



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:36 PM UTC

PDB ID : 4MZ8 / pdb_00004mz8
Title : Crystal Structure of the Inosine 5'-monophosphate Dehydrogenase, with an Internal Deletion of CBS Domain from Campylobacter jejuni complexed with inhibitor compound C91
Authors : Kim, Y.; Makowska-Grzyska, M.; Gu, M.; Gorla, S.K.; Hedstrom, L.; Anderson, W.F.; Joachimiak, A.; CSGID; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2013-09-29
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<https://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)

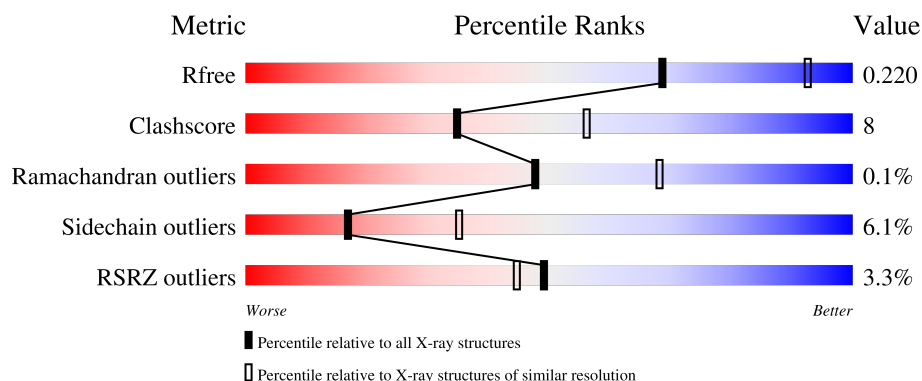
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	406	0% 75% 11% • 13%
1	B	406	0% 78% 8% • 13%
1	C	406	2% 65% 18% • 14%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	D	406	7% 60% 22% • 14%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 11176 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 Inosine-5'-monophosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	5	0
			2669	1680	473	502	14			
1	B	354	Total	C	N	O	S	0	7	0
			2691	1691	476	509	15			
1	C	349	Total	C	N	O	S	0	3	0
			2619	1643	463	500	13			
1	D	350	Total	C	N	O	S	0	1	0
			2607	1642	460	491	14			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	expression tag	UNP Q0P9J4
A	-22	HIS	-	expression tag	UNP Q0P9J4
A	-21	HIS	-	expression tag	UNP Q0P9J4
A	-20	HIS	-	expression tag	UNP Q0P9J4
A	-19	HIS	-	expression tag	UNP Q0P9J4
A	-18	HIS	-	expression tag	UNP Q0P9J4
A	-17	HIS	-	expression tag	UNP Q0P9J4
A	-16	SER	-	expression tag	UNP Q0P9J4
A	-15	SER	-	expression tag	UNP Q0P9J4
A	-14	GLY	-	expression tag	UNP Q0P9J4
A	-13	VAL	-	expression tag	UNP Q0P9J4
A	-12	ASP	-	expression tag	UNP Q0P9J4
A	-11	LEU	-	expression tag	UNP Q0P9J4
A	-10	GLY	-	expression tag	UNP Q0P9J4
A	-9	THR	-	expression tag	UNP Q0P9J4
A	-8	GLU	-	expression tag	UNP Q0P9J4
A	-7	ASN	-	expression tag	UNP Q0P9J4
A	-6	LEU	-	expression tag	UNP Q0P9J4
A	-5	TYR	-	expression tag	UNP Q0P9J4
A	-4	PHE	-	expression tag	UNP Q0P9J4
A	-3	GLN	-	expression tag	UNP Q0P9J4

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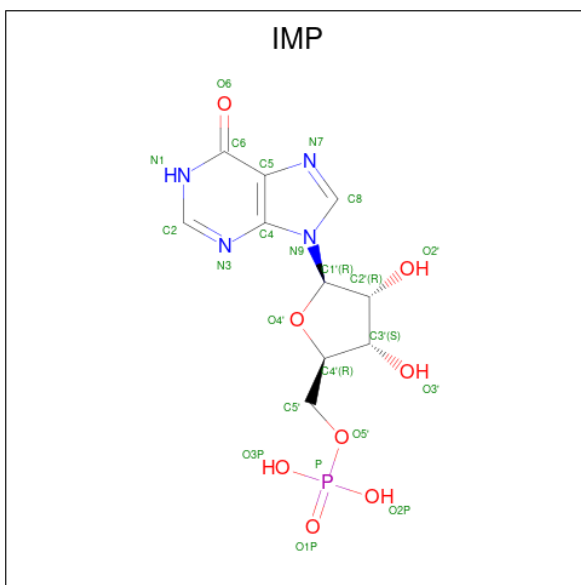
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q0P9J4
A	-1	ASN	-	expression tag	UNP Q0P9J4
A	0	ALA	-	expression tag	UNP Q0P9J4
A	92	GLY	-	linker	UNP Q0P9J4
B	-23	MET	-	expression tag	UNP Q0P9J4
B	-22	HIS	-	expression tag	UNP Q0P9J4
B	-21	HIS	-	expression tag	UNP Q0P9J4
B	-20	HIS	-	expression tag	UNP Q0P9J4
B	-19	HIS	-	expression tag	UNP Q0P9J4
B	-18	HIS	-	expression tag	UNP Q0P9J4
B	-17	HIS	-	expression tag	UNP Q0P9J4
B	-16	SER	-	expression tag	UNP Q0P9J4
B	-15	SER	-	expression tag	UNP Q0P9J4
B	-14	GLY	-	expression tag	UNP Q0P9J4
B	-13	VAL	-	expression tag	UNP Q0P9J4
B	-12	ASP	-	expression tag	UNP Q0P9J4
B	-11	LEU	-	expression tag	UNP Q0P9J4
B	-10	GLY	-	expression tag	UNP Q0P9J4
B	-9	THR	-	expression tag	UNP Q0P9J4
B	-8	GLU	-	expression tag	UNP Q0P9J4
B	-7	ASN	-	expression tag	UNP Q0P9J4
B	-6	LEU	-	expression tag	UNP Q0P9J4
B	-5	TYR	-	expression tag	UNP Q0P9J4
B	-4	PHE	-	expression tag	UNP Q0P9J4
B	-3	GLN	-	expression tag	UNP Q0P9J4
B	-2	SER	-	expression tag	UNP Q0P9J4
B	-1	ASN	-	expression tag	UNP Q0P9J4
B	0	ALA	-	expression tag	UNP Q0P9J4
B	92	GLY	-	linker	UNP Q0P9J4
C	-23	MET	-	expression tag	UNP Q0P9J4
C	-22	HIS	-	expression tag	UNP Q0P9J4
C	-21	HIS	-	expression tag	UNP Q0P9J4
C	-20	HIS	-	expression tag	UNP Q0P9J4
C	-19	HIS	-	expression tag	UNP Q0P9J4
C	-18	HIS	-	expression tag	UNP Q0P9J4
C	-17	HIS	-	expression tag	UNP Q0P9J4
C	-16	SER	-	expression tag	UNP Q0P9J4
C	-15	SER	-	expression tag	UNP Q0P9J4
C	-14	GLY	-	expression tag	UNP Q0P9J4
C	-13	VAL	-	expression tag	UNP Q0P9J4
C	-12	ASP	-	expression tag	UNP Q0P9J4
C	-11	LEU	-	expression tag	UNP Q0P9J4

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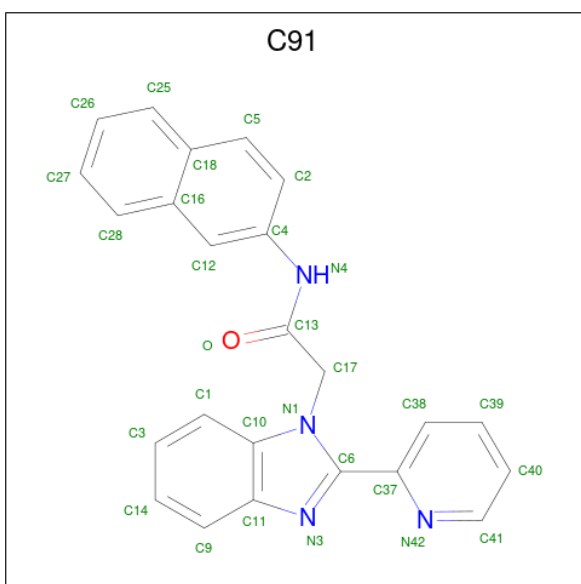
Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	GLY	-	expression tag	UNP Q0P9J4
C	-9	THR	-	expression tag	UNP Q0P9J4
C	-8	GLU	-	expression tag	UNP Q0P9J4
C	-7	ASN	-	expression tag	UNP Q0P9J4
C	-6	LEU	-	expression tag	UNP Q0P9J4
C	-5	TYR	-	expression tag	UNP Q0P9J4
C	-4	PHE	-	expression tag	UNP Q0P9J4
C	-3	GLN	-	expression tag	UNP Q0P9J4
C	-2	SER	-	expression tag	UNP Q0P9J4
C	-1	ASN	-	expression tag	UNP Q0P9J4
C	0	ALA	-	expression tag	UNP Q0P9J4
C	92	GLY	-	linker	UNP Q0P9J4
D	-23	MET	-	expression tag	UNP Q0P9J4
D	-22	HIS	-	expression tag	UNP Q0P9J4
D	-21	HIS	-	expression tag	UNP Q0P9J4
D	-20	HIS	-	expression tag	UNP Q0P9J4
D	-19	HIS	-	expression tag	UNP Q0P9J4
D	-18	HIS	-	expression tag	UNP Q0P9J4
D	-17	HIS	-	expression tag	UNP Q0P9J4
D	-16	SER	-	expression tag	UNP Q0P9J4
D	-15	SER	-	expression tag	UNP Q0P9J4
D	-14	GLY	-	expression tag	UNP Q0P9J4
D	-13	VAL	-	expression tag	UNP Q0P9J4
D	-12	ASP	-	expression tag	UNP Q0P9J4
D	-11	LEU	-	expression tag	UNP Q0P9J4
D	-10	GLY	-	expression tag	UNP Q0P9J4
D	-9	THR	-	expression tag	UNP Q0P9J4
D	-8	GLU	-	expression tag	UNP Q0P9J4
D	-7	ASN	-	expression tag	UNP Q0P9J4
D	-6	LEU	-	expression tag	UNP Q0P9J4
D	-5	TYR	-	expression tag	UNP Q0P9J4
D	-4	PHE	-	expression tag	UNP Q0P9J4
D	-3	GLN	-	expression tag	UNP Q0P9J4
D	-2	SER	-	expression tag	UNP Q0P9J4
D	-1	ASN	-	expression tag	UNP Q0P9J4
D	0	ALA	-	expression tag	UNP Q0P9J4
D	92	GLY	-	linker	UNP Q0P9J4

- Molecule 2 is INOSINIC ACID (CCD ID: IMP) (formula: C₁₀H₁₃N₄O₈P).



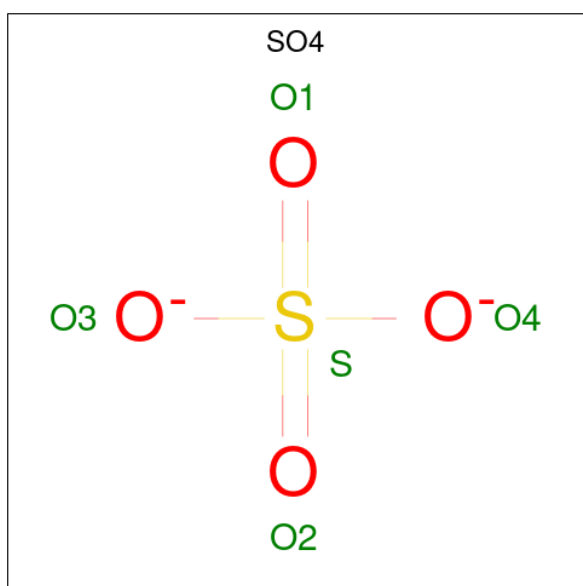
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	4	8	1		

- Molecule 3 is N-(naphthalen-2-yl)-2-[2-(pyridin-2-yl)-1H-benzimidazol-1-yl]acetamide (CCD ID: C91) (formula: C₂₄H₁₈N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			29	24	4	1		
3	B	1	Total	C	N	O	0	0
			29	24	4	1		
3	C	1	Total	C	N	O	0	0
			29	24	4	1		
3	D	1	Total	C	N	O	0	0
			29	24	4	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



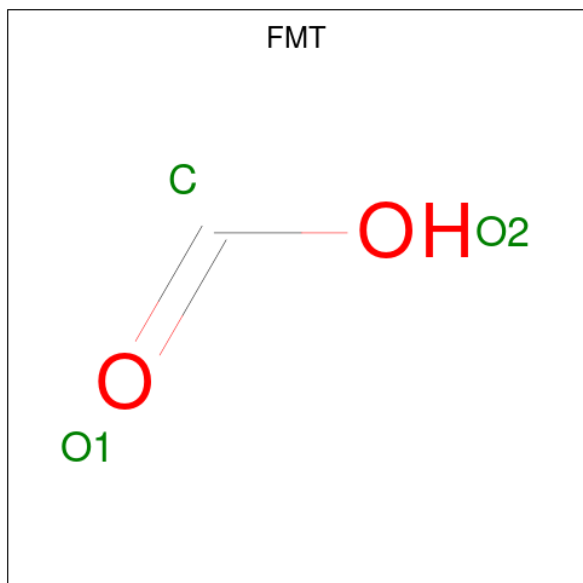
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



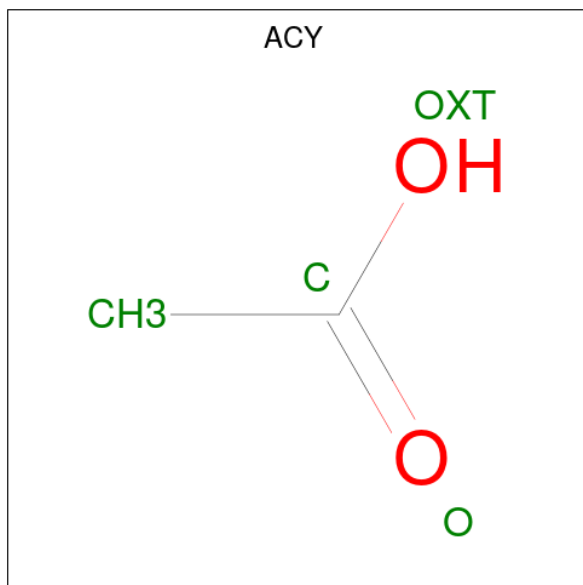
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



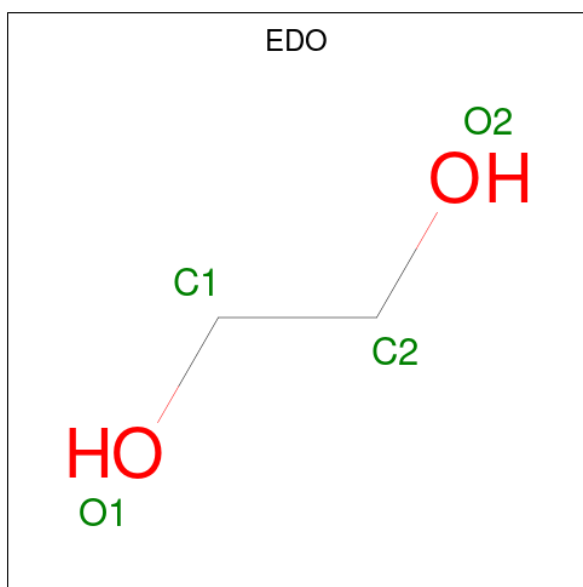
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 7 is ACETIC ACID (CCD ID: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

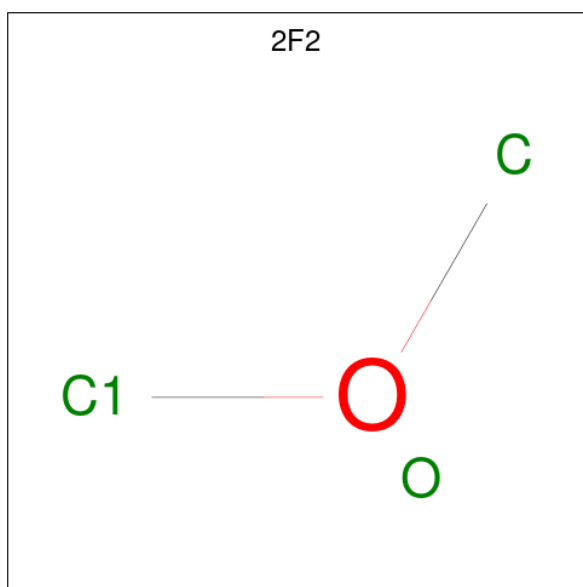


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Cl	0	0
			1	1		
9	B	1	Total	Cl	0	0
			1	1		
9	C	3	Total	Cl	0	0
			3	3		

- Molecule 10 is dimethyl ether (CCD ID: 2F2) (formula: C₂H₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			3	2	1		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	107	Total	O	0	0
			107	107		
11	B	114	Total	O	0	0
			114	114		
11	C	46	Total	O	0	0
			46	46		
11	D	27	Total	O	0	0
			27	27		

- Molecule 1: Inosine-5'-monophosphate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.46Å 114.46Å 256.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.23 – 2.50 39.23 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.23-2.50) 99.7 (39.23-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1367)	Depositor
R, R_{free}	0.176 , 0.217 0.183 , 0.220	Depositor DCC
R_{free} test set	3448 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11176	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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: 2F2, EDO, SO4, FMT, ACY, IMP, C91, GOL, CL

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	0.54	0/2704	0.87	2/3646 (0.1%)
1	B	0.54	0/2726	0.86	4/3676 (0.1%)
1	C	0.44	0/2653	0.88	5/3578 (0.1%)
1	D	0.42	0/2641	0.88	3/3561 (0.1%)
All	All	0.49	0/10724	0.87	14/14461 (0.1%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	296	GLY	CA-C-N	-8.14	111.75	120.47
1	C	296	GLY	C-N-CA	-8.14	111.75	120.47
1	A	296	GLY	CA-C-N	-6.83	112.67	120.04
1	A	296	GLY	C-N-CA	-6.83	112.67	120.04
1	D	417	VAL	CA-C-N	-6.40	113.39	119.85

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2669	0	2759	30	0
1	B	2691	0	2770	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2619	0	2681	42	0
1	D	2607	0	2694	67	0
2	A	23	0	11	1	0
2	B	23	0	11	2	0
2	C	23	0	11	3	0
2	D	23	0	11	2	0
3	A	29	0	18	2	0
3	B	29	0	18	5	0
3	C	29	0	18	1	0
3	D	29	0	18	2	0
4	A	5	0	0	0	0
4	B	10	0	0	0	0
4	C	10	0	0	0	0
4	D	5	0	0	1	0
5	A	6	0	8	0	0
5	B	12	0	16	0	0
5	D	6	0	8	1	0
6	A	3	0	1	0	0
6	B	3	0	1	0	0
7	A	4	0	3	0	0
7	B	4	0	3	1	0
8	A	4	0	6	1	0
8	B	8	0	12	2	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	C	3	0	0	0	0
10	A	3	0	6	0	0
11	A	107	0	0	2	0
11	B	114	0	0	0	0
11	C	46	0	0	1	0
11	D	27	0	0	2	0
All	All	11176	0	11084	165	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 165 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:434:LEU:HG	1:B:438:MET:HE2	1.52	0.91
1:A:434:LEU:HG	1:A:438:MET:HE2	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:ILE:HG22	1:B:438:MET:HE1	1.54	0.86
1:A:29:ILE:HG22	1:A:438:MET:HE1	1.65	0.79
1:B:246:ALA:H	8:B:509:EDO:H12	1.50	0.76

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	351/406 (86%)	343 (98%)	8 (2%)	0	100	100
1	B	354/406 (87%)	344 (97%)	10 (3%)	0	100	100
1	C	346/406 (85%)	332 (96%)	13 (4%)	1 (0%)	36	55
1	D	345/406 (85%)	330 (96%)	14 (4%)	1 (0%)	36	55
All	All	1396/1624 (86%)	1349 (97%)	45 (3%)	2 (0%)	48	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	294	GLY
1	C	249	HIS

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	283/323 (88%)	272 (96%)	11 (4%)	28	55
1	B	286/323 (88%)	281 (98%)	5 (2%)	53	78
1	C	277/323 (86%)	251 (91%)	26 (9%)	8	18
1	D	276/323 (85%)	250 (91%)	26 (9%)	8	18
All	All	1122/1292 (87%)	1054 (94%)	68 (6%)	17	35

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	270	ILE
1	D	300	ILE
1	D	456	VAL
1	C	228	ASP
1	C	224	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	391	GLN
1	D	209	ASN
1	D	226	GLN
1	B	247	HIS
1	C	70	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 31 ligands modelled in this entry, 5 are monoatomic - leaving 26 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
5	GOL	D	504	-	5,5,5	0.40	0	5,5,5	0.34	0
2	IMP	C	501	-	25,25,25	1.05	1 (4%)	37,38,38	1.98	9 (24%)
6	FMT	A	505	-	2,2,2	0.71	0	1,1,1	0.34	0
7	ACY	B	506	-	3,3,3	0.83	0	3,3,3	0.76	0
7	ACY	A	506	-	3,3,3	0.82	0	3,3,3	0.82	0
5	GOL	A	504	-	5,5,5	0.35	0	5,5,5	0.58	0
2	IMP	D	501	-	25,25,25	1.17	1 (4%)	37,38,38	2.02	9 (24%)
4	SO4	C	506	-	4,4,4	0.22	0	6,6,6	0.09	0
3	C91	C	502	-	33,33,33	2.06	11 (33%)	46,46,46	1.73	11 (23%)
3	C91	B	502	-	33,33,33	2.04	13 (39%)	46,46,46	1.61	8 (17%)
3	C91	A	502	-	33,33,33	2.00	12 (36%)	46,46,46	1.57	9 (19%)
2	IMP	A	501	-	25,25,25	1.11	1 (4%)	37,38,38	1.87	11 (29%)
4	SO4	A	503	-	4,4,4	0.26	0	6,6,6	0.16	0
3	C91	D	502	-	33,33,33	2.12	12 (36%)	46,46,46	1.75	13 (28%)
4	SO4	C	503	-	4,4,4	0.24	0	6,6,6	0.20	0
4	SO4	D	503	-	4,4,4	0.24	0	6,6,6	0.15	0
4	SO4	B	503	-	4,4,4	0.24	0	6,6,6	0.28	0
8	EDO	A	507	-	3,3,3	0.48	0	2,2,2	0.34	0
10	2F2	A	509	-	2,2,2	0.08	0	1,1,1	0.24	0
8	EDO	B	508	-	3,3,3	0.48	0	2,2,2	0.34	0
5	GOL	B	507	-	5,5,5	0.44	0	5,5,5	0.47	0
5	GOL	B	511	-	5,5,5	0.35	0	5,5,5	0.25	0
8	EDO	B	509	-	3,3,3	0.51	0	2,2,2	0.31	0
4	SO4	B	505	-	4,4,4	0.25	0	6,6,6	0.07	0
2	IMP	B	501	-	25,25,25	1.13	1 (4%)	37,38,38	1.86	9 (24%)
6	FMT	B	510	-	2,2,2	0.71	0	1,1,1	0.29	0

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
5	GOL	D	504	-	-	2/4/4/4	-
3	C91	D	502	-	-	0/12/12/12	0/5/5/5
2	IMP	C	501	-	-	5/10/26/26	0/3/3/3
8	EDO	A	507	-	-	0/1/1/1	-
3	C91	C	502	-	-	0/12/12/12	0/5/5/5
3	C91	B	502	-	-	0/12/12/12	0/5/5/5
8	EDO	B	508	-	-	0/1/1/1	-
5	GOL	B	507	-	-	3/4/4/4	-
5	GOL	B	511	-	-	3/4/4/4	-
3	C91	A	502	-	-	0/12/12/12	0/5/5/5
5	GOL	A	504	-	-	2/4/4/4	-
8	EDO	B	509	-	-	1/1/1/1	-
2	IMP	B	501	-	-	1/10/26/26	0/3/3/3
2	IMP	D	501	-	-	5/10/26/26	0/3/3/3
2	IMP	A	501	-	-	0/10/26/26	0/3/3/3

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	502	C91	C37-C6	5.90	1.55	1.47
3	D	502	C91	C37-C6	5.76	1.55	1.47
2	D	501	IMP	C2-N3	4.79	1.38	1.30
2	B	501	IMP	C2-N3	4.62	1.38	1.30
3	A	502	C91	C37-C6	4.62	1.53	1.47

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	IMP	C5-C6-N1	5.98	119.38	110.78
2	C	501	IMP	C5-C6-N1	5.67	118.94	110.78
2	B	501	IMP	C5-C6-N1	5.46	118.62	110.78
2	A	501	IMP	C5-C6-N1	5.15	118.19	110.78
3	C	502	C91	N1-C6-N3	-4.99	107.97	112.96

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	501	IMP	C5'-O5'-P-O1P

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Mol	Chain	Res	Type	Atoms
2	C	501	IMP	C5'-O5'-P-O2P
2	C	501	IMP	C5'-O5'-P-O3P
2	C	501	IMP	C3'-C4'-C5'-O5'
2	D	501	IMP	C5'-O5'-P-O1P

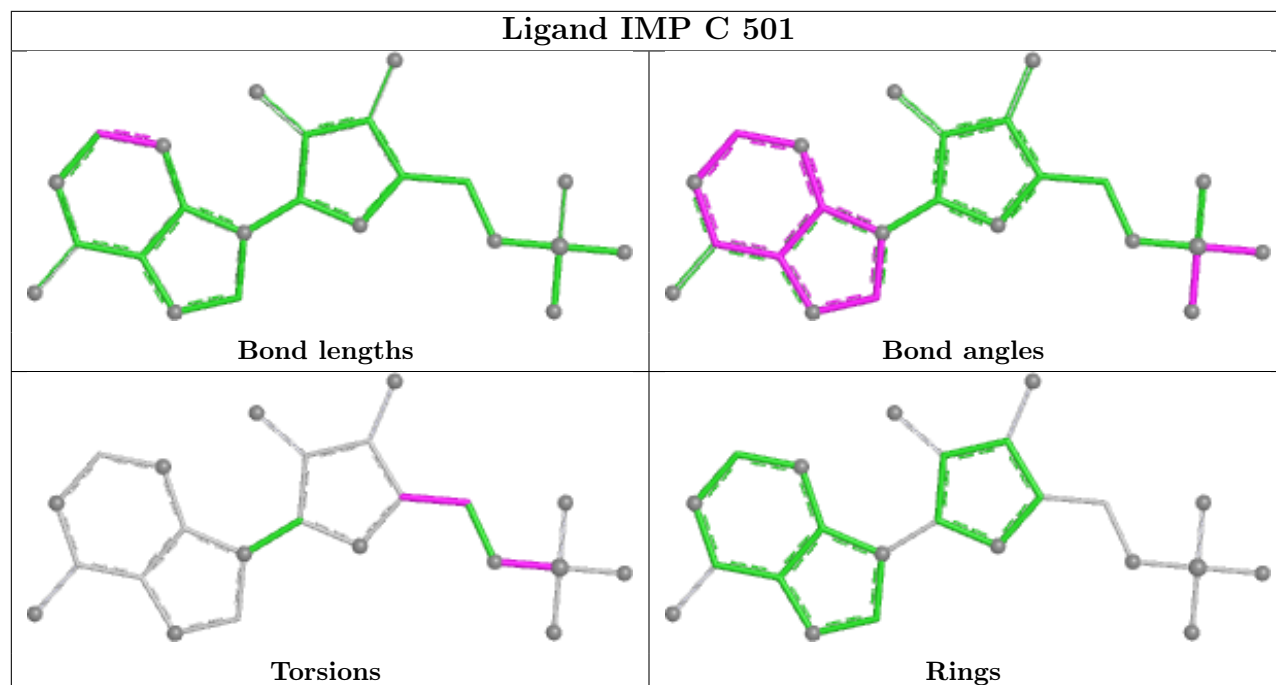
There are no ring outliers.

13 monomers are involved in 22 short contacts:

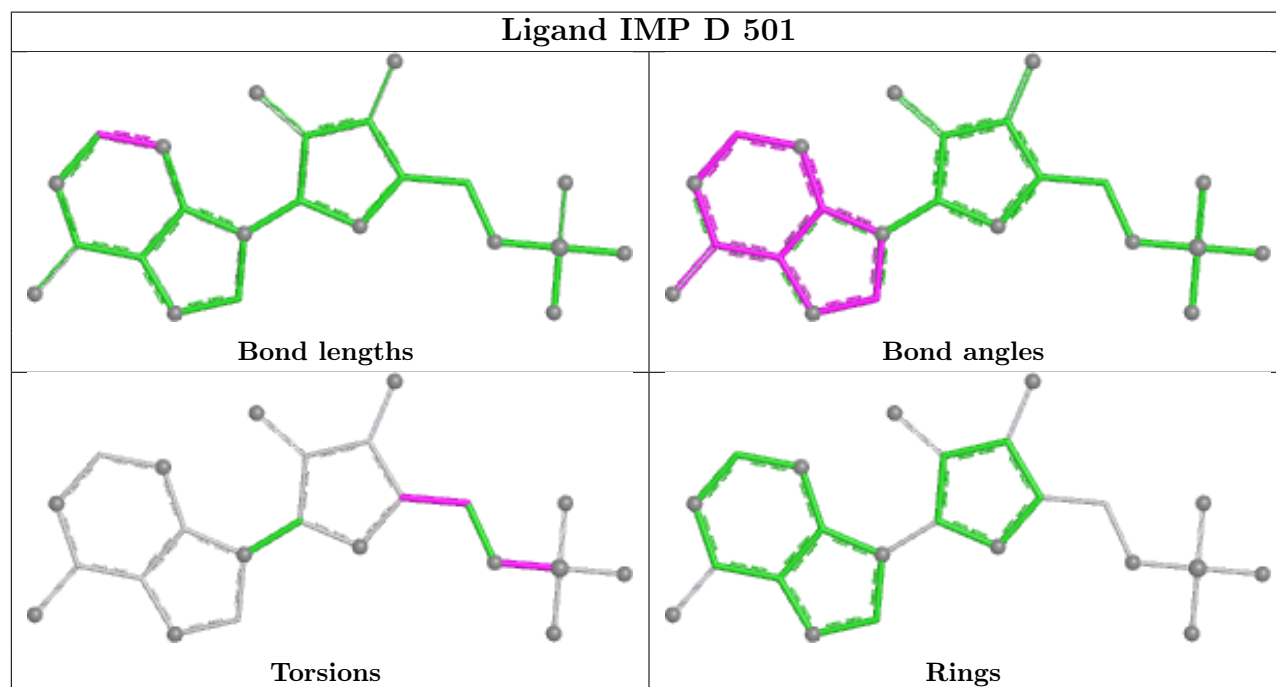
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	504	GOL	1	0
2	C	501	IMP	3	0
7	B	506	ACY	1	0
2	D	501	IMP	2	0
3	C	502	C91	1	0
3	B	502	C91	5	0
3	A	502	C91	2	0
2	A	501	IMP	1	0
3	D	502	C91	2	0
4	D	503	SO4	1	0
8	A	507	EDO	1	0
8	B	509	EDO	2	0
2	B	501	IMP	2	0

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.

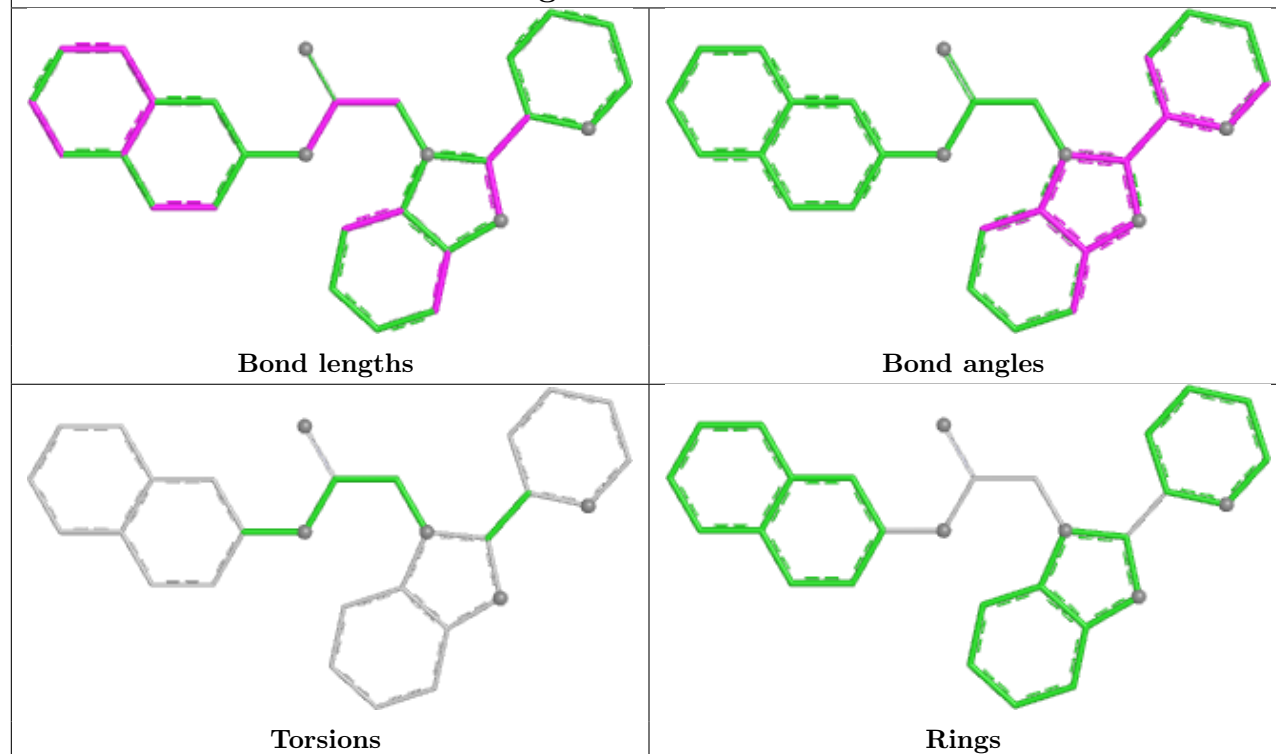
Ligand IMP C 501



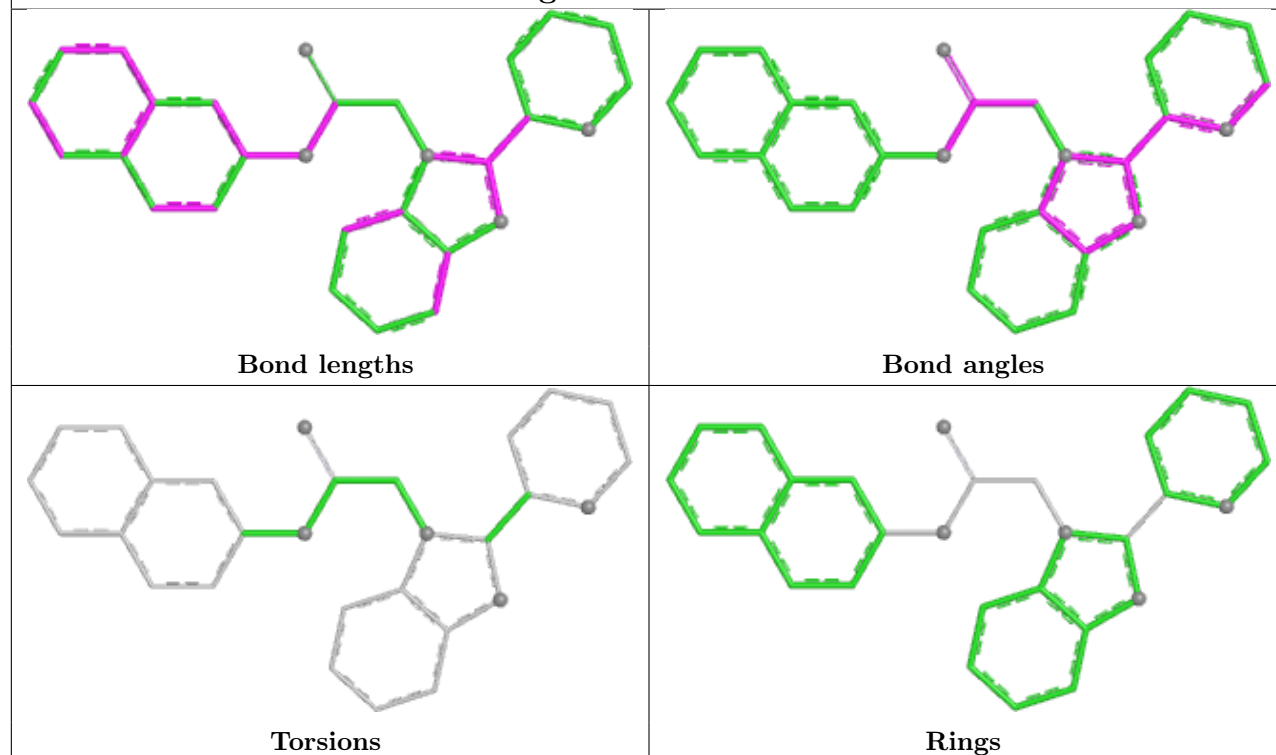
Ligand IMP D 501



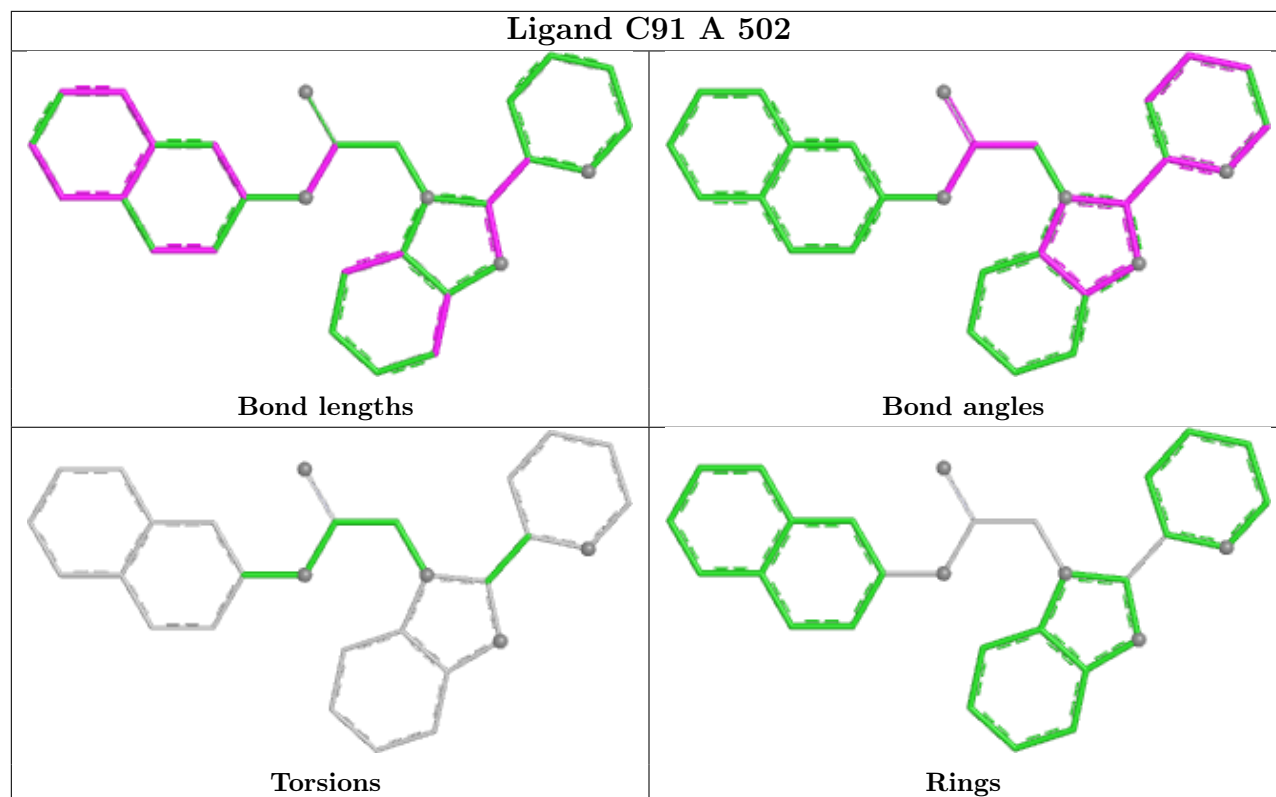
Ligand C91 C 502



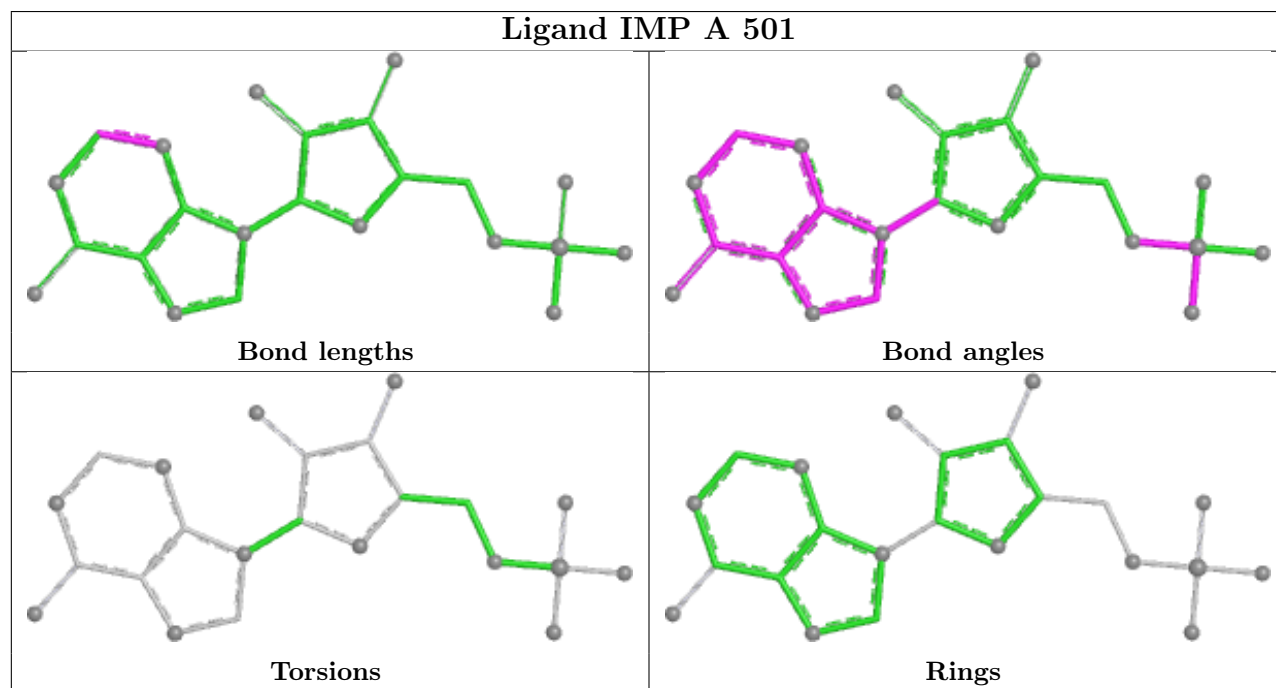
Ligand C91 B 502

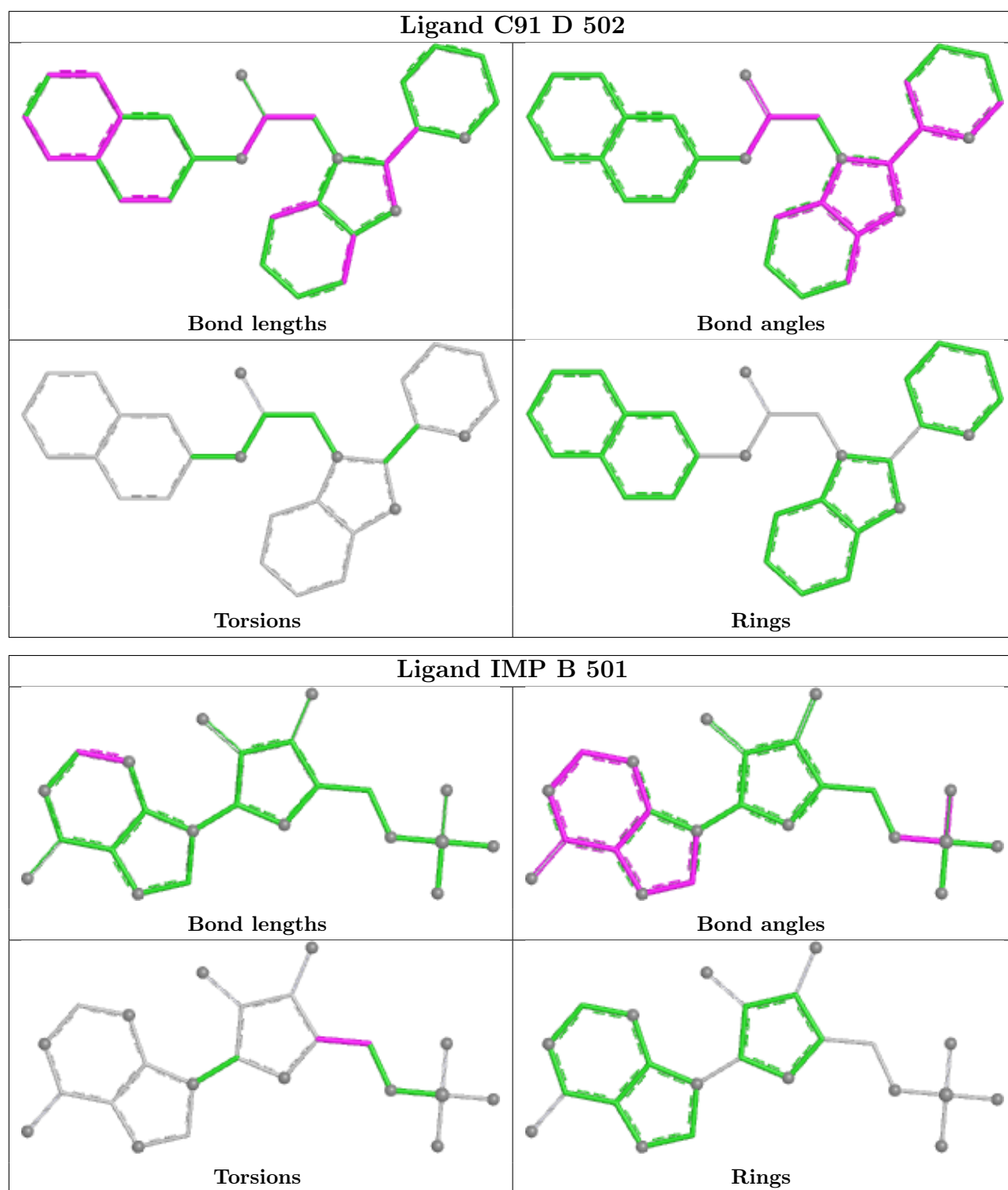


Ligand C91 A 502



Ligand IMP A 501





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [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	353/406 (86%)	-0.49	4 (1%) 78 75	21, 43, 69, 112	5 (1%)
1	B	354/406 (87%)	-0.54	4 (1%) 78 75	18, 44, 67, 120	7 (1%)
1	C	349/406 (85%)	0.26	10 (2%) 53 49	22, 78, 110, 134	3 (0%)
1	D	350/406 (86%)	0.69	29 (8%) 17 15	39, 94, 124, 140	1 (0%)
All	All	1406/1624 (86%)	-0.02	47 (3%) 49 45	18, 60, 114, 140	16 (1%)

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	408[A]	LEU	9.7
1	B	408[A]	LEU	6.8
1	C	482	VAL	4.6
1	C	11[A]	GLU	4.1
1	C	408	LEU	3.4

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

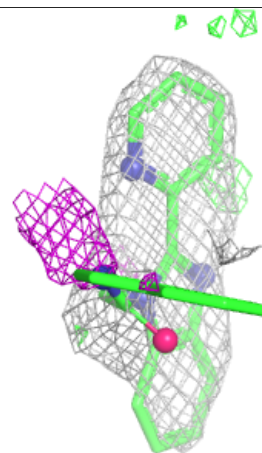
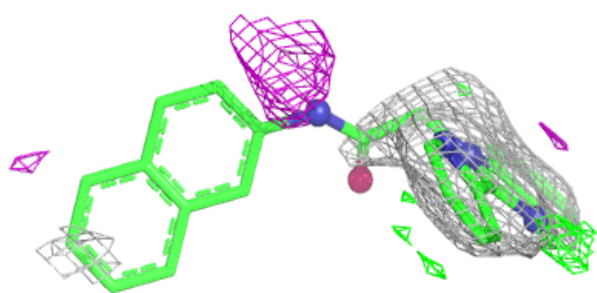
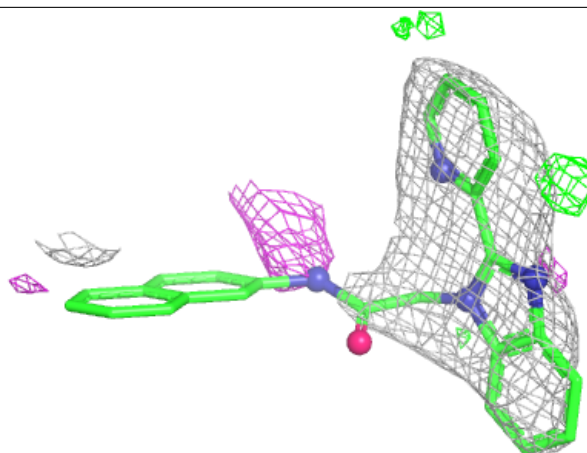
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	ACY	A	506	4/4	0.70	0.21	77,80,80,82	0
8	EDO	A	507	4/4	0.72	0.21	78,79,79,80	0
4	SO4	B	505	5/5	0.75	0.08	117,119,121,121	0
5	GOL	D	504	6/6	0.75	0.14	79,83,85,86	0
7	ACY	B	506	4/4	0.78	0.26	83,84,84,84	0
3	C91	C	502	29/29	0.78	0.24	99,116,145,145	0
5	GOL	B	511	6/6	0.79	0.17	74,75,78,80	0
10	2F2	A	509	3/3	0.80	0.20	48,48,54,54	0
3	C91	D	502	29/29	0.82	0.18	92,94,96,97	0
5	GOL	B	507	6/6	0.82	0.24	58,66,69,75	0
8	EDO	B	508	4/4	0.83	0.15	55,57,59,63	0
6	FMT	A	505	3/3	0.84	0.19	61,61,62,63	0
5	GOL	A	504	6/6	0.84	0.14	71,73,77,80	0
6	FMT	B	510	3/3	0.86	0.12	54,54,55,56	0
4	SO4	C	506	5/5	0.86	0.09	128,130,131,131	0
9	CL	B	504	1/1	0.90	0.13	85,85,85,85	0
9	CL	C	505	1/1	0.90	0.14	88,88,88,88	0
8	EDO	B	509	4/4	0.90	0.11	54,57,62,64	0
4	SO4	D	503	5/5	0.91	0.20	83,84,85,86	0
3	C91	A	502	29/29	0.92	0.11	50,63,76,78	0
2	IMP	D	501	23/23	0.92	0.10	40,58,70,77	0
3	C91	B	502	29/29	0.94	0.09	41,60,62,63	0
9	CL	C	504	1/1	0.94	0.16	81,81,81,81	0
4	SO4	C	503	5/5	0.94	0.16	68,69,70,72	0
4	SO4	B	503	5/5	0.94	0.13	75,77,77,80	0
2	IMP	C	501	23/23	0.95	0.08	47,53,63,67	0
9	CL	C	507	1/1	0.95	0.09	79,79,79,79	1
4	SO4	A	503	5/5	0.95	0.12	68,72,78,78	0
2	IMP	A	501	23/23	0.98	0.05	28,33,38,41	0
2	IMP	B	501	23/23	0.98	0.05	26,39,44,46	0
9	CL	A	508	1/1	0.99	0.19	70,70,70,70	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.

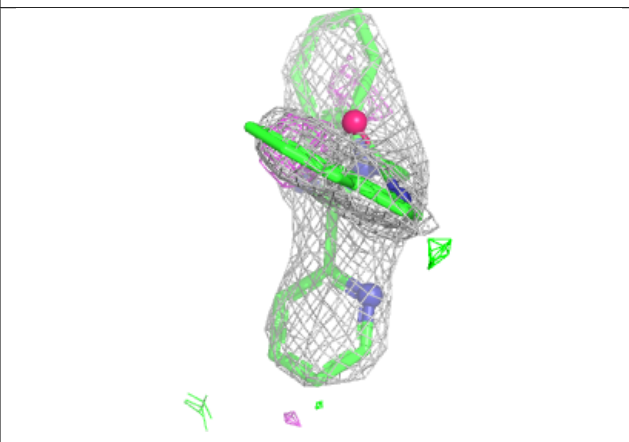
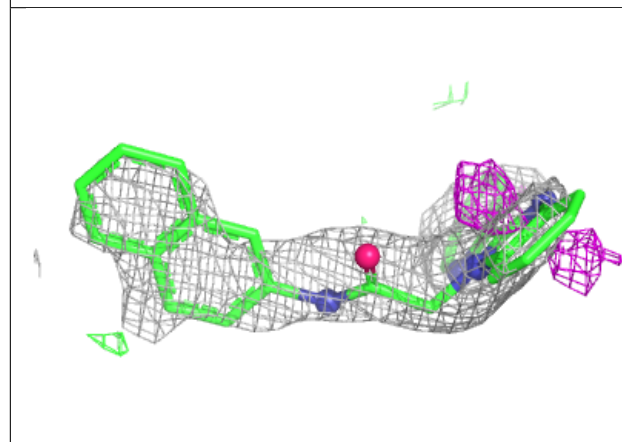
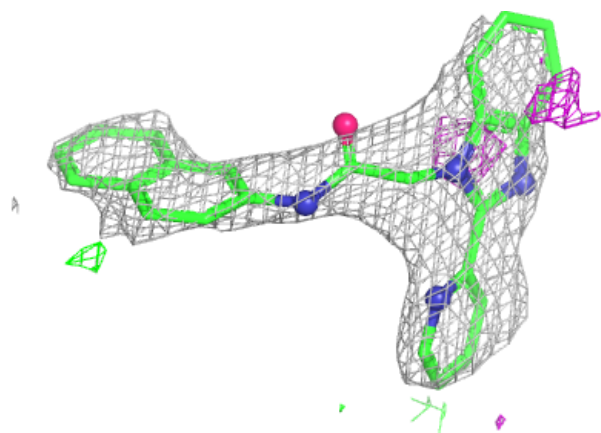
Electron density around C91 C 502:

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



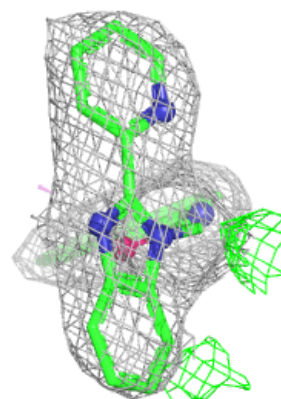
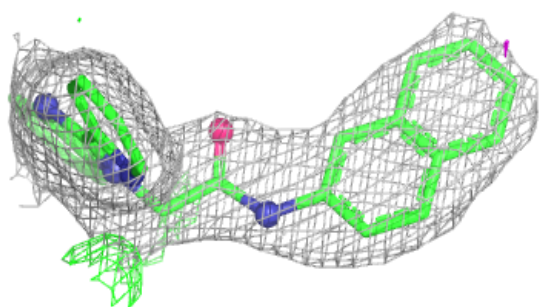
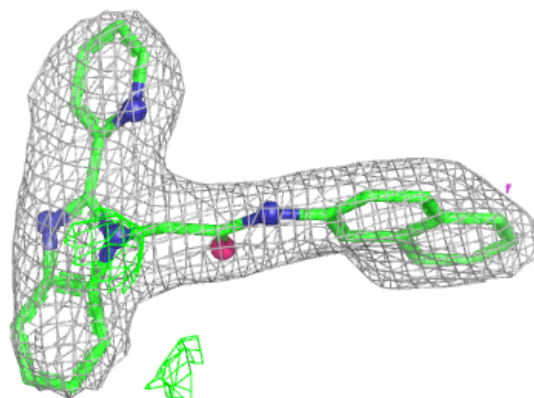
Electron density around C91 D 502:

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and green (positive)

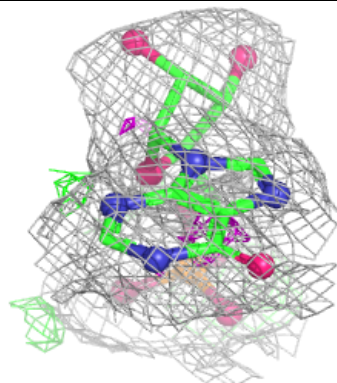
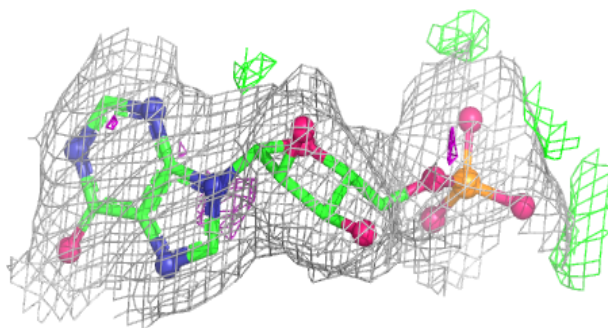
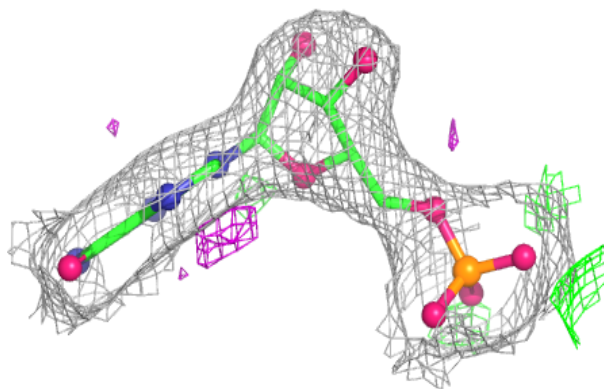


Electron density around C91 A 502:

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

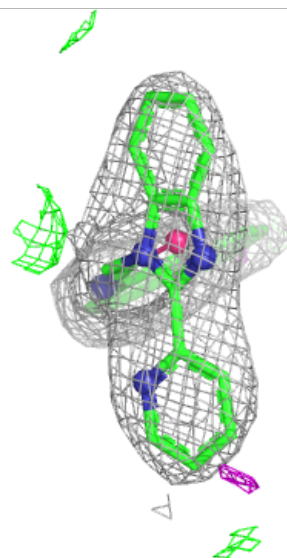
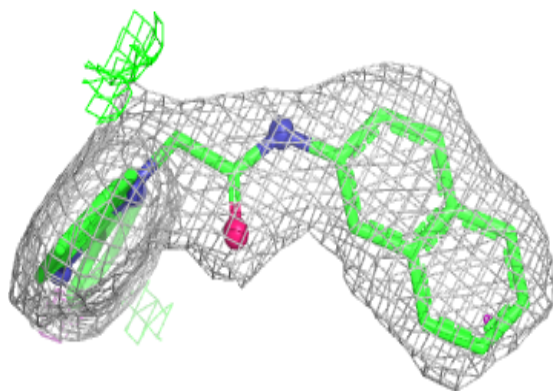
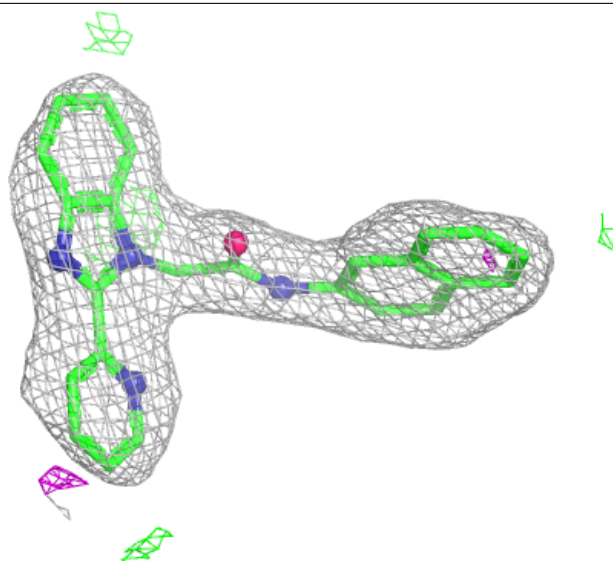
**Electron density around IMP D 501:**

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and green (positive)



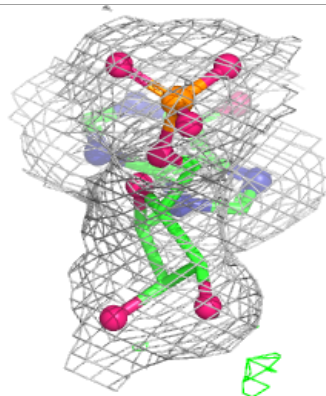
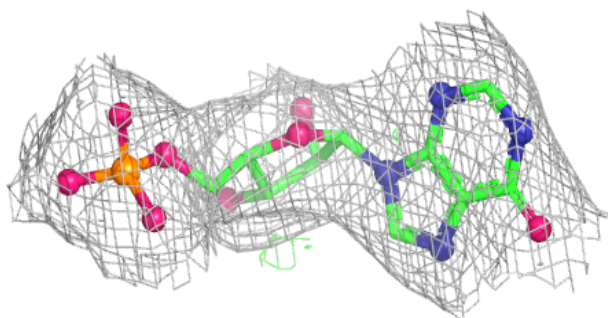
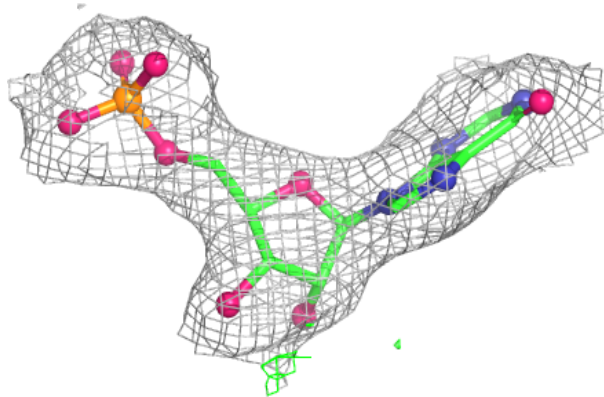
Electron density around C91 B 502:

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and green (positive)

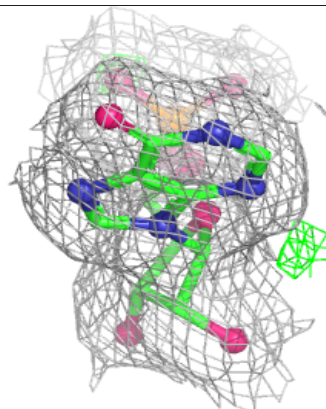
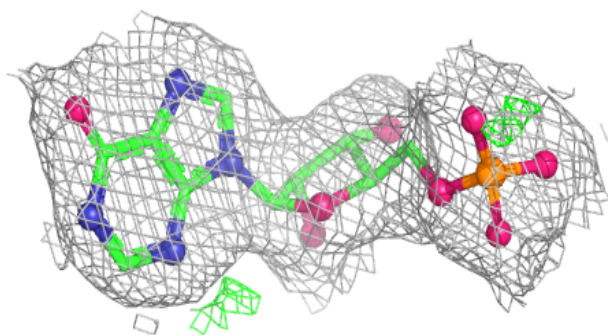
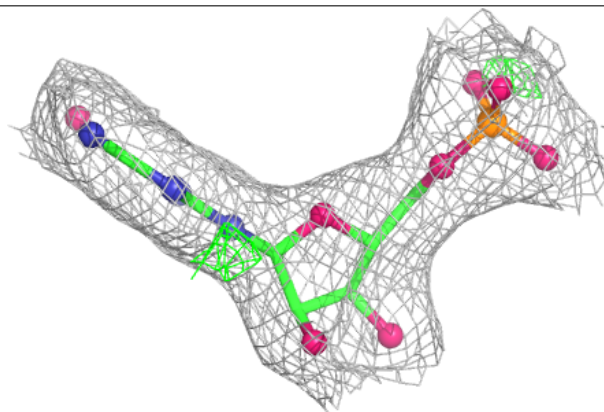


Electron density around IMP C 501:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

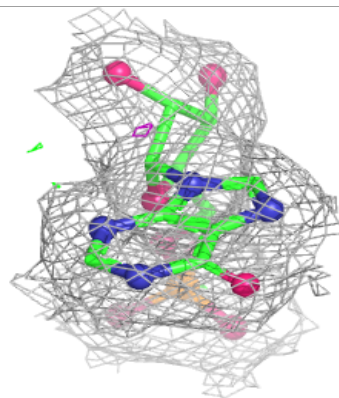
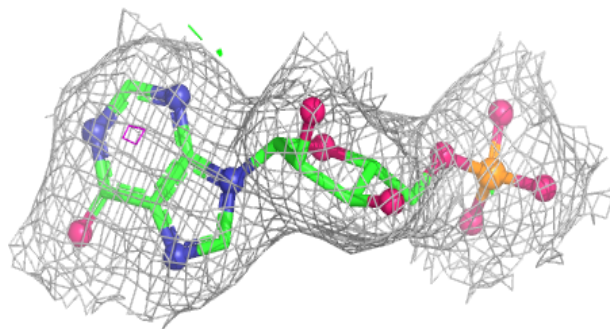
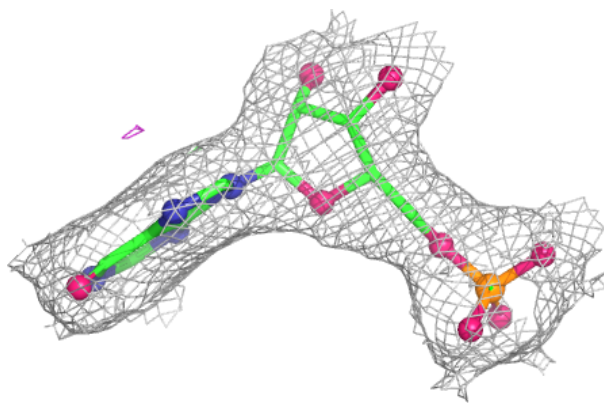
**Electron density around IMP A 501:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around IMP B 501:

$2mF_o-DF_c$ (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.