



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 11:57 AM UTC

PDB ID : 3SEQ / pdb_00003seq
Title : Crystal structure of C176A mutant of glutamine-dependent NAD⁺ synthetase from *M. tuberculosis* in complex with AMPCPP and NaAD⁺
Authors : Chuenchor, W.; Gerratana, B.
Deposited on : 2011-06-10
Resolution : 2.73 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

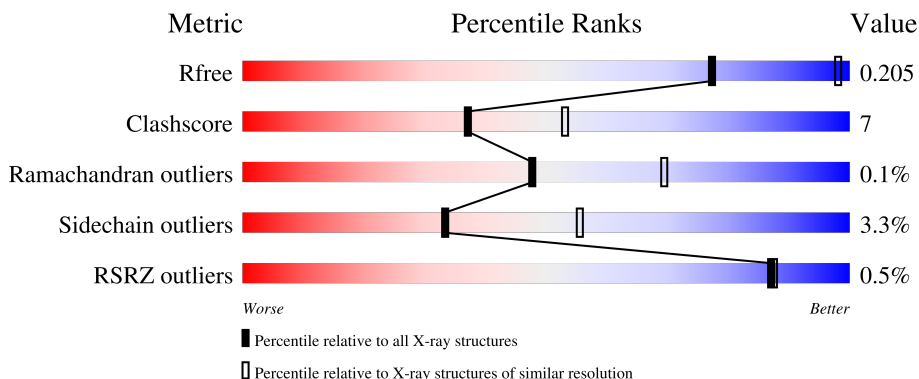
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	680	 82% 14% ..
1	B	680	 81% 14% ..
1	C	680	 79% 14% ..
1	D	680	 80% 14% ..

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 20820 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 Glutamine-dependent NAD(+) synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	661	5102	3234	905	948	15	0	0	0
1	B	658	5063	3215	894	939	15	0	0	0
1	C	650	4992	3171	885	921	15	0	0	0
1	D	650	5002	3174	887	926	15	0	0	0

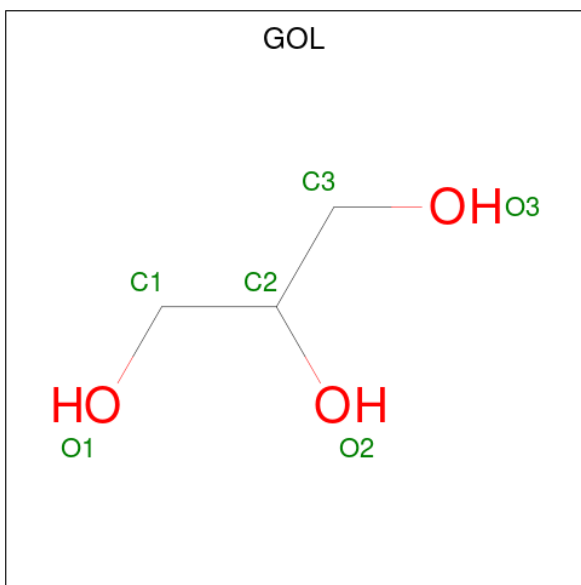
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P0A5L6
A	176	ALA	CYS	engineered mutation	UNP P0A5L6
B	0	SER	-	expression tag	UNP P0A5L6
B	176	ALA	CYS	engineered mutation	UNP P0A5L6
C	0	SER	-	expression tag	UNP P0A5L6
C	176	ALA	CYS	engineered mutation	UNP P0A5L6
D	0	SER	-	expression tag	UNP P0A5L6
D	176	ALA	CYS	engineered mutation	UNP P0A5L6

- Molecule 2 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (CCD ID: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	N	O	P	0	0
			44	21	6	15	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	6	15	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	6	15	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	6	15	2		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

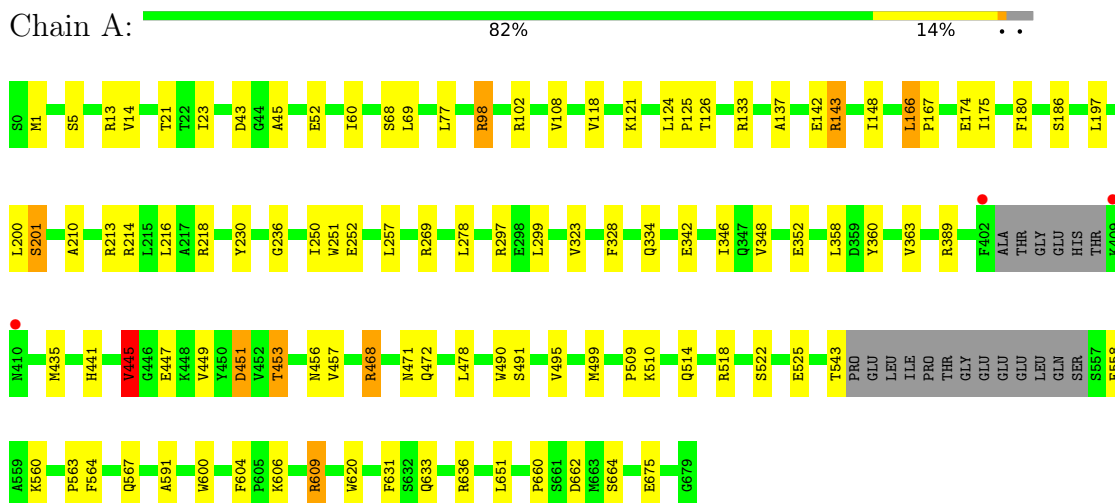
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	96	Total	O	0	0
			96	96		
5	B	92	Total	O	0	0
			92	92		
5	C	73	Total	O	0	0
			73	73		
5	D	88	Total	O	0	0
			88	88		

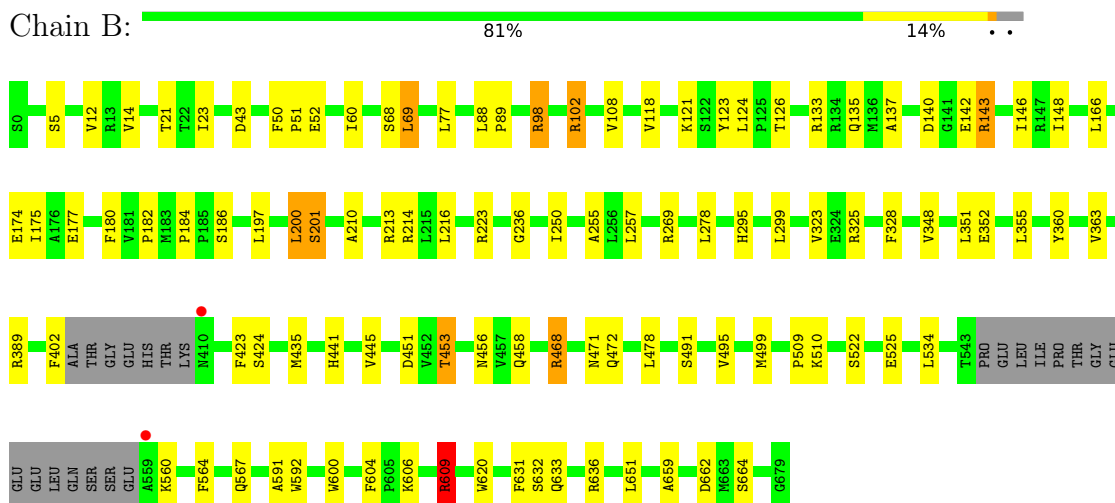
3 Residue-property plots [i](#)

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.

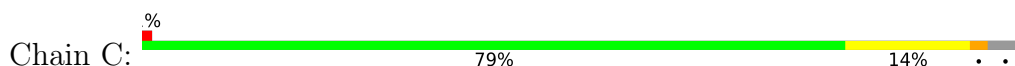
- Molecule 1: Glutamine-dependent NAD(+) synthetase



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4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	178.17Å 178.17Å 214.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.09 – 2.73 40.09 – 2.73	Depositor EDS
% Data completeness (in resolution range)	96.3 (40.09-2.73) 91.5 (40.09-2.73)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.80 (at 2.73Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.163 , 0.212 0.156 , 0.205	Depositor DCC
R_{free} test set	4400 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	37.4	Xtrriage
Anisotropy	1.061	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20820	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.11% 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: APC, DND, GOL

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	0.80	0/5222	1.01	7/7099 (0.1%)
1	B	0.79	1/5183 (0.0%)	1.00	11/7049 (0.2%)
1	C	0.78	1/5108 (0.0%)	0.98	6/6941 (0.1%)
1	D	0.79	0/5118	1.02	7/6955 (0.1%)
All	All	0.79	2/20631 (0.0%)	1.00	31/28044 (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	C	0	1
1	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	25	ASP	CA-C	5.39	1.58	1.52
1	B	255	ALA	CA-CB	-5.26	1.45	1.53

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	631	PHE	N-CA-C	7.71	119.33	111.07
1	B	560	LYS	N-CA-C	-7.51	104.15	113.38
1	A	166	LEU	CA-C-N	7.23	126.94	119.56
1	A	166	LEU	C-N-CA	7.23	126.94	119.56
1	D	453	THR	N-CA-C	-7.21	103.45	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	166	LEU	CA-C-N	7.11	126.81	119.56
1	D	166	LEU	C-N-CA	7.11	126.81	119.56
1	D	609	ARG	CA-C-N	6.68	126.60	119.85
1	D	609	ARG	C-N-CA	6.68	126.60	119.85
1	B	166	LEU	CA-C-N	6.58	126.27	119.56
1	B	166	LEU	C-N-CA	6.58	126.27	119.56
1	B	631	PHE	N-CA-C	6.27	118.11	111.28
1	B	659	ALA	N-CA-C	6.25	113.85	108.22
1	C	631	PHE	N-CA-C	6.20	117.70	111.07
1	B	456	ASN	N-CA-C	5.90	117.80	111.36
1	C	609	ARG	CA-C-N	5.86	125.77	119.85
1	C	609	ARG	C-N-CA	5.86	125.77	119.85
1	C	166	LEU	CA-C-N	5.62	125.30	119.56
1	C	166	LEU	C-N-CA	5.62	125.30	119.56
1	B	184	PRO	CA-C-N	5.59	125.69	119.32
1	B	184	PRO	C-N-CA	5.59	125.69	119.32
1	B	609	ARG	CA-C-N	5.54	125.45	119.85
1	B	609	ARG	C-N-CA	5.54	125.45	119.85
1	D	659	ALA	N-CA-C	5.44	113.12	108.22
1	B	102	ARG	N-CA-C	5.38	116.82	109.18
1	A	456	ASN	N-CA-C	5.26	117.10	111.36
1	A	445	VAL	N-CA-C	-5.22	107.63	112.43
1	A	441	HIS	CA-C-N	5.11	125.40	119.47
1	A	441	HIS	C-N-CA	5.11	125.40	119.47
1	D	631	PHE	N-CA-C	5.09	116.52	111.07
1	C	561	VAL	N-CA-C	5.06	117.05	112.29

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	452	VAL	Peptide
1	D	452	VAL	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5102	0	4976	72	1
1	B	5063	0	4930	72	0
1	C	4992	0	4868	77	0
1	D	5002	0	4878	78	1
2	A	31	0	14	2	0
2	B	31	0	14	2	0
2	C	31	0	14	3	0
2	D	31	0	14	2	0
3	A	44	0	25	4	0
3	B	44	0	25	1	0
3	C	44	0	25	1	0
3	D	44	0	25	2	0
4	B	6	0	8	1	0
4	D	6	0	8	0	0
5	A	96	0	0	6	0
5	B	92	0	0	2	0
5	C	73	0	0	2	0
5	D	88	0	0	4	0
All	All	20820	0	19824	286	1

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 7.

All (286) 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:D:98:ARG:HG2	1:D:98:ARG:HH11	1.29	0.96
1:D:633:GLN:OE1	1:D:636:ARG:NH1	2.04	0.90
1:B:98:ARG:HG2	1:B:98:ARG:HH11	1.37	0.90
1:A:98:ARG:HG2	1:A:98:ARG:HH11	1.35	0.88
1:A:633:GLN:OE1	1:A:636:ARG:NH1	2.06	0.88
1:A:468:ARG:NH2	1:D:495:VAL:O	2.08	0.87
1:B:451:ASP:HB3	1:B:453:THR:H	1.40	0.87
1:C:98:ARG:HH11	1:C:98:ARG:HG2	1.38	0.86
1:C:633:GLN:OE1	1:C:636:ARG:NH1	2.07	0.86
1:B:633:GLN:OE1	1:B:636:ARG:NH1	2.10	0.84
1:B:468:ARG:NH2	1:C:495:VAL:O	2.11	0.83
1:D:143:ARG:HG2	1:D:143:ARG:HH11	1.43	0.83
1:B:143:ARG:HG2	1:B:143:ARG:HH11	1.44	0.83
1:B:495:VAL:O	1:C:468:ARG:NH2	2.13	0.82
2:D:680:APC:H3'	2:D:680:APC:H3A1	1.68	0.76
1:A:606:LYS:HA	1:A:609:ARG:HD3	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:VAL:HG13	1:B:478:LEU:HD13	1.68	0.75
1:B:135:GLN:OE1	4:B:682:GOL:O2	2.03	0.75
1:A:143:ARG:HH11	1:A:143:ARG:HG2	1.52	0.75
1:D:606:LYS:HA	1:D:609:ARG:HD3	1.68	0.74
1:A:495:VAL:O	1:D:468:ARG:NH2	2.21	0.73
1:C:143:ARG:HG2	1:C:143:ARG:HH11	1.53	0.73
1:A:102:ARG:HD3	1:A:137:ALA:HB2	1.71	0.73
1:B:102:ARG:HD3	1:B:137:ALA:HB2	1.70	0.73
1:B:606:LYS:HA	1:B:609:ARG:HD3	1.69	0.73
1:A:363:VAL:HG13	1:A:478:LEU:HD13	1.71	0.72
1:D:452:VAL:N	1:D:454:PHE:HB3	2.04	0.72
1:A:468:ARG:NH1	1:A:471:ASN:OD1	2.24	0.71
1:A:252:GLU:OE2	5:A:725:HOH:O	2.08	0.71
1:A:297:ARG:NH2	1:B:142:GLU:OE2	2.23	0.70
1:C:606:LYS:HA	1:C:609:ARG:HD3	1.72	0.70
1:D:363:VAL:HG13	1:D:478:LEU:HD13	1.74	0.70
1:D:102:ARG:HD3	1:D:137:ALA:HB2	1.73	0.70
1:D:525:GLU:HB2	5:D:728:HOH:O	1.90	0.69
1:B:468:ARG:NH1	1:B:471:ASN:OD1	2.25	0.69
1:C:363:VAL:HG13	1:C:478:LEU:HD13	1.73	0.69
1:B:525:GLU:HA	1:B:525:GLU:OE1	1.94	0.67
1:C:468:ARG:NH1	1:C:471:ASN:OD1	2.26	0.66
1:D:525:GLU:HA	1:D:525:GLU:OE1	1.96	0.65
1:A:451:ASP:HB3	1:A:453:THR:H	1.60	0.65
1:A:525:GLU:OE1	1:A:525:GLU:HA	1.95	0.64
1:D:468:ARG:NH1	1:D:471:ASN:OD1	2.27	0.64
1:C:525:GLU:OE1	1:C:525:GLU:HA	1.96	0.64
1:C:102:ARG:HD3	1:C:137:ALA:HB2	1.81	0.63
1:D:143:ARG:HG2	1:D:143:ARG:NH1	2.14	0.61
1:A:98:ARG:HG2	1:A:98:ARG:NH1	2.11	0.60
1:C:297:ARG:NH2	1:D:142:GLU:OE2	2.34	0.60
1:A:636:ARG:HD3	1:A:651:LEU:HB3	1.84	0.60
1:C:98:ARG:HG2	1:C:98:ARG:NH1	2.12	0.59
1:B:636:ARG:HD3	1:B:651:LEU:HB3	1.84	0.59
1:C:452:VAL:N	1:C:454:PHE:H	2.01	0.58
1:B:451:ASP:HB3	1:B:453:THR:N	2.13	0.58
1:D:21:THR:O	1:D:236:GLY:HA3	2.03	0.58
1:D:567:GLN:HA	1:D:567:GLN:OE1	2.04	0.58
1:C:323:VAL:HG12	1:C:591:ALA:HB2	1.85	0.58
1:B:472:GLN:HB2	1:C:453:THR:HG21	1.84	0.58
1:C:121:LYS:HD2	1:C:175:ILE:HG22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:632:SER:OG	1:C:636:ARG:NH2	2.37	0.58
2:C:680:APC:H3'	2:C:680:APC:H3A1	1.85	0.57
1:B:98:ARG:HG2	1:B:98:ARG:NH1	2.14	0.57
1:B:143:ARG:HG2	1:B:143:ARG:NH1	2.13	0.57
1:D:98:ARG:HG2	1:D:98:ARG:NH1	2.07	0.57
1:D:186:SER:HB2	1:D:197:LEU:HD13	1.87	0.57
1:A:186:SER:HB2	1:A:197:LEU:HD13	1.87	0.56
1:D:23:ILE:HB	1:D:60:ILE:HG22	1.87	0.56
1:B:43:ASP:OD2	1:B:269:ARG:NH2	2.38	0.56
1:A:567:GLN:OE1	1:A:567:GLN:HA	2.06	0.56
1:C:636:ARG:HD3	1:C:651:LEU:HB3	1.88	0.56
1:A:210:ALA:HA	1:A:213:ARG:HD2	1.89	0.55
1:C:21:THR:O	1:C:236:GLY:HA3	2.06	0.55
1:A:143:ARG:HG2	1:A:143:ARG:NH1	2.20	0.55
1:A:453:THR:HG21	1:D:472:GLN:HB2	1.88	0.55
1:A:510:LYS:HD2	1:A:564:PHE:CD2	2.42	0.55
1:B:453:THR:HG21	1:C:472:GLN:HB2	1.88	0.54
1:D:523:ALA:HB3	5:D:728:HOH:O	2.07	0.54
1:A:14:VAL:HG23	1:A:250:ILE:HD13	1.90	0.54
1:B:632:SER:OG	1:B:636:ARG:NH2	2.41	0.54
1:C:186:SER:HB2	1:C:197:LEU:HD13	1.90	0.54
1:A:389:ARG:CD	5:A:753:HOH:O	2.56	0.54
1:A:604:PHE:O	1:A:609:ARG:HD2	2.08	0.54
1:B:77:LEU:HD11	1:B:108:VAL:HG11	1.89	0.54
1:A:389:ARG:HD3	5:A:753:HOH:O	2.07	0.54
1:C:14:VAL:HG23	1:C:250:ILE:HD13	1.90	0.54
1:C:143:ARG:HG2	1:C:143:ARG:NH1	2.21	0.54
1:B:323:VAL:HG12	1:B:591:ALA:HB2	1.90	0.53
1:C:23:ILE:HB	1:C:60:ILE:HG22	1.90	0.53
1:D:510:LYS:HD2	1:D:564:PHE:CD2	2.43	0.53
2:A:680:APC:H3A2	2:A:680:APC:O2G	2.09	0.53
1:C:210:ALA:O	1:C:214:ARG:HG3	2.08	0.53
1:A:23:ILE:HB	1:A:60:ILE:HG22	1.90	0.53
1:D:604:PHE:O	1:D:609:ARG:HD2	2.09	0.53
1:B:23:ILE:HB	1:B:60:ILE:HG22	1.91	0.53
1:A:200:LEU:HD12	1:A:200:LEU:N	2.23	0.53
1:D:620:TRP:HA	1:D:620:TRP:CE3	2.43	0.52
1:C:620:TRP:HA	1:C:620:TRP:CE3	2.44	0.52
1:D:98:ARG:HH11	1:D:98:ARG:CG	2.10	0.52
1:D:323:VAL:HG12	1:D:591:ALA:HB2	1.91	0.52
1:A:121:LYS:HD2	1:A:175:ILE:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:THR:O	1:B:236:GLY:HA3	2.10	0.52
1:B:52:GLU:HB2	1:B:201:SER:C	2.35	0.52
1:C:77:LEU:HD11	1:C:108:VAL:HG11	1.92	0.51
1:C:43:ASP:OD2	1:C:269:ARG:NH2	2.41	0.51
1:C:210:ALA:HA	1:C:213:ARG:HD2	1.91	0.51
1:A:180:PHE:CD2	1:A:216:LEU:CD1	2.93	0.51
2:B:680:APC:H3A2	2:B:680:APC:O2G	2.11	0.51
1:C:200:LEU:N	1:C:200:LEU:HD12	2.26	0.51
1:C:218:ARG:HG3	1:C:251:TRP:CZ3	2.44	0.51
1:D:636:ARG:HD3	1:D:651:LEU:HB3	1.92	0.51
1:A:472:GLN:HB2	1:D:453:THR:HG21	1.92	0.51
1:B:499:MET:HE3	1:C:499:MET:HE3	1.93	0.51
1:B:662:ASP:N	1:B:662:ASP:OD1	2.43	0.51
1:C:510:LYS:HD2	1:C:564:PHE:CD2	2.45	0.51
1:C:662:ASP:OD1	1:C:662:ASP:N	2.44	0.51
1:C:567:GLN:OE1	1:C:567:GLN:HA	2.11	0.51
1:D:210:ALA:O	1:D:214:ARG:HG3	2.11	0.51
1:B:50:PHE:HB3	1:B:51:PRO:CD	2.41	0.50
1:D:200:LEU:HD12	1:D:200:LEU:N	2.27	0.50
1:B:402:PHE:HD2	1:B:458:GLN:NE2	2.10	0.50
1:D:43:ASP:OD2	1:D:269:ARG:NH2	2.41	0.50
1:D:210:ALA:HA	1:D:213:ARG:HD2	1.93	0.50
1:A:210:ALA:O	1:A:214:ARG:HG3	2.11	0.50
1:B:510:LYS:HD2	1:B:564:PHE:CD2	2.47	0.50
1:A:21:THR:O	1:A:236:GLY:HA3	2.11	0.50
1:B:121:LYS:HD2	1:B:175:ILE:HG22	1.92	0.50
1:D:1:MET:HB3	1:D:675:GLU:OE1	2.11	0.50
1:B:174:GLU:HG2	5:B:694:HOH:O	2.11	0.49
1:B:441:HIS:HE2	1:B:451:ASP:HB2	1.77	0.49
1:D:374:THR:HG23	1:D:415:LEU:HD22	1.94	0.49
1:B:186:SER:HB2	1:B:197:LEU:HD13	1.95	0.49
1:A:451:ASP:HB3	1:A:453:THR:N	2.27	0.49
1:A:620:TRP:CE3	1:A:620:TRP:HA	2.47	0.49
1:D:328:PHE:CG	1:D:509:PRO:HG3	2.47	0.49
1:C:360:TYR:HB3	1:C:389:ARG:HD2	1.94	0.49
1:D:600:TRP:CD2	1:D:609:ARG:HG2	2.47	0.49
1:A:126:THR:OG1	1:A:133:ARG:HB2	2.12	0.49
1:B:180:PHE:CD2	1:B:216:LEU:CD1	2.96	0.49
1:C:1:MET:HB3	1:C:675:GLU:OE1	2.13	0.49
1:B:200:LEU:N	1:B:200:LEU:HD12	2.29	0.48
1:B:620:TRP:HA	1:B:620:TRP:CE3	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:ALA:O	1:B:214:ARG:HG3	2.14	0.48
1:C:633:GLN:HA	1:C:636:ARG:NH1	2.28	0.48
1:B:360:TYR:HB3	1:B:389:ARG:HD2	1.94	0.48
1:B:604:PHE:O	1:B:609:ARG:HD2	2.14	0.48
1:D:147:ARG:NH1	1:D:152:ASP:OD2	2.45	0.47
1:D:635:LYS:NZ	3:D:681:DND:O11	2.47	0.47
1:A:558:GLU:CD	1:A:563:PRO:HA	2.39	0.47
1:B:510:LYS:HE3	1:B:564:PHE:CE2	2.49	0.47
1:C:180:PHE:CD2	1:C:216:LEU:CD1	2.98	0.47
1:A:1:MET:HB3	1:A:675:GLU:OE1	2.15	0.47
1:B:348:VAL:O	1:B:352:GLU:HG3	2.13	0.47
1:D:12:VAL:HG13	1:D:12:VAL:O	2.12	0.47
1:A:633:GLN:HA	1:A:636:ARG:NH1	2.30	0.47
1:C:121:LYS:HD2	1:C:175:ILE:CG2	2.44	0.47
1:D:510:LYS:HE3	1:D:564:PHE:CE2	2.49	0.47
1:A:200:LEU:HD12	1:A:200:LEU:H	1.80	0.47
1:A:435:MET:SD	1:A:457:VAL:HG13	2.54	0.47
1:A:468:ARG:HA	1:A:468:ARG:HD3	1.51	0.47
1:D:77:LEU:HD11	1:D:108:VAL:HG11	1.97	0.47
1:B:468:ARG:HA	1:B:468:ARG:HD3	1.45	0.47
3:B:681:DND:N6A	1:C:358:LEU:HD21	2.30	0.47
1:D:183:MET:HB3	5:D:707:HOH:O	2.15	0.46
1:C:328:PHE:CG	1:C:509:PRO:HG3	2.50	0.46
1:D:118:VAL:HG21	1:D:148:ILE:CD1	2.46	0.46
1:D:180:PHE:CD2	1:D:216:LEU:CD1	2.98	0.46
1:C:490:TRP:CZ2	1:C:557:SER:HA	2.51	0.46
1:C:452:VAL:C	1:C:454:PHE:N	2.72	0.46
1:A:118:VAL:HG21	1:A:148:ILE:CD1	2.46	0.46
1:A:121:LYS:HD2	1:A:175:ILE:CG2	2.46	0.46
1:B:567:GLN:HA	1:B:567:GLN:OE1	2.15	0.46
1:A:328:PHE:CG	1:A:509:PRO:HG3	2.52	0.45
1:B:210:ALA:HA	1:B:213:ARG:HD2	1.98	0.45
1:C:124:LEU:HA	1:C:125:PRO:HD2	1.85	0.45
1:D:374:THR:HG23	1:D:415:LEU:CD2	2.46	0.45
1:B:445:VAL:HG23	1:B:445:VAL:O	2.16	0.45
1:D:230:TYR:CD1	1:D:230:TYR:C	2.94	0.45
1:D:328:PHE:CD2	1:D:509:PRO:HG3	2.51	0.45
1:A:43:ASP:OD2	1:A:269:ARG:NH2	2.44	0.45
1:B:140:ASP:HB2	1:D:295:HIS:ND1	2.31	0.45
1:D:14:VAL:HG23	1:D:250:ILE:HD13	1.99	0.45
2:A:680:APC:O2A	3:A:681:DND:C7N	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:ARG:HB3	1:B:592:TRP:CZ2	2.52	0.45
1:B:278:LEU:HD23	1:B:278:LEU:C	2.42	0.45
1:B:88:LEU:N	1:B:89:PRO:CD	2.81	0.44
1:B:126:THR:OG1	1:B:133:ARG:HB2	2.16	0.44
1:B:351:LEU:O	1:B:355:LEU:HG	2.17	0.44
1:C:52:GLU:HB2	1:C:201:SER:C	2.42	0.44
1:D:452:VAL:N	1:D:455:GLU:H	2.15	0.44
1:A:180:PHE:CD2	1:A:216:LEU:HD13	2.52	0.44
1:D:557:SER:C	1:D:559:ALA:N	2.71	0.44
1:A:514:GLN:HE21	1:A:518:ARG:HH21	1.65	0.44
1:C:26:PRO:HA	1:C:55:LEU:O	2.17	0.44
1:C:166:LEU:N	1:C:167:PRO:HD3	2.32	0.44
1:A:600:TRP:CD2	1:A:609:ARG:HG2	2.52	0.44
1:C:490:TRP:NE1	3:C:681:DND:H13	2.33	0.44
1:D:50:PHE:HB3	1:D:51:PRO:CD	2.48	0.44
1:A:510:LYS:HE3	1:A:564:PHE:CE2	2.52	0.44
1:C:510:LYS:HE3	1:C:564:PHE:CE2	2.52	0.44
1:A:77:LEU:HD11	1:A:108:VAL:HG11	2.00	0.44
1:C:468:ARG:HD3	1:C:468:ARG:HA	1.46	0.44
1:B:328:PHE:CG	1:B:509:PRO:HG3	2.52	0.44
1:D:224:CYS:O	1:D:225:LEU:C	2.61	0.44
1:A:662:ASP:OD1	1:A:662:ASP:N	2.50	0.44
1:D:360:TYR:HB3	1:D:389:ARG:HD2	2.00	0.44
1:C:491:SER:HB3	1:C:498:GLN:HB2	2.01	0.43
1:C:663:MET:HG2	1:C:664:SER:O	2.18	0.43
1:A:323:VAL:HG12	1:A:591:ALA:HB2	2.01	0.43
1:A:348:VAL:O	1:A:352:GLU:HG3	2.18	0.43
1:D:600:TRP:CE2	1:D:609:ARG:HG2	2.54	0.43
1:B:12:VAL:O	1:B:12:VAL:HG13	2.18	0.43
1:A:102:ARG:HB3	5:A:699:HOH:O	2.18	0.43
1:B:471:ASN:HB2	1:C:453:THR:HG23	2.01	0.43
1:C:50:PHE:HB3	1:C:51:PRO:CD	2.48	0.43
1:A:52:GLU:HB2	1:A:201:SER:C	2.44	0.43
1:B:121:LYS:HD2	1:B:175:ILE:CG2	2.49	0.43
1:C:660:PRO:HG3	1:D:60:ILE:HA	1.99	0.43
1:D:402:PHE:HD2	1:D:454:PHE:CZ	2.37	0.43
1:D:633:GLN:HA	1:D:636:ARG:NH1	2.34	0.43
1:A:166:LEU:N	1:A:167:PRO:HD3	2.34	0.43
1:B:118:VAL:HG21	1:B:148:ILE:CD1	2.48	0.43
1:D:241:ASP:C	1:D:242:LEU:HG	2.44	0.43
1:D:325:ARG:HB3	1:D:592:TRP:CZ2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:PHE:CD2	1:C:216:LEU:HD13	2.54	0.43
1:C:604:PHE:O	1:C:609:ARG:HD2	2.19	0.43
1:D:166:LEU:N	1:D:167:PRO:HD3	2.34	0.43
1:D:180:PHE:CD2	1:D:216:LEU:HD13	2.52	0.43
1:C:92:VAL:CG1	1:C:200:LEU:HD11	2.49	0.42
1:C:399:LEU:N	2:C:680:APC:N1	2.55	0.42
1:C:352:GLU:OE2	1:C:386:ARG:HD3	2.19	0.42
1:A:342:GLU:O	1:A:346:ILE:HG13	2.19	0.42
1:A:449:VAL:O	1:A:449:VAL:HG12	2.19	0.42
1:B:14:VAL:HG23	1:B:250:ILE:HD13	2.02	0.42
1:D:121:LYS:HD2	1:D:175:ILE:HG22	2.01	0.42
1:A:490:TRP:NE1	3:A:681:DND:H13	2.34	0.42
1:A:499:MET:HE3	1:D:499:MET:HE3	2.01	0.42
3:A:681:DND:N6A	1:D:358:LEU:HD21	2.33	0.42
1:C:128:ARG:HH11	1:C:128:ARG:HD2	1.71	0.42
1:D:663:MET:HG2	1:D:664:SER:O	2.20	0.42
1:D:621:LEU:HA	5:D:722:HOH:O	2.19	0.42
1:B:435:MET:HG3	1:C:465:TYR:CE1	2.54	0.42
1:C:600:TRP:CD2	1:C:609:ARG:HG2	2.55	0.42
1:A:23:ILE:HB	1:A:60:ILE:CG2	2.50	0.42
1:A:389:ARG:HD2	5:A:753:HOH:O	2.19	0.42
1:B:600:TRP:CD2	1:B:609:ARG:HG2	2.55	0.42
1:D:378:ILE:HD13	1:D:378:ILE:HA	1.91	0.42
1:A:660:PRO:HG3	1:B:60:ILE:HA	2.02	0.41
3:A:681:DND:O2B	1:D:475:GLY:O	2.37	0.41
1:B:534:LEU:HA	1:B:534:LEU:HD23	1.78	0.41
1:C:136:MET:HE3	1:C:136:MET:HB2	1.88	0.41
1:D:525:GLU:OE1	1:D:525:GLU:CA	2.65	0.41
1:C:218:ARG:HG3	1:C:251:TRP:CE3	2.55	0.41
1:B:402:PHE:CD2	1:B:458:GLN:CD	2.98	0.41
1:D:257:LEU:HA	1:D:257:LEU:HD12	1.76	0.41
1:C:118:VAL:HG21	1:C:148:ILE:CD1	2.50	0.41
1:B:69:LEU:O	1:B:69:LEU:HG	2.18	0.41
1:A:445:VAL:O	1:A:445:VAL:CG1	2.68	0.41
1:B:182:PRO:HG2	1:D:191:LEU:HD21	2.02	0.41
1:C:26:PRO:HD2	5:C:796:HOH:O	2.20	0.41
1:D:52:GLU:HB2	1:D:201:SER:C	2.46	0.41
1:D:662:ASP:N	1:D:662:ASP:OD1	2.54	0.41
1:C:453:THR:O	1:C:457:VAL:HG23	2.21	0.41
2:B:680:APC:H3A2	2:B:680:APC:H5'2	1.73	0.41
1:C:397:PHE:O	2:C:680:APC:H2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:516:LEU:O	1:C:520:VAL:HG23	2.20	0.41
1:D:366:GLY:O	2:D:680:APC:O2'	2.35	0.41
1:A:13:ARG:HB3	1:A:45:ALA:HA	2.03	0.41
1:A:230:TYR:CD1	1:A:230:TYR:C	2.98	0.41
1:B:295:HIS:ND1	1:D:140:ASP:HB2	2.36	0.41
1:B:423:PHE:CG	1:B:424:SER:N	2.89	0.41
1:C:92:VAL:HG11	1:C:200:LEU:HD11	2.02	0.41
1:D:676:VAL:HA	1:D:677:PRO:HD3	1.97	0.41
1:A:124:LEU:HA	1:A:125:PRO:HD2	1.89	0.40
1:B:146:ILE:HD13	1:B:146:ILE:HG21	1.88	0.40
1:A:358:LEU:HD21	3:D:681:DND:N6A	2.37	0.40
1:B:223:ARG:HD3	5:B:753:HOH:O	2.20	0.40
1:A:174:GLU:HG2	5:A:756:HOH:O	2.21	0.40
1:C:613:SER:OG	1:C:616:GLU:HG3	2.20	0.40
1:C:676:VAL:HA	1:C:677:PRO:HD3	1.96	0.40
1:D:352:GLU:OE2	1:D:386:ARG:HB2	2.22	0.40
1:B:123:TYR:C	1:B:124:LEU:HD12	2.46	0.40
1:B:600:TRP:CE2	1:B:609:ARG:HG2	2.57	0.40
1:C:325:ARG:HB3	1:C:592:TRP:CZ2	2.56	0.40
1:A:218:ARG:HG3	1:A:251:TRP:CZ3	2.57	0.40
1:A:278:LEU:HD23	1:A:278:LEU:C	2.47	0.40
1:A:360:TYR:HB3	1:A:389:ARG:HD2	2.02	0.40
1:C:342:GLU:O	1:C:346:ILE:HG13	2.21	0.40
1:C:621:LEU:HA	5:C:784:HOH:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:GLU:OE2	1:D:297:ARG:NH2[8_555]	2.15	0.05

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	655/680 (96%)	631 (96%)	24 (4%)	0	100	100
1	B	652/680 (96%)	626 (96%)	25 (4%)	1 (0%)	43	62
1	C	642/680 (94%)	618 (96%)	23 (4%)	1 (0%)	43	62
1	D	642/680 (94%)	621 (97%)	20 (3%)	1 (0%)	43	62
All	All	2591/2720 (95%)	2496 (96%)	92 (4%)	3 (0%)	48	69

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	177	GLU
1	D	177	GLU
1	B	177	GLU

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	525/548 (96%)	505 (96%)	20 (4%)	29	51
1	B	517/548 (94%)	502 (97%)	15 (3%)	37	59
1	C	509/548 (93%)	492 (97%)	17 (3%)	33	55
1	D	512/548 (93%)	495 (97%)	17 (3%)	33	55
All	All	2063/2192 (94%)	1994 (97%)	69 (3%)	33	55

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	68	SER
1	A	69	LEU
1	A	98	ARG
1	A	143	ARG
1	A	201	SER

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Mol	Chain	Res	Type
1	A	257	LEU
1	A	299	LEU
1	A	334	GLN
1	A	445	VAL
1	A	447	GLU
1	A	451	ASP
1	A	453	THR
1	A	468	ARG
1	A	491	SER
1	A	522	SER
1	A	543	THR
1	A	560	LYS
1	A	609	ARG
1	A	664	SER
1	B	5	SER
1	B	68	SER
1	B	69	LEU
1	B	98	ARG
1	B	143	ARG
1	B	200	LEU
1	B	201	SER
1	B	257	LEU
1	B	299	LEU
1	B	453	THR
1	B	468	ARG
1	B	491	SER
1	B	522	SER
1	B	609	ARG
1	B	664	SER
1	C	21	THR
1	C	68	SER
1	C	69	LEU
1	C	98	ARG
1	C	143	ARG
1	C	200	LEU
1	C	201	SER
1	C	257	LEU
1	C	299	LEU
1	C	409	LYS
1	C	453	THR
1	C	468	ARG
1	C	491	SER

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Mol	Chain	Res	Type
1	C	522	SER
1	C	596	GLU
1	C	609	ARG
1	C	664	SER
1	D	21	THR
1	D	69	LEU
1	D	98	ARG
1	D	143	ARG
1	D	201	SER
1	D	257	LEU
1	D	299	LEU
1	D	334	GLN
1	D	410	ASN
1	D	452	VAL
1	D	453	THR
1	D	468	ARG
1	D	491	SER
1	D	522	SER
1	D	596	GLU
1	D	609	ARG
1	D	664	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	HIS
1	A	172	HIS
1	A	292	ASN
1	A	514	GLN
1	A	573	GLN
1	B	345	ASN
1	B	456	ASN
1	B	514	GLN
1	B	573	GLN
1	C	101	HIS
1	C	172	HIS
1	C	456	ASN
1	C	472	GLN
1	C	573	GLN
1	C	619	HIS
1	D	172	HIS
1	D	573	GLN

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Mol	Chain	Res	Type
1	D	619	HIS

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](#)

10 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	GOL	B	682	-	5,5,5	0.41	0	5,5,5	0.19	0
3	DND	A	681	-	46,48,48	1.28	5 (10%)	64,73,73	1.60	7 (10%)
3	DND	C	681	-	46,48,48	1.48	5 (10%)	64,73,73	1.66	11 (17%)
4	GOL	D	682	-	5,5,5	0.81	0	5,5,5	0.43	0
2	APC	D	680	-	29,33,33	1.41	3 (10%)	44,52,52	1.79	9 (20%)
3	DND	D	681	-	46,48,48	1.65	4 (8%)	64,73,73	1.84	9 (14%)
2	APC	C	680	-	29,33,33	1.38	4 (13%)	44,52,52	1.80	12 (27%)
2	APC	B	680	-	29,33,33	1.44	3 (10%)	44,52,52	1.84	9 (20%)
3	DND	B	681	-	46,48,48	1.33	3 (6%)	64,73,73	1.69	9 (14%)
2	APC	A	680	-	29,33,33	1.32	5 (17%)	44,52,52	1.79	9 (20%)

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	GOL	B	682	-	-	4/4/4/4	-
3	DND	A	681	-	-	14/30/62/62	0/5/5/5
3	DND	C	681	-	-	15/30/62/62	0/5/5/5
4	GOL	D	682	-	-	0/4/4/4	-
2	APC	D	680	-	-	7/19/38/38	0/3/3/3
3	DND	D	681	-	-	15/30/62/62	0/5/5/5
2	APC	C	680	-	-	6/19/38/38	0/3/3/3
2	APC	B	680	-	-	11/19/38/38	0/3/3/3
3	DND	B	681	-	-	14/30/62/62	0/5/5/5
2	APC	A	680	-	-	4/19/38/38	0/3/3/3

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	681	DND	PN-O3P	6.83	1.66	1.59
3	D	681	DND	PA-O3P	5.95	1.65	1.59
3	C	681	DND	PA-O3P	5.57	1.65	1.59
3	C	681	DND	PN-O3P	5.42	1.65	1.59
3	B	681	DND	PN-O3P	4.90	1.64	1.59
2	D	680	APC	PB-O3B	4.38	1.63	1.58
2	C	680	APC	PB-O3B	4.28	1.63	1.58
2	B	680	APC	PB-O3B	4.12	1.63	1.58
3	A	681	DND	PN-O3P	4.09	1.63	1.59
3	B	681	DND	PA-O3P	3.83	1.63	1.59
3	A	681	DND	PA-O3P	3.78	1.63	1.59
2	A	680	APC	PB-O3B	3.60	1.62	1.58
2	B	680	APC	C5-C6	3.24	1.50	1.41
3	C	681	DND	C5A-C6A	3.11	1.49	1.41
3	B	681	DND	C5A-C6A	3.10	1.49	1.41
2	A	680	APC	C5-C6	3.06	1.49	1.41
2	D	680	APC	C5-C6	2.98	1.49	1.41
3	D	681	DND	C5A-C6A	2.85	1.48	1.41
3	A	681	DND	O4D-C1D	2.75	1.44	1.40
3	A	681	DND	C5A-C6A	2.62	1.48	1.41
2	C	680	APC	C5-C6	2.62	1.48	1.41
3	A	681	DND	C8A-N7A	2.38	1.36	1.31
3	D	681	DND	C5A-N7A	-2.27	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	680	APC	PA-O2A	-2.17	1.51	1.56
2	B	680	APC	C8-N7	2.14	1.35	1.31
3	C	681	DND	C8A-N7A	2.09	1.35	1.31
2	D	680	APC	C8-N7	2.06	1.35	1.31
2	A	680	APC	C8-N7	2.06	1.35	1.31
2	C	680	APC	PA-O2A	-2.02	1.51	1.56
3	C	681	DND	C4A-N9A	-2.02	1.33	1.37
2	A	680	APC	C4-N9	-2.02	1.33	1.37
2	C	680	APC	C8-N7	2.00	1.35	1.31

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	681	DND	C5A-C4A-N3A	-6.23	118.14	126.72
3	D	681	DND	C5A-C4A-N3A	-6.05	118.39	126.72
3	D	681	DND	N1A-C2A-N3A	-5.78	119.84	128.58
2	B	680	APC	C5-C4-N3	-5.76	118.79	126.72
3	A	681	DND	C5A-C4A-N3A	-5.50	119.14	126.72
3	D	681	DND	C2A-N3A-C4A	5.10	124.30	111.83
3	A	681	DND	N1A-C2A-N3A	-5.08	120.89	128.58
3	C	681	DND	N1A-C2A-N3A	-4.99	121.03	128.58
2	D	680	APC	C5-C4-N3	-4.95	119.90	126.72
3	B	681	DND	N1A-C2A-N3A	-4.86	121.22	128.58
3	B	681	DND	C2A-N3A-C4A	4.82	123.59	111.83
2	A	680	APC	C5-C4-N3	-4.52	120.49	126.72
3	A	681	DND	C2A-N3A-C4A	4.52	122.87	111.83
2	C	680	APC	C5-C4-N3	-4.36	120.71	126.72
3	C	681	DND	C5A-C4A-N3A	-4.34	120.74	126.72
3	B	681	DND	N3A-C4A-N9A	4.24	134.38	127.17
3	C	681	DND	C2A-N3A-C4A	4.20	122.10	111.83
3	D	681	DND	N3A-C4A-N9A	4.20	134.32	127.17
2	A	680	APC	N3-C2-N1	-4.19	122.24	128.58
2	B	680	APC	N3-C4-N9	4.04	134.04	127.17
2	D	680	APC	N3-C2-N1	-4.02	122.49	128.58
3	D	681	DND	N9A-C8A-N7A	-3.94	108.35	113.94
2	B	680	APC	N3-C2-N1	-3.87	122.73	128.58
3	D	681	DND	O12-PN-O3P	3.85	117.68	107.27
2	B	680	APC	C2-N3-C4	3.83	121.18	111.83
3	A	681	DND	N3A-C4A-N9A	3.82	133.66	127.17
3	C	681	DND	O12-PN-O3P	3.79	117.53	107.27
2	C	680	APC	N3-C2-N1	-3.79	122.84	128.58
2	D	680	APC	C2-N3-C4	3.65	120.74	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	680	APC	C2-N3-C4	3.64	120.73	111.83
3	C	681	DND	N9A-C8A-N7A	-3.55	108.90	113.94
2	D	680	APC	N3-C4-N9	3.50	133.12	127.17
2	A	680	APC	C2'-C1'-N9	-3.42	104.81	113.30
2	C	680	APC	N3-C4-N9	3.38	132.92	127.17
2	C	680	APC	O5'-C5'-C4'	3.38	120.49	108.99
2	C	680	APC	C2-N3-C4	3.38	120.07	111.83
3	C	681	DND	C4A-N9A-C8A	3.37	109.28	105.74
2	A	680	APC	O2B-PB-O1B	3.37	120.93	109.95
3	D	681	DND	C5A-N7A-C8A	3.21	108.49	103.45
2	A	680	APC	N3-C4-N9	3.21	132.62	127.17
3	B	681	DND	N9A-C8A-N7A	-3.09	109.56	113.94
3	C	681	DND	N3A-C4A-N9A	3.06	132.38	127.17
2	C	680	APC	O1A-PA-C3A	2.98	116.91	109.05
2	B	680	APC	O2B-PB-O1B	2.96	119.57	109.95
2	A	680	APC	N9-C8-N7	-2.92	109.79	113.94
2	C	680	APC	N9-C8-N7	-2.76	110.02	113.94
3	A	681	DND	N9A-C8A-N7A	-2.76	110.02	113.94
2	C	680	APC	O2B-PB-O1B	2.67	118.65	109.95
2	B	680	APC	N9-C8-N7	-2.64	110.18	113.94
2	A	680	APC	C4-N9-C8	2.62	108.49	105.74
3	B	681	DND	C4D-O4D-C1D	2.62	112.32	109.92
3	D	681	DND	C4A-C5A-N7A	-2.60	107.61	110.58
3	C	681	DND	C6N-N1N-C2N	-2.60	119.67	121.88
2	C	680	APC	C4-N9-C8	2.57	108.43	105.74
3	B	681	DND	C5A-N7A-C8A	2.55	107.45	103.45
2	B	680	APC	O5'-C5'-C4'	2.48	117.43	108.99
2	D	680	APC	N9-C8-N7	-2.46	110.45	113.94
2	D	680	APC	O2A-PA-O1A	2.44	117.89	109.95
2	C	680	APC	O4'-C4'-C5'	2.43	117.12	109.33
2	B	680	APC	C4-C5-N7	-2.43	107.81	110.58
3	D	681	DND	C4A-N9A-C8A	2.40	108.26	105.74
2	D	680	APC	O1B-PB-C3A	-2.39	102.76	109.05
3	B	681	DND	C4A-C5A-N7A	-2.38	107.86	110.58
3	A	681	DND	C6N-N1N-C2N	-2.33	119.89	121.88
3	B	681	DND	O8N-C7N-C3N	2.33	120.83	114.84
3	C	681	DND	O2D-C2D-C3D	-2.33	104.36	111.82
2	B	680	APC	C5-N7-C8	2.29	107.05	103.45
2	C	680	APC	O2A-PA-O1A	2.26	117.32	109.95
3	A	681	DND	O12-PN-O3P	2.24	113.32	107.27
2	D	680	APC	O3G-PG-O2G	2.23	116.16	107.80
2	D	680	APC	O2B-PB-O1B	2.10	116.80	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	680	APC	N6-C6-N1	2.07	122.99	118.38
3	C	681	DND	C5A-N7A-C8A	2.04	106.65	103.45
3	C	681	DND	C4A-C5A-N7A	-2.01	108.28	110.58
2	A	680	APC	O3G-PG-O2G	2.01	115.34	107.80

There are no chirality outliers.

All (90) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	680	APC	PB-C3A-PA-O1A
2	A	680	APC	C5'-O5'-PA-C3A
2	B	680	APC	PB-O3B-PG-O2G
2	B	680	APC	PB-C3A-PA-O1A
2	B	680	APC	PB-C3A-PA-O2A
2	B	680	APC	C5'-O5'-PA-O1A
2	B	680	APC	C5'-O5'-PA-C3A
2	C	680	APC	PA-C3A-PB-O1B
2	C	680	APC	PA-C3A-PB-O2B
2	C	680	APC	PA-C3A-PB-O3B
2	C	680	APC	PB-C3A-PA-O1A
2	D	680	APC	PA-C3A-PB-O1B
2	D	680	APC	PA-C3A-PB-O2B
2	D	680	APC	PA-C3A-PB-O3B
2	D	680	APC	C5'-O5'-PA-O1A
3	A	681	DND	C5D-O5D-PN-O11
3	A	681	DND	O4D-C1D-N1N-C6N
3	A	681	DND	C2N-C3N-C7N-O7N
3	A	681	DND	C2N-C3N-C7N-O8N
3	B	681	DND	PN-O3P-PA-O5B
3	B	681	DND	O4D-C1D-N1N-C6N
3	B	681	DND	O4D-C1D-N1N-C2N
3	B	681	DND	C2D-C1D-N1N-C6N
3	B	681	DND	C2D-C1D-N1N-C2N
3	C	681	DND	PN-O3P-PA-O5B
3	C	681	DND	C3D-C4D-C5D-O5D
3	C	681	DND	C2N-C3N-C7N-O7N
3	C	681	DND	C2N-C3N-C7N-O8N
3	D	681	DND	C5D-O5D-PN-O11
3	D	681	DND	O4D-C1D-N1N-C6N
3	D	681	DND	O4D-C1D-N1N-C2N
3	D	681	DND	C2D-C1D-N1N-C6N
3	D	681	DND	C2D-C1D-N1N-C2N

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Mol	Chain	Res	Type	Atoms
3	D	681	DND	C2N-C3N-C7N-O7N
3	D	681	DND	C2N-C3N-C7N-O8N
4	B	682	GOL	O1-C1-C2-C3
3	C	681	DND	C4N-C3N-C7N-O7N
3	A	681	DND	C4N-C3N-C7N-O7N
3	A	681	DND	C4N-C3N-C7N-O8N
3	D	681	DND	C4N-C3N-C7N-O7N
3	C	681	DND	C4N-C3N-C7N-O8N
3	D	681	DND	C4N-C3N-C7N-O8N
2	B	680	APC	O4'-C4'-C5'-O5'
2	C	680	APC	O4'-C4'-C5'-O5'
3	A	681	DND	O4D-C4D-C5D-O5D
3	C	681	DND	O4D-C4D-C5D-O5D
3	A	681	DND	C3D-C4D-C5D-O5D
4	B	682	GOL	C1-C2-C3-O3
4	B	682	GOL	O1-C1-C2-O2
4	B	682	GOL	O2-C2-C3-O3
2	B	680	APC	C3'-C4'-C5'-O5'
2	C	680	APC	C3'-C4'-C5'-O5'
3	A	681	DND	PN-O3P-PA-O5B
3	D	681	DND	PN-O3P-PA-O5B
3	C	681	DND	C2B-C1B-N9A-C8A
3	C	681	DND	C4B-C5B-O5B-PA
3	B	681	DND	C4N-C3N-C7N-O7N
3	B	681	DND	C4N-C3N-C7N-O8N
2	A	680	APC	PB-C3A-PA-O2A
2	B	680	APC	PA-C3A-PB-O2B
3	A	681	DND	C5D-O5D-PN-O3P
3	B	681	DND	C5B-O5B-PA-O13
3	C	681	DND	C5D-O5D-PN-O11
3	C	681	DND	C5D-O5D-PN-O12
3	C	681	DND	C5D-O5D-PN-O3P
3	C	681	DND	C5B-O5B-PA-O13
3	D	681	DND	C5D-O5D-PN-O12
3	D	681	DND	C5D-O5D-PN-O3P
3	A	681	DND	C4B-C5B-O5B-PA
3	B	681	DND	C4B-C5B-O5B-PA
3	D	681	DND	C4B-C5B-O5B-PA
3	D	681	DND	C2B-C1B-N9A-C8A
3	B	681	DND	O4D-C4D-C5D-O5D
3	A	681	DND	O4D-C1D-N1N-C2N
2	B	680	APC	C5'-O5'-PA-O2A

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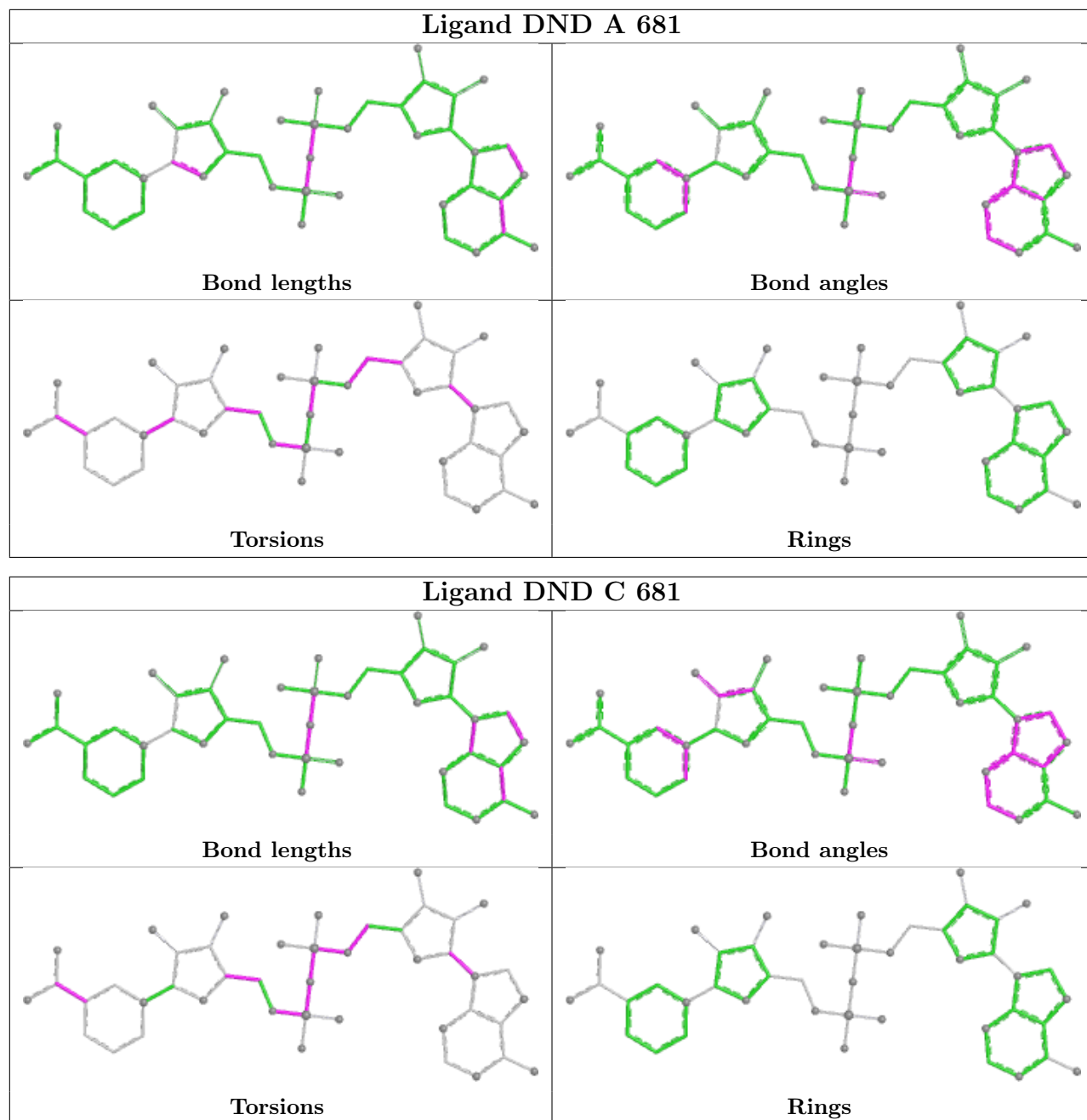
Mol	Chain	Res	Type	Atoms
2	D	680	APC	PB-C3A-PA-O1A
2	D	680	APC	C5'-O5'-PA-O2A
2	B	680	APC	PB-O3B-PG-O1G
2	B	680	APC	PB-O3B-PG-O3G
3	B	681	DND	C2N-C3N-C7N-O7N
3	B	681	DND	C2N-C3N-C7N-O8N
3	C	681	DND	O4B-C1B-N9A-C8A
3	D	681	DND	O4D-C4D-C5D-O5D
3	A	681	DND	C2B-C1B-N9A-C8A
2	A	680	APC	PB-O3B-PG-O1G
3	A	681	DND	C3B-C4B-C5B-O5B
3	B	681	DND	C2B-C1B-N9A-C8A
2	D	680	APC	C4'-C5'-O5'-PA
3	B	681	DND	PA-O3P-PN-O12
3	C	681	DND	PA-O3P-PN-O12

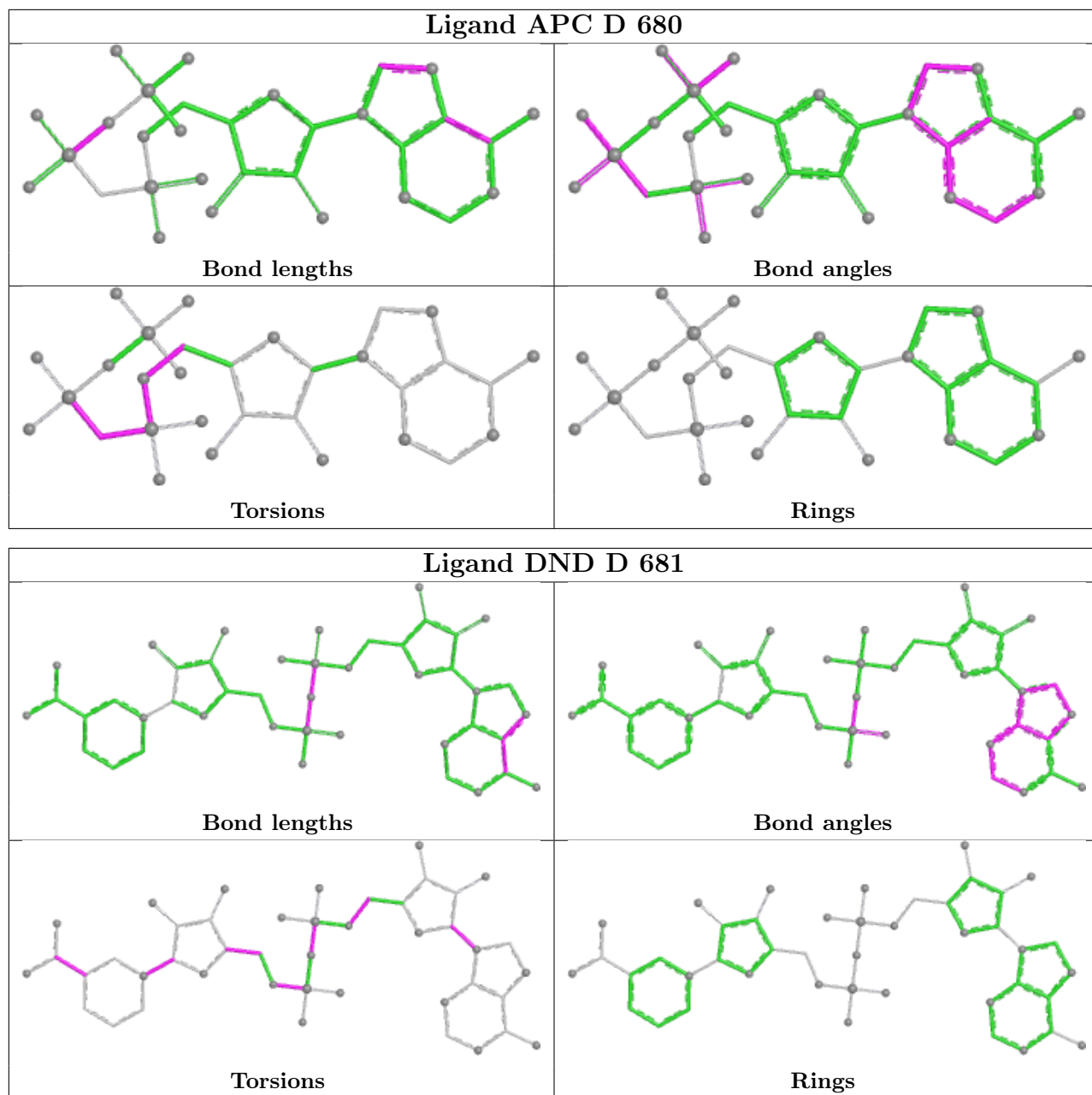
There are no ring outliers.

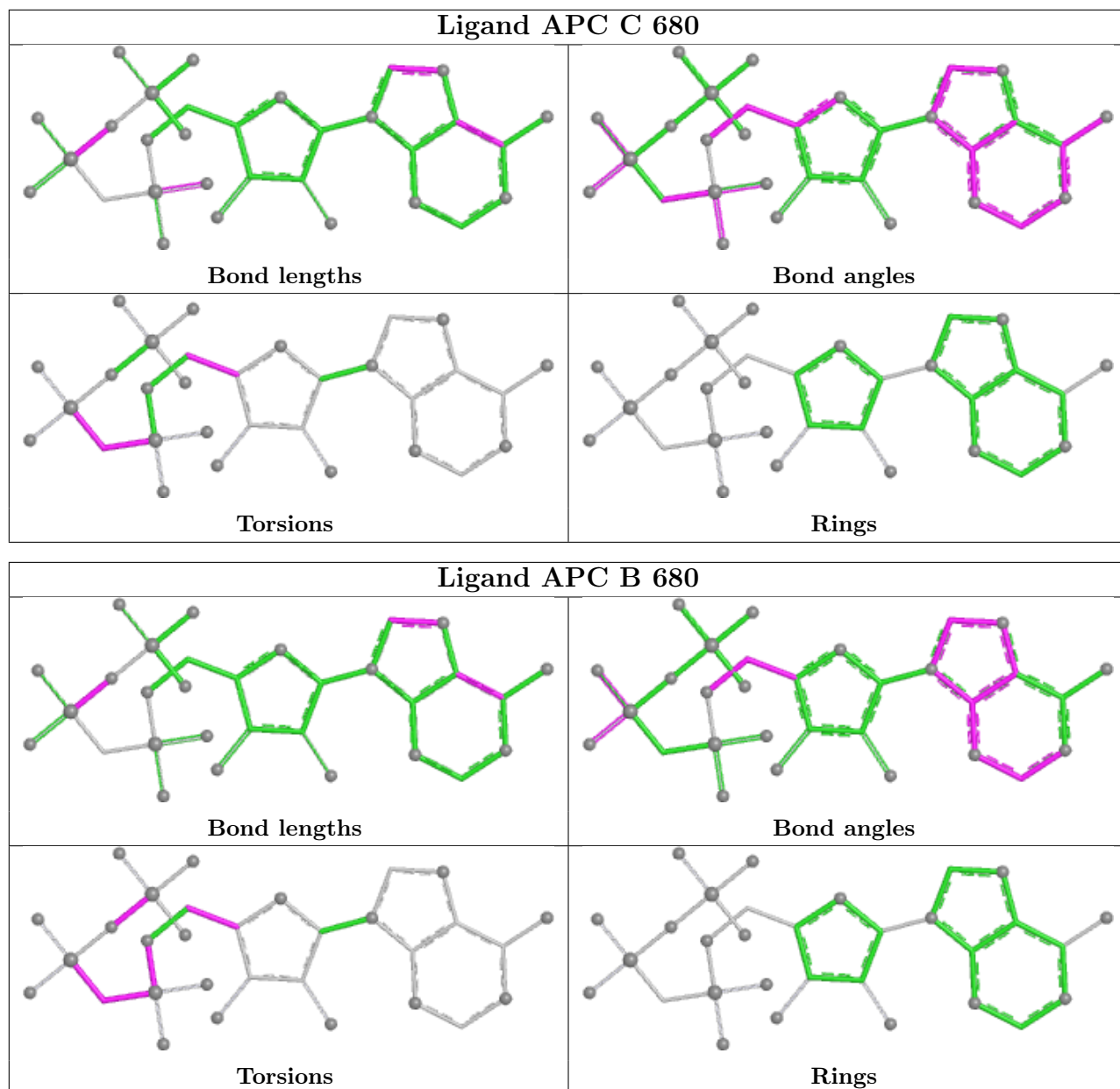
9 monomers are involved in 17 short contacts:

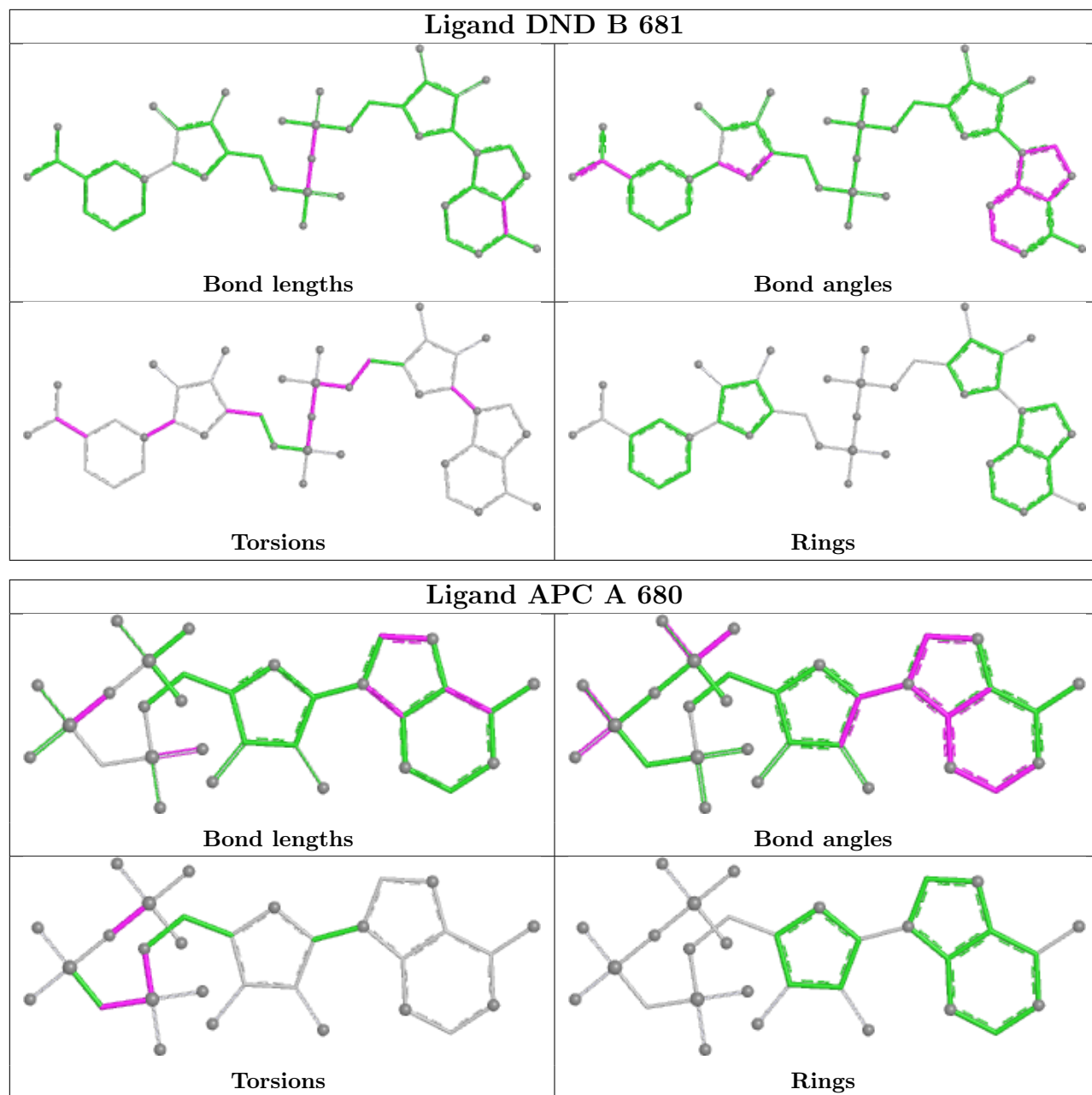
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	682	GOL	1	0
3	A	681	DND	4	0
3	C	681	DND	1	0
2	D	680	APC	2	0
3	D	681	DND	2	0
2	C	680	APC	3	0
2	B	680	APC	2	0
3	B	681	DND	1	0
2	A	680	APC	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	661/680 (97%)	-0.78	3 (0%) 87 87	13, 30, 56, 87	0
1	B	658/680 (96%)	-0.80	2 (0%) 90 91	14, 30, 55, 87	0
1	C	650/680 (95%)	-0.77	4 (0%) 85 85	17, 32, 56, 89	0
1	D	650/680 (95%)	-0.76	4 (0%) 85 85	14, 30, 55, 90	0
All	All	2619/2720 (96%)	-0.78	13 (0%) 87 87	13, 30, 56, 90	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	402	PHE	4.8
1	A	409	LYS	4.5
1	B	410	ASN	4.4
1	C	452	VAL	4.1
1	A	410	ASN	4.0
1	D	409	LYS	3.7
1	B	559	ALA	3.6
1	C	409	LYS	3.4
1	D	606	LYS	3.2
1	D	605	PRO	3.0
1	D	452	VAL	2.6
1	C	402	PHE	2.5
1	C	558	GLU	2.3

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](#)

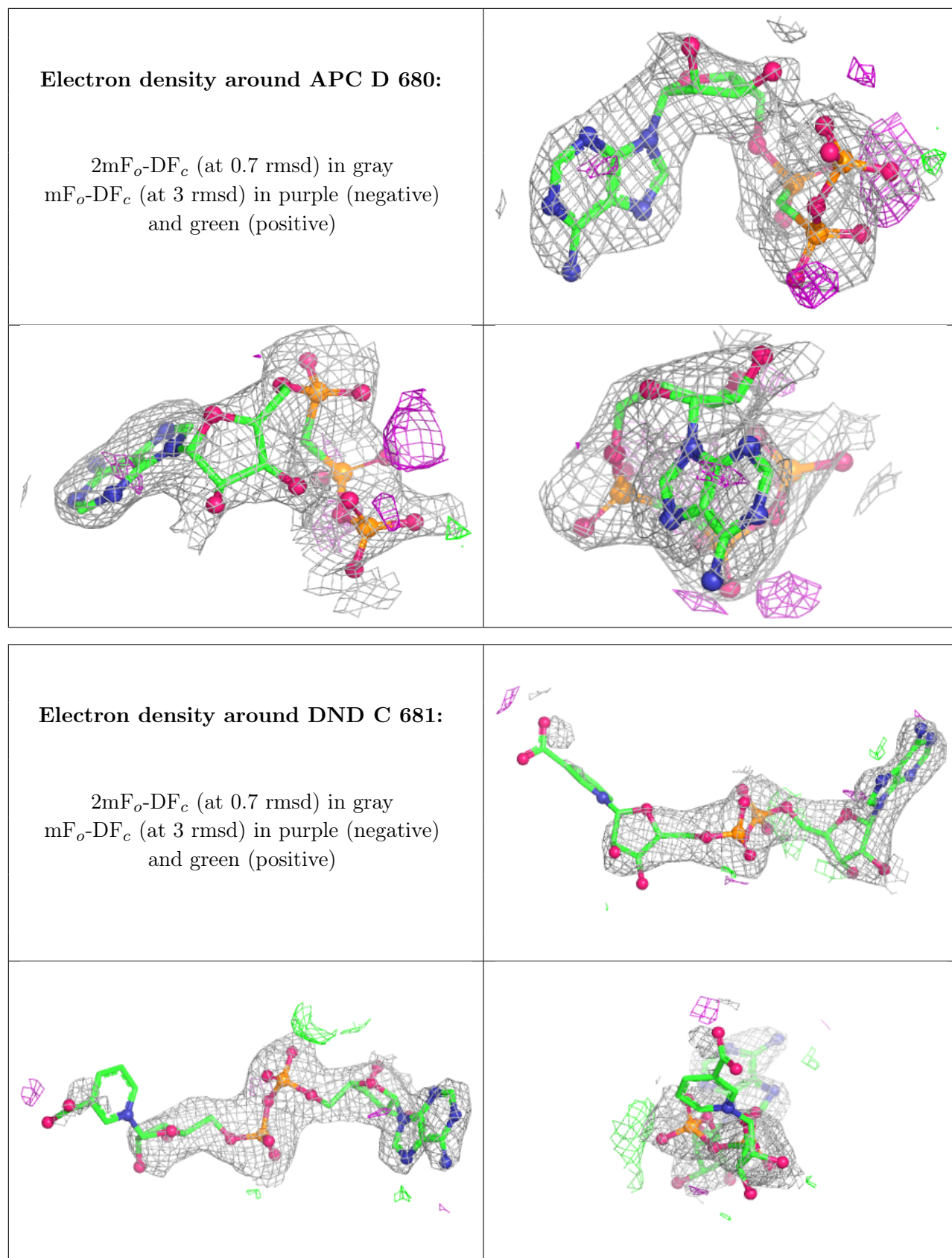
There are no oligosaccharides in this entry.

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.

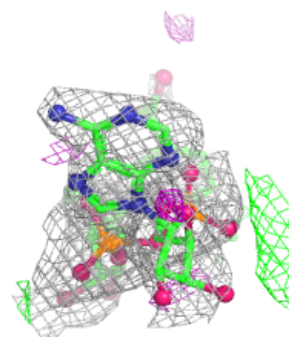
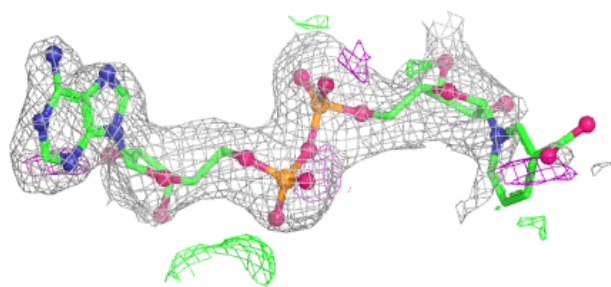
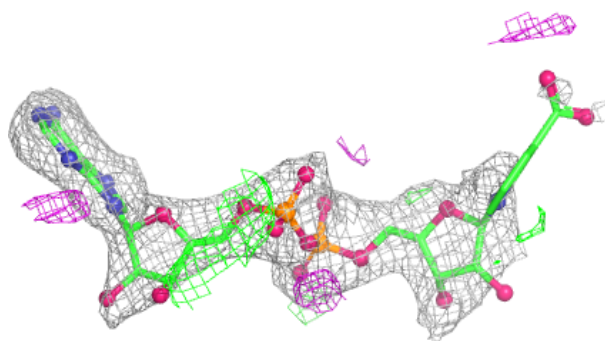
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	D	682	6/6	0.81	0.15	36,68,74,81	0
2	APC	D	680	31/31	0.89	0.10	41,63,114,119	0
3	DND	C	681	44/44	0.91	0.12	39,73,144,154	0
3	DND	D	681	44/44	0.91	0.13	27,65,132,135	0
3	DND	B	681	44/44	0.91	0.12	27,79,151,156	0
2	APC	B	680	31/31	0.92	0.08	38,59,112,160	0
2	APC	C	680	31/31	0.93	0.07	37,61,103,140	0
3	DND	A	681	44/44	0.93	0.11	31,59,121,140	0
4	GOL	B	682	6/6	0.94	0.11	38,48,57,60	0
2	APC	A	680	31/31	0.94	0.07	32,59,102,161	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.

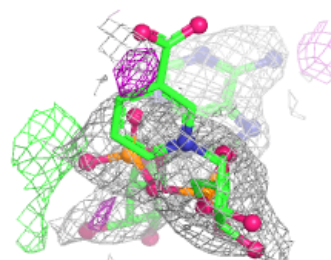
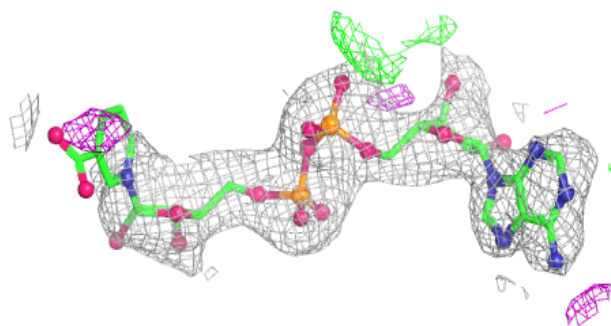
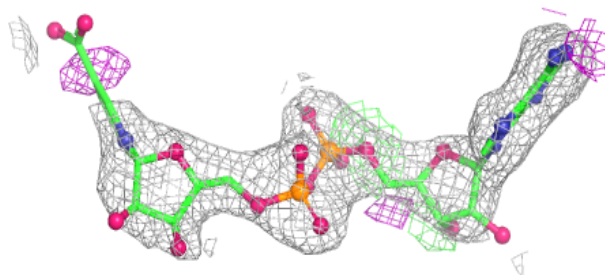


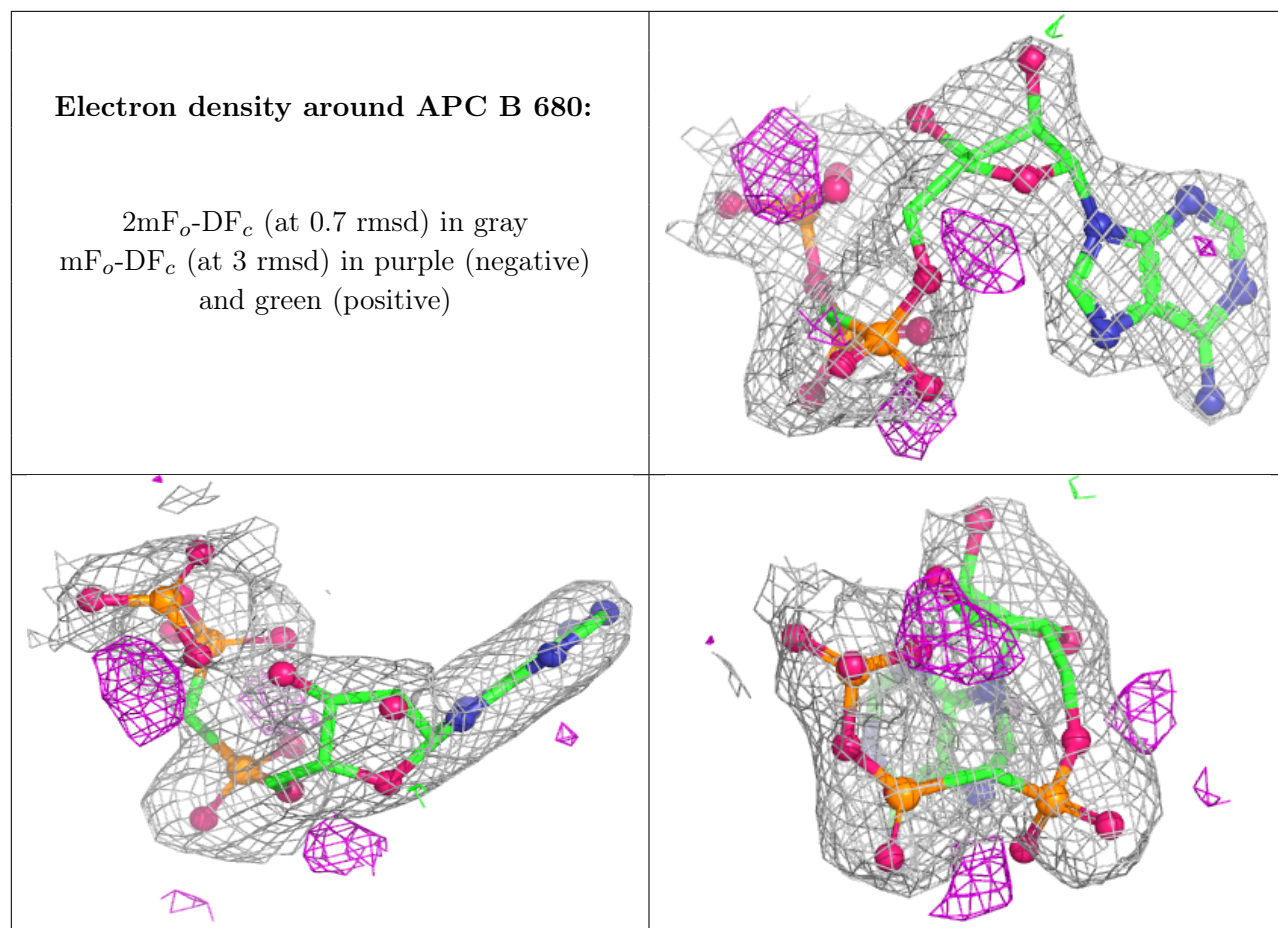
Electron density around DND D 681:

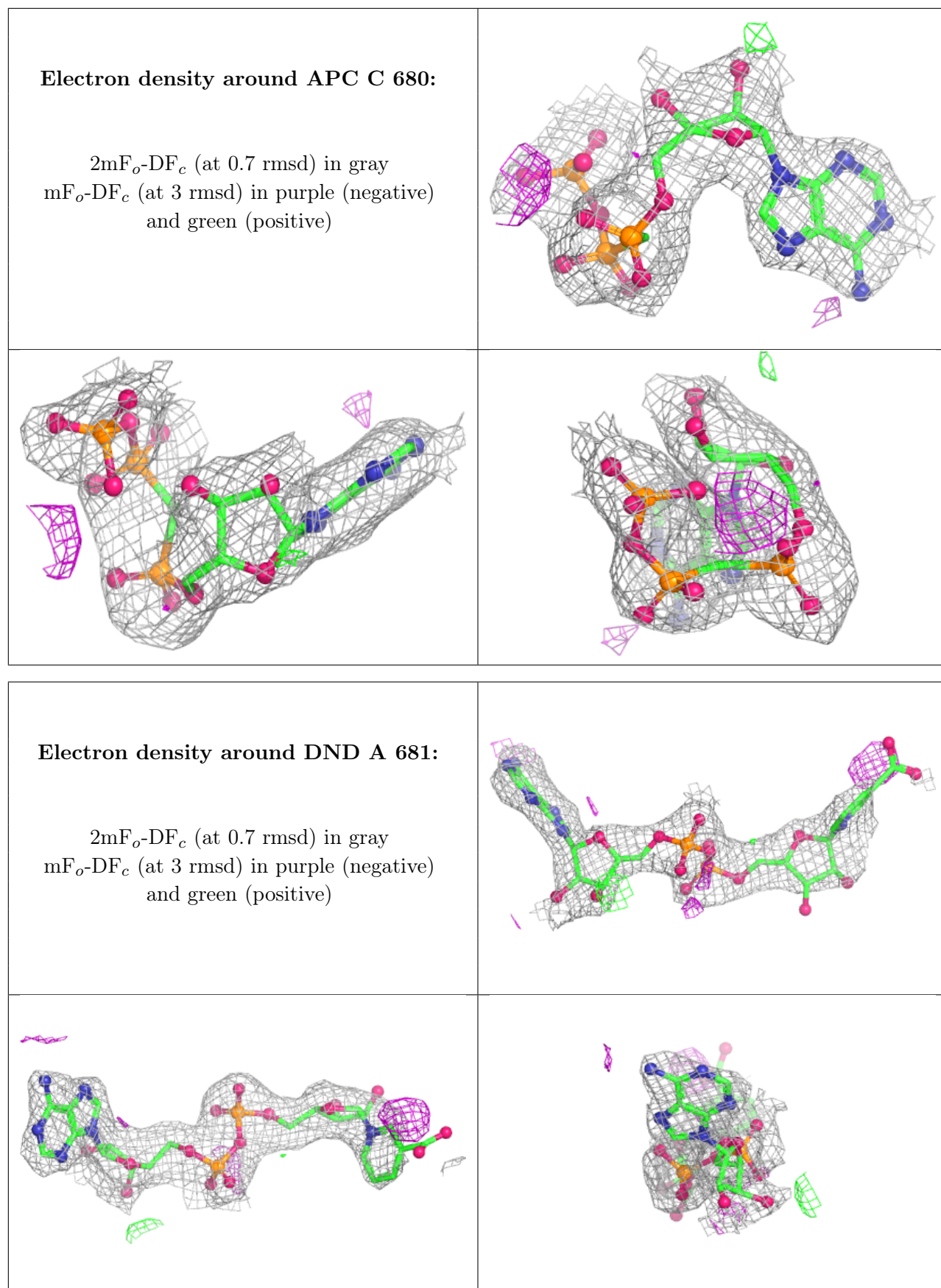
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

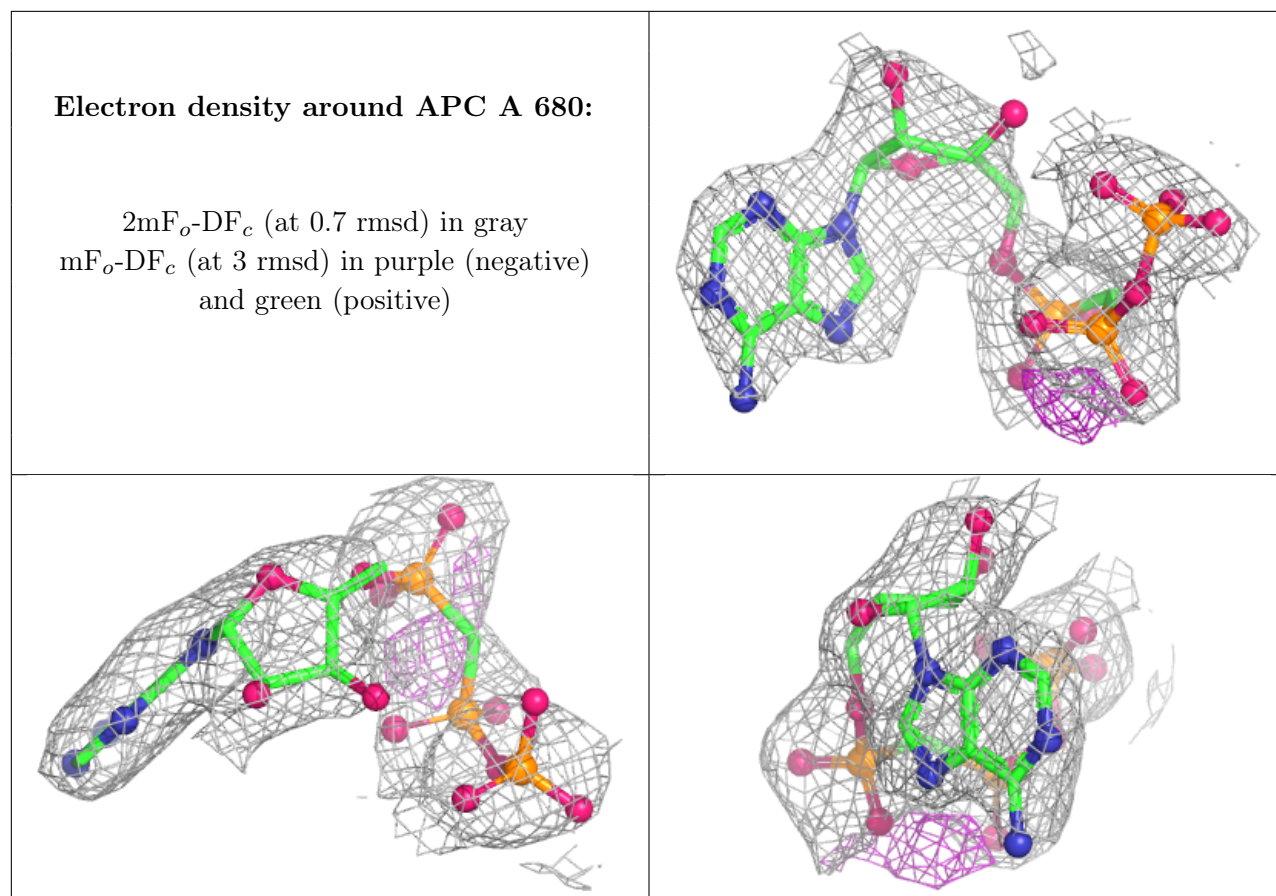
**Electron density around DND B 681:**

$2mF_o-DF_c$ (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.