Full wwPDB X-ray Structure Validation Report (i)

Nov 15, 2023 – 10:57 AM JST

PDB ID	:	6IYK
Title	:	The structure of EntE with 2-nitrobenzoyl adenylate analog
Authors	:	Miyanaga, A.; Ishikawa, F.
Deposited on	:	2018-12-17
Resolution	:	2.45 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 (i) 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 (i)) were used in the production of this report:

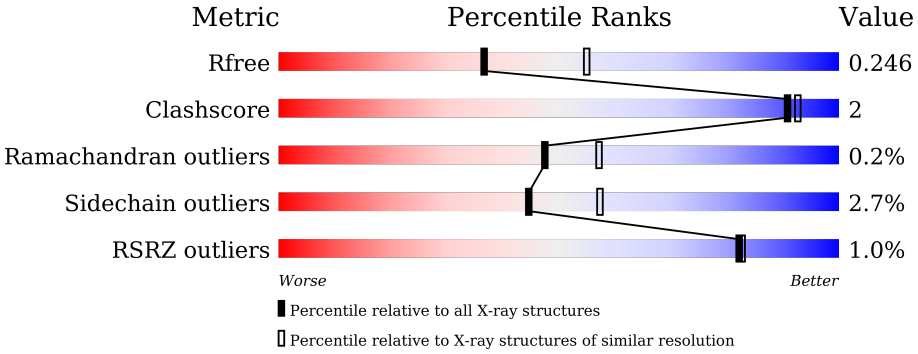
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

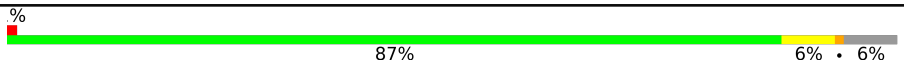
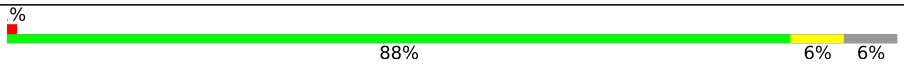
The reported resolution of this entry is 2.45 Å.

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}	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	556	
1	B	556	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8380 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 2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	521	4054	2565	706	768	15	0	0	0
1	B	523	4070	2575	709	771	15	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLY	ASN	engineered mutation	UNP A0A0E1LUI6
A	537	THR	-	expression tag	UNP A0A0E1LUI6
A	538	ASN	-	expression tag	UNP A0A0E1LUI6
A	539	SER	-	expression tag	UNP A0A0E1LUI6
A	540	SER	-	expression tag	UNP A0A0E1LUI6
A	541	SER	-	expression tag	UNP A0A0E1LUI6
A	542	VAL	-	expression tag	UNP A0A0E1LUI6
A	543	ASP	-	expression tag	UNP A0A0E1LUI6
A	544	LYS	-	expression tag	UNP A0A0E1LUI6
A	545	LEU	-	expression tag	UNP A0A0E1LUI6
A	546	ALA	-	expression tag	UNP A0A0E1LUI6
A	547	ALA	-	expression tag	UNP A0A0E1LUI6
A	548	ALA	-	expression tag	UNP A0A0E1LUI6
A	549	LEU	-	expression tag	UNP A0A0E1LUI6
A	550	GLU	-	expression tag	UNP A0A0E1LUI6
A	551	HIS	-	expression tag	UNP A0A0E1LUI6
A	552	HIS	-	expression tag	UNP A0A0E1LUI6
A	553	HIS	-	expression tag	UNP A0A0E1LUI6
A	554	HIS	-	expression tag	UNP A0A0E1LUI6
A	555	HIS	-	expression tag	UNP A0A0E1LUI6
A	556	HIS	-	expression tag	UNP A0A0E1LUI6
B	235	GLY	ASN	engineered mutation	UNP A0A0E1LUI6
B	537	THR	-	expression tag	UNP A0A0E1LUI6
B	538	ASN	-	expression tag	UNP A0A0E1LUI6

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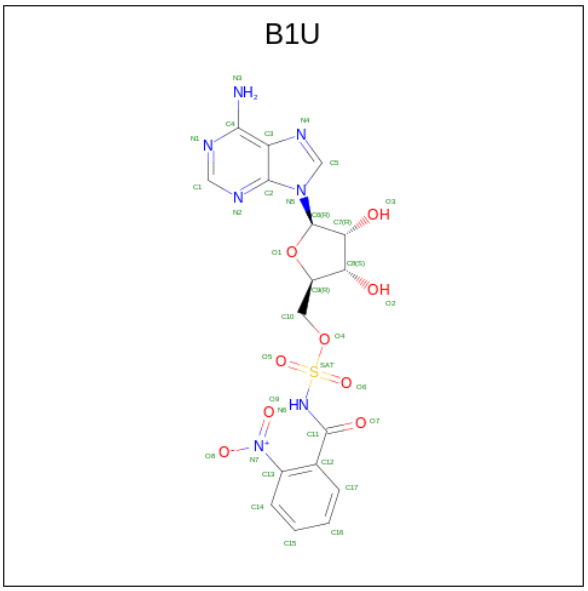
Chain	Residue	Modelled	Actual	Comment	Reference
B	539	SER	-	expression tag	UNP A0A0E1LUI6
B	540	SER	-	expression tag	UNP A0A0E1LUI6
B	541	SER	-	expression tag	UNP A0A0E1LUI6
B	542	VAL	-	expression tag	UNP A0A0E1LUI6
B	543	ASP	-	expression tag	UNP A0A0E1LUI6
B	544	LYS	-	expression tag	UNP A0A0E1LUI6
B	545	LEU	-	expression tag	UNP A0A0E1LUI6
B	546	ALA	-	expression tag	UNP A0A0E1LUI6
B	547	ALA	-	expression tag	UNP A0A0E1LUI6
B	548	ALA	-	expression tag	UNP A0A0E1LUI6
B	549	LEU	-	expression tag	UNP A0A0E1LUI6
B	550	GLU	-	expression tag	UNP A0A0E1LUI6
B	551	HIS	-	expression tag	UNP A0A0E1LUI6
B	552	HIS	-	expression tag	UNP A0A0E1LUI6
B	553	HIS	-	expression tag	UNP A0A0E1LUI6
B	554	HIS	-	expression tag	UNP A0A0E1LUI6
B	555	HIS	-	expression tag	UNP A0A0E1LUI6
B	556	HIS	-	expression tag	UNP A0A0E1LUI6

- Molecule 2 is 5'-O-[(2-nitrobenzene-1-carbonyl)sulfamoyl]adenosine (three-letter code: B1U) (formula: $C_{17}H_{17}N_7O_9S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	34	17	7	9	1	0	0
			Total	C	N	O	S		
2	B	1	34	17	7	9	1	0	0

- Molecule 3 is water.

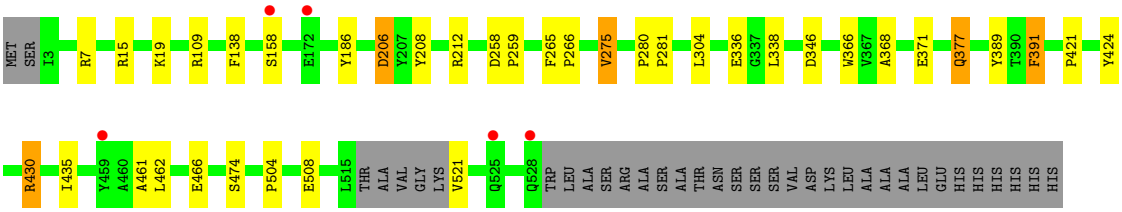
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	96	96	96	0	0
			Total	O		
3	B	92	92	92	0	0

3 Residue-property plots (i)

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

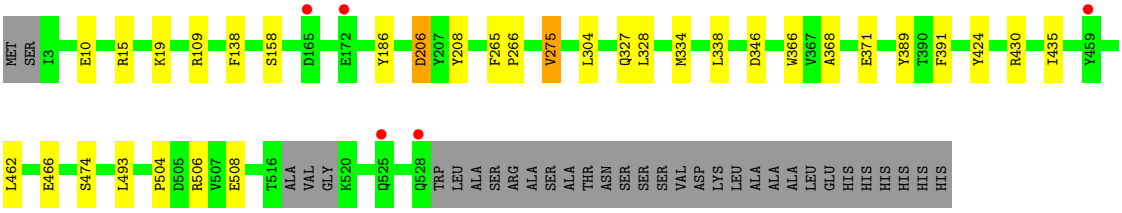
• Molecule 1: 2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex

Chain A:



• Molecule 1: 2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	124.50Å 57.22Å 171.65Å 90.00° 96.31° 90.00°	Depositor
Resolution (Å)	45.34 – 2.45 43.48 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.34-2.45) 99.7 (43.48-2.45)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.42 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.189 , 0.241 0.195 , 0.246	Depositor DCC
R_{free} test set	2235 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	33.8	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 34.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8380	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.80 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0427e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: B1U

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	0.64	0/4140	0.77	3/5627 (0.1%)
1	B	0.64	0/4156	0.78	1/5648 (0.0%)
All	All	0.64	0/8296	0.77	4/11275 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	430	ARG	NE-CZ-NH1	-7.62	116.49	120.30
1	A	430	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	A	7	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	A	212	ARG	NE-CZ-NH2	-5.24	117.68	120.30

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	4054	0	4004	15	0
1	B	4070	0	4024	12	0
2	A	34	0	0	0	0
2	B	34	0	0	1	0
3	A	96	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	92	0	0	0	0
All	All	8380	0	8028	27	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 2.

All (27) 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:461:ALA:HB2	1:A:521:VAL:HG11	1.77	0.65
1:B:265:PHE:HB2	1:B:266:PRO:HD3	1.84	0.60
1:A:109:ARG:HG2	1:A:138:PHE:CE1	2.41	0.56
1:A:265:PHE:HB2	1:A:266:PRO:HD3	1.86	0.56
1:B:109:ARG:HG2	1:B:138:PHE:CE1	2.41	0.55
1:B:506:ARG:NH1	1:B:508:GLU:OE2	2.43	0.51
1:A:366:TRP:CZ3	1:A:368:ALA:HB2	2.47	0.50
1:A:377:GLN:HE22	1:A:421:PRO:HG3	1.77	0.49
1:B:366:TRP:CZ3	1:B:368:ALA:HB2	2.48	0.48
1:A:206:ASP:HB2	1:A:389:TYR:HA	1.98	0.46
1:B:334:MET:C	2:B:601:B1U:O8	2.54	0.46
1:A:430:ARG:HD3	3:A:729:HOH:O	2.18	0.44
1:B:206:ASP:HB2	1:B:389:TYR:HA	2.00	0.43
1:A:435:ILE:HD12	1:A:462:LEU:HD23	2.00	0.43
1:A:346:ASP:OD1	1:A:424:TYR:OH	2.34	0.42
1:B:474:SER:OG	1:B:504:PRO:HA	2.20	0.42
1:B:275:VAL:HA	1:B:304:LEU:O	2.20	0.41
1:A:258:ASP:HB2	1:A:259:PRO:HD2	2.02	0.41
1:A:474:SER:OG	1:A:504:PRO:HA	2.21	0.41
1:B:327:GLN:HG3	1:B:328:LEU:N	2.36	0.41
1:A:275:VAL:HA	1:A:304:LEU:O	2.21	0.41
1:B:493:LEU:HD23	1:B:493:LEU:HA	1.95	0.41
1:A:435:ILE:HD12	1:A:462:LEU:CD2	2.50	0.41
1:B:435:ILE:HD12	1:B:462:LEU:HD23	2.03	0.40
1:B:346:ASP:OD1	1:B:424:TYR:OH	2.34	0.40
1:A:336:GLU:HB3	1:A:391:PHE:CE1	2.56	0.40
1:A:280:PRO:N	1:A:281:PRO:HD2	2.37	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	517/556 (93%)	509 (98%)	7 (1%)	1 (0%)	47	57
1	B	519/556 (93%)	507 (98%)	11 (2%)	1 (0%)	47	57
All	All	1036/1112 (93%)	1016 (98%)	18 (2%)	2 (0%)	47	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	338	LEU
1	B	338	LEU

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	430/457 (94%)	418 (97%)	12 (3%)	43	56
1	B	432/457 (94%)	421 (98%)	11 (2%)	47	60
All	All	862/914 (94%)	839 (97%)	23 (3%)	44	57

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ARG
1	A	19	LYS
1	A	158	SER
1	A	186	TYR

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Mol	Chain	Res	Type
1	A	206	ASP
1	A	208	TYR
1	A	275	VAL
1	A	371	GLU
1	A	377	GLN
1	A	391	PHE
1	A	466	GLU
1	A	508	GLU
1	B	10	GLU
1	B	15	ARG
1	B	19	LYS
1	B	158	SER
1	B	186	TYR
1	B	206	ASP
1	B	208	TYR
1	B	275	VAL
1	B	371	GLU
1	B	391	PHE
1	B	466	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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	B1U	B	601	-	33,37,37	3.94	12 (36%)	37,55,55	2.32	11 (29%)
2	B1U	A	601	-	33,37,37	3.94	10 (30%)	37,55,55	2.24	10 (27%)

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	B1U	B	601	-	-	5/16/39/39	0/4/4/4
2	B1U	A	601	-	-	7/16/39/39	0/4/4/4

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	B1U	O5-SAT	13.57	1.54	1.42
2	B	601	B1U	O6-SAT	11.53	1.52	1.42
2	A	601	B1U	O6-SAT	11.00	1.51	1.42
2	B	601	B1U	O5-SAT	10.33	1.51	1.42
2	B	601	B1U	O9-N7	8.93	1.38	1.22
2	A	601	B1U	C13-N7	-8.93	1.29	1.45
2	B	601	B1U	C13-N7	-8.57	1.30	1.45
2	A	601	B1U	C1-N2	5.49	1.41	1.32
2	B	601	B1U	C1-N2	4.69	1.39	1.32
2	B	601	B1U	C1-N1	4.31	1.41	1.33
2	A	601	B1U	SAT-N6	4.26	1.67	1.59
2	A	601	B1U	O9-N7	4.02	1.29	1.22
2	B	601	B1U	O1-C6	3.92	1.46	1.41
2	A	601	B1U	C12-C11	-3.80	1.42	1.50
2	A	601	B1U	C1-N1	3.61	1.40	1.33
2	B	601	B1U	O4-SAT	-3.52	1.52	1.59
2	B	601	B1U	C11-N6	-3.44	1.35	1.39
2	B	601	B1U	C12-C11	-3.24	1.43	1.50
2	A	601	B1U	C11-N6	-2.71	1.35	1.39
2	A	601	B1U	C3-C2	-2.70	1.33	1.40
2	B	601	B1U	C3-C2	-2.26	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	B1U	C4-C3	-2.18	1.35	1.43

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	B1U	O6-SAT-O5	-7.48	109.10	120.76
2	B	601	B1U	O6-SAT-O5	-6.75	110.24	120.76
2	A	601	B1U	N2-C1-N1	-6.63	118.31	128.68
2	B	601	B1U	N2-C1-N1	-5.68	119.80	128.68
2	B	601	B1U	C14-C13-N7	-4.69	111.46	116.47
2	B	601	B1U	C14-C13-C12	4.66	126.26	119.33
2	B	601	B1U	C10-O4-SAT	4.12	125.88	117.37
2	A	601	B1U	C14-C13-C12	3.59	124.68	119.33
2	B	601	B1U	C17-C12-C13	-3.19	113.96	118.40
2	A	601	B1U	C17-C12-C13	-2.88	114.39	118.40
2	B	601	B1U	O9-N7-C13	-2.65	114.50	119.03
2	A	601	B1U	C14-C13-N7	-2.53	113.77	116.47
2	A	601	B1U	C13-C12-C11	2.53	129.48	123.58
2	B	601	B1U	O4-SAT-O6	2.53	113.31	105.59
2	B	601	B1U	C13-C12-C11	2.52	129.46	123.58
2	A	601	B1U	C2-C3-N4	-2.47	106.82	109.40
2	A	601	B1U	O4-SAT-N6	2.46	112.46	105.60
2	B	601	B1U	C12-C11-N6	2.18	117.40	114.34
2	B	601	B1U	C3-C4-N3	-2.12	117.13	120.35
2	A	601	B1U	C10-O4-SAT	2.12	121.75	117.37
2	A	601	B1U	C12-C11-N6	2.11	117.31	114.34

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	B1U	C14-C13-N7-O9
2	A	601	B1U	C12-C13-N7-O9
2	A	601	B1U	N6-C11-C12-C13
2	A	601	B1U	C10-O4-SAT-N6
2	B	601	B1U	C14-C13-N7-O9
2	B	601	B1U	C12-C13-N7-O9
2	B	601	B1U	N6-C11-C12-C13
2	A	601	B1U	C10-O4-SAT-O6
2	A	601	B1U	O7-C11-C12-C13
2	A	601	B1U	C10-O4-SAT-O5
2	B	601	B1U	O7-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
2	B	601	B1U	O4-C10-C9-C8

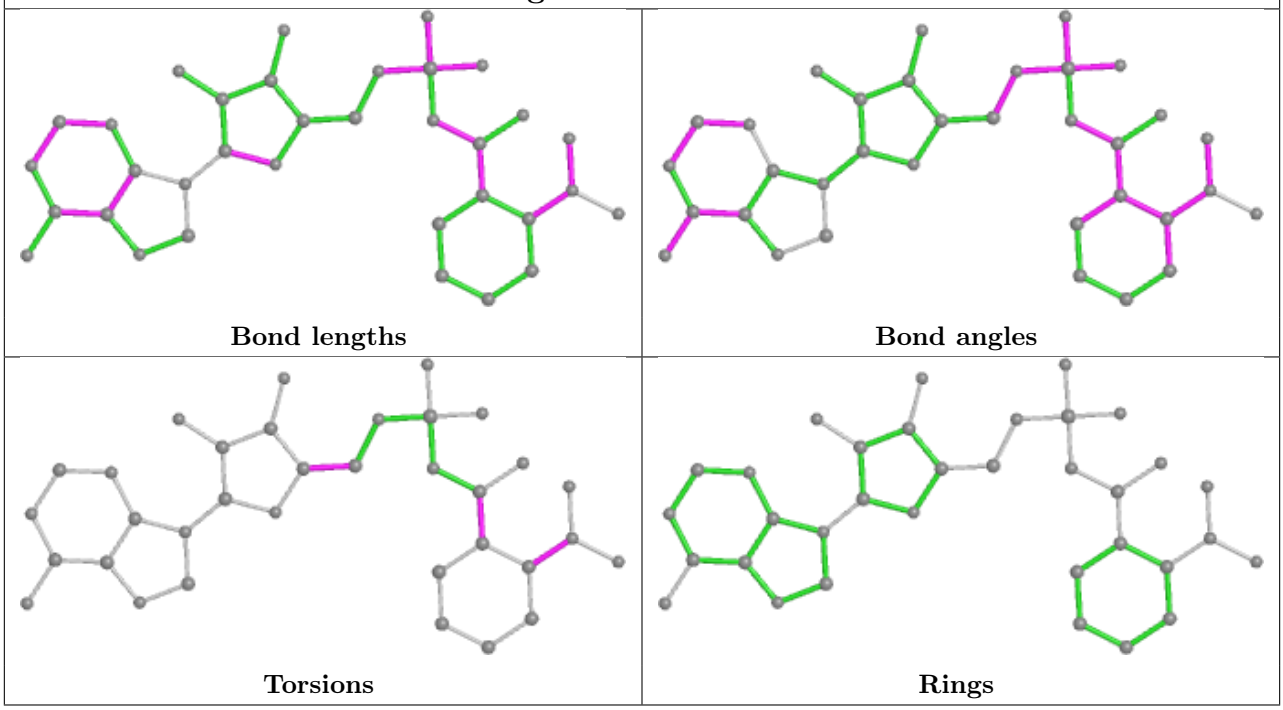
There are no ring outliers.

1 monomer is involved in 1 short contact:

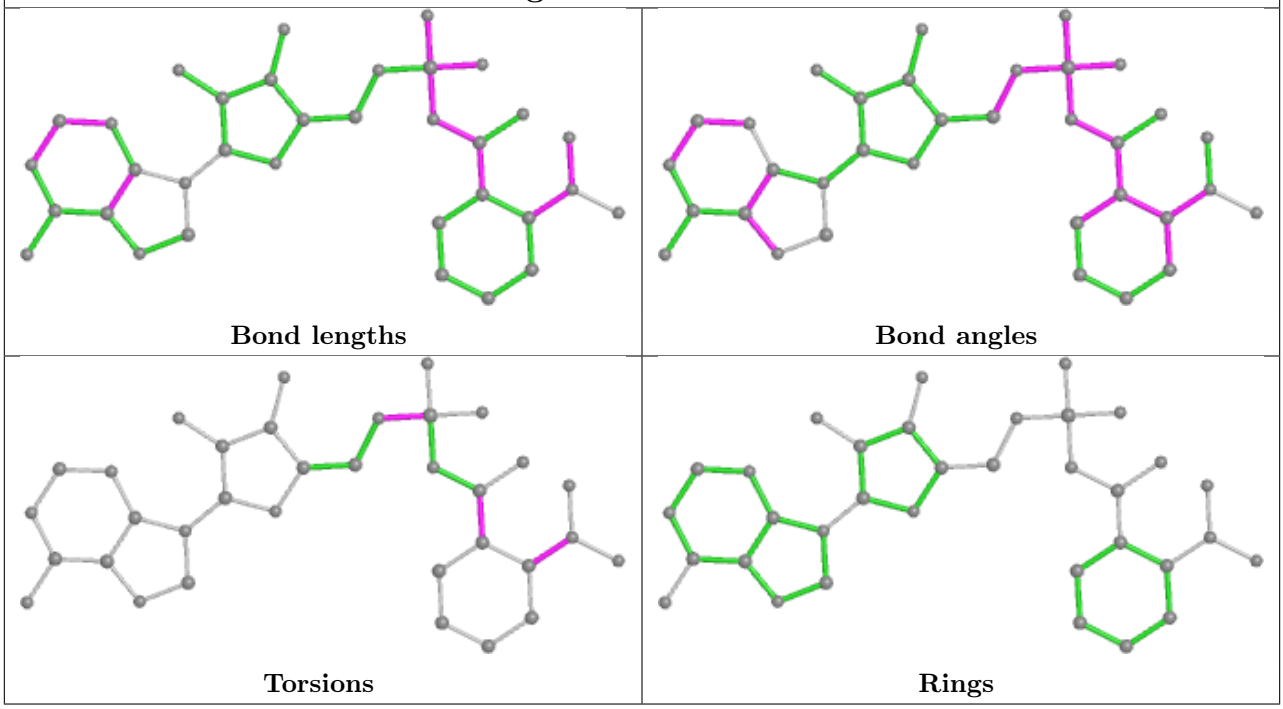
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	B1U	1	0

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 B1U B 601



Ligand B1U A 601



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)

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	521/556 (93%)	-0.40	5 (0%)	82	83	21, 31, 52, 80	0
1	B	523/556 (94%)	-0.38	5 (0%)	82	83	17, 31, 53, 102	0
All	All	1044/1112 (93%)	-0.39	10 (0%)	82	83	17, 31, 53, 102	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	GLU	3.5
1	A	158	SER	3.4
1	B	459	TYR	2.8
1	B	525	GLN	2.6
1	A	459	TYR	2.6
1	B	165	ASP	2.3
1	A	525	GLN	2.3
1	A	528	GLN	2.2
1	A	172	GLU	2.2
1	B	528	GLN	2.1

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)

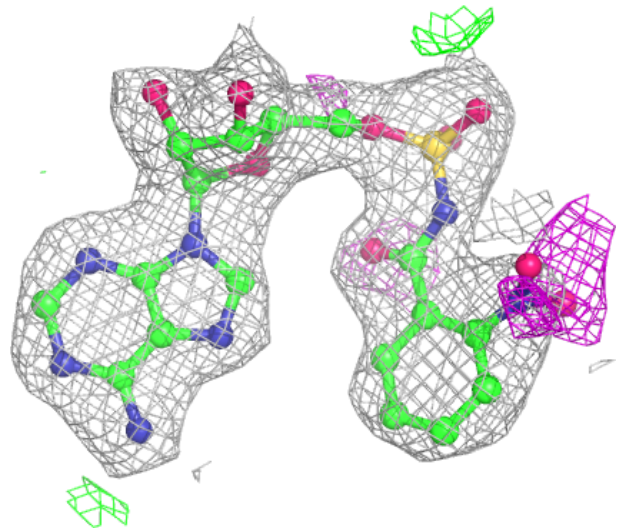
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

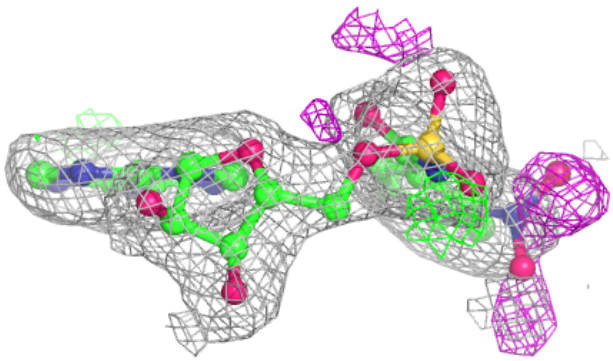
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	B1U	B	601	34/34	0.97	0.13	20,25,43,53	0
2	B1U	A	601	34/34	0.98	0.12	21,24,41,61	0

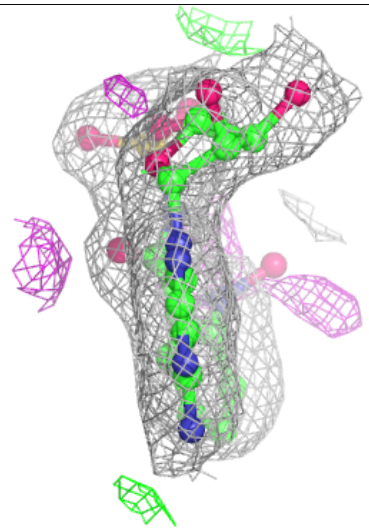
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around B1U 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)

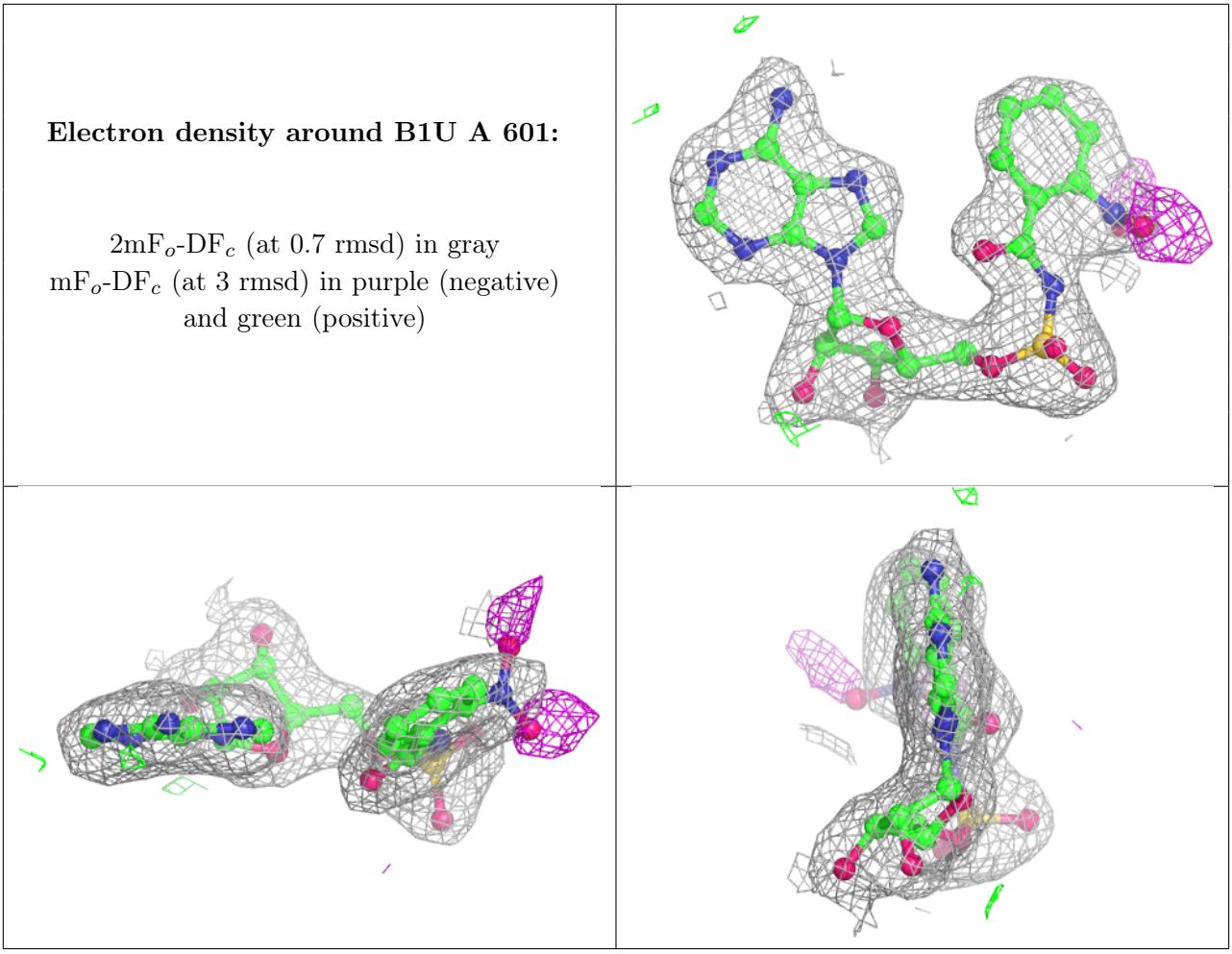






Electron density around B1U A 601:

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 (i)

There are no such residues in this entry.