Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:49 AM UTC

PDB ID	:	6HQ4 / pdb_00006hq4
Title	:	Structure of EAL enzyme Bd1971 - cAMP bound form
Authors	:	Lovering, A.L.; Cadby, I.T.
Deposited on	:	2018-09-24
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:

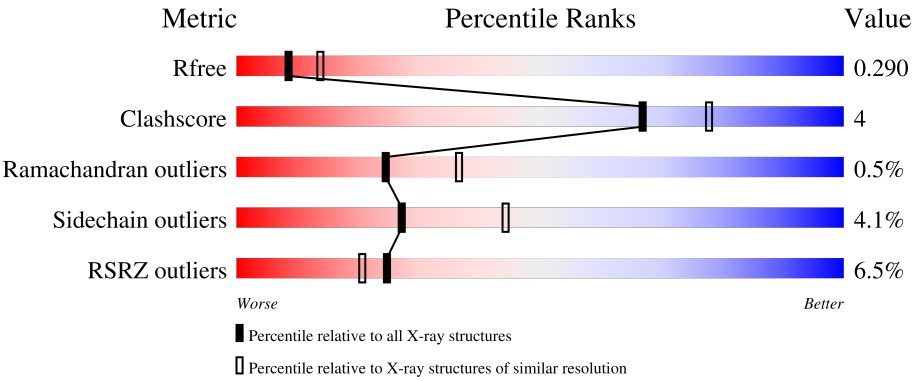
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

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 <=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	397	7% 86% 7% • 6%
1	B	397	5% 83% 9% • 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5970 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.

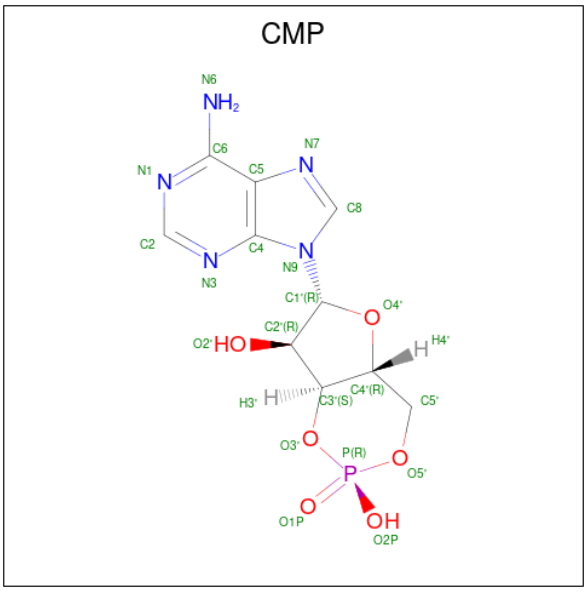
- Molecule 1 is a protein called EAL Enzyme Bd1971.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	0	0
			2986	1899	518	554	15			
1	B	368	Total	C	N	O	S	0	0	0
			2938	1869	507	547	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	401	LYS	-	expression tag	UNP Q6MLN6
A	402	LEU	-	expression tag	UNP Q6MLN6
B	401	LYS	-	expression tag	UNP Q6MLN6
B	402	LEU	-	expression tag	UNP Q6MLN6

- Molecule 2 is ADENOSINE-3',5'-CYCLIC-MONOPHOSPHATE (CCD ID: CMP) (formula: $C_{10}H_{12}N_5O_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

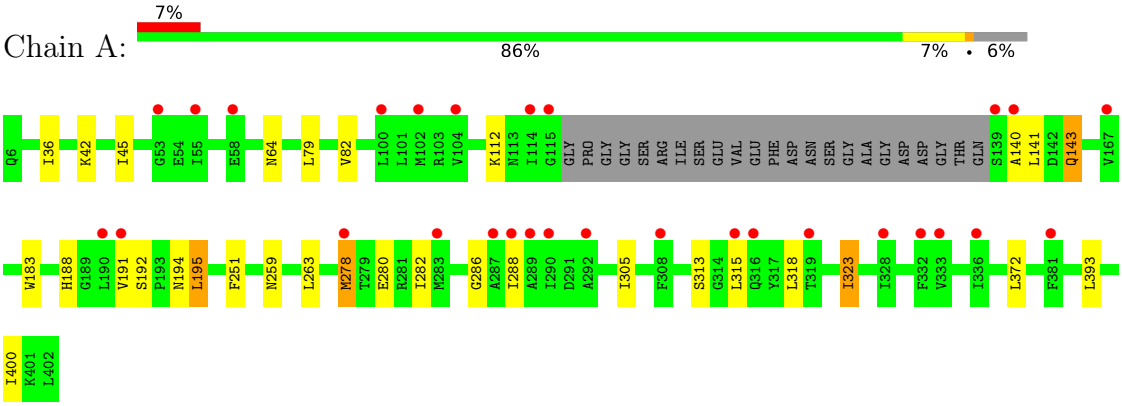
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

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.

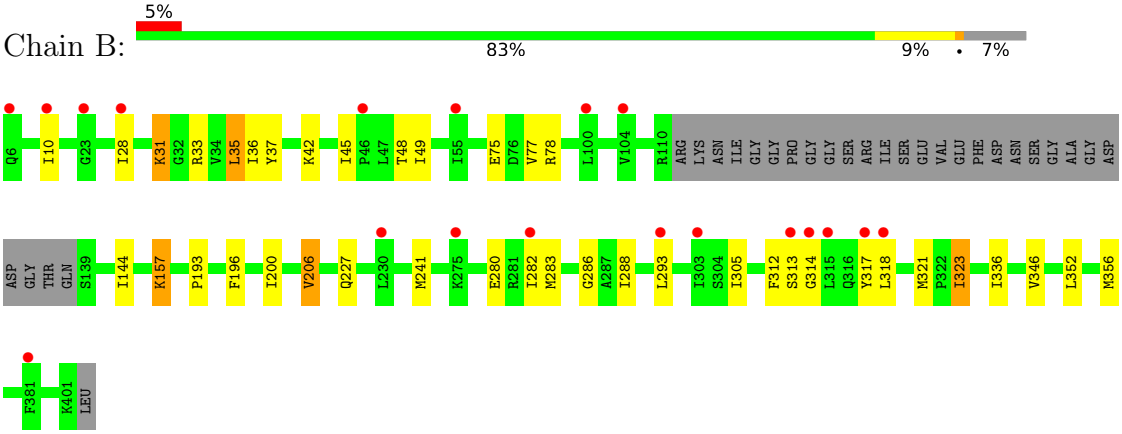
• Molecule 1: EAL Enzyme Bd1971

Chain A:



• Molecule 1: EAL Enzyme Bd1971

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	82.38Å 82.38Å 131.32Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.66 – 2.63 65.66 – 2.63	Depositor EDS
% Data completeness (in resolution range)	99.5 (65.66-2.63) 99.5 (65.66-2.63)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.52 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.240 , 0.286 0.244 , 0.290	Depositor DCC
R_{free} test set	1483 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	78.2	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 45.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.012 for -h,-k,l 0.047 for h,-h-k,-l 0.024 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5970	wwPDB-VP
Average B, all atoms (Å^2)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, CMP

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	0.44	0/3029	0.75	2/4076 (0.0%)
1	B	0.45	0/2981	0.74	1/4013 (0.0%)
All	All	0.45	0/6010	0.74	3/8089 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	393	LEU	N-CA-C	-7.52	98.68	109.96
1	A	400	ILE	CB-CA-C	-5.19	105.24	112.04
1	B	206	VAL	CB-CA-C	-5.04	104.36	112.16

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	2986	0	3060	12	0
1	B	2938	0	3003	33	0
2	A	22	0	11	1	0
2	B	22	0	11	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5970	0	6085	44	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 4.

All (44) 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)
2:B:901:CMP:C2	2:B:901:CMP:H2	0.97	1.49
2:A:901:CMP:H2	2:A:901:CMP:C2	0.97	1.47
1:B:336:ILE:HD11	1:B:346:VAL:HG21	1.60	0.81
1:A:183:TRP:CE3	1:A:188:HIS:HB2	2.26	0.70
1:B:321:MET:HB3	1:B:323:ILE:HD13	1.77	0.65
1:B:283:MET:HB2	1:B:317:TYR:CE2	2.35	0.61
1:A:251:PHE:CD1	1:A:278:MET:HE1	2.35	0.61
1:B:200:ILE:O	1:B:206:VAL:HG13	2.00	0.61
1:A:141:LEU:HD11	1:B:28:ILE:HG21	1.89	0.55
1:A:251:PHE:CE1	1:A:278:MET:HE1	2.45	0.52
1:B:312:PHE:CE1	1:B:317:TYR:CZ	2.98	0.51
1:B:318:LEU:HD21	1:B:356:MET:CE	2.40	0.51
1:B:314:GLY:O	1:B:318:LEU:N	2.41	0.51
1:B:193:PRO:HA	1:B:196:PHE:CE2	2.47	0.49
1:B:318:LEU:CD2	1:B:356:MET:HE1	2.42	0.49
1:B:321:MET:HB3	1:B:323:ILE:CD1	2.43	0.49
1:A:82:VAL:HG22	1:B:144:ILE:HG21	1.94	0.48
1:B:318:LEU:CD2	1:B:356:MET:SD	3.02	0.48
1:B:293:LEU:HD13	1:B:321:MET:HG2	1.95	0.48
1:B:352:LEU:HG	1:B:356:MET:HE2	1.95	0.48
1:B:280:GLU:OE2	1:B:314:GLY:CA	2.62	0.47
1:B:305:ILE:HG12	1:B:323:ILE:HG13	1.97	0.47
1:B:157:LYS:HA	1:B:157:LYS:HE3	1.95	0.46
1:B:49:ILE:HD12	1:B:49:ILE:N	2.30	0.46
1:A:183:TRP:CD2	1:A:188:HIS:HB2	2.50	0.46
1:A:305:ILE:HG12	1:A:323:ILE:HG13	1.98	0.45
1:B:33:ARG:NH2	1:B:75:GLU:OE1	2.49	0.44
1:B:283:MET:HB2	1:B:317:TYR:CZ	2.51	0.44
1:B:318:LEU:CD2	1:B:356:MET:CE	2.95	0.44
1:A:313:SER:HB3	1:B:313:SER:HA	2.00	0.43
1:A:36:ILE:HD12	1:A:36:ILE:N	2.34	0.43
1:B:31:LYS:CD	1:B:78:ARG:HB3	2.47	0.43
1:A:194:ASN:O	1:A:195:LEU:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:THR:C	1:B:49:ILE:HD12	2.44	0.43
1:B:280:GLU:OE2	1:B:314:GLY:N	2.52	0.42
1:A:259:ASN:O	1:A:263:LEU:HD23	2.19	0.42
1:B:35:LEU:HD13	1:B:37:TYR:CD1	2.55	0.42
1:B:321:MET:HE2	1:B:323:ILE:HD11	2.02	0.42
1:B:157:LYS:HA	1:B:157:LYS:CE	2.50	0.42
1:B:318:LEU:HD22	1:B:356:MET:HE1	2.02	0.42
1:B:36:ILE:N	1:B:36:ILE:HD12	2.35	0.41
1:A:140:ALA:O	1:A:143:GLN:HG2	2.19	0.41
1:B:200:ILE:O	1:B:206:VAL:CG1	2.65	0.41
1:B:318:LEU:HD23	1:B:318:LEU:O	2.21	0.40

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	370/397 (93%)	359 (97%)	8 (2%)	3 (1%)	16 24
1	B	364/397 (92%)	356 (98%)	7 (2%)	1 (0%)	36 50
All	All	734/794 (92%)	715 (97%)	15 (2%)	4 (0%)	24 36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	191	VAL
1	A	192	SER
1	A	286	GLY
1	B	286	GLY

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	331/347 (95%)	316 (96%)	15 (4%)	24 40
1	B	326/347 (94%)	314 (96%)	12 (4%)	30 49
All	All	657/694 (95%)	630 (96%)	27 (4%)	27 44

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	LYS
1	A	45	ILE
1	A	64	ASN
1	A	79	LEU
1	A	112	LYS
1	A	143	GLN
1	A	195	LEU
1	A	278	MET
1	A	280	GLU
1	A	282	ILE
1	A	288	ILE
1	A	315	LEU
1	A	318	LEU
1	A	323	ILE
1	A	372	LEU
1	B	10	ILE
1	B	31	LYS
1	B	35	LEU
1	B	42	LYS
1	B	45	ILE
1	B	77	VAL
1	B	157	LYS
1	B	227	GLN
1	B	241	MET
1	B	282	ILE
1	B	288	ILE
1	B	323	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	ASN
1	A	149	GLN
1	A	194	ASN
1	A	245	ASN
1	A	354	HIS
1	A	367	HIS
1	B	65	GLN
1	B	66	ASN
1	B	143	GLN
1	B	188	HIS
1	B	227	GLN
1	B	245	ASN
1	B	250	GLN

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	CMP	A	901	-	25,25,25	1.73	6 (24%)	37,39,39	2.24	13 (35%)
2	CMP	B	901	-	25,25,25	1.79	6 (24%)	37,39,39	2.22	12 (32%)

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	CMP	A	901	-	-	0/4/31/31	0/4/4/4
2	CMP	B	901	-	-	0/4/31/31	0/4/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	CMP	C5-C4	4.70	1.47	1.39
2	A	901	CMP	C5-C4	4.43	1.47	1.39
2	B	901	CMP	P-O5'	4.09	1.62	1.57
2	A	901	CMP	P-O5'	3.79	1.62	1.57
2	B	901	CMP	C5-C6	2.58	1.48	1.41
2	A	901	CMP	C5-N7	-2.57	1.34	1.39
2	A	901	CMP	C5-C6	2.54	1.48	1.41
2	B	901	CMP	P-O3'	2.42	1.61	1.57
2	B	901	CMP	C5-N7	-2.42	1.34	1.39
2	A	901	CMP	P-O3'	2.34	1.61	1.57
2	B	901	CMP	C8-N7	2.29	1.36	1.31
2	A	901	CMP	C8-N7	2.14	1.35	1.31

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	901	CMP	C5-C4-N3	-6.05	118.38	126.72
2	B	901	CMP	C5-C4-N3	-5.84	118.67	126.72
2	A	901	CMP	N3-C4-N9	4.86	135.44	127.17
2	B	901	CMP	N3-C4-N9	4.63	135.04	127.17
2	B	901	CMP	O3'-C3'-C4'	-4.18	107.55	110.71
2	B	901	CMP	O3'-C3'-C2'	4.04	119.56	115.61
2	A	901	CMP	C2-N3-C4	3.97	121.52	111.83
2	A	901	CMP	O3'-C3'-C2'	3.95	119.48	115.61
2	B	901	CMP	C2-N3-C4	3.85	121.22	111.83
2	B	901	CMP	N3-C2-N1	-3.69	122.99	128.58
2	A	901	CMP	O3'-C3'-C4'	-3.67	107.94	110.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	901	CMP	N3-C2-N1	-3.66	123.04	128.58
2	B	901	CMP	O2P-P-O1P	3.60	119.61	108.56
2	B	901	CMP	C4-C5-N7	-3.12	107.02	110.58
2	A	901	CMP	C4-C5-N7	-3.09	107.05	110.58
2	A	901	CMP	O2P-P-O1P	3.07	118.00	108.56
2	A	901	CMP	C4-N9-C8	2.54	108.40	105.74
2	A	901	CMP	C5-N7-C8	2.46	107.32	103.45
2	B	901	CMP	C5-N7-C8	2.37	107.17	103.45
2	A	901	CMP	O5'-P-O3'	-2.32	102.60	105.70
2	B	901	CMP	C4-N9-C8	2.30	108.16	105.74
2	B	901	CMP	C5'-C4'-C3'	-2.27	108.30	112.56
2	A	901	CMP	N9-C8-N7	-2.03	111.05	113.94
2	A	901	CMP	C5'-C4'-C3'	-2.01	108.78	112.56
2	B	901	CMP	C2-N1-C6	2.00	122.02	118.73

There are no chirality outliers.

There are no torsion outliers.

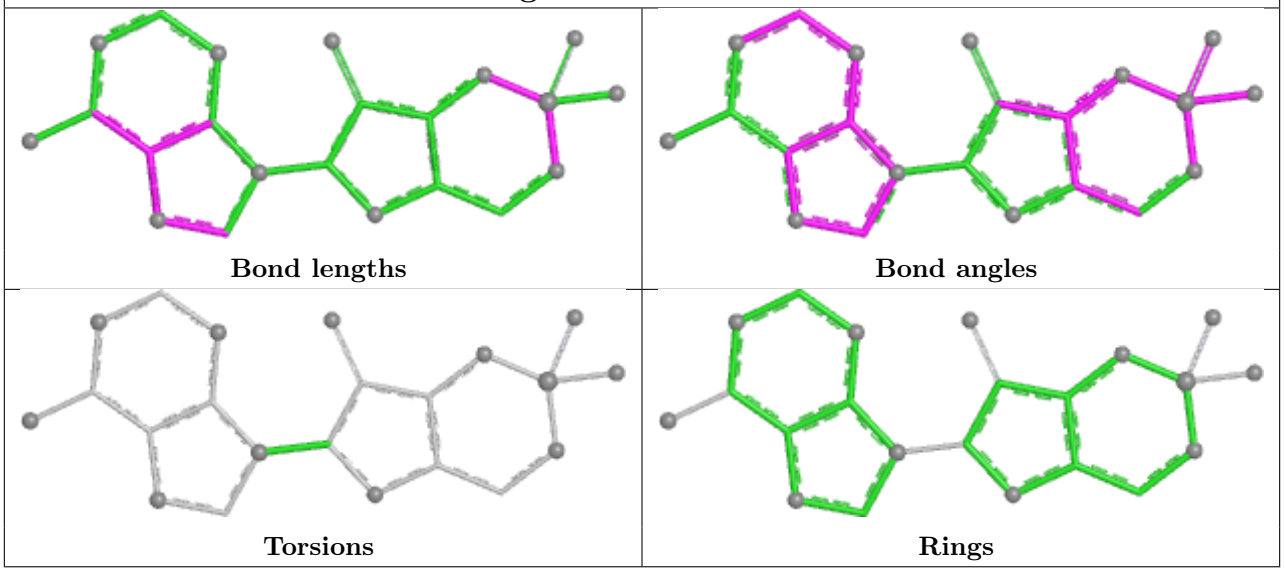
There are no ring outliers.

2 monomers are involved in 2 short contacts:

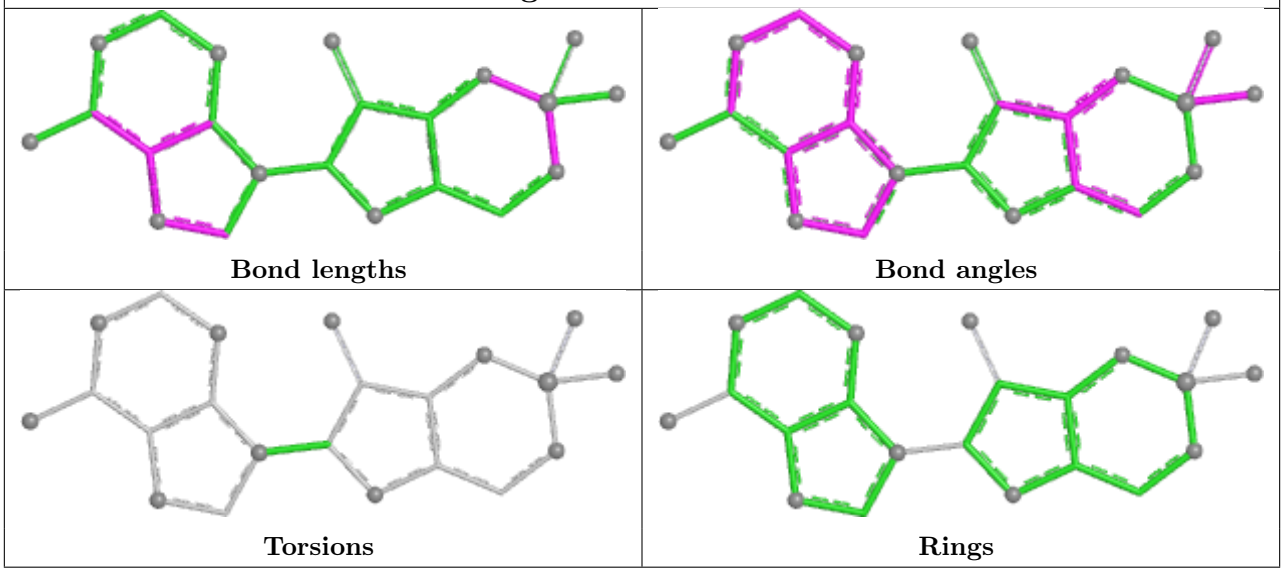
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	CMP	1	0
2	B	901	CMP	1	0

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 then 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 CMP A 901



Ligand CMP B 901



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, 95^{th} 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	374/397 (94%)	0.51	29 (7%)	19	15	66, 91, 126, 159	1 (0%)
1	B	368/397 (92%)	0.54	19 (5%)	33	27	66, 98, 148, 177	1 (0%)
All	All	742/794 (93%)	0.52	48 (6%)	25	21	66, 94, 145, 177	2 (0%)

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	315	LEU	7.4
1	B	314	GLY	3.6
1	B	6	GLN	3.5
1	A	328	ILE	3.4
1	A	190	LEU	3.4
1	A	100	LEU	2.9
1	A	55	ILE	2.9
1	A	139	SER	2.9
1	A	289	ALA	2.8
1	A	167	VAL	2.8
1	A	336	ILE	2.8
1	A	315	LEU	2.8
1	A	104	VAL	2.8
1	B	313	SER	2.7
1	B	317	TYR	2.7
1	B	100	LEU	2.7
1	A	290	ILE	2.7
1	A	288	ILE	2.7
1	B	303	ILE	2.7
1	B	46	PRO	2.7
1	A	287	ALA	2.5
1	A	53	GLY	2.5
1	A	278	MET	2.5
1	B	275	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	283	MET	2.4
1	B	282	ILE	2.3
1	A	308	PHE	2.3
1	A	292	ALA	2.3
1	B	10	ILE	2.3
1	B	28	ILE	2.3
1	A	102	MET	2.3
1	B	230	LEU	2.3
1	A	332	PHE	2.3
1	A	58	GLU	2.2
1	B	55	ILE	2.2
1	A	114	ILE	2.2
1	B	381	PHE	2.2
1	B	104	VAL	2.2
1	A	316	GLN	2.2
1	B	293	LEU	2.2
1	B	318	LEU	2.1
1	A	333	VAL	2.1
1	A	191	VAL	2.1
1	A	381	PHE	2.1
1	A	319	THR	2.1
1	A	115	GLY	2.1
1	B	23	GLY	2.1
1	A	140	ALA	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)

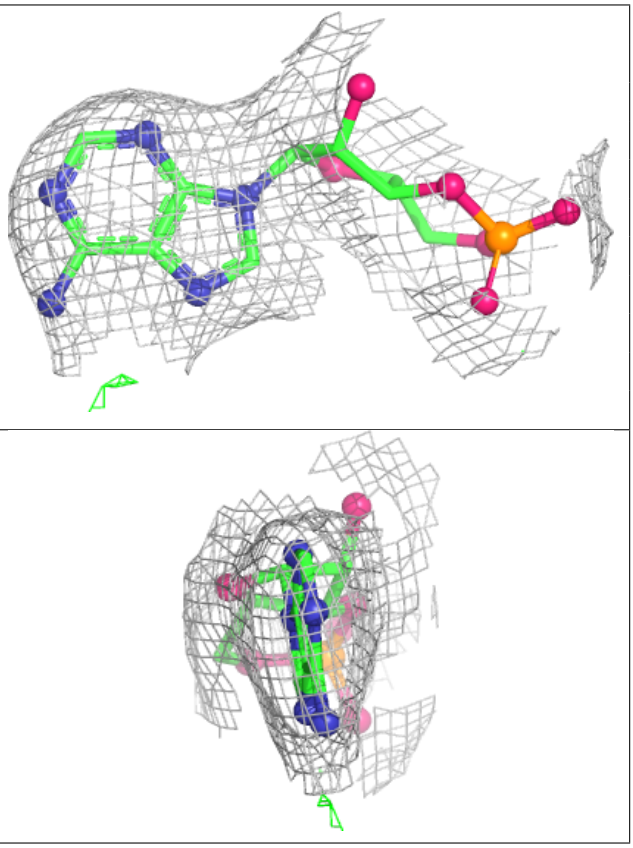
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

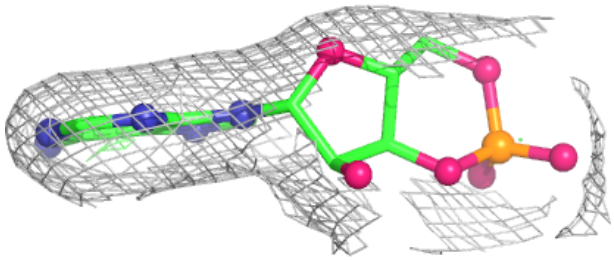
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	B	902	1/1	0.68	0.18	82,82,82,82	0
3	MG	A	902	1/1	0.88	0.12	72,72,72,72	0
2	CMP	B	901	22/22	0.91	0.09	100,106,110,115	0
2	CMP	A	901	22/22	0.93	0.09	74,77,81,87	0

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

Electron density around CMP B 901:

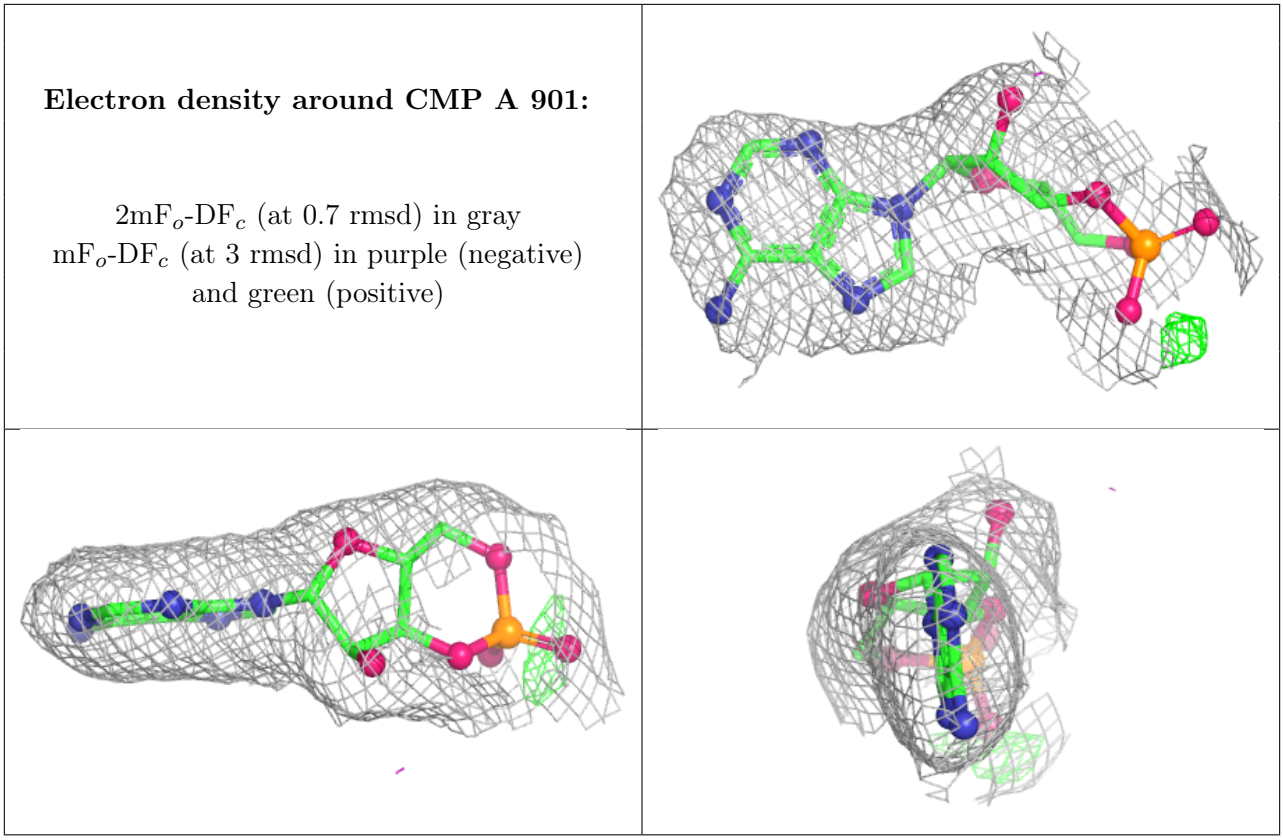
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around CMP A 901:

$2mF_o$-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.