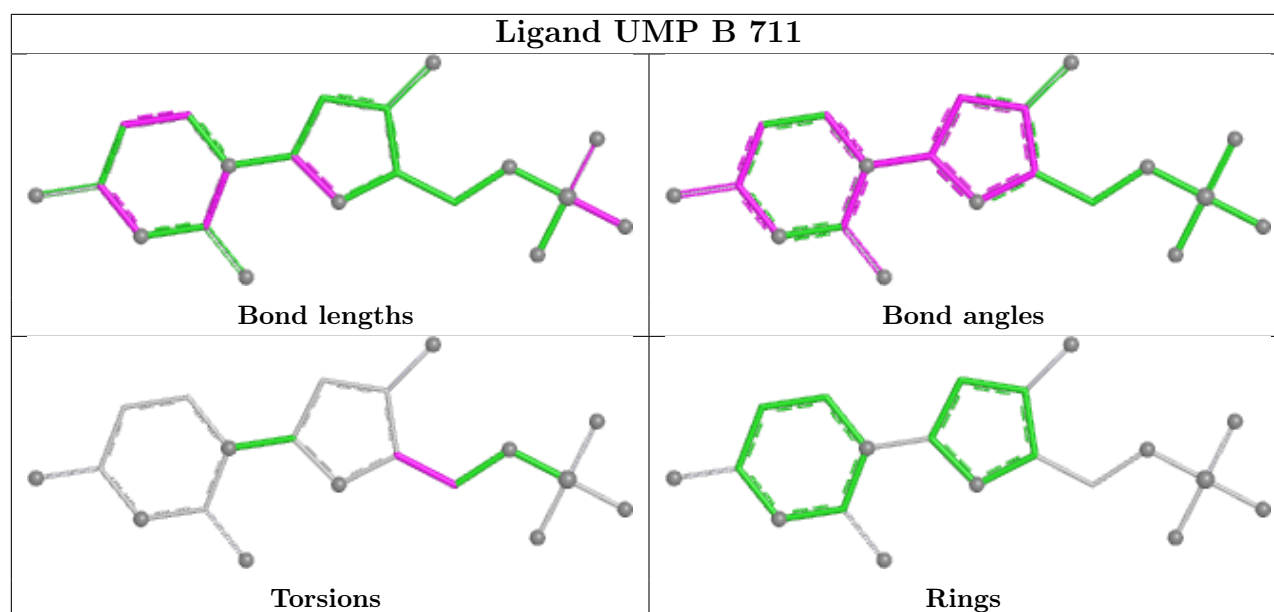
There are no ring outliers.

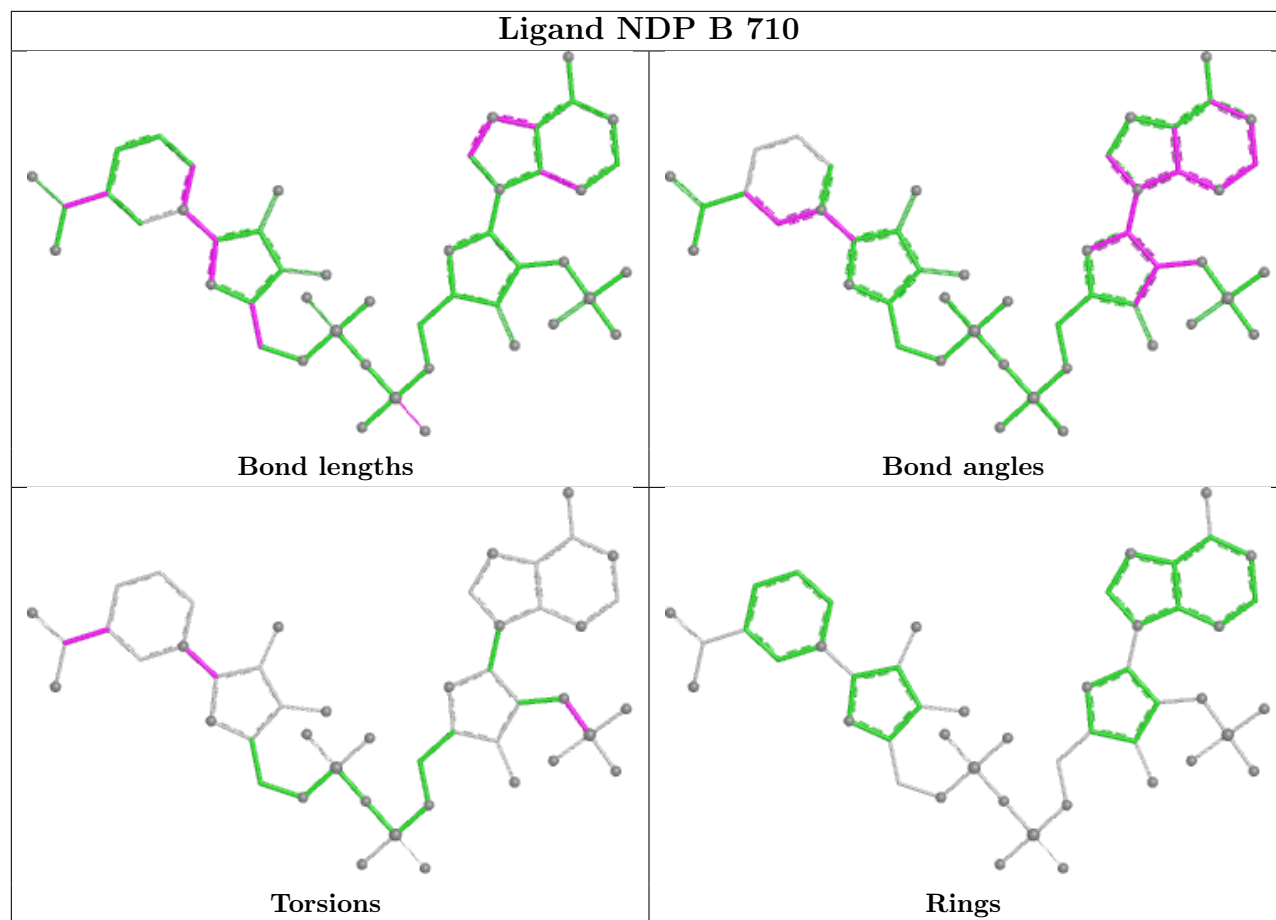
3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	609	CP6	1	0
3	A	610	NDP	5	0
3	B	710	NDP	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	546/608 (89%)	-0.23	16 (2%) 53 50	21, 35, 86, 90	0
1	B	544/608 (89%)	0.21	40 (7%) 20 17	21, 43, 90, 90	0
All	All	1090/1216 (89%)	-0.01	56 (5%) 33 30	21, 37, 90, 90	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	307	ILE	4.4
1	B	29	ASN	4.2
1	B	26	GLY	3.9
1	A	608	ALA	3.8
1	B	608	ALA	3.7
1	B	86	VAL	3.6
1	A	2	MET	3.5
1	B	136	PHE	3.0
1	B	151	VAL	3.0
1	A	307	ILE	2.9
1	A	1	MET	2.9
1	B	285	GLU	2.9
1	B	347	GLY	2.9
1	B	82	ASN	2.8
1	A	304	LYS	2.8
1	B	81	LEU	2.7
1	B	607	ALA	2.6
1	B	308	HIS	2.6
1	A	231	ASN	2.6
1	A	343	SER	2.5
1	B	346	THR	2.5
1	B	112	ILE	2.4
1	B	152	LEU	2.4
1	B	28	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	6	CYS	2.4
1	A	310	ASN	2.3
1	B	142	ILE	2.3
1	A	305	ASN	2.3
1	A	346	THR	2.2
1	B	27	LYS	2.2
1	B	309	PRO	2.2
1	B	75	TYR	2.2
1	B	79	LYS	2.2
1	B	606	MET	2.2
1	A	26	GLY	2.2
1	B	70	TYR	2.2
1	B	164	ILE	2.2
1	B	127	LEU	2.1
1	B	200	ILE	2.1
1	B	140	VAL	2.1
1	A	27	LYS	2.1
1	B	73	LEU	2.1
1	B	78	CYS	2.1
1	B	168	VAL	2.0
1	A	24	ASN	2.0
1	B	157	ASN	2.0
1	B	303	ASN	2.0
1	A	284	ASP	2.0
1	B	61	VAL	2.0
1	B	13	ALA	2.0
1	B	149	LEU	2.0
1	B	286	GLU	2.0
1	A	303	ASN	2.0
1	B	66	ASN	2.0
1	A	344	ASP	2.0
1	B	10	ASP	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](#)

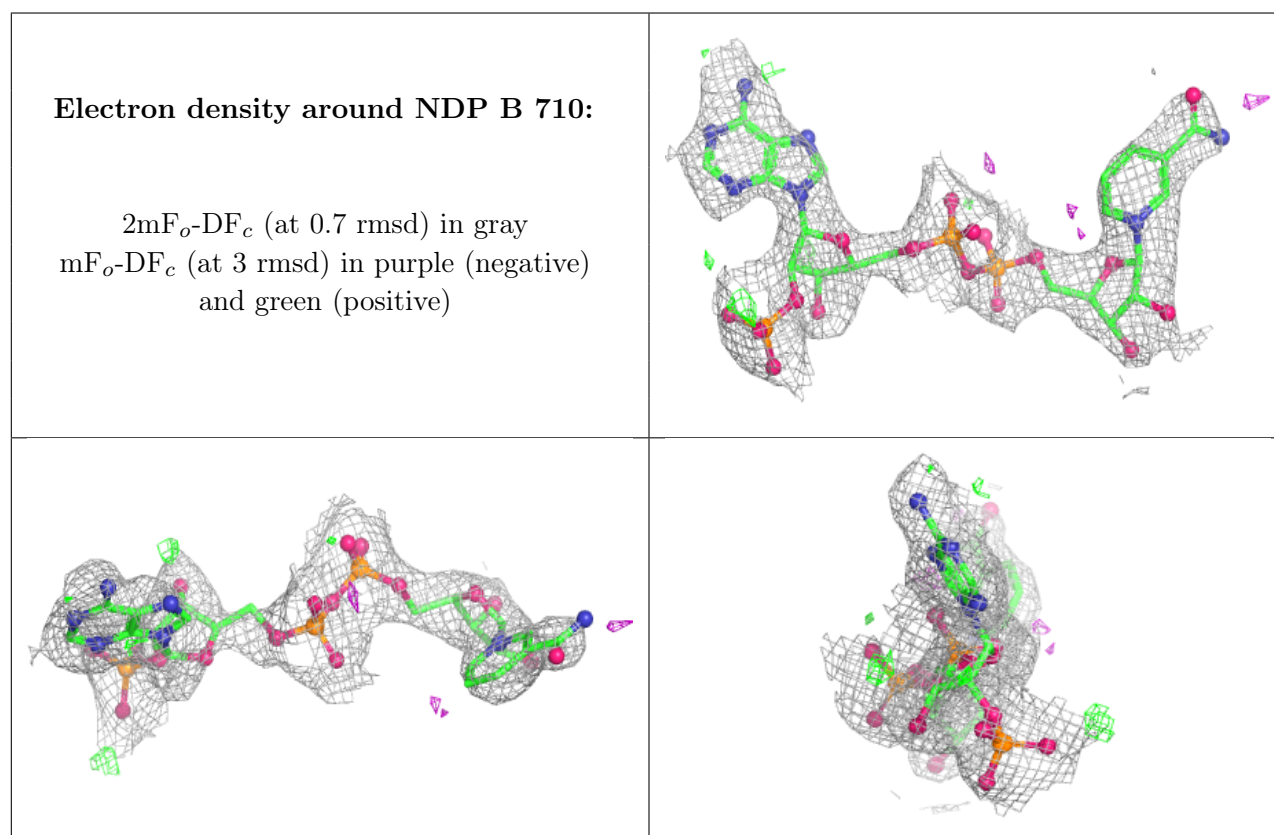
There are no oligosaccharides in this entry.

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.

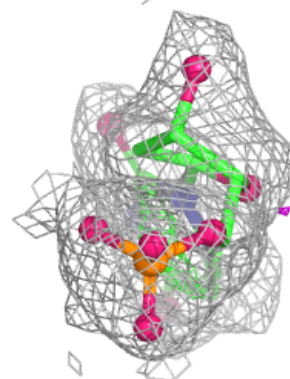
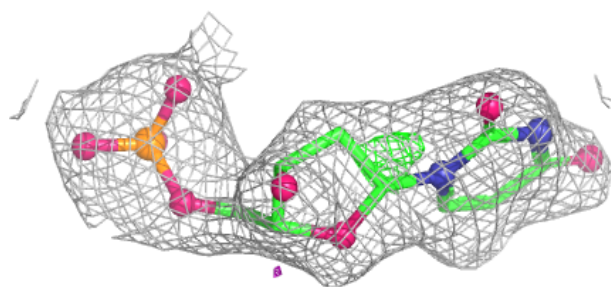
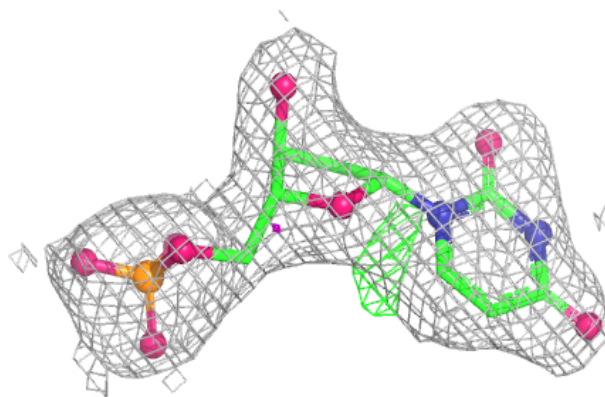
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NDP	B	710	48/48	0.82	0.13	81,86,89,89	0
2	CP6	B	709	17/17	0.88	0.14	66,69,73,74	0
4	UMP	B	711	20/20	0.94	0.08	38,42,44,45	0
2	CP6	A	609	17/17	0.95	0.07	23,25,34,39	0
4	UMP	A	611	20/20	0.96	0.07	33,39,48,49	0
3	NDP	A	610	48/48	0.97	0.07	25,36,39,40	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.

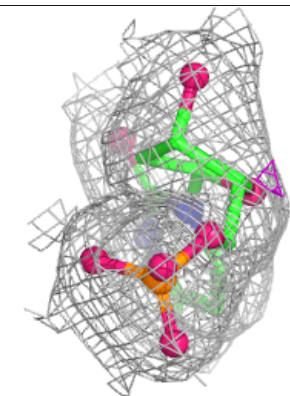
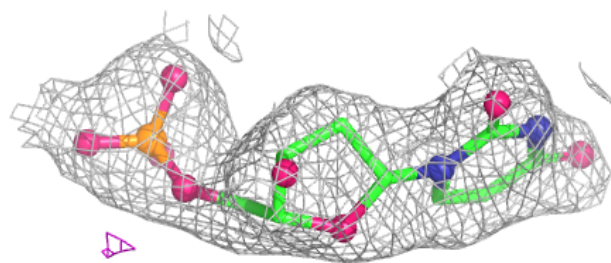
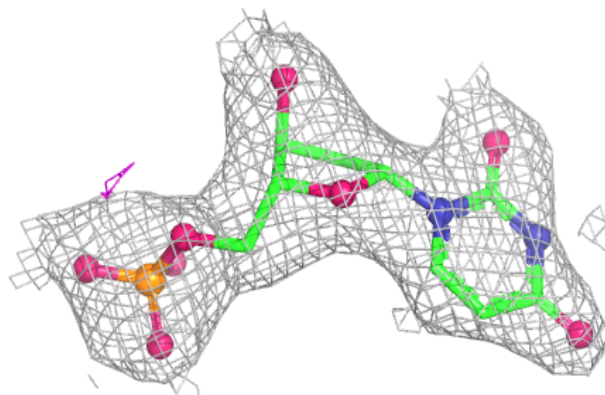


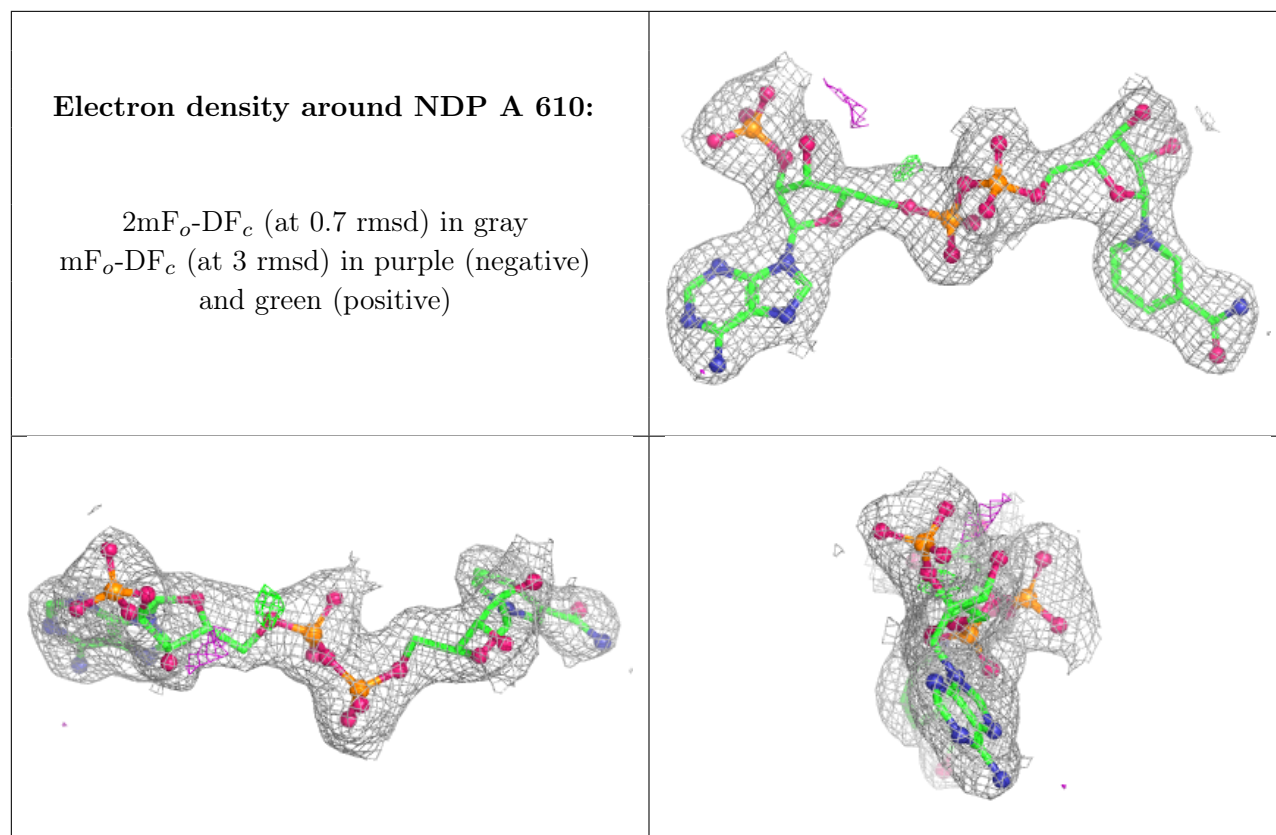
Electron density around UMP B 711:

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

**Electron density around UMP A 611:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.