



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 14, 2024 – 06:30 PM EST

PDB ID : 1B3O
Title : TERNARY COMPLEX OF HUMAN TYPE-II INOSINE MONOPHOSPHATE DEHYDROGENASE WITH 6-CL-IMP AND SELENAZOLE ADENINE DINUCLEOTIDE
Authors : Colby, T.D.; Vanderveen, K.; Strickler, M.D.; Goldstein, B.M.
Deposited on : 1998-12-14
Resolution : 2.90 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	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

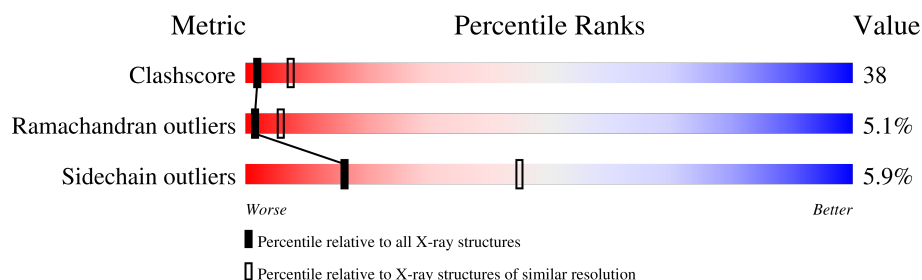
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
Clashscore	180529	2564 (2.90-2.90)
Ramachandran outliers	177936	2514 (2.90-2.90)
Sidechain outliers	177891	2516 (2.90-2.90)

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.

Note EDS failed to run properly.

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

2 Entry composition [i](#)

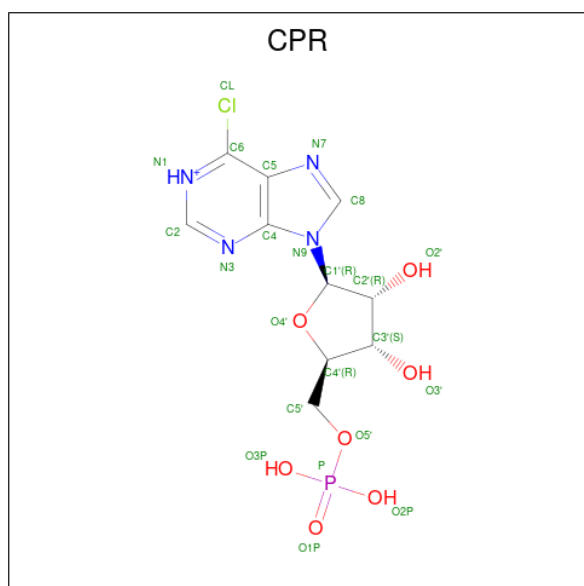
There are 5 unique types of molecules in this entry. The entry contains 5536 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (INOSINE MONOPHOSPHATE DEHYDROGENASE 2).

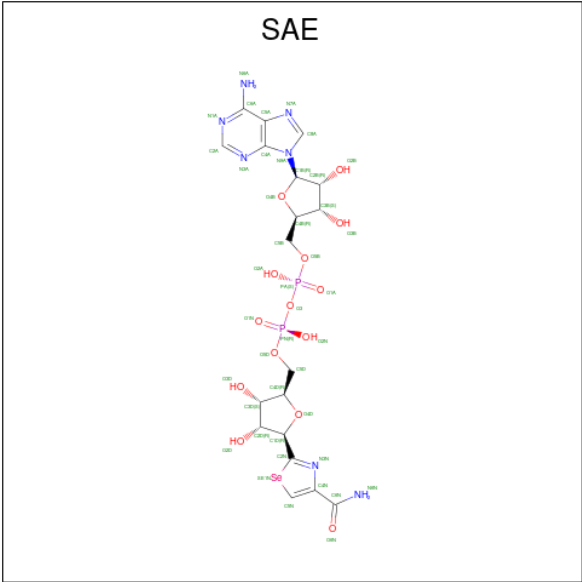
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	3
			2275	1434	389	439	13			
1	B	414	Total	C	N	O	S	0	0	4
			3085	1941	535	591	18			

- Molecule 2 is 6-CHLOROPURINE RIBOSIDE, 5'-MONOPHOSPHATE (three-letter code: CPR) (formula: $C_{10}H_{13}ClN_4O_7P$).



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

- Molecule 3 is SELENAZOLE-4-CARBOXYAMIDE-ADENINE DINUCLEOTIDE (three-letter code: SAE) (formula: $C_{19}H_{25}N_7O_{14}P_2Se$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	Se	0	0
			43	19	7	14	2	1		
3	B	1	Total	C	N	O	P	Se	0	0
			43	19	7	14	2	1		

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	15	Total	X	15	0
			15	15		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	11	Total	O	0	0
			11	11		
5	B	20	Total	O	0	0
			20	20		



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	142.26Å 142.26Å 174.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.90	Depositor
% Data completeness (in resolution range)	86.4 (100.00-2.90)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.85Å)	Xtriage
Refinement program	CNS 0.3	Depositor
R, R_{free}	0.244 , 0.270	Depositor
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.068	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.039 for -h,k,-l	Xtriage
Total number of atoms	5536	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UNX, CPR, SAE

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	0.49	0/2308	0.77	0/3122
1	B	0.58	0/3125	0.85	2/4224 (0.0%)
All	All	0.54	0/5433	0.82	2/7346 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	181	LYS	N-CA-C	6.40	128.27	111.00
1	B	231	ARG	NE-CZ-NH1	-5.02	117.79	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	TYR	Sidechain

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	2275	0	2294	129	0
1	B	3085	0	3161	285	0
2	A	22	0	11	1	0
2	B	22	0	11	2	0
3	A	43	0	23	4	0
3	B	43	0	23	4	0
4	B	15	0	0	0	0
5	A	11	0	0	0	0
5	B	20	0	0	0	0
All	All	5536	0	5523	417	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 38.

The worst 5 of 417 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:105:ARG:HH12	1:B:109:LYS:HG2	1.18	1.06
1:B:181:LYS:HE2	1:B:181:LYS:H	1.20	1.01
1:B:224:ARG:HB3	1:B:227:LEU:HD11	1.46	0.97
1:B:227:LEU:HD13	1:B:228:LYS:N	1.80	0.96
1:B:198:ASN:HA	1:B:201:LEU:HD12	1.44	0.95

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	299/514 (58%)	249 (83%)	39 (13%)	11 (4%)	2 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	406/514 (79%)	304 (75%)	77 (19%)	25 (6%)	1	3
All	All	705/1028 (69%)	553 (78%)	116 (16%)	36 (5%)	1	6

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	VAL
1	A	14	PRO
1	A	17	GLY
1	A	76	ALA
1	A	450	LYS

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	242/420 (58%)	237 (98%)	5 (2%)	48	78
1	B	333/420 (79%)	304 (91%)	29 (9%)	8	27
All	All	575/840 (68%)	541 (94%)	34 (6%)	16	45

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	277	GLN
1	B	291	LYS
1	B	471	ILE
1	B	126	ARG
1	B	124	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	94	ASN
1	B	277	GLN

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Mol	Chain	Res	Type
1	B	478	GLN
1	B	265	GLN
1	B	283	GLN

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 19 ligands modelled in this entry, 15 are unknown - leaving 4 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	$\# Z > 2$
3	SAE	A	600	-	39,47,47	1.24	2 (5%)	44,72,72	2.26	13 (29%)
2	CPR	A	631	-	19,24,25	1.44	3 (15%)	17,36,38	1.73	4 (23%)
2	CPR	B	631	-	19,24,25	1.56	5 (26%)	17,36,38	1.97	4 (23%)
3	SAE	B	601	-	39,47,47	1.25	2 (5%)	44,72,72	2.26	13 (29%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SAE	A	600	-	-	4/18/62/62	0/5/5/5
2	CPR	A	631	-	-	5/6/26/26	0/3/3/3
2	CPR	B	631	-	-	0/6/26/26	0/3/3/3
3	SAE	B	601	-	-	4/18/62/62	0/5/5/5

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	SAE	O4B-C1B	4.89	1.47	1.40
3	A	600	SAE	O4B-C1B	4.85	1.47	1.40
2	A	631	CPR	C2-N3	3.27	1.37	1.32
2	B	631	CPR	O4'-C1'	2.95	1.44	1.40
2	B	631	CPR	C2-N3	2.90	1.36	1.32

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	SAE	N3A-C2A-N1A	-6.72	119.56	128.67
3	A	600	SAE	N3A-C2A-N1A	-6.69	119.59	128.67
3	B	601	SAE	C4B-O4B-C1B	-6.38	104.08	109.92
3	A	600	SAE	C4B-O4B-C1B	-6.37	104.09	109.92
2	B	631	CPR	O4'-C1'-N9	5.61	116.18	108.75

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

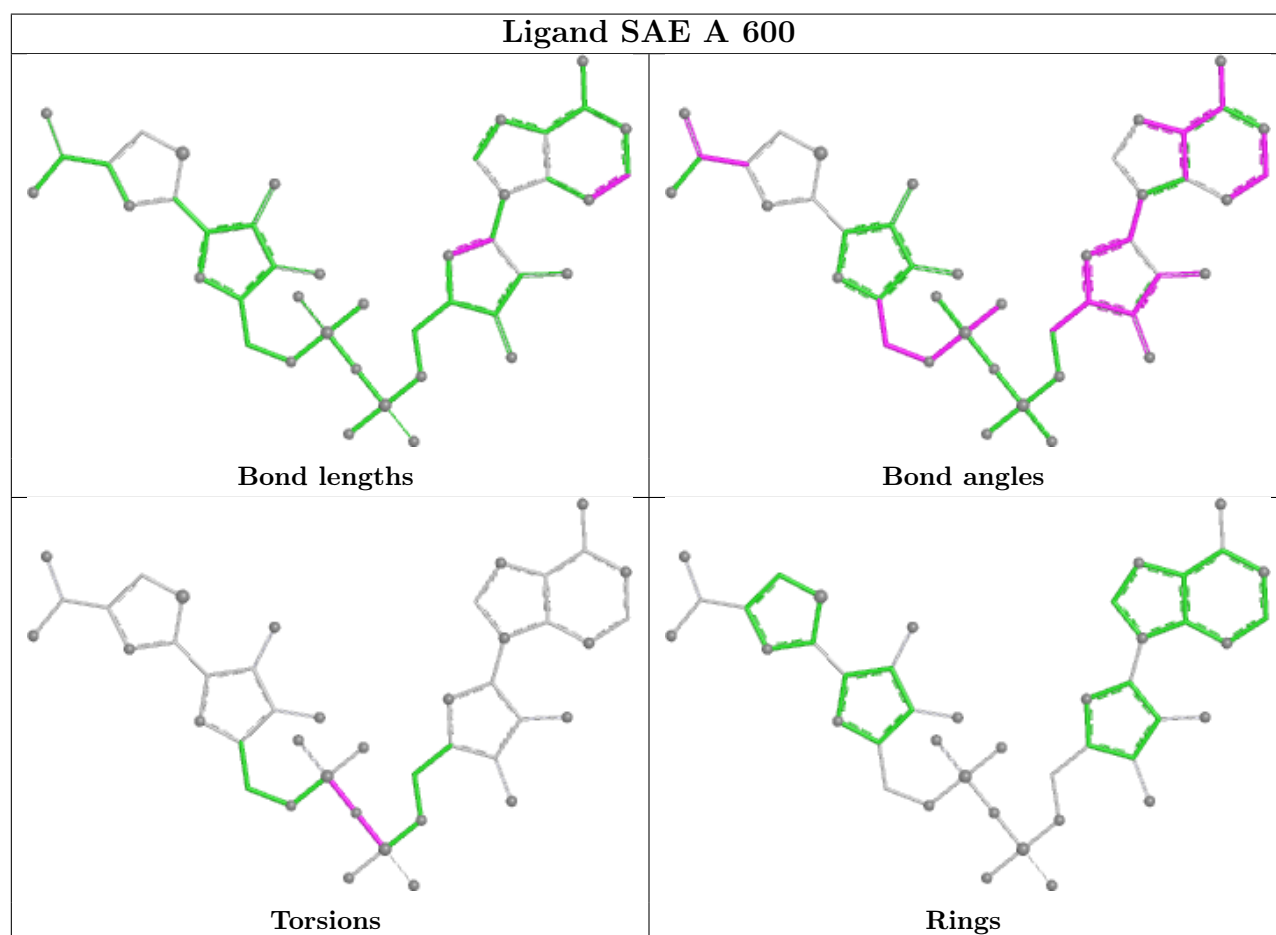
Mol	Chain	Res	Type	Atoms
2	A	631	CPR	C5'-O5'-P-O2P
2	A	631	CPR	C5'-O5'-P-O3P
2	A	631	CPR	C3'-C4'-C5'-O5'
2	A	631	CPR	C5'-O5'-P-O1P
3	A	600	SAE	PN-O3-PA-O5B

There are no ring outliers.

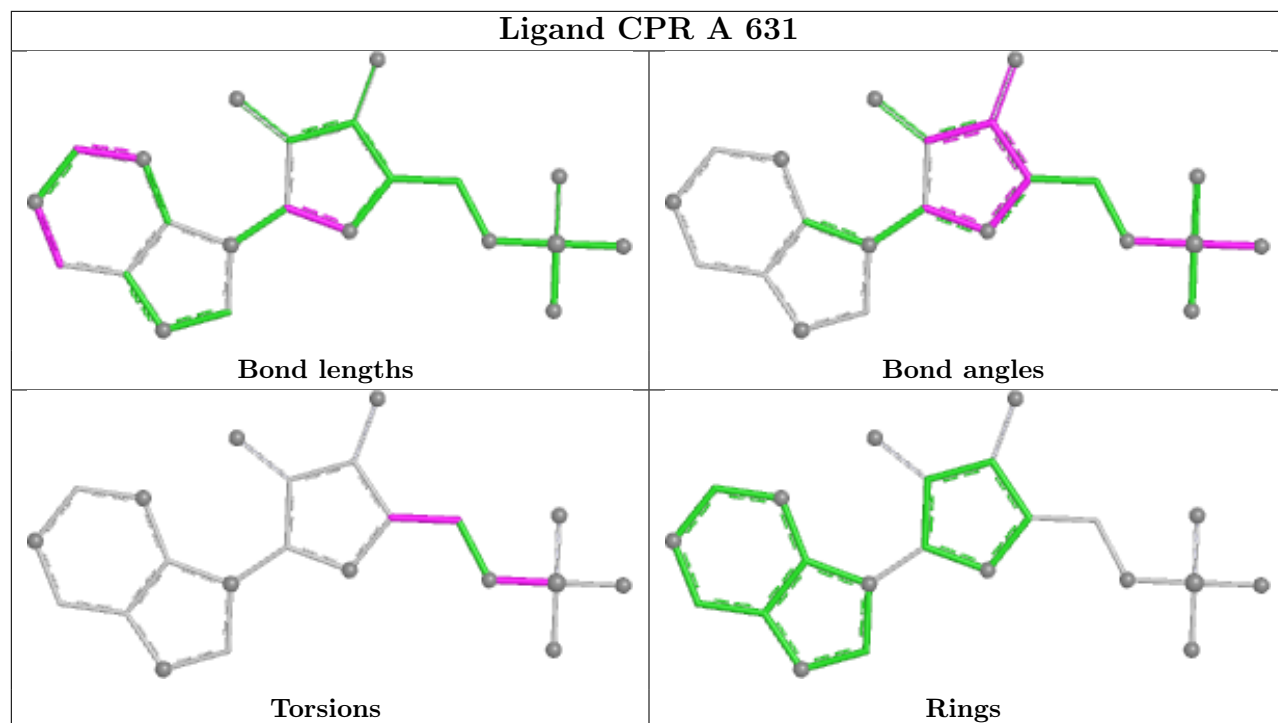
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	SAE	4	0
2	A	631	CPR	1	0
2	B	631	CPR	2	0
3	B	601	SAE	4	0

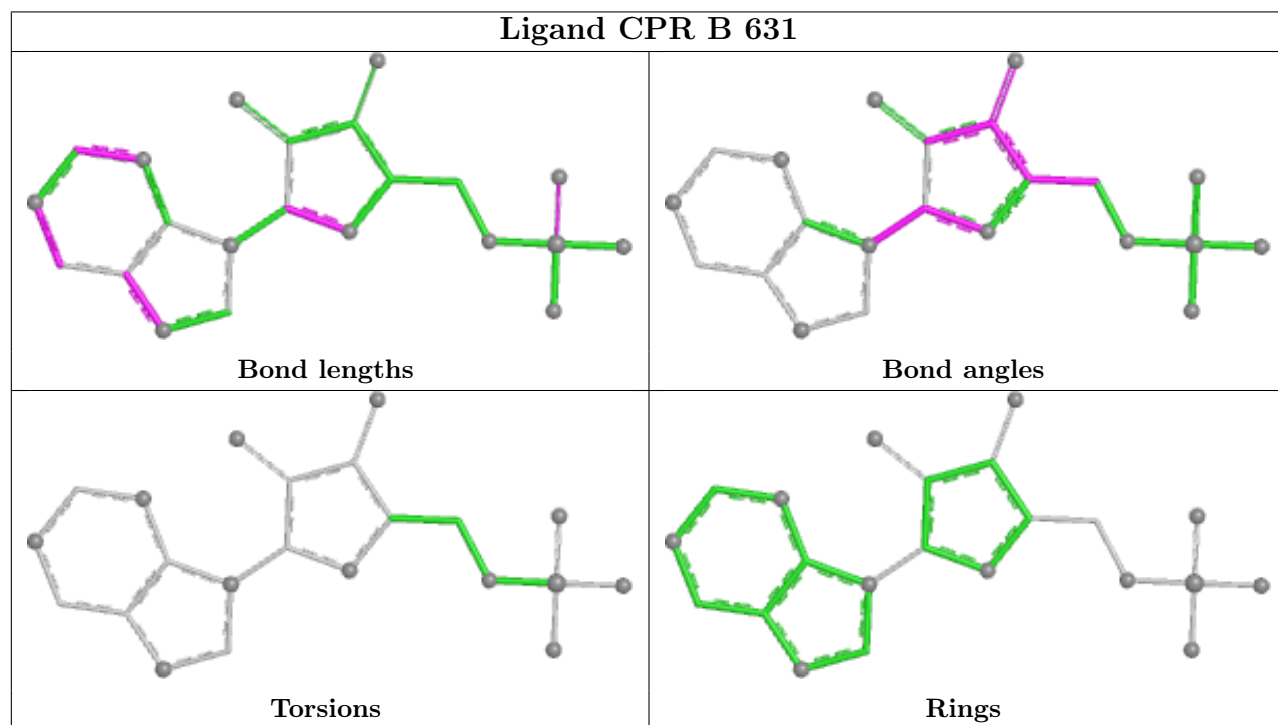
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

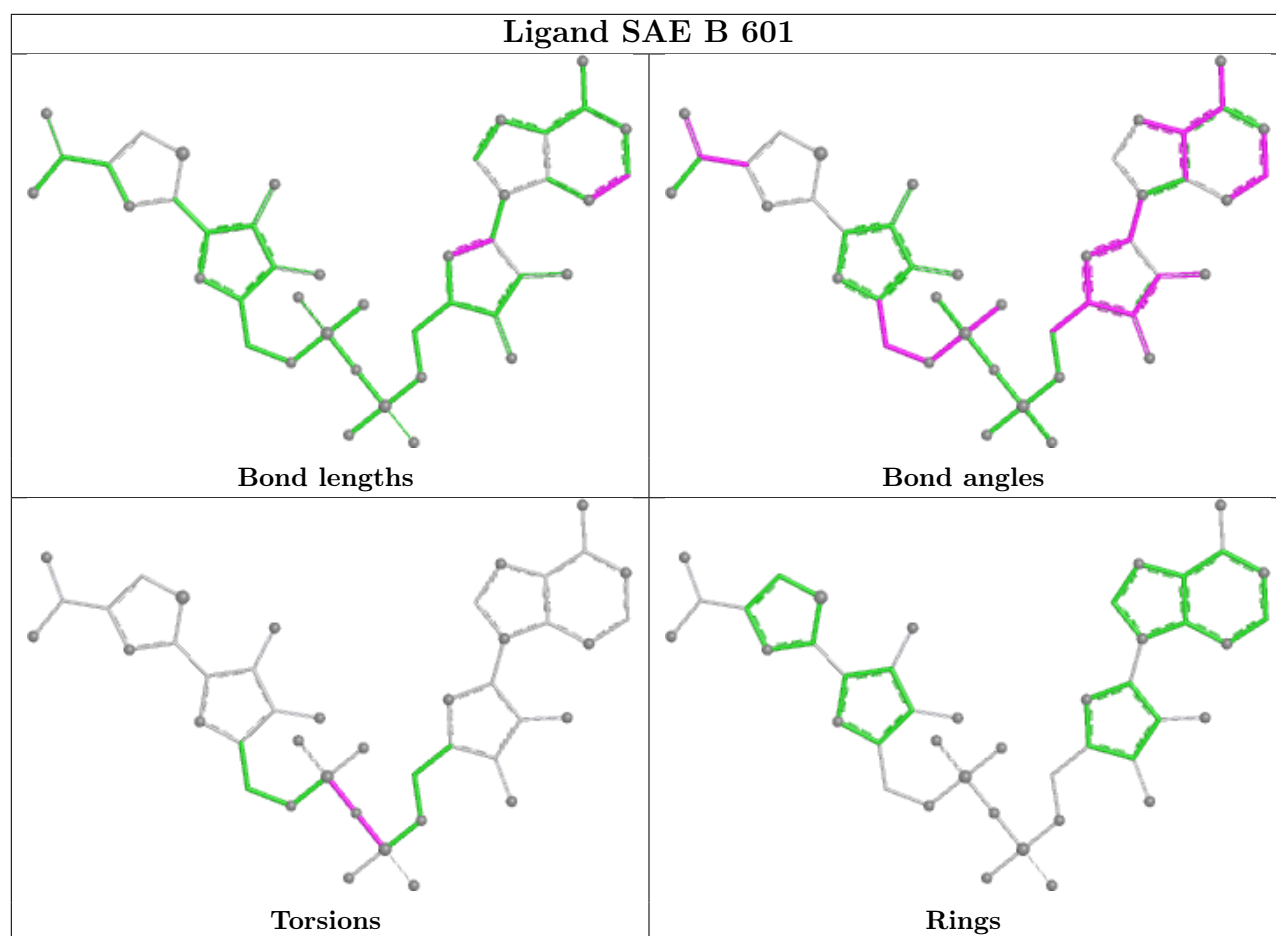


Ligand CPR A 631



Ligand CPR B 631





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

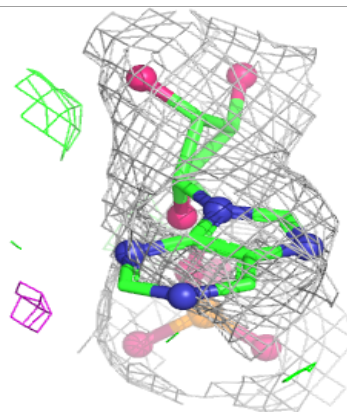
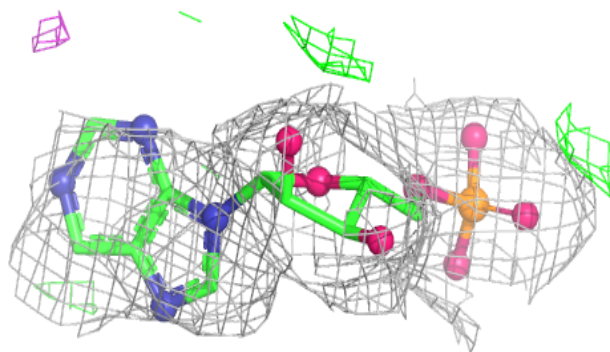
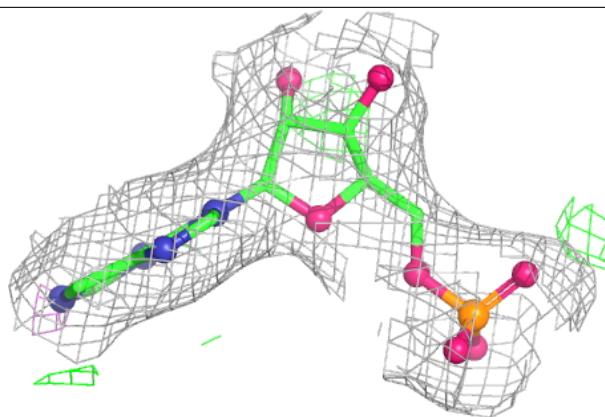
6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

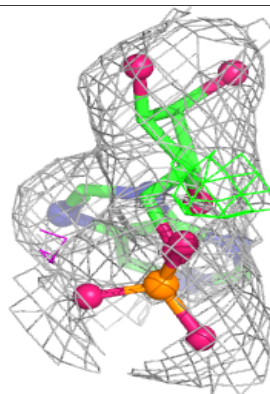
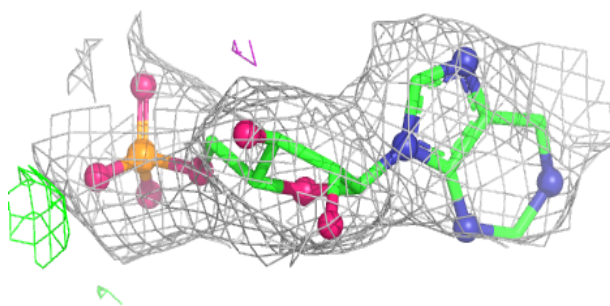
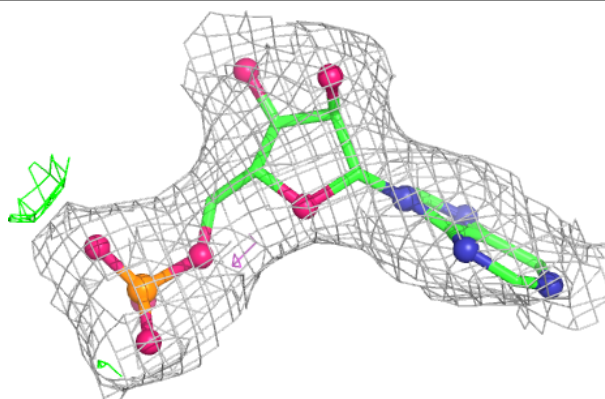
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CPR A 631:

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

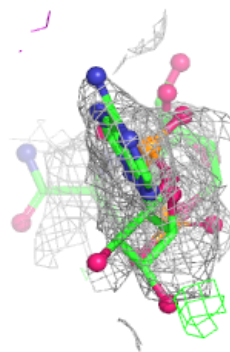
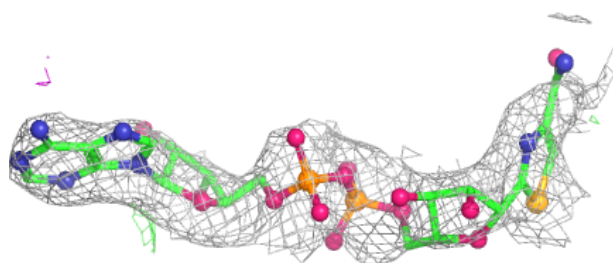
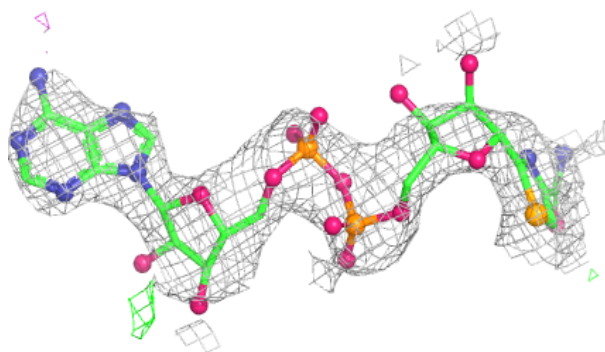
**Electron density around CPR B 631:**

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

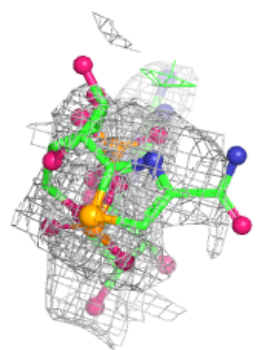
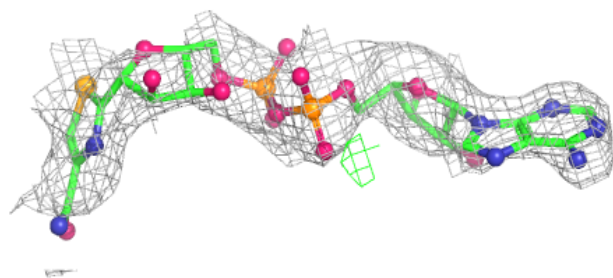
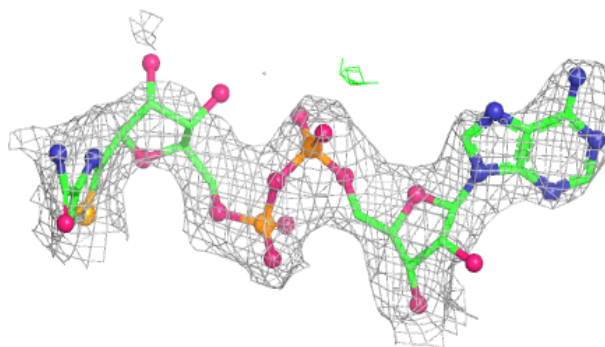


Electron density around SAE A 600:

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

**Electron density around SAE B 601:**

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



6.5 Other polymers

EDS failed to run properly - this section is therefore empty.