



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 01:43 PM EDT

PDB ID : 3DG8
Title : Quadruple mutant (N51I+C59R+S108N+I164L) Plasmodium falciparum dihydrofolate reductase-thymidylate synthase (PfDHFR-TS) complexed with RJF670, NADPH, and dUMP
Authors : Dasgupta, T.; Chitnumsub, P.; Maneeruttanarungroj, C.; Kamchonwongpaisan, S.; Nichols, S.; Lyons, T.M.; Tirado-Rives, J.; Jorgensen, W.L.; Yuthavong, Y.; Anderson, K.S.
Deposited on : 2008-06-13
Resolution : 2.58 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

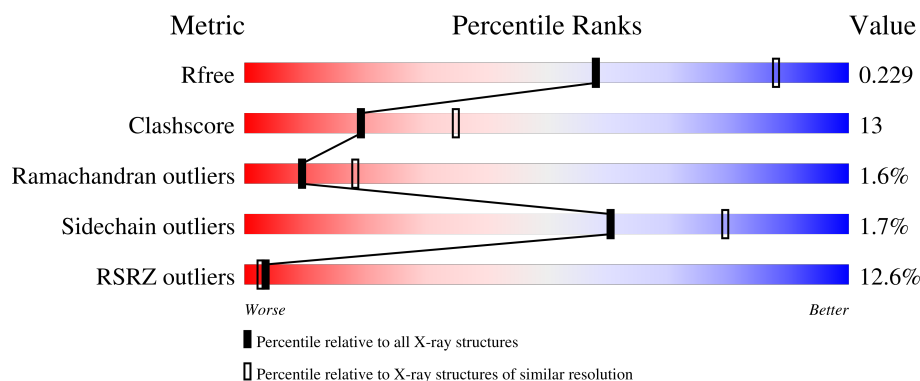
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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}	130704	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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	280	<div> <div>9%</div> <div>59%</div> <div>18%</div> <div>21%</div> </div>
1	B	280	<div> <div>27%</div> <div>44%</div> <div>32%</div> <div>21%</div> </div>
2	C	328	<div> <div>6%</div> <div>81%</div> <div>16%</div> <div>..</div> </div>
2	D	328	<div> <div>5%</div> <div>81%</div> <div>17%</div> <div>..</div> </div>

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
3	RJ6	B	609	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9527 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	221	Total	C	N	O	S	0	0	0
			1837	1190	297	338	12			
1	B	221	Total	C	N	O	S	0	0	0
			1834	1189	297	336	12			

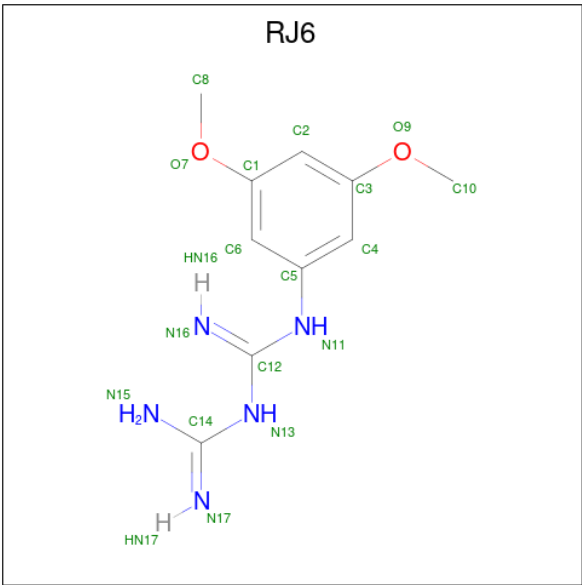
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ILE	ASN	engineered mutation	UNP Q8I1R6
A	59	ARG	CYS	engineered mutation	UNP Q8I1R6
A	108	ASN	SER	engineered mutation	UNP Q8I1R6
A	164	LEU	ILE	engineered mutation	UNP Q8I1R6
B	51	ILE	ASN	engineered mutation	UNP Q8I1R6
B	59	ARG	CYS	engineered mutation	UNP Q8I1R6
B	108	ASN	SER	engineered mutation	UNP Q8I1R6
B	164	LEU	ILE	engineered mutation	UNP Q8I1R6

- Molecule 2 is a protein called Bifunctional dihydrofolate reductase-thymidylate synthase.

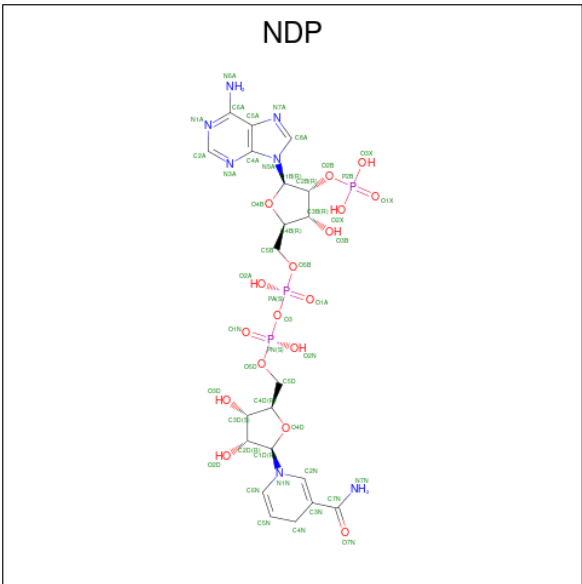
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	326	Total	C	N	O	S	0	0	0
			2713	1747	456	495	15			
2	D	326	Total	C	N	O	S	0	0	0
			2713	1747	456	495	15			

- Molecule 3 is N-(3,5-dimethoxyphenyl)imidodicarbonimidic diamide (three-letter code: RJ6) (formula: C₁₀H₁₅N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	10	5	2		
3	B	1	Total	C	N	O	0	0
			17	10	5	2		

- Molecule 4 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



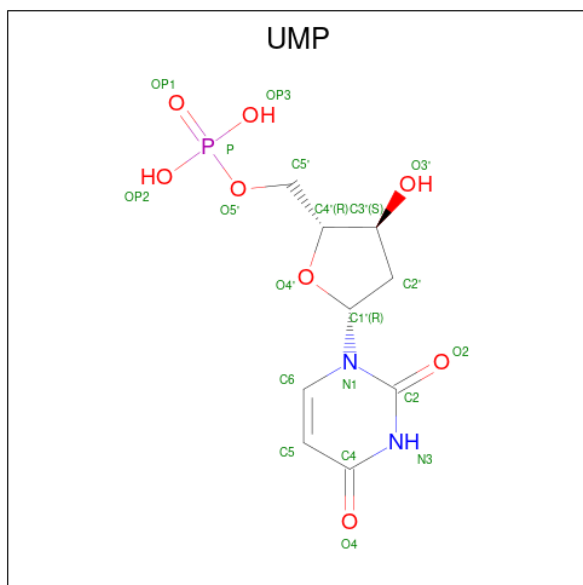
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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

- Molecule 5 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula: $C_9H_{13}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
5	D	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

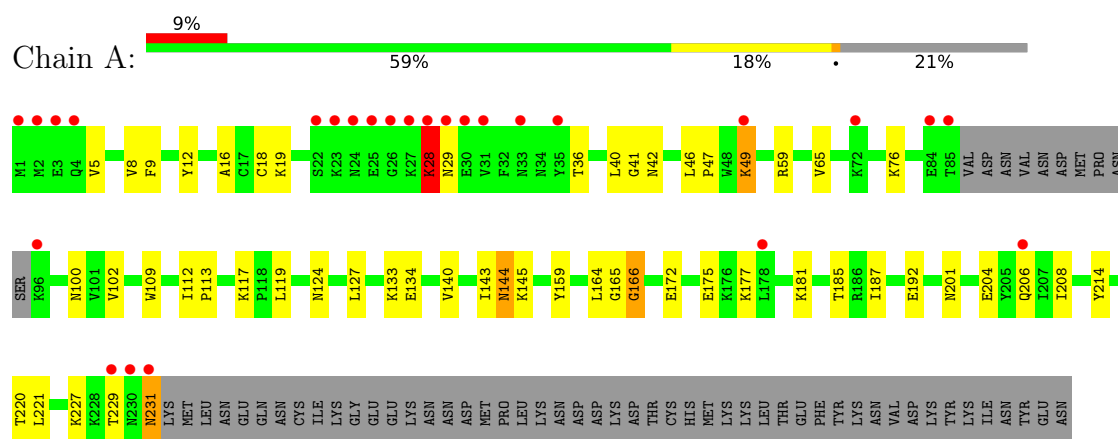
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	40	Total	O	0	0
			40	40		
6	B	7	Total	O	0	0
			7	7		
6	C	93	Total	O	0	0
			93	93		
6	D	120	Total	O	0	0
			120	120		

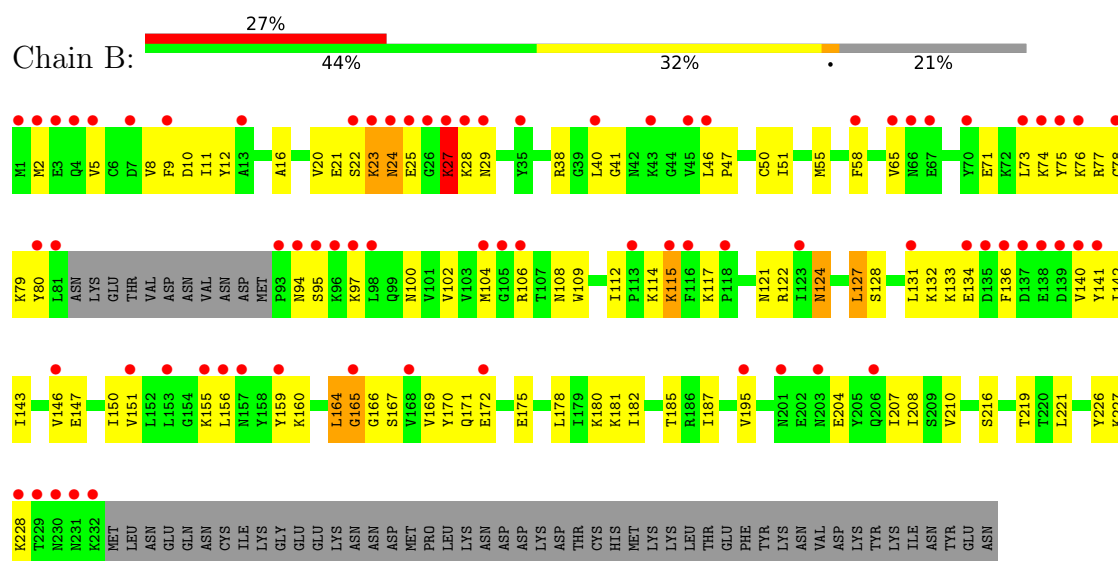
3 Residue-property plots

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.

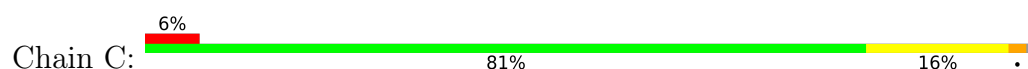
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

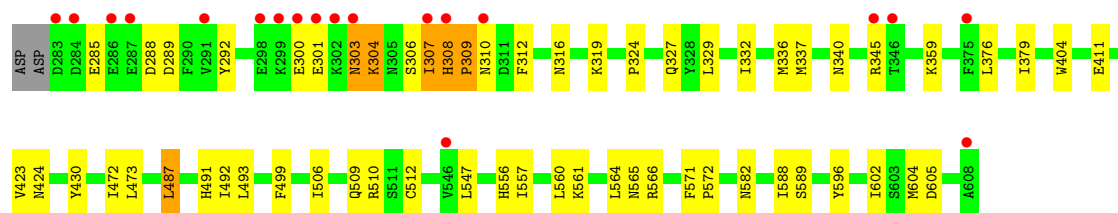


- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

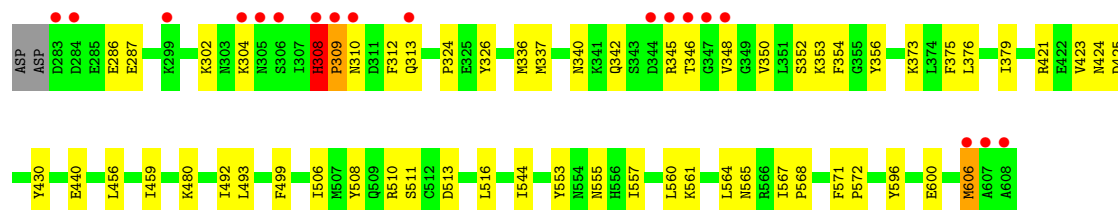
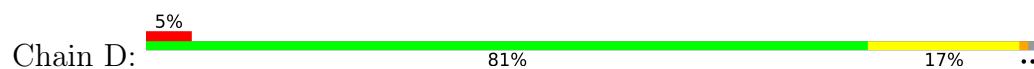


- Molecule 2: Bifunctional dihydrofolate reductase-thymidylate synthase





● Molecule 2: Bifunctional dihydrofolate reductase-thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.52Å 155.40Å 165.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.43 – 2.58 49.43 – 2.58	Depositor EDS
% Data completeness (in resolution range)	97.6 (49.43-2.58) 97.3 (49.43-2.58)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.86 (at 2.58Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.199 , 0.239 0.190 , 0.229	Depositor DCC
R_{free} test set	2322 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.5	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	0.94	EDS
Total number of atoms	9527	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 3.78% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: RJ6, 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	0.39	0/1871	0.66	3/2515 (0.1%)
1	B	0.35	0/1869	0.62	1/2512 (0.0%)
2	C	0.38	0/2784	0.64	0/3766
2	D	0.38	0/2784	0.65	1/3766 (0.0%)
All	All	0.38	0/9308	0.64	5/12559 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	166	GLY	N-CA-C	-8.11	92.82	113.10
1	B	27	LYS	N-CA-C	6.12	127.52	111.00
1	A	165	GLY	N-CA-C	5.59	127.07	113.10
1	A	28	LYS	N-CA-C	5.54	125.96	111.00
2	D	308	HIS	N-CA-C	5.02	124.57	111.00

There are no chirality outliers.

There are no planarity outliers.

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	A	1837	0	1873	46	0
1	B	1834	0	1873	97	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	2713	0	2638	52	0
2	D	2713	0	2638	49	0
3	A	17	0	13	6	0
3	B	17	0	13	3	0
4	A	48	0	26	7	0
4	B	48	0	26	6	0
5	C	20	0	11	0	0
5	D	20	0	11	1	0
6	A	40	0	0	0	0
6	B	7	0	0	0	0
6	C	93	0	0	1	0
6	D	120	0	0	4	0
All	All	9527	0	9122	237	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 13.

All (237) 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:HD2	1:B:114:LYS:H	1.09	1.12
1:B:133:LYS:H	1:B:133:LYS:HD2	1.36	0.90
2:D:376:LEU:HD22	2:D:379:ILE:HD11	1.56	0.86
2:C:308:HIS:O	2:C:310:ASN:N	2.08	0.86
2:C:332:ILE:HD13	2:C:560:LEU:HD22	1.58	0.85
1:B:12:TYR:HE2	1:B:160:LYS:HD3	1.44	0.80
2:D:309:PRO:HG3	2:D:337:MET:HE1	1.62	0.79
1:A:28:LYS:HD2	1:A:29:ASN:HD22	1.45	0.78
2:C:376:LEU:HD22	2:C:379:ILE:HD11	1.65	0.78
1:B:114:LYS:H	1:B:114:LYS:CD	1.91	0.77
1:B:8:VAL:HA	1:B:76:LYS:HD3	1.65	0.77
1:B:5:VAL:HG11	1:B:150:ILE:HD12	1.67	0.77
1:B:104:MET:HA	1:B:165:GLY:HA2	1.68	0.76
2:C:306:SER:C	2:C:308:HIS:H	1.88	0.75
1:A:164:LEU:HD13	3:A:609:RJ6:H8A	1.69	0.75
2:D:308:HIS:O	2:D:310:ASN:N	2.20	0.74
2:C:306:SER:O	2:C:308:HIS:N	2.19	0.74
2:D:336:MET:HE2	2:D:557:ILE:HG23	1.70	0.74
1:B:182:ILE:HB	1:B:226:TYR:HB2	1.70	0.73
1:B:112:ILE:HB	1:B:117:LYS:HD3	1.71	0.72
1:B:124:ASN:N	1:B:124:ASN:HD22	1.85	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:LYS:HD2	1:B:114:LYS:N	1.95	0.71
1:A:28:LYS:HD2	1:A:29:ASN:ND2	2.07	0.70
1:B:22:SER:O	1:B:23:LYS:HB2	1.91	0.70
3:A:609:RJ6:HN15	3:A:609:RJ6:HN11	1.41	0.69
1:A:19:LYS:HG2	1:A:36:THR:HG22	1.75	0.69
1:A:8:VAL:HA	1:A:76:LYS:HD3	1.74	0.68
2:D:312:PHE:HA	2:D:565:ASN:HD21	1.59	0.67
1:B:127:LEU:HD23	1:B:143:ILE:HG13	1.75	0.67
1:A:41:GLY:HA2	1:A:47:PRO:HD3	1.77	0.67
3:A:609:RJ6:H10	4:A:610:NDP:O2D	1.97	0.65
1:B:106:ARG:HG3	1:B:131:LEU:HD11	1.77	0.65
1:B:46:LEU:HG	3:B:609:RJ6:H10A	1.77	0.65
1:A:124:ASN:HB2	1:A:140:VAL:HG12	1.78	0.64
1:B:171:GLN:O	1:B:175:GLU:HG3	1.98	0.63
2:C:307:ILE:HG23	2:C:561:LYS:HE2	1.80	0.63
1:A:28:LYS:CD	1:A:29:ASN:HD22	2.12	0.63
1:A:166:GLY:HA3	4:A:610:NDP:PA	2.38	0.63
1:B:133:LYS:H	1:B:133:LYS:CD	2.11	0.63
2:C:303:ASN:C	2:C:303:ASN:HD22	2.02	0.63
1:B:25:GLU:C	1:B:27:LYS:H	2.01	0.63
1:B:136:PHE:CD2	1:B:142:ILE:HD11	2.34	0.63
2:D:376:LEU:HD22	2:D:379:ILE:CD1	2.26	0.62
1:B:167:SER:HB3	4:B:610:NDP:O2N	2.00	0.62
2:D:310:ASN:O	2:D:313:GLN:HG3	1.98	0.62
2:D:308:HIS:N	2:D:309:PRO:HD2	2.15	0.62
1:B:208:ILE:HD13	1:B:227:LYS:HD2	1.82	0.62
2:C:512:CYS:SG	2:C:547:LEU:HD22	2.40	0.61
2:D:480:LYS:HE2	6:D:1167:HOH:O	2.01	0.61
2:C:336:MET:HE2	2:C:557:ILE:HG23	1.81	0.61
1:B:151:VAL:HG12	1:B:155:LYS:HE2	1.83	0.61
2:D:423:VAL:O	2:D:424:ASN:HB2	2.00	0.60
1:A:46:LEU:HG	3:A:609:RJ6:H10A	1.82	0.60
2:C:303:ASN:O	2:C:304:LYS:HB2	2.00	0.60
2:D:309:PRO:HA	2:D:312:PHE:CD2	2.37	0.59
1:A:201:ASN:HB3	1:A:204:GLU:HG3	1.84	0.59
1:B:21:GLU:C	1:B:23:LYS:H	2.04	0.59
2:D:421:ARG:HH11	2:D:421:ARG:HG2	1.68	0.59
2:C:376:LEU:HD22	2:C:379:ILE:CD1	2.32	0.59
2:D:312:PHE:CE1	2:D:561:LYS:HG2	2.37	0.58
2:D:324:PRO:HB2	2:D:571:PHE:HE2	1.68	0.58
1:A:127:LEU:HD23	1:A:143:ILE:HG13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:493:LEU:C	2:C:493:LEU:HD12	2.23	0.58
1:B:133:LYS:HD2	1:B:133:LYS:N	2.15	0.58
2:C:319:LYS:HG2	2:D:286:GLU:HG2	1.84	0.58
1:B:78:CYS:C	1:B:80:TYR:H	2.06	0.57
1:B:210:VAL:HG21	2:D:326:TYR:HE2	1.69	0.57
2:C:306:SER:O	2:C:309:PRO:HD2	2.03	0.57
2:C:491:HIS:HD2	2:C:509:GLN:HG3	1.69	0.57
2:C:301:GLU:OE1	2:C:301:GLU:HA	2.05	0.57
1:B:58:PHE:HZ	1:B:164:LEU:HD13	1.69	0.57
1:B:12:TYR:CE2	1:B:160:LYS:HD3	2.34	0.57
2:D:506:ILE:HG12	2:D:544:ILE:HB	1.86	0.57
1:A:144:ASN:ND2	1:A:145:LYS:HG3	2.21	0.55
1:B:131:LEU:HB3	1:B:136:PHE:HE2	1.69	0.55
2:C:404:TRP:CZ3	2:C:487:LEU:HD21	2.41	0.55
1:B:65:VAL:HG13	1:B:159:TYR:HB2	1.88	0.55
2:C:300:GLU:HA	2:C:303:ASN:HB2	1.89	0.55
1:A:102:VAL:HB	1:A:164:LEU:HD11	1.88	0.55
2:C:582:ASN:HB3	6:C:1037:HOH:O	2.06	0.55
2:C:492:ILE:HD11	2:C:510:ARG:HD3	1.88	0.54
2:C:306:SER:C	2:C:308:HIS:N	2.59	0.54
1:A:49:LYS:H	1:A:49:LYS:HD3	1.71	0.54
1:A:177:LYS:NZ	1:A:204:GLU:OE1	2.41	0.54
1:B:95:SER:C	1:B:97:LYS:H	2.11	0.54
2:D:572:PRO:HB3	2:D:596:TYR:HA	1.88	0.54
1:A:201:ASN:CG	1:A:204:GLU:HG3	2.28	0.53
2:D:304:LYS:HB3	6:D:1189:HOH:O	2.07	0.53
1:B:166:GLY:H	1:B:169:VAL:HB	1.73	0.53
2:C:312:PHE:HA	2:C:565:ASN:HD21	1.74	0.53
1:B:102:VAL:HG11	1:B:122:ARG:HD2	1.91	0.53
2:D:302:LYS:HB2	6:D:1182:HOH:O	2.08	0.53
1:A:164:LEU:CD1	3:A:609:RJ6:H8A	2.39	0.53
1:A:16:ALA:HA	1:A:185:THR:HB	1.91	0.53
1:A:112:ILE:HB	1:A:117:LYS:HD3	1.90	0.52
1:B:132:LYS:HD2	1:B:134:GLU:CD	2.30	0.52
1:B:146:VAL:HG22	1:B:172:GLU:OE2	2.08	0.52
1:B:171:GLN:HE21	1:B:175:GLU:CD	2.13	0.52
1:B:169:VAL:HG23	4:B:610:NDP:O1A	2.10	0.52
1:B:95:SER:C	1:B:97:LYS:N	2.62	0.52
2:C:308:HIS:N	2:C:309:PRO:HD2	2.24	0.51
1:A:214:TYR:O	1:A:220:THR:HA	2.10	0.51
1:B:164:LEU:HD12	3:B:609:RJ6:H8A	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:ILE:HD13	1:B:187:ILE:HD12	1.93	0.51
2:C:309:PRO:HG3	2:C:337:MET:CE	2.41	0.51
1:B:124:ASN:N	1:B:124:ASN:ND2	2.57	0.50
1:B:216:SER:O	1:B:219:THR:HG22	2.12	0.50
2:C:566:ARG:NH1	2:C:602:ILE:HD11	2.27	0.50
1:B:171:GLN:HG3	1:B:175:GLU:OE2	2.12	0.50
2:D:302:LYS:HZ1	2:D:340:ASN:HA	1.77	0.50
1:A:100:ASN:OD1	1:A:159:TYR:HB3	2.11	0.50
1:B:71:GLU:OE2	1:B:74:LYS:HD3	2.11	0.50
2:D:373:LYS:HE2	2:D:375:PHE:CE1	2.46	0.50
1:A:172:GLU:HA	1:A:175:GLU:HG2	1.93	0.50
1:A:59:ARG:HG2	1:A:59:ARG:HH11	1.77	0.50
1:B:204:GLU:O	1:B:228:LYS:HD2	2.11	0.50
2:C:572:PRO:HB3	2:C:596:TYR:HA	1.93	0.49
2:D:302:LYS:NZ	2:D:340:ASN:HA	2.26	0.49
1:B:109:TRP:CE2	1:B:117:LYS:HD2	2.46	0.49
2:C:329:LEU:HD22	2:C:564:LEU:HD12	1.95	0.49
1:B:8:VAL:HG13	1:B:76:LYS:HG2	1.94	0.48
2:C:345:ARG:HH11	2:C:345:ARG:HG2	1.79	0.48
1:A:49:LYS:HD3	1:A:49:LYS:N	2.28	0.48
2:D:421:ARG:HD2	2:D:425:ASP:CG	2.34	0.48
2:C:506:ILE:HG13	2:D:354:PHE:CE2	2.49	0.48
1:A:119:LEU:HD11	3:A:609:RJ6:C8	2.44	0.48
2:D:309:PRO:HG3	2:D:337:MET:CE	2.38	0.48
2:D:492:ILE:HD11	2:D:510:ARG:HD3	1.96	0.48
1:B:136:PHE:HD2	1:B:142:ILE:HD11	1.78	0.47
1:B:127:LEU:HG	1:B:143:ILE:HD11	1.95	0.47
1:A:201:ASN:CB	1:A:204:GLU:HG3	2.43	0.47
2:D:493:LEU:HD12	2:D:493:LEU:C	2.35	0.47
1:B:78:CYS:C	1:B:80:TYR:N	2.68	0.47
2:C:404:TRP:HZ3	2:C:487:LEU:HD21	1.80	0.47
2:D:511:SER:OG	5:D:611:UMP:H3'	2.15	0.47
1:B:40:LEU:O	4:B:610:NDP:H2N	2.15	0.47
1:B:122:ARG:O	1:B:124:ASN:ND2	2.48	0.47
1:B:207:ILE:HB	2:D:567:ILE:HD13	1.96	0.47
1:B:11:ILE:HB	1:B:178:LEU:O	2.16	0.46
2:C:423:VAL:O	2:C:424:ASN:HB2	2.15	0.46
2:C:324:PRO:HB2	2:C:571:PHE:HE2	1.81	0.46
2:D:513:ASP:OD2	2:D:516:LEU:HB2	2.16	0.46
1:B:75:TYR:CE1	1:B:79:LYS:HD2	2.50	0.46
1:B:102:VAL:HG23	1:B:102:VAL:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:307:ILE:HG22	2:C:307:ILE:O	2.16	0.46
2:C:309:PRO:HA	2:C:312:PHE:CD2	2.50	0.46
1:B:73:LEU:HD13	1:B:77:ARG:NH2	2.31	0.46
2:D:342:GLN:NE2	2:D:352:SER:OG	2.48	0.46
1:B:10:ASP:OD2	1:B:73:LEU:HD22	2.16	0.46
1:B:21:GLU:C	1:B:23:LYS:N	2.69	0.45
1:A:144:ASN:ND2	1:A:144:ASN:H	2.14	0.45
1:B:108:ASN:HB2	4:B:610:NDP:O2A	2.16	0.45
1:B:102:VAL:HG23	1:B:124:ASN:HA	1.97	0.45
2:D:350:VAL:HG12	2:D:553:TYR:CD1	2.50	0.45
1:B:41:GLY:N	1:B:195:VAL:HG23	2.30	0.45
2:C:499:PHE:CE1	2:D:340:ASN:HB3	2.52	0.45
1:B:165:GLY:HA3	1:B:169:VAL:HB	1.97	0.45
2:C:487:LEU:N	2:C:487:LEU:HD23	2.31	0.45
1:B:28:LYS:CG	1:B:29:ASN:H	2.30	0.45
1:B:95:SER:O	1:B:97:LYS:N	2.49	0.45
1:B:77:ARG:O	1:B:80:TYR:HB3	2.16	0.45
1:B:147:GLU:OE1	1:B:147:GLU:N	2.49	0.45
2:C:289:ASP:HA	2:C:292:TYR:CD2	2.52	0.45
2:C:312:PHE:HB2	2:C:316:ASN:ND2	2.32	0.45
1:A:65:VAL:HA	1:A:159:TYR:CD2	2.52	0.44
1:B:5:VAL:HG13	1:B:9:PHE:CD2	2.52	0.44
1:B:16:ALA:HA	1:B:185:THR:HB	1.99	0.44
1:A:206:GLN:HE21	1:A:229:THR:HG21	1.83	0.44
2:C:303:ASN:O	2:C:304:LYS:CB	2.65	0.44
2:C:307:ILE:CG2	2:C:561:LYS:HE2	2.47	0.44
2:C:340:ASN:HB3	2:D:499:PHE:CE1	2.52	0.44
1:B:41:GLY:H	1:B:195:VAL:HG23	1.83	0.44
2:C:509:GLN:HB3	2:C:512:CYS:SG	2.58	0.44
2:D:309:PRO:HA	2:D:312:PHE:HD2	1.80	0.44
1:B:25:GLU:C	1:B:27:LYS:N	2.70	0.44
1:B:180:LYS:HE2	2:C:285:GLU:OE1	2.17	0.44
1:B:121:ASN:N	1:B:121:ASN:ND2	2.64	0.44
1:B:41:GLY:HA2	1:B:47:PRO:HD3	2.00	0.44
1:A:172:GLU:OE2	4:A:610:NDP:N7A	2.51	0.43
1:B:127:LEU:HA	1:B:143:ILE:HG13	2.00	0.43
2:D:312:PHE:HE1	2:D:561:LYS:HG2	1.80	0.43
1:A:42:ASN:HB2	1:A:192:GLU:O	2.18	0.43
1:B:100:ASN:OD1	1:B:159:TYR:HB3	2.18	0.43
1:B:121:ASN:N	1:B:121:ASN:HD22	2.15	0.43
1:A:127:LEU:O	4:A:610:NDP:H1B	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:493:LEU:CD2	2:D:492:ILE:HG21	2.48	0.43
2:D:567:ILE:HA	2:D:568:PRO:HD3	1.88	0.43
1:B:23:LYS:O	1:B:24:ASN:ND2	2.51	0.43
1:B:210:VAL:HG23	1:B:210:VAL:O	2.19	0.43
2:D:353:LYS:HG3	2:D:356:TYR:OH	2.18	0.43
2:D:421:ARG:HG2	2:D:421:ARG:NH1	2.31	0.43
2:D:600:GLU:HG3	6:D:1084:HOH:O	2.17	0.43
1:A:102:VAL:HB	1:A:164:LEU:CD1	2.49	0.43
2:C:411:GLU:H	2:C:411:GLU:CD	2.21	0.43
2:D:508:TYR:CD1	2:D:508:TYR:C	2.92	0.42
1:A:133:LYS:HG3	1:A:134:GLU:N	2.33	0.42
1:A:166:GLY:HA3	4:A:610:NDP:O1A	2.19	0.42
1:B:164:LEU:CD1	3:B:609:RJ6:H8A	2.50	0.42
2:C:556:HIS:HA	2:C:604:MET:O	2.20	0.42
1:A:231:ASN:HD22	1:A:231:ASN:HA	1.53	0.42
1:B:12:TYR:CD1	1:B:181:LYS:HB2	2.55	0.42
1:B:115:LYS:H	1:B:115:LYS:HG2	1.62	0.42
2:C:492:ILE:HG21	2:D:493:LEU:CD2	2.49	0.42
2:D:346:THR:OG1	2:D:348:VAL:HG23	2.19	0.42
1:B:23:LYS:HD2	1:B:23:LYS:HA	1.90	0.42
1:B:181:LYS:HE3	1:B:227:LYS:NZ	2.35	0.42
1:B:141:TYR:CE2	1:B:156:LEU:HD11	2.54	0.42
1:A:40:LEU:O	4:A:610:NDP:H2N	2.19	0.42
2:C:327:GLN:NE2	2:C:359:LYS:O	2.47	0.42
2:D:310:ASN:O	2:D:313:GLN:NE2	2.46	0.42
1:B:127:LEU:HD22	4:B:610:NDP:C2A	2.49	0.42
1:A:18:CYS:HA	1:A:187:ILE:HB	2.02	0.42
1:A:112:ILE:HA	1:A:113:PRO:HD3	1.94	0.42
1:B:27:LYS:O	1:B:28:LYS:HB2	2.20	0.42
1:A:208:ILE:HD13	1:A:227:LYS:HB2	2.01	0.42
1:B:50:CYS:SG	1:B:55:MET:CE	3.08	0.41
1:A:109:TRP:CE2	1:A:117:LYS:HD2	2.56	0.41
1:A:166:GLY:HA3	4:A:610:NDP:O2A	2.20	0.41
1:B:20:VAL:CG2	1:B:38:ARG:NH2	2.83	0.41
1:B:106:ARG:HG2	1:B:106:ARG:HH11	1.85	0.41
1:B:221:LEU:HD23	1:B:221:LEU:N	2.34	0.41
2:D:336:MET:HE3	2:D:560:LEU:HB2	2.02	0.41
1:A:12:TYR:HD1	1:A:181:LYS:HB2	1.85	0.41
2:C:308:HIS:N	2:C:309:PRO:CD	2.84	0.41
1:A:5:VAL:HG13	1:A:9:PHE:HD2	1.86	0.41
1:B:94:ASN:O	1:B:95:SER:OG	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:472:ILE:C	2:C:473:LEU:HD12	2.41	0.41
1:B:109:TRP:CZ2	1:B:117:LYS:HD2	2.56	0.41
1:B:171:GLN:HE21	1:B:175:GLU:CG	2.35	0.40
1:A:221:LEU:HD23	1:A:221:LEU:N	2.36	0.40
1:B:170:TYR:OH	4:B:610:NDP:H41N	2.20	0.40
2:C:309:PRO:HG3	2:C:337:MET:HE2	2.02	0.40
1:B:50:CYS:SG	1:B:55:MET:HE1	2.61	0.40
2:C:588:ILE:HG23	2:C:589:SER:N	2.36	0.40
2:D:336:MET:CE	2:D:557:ILE:HG23	2.47	0.40
1:B:106:ARG:HD3	1:B:128:SER:OG	2.21	0.40
2:D:456:LEU:O	2:D:459:ILE:HG13	2.22	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	217/280 (78%)	200 (92%)	16 (7%)	1 (0%)	29	50
1	B	217/280 (78%)	184 (85%)	27 (12%)	6 (3%)	5	7
2	C	324/328 (99%)	301 (93%)	18 (6%)	5 (2%)	10	20
2	D	324/328 (99%)	301 (93%)	18 (6%)	5 (2%)	10	20
All	All	1082/1216 (89%)	986 (91%)	79 (7%)	17 (2%)	9	18

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	B	24	ASN
1	B	27	LYS
2	C	304	LYS

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Mol	Chain	Res	Type
2	C	307	ILE
2	C	308	HIS
2	C	309	PRO
2	D	308	HIS
2	D	309	PRO
2	D	345	ARG
1	B	23	LYS
1	B	115	LYS
1	B	165	GLY
2	D	606	MET
2	C	430	TYR
2	D	430	TYR
1	B	140	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	210/268 (78%)	206 (98%)	4 (2%)	57	77
1	B	210/268 (78%)	206 (98%)	4 (2%)	57	77
2	C	300/302 (99%)	296 (99%)	4 (1%)	69	85
2	D	300/302 (99%)	295 (98%)	5 (2%)	60	79
All	All	1020/1140 (90%)	1003 (98%)	17 (2%)	60	79

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	49	LYS
1	A	144	ASN
1	A	231	ASN
1	B	2	MET
1	B	124	ASN
1	B	127	LEU
1	B	164	LEU

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Mol	Chain	Res	Type
2	C	288	ASP
2	C	303	ASN
2	C	487	LEU
2	C	605	ASP
2	D	287	GLU
2	D	440	GLU
2	D	555	ASN
2	D	564	LEU
2	D	606	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	ASN
1	A	99	GLN
1	A	144	ASN
1	A	206	GLN
1	A	231	ASN
1	B	24	ASN
1	B	99	GLN
1	B	121	ASN
1	B	171	GLN
2	C	303	ASN
2	C	316	ASN
2	C	394	ASN
2	C	415	ASN
2	C	424	ASN
2	C	554	ASN
2	C	555	ASN
2	D	316	ASN
2	D	342	GLN
2	D	394	ASN
2	D	407	ASN
2	D	415	ASN
2	D	424	ASN

5.3.3 RNA ⓘ

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 monosaccharides 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$
3	RJ6	B	609	-	16,17,17	1.10	2 (12%)	21,22,22	3.13	7 (33%)
5	UMP	C	611	-	18,21,21	2.18	5 (27%)	21,31,31	1.81	6 (28%)
4	NDP	A	610	-	45,52,52	1.73	9 (20%)	53,80,80	1.52	10 (18%)
3	RJ6	A	609	-	16,17,17	1.17	3 (18%)	21,22,22	2.69	6 (28%)
5	UMP	D	611	-	18,21,21	2.14	6 (33%)	21,31,31	1.85	6 (28%)
4	NDP	B	610	-	45,52,52	1.68	8 (17%)	53,80,80	1.64	13 (24%)

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	RJ6	B	609	-	-	2/12/12/12	0/1/1/1
5	UMP	C	611	-	-	1/7/22/22	0/2/2/2
4	NDP	A	610	-	-	2/30/77/77	0/5/5/5
3	RJ6	A	609	-	-	3/12/12/12	0/1/1/1
5	UMP	D	611	-	-	2/7/22/22	0/2/2/2
4	NDP	B	610	-	-	5/30/77/77	0/5/5/5

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	611	UMP	C4-N3	5.85	1.43	1.33
5	D	611	UMP	C4-N3	5.84	1.43	1.33
5	C	611	UMP	O4'-C1'	4.47	1.52	1.42
4	A	610	NDP	C4N-C3N	-4.43	1.41	1.49
4	A	610	NDP	C2N-C3N	4.41	1.47	1.34
5	D	611	UMP	O4'-C1'	4.25	1.51	1.42
4	A	610	NDP	C4N-C5N	-4.25	1.37	1.48
4	B	610	NDP	C4N-C3N	-4.20	1.41	1.49
4	B	610	NDP	C4N-C5N	-4.16	1.38	1.48
4	B	610	NDP	C2N-C3N	3.95	1.46	1.34
4	B	610	NDP	C6N-C5N	3.21	1.39	1.33
4	A	610	NDP	C6N-C5N	3.03	1.38	1.33
4	B	610	NDP	C4A-N3A	2.90	1.39	1.35
4	A	610	NDP	P2B-O2B	-2.82	1.54	1.59
3	B	609	RJ6	C5-N11	-2.67	1.36	1.41
5	C	611	UMP	O4'-C4'	2.53	1.50	1.45
4	B	610	NDP	C3B-C2B	-2.47	1.47	1.52
5	D	611	UMP	P-OP3	-2.38	1.45	1.54
5	C	611	UMP	P-OP3	-2.33	1.45	1.54
4	A	610	NDP	C3B-C2B	-2.33	1.47	1.52
3	B	609	RJ6	C14-N13	-2.32	1.34	1.37
5	D	611	UMP	O4'-C4'	2.25	1.50	1.45
4	B	610	NDP	C3B-C4B	-2.25	1.47	1.53
4	A	610	NDP	C4A-N3A	2.23	1.38	1.35
4	B	610	NDP	P2B-O2B	-2.22	1.55	1.59
3	A	609	RJ6	C5-N11	-2.22	1.37	1.41
3	A	609	RJ6	C14-N13	-2.21	1.34	1.37
3	A	609	RJ6	C2-C3	-2.13	1.35	1.38
5	D	611	UMP	C2-N3	2.09	1.42	1.38
4	A	610	NDP	C2D-C1D	2.08	1.60	1.53
4	A	610	NDP	C3B-C4B	-2.05	1.47	1.53
5	D	611	UMP	P-OP2	-2.05	1.46	1.54
5	C	611	UMP	P-OP2	-2.02	1.47	1.54

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	609	RJ6	C8-O7-C1	8.80	136.60	117.51
3	B	609	RJ6	C8-O7-C1	8.01	134.88	117.51
3	B	609	RJ6	C10-O9-C3	7.81	134.46	117.51
3	B	609	RJ6	C14-N13-C12	5.23	133.92	125.21
3	A	609	RJ6	C3-C2-C1	4.72	125.59	118.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	609	RJ6	C3-C2-C1	4.43	125.15	118.48
4	A	610	NDP	C3N-C2N-N1N	-4.42	116.79	123.10
3	A	609	RJ6	C14-N13-C12	4.22	132.24	125.21
4	B	610	NDP	C3N-C2N-N1N	-4.21	117.09	123.10
5	D	611	UMP	C2'-C1'-N1	4.00	123.50	114.27
5	D	611	UMP	O4'-C1'-C2'	-3.78	99.11	106.25
4	B	610	NDP	C1D-N1N-C2N	-3.77	114.83	121.11
4	A	610	NDP	C3B-C2B-C1B	-3.63	96.07	102.89
5	C	611	UMP	C5-C4-N3	-3.59	115.41	123.31
5	C	611	UMP	O4'-C1'-C2'	-3.57	99.50	106.25
5	D	611	UMP	C5-C4-N3	-3.43	115.76	123.31
4	B	610	NDP	O3B-C3B-C4B	3.38	120.81	111.05
5	C	611	UMP	C2'-C1'-N1	3.26	121.78	114.27
4	A	610	NDP	C1D-N1N-C2N	-3.12	115.92	121.11
4	B	610	NDP	O7N-C7N-N7N	-2.97	115.93	122.88
4	B	610	NDP	O3B-C3B-C2B	2.87	119.31	111.17
4	A	610	NDP	O7N-C7N-N7N	-2.84	116.24	122.88
3	B	609	RJ6	C6-C1-C2	-2.79	116.54	120.98
5	D	611	UMP	O4'-C4'-C3'	-2.77	99.20	105.67
3	B	609	RJ6	C5-N11-C12	2.74	134.20	126.57
4	B	610	NDP	C2B-C3B-C4B	2.74	107.94	101.99
3	A	609	RJ6	C4-C3-C2	-2.66	116.74	120.98
5	C	611	UMP	O4'-C4'-C3'	-2.63	99.54	105.67
4	B	610	NDP	C3B-C2B-C1B	-2.62	97.97	102.89
3	B	609	RJ6	C4-C3-C2	-2.61	116.83	120.98
4	A	610	NDP	O3B-C3B-C4B	2.54	118.40	111.05
4	A	610	NDP	O3B-C3B-C2B	2.53	118.34	111.17
5	C	611	UMP	C4'-O4'-C1'	2.45	115.36	109.45
3	A	609	RJ6	C6-C1-C2	-2.44	117.09	120.98
5	D	611	UMP	C4'-O4'-C1'	2.40	115.24	109.45
3	A	609	RJ6	C10-O9-C3	2.35	122.60	117.51
4	B	610	NDP	O4B-C1B-C2B	2.27	110.53	106.59
4	B	610	NDP	N3A-C2A-N1A	-2.27	125.13	128.68
4	A	610	NDP	PN-O3-PA	2.25	140.56	132.83
4	B	610	NDP	O2B-C2B-C3B	2.25	119.82	111.68
4	B	610	NDP	C2D-C3D-C4D	2.16	106.84	102.64
4	B	610	NDP	C3D-C2D-C1D	-2.14	97.36	101.43
4	A	610	NDP	N3A-C2A-N1A	-2.12	125.36	128.68
4	B	610	NDP	O2A-PA-O1A	2.11	122.69	112.24
4	A	610	NDP	O2N-PN-O1N	2.11	122.67	112.24
4	A	610	NDP	O2A-PA-O1A	2.09	122.57	112.24
5	C	611	UMP	C2'-C3'-C4'	2.07	107.07	102.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	611	UMP	O5'-P-OP1	2.02	112.15	106.47

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	611	UMP	C3'-C4'-C5'-O5'
5	D	611	UMP	O4'-C4'-C5'-O5'
4	B	610	NDP	O4D-C1D-N1N-C2N
4	A	610	NDP	O4D-C1D-N1N-C2N
3	B	609	RJ6	C4-C5-N11-C12
3	A	609	RJ6	C4-C5-N11-C12
3	B	609	RJ6	C6-C5-N11-C12
3	A	609	RJ6	C6-C5-N11-C12
3	A	609	RJ6	C2-C3-O9-C10
4	B	610	NDP	C2B-O2B-P2B-O1X
4	B	610	NDP	C2B-O2B-P2B-O2X
4	B	610	NDP	C2B-O2B-P2B-O3X
5	C	611	UMP	O4'-C4'-C5'-O5'
4	A	610	NDP	C2N-C3N-C7N-N7N
4	B	610	NDP	C2N-C3N-C7N-N7N

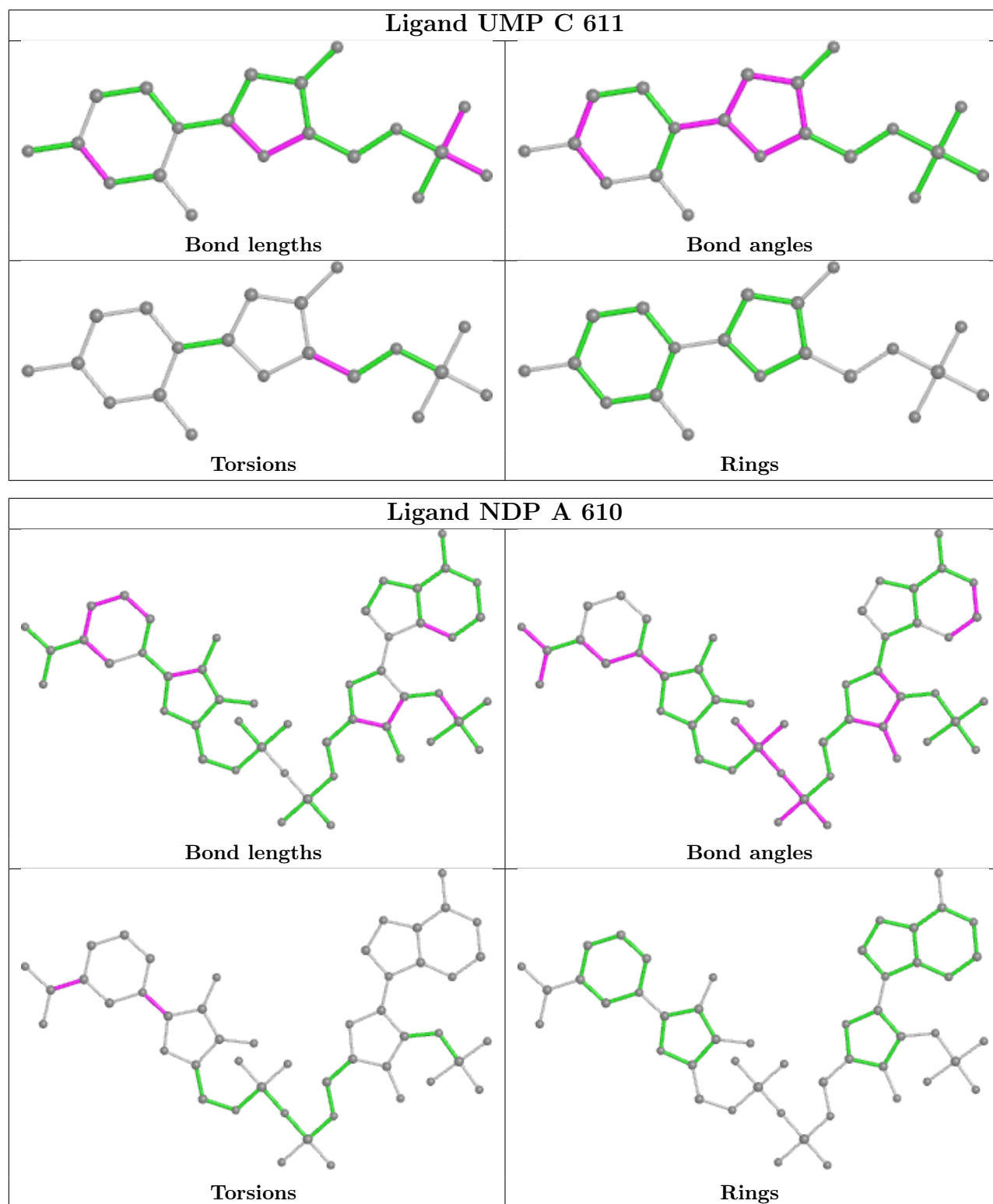
There are no ring outliers.

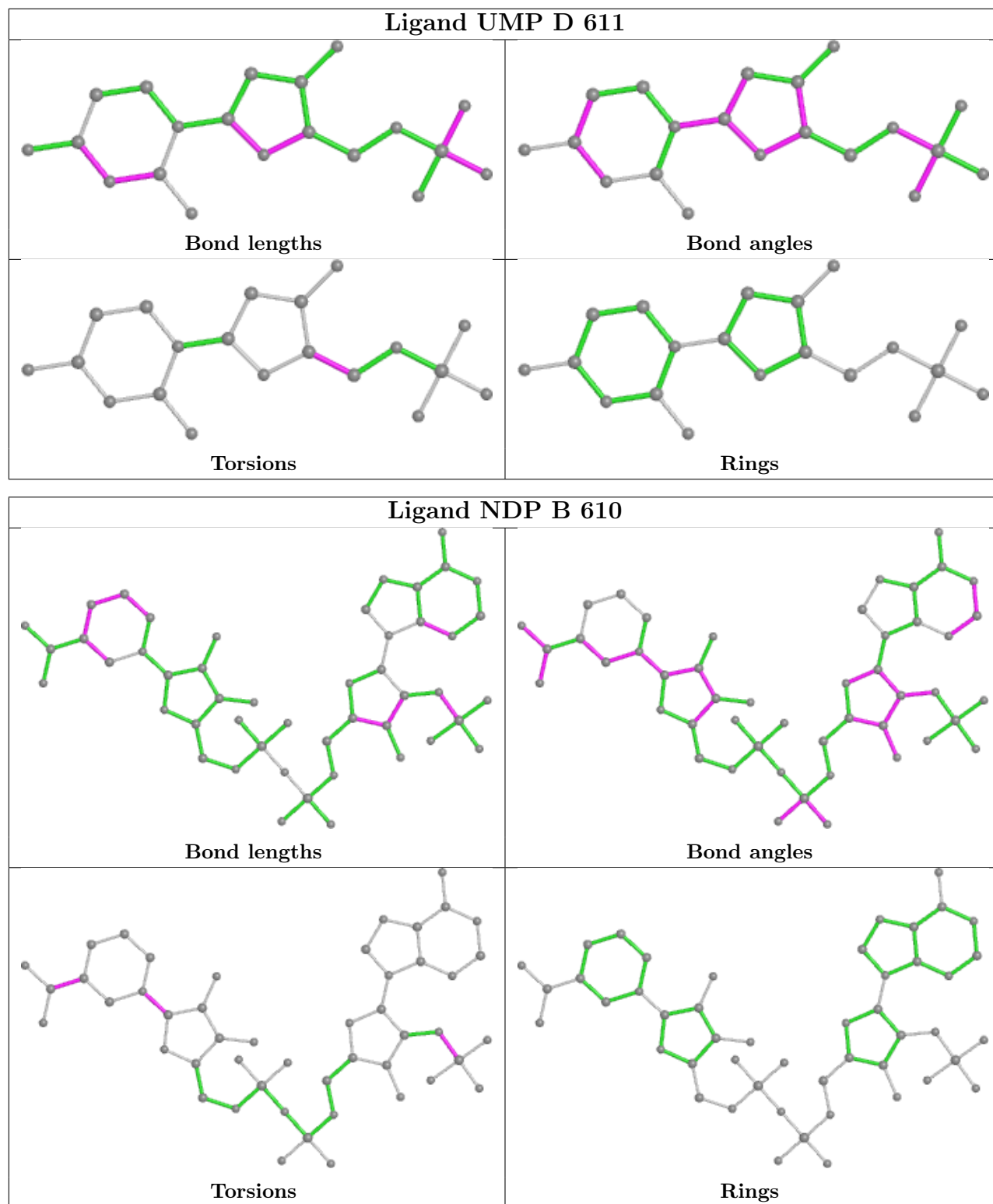
5 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	609	RJ6	3	0
4	A	610	NDP	7	0
3	A	609	RJ6	6	0
5	D	611	UMP	1	0
4	B	610	NDP	6	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 ⓘ

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	221/280 (78%)	0.56	26 (11%) 4 3	22, 41, 86, 90	0
1	B	221/280 (78%)	1.96	75 (33%) 0 0	30, 81, 90, 90	0
2	C	326/328 (99%)	0.29	19 (5%) 23 19	22, 31, 74, 90	0
2	D	326/328 (99%)	0.13	18 (5%) 25 21	19, 28, 73, 90	0
All	All	1094/1216 (89%)	0.64	138 (12%) 3 3	19, 36, 90, 90	0

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	MET	12.3
1	A	1	MET	12.0
1	B	1	MET	11.3
1	A	2	MET	10.2
1	B	95	SER	9.4
1	B	231	ASN	9.1
1	B	3	GLU	8.6
1	B	27	LYS	8.6
1	B	93	PRO	8.2
1	B	94	ASN	7.9
1	B	29	ASN	7.6
1	B	136	PHE	7.2
1	B	232	LYS	6.6
1	B	26	GLY	6.5
2	D	345	ARG	6.3
1	B	9	PHE	6.2
1	B	23	LYS	6.1
1	B	96	LYS	6.1
1	A	85	THR	5.9
1	B	165	GLY	5.7
1	A	31	VAL	5.6

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Mol	Chain	Res	Type	RSRZ
1	B	75	TYR	5.6
1	B	25	GLU	5.6
1	B	70	TYR	5.5
1	B	97	LYS	5.4
2	C	299	LYS	5.4
1	A	231	ASN	5.4
1	B	81	LEU	5.4
1	B	24	ASN	5.4
2	C	301	GLU	5.3
1	B	76	LYS	5.1
1	B	138	GLU	4.9
1	B	157	ASN	4.9
2	C	303	ASN	4.9
2	D	283	ASP	4.8
1	A	29	ASN	4.8
1	A	23	LYS	4.7
1	B	5	VAL	4.7
1	B	116	PHE	4.7
1	A	25	GLU	4.6
2	C	307	ILE	4.5
1	B	28	LYS	4.4
1	A	26	GLY	4.4
1	A	230	ASN	4.4
1	B	159	TYR	4.4
1	B	139	ASP	4.2
2	C	300	GLU	4.2
2	D	305	ASN	4.1
1	B	134	GLU	4.0
1	A	96	LYS	3.9
1	A	24	ASN	3.9
1	B	73	LEU	3.8
1	A	28	LYS	3.8
2	D	607	ALA	3.8
1	B	131	LEU	3.8
1	B	141	TYR	3.7
2	D	608	ALA	3.7
1	B	137	ASP	3.6
2	D	348	VAL	3.6
1	A	27	LYS	3.6
1	A	30	GLU	3.5
1	B	22	SER	3.4
2	D	309	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	66	ASN	3.3
1	B	35	TYR	3.3
2	C	283	ASP	3.3
1	B	118	PRO	3.1
1	B	230	ASN	3.1
2	D	284	ASP	3.1
2	C	302	LYS	3.1
1	A	3	GLU	3.1
1	B	156	LEU	3.1
2	D	299	LYS	3.0
2	C	608	ALA	3.0
1	B	67	GLU	3.0
1	B	4	GLN	3.0
1	A	22	SER	2.9
1	B	45	VAL	2.9
1	B	135	ASP	2.9
2	D	606	MET	2.8
2	D	346	THR	2.8
1	B	151	VAL	2.7
1	B	80	TYR	2.7
1	A	4	GLN	2.7
1	B	140	VAL	2.7
1	A	229	THR	2.7
1	B	7	ASP	2.6
1	B	58	PHE	2.6
2	D	308	HIS	2.5
2	D	310	ASN	2.5
1	B	155	LYS	2.5
2	D	304	LYS	2.5
1	A	84	GLU	2.5
1	B	115	LYS	2.5
1	B	228	LYS	2.5
2	C	310	ASN	2.5
2	C	284	ASP	2.4
1	B	65	VAL	2.4
1	B	105	GLY	2.4
2	D	306	SER	2.4
1	B	74	LYS	2.4
1	B	146	VAL	2.4
1	B	40	LEU	2.4
1	B	104	MET	2.3
1	B	168	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	123	ILE	2.3
1	B	46	LEU	2.3
2	C	298	GLU	2.3
2	C	375	PHE	2.3
1	B	98	LEU	2.3
2	C	308	HIS	2.3
2	D	347	GLY	2.3
1	B	113	PRO	2.2
1	A	33	ASN	2.2
1	B	229	THR	2.2
2	C	546	VAL	2.2
1	A	206	GLN	2.1
1	B	106	ARG	2.1
1	B	172	GLU	2.1
1	A	72	LYS	2.1
2	D	313	GLN	2.1
1	A	35	TYR	2.1
2	C	286	GLU	2.1
2	C	287	GLU	2.1
1	B	203	ASN	2.1
1	B	78	CYS	2.1
1	B	201	ASN	2.1
1	B	13	ALA	2.1
1	B	206	GLN	2.1
2	C	346	THR	2.1
1	A	178	LEU	2.1
2	C	345	ARG	2.1
1	A	49	LYS	2.0
1	B	43	LYS	2.0
1	B	195	VAL	2.0
2	C	291	VAL	2.0
1	B	153	LEU	2.0
2	D	344	ASP	2.0

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

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

6.3 Carbohydrates ⓘ

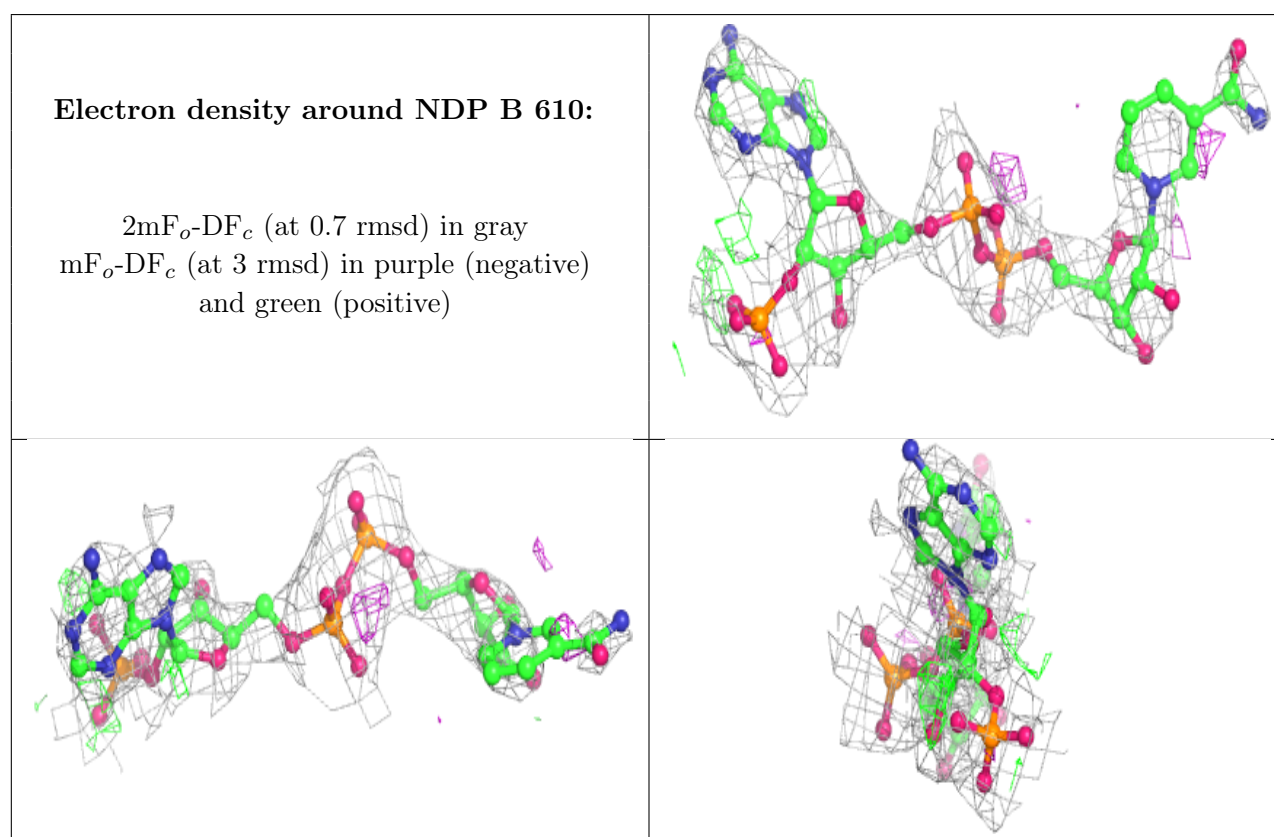
There are no monosaccharides in this entry.

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.

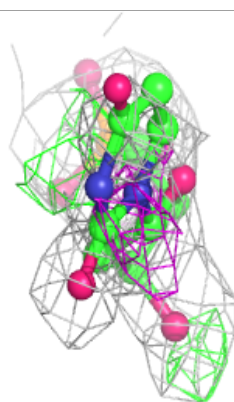
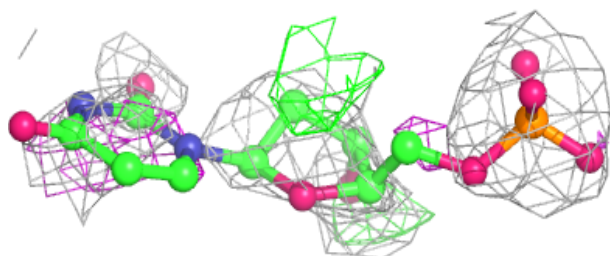
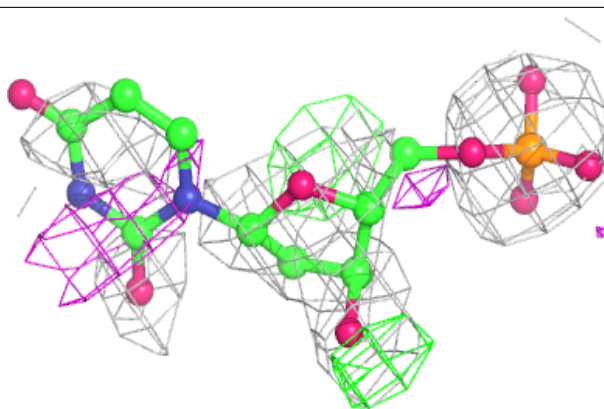
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	RJ6	B	609	17/17	0.67	0.46	85,89,90,90	0
4	NDP	B	610	48/48	0.83	0.28	87,90,90,90	0
5	UMP	D	611	20/20	0.84	0.42	75,86,90,90	0
5	UMP	C	611	20/20	0.87	0.31	76,87,90,90	0
3	RJ6	A	609	17/17	0.88	0.29	37,51,60,62	0
4	NDP	A	610	48/48	0.96	0.19	40,44,59,60	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.

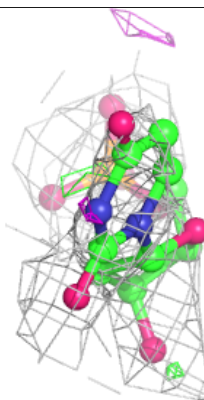
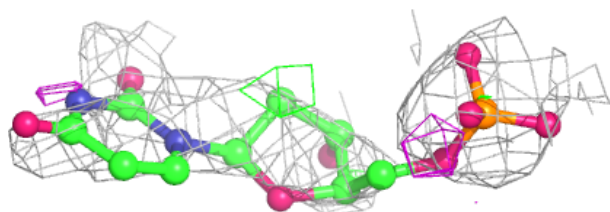
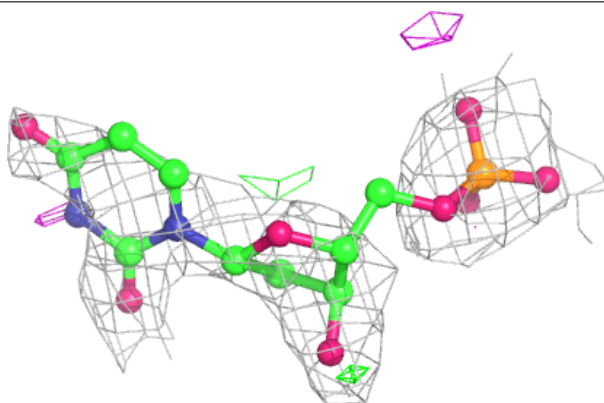


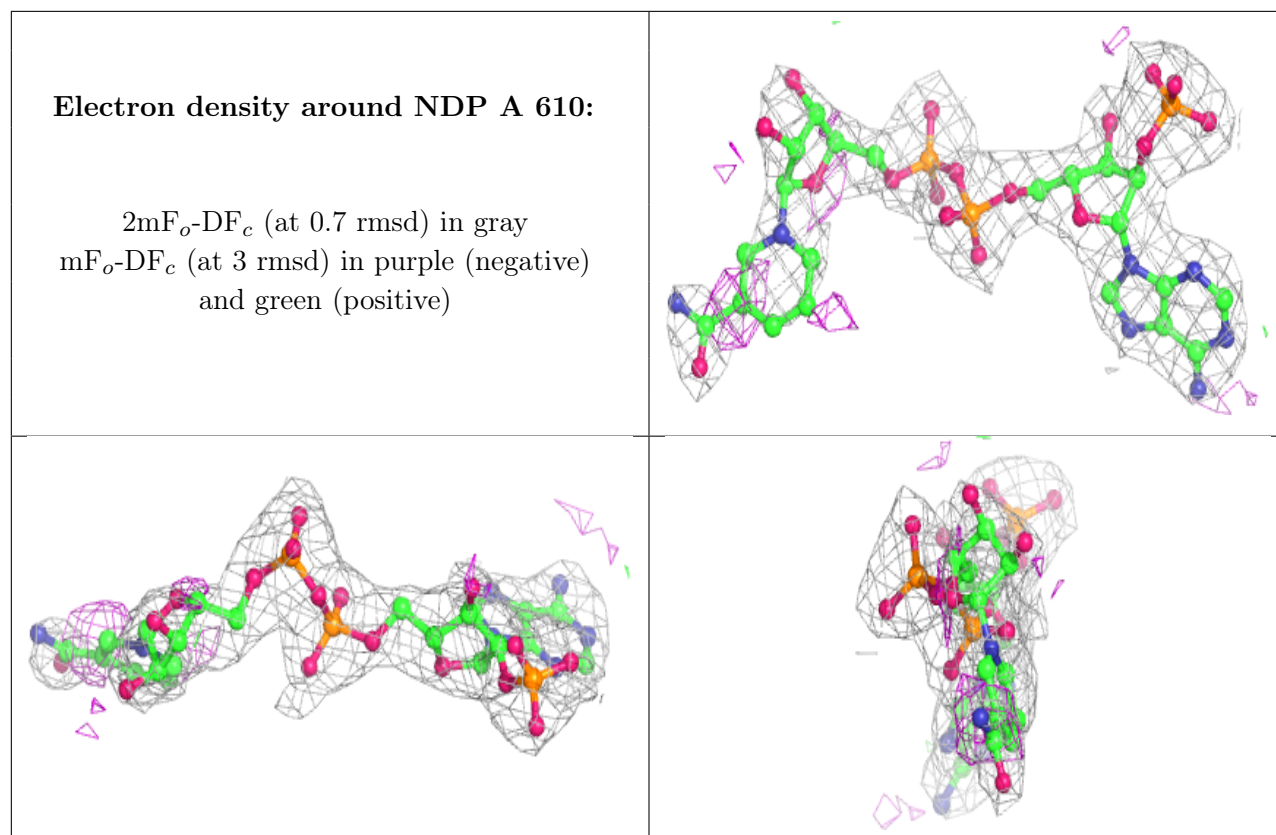
Electron density around UMP D 611:

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

**Electron density around UMP C 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 [i](#)

There are no such residues in this entry.