



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 15, 2024 – 04:06 AM EST

PDB ID : 1JCN
Title : BINARY COMPLEX OF HUMAN TYPE-I INOSINE MONOPHOSPHATE
DEHYDROGENASE WITH 6-CL-IMP
Authors : Risal, D.; Strickler, M.D.; Goldstein, B.M.
Deposited on : 2001-06-11
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

<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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

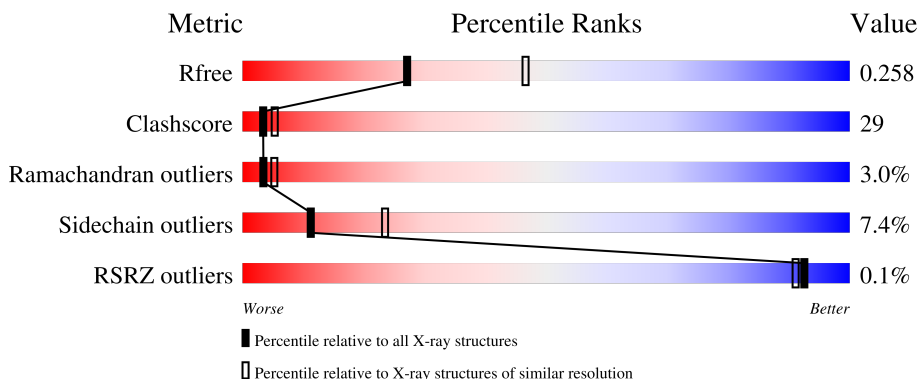
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

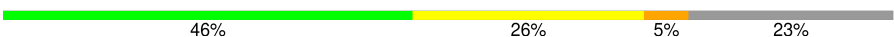
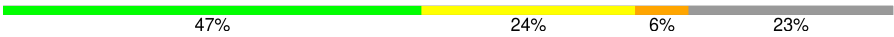
The reported resolution of this entry is 2.50 Å.

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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (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.

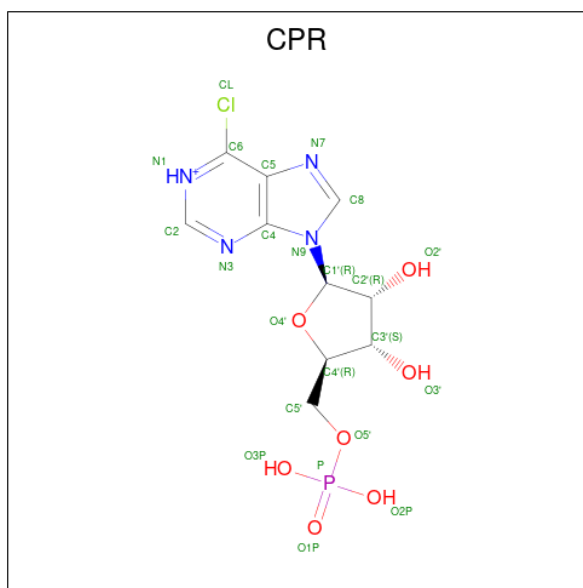
Mol	Chain	Length	Quality of chain
1	A	514	
1	B	514	

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 MONOPHOSPHATE DEHYDROGENASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total 2939	C 1855	N 506	O 560	S 18	0	0	0
1	B	395	Total 2939	C 1855	N 506	O 560	S 18	0	0	0

- Molecule 2 is 6-CHLOROPURINE RIBOSIDE, 5'-MONOPHOSPHATE (three-letter code: CPR) (formula: $\text{C}_{10}\text{H}_{13}\text{ClN}_4\text{O}_7\text{P}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 22	C 10	N 4	O 7	P 1	0	0
2	B	1	Total 22	C 10	N 4	O 7	P 1	0	0

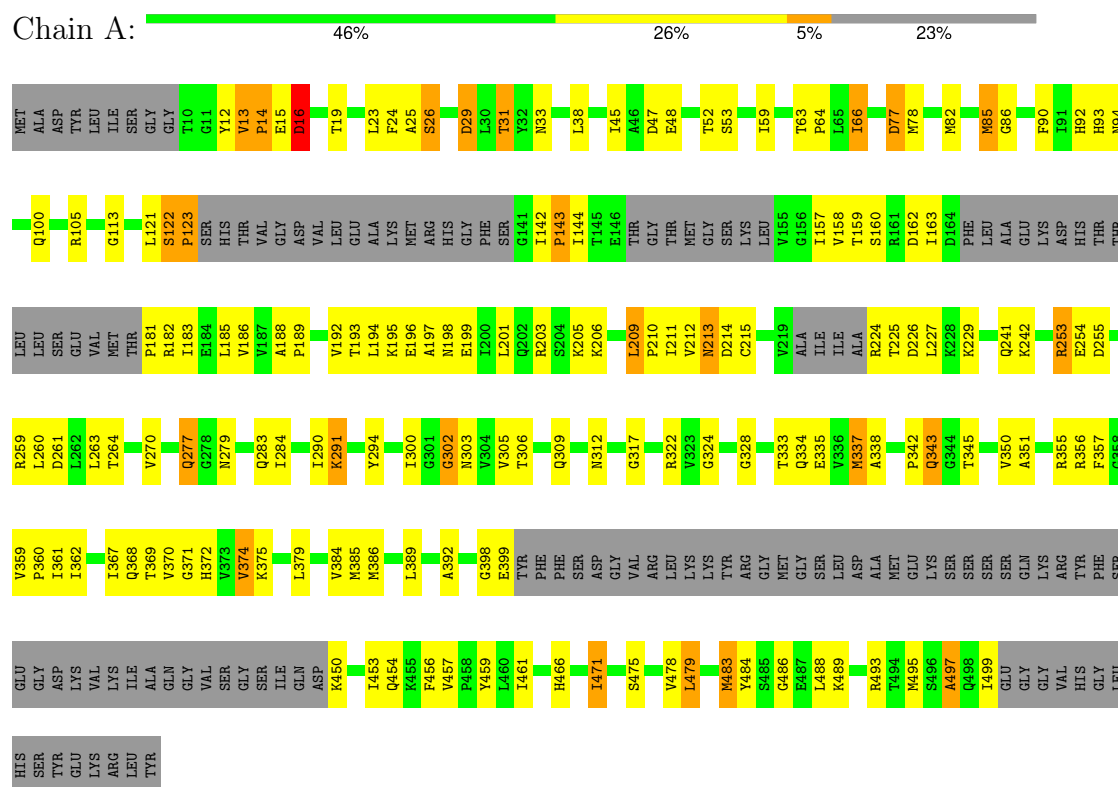
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	142	Total 142	O 142	0	0
3	B	152	Total 152	O 152	0	0

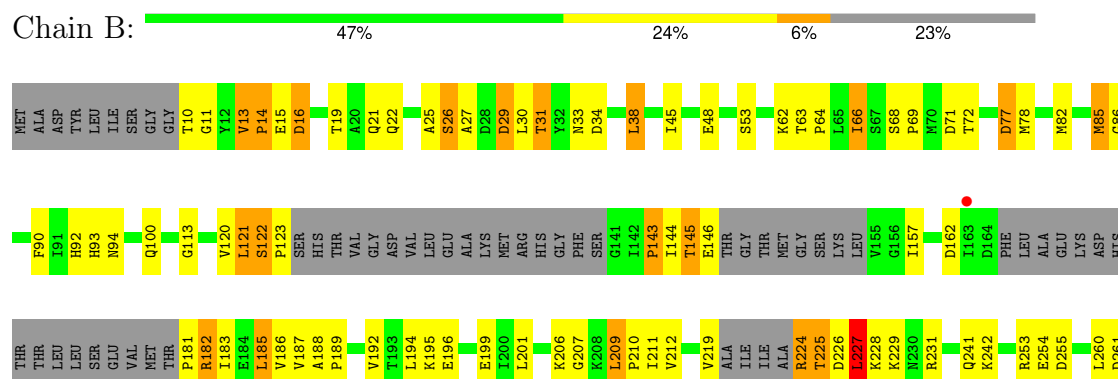
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: INOSINE MONOPHOSPHATE DEHYDROGENASE I



• Molecule 1: INOSINE MONOPHOSPHATE DEHYDROGENASE I



L262	L263	L264	V270	Q277	G278	N279	Q283	I284	V287	I290	K291	Y294	P295	H296	I300	G301	G302	N303	V304	V305	Q309	N312	L313	G317	V318	R322	G328	T333	Q334	E335	P342	Q343	G344	T345	V350	A351	R355	R356	F357	I361	I362										
I367	Q368	T369	V370	G371	H372	V373	V374	K375	A378	L379	V384	K385	M386	L389	L390	A391	A392	G398	E399	TYR	PHE	PHE	SER	SER	ASP	GLY	VAL	ARG	ARG	LEU	LYS	LYS	TYR	ARG	GLN	LYS	ARG	TYR	PHE	SER	GLU	GLY	ASP								
LYS	VAL	LYS	ILE	ALA	GLN	GLY	VAL	SER	GLY	SER	ILE	GLN	ASP	R450	Q454	K455	F456	V457	P458	Y459	I471	S475	V478	L479	M483	Y484	S485	G486	K489	R493	T494	M495	S496	A497	Q498	I499	GLU	GLY	GLY	VAL	HIS	GLY	LEU	HIS	SER	TYR	GLU	LYS	ARG	LEU	TYR

4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	148.11Å 148.11Å 122.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.74 – 2.50 39.74 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.4 (39.74-2.50) 97.5 (39.74-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.238 , 0.271 0.227 , 0.258	Depositor DCC
R_{free} test set	4483 reflections (9.94%)	wwPDB-VP
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.460 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6216	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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: CPR

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	0.37	0/2977	0.61	1/4023 (0.0%)
1	B	0.37	0/2977	0.62	1/4023 (0.0%)
All	All	0.37	0/5954	0.62	2/8046 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	PRO	N-CA-CB	5.42	109.80	103.30
1	B	143	PRO	N-CA-CB	5.23	109.57	103.30

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	2939	0	2967	200	0
1	B	2939	0	2967	162	0
2	A	22	0	11	2	0
2	B	22	0	11	1	0
3	A	142	0	0	11	0
3	B	152	0	0	10	0
All	All	6216	0	5956	350	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 29.

The worst 5 of 350 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:13:VAL:HB	1:A:14:PRO:HD3	1.31	1.12
1:B:13:VAL:HB	1:B:14:PRO:HD3	1.24	1.09
1:A:192:VAL:HG13	1:A:224:ARG:HH22	1.20	1.03
1:B:471:ILE:HD11	1:B:479:LEU:HG	1.44	0.99
1:A:29:ASP:HB3	1:A:342:PRO:HG2	1.44	0.98

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	383/514 (74%)	342 (89%)	31 (8%)	10 (3%)	4	7
1	B	383/514 (74%)	339 (88%)	31 (8%)	13 (3%)	3	4
All	All	766/1028 (74%)	681 (89%)	62 (8%)	23 (3%)	3	5

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	SER
1	A	122	SER
1	A	229	LYS
1	B	26	SER
1	B	122	SER

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	311/420 (74%)	289 (93%)	22 (7%)	12	25
1	B	311/420 (74%)	287 (92%)	24 (8%)	10	22
All	All	622/840 (74%)	576 (93%)	46 (7%)	11	23

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	85	MET
1	B	270	VAL
1	B	93	HIS
1	B	209	LEU
1	B	283	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	92	HIS
1	B	372	HIS
1	B	109	ASN
1	B	309	GLN
1	B	94	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
2	CPR	A	631	-	19,24,25	3.95	10 (52%)	17,36,38	2.09	5 (29%)
2	CPR	B	631	-	19,24,25	4.04	9 (47%)	17,36,38	2.08	6 (35%)

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	CPR	A	631	-	-	0/6/26/26	0/3/3/3
2	CPR	B	631	-	-	0/6/26/26	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	631	CPR	O4'-C1'	14.51	1.59	1.40
2	A	631	CPR	O4'-C1'	13.95	1.59	1.40
2	B	631	CPR	C4-N3	4.19	1.41	1.35
2	B	631	CPR	C2-N3	4.15	1.38	1.32
2	A	631	CPR	C4-N3	4.01	1.41	1.35

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	631	CPR	O4'-C4'-C5'	-4.79	93.98	109.33
2	B	631	CPR	O4'-C4'-C5'	-4.59	94.64	109.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	631	CPR	O3'-C3'-C2'	3.63	123.47	111.82
2	B	631	CPR	O3'-C3'-C2'	3.34	122.51	111.82
2	A	631	CPR	O4'-C1'-N9	3.06	112.80	108.75

There are no chirality outliers.

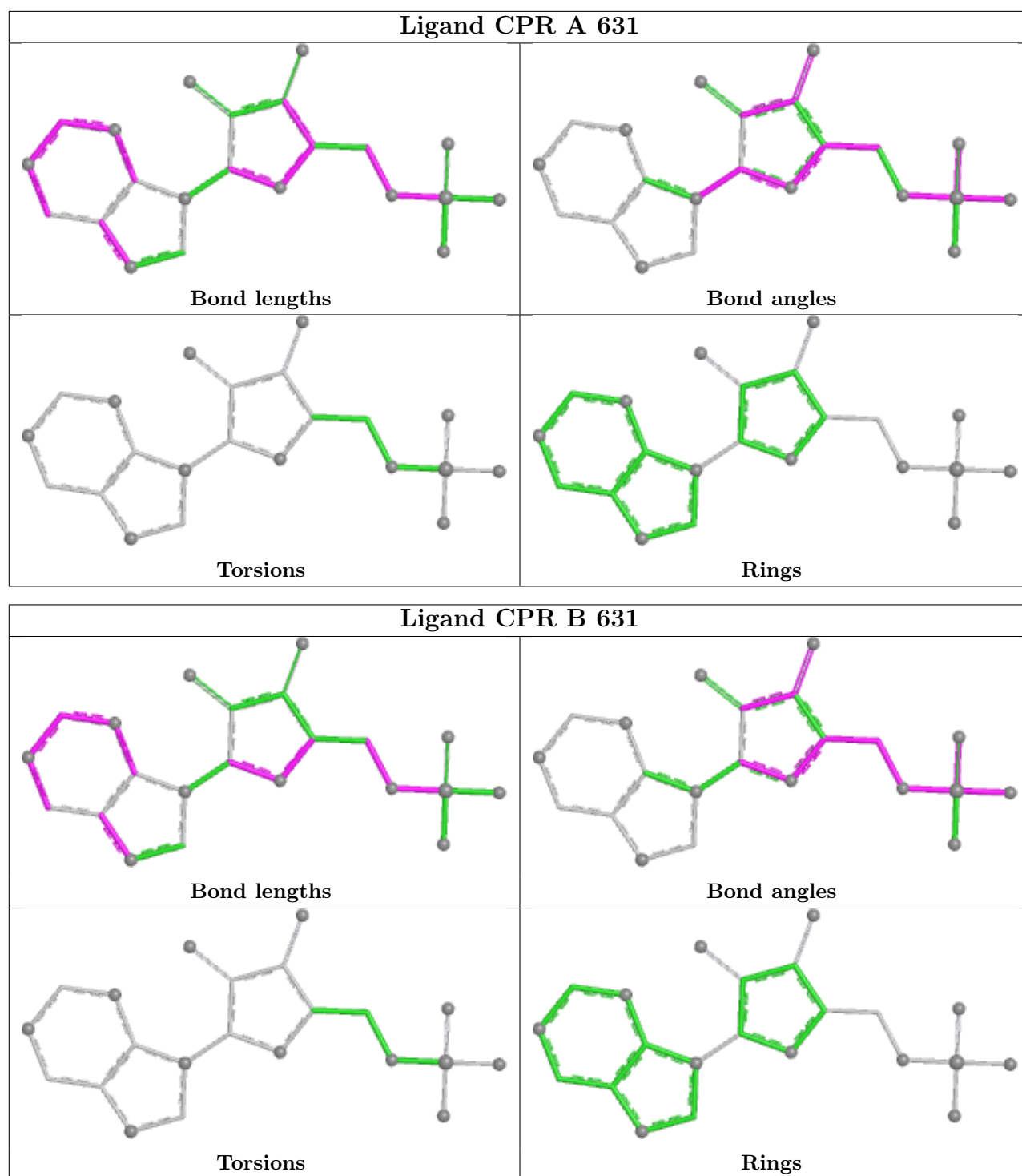
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	631	CPR	2	0
2	B	631	CPR	1	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 ⓘ

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	395/514 (76%)	-1.22	0 100 100	12, 28, 93, 109	0
1	B	395/514 (76%)	-1.20	1 (0%) 90 88	13, 28, 94, 105	0
All	All	790/1028 (76%)	-1.21	1 (0%) 92 91	12, 28, 93, 109	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	ILE	2.4

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 monosaccharides in this entry.

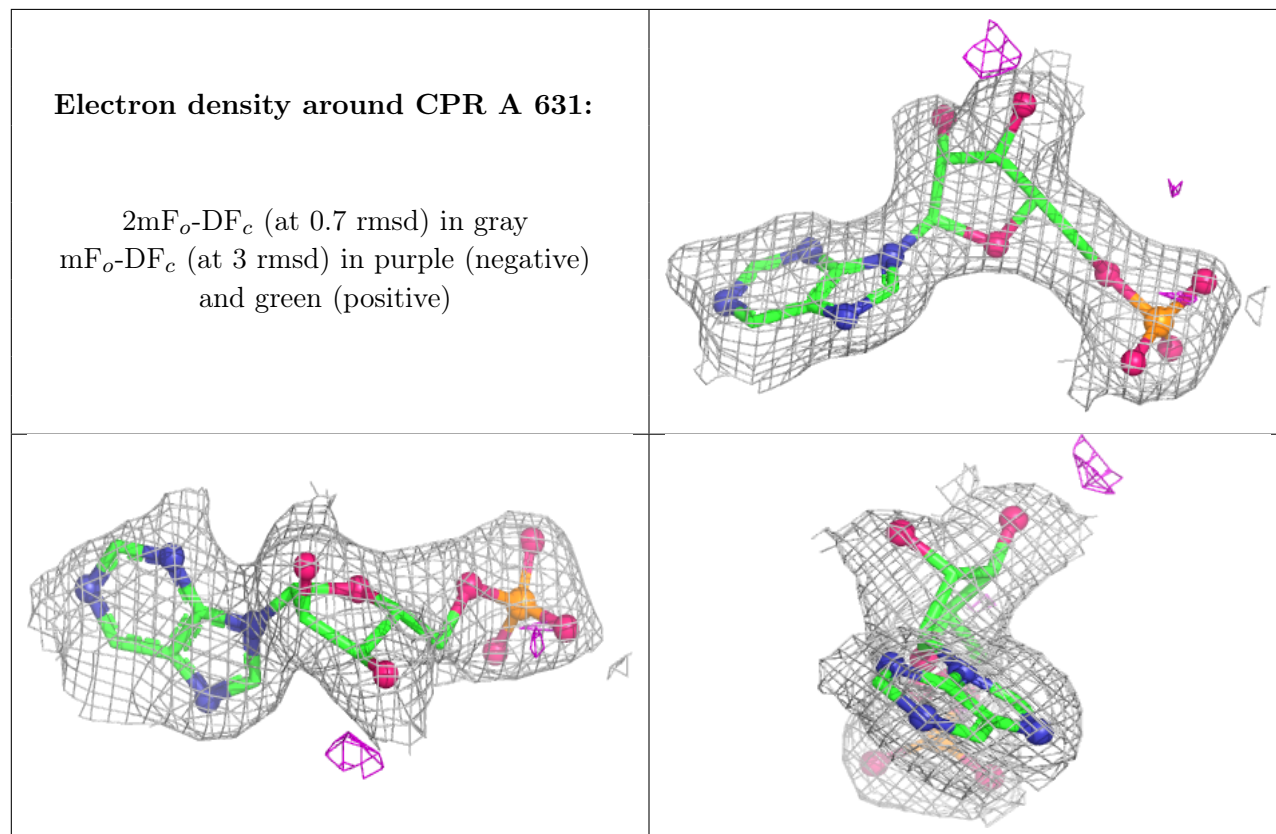
6.4 Ligands [i](#)

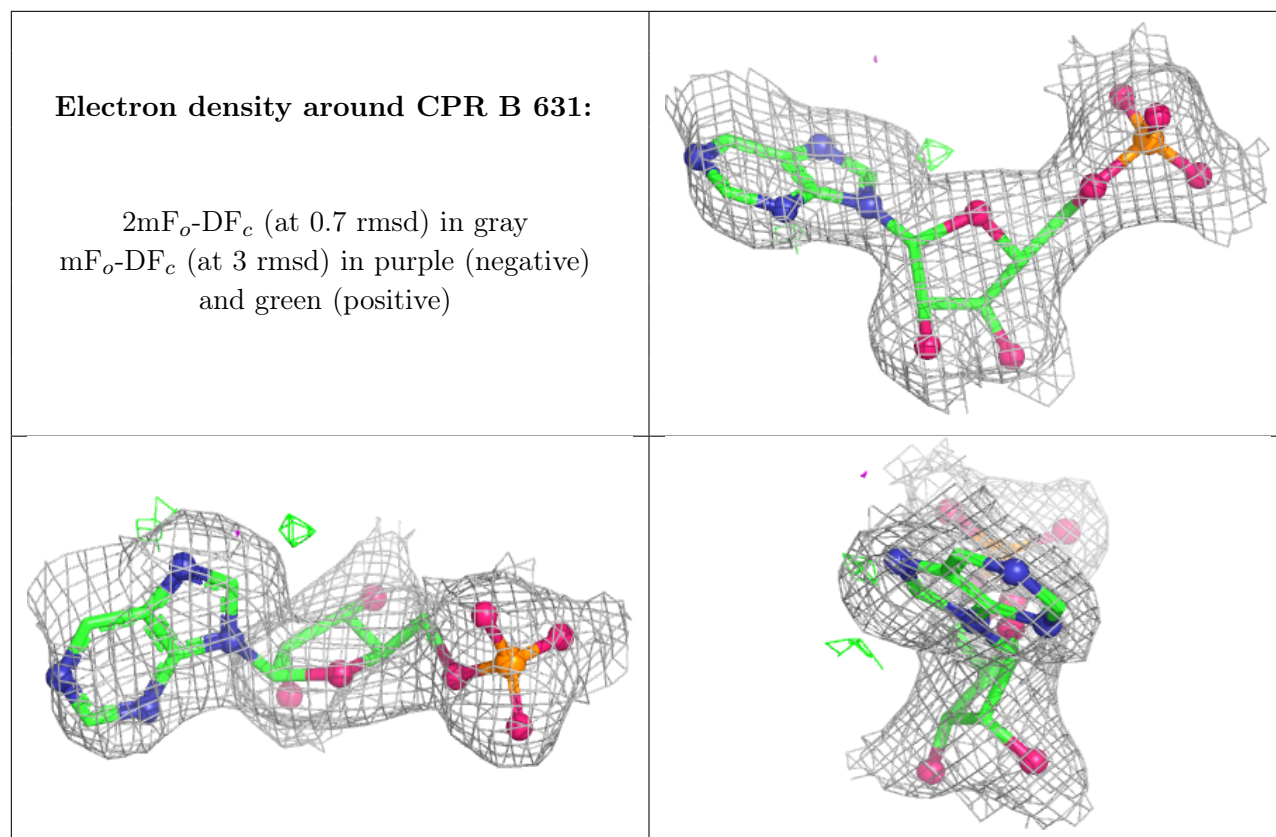
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CPR	A	631	22/23	0.99	0.04	22,29,48,50	0
2	CPR	B	631	22/23	1.00	0.03	20,28,46,48	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.