



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 06:08 PM EDT

PDB ID : 4TM4 / pdb_00004tm4
Title : Kutzneria sp. 744 ornithine N-hydroxylase, KtzI-FADox-red-NADP+-Br
Authors : Setser, J.W.; Drennan, C.L.
Deposited on : 2014-05-30
Resolution : 2.63 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

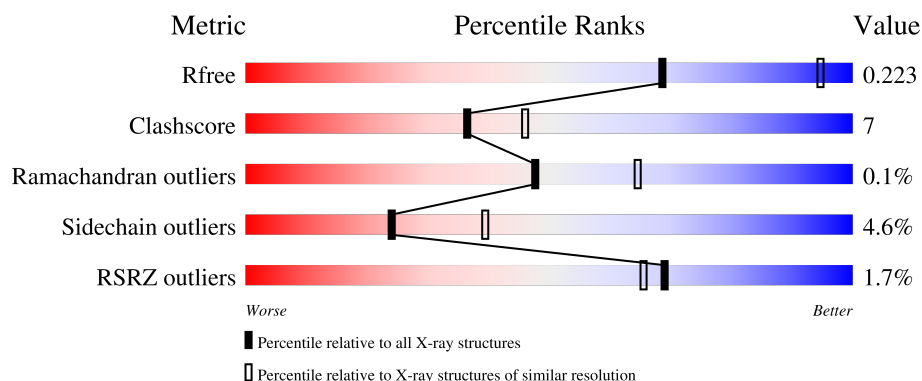
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.63 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	2053 (2.66-2.62)
Clashscore	190562	2097 (2.66-2.62)
Ramachandran outliers	187476	2066 (2.66-2.62)
Sidechain outliers	187428	2066 (2.66-2.62)
RSRZ outliers	180081	2052 (2.66-2.62)

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	443	
1	B	443	
1	C	443	
1	D	443	

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
4	BR	A	506	-	-	X	-
4	BR	D	509	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13418 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 KtzI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	0	0
			3189	2007	568	604	10			
1	B	415	Total	C	N	O	S	0	0	0
			3193	2009	569	605	10			
1	C	414	Total	C	N	O	S	0	0	0
			3153	1987	558	598	10			
1	D	414	Total	C	N	O	S	0	0	0
			3190	2007	573	600	10			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP A8CF85
A	-17	GLY	-	expression tag	UNP A8CF85
A	-16	SER	-	expression tag	UNP A8CF85
A	-15	SER	-	expression tag	UNP A8CF85
A	-14	HIS	-	expression tag	UNP A8CF85
A	-13	HIS	-	expression tag	UNP A8CF85
A	-12	HIS	-	expression tag	UNP A8CF85
A	-11	HIS	-	expression tag	UNP A8CF85
A	-10	HIS	-	expression tag	UNP A8CF85
A	-9	HIS	-	expression tag	UNP A8CF85
A	-8	SER	-	expression tag	UNP A8CF85
A	-7	SER	-	expression tag	UNP A8CF85
A	-6	GLY	-	expression tag	UNP A8CF85
A	-5	LEU	-	expression tag	UNP A8CF85
A	-4	VAL	-	expression tag	UNP A8CF85
A	-3	PRO	-	expression tag	UNP A8CF85
A	-2	ARG	-	expression tag	UNP A8CF85
A	-1	GLY	-	expression tag	UNP A8CF85
A	0	SER	-	expression tag	UNP A8CF85
A	1	HIS	-	expression tag	UNP A8CF85
A	2	MET	-	expression tag	UNP A8CF85

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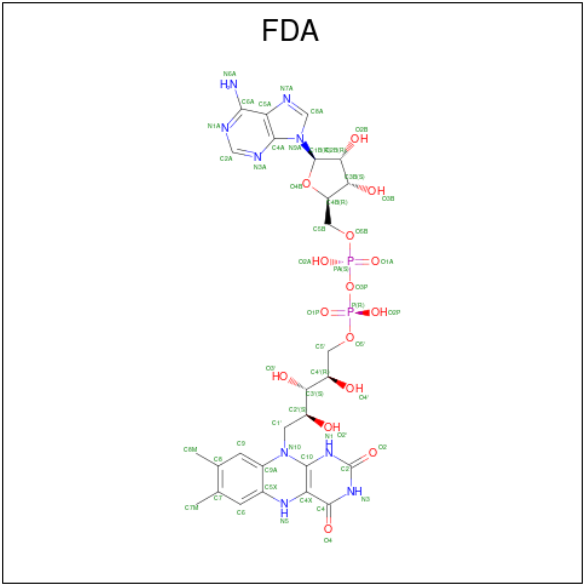
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	MET	-	initiating methionine	UNP A8CF85
B	-17	GLY	-	expression tag	UNP A8CF85
B	-16	SER	-	expression tag	UNP A8CF85
B	-15	SER	-	expression tag	UNP A8CF85
B	-14	HIS	-	expression tag	UNP A8CF85
B	-13	HIS	-	expression tag	UNP A8CF85
B	-12	HIS	-	expression tag	UNP A8CF85
B	-11	HIS	-	expression tag	UNP A8CF85
B	-10	HIS	-	expression tag	UNP A8CF85
B	-9	HIS	-	expression tag	UNP A8CF85
B	-8	SER	-	expression tag	UNP A8CF85
B	-7	SER	-	expression tag	UNP A8CF85
B	-6	GLY	-	expression tag	UNP A8CF85
B	-5	LEU	-	expression tag	UNP A8CF85
B	-4	VAL	-	expression tag	UNP A8CF85
B	-3	PRO	-	expression tag	UNP A8CF85
B	-2	ARG	-	expression tag	UNP A8CF85
B	-1	GLY	-	expression tag	UNP A8CF85
B	0	SER	-	expression tag	UNP A8CF85
B	1	HIS	-	expression tag	UNP A8CF85
B	2	MET	-	expression tag	UNP A8CF85
C	-18	MET	-	initiating methionine	UNP A8CF85
C	-17	GLY	-	expression tag	UNP A8CF85
C	-16	SER	-	expression tag	UNP A8CF85
C	-15	SER	-	expression tag	UNP A8CF85
C	-14	HIS	-	expression tag	UNP A8CF85
C	-13	HIS	-	expression tag	UNP A8CF85
C	-12	HIS	-	expression tag	UNP A8CF85
C	-11	HIS	-	expression tag	UNP A8CF85
C	-10	HIS	-	expression tag	UNP A8CF85
C	-9	HIS	-	expression tag	UNP A8CF85
C	-8	SER	-	expression tag	UNP A8CF85
C	-7	SER	-	expression tag	UNP A8CF85
C	-6	GLY	-	expression tag	UNP A8CF85
C	-5	LEU	-	expression tag	UNP A8CF85
C	-4	VAL	-	expression tag	UNP A8CF85
C	-3	PRO	-	expression tag	UNP A8CF85
C	-2	ARG	-	expression tag	UNP A8CF85
C	-1	GLY	-	expression tag	UNP A8CF85
C	0	SER	-	expression tag	UNP A8CF85
C	1	HIS	-	expression tag	UNP A8CF85
C	2	MET	-	expression tag	UNP A8CF85

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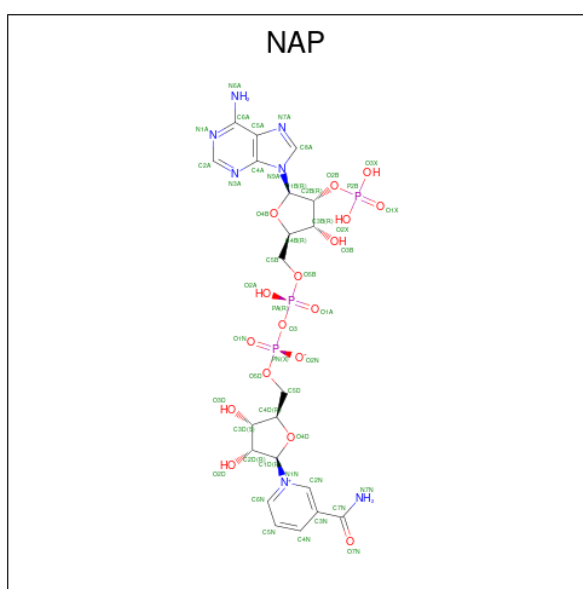
Chain	Residue	Modelled	Actual	Comment	Reference
D	-18	MET	-	initiating methionine	UNP A8CF85
D	-17	GLY	-	expression tag	UNP A8CF85
D	-16	SER	-	expression tag	UNP A8CF85
D	-15	SER	-	expression tag	UNP A8CF85
D	-14	HIS	-	expression tag	UNP A8CF85
D	-13	HIS	-	expression tag	UNP A8CF85
D	-12	HIS	-	expression tag	UNP A8CF85
D	-11	HIS	-	expression tag	UNP A8CF85
D	-10	HIS	-	expression tag	UNP A8CF85
D	-9	HIS	-	expression tag	UNP A8CF85
D	-8	SER	-	expression tag	UNP A8CF85
D	-7	SER	-	expression tag	UNP A8CF85
D	-6	GLY	-	expression tag	UNP A8CF85
D	-5	LEU	-	expression tag	UNP A8CF85
D	-4	VAL	-	expression tag	UNP A8CF85
D	-3	PRO	-	expression tag	UNP A8CF85
D	-2	ARG	-	expression tag	UNP A8CF85
D	-1	GLY	-	expression tag	UNP A8CF85
D	0	SER	-	expression tag	UNP A8CF85
D	1	HIS	-	expression tag	UNP A8CF85
D	2	MET	-	expression tag	UNP A8CF85

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



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		
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	10	Total	Br	0	0
			10	10		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	6	Total 6	Br 6	0	0
4	C	8	Total 8	Br 8	0	0
4	D	7	Total 7	Br 7	0	0

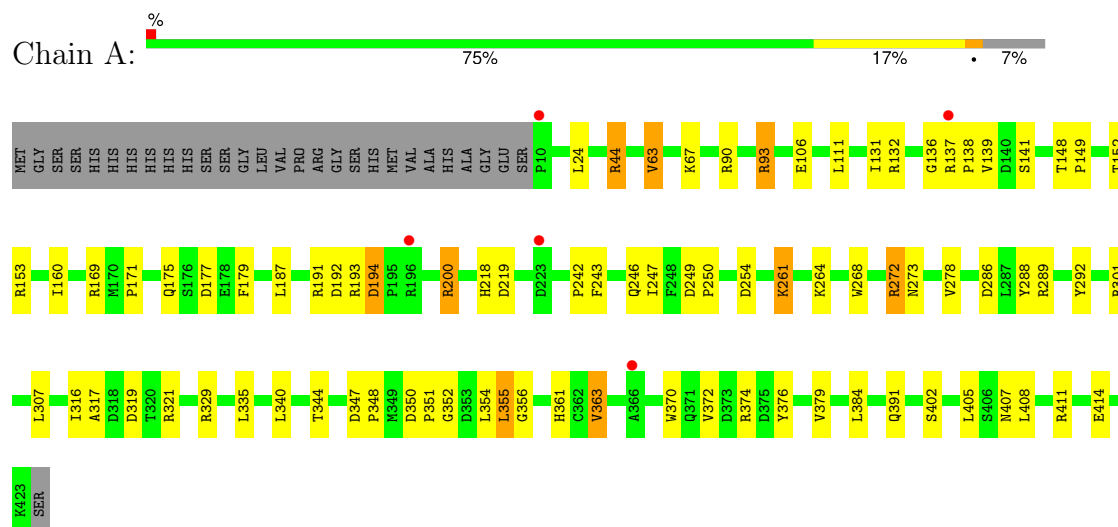
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	68	Total 68	O 68	0	0
5	B	68	Total 68	O 68	0	0
5	C	59	Total 59	O 59	0	0
5	D	63	Total 63	O 63	0	0

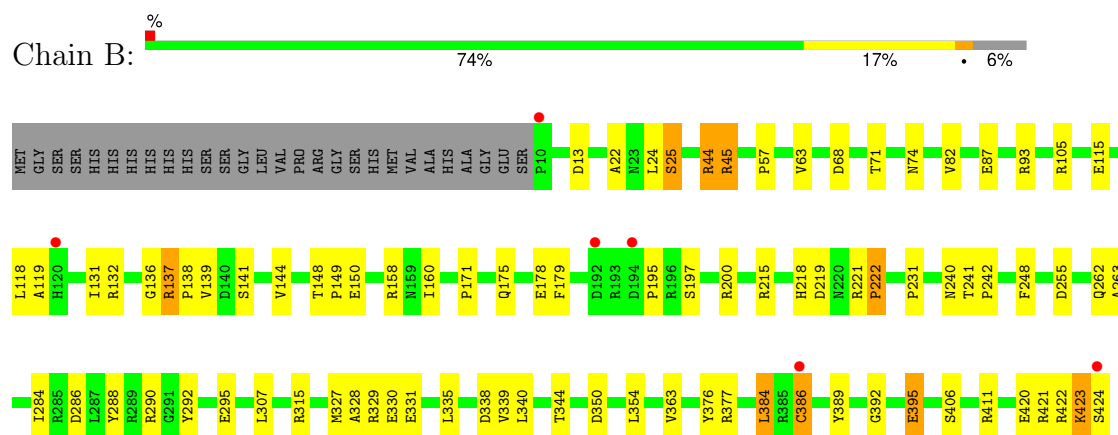
3 Residue-property plots [i](#)

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.

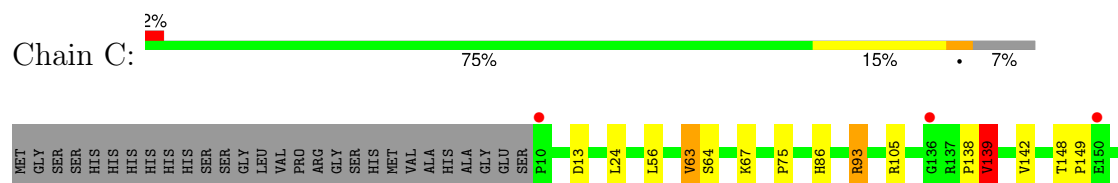
• Molecule 1: KtzI

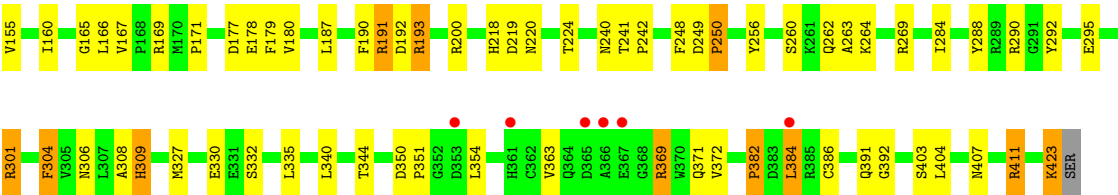


• Molecule 1: KtzI

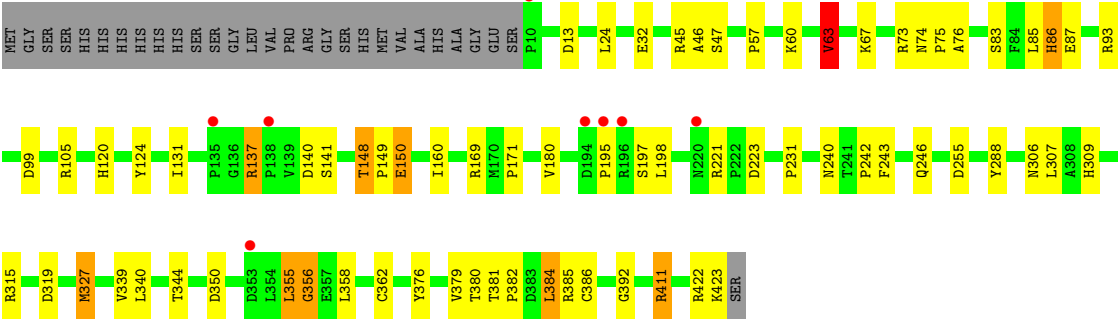
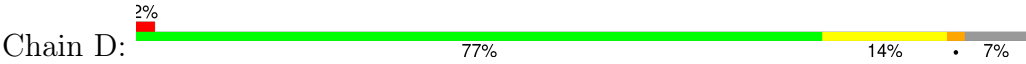


• Molecule 1: KtzI





● Molecule 1: KtzI



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.39Å 151.96Å 163.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.12 – 2.63 46.12 – 2.63	Depositor EDS
% Data completeness (in resolution range)	98.9 (46.12-2.63) 98.9 (46.12-2.63)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.193 , 0.223 0.198 , 0.223	Depositor DCC
R_{free} test set	3067 reflections (3.79%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.781	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 27.0	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	13418	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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: BR, NAP, FDA

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	1.01	7/3268 (0.2%)	0.98	9/4455 (0.2%)
1	B	1.01	13/3271 (0.4%)	0.96	7/4459 (0.2%)
1	C	1.10	21/3231 (0.6%)	1.00	11/4410 (0.2%)
1	D	1.10	17/3269 (0.5%)	1.03	16/4456 (0.4%)
All	All	1.06	58/13039 (0.4%)	0.99	43/17780 (0.2%)

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	221	ARG	C-N	8.71	1.40	1.33
1	B	350	ASP	C-O	-8.38	1.18	1.25
1	B	263	ALA	C-O	-7.36	1.15	1.24
1	C	304	PHE	C-O	-7.23	1.15	1.24
1	D	350	ASP	C-O	-7.11	1.19	1.25
1	C	308	ALA	C-O	-6.82	1.15	1.23
1	B	144	VAL	C-O	-6.75	1.17	1.24
1	C	169	ARG	C-O	-6.72	1.16	1.24
1	C	179	PHE	C-O	-6.33	1.15	1.24
1	B	137	ARG	C-O	-6.26	1.16	1.24
1	C	309	HIS	CA-C	-6.21	1.45	1.52
1	B	25	SER	C-O	-6.09	1.16	1.24
1	C	177	ASP	C-O	-6.02	1.17	1.24
1	D	221	ARG	CA-C	-5.98	1.46	1.52
1	C	180	VAL	C-O	-5.97	1.17	1.24
1	B	255	ASP	C-O	-5.94	1.17	1.24
1	C	330	GLU	C-O	-5.94	1.16	1.23
1	A	219	ASP	C-O	-5.76	1.16	1.24
1	D	362	CYS	C-O	-5.72	1.17	1.24
1	D	381	THR	C-N	5.71	1.40	1.34
1	D	85	LEU	C-O	-5.70	1.17	1.24
1	D	76	ALA	C-O	-5.70	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	219	ASP	C-O	-5.67	1.16	1.24
1	C	155	VAL	C-O	-5.62	1.18	1.24
1	A	350	ASP	C-N	5.62	1.40	1.33
1	B	339	VAL	C-O	-5.61	1.18	1.24
1	C	249	ASP	C-N	5.58	1.41	1.33
1	D	99	ASP	C-O	-5.51	1.17	1.24
1	C	301	ARG	C-O	-5.46	1.17	1.24
1	D	148	THR	C-N	5.45	1.40	1.34
1	A	372	VAL	C-O	-5.45	1.18	1.24
1	B	74	ASN	C-N	5.43	1.40	1.34
1	A	286	ASP	C-O	-5.41	1.17	1.24
1	D	306	ASN	C-O	-5.38	1.16	1.23
1	C	224	THR	C-O	-5.34	1.17	1.23
1	A	200	ARG	C-O	-5.34	1.18	1.24
1	A	177	ASP	C-O	-5.33	1.20	1.24
1	D	221	ARG	C-O	-5.33	1.18	1.24
1	C	250	PRO	N-CD	5.33	1.55	1.47
1	C	200	ARG	C-O	-5.32	1.18	1.24
1	C	382	PRO	N-CD	5.31	1.55	1.47
1	B	338	ASP	C-O	-5.30	1.17	1.24
1	B	119	ALA	C-O	-5.29	1.17	1.24
1	D	195	PRO	N-CD	5.28	1.55	1.47
1	D	149	PRO	N-CD	5.28	1.55	1.47
1	C	332	SER	C-O	-5.27	1.17	1.23
1	D	169	ARG	C-O	-5.25	1.17	1.24
1	D	45	ARG	C-O	-5.24	1.16	1.23
1	D	63	VAL	C-O	-5.22	1.18	1.24
1	C	351	PRO	N-CD	5.19	1.55	1.47
1	D	382	PRO	N-CD	5.18	1.54	1.47
1	C	304	PHE	CA-C	-5.15	1.46	1.52
1	B	222	PRO	C-O	-5.15	1.18	1.23
1	D	180	VAL	C-O	-5.13	1.18	1.24
1	A	152	THR	C-O	-5.09	1.17	1.23
1	C	372	VAL	C-O	-5.07	1.18	1.23
1	C	256	TYR	C-O	-5.06	1.18	1.24
1	C	309	HIS	C-O	-5.02	1.17	1.23

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	139	VAL	N-CA-C	9.60	121.51	108.84
1	A	402	SER	N-CA-C	8.88	120.57	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	165	GLY	N-CA-C	8.49	122.57	111.70
1	A	352	GLY	N-CA-C	7.18	122.85	114.16
1	A	355	LEU	N-CA-C	7.01	119.78	111.71
1	A	350	ASP	CA-C-N	-6.97	112.45	119.56
1	A	350	ASP	C-N-CA	-6.97	112.45	119.56
1	D	120	HIS	N-CA-C	6.76	119.67	110.55
1	D	148	THR	CA-C-N	-6.69	112.91	119.87
1	D	148	THR	C-N-CA	-6.69	112.91	119.87
1	A	191	ARG	N-CA-C	6.61	118.57	111.36
1	C	220	ASN	N-CA-C	6.52	121.36	113.41
1	B	221	ARG	CA-C-N	-6.51	113.45	121.00
1	B	221	ARG	C-N-CA	-6.51	113.45	121.00
1	B	74	ASN	CA-C-N	-6.31	113.19	119.56
1	B	74	ASN	C-N-CA	-6.31	113.19	119.56
1	B	392	GLY	N-CA-C	-6.24	106.03	111.95
1	A	317	ALA	CA-C-N	-6.04	113.61	122.86
1	A	317	ALA	C-N-CA	-6.04	113.61	122.86
1	D	356	GLY	N-CA-C	6.02	127.44	113.18
1	D	350	ASP	CA-C-N	-5.98	113.52	119.56
1	D	350	ASP	C-N-CA	-5.98	113.52	119.56
1	C	138	PRO	CB-CA-C	-5.98	97.06	112.00
1	B	423	LYS	N-CA-C	-5.90	104.93	111.36
1	D	392	GLY	N-CA-C	-5.81	106.43	111.95
1	A	363	VAL	N-CA-C	5.63	116.84	108.23
1	D	86	HIS	N-CA-C	5.62	117.09	111.07
1	D	63	VAL	CB-CA-C	5.61	119.45	110.82
1	C	167	VAL	N-CA-C	5.56	114.00	107.77
1	D	381	THR	CA-C-N	-5.49	114.11	120.04
1	D	381	THR	C-N-CA	-5.49	114.11	120.04
1	C	350	ASP	CA-C-N	-5.49	113.38	119.19
1	C	350	ASP	C-N-CA	-5.49	113.38	119.19
1	C	64	SER	N-CA-C	5.37	117.22	110.24
1	D	379	VAL	N-CA-C	5.31	115.91	108.89
1	D	355	LEU	N-CA-C	5.29	119.72	113.16
1	D	74	ASN	CA-C-N	-5.29	113.23	119.84
1	D	74	ASN	C-N-CA	-5.29	113.23	119.84
1	C	219	ASP	N-CA-C	5.28	117.94	111.82
1	D	46	ALA	N-CA-C	5.17	118.69	112.38
1	C	392	GLY	N-CA-C	-5.12	107.09	111.95
1	B	363	VAL	N-CA-C	5.06	115.57	108.89
1	C	177	ASP	N-CA-CB	-5.00	102.69	111.49

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	3189	0	3015	54	0
1	B	3193	0	3016	55	0
1	C	3153	0	2953	46	0
1	D	3190	0	3020	49	0
2	A	53	0	29	4	0
2	B	53	0	30	2	0
2	C	53	0	30	0	0
2	D	53	0	30	0	0
3	A	48	0	25	0	0
3	B	48	0	25	0	0
3	C	48	0	25	0	0
3	D	48	0	25	0	0
4	A	10	0	0	4	0
4	B	6	0	0	1	0
4	C	8	0	0	0	0
4	D	7	0	0	4	0
5	A	68	0	0	2	0
5	B	68	0	0	2	0
5	C	59	0	0	3	0
5	D	63	0	0	3	0
All	All	13418	0	12223	183	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 7.

All (183) 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:A:63:VAL:HG22	1:A:67:LYS:HD2	1.48	0.93
1:D:137:ARG:HG2	1:D:137:ARG:HH11	1.36	0.91
1:D:380:THR:HG21	1:D:384:LEU:HD12	1.55	0.87
1:A:193:ARG:HG2	1:A:193:ARG:HH11	1.38	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:VAL:HB	1:C:384:LEU:HD23	1.54	0.86
1:A:414:GLU:OE1	4:A:506:BR:BR	2.50	0.85
1:C:139:VAL:HB	1:C:384:LEU:CD2	2.06	0.84
1:B:218:HIS:CE1	1:B:290:ARG:HG2	2.21	0.75
1:D:380:THR:CG2	1:D:384:LEU:HD12	2.16	0.75
1:A:194:ASP:OD2	1:A:194:ASP:N	2.18	0.73
1:C:93:ARG:NH2	5:C:648:HOH:O	2.21	0.73
1:A:169:ARG:NH1	1:A:344:THR:O	2.23	0.71
1:A:44:ARG:HG2	2:A:501:FDA:C4A	2.21	0.70
1:B:132:ARG:CB	1:B:132:ARG:HH11	2.04	0.70
1:A:192:ASP:OD1	1:A:193:ARG:NH1	2.24	0.70
1:B:240:ASN:ND2	5:B:663:HOH:O	2.25	0.69
1:D:13:ASP:OD1	1:D:423:LYS:HE2	1.92	0.69
1:B:179:PHE:CD2	1:B:315:ARG:HD3	2.28	0.69
1:D:240:ASN:ND2	5:D:658:HOH:O	2.27	0.67
1:D:380:THR:HG21	1:D:384:LEU:CD1	2.24	0.67
1:B:377:ARG:NH2	1:B:422:ARG:CZ	2.58	0.67
1:C:218:HIS:CD2	1:C:301:ARG:NH1	2.63	0.66
1:D:198:LEU:CD2	1:D:339:VAL:HG23	2.26	0.66
1:A:90:ARG:NH2	1:A:106:GLU:OE2	2.28	0.66
1:A:273:ASN:HB2	5:A:665:HOH:O	1.95	0.66
1:B:148:THR:HB	1:B:149:PRO:HD2	1.78	0.66
1:B:141:SER:HA	1:B:386:CYS:SG	2.36	0.65
1:B:13:ASP:OD1	1:B:423:LYS:NZ	2.29	0.65
1:A:63:VAL:CG2	1:A:67:LYS:HD2	2.25	0.65
1:A:93:ARG:HD2	1:C:292:TYR:HD2	1.61	0.64
1:D:198:LEU:HD22	1:D:339:VAL:CG2	2.27	0.64
1:A:148:THR:HB	1:A:149:PRO:HD2	1.78	0.64
1:A:261:LYS:HE3	1:A:264:LYS:HD2	1.79	0.64
1:B:377:ARG:HH21	1:B:422:ARG:NH2	1.96	0.64
1:B:423:LYS:O	1:B:424:SER:CB	2.46	0.63
1:D:148:THR:OG1	1:D:150:GLU:HG2	1.98	0.63
1:A:218:HIS:CD2	1:A:301:ARG:NH2	2.67	0.63
1:C:148:THR:HB	1:C:149:PRO:HD2	1.79	0.62
1:B:132:ARG:HB2	1:B:132:ARG:NH1	2.14	0.62
1:A:44:ARG:HD2	2:A:501:FDA:O2B	1.99	0.62
1:A:193:ARG:HG2	1:A:193:ARG:NH1	2.09	0.61
1:B:295:GLU:OE2	1:D:93:ARG:NH1	2.34	0.60
1:B:377:ARG:NH2	1:B:422:ARG:NH2	2.50	0.60
1:D:198:LEU:CD2	1:D:339:VAL:CG2	2.79	0.60
1:C:86:HIS:CG	1:D:75:PRO:HG3	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:307:LEU:HD12	4:D:508:BR:BR	2.57	0.59
1:D:63:VAL:HG13	1:D:67:LYS:HB2	1.85	0.58
1:A:44:ARG:HG2	2:A:501:FDA:N3A	2.19	0.57
1:A:200:ARG:NH1	1:A:319:ASP:OD1	2.20	0.57
1:A:405:LEU:HD22	1:A:408:LEU:HD11	1.85	0.57
1:D:32:GLU:OE1	1:D:73:ARG:NH2	2.37	0.57
1:B:132:ARG:HH11	1:B:132:ARG:HB2	1.66	0.56
1:D:198:LEU:HD22	1:D:339:VAL:HG23	1.85	0.56
1:B:44:ARG:HD2	2:B:501:FDA:C4A	2.36	0.56
1:C:63:VAL:HG22	1:C:67:LYS:CD	2.36	0.56
1:D:137:ARG:HG2	1:D:137:ARG:NH1	2.11	0.56
1:C:178:GLU:O	1:C:193:ARG:NH1	2.36	0.55
1:B:329:ARG:O	1:B:330:GLU:HB2	2.07	0.54
1:A:131:ILE:HD13	1:A:160:ILE:HD13	1.90	0.54
1:B:242:PRO:HB2	1:C:288:TYR:CD1	2.43	0.54
1:C:363:VAL:O	1:C:371:GLN:HG3	2.08	0.54
1:A:93:ARG:HD2	1:C:292:TYR:CD2	2.42	0.54
1:C:190:PHE:O	1:C:191:ARG:C	2.50	0.53
1:D:140:ASP:C	1:D:386:CYS:SG	2.91	0.53
1:C:63:VAL:HG22	1:C:67:LYS:HD3	1.91	0.53
1:B:131:ILE:HD13	1:B:160:ILE:HD13	1.90	0.53
1:A:249:ASP:OD2	1:A:250:PRO:HD2	2.09	0.53
1:A:351:PRO:HG2	1:A:370:TRP:CD1	2.43	0.53
1:D:243:PHE:O	1:D:246:GLN:HB2	2.09	0.53
1:B:376:TYR:CE1	1:B:411:ARG:HG3	2.44	0.53
1:B:139:VAL:HB	1:B:384:LEU:HD23	1.91	0.52
1:D:137:ARG:HH11	1:D:137:ARG:CG	2.13	0.52
1:A:179:PHE:HD2	4:A:510:BR:BR	2.47	0.52
1:A:292:TYR:HD2	1:C:93:ARG:HD2	1.75	0.52
1:C:139:VAL:HB	1:C:384:LEU:HD21	1.90	0.51
1:A:363:VAL:HG21	1:A:379:VAL:HG12	1.93	0.51
1:D:60:LYS:NZ	5:D:641:HOH:O	2.25	0.51
1:B:44:ARG:HG2	1:B:45:ARG:N	2.25	0.51
1:B:288:TYR:CG	1:C:242:PRO:HB2	2.46	0.51
1:B:44:ARG:HG2	1:B:45:ARG:HG2	1.92	0.50
1:B:288:TYR:CD1	1:C:242:PRO:HB2	2.46	0.50
1:B:292:TYR:HD2	1:D:93:ARG:HG2	1.75	0.50
1:A:171:PRO:HG3	1:A:344:THR:HG21	1.92	0.50
1:C:240:ASN:ND2	5:C:656:HOH:O	2.36	0.50
1:D:231:PRO:O	1:D:307:LEU:HA	2.12	0.50
1:A:132:ARG:NH1	1:A:132:ARG:HB2	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ASN:O	1:A:278:VAL:HG21	2.12	0.49
1:D:197:SER:O	1:D:198:LEU:HG	2.13	0.49
1:D:57:PRO:HB2	4:D:506:BR:BR	2.68	0.49
1:A:243:PHE:O	1:A:246:GLN:HB2	2.12	0.49
1:D:63:VAL:HG22	1:D:67:LYS:HD2	1.95	0.49
1:C:56:LEU:HD23	1:C:187:LEU:HD11	1.94	0.48
1:A:391:GLN:HB3	1:A:411:ARG:HH21	1.77	0.48
1:D:315:ARG:HD2	1:D:319:ASP:O	2.13	0.48
1:C:218:HIS:CE1	1:C:290:ARG:HB3	2.49	0.48
1:D:422:ARG:HG2	1:D:422:ARG:HH11	1.79	0.48
1:D:355:LEU:O	1:D:358:LEU:N	2.47	0.48
1:A:137:ARG:HA	1:A:138:PRO:C	2.39	0.47
1:B:22:ALA:O	1:B:25:SER:HB3	2.13	0.47
1:D:243:PHE:HB2	5:D:601:HOH:O	2.14	0.47
1:B:376:TYR:CZ	1:B:411:ARG:HG3	2.49	0.47
1:C:193:ARG:HG2	1:C:193:ARG:HH21	1.80	0.47
1:A:307:LEU:HD12	4:D:509:BR:BR	2.70	0.47
1:B:195:PRO:C	1:B:197:SER:H	2.23	0.47
1:D:131:ILE:HD13	1:D:160:ILE:HD13	1.96	0.47
1:A:218:HIS:CD2	1:A:301:ARG:HH21	2.31	0.47
1:A:242:PRO:HB2	1:D:288:TYR:CG	2.50	0.47
1:C:75:PRO:HD3	1:D:86:HIS:CD2	2.50	0.47
1:C:391:GLN:HB3	1:C:411:ARG:NH1	2.29	0.47
1:B:132:ARG:CB	1:B:132:ARG:NH1	2.73	0.47
1:B:171:PRO:HG3	1:B:344:THR:HG21	1.96	0.47
1:D:223:ASP:OD2	1:D:223:ASP:N	2.48	0.46
1:B:384:LEU:HD22	1:B:386:CYS:H	1.80	0.46
1:B:179:PHE:HD2	1:B:315:ARG:HD3	1.80	0.46
1:C:193:ARG:HH21	1:C:193:ARG:CG	2.29	0.46
1:B:82:VAL:HG23	5:B:602:HOH:O	2.16	0.46
1:B:328:ALA:HA	1:C:263:ALA:HB2	1.98	0.46
1:A:44:ARG:CG	2:A:501:FDA:N3A	2.79	0.46
1:A:153:ARG:NH2	4:A:508:BR:BR	2.94	0.46
1:A:407:ASN:ND2	4:A:506:BR:BR	3.04	0.45
1:B:241:THR:HB	1:C:284:ILE:HG21	1.98	0.45
1:B:377:ARG:NH2	1:B:422:ARG:NH1	2.65	0.45
1:D:83:SER:O	1:D:87:GLU:HG3	2.16	0.45
1:C:304:PHE:HB3	1:C:306:ASN:ND2	2.31	0.45
1:D:198:LEU:HD22	1:D:339:VAL:HG21	1.97	0.45
1:A:316:ILE:HD12	1:A:321:ARG:HD2	1.97	0.45
1:D:137:ARG:NH1	1:D:137:ARG:CG	2.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ARG:NE	1:C:295:GLU:OE2	2.41	0.45
1:D:171:PRO:HG3	1:D:344:THR:HG21	1.99	0.45
1:A:361:HIS:CB	1:A:384:LEU:HG	2.47	0.45
1:C:260:SER:O	1:C:264:LYS:HG3	2.18	0.44
1:D:197:SER:C	1:D:198:LEU:HG	2.42	0.44
1:B:136:GLY:C	1:B:137:ARG:HG2	2.43	0.44
1:B:231:PRO:O	1:B:307:LEU:HA	2.18	0.44
1:B:377:ARG:HD3	1:B:389:TYR:CZ	2.52	0.44
1:B:178:GLU:HG2	1:B:179:PHE:CE1	2.53	0.44
1:B:262:GLN:NE2	1:C:327:MET:HG2	2.33	0.44
1:C:63:VAL:HG22	1:C:67:LYS:HD2	1.99	0.44
1:C:171:PRO:HG3	1:C:344:THR:HG21	1.98	0.44
1:A:139:VAL:CG1	1:A:141:SER:O	2.66	0.43
1:B:242:PRO:HB2	1:C:288:TYR:CG	2.53	0.43
1:D:141:SER:N	1:D:386:CYS:SG	2.91	0.43
1:B:150:GLU:H	1:B:150:GLU:CD	2.26	0.43
1:D:376:TYR:CZ	1:D:411:ARG:HG3	2.53	0.43
1:C:13:ASP:OD1	1:C:423:LYS:NZ	2.49	0.43
1:C:369:ARG:HE	1:C:369:ARG:HB2	1.65	0.43
1:B:44:ARG:HD3	2:B:501:FDA:O2B	2.19	0.43
1:B:215:ARG:HD2	1:B:286:ASP:OD2	2.19	0.43
1:C:250:PRO:HG3	1:C:407:ASN:OD1	2.18	0.43
1:D:47:SER:HA	1:D:124:TYR:CD1	2.54	0.42
1:A:193:ARG:NH1	1:A:193:ARG:CG	2.73	0.42
1:A:169:ARG:NH2	5:A:627:HOH:O	2.53	0.42
1:A:90:ARG:HD2	1:C:295:GLU:HG2	2.01	0.42
1:D:141:SER:CA	1:D:386:CYS:SG	3.08	0.42
1:A:288:TYR:CD1	1:D:242:PRO:HB2	2.55	0.42
1:B:284:ILE:HG21	1:C:241:THR:HB	2.02	0.42
1:C:187:LEU:HD23	1:C:187:LEU:HA	1.79	0.42
1:A:254:ASP:OD1	1:A:374:ARG:NH2	2.51	0.42
1:A:218:HIS:CG	1:A:301:ARG:NH2	2.88	0.41
1:A:268:TRP:O	1:A:272:ARG:HB3	2.19	0.41
1:C:142:VAL:HG13	1:C:386:CYS:SG	2.60	0.41
1:A:347:ASP:HA	1:A:348:PRO:HD3	1.89	0.41
1:B:115:GLU:O	1:B:118:LEU:HB2	2.20	0.41
1:B:248:PHE:HB3	1:B:406:SER:HB2	2.02	0.41
1:C:411:ARG:NH1	5:C:618:HOH:O	2.53	0.41
1:A:355:LEU:O	1:A:356:GLY:C	2.64	0.41
1:A:376:TYR:CE2	1:A:411:ARG:HD2	2.54	0.41
1:B:68:ASP:CG	1:B:71:THR:HG1	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:255:ASP:HB3	4:D:509:BR:BR	2.75	0.41
1:D:422:ARG:HG2	1:D:422:ARG:NH1	2.36	0.41
1:A:24:LEU:HD23	1:A:111:LEU:HD22	2.03	0.41
1:A:187:LEU:HA	1:A:187:LEU:HD23	1.75	0.40
1:B:292:TYR:CD2	1:D:93:ARG:HG2	2.55	0.40
1:B:395:GLU:H	1:B:395:GLU:HG2	1.54	0.40
1:D:198:LEU:CD2	1:D:339:VAL:HG21	2.49	0.40
1:B:158:ARG:O	1:B:386:CYS:SG	2.77	0.40
1:C:166:LEU:HD21	1:C:403:SER:HB2	2.02	0.40
1:B:57:PRO:HB2	4:B:504:BR:BR	2.77	0.40
1:C:248:PHE:CE1	1:C:404:LEU:HD12	2.57	0.40
1:D:309:HIS:CE1	1:D:327:MET:HE2	2.55	0.40
1:B:137:ARG:HA	1:B:138:PRO:C	2.46	0.40
1:B:327:MET:HG2	1:C:262:GLN:NE2	2.36	0.40
1:C:63:VAL:CG2	1:C:67:LYS:HD3	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	412/443 (93%)	391 (95%)	20 (5%)	1 (0%)	43	58
1	B	413/443 (93%)	396 (96%)	17 (4%)	0	100	100
1	C	412/443 (93%)	389 (94%)	23 (6%)	0	100	100
1	D	412/443 (93%)	390 (95%)	21 (5%)	1 (0%)	43	58
All	All	1649/1772 (93%)	1566 (95%)	81 (5%)	2 (0%)	48	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	GLY
1	D	356	GLY

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	332/372 (89%)	319 (96%)	13 (4%)	28	47
1	B	331/372 (89%)	312 (94%)	19 (6%)	18	31
1	C	323/372 (87%)	304 (94%)	19 (6%)	18	29
1	D	331/372 (89%)	321 (97%)	10 (3%)	36	56
All	All	1317/1488 (88%)	1256 (95%)	61 (5%)	24	39

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	63	VAL
1	A	93	ARG
1	A	175	GLN
1	A	194	ASP
1	A	247	ILE
1	A	261	LYS
1	A	272	ARG
1	A	289	ARG
1	A	329	ARG
1	A	335	LEU
1	A	340	LEU
1	A	354	LEU
1	B	24	LEU
1	B	44	ARG
1	B	45	ARG
1	B	63	VAL
1	B	87	GLU
1	B	93	ARG
1	B	105	ARG

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Mol	Chain	Res	Type
1	B	175	GLN
1	B	200	ARG
1	B	222	PRO
1	B	331	GLU
1	B	335	LEU
1	B	340	LEU
1	B	354	LEU
1	B	384	LEU
1	B	386	CYS
1	B	395	GLU
1	B	420	GLU
1	B	421	ARG
1	C	24	LEU
1	C	63	VAL
1	C	93	ARG
1	C	105	ARG
1	C	139	VAL
1	C	160	ILE
1	C	191	ARG
1	C	192	ASP
1	C	193	ARG
1	C	269	ARG
1	C	309	HIS
1	C	335	LEU
1	C	340	LEU
1	C	354	LEU
1	C	369	ARG
1	C	382	PRO
1	C	384	LEU
1	C	411	ARG
1	C	423	LYS
1	D	24	LEU
1	D	63	VAL
1	D	105	ARG
1	D	137	ARG
1	D	150	GLU
1	D	327	MET
1	D	340	LEU
1	D	384	LEU
1	D	385	ARG
1	D	411	ARG

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	86	HIS
1	A	240	ASN
1	A	273	ASN
1	A	306	ASN
1	B	62	GLN
1	B	86	HIS
1	B	189	HIS
1	B	240	ASN
1	B	262	GLN
1	B	306	ASN
1	B	309	HIS
1	C	86	HIS
1	C	262	GLN
1	D	86	HIS
1	D	98	HIS
1	D	227	HIS
1	D	240	ASN
1	D	246	GLN
1	D	262	GLN
1	D	306	ASN
1	D	309	HIS
1	D	361	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](#)

Of 39 ligands modelled in this entry, 31 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FDA	C	501	-	57,58,58	2.26	19 (33%)	78,89,89	2.59	25 (32%)
2	FDA	B	501	-	57,58,58	2.16	19 (33%)	78,89,89	2.57	25 (32%)
2	FDA	D	501	-	57,58,58	2.14	16 (28%)	78,89,89	1.59	13 (16%)
2	FDA	A	501	-	57,58,58	2.25	20 (35%)	78,89,89	2.06	20 (25%)
3	NAP	C	502	-	50,52,52	1.72	9 (18%)	71,80,80	1.67	16 (22%)
3	NAP	B	502	-	50,52,52	1.57	6 (12%)	71,80,80	1.70	16 (22%)
3	NAP	A	502	-	50,52,52	1.60	7 (14%)	71,80,80	1.70	15 (21%)
3	NAP	D	502	-	50,52,52	1.45	7 (14%)	71,80,80	2.07	16 (22%)

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
2	FDA	C	501	-	-	5/34/50/50	0/6/6/6
2	FDA	B	501	-	-	9/34/50/50	0/6/6/6
2	FDA	D	501	-	-	8/34/50/50	0/6/6/6
2	FDA	A	501	-	-	3/34/50/50	0/6/6/6
3	NAP	C	502	-	-	4/35/67/67	0/5/5/5
3	NAP	B	502	-	-	4/35/67/67	0/5/5/5
3	NAP	A	502	-	-	5/35/67/67	0/5/5/5
3	NAP	D	502	-	-	7/35/67/67	0/5/5/5

All (103) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FDA	C6A-N6A	5.63	1.48	1.34
2	C	501	FDA	C6A-N6A	5.61	1.48	1.34
2	B	501	FDA	C6A-N6A	5.61	1.48	1.34
3	C	502	NAP	PN-O3	-5.53	1.53	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	FDA	O2B-C2B	-5.51	1.29	1.43
2	A	501	FDA	O2B-C2B	-5.50	1.29	1.43
2	D	501	FDA	C6A-N6A	5.41	1.48	1.34
2	D	501	FDA	O2B-C2B	-5.15	1.30	1.43
2	B	501	FDA	O2B-C2B	-5.11	1.30	1.43
2	A	501	FDA	PA-O3P	-4.80	1.54	1.59
3	A	502	NAP	C6A-N6A	4.78	1.46	1.34
3	D	502	NAP	C6A-N6A	4.68	1.46	1.34
3	B	502	NAP	C6A-N6A	4.62	1.46	1.34
3	B	502	NAP	C3B-C2B	-4.56	1.43	1.53
3	C	502	NAP	C7N-N7N	4.56	1.41	1.33
3	A	502	NAP	PN-O3	-4.55	1.54	1.59
2	B	501	FDA	C10-N1	4.29	1.44	1.37
2	D	501	FDA	C2-N1	4.27	1.44	1.37
2	C	501	FDA	C10-N1	4.27	1.44	1.37
2	B	501	FDA	C2-N1	4.26	1.44	1.37
2	A	501	FDA	C2-N3	4.22	1.44	1.37
2	D	501	FDA	C10-N1	4.21	1.44	1.37
2	D	501	FDA	C9A-N10	-4.15	1.34	1.41
2	A	501	FDA	C9A-N10	-4.12	1.34	1.41
2	C	501	FDA	C2-N1	4.09	1.44	1.37
3	C	502	NAP	C6A-N6A	4.08	1.44	1.34
3	A	502	NAP	C7N-N7N	4.03	1.40	1.33
2	C	501	FDA	P-O3P	3.99	1.63	1.59
3	D	502	NAP	C2D-C3D	-3.97	1.42	1.53
3	A	502	NAP	C3B-C2B	-3.92	1.44	1.53
2	A	501	FDA	C10-N1	3.91	1.44	1.37
3	B	502	NAP	C7N-N7N	3.91	1.40	1.33
2	B	501	FDA	C2-N3	3.83	1.43	1.37
2	C	501	FDA	C2B-C3B	-3.82	1.43	1.53
2	D	501	FDA	C2B-C3B	-3.81	1.43	1.53
2	D	501	FDA	C2-N3	3.79	1.43	1.37
3	B	502	NAP	C2D-C3D	-3.79	1.43	1.53
3	C	502	NAP	C3B-C2B	-3.74	1.44	1.53
2	A	501	FDA	C2B-C3B	-3.67	1.43	1.53
2	A	501	FDA	C2-N1	3.65	1.43	1.37
2	B	501	FDA	C5X-N5	-3.65	1.33	1.39
2	C	501	FDA	C9A-N10	-3.63	1.34	1.41
2	B	501	FDA	O3'-C3'	-3.58	1.34	1.43
3	C	502	NAP	C2D-C3D	-3.53	1.43	1.53
2	B	501	FDA	C2B-C3B	-3.51	1.43	1.53
3	D	502	NAP	C7N-N7N	3.47	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FDA	O2'-C2'	-3.47	1.36	1.43
2	C	501	FDA	C5X-N5	-3.47	1.34	1.39
2	B	501	FDA	C9A-N10	-3.43	1.35	1.41
2	D	501	FDA	O3'-C3'	-3.42	1.34	1.43
2	D	501	FDA	PA-O3P	-3.38	1.55	1.59
2	C	501	FDA	C2-N3	3.38	1.43	1.37
2	B	501	FDA	PA-O1A	3.38	1.62	1.50
2	C	501	FDA	O2'-C2'	-3.31	1.36	1.43
3	D	502	NAP	C3B-C2B	-3.28	1.45	1.53
2	D	501	FDA	O4'-C4'	-3.24	1.36	1.43
2	C	501	FDA	O3'-C3'	-3.23	1.35	1.43
3	A	502	NAP	C2D-C3D	-3.23	1.44	1.53
2	B	501	FDA	O2'-C2'	-3.19	1.36	1.43
2	C	501	FDA	PA-O1A	3.12	1.61	1.50
2	A	501	FDA	O4'-C4'	-3.11	1.36	1.43
3	B	502	NAP	PN-O3	-3.09	1.56	1.59
2	A	501	FDA	O3'-C3'	-3.06	1.35	1.43
2	A	501	FDA	C1'-N10	3.05	1.55	1.47
2	C	501	FDA	O4'-C4'	-3.04	1.37	1.43
2	D	501	FDA	O2'-C2'	-2.98	1.37	1.43
2	A	501	FDA	C5X-N5	-2.97	1.34	1.39
2	D	501	FDA	C5X-N5	-2.95	1.34	1.39
2	B	501	FDA	P-O3P	2.84	1.62	1.59
2	C	501	FDA	C1'-N10	2.83	1.54	1.47
2	B	501	FDA	O4'-C4'	-2.83	1.37	1.43
3	C	502	NAP	O4D-C4D	-2.73	1.38	1.45
2	D	501	FDA	C1'-C2'	-2.70	1.48	1.52
2	C	501	FDA	C8A-N7A	2.57	1.36	1.31
2	A	501	FDA	O4B-C1B	-2.55	1.36	1.42
2	A	501	FDA	PA-O1A	2.53	1.59	1.50
3	C	502	NAP	O4D-C1D	2.52	1.44	1.40
3	D	502	NAP	C5A-N7A	-2.48	1.34	1.39
3	D	502	NAP	PA-O3	2.48	1.62	1.59
3	B	502	NAP	O4D-C1D	2.43	1.44	1.40
2	C	501	FDA	O4B-C1B	-2.40	1.36	1.42
2	A	501	FDA	C4X-C4	2.38	1.49	1.41
3	C	502	NAP	C5A-N7A	-2.37	1.34	1.39
2	D	501	FDA	PA-O1A	2.31	1.58	1.50
2	B	501	FDA	C4X-C4	2.30	1.48	1.41
2	B	501	FDA	C1'-N10	2.28	1.53	1.47
3	A	502	NAP	O4D-C4D	-2.24	1.40	1.45
2	C	501	FDA	C5'-C4'	2.23	1.54	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FDA	C5A-N7A	-2.22	1.35	1.39
2	D	501	FDA	O4B-C1B	-2.21	1.36	1.42
2	C	501	FDA	C5X-C9A	-2.18	1.38	1.40
2	A	501	FDA	C5X-C9A	-2.17	1.38	1.40
2	C	501	FDA	C4X-C4	2.16	1.48	1.41
2	B	501	FDA	C1'-C2'	-2.13	1.49	1.52
2	A	501	FDA	C5'-C4'	2.11	1.54	1.51
3	D	502	NAP	O4D-C4D	-2.11	1.40	1.45
2	A	501	FDA	O2-C2	2.08	1.27	1.23
3	C	502	NAP	C8A-N9A	-2.07	1.34	1.37
2	D	501	FDA	C8A-N7A	2.05	1.35	1.31
2	B	501	FDA	C8A-N7A	2.02	1.35	1.31
3	A	502	NAP	O4D-C1D	2.02	1.43	1.40
2	B	501	FDA	C5X-C9A	-2.01	1.38	1.40
2	B	501	FDA	O4B-C1B	-2.01	1.37	1.42

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	FDA	O3P-PA-O1A	-9.69	81.55	110.70
2	B	501	FDA	O3P-PA-O1A	-9.40	82.43	110.70
2	B	501	FDA	O2A-PA-O3P	-8.52	84.24	107.27
2	B	501	FDA	O5'-P-O1P	-8.26	76.18	108.94
3	D	502	NAP	O2A-PA-O3	-7.86	86.02	107.27
2	A	501	FDA	O5'-P-O1P	-7.31	79.96	108.94
2	C	501	FDA	O5'-P-O1P	-7.18	80.49	108.94
2	C	501	FDA	O2A-PA-O3P	-6.44	89.88	107.27
3	D	502	NAP	O3-PA-O1A	-5.76	93.37	110.70
3	C	502	NAP	C5A-C4A-N3A	-5.74	118.81	126.72
2	C	501	FDA	O2P-P-O3P	5.58	122.36	107.27
3	D	502	NAP	C5A-C4A-N3A	-5.42	119.25	126.72
2	C	501	FDA	O2P-P-O5'	-5.37	83.23	107.57
3	B	502	NAP	N3A-C2A-N1A	-5.25	120.63	128.58
3	A	502	NAP	C5A-C4A-N3A	-5.19	119.58	126.72
3	A	502	NAP	N3A-C2A-N1A	-5.14	120.80	128.58
2	C	501	FDA	C4-N3-C2	-5.09	119.36	126.37
2	A	501	FDA	C4-N3-C2	-4.90	119.63	126.37
3	D	502	NAP	N3A-C2A-N1A	-4.76	121.37	128.58
2	A	501	FDA	N3A-C2A-N1A	-4.72	121.43	128.58
2	A	501	FDA	O2P-P-O5'	-4.61	86.67	107.57
3	B	502	NAP	C5A-C4A-N3A	-4.57	120.42	126.72
2	C	501	FDA	N3A-C2A-N1A	-4.45	121.85	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	FDA	O3P-P-O1P	4.38	123.88	110.70
2	B	501	FDA	O2P-P-O5'	-4.38	87.72	107.57
2	A	501	FDA	O3P-P-O1P	4.26	123.52	110.70
2	D	501	FDA	N3A-C2A-N1A	-4.25	122.15	128.58
2	B	501	FDA	C4-N3-C2	-4.20	120.58	126.37
2	B	501	FDA	O2P-P-O3P	4.19	118.59	107.27
2	C	501	FDA	C5A-C4A-N3A	-4.17	120.97	126.72
3	C	502	NAP	N3A-C4A-N9A	4.14	134.22	127.17
2	A	501	FDA	C5A-C4A-N3A	-4.07	121.12	126.72
2	D	501	FDA	C5A-C4A-N3A	-4.06	121.13	126.72
2	D	501	FDA	C4-N3-C2	-4.01	120.84	126.37
2	B	501	FDA	C5A-C4A-N3A	-3.95	121.28	126.72
2	A	501	FDA	N9A-C8A-N7A	-3.86	108.45	113.94
3	C	502	NAP	C2B-C1B-N9A	3.86	120.11	113.75
2	B	501	FDA	N3A-C2A-N1A	-3.86	122.73	128.58
2	C	501	FDA	N9A-C8A-N7A	-3.72	108.66	113.94
2	C	501	FDA	O5B-PA-O1A	3.69	123.55	108.94
3	A	502	NAP	C2B-C1B-N9A	3.64	119.74	113.75
2	C	501	FDA	O3P-P-O1P	3.64	121.64	110.70
2	B	501	FDA	N9A-C8A-N7A	-3.59	108.84	113.94
3	A	502	NAP	C3N-C7N-N7N	3.58	122.15	117.74
2	B	501	FDA	O5'-C5'-C4'	3.57	118.89	109.36
3	A	502	NAP	C2A-N3A-C4A	3.57	120.55	111.83
3	D	502	NAP	C2A-N3A-C4A	3.55	120.50	111.83
3	C	502	NAP	N3A-C2A-N1A	-3.51	123.26	128.58
3	D	502	NAP	N9A-C8A-N7A	-3.51	108.96	113.94
2	C	501	FDA	O3'-C3'-C2'	-3.50	100.97	108.93
2	D	501	FDA	N9A-C8A-N7A	-3.44	109.06	113.94
3	B	502	NAP	C2B-C1B-N9A	3.42	119.38	113.75
3	A	502	NAP	N9A-C8A-N7A	-3.40	109.12	113.94
3	B	502	NAP	C2A-N3A-C4A	3.39	120.12	111.83
3	D	502	NAP	N3A-C4A-N9A	3.34	132.86	127.17
3	B	502	NAP	N9A-C8A-N7A	-3.34	109.19	113.94
2	C	501	FDA	O4-C4-C4X	-3.31	119.27	127.26
3	D	502	NAP	C5A-N7A-C8A	3.30	108.64	103.45
3	A	502	NAP	N3A-C4A-N9A	3.30	132.77	127.17
2	C	501	FDA	N3-C2-N1	3.21	120.79	115.74
3	B	502	NAP	C2N-C3N-C4N	3.20	121.98	118.26
2	A	501	FDA	C5A-N7A-C8A	3.18	108.45	103.45
2	C	501	FDA	C4A-C5A-N7A	-3.18	106.95	110.58
2	B	501	FDA	N3-C2-N1	3.17	120.72	115.74
2	A	501	FDA	O2P-P-O3P	3.14	115.77	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	NAP	N3A-C4A-N9A	3.13	132.50	127.17
3	D	502	NAP	C4A-C5A-N7A	-3.11	107.03	110.58
2	A	501	FDA	C2A-N3A-C4A	3.08	119.36	111.83
2	C	501	FDA	C5A-N7A-C8A	3.08	108.29	103.45
3	C	502	NAP	C2N-C3N-C4N	3.08	121.84	118.26
2	C	501	FDA	C2A-N3A-C4A	3.06	119.30	111.83
2	C	501	FDA	O3'-C3'-C4'	3.05	115.86	108.93
3	C	502	NAP	C2A-N3A-C4A	3.04	119.25	111.83
3	D	502	NAP	O5B-C5B-C4B	3.02	119.27	108.99
3	C	502	NAP	O7N-C7N-C3N	-3.01	115.92	119.60
2	B	501	FDA	C4A-C5A-N7A	-3.01	107.14	110.58
2	B	501	FDA	O5B-PA-O1A	2.99	120.78	108.94
3	D	502	NAP	O5B-PA-O1A	2.98	120.75	108.94
3	B	502	NAP	C6N-N1N-C2N	-2.97	119.35	121.88
2	D	501	FDA	C2A-N3A-C4A	2.91	118.93	111.83
3	B	502	NAP	O4B-C4B-C5B	2.90	118.64	109.33
2	D	501	FDA	N3-C2-N1	2.90	120.30	115.74
3	B	502	NAP	C5N-C4N-C3N	-2.90	117.51	120.36
2	A	501	FDA	N3A-C4A-N9A	2.89	132.09	127.17
2	C	501	FDA	C4X-C4-N3	2.89	120.07	112.13
2	B	501	FDA	C4A-N9A-C8A	2.86	108.74	105.74
3	D	502	NAP	O2A-PA-O5B	2.85	120.50	107.57
2	A	501	FDA	C4A-N9A-C8A	2.81	108.69	105.74
2	D	501	FDA	C4A-C5A-N7A	-2.81	107.37	110.58
2	A	501	FDA	O5'-C5'-C4'	2.79	116.82	109.36
3	C	502	NAP	C4A-C5A-N7A	-2.79	107.39	110.58
2	B	501	FDA	C2A-N3A-C4A	2.79	118.65	111.83
2	D	501	FDA	C4A-N9A-C8A	2.79	108.66	105.74
2	D	501	FDA	O4-C4-C4X	-2.78	120.56	127.26
2	D	501	FDA	C5A-N7A-C8A	2.76	107.78	103.45
2	B	501	FDA	C5A-N7A-C8A	2.75	107.78	103.45
3	A	502	NAP	C4A-C5A-N7A	-2.74	107.45	110.58
2	C	501	FDA	C5'-C4'-C3'	2.74	117.38	112.22
2	A	501	FDA	N3-C2-N1	2.73	120.04	115.74
2	C	501	FDA	C4A-N9A-C8A	2.73	108.60	105.74
2	C	501	FDA	O5B-C5B-C4B	2.71	118.22	108.99
2	A	501	FDA	C4X-C4-N3	2.71	119.56	112.13
2	B	501	FDA	O5B-C5B-C4B	2.70	118.20	108.99
2	D	501	FDA	N3A-C4A-N9A	2.70	131.75	127.17
3	C	502	NAP	C3N-C7N-N7N	2.67	121.03	117.74
3	C	502	NAP	C5N-C4N-C3N	-2.65	117.75	120.36
3	A	502	NAP	C5A-N7A-C8A	2.65	107.62	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	502	NAP	C5A-N7A-C8A	2.64	107.60	103.45
2	A	501	FDA	O4-C4-C4X	-2.64	120.89	127.26
2	B	501	FDA	C4X-C4-N3	2.61	119.29	112.13
2	B	501	FDA	O3B-C3B-C4B	-2.61	103.60	111.08
2	A	501	FDA	C4A-C5A-N7A	-2.60	107.60	110.58
3	D	502	NAP	O4B-C1B-N9A	2.60	113.08	108.09
2	B	501	FDA	C1'-C2'-C3'	2.59	116.68	109.66
2	C	501	FDA	N3A-C4A-N9A	2.57	131.54	127.17
2	D	501	FDA	C4X-C4-N3	2.56	119.15	112.13
3	B	502	NAP	C5A-N7A-C8A	2.55	107.45	103.45
3	D	502	NAP	C2B-C1B-N9A	2.55	117.94	113.75
3	B	502	NAP	C4A-N9A-C8A	2.52	108.38	105.74
3	D	502	NAP	C2N-C3N-C4N	2.50	121.17	118.26
3	A	502	NAP	O7N-C7N-C3N	-2.46	116.59	119.60
3	C	502	NAP	N9A-C8A-N7A	-2.45	110.45	113.94
3	D	502	NAP	O2N-PN-O3	2.41	113.79	107.27
3	C	502	NAP	O5D-C5D-C4D	2.41	117.19	108.99
2	C	501	FDA	C5X-C9A-N10	2.40	120.73	118.01
2	B	501	FDA	N3A-C4A-N9A	2.38	131.22	127.17
3	B	502	NAP	C4D-O4D-C1D	-2.36	107.76	109.92
3	B	502	NAP	C4A-C5A-N7A	-2.36	107.89	110.58
2	D	501	FDA	O4B-C4B-C5B	2.32	116.77	109.33
3	A	502	NAP	C2N-C3N-C4N	2.32	120.95	118.26
3	A	502	NAP	C4A-N9A-C8A	2.31	108.16	105.74
2	C	501	FDA	C2'-C1'-N10	2.30	121.07	110.20
3	B	502	NAP	O5D-C5D-C4D	2.27	116.72	108.99
2	A	501	FDA	C1'-C2'-C3'	2.16	115.52	109.66
3	C	502	NAP	C6A-C5A-C4A	2.12	120.07	117.18
3	C	502	NAP	C6N-N1N-C2N	-2.10	120.09	121.88
3	B	502	NAP	O2A-PA-O3	2.10	112.95	107.27
2	A	501	FDA	O4B-C1B-C2B	-2.09	102.13	106.62
2	A	501	FDA	C5'-C4'-C3'	2.08	116.14	112.22
2	B	501	FDA	O4B-C4B-C5B	2.05	115.91	109.33
2	B	501	FDA	O2A-PA-O1A	2.04	121.95	112.44
3	A	502	NAP	C4D-O4D-C1D	-2.03	108.06	109.92
3	A	502	NAP	O5D-C5D-C4D	2.02	115.89	108.99
3	C	502	NAP	O4B-C4B-C5B	2.01	115.78	109.33
2	B	501	FDA	O4-C4-C4X	-2.01	122.41	127.26
3	A	502	NAP	O4B-C4B-C5B	2.01	115.77	109.33

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	FDA	C5B-O5B-PA-O3P
2	C	501	FDA	C5B-O5B-PA-O3P
3	D	502	NAP	C5B-O5B-PA-O3
2	B	501	FDA	C2'-C3'-C4'-C5'
2	B	501	FDA	O4B-C4B-C5B-O5B
2	C	501	FDA	O4B-C4B-C5B-O5B
2	D	501	FDA	O4B-C4B-C5B-O5B
2	D	501	FDA	C3B-C4B-C5B-O5B
3	D	502	NAP	O4B-C4B-C5B-O5B
2	B	501	FDA	O3'-C3'-C4'-C5'
2	A	501	FDA	O4B-C4B-C5B-O5B
2	B	501	FDA	C3B-C4B-C5B-O5B
3	D	502	NAP	C3B-C4B-C5B-O5B
2	C	501	FDA	C3B-C4B-C5B-O5B
2	B	501	FDA	C2'-C3'-C4'-O4'
2	A	501	FDA	C3B-C4B-C5B-O5B
2	B	501	FDA	O3'-C3'-C4'-O4'
3	A	502	NAP	O4B-C4B-C5B-O5B
3	D	502	NAP	C2B-O2B-P2B-O1X
2	D	501	FDA	C2'-C3'-C4'-C5'
2	D	501	FDA	O3'-C3'-C4'-C5'
3	B	502	NAP	PN-O3-PA-O1A
2	C	501	FDA	C2'-C3'-C4'-C5'
2	A	501	FDA	P-O3P-PA-O5B
2	B	501	FDA	P-O3P-PA-O5B
2	C	501	FDA	P-O3P-PA-O5B
2	D	501	FDA	PA-O3P-P-O5'
3	B	502	NAP	PA-O3-PN-O5D
3	C	502	NAP	PA-O3-PN-O5D
2	D	501	FDA	C5B-O5B-PA-O1A
2	D	501	FDA	C5B-O5B-PA-O2A
2	D	501	FDA	C5B-O5B-PA-O3P
3	A	502	NAP	C5B-O5B-PA-O2A
3	A	502	NAP	C5B-O5B-PA-O3
3	C	502	NAP	C5B-O5B-PA-O1A
3	D	502	NAP	C5B-O5B-PA-O1A
3	C	502	NAP	PN-O3-PA-O2A
3	A	502	NAP	C3B-C4B-C5B-O5B
3	A	502	NAP	C2B-O2B-P2B-O1X
3	C	502	NAP	PN-O3-PA-O1A
2	B	501	FDA	C3'-C4'-C5'-O5'
3	B	502	NAP	PN-O3-PA-O2A
3	B	502	NAP	O4B-C4B-C5B-O5B

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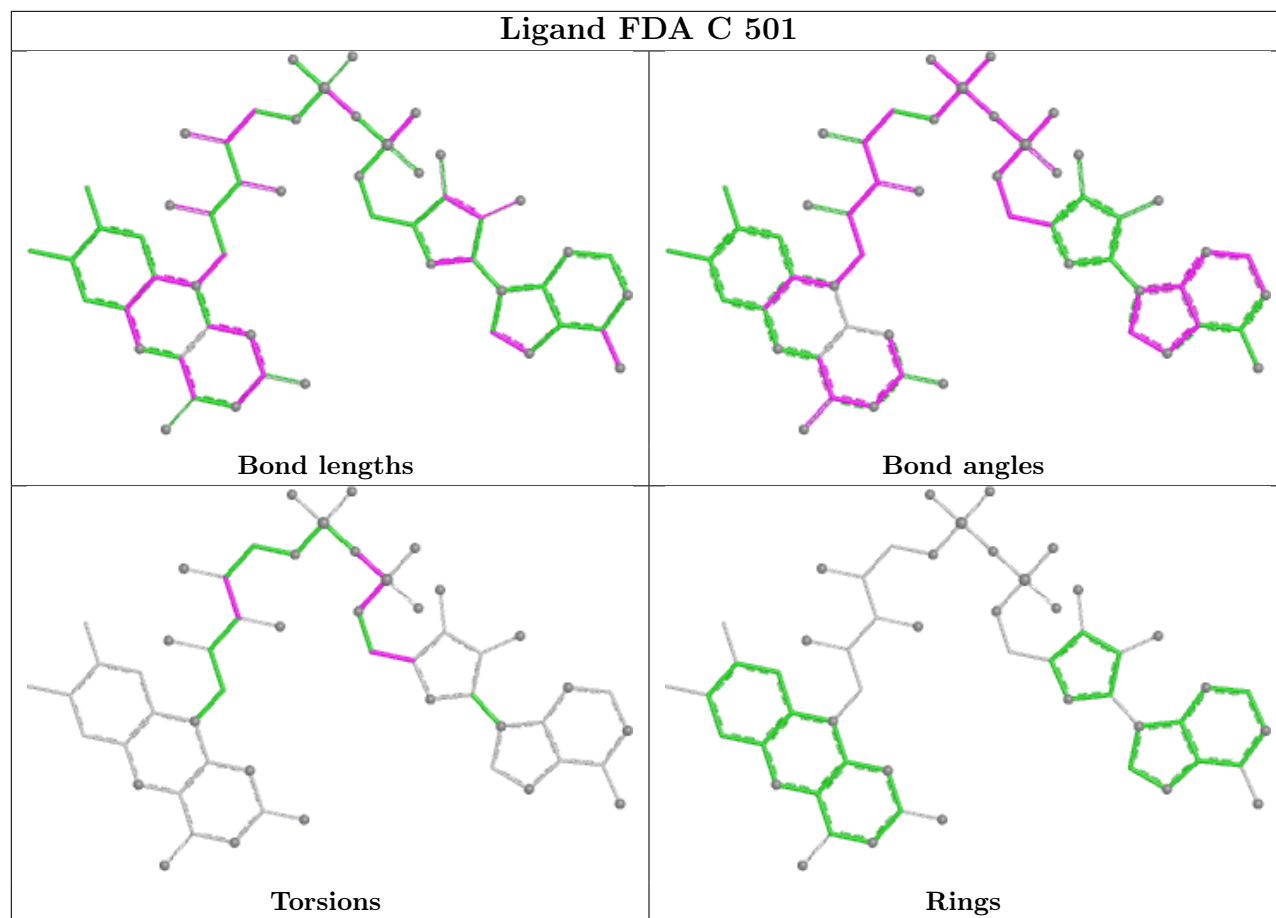
Mol	Chain	Res	Type	Atoms
3	D	502	NAP	O4B-C1B-N9A-C8A
3	D	502	NAP	PN-O3-PA-O2A

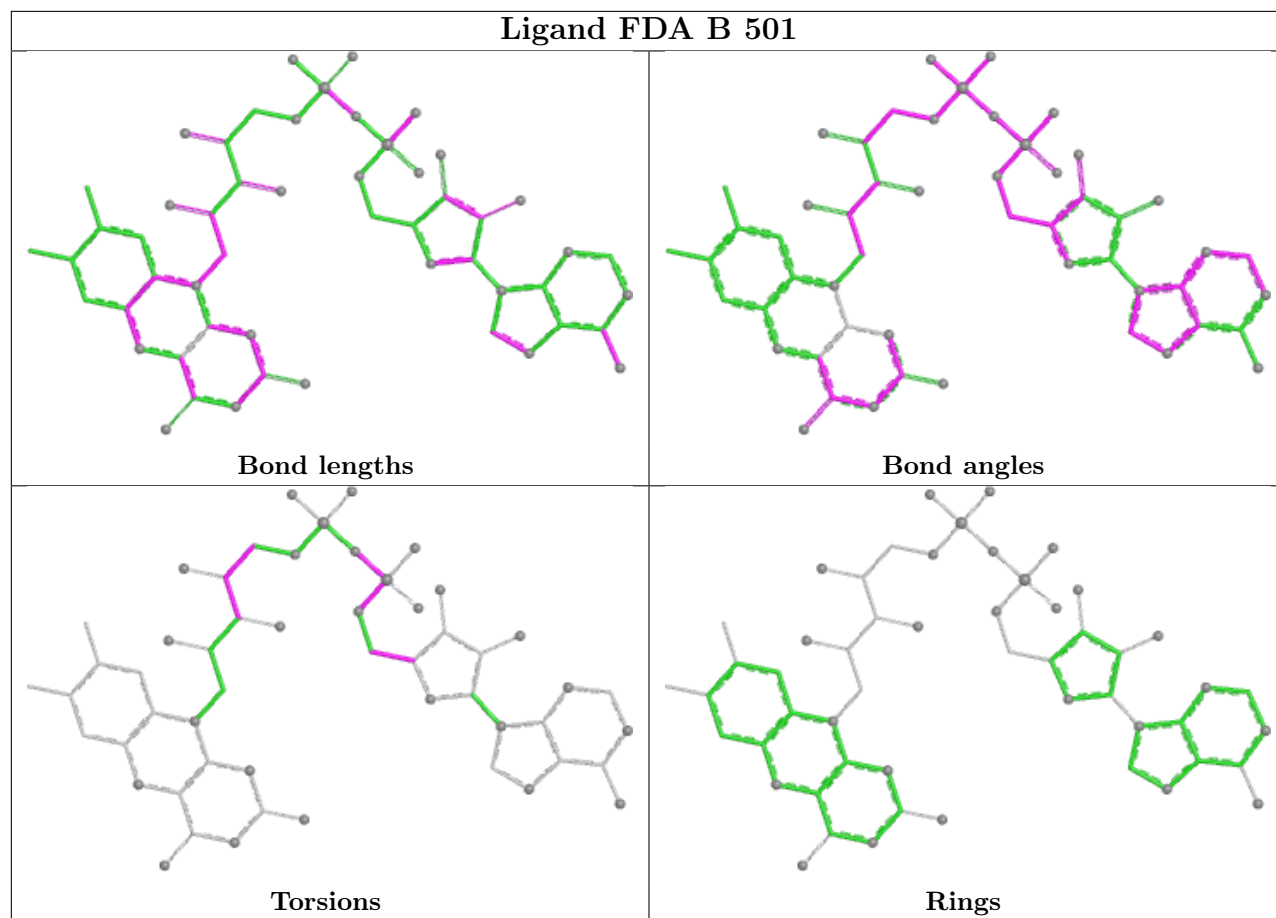
There are no ring outliers.

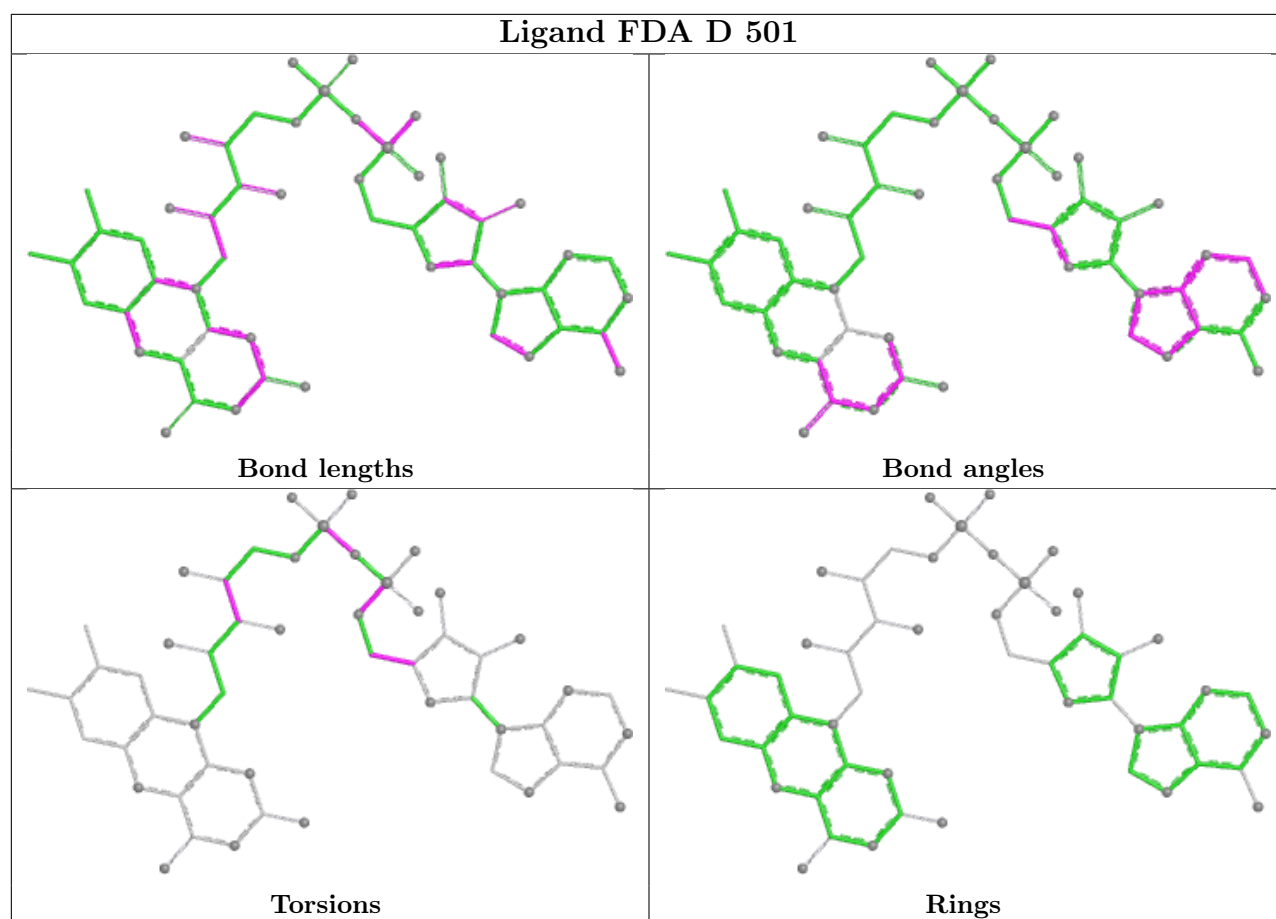
2 monomers are involved in 6 short contacts:

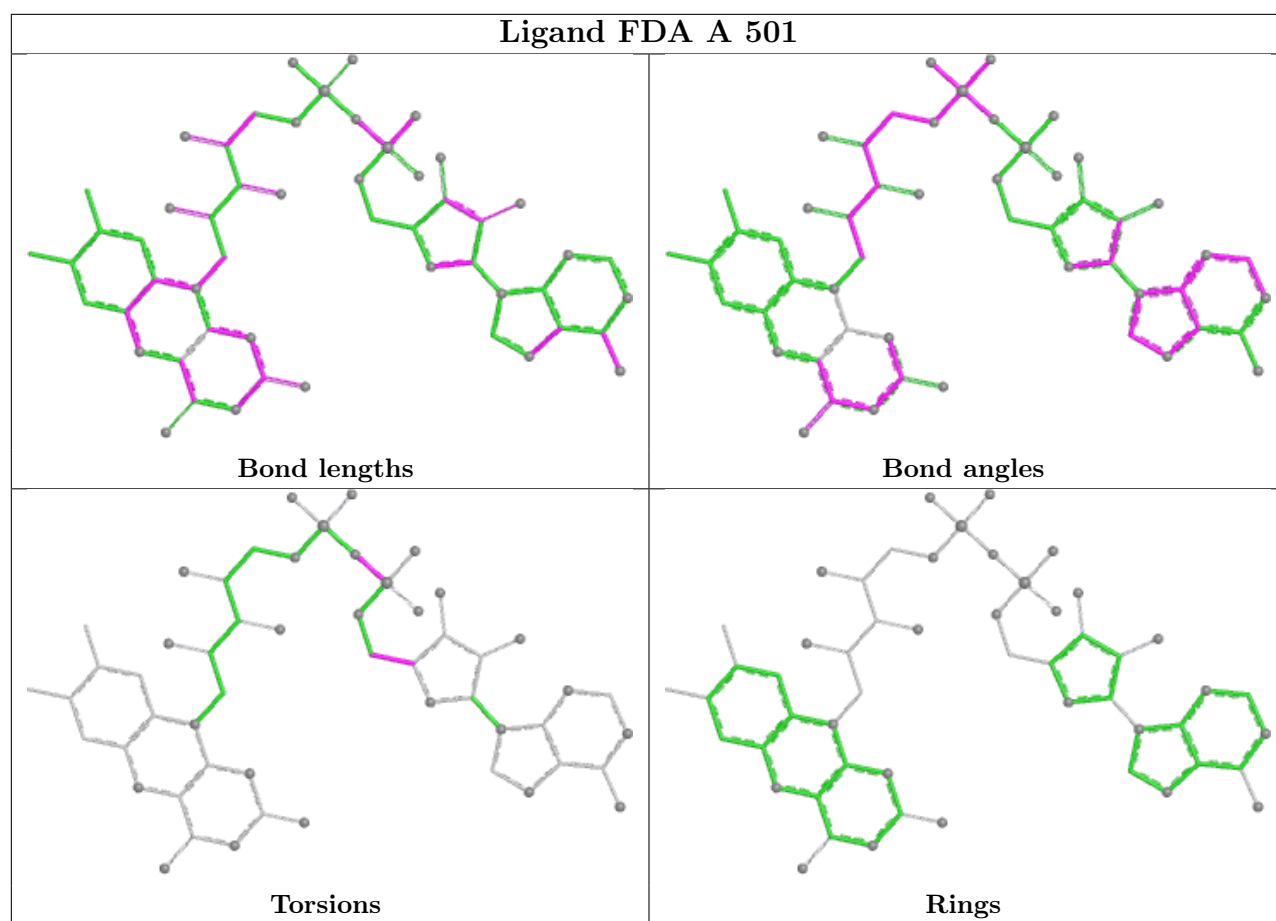
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	FDA	2	0
2	A	501	FDA	4	0

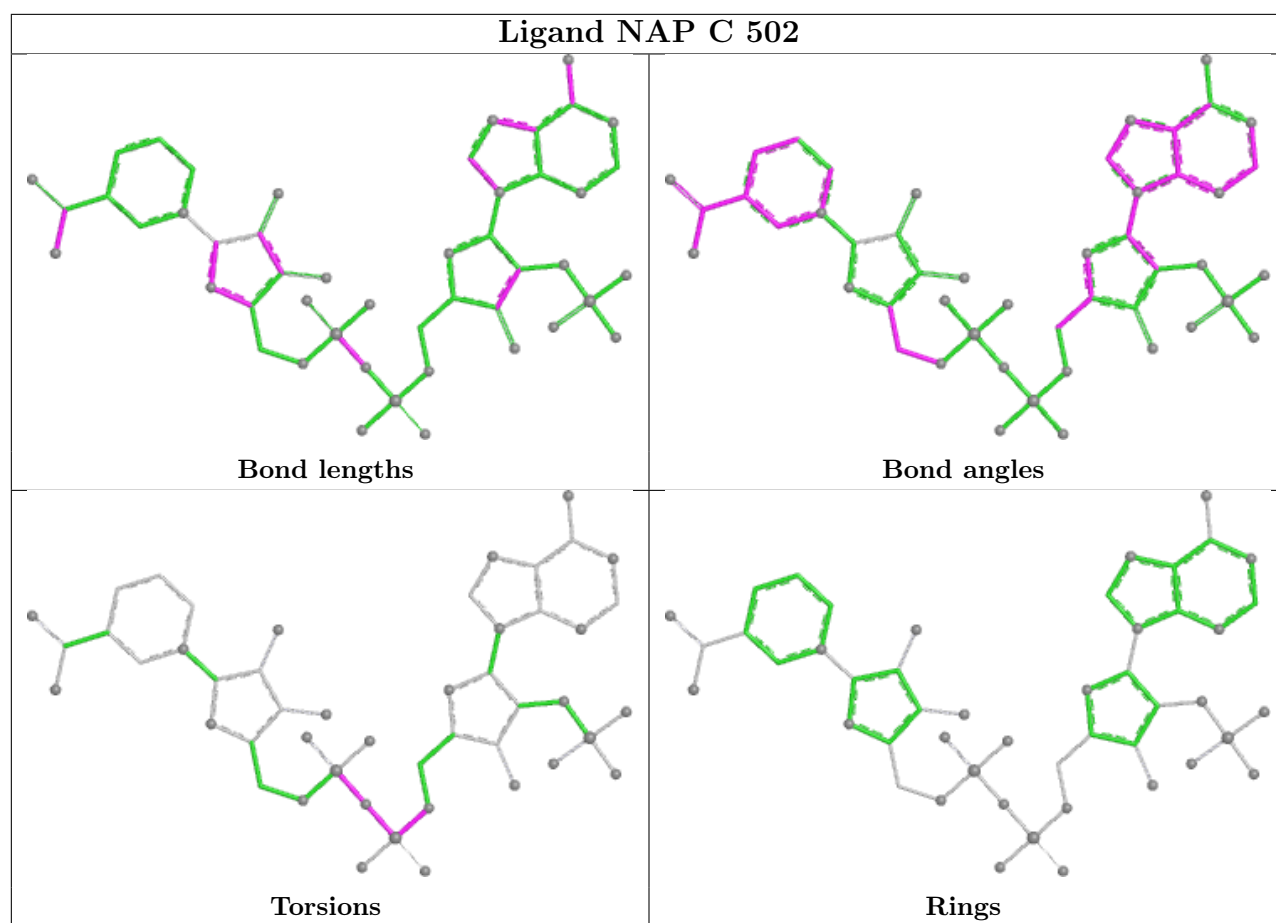
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

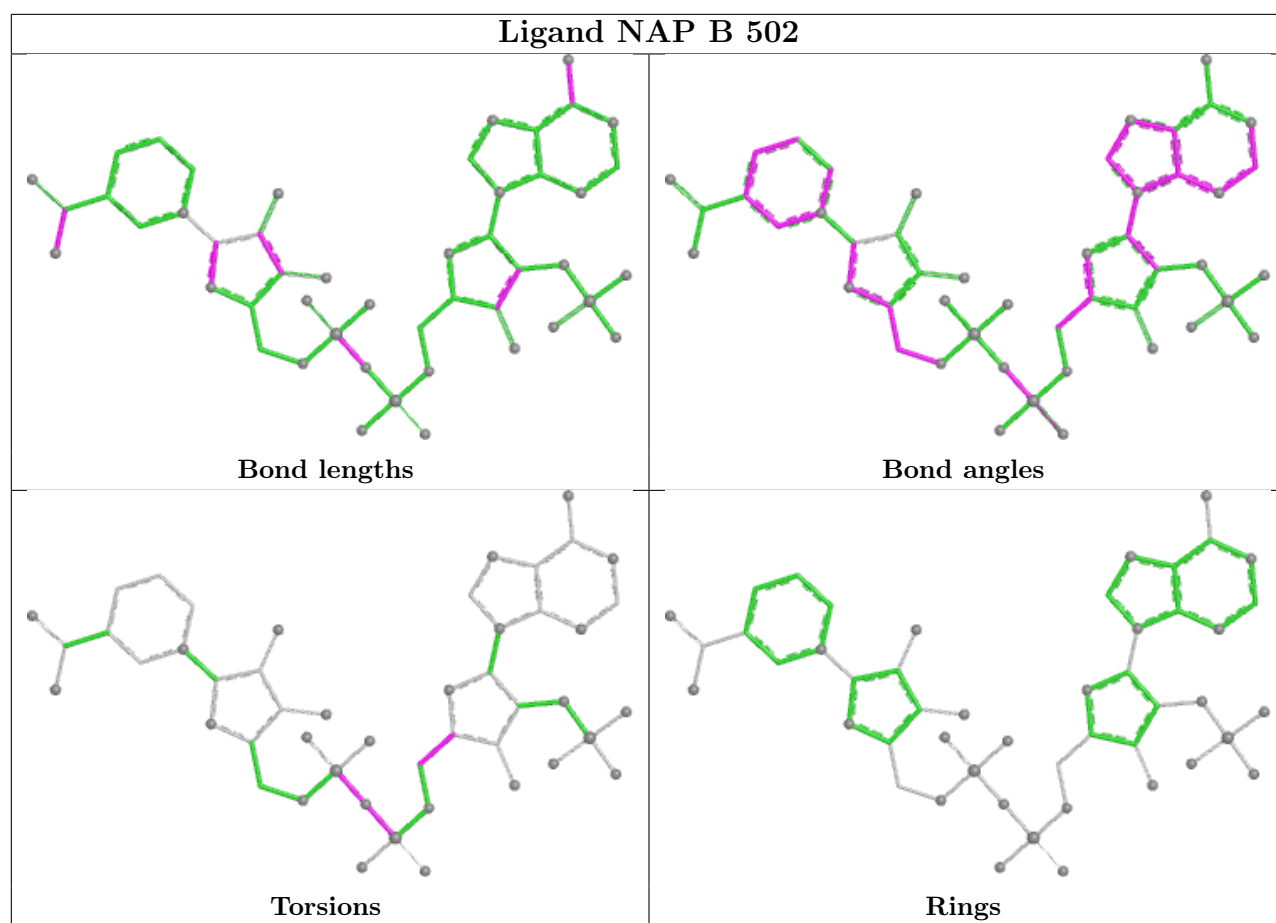


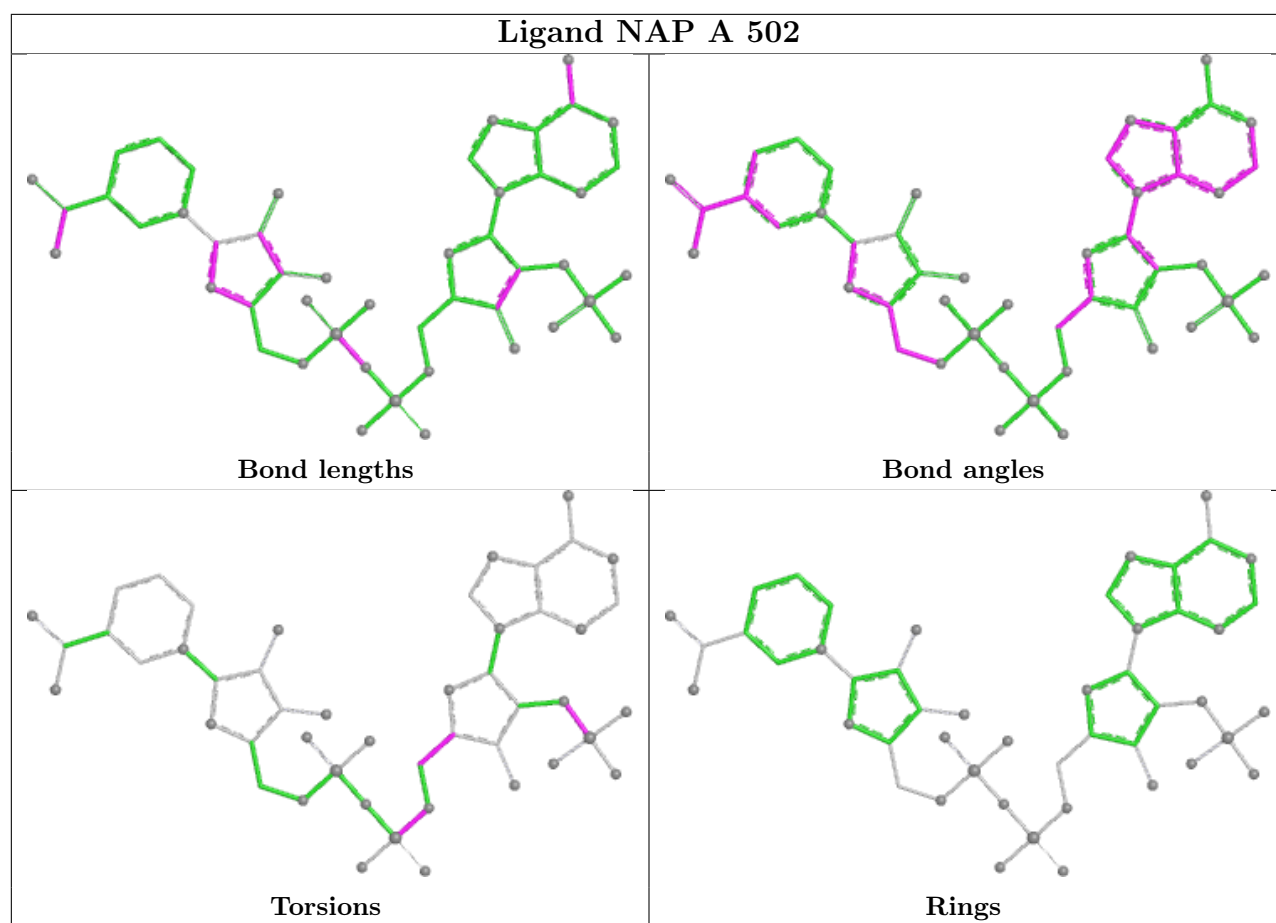


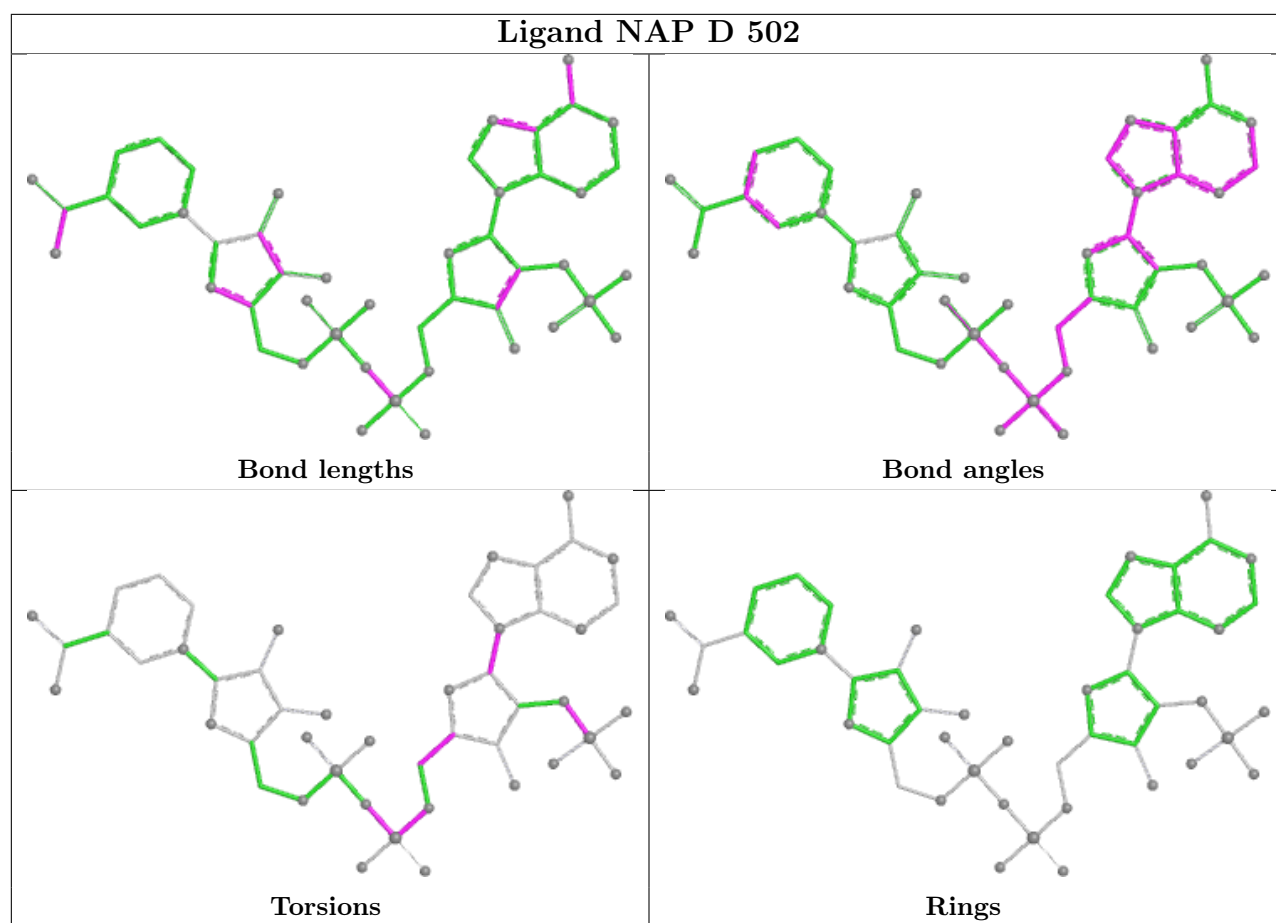












5.7 Other polymers [i](#)

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	414/443 (93%)	-0.22	5 (1%) 76 73	18, 31, 58, 83	0
1	B	415/443 (93%)	-0.23	6 (1%) 73 70	20, 32, 61, 82	0
1	C	414/443 (93%)	-0.17	9 (2%) 62 58	16, 32, 63, 83	0
1	D	414/443 (93%)	-0.16	8 (1%) 66 62	22, 33, 64, 98	0
All	All	1657/1772 (93%)	-0.20	28 (1%) 69 65	16, 32, 62, 98	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	10	PRO	5.0
1	B	386	CYS	4.0
1	A	137	ARG	3.7
1	B	424	SER	3.7
1	D	195	PRO	3.3
1	B	120	HIS	3.2
1	A	10	PRO	3.1
1	C	10	PRO	3.1
1	D	135	PRO	3.1
1	B	10	PRO	3.1
1	C	361	HIS	2.7
1	D	220	ASN	2.6
1	B	192	ASP	2.6
1	C	384	LEU	2.6
1	A	366	ALA	2.6
1	C	353	ASP	2.5
1	D	353	ASP	2.5
1	C	366	ALA	2.5
1	D	194	ASP	2.4
1	D	138	PRO	2.4
1	A	223	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	196	ARG	2.3
1	C	367	GLU	2.2
1	C	365	ASP	2.2
1	D	196	ARG	2.1
1	C	136	GLY	2.1
1	B	194	ASP	2.1
1	C	150	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BR	A	508	1/1	0.91	0.08	56,56,56,56	1
4	BR	A	512	1/1	0.91	0.08	60,60,60,60	1
4	BR	D	509	1/1	0.92	0.07	51,51,51,51	1
4	BR	A	510	1/1	0.93	0.07	51,51,51,51	1
4	BR	D	506	1/1	0.94	0.08	47,47,47,47	1
4	BR	B	504	1/1	0.95	0.06	37,37,37,37	1
4	BR	C	509	1/1	0.96	0.09	33,33,33,33	1
4	BR	C	510	1/1	0.96	0.10	33,33,33,33	1
4	BR	D	503	1/1	0.96	0.04	36,36,36,36	1
2	FDA	C	501	53/53	0.96	0.06	19,27,40,43	0
2	FDA	D	501	53/53	0.96	0.06	23,28,33,40	0
3	NAP	C	502	48/48	0.97	0.06	16,22,29,37	0
4	BR	B	507	1/1	0.97	0.04	38,38,38,38	1
4	BR	C	503	1/1	0.97	0.06	39,39,39,39	1
4	BR	C	506	1/1	0.97	0.06	42,42,42,42	1
4	BR	A	503	1/1	0.97	0.06	37,37,37,37	1

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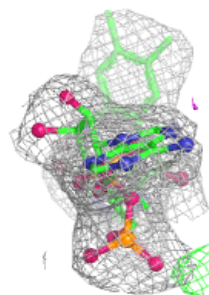
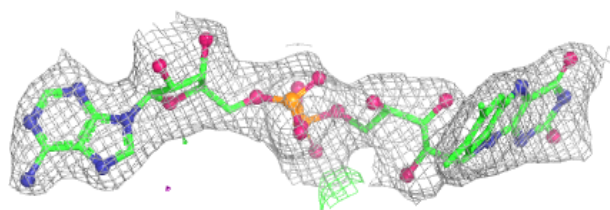
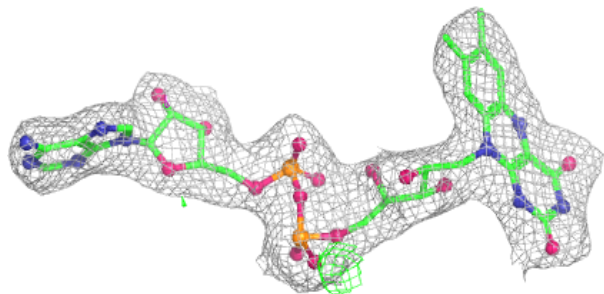
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BR	A	507	1/1	0.97	0.04	24,24,24,24	1
2	FDA	A	501	53/53	0.97	0.06	18,24,34,36	0
2	FDA	B	501	53/53	0.97	0.06	21,27,33,36	0
3	NAP	B	502	48/48	0.97	0.05	17,28,36,43	0
4	BR	A	505	1/1	0.98	0.04	34,34,34,34	1
4	BR	C	504	1/1	0.98	0.03	31,31,31,31	1
4	BR	C	505	1/1	0.98	0.07	45,45,45,45	1
4	BR	A	511	1/1	0.98	0.04	32,32,32,32	1
4	BR	C	507	1/1	0.98	0.03	32,32,32,32	1
4	BR	C	508	1/1	0.98	0.04	39,39,39,39	1
3	NAP	D	502	48/48	0.98	0.05	21,27,36,43	0
4	BR	B	503	1/1	0.98	0.03	27,27,27,27	1
3	NAP	A	502	48/48	0.98	0.04	18,23,30,33	0
4	BR	A	509	1/1	0.98	0.03	31,31,31,31	1
4	BR	B	508	1/1	0.98	0.04	39,39,39,39	1
4	BR	A	506	1/1	0.99	0.02	27,27,27,27	1
4	BR	B	505	1/1	0.99	0.02	28,28,28,28	1
4	BR	D	504	1/1	0.99	0.03	26,26,26,26	1
4	BR	D	505	1/1	0.99	0.03	29,29,29,29	1
4	BR	B	506	1/1	0.99	0.04	33,33,33,33	1
4	BR	D	507	1/1	0.99	0.03	37,37,37,37	1
4	BR	D	508	1/1	0.99	0.03	55,55,55,55	1
4	BR	A	504	1/1	0.99	0.02	20,20,20,20	1

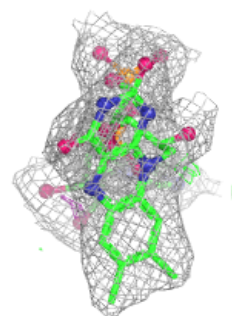
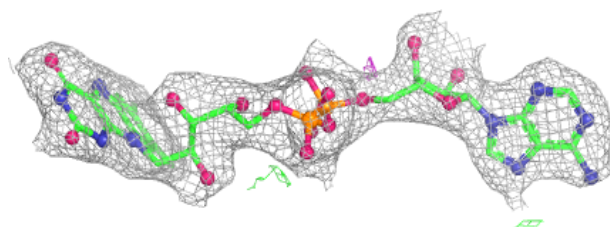
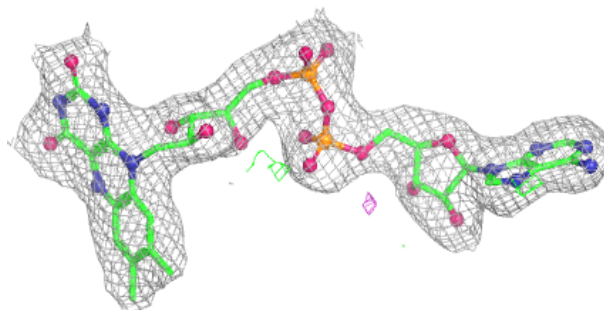
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FDA C 501:

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

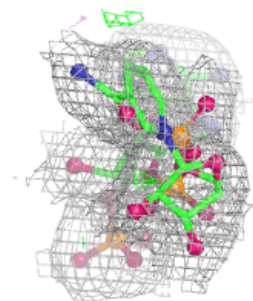
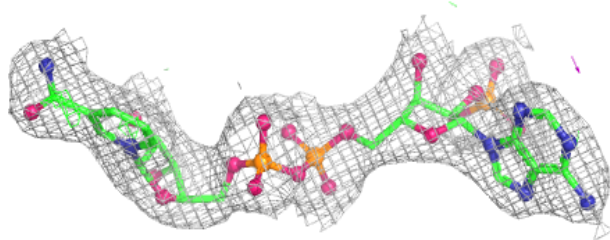
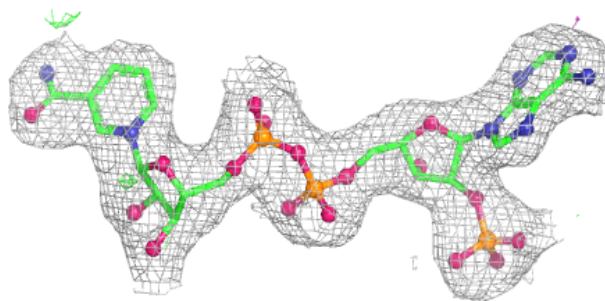
**Electron density around FDA D 501:**

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

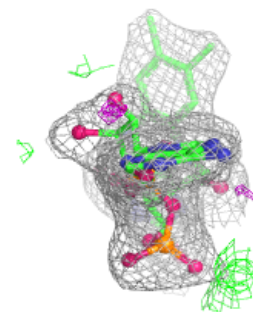
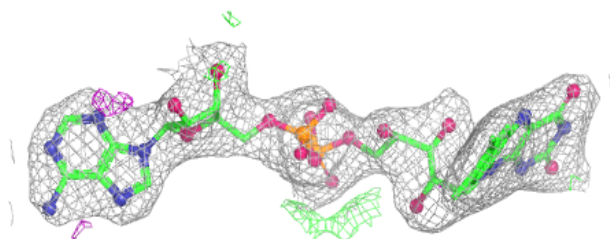
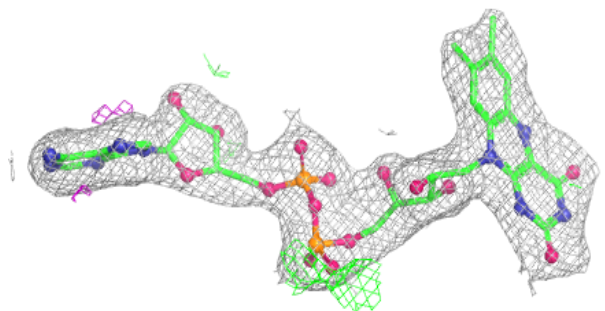


Electron density around NAP C 502:

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

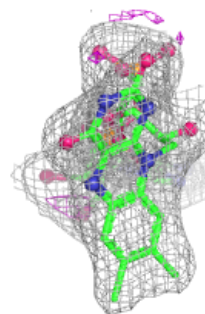
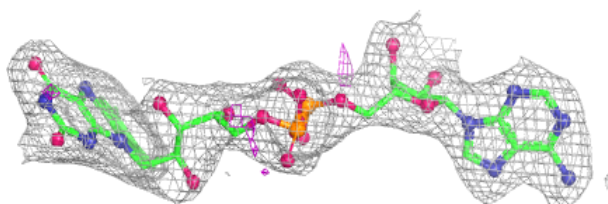
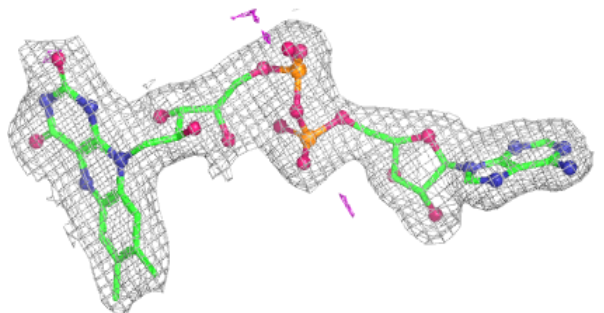
**Electron density around FDA A 501:**

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and green (positive)

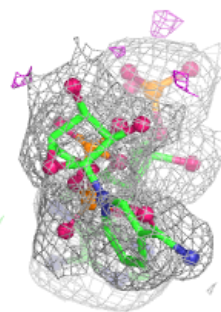
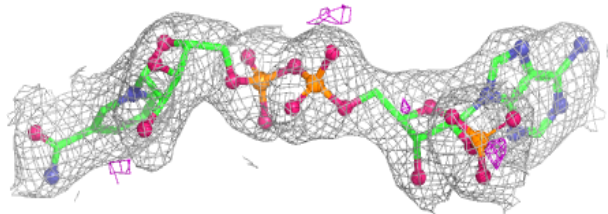
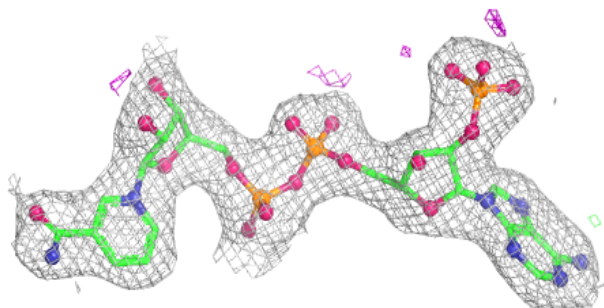


Electron density around FDA B 501:

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and green (positive)

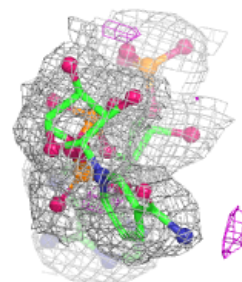
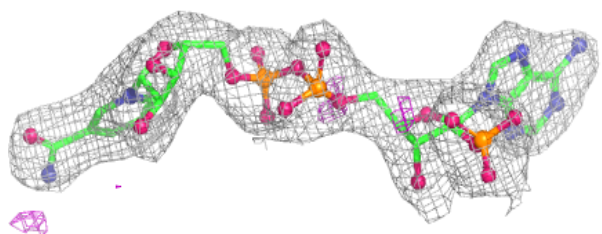
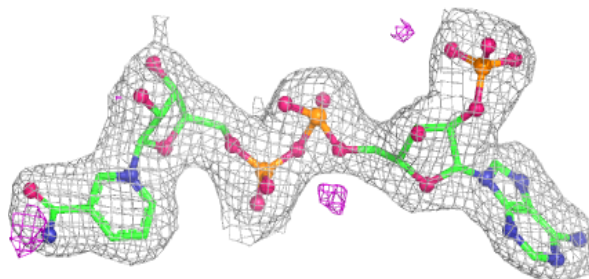
**Electron density around NAP B 502:**

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

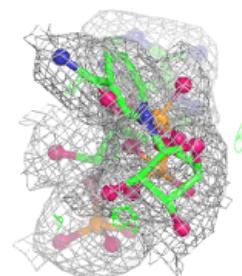
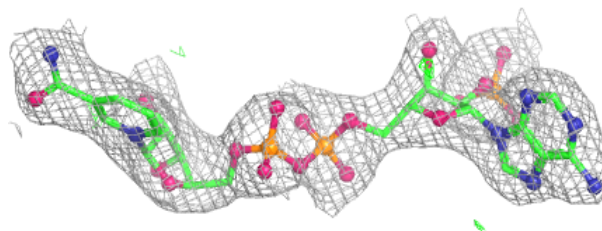
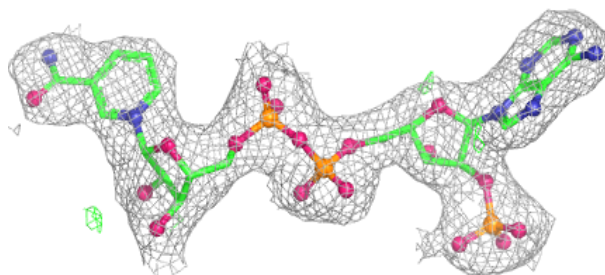


Electron density around NAP D 502:

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

**Electron density around NAP A 502:**

$2mF_o-DF_c$ (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.