Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2023 – 10:24 AM EDT

PDB ID	:	6EC8
Title	:	Glutamylation domain, TbtB, from thiomuracin biosynthesis bound to 5'-pho sphodesmethylglutamycin
Authors	:	Cogan, D.P.; Nair, S.K.
Deposited on	:	2018-08-07
Resolution	:	2.15 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:

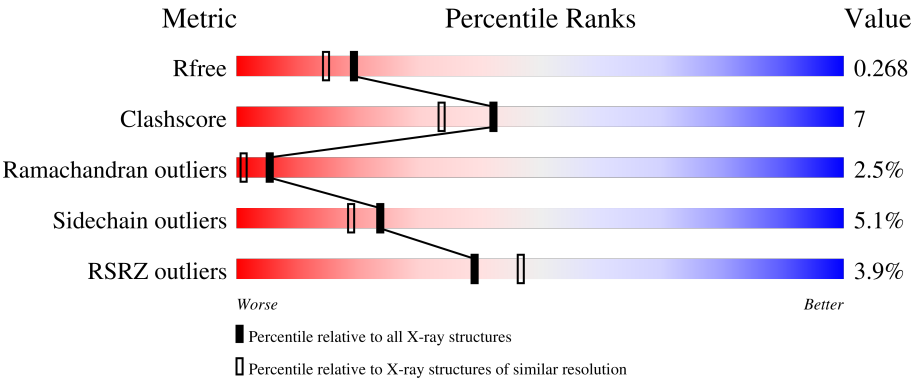
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.15 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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	861	4% 76% 14% · 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6626 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.

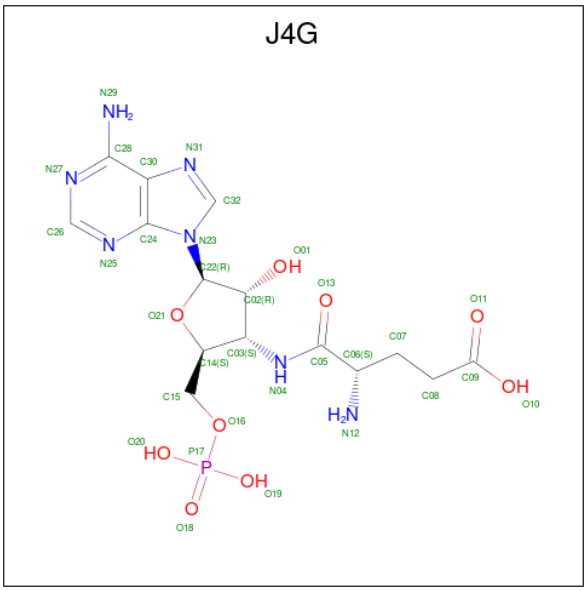
- Molecule 1 is a protein called Lantibiotic dehydratase domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	803	Total	C	N	O	S	0	1	0
			6306	4002	1186	1102	16			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP D6Y502
A	-1	GLY	-	expression tag	UNP D6Y502
A	0	SER	-	expression tag	UNP D6Y502

- Molecule 2 is 3'-deoxy-3'-[(L-alpha-glutamyl)amino]adenosine 5'-(dihydrogen phosphate) (three-letter code: J4G) (formula: $C_{15}H_{22}N_7O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	1
			64	30	14	18	2		

- Molecule 3 is water.

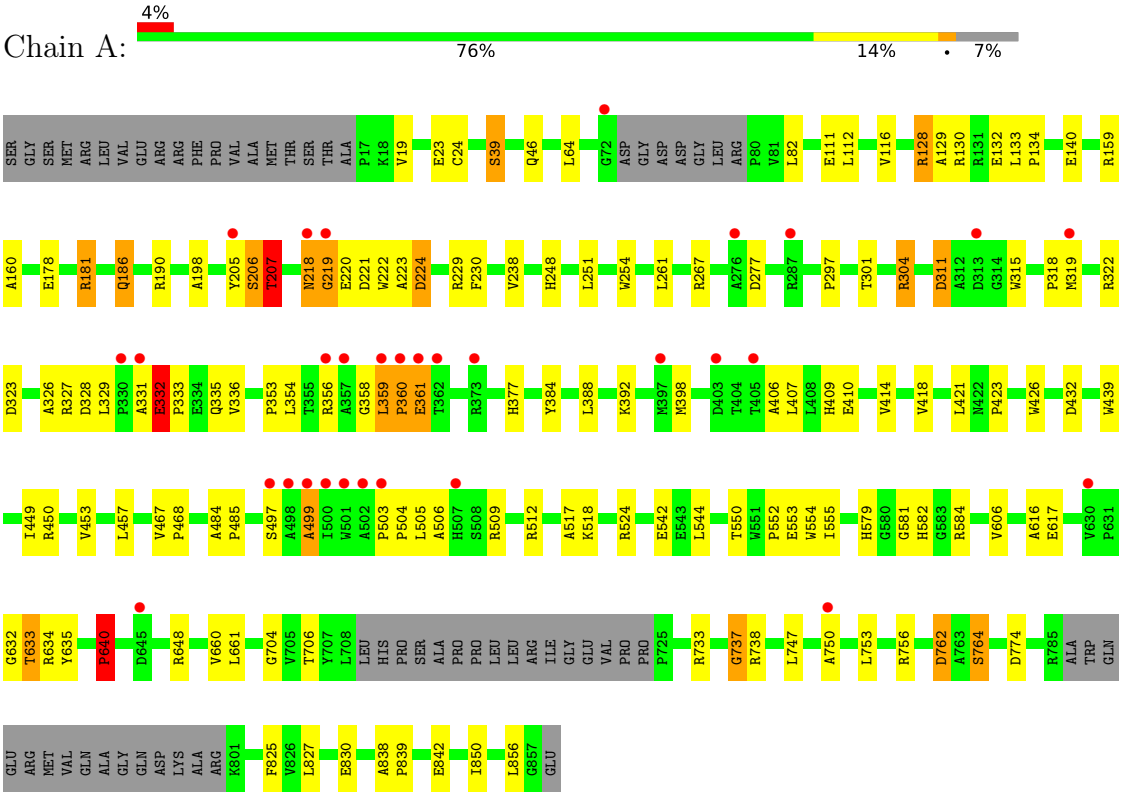
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	256	Total	O	0	0
			256	256		

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: Lantibiotic dehydratase domain protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	44.50Å 96.10Å 107.13Å 90.00° 98.84° 90.00°	Depositor
Resolution (Å)	71.00 – 2.15 71.15 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.1 (71.00-2.15) 99.1 (71.15-2.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.25 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.213 , 0.266 0.222 , 0.268	Depositor DCC
R_{free} test set	2430 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	37.9	Xtriage
Anisotropy	0.649	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.2	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	6626	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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: J4G

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	0.77	0/6458	0.93	3/8787 (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	359	LEU	C-N-CD	-5.53	108.43	120.60
1	A	223	ALA	C-N-CA	5.39	135.18	121.70
1	A	762	ASP	N-CA-C	5.18	124.98	111.00

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	6306	0	6396	88	0
2	A	64	0	0	0	0
3	A	256	0	0	3	0
All	All	6626	0	6396	88	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 7.

All (88) 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:359:LEU:HB3	1:A:360:PRO:HD2	1.47	0.94
1:A:633:THR:CG2	1:A:635:TYR:O	2.16	0.94
1:A:160:ALA:HB2	1:A:207:THR:HB	1.51	0.91
1:A:318:PRO:O	1:A:322:ARG:HG3	1.71	0.90
1:A:224:ASP:OD2	1:A:229:ARG:NH2	2.05	0.88
1:A:205:TYR:O	1:A:206:SER:CB	2.22	0.86
1:A:358:GLY:C	1:A:359:LEU:HD23	1.97	0.85
1:A:359:LEU:CB	1:A:360:PRO:HD2	2.06	0.82
1:A:633:THR:HG22	1:A:635:TYR:O	1.82	0.80
1:A:359:LEU:HD23	1:A:359:LEU:N	2.04	0.72
1:A:205:TYR:O	1:A:206:SER:HB3	1.89	0.70
1:A:332:GLU:HG3	1:A:335:GLN:HE21	1.57	0.70
1:A:616:ALA:HA	1:A:633:THR:HG21	1.74	0.70
1:A:219:GLY:O	1:A:221:ASP:N	2.28	0.66
1:A:737:GLY:O	1:A:738:ARG:HB2	1.97	0.65
1:A:254:TRP:CD2	1:A:359:LEU:HD13	2.33	0.64
1:A:159:ARG:CZ	1:A:238:VAL:HG21	2.27	0.64
1:A:254:TRP:CE3	1:A:359:LEU:HD13	2.35	0.62
1:A:297:PRO:O	1:A:301:THR:HG23	1.98	0.62
1:A:353:PRO:CG	1:A:359:LEU:HD22	2.29	0.62
1:A:756:ARG:HH21	1:A:762:ASP:HA	1.65	0.62
1:A:23:GLU:HG2	1:A:850:ILE:HG22	1.81	0.61
1:A:159:ARG:NH2	1:A:238:VAL:HG21	2.14	0.61
1:A:579:HIS:CE1	1:A:584:ARG:HG2	2.37	0.60
1:A:267:ARG:NH2	1:A:640:PRO:O	2.35	0.59
1:A:205:TYR:O	1:A:206:SER:OG	2.20	0.59
1:A:329:LEU:HA	3:A:1026:HOH:O	2.04	0.58
1:A:319:MET:HA	1:A:322:ARG:HD3	1.85	0.57
1:A:318:PRO:O	1:A:322:ARG:CG	2.48	0.57
1:A:186:GLN:NE2	1:A:190:ARG:HH11	2.03	0.56
1:A:439:TRP:CE2	1:A:544:LEU:HD22	2.40	0.56
1:A:301:THR:HG22	1:A:304:ARG:NH2	2.21	0.55
1:A:254:TRP:CD2	1:A:359:LEU:CD1	2.91	0.54
1:A:353:PRO:CB	1:A:359:LEU:HD22	2.38	0.54
1:A:552:PRO:HD2	1:A:555:ILE:HD12	1.90	0.54
1:A:384:TYR:OH	1:A:410:GLU:OE2	2.21	0.54
1:A:360:PRO:O	1:A:361:GLU:HB2	2.08	0.53
1:A:323:ASP:O	1:A:326:ALA:N	2.42	0.53
1:A:617:GLU:H	1:A:633:THR:HG21	1.74	0.52
1:A:581:GLY:O	1:A:582:HIS:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:LEU:HB2	1:A:517:ALA:HB2	1.90	0.52
1:A:39:SER:OG	1:A:140:GLU:OE1	2.28	0.51
1:A:384:TYR:CZ	1:A:388:LEU:HD11	2.46	0.51
1:A:358:GLY:O	1:A:359:LEU:HD23	2.11	0.51
1:A:432:ASP:OD2	1:A:737:GLY:O	2.29	0.50
1:A:353:PRO:HB3	1:A:359:LEU:HD22	1.92	0.50
1:A:301:THR:HG22	1:A:304:ARG:HH22	1.76	0.49
1:A:542:GLU:HG2	3:A:1009:HOH:O	2.12	0.49
1:A:178:GLU:O	1:A:181:ARG:HB3	2.14	0.48
1:A:499:ALA:HB1	1:A:504:PRO:HD3	1.95	0.48
1:A:160:ALA:CB	1:A:207:THR:HB	2.34	0.48
1:A:392:LYS:HD3	1:A:407:LEU:HD12	1.95	0.48
1:A:248:HIS:HE1	3:A:1189:HOH:O	1.97	0.47
1:A:414:VAL:HG21	1:A:418:VAL:CG1	2.43	0.47
1:A:133:LEU:N	1:A:134:PRO:HD2	2.29	0.47
1:A:457:LEU:HD23	1:A:661:LEU:HG	1.96	0.47
1:A:24:CYS:HB3	1:A:198:ALA:O	2.15	0.46
1:A:332:GLU:N	1:A:332:GLU:OE2	2.48	0.46
1:A:19:VAL:HG11	1:A:421:LEU:HD11	1.98	0.46
1:A:332:GLU:HG2	1:A:335:GLN:CG	2.47	0.45
1:A:505:LEU:O	1:A:506:ALA:HB3	2.18	0.44
1:A:606:VAL:HG23	1:A:632:GLY:O	2.17	0.44
1:A:384:TYR:CE2	1:A:388:LEU:HD11	2.51	0.44
1:A:222:TRP:C	1:A:224:ASP:N	2.69	0.44
1:A:64:LEU:HD11	1:A:82:LEU:HD22	1.99	0.44
1:A:318:PRO:O	1:A:322:ARG:CD	2.65	0.44
1:A:353:PRO:HG2	1:A:359:LEU:CD2	2.48	0.44
1:A:737:GLY:O	1:A:738:ARG:CB	2.62	0.43
1:A:616:ALA:HA	1:A:633:THR:CG2	2.46	0.43
1:A:230:PHE:HZ	1:A:850:ILE:HD13	1.82	0.43
1:A:331:ALA:C	1:A:332:GLU:OE2	2.57	0.43
1:A:484:ALA:HB1	1:A:485:PRO:HD2	2.00	0.43
1:A:128:ARG:CD	1:A:129:ALA:N	2.82	0.43
1:A:423:PRO:O	1:A:426:TRP:O	2.37	0.43
1:A:450:ARG:NH1	1:A:704:GLY:O	2.52	0.42
1:A:112:LEU:O	1:A:116:VAL:HG23	2.20	0.42
1:A:361:GLU:HG2	1:A:361:GLU:O	2.19	0.42
1:A:838:ALA:HA	1:A:839:PRO:HD3	1.93	0.42
1:A:130:ARG:NH2	1:A:764:SER:HB2	2.36	0.41
1:A:512:ARG:HD2	1:A:554:TRP:NE1	2.35	0.41
1:A:747:LEU:HD11	1:A:825:PHE:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:ILE:O	1:A:453:VAL:HG23	2.21	0.41
1:A:311:ASP:HB2	1:A:315:TRP:O	2.21	0.41
1:A:159:ARG:NH1	1:A:238:VAL:HG21	2.35	0.40
1:A:333:PRO:HA	1:A:336:VAL:HG12	2.02	0.40
1:A:467:VAL:O	1:A:468:PRO:C	2.60	0.40
1:A:733:ARG:HD3	1:A:830:GLU:OE2	2.19	0.40
1:A:327:ARG:NH1	1:A:328:ASP:OD1	2.54	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	796/861 (92%)	739 (93%)	37 (5%)	20 (2%)	5 1

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	206	SER
1	A	207	THR
1	A	218	ASN
1	A	219	GLY
1	A	356	ARG
1	A	360	PRO
1	A	361	GLU
1	A	497	SER
1	A	737	GLY
1	A	750	ALA
1	A	277	ASP
1	A	398	MET
1	A	640	PRO
1	A	220	GLU

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Mol	Chain	Res	Type
1	A	224	ASP
1	A	499	ALA
1	A	332	GLU
1	A	406	ALA
1	A	503	PRO
1	A	377	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	646/698 (93%)	613 (95%)	33 (5%)	24 19

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	SER
1	A	46	GLN
1	A	111	GLU
1	A	128	ARG
1	A	132	GLU
1	A	181	ARG
1	A	186	GLN
1	A	207	THR
1	A	218	ASN
1	A	251	LEU
1	A	261	LEU
1	A	304	ARG
1	A	311	ASP
1	A	332	GLU
1	A	354	LEU
1	A	409	HIS
1	A	509	ARG
1	A	518	LYS
1	A	524	ARG
1	A	550	THR

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Mol	Chain	Res	Type
1	A	553	GLU
1	A	633	THR
1	A	634	ARG
1	A	640	PRO
1	A	648	ARG
1	A	660	VAL
1	A	706	THR
1	A	753	LEU
1	A	764	SER
1	A	774	ASP
1	A	827	LEU
1	A	842	GLU
1	A	856	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	186	GLN
1	A	335	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 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	J4G	A	901[A]	-	31,34,34	4.26	10 (32%)	32,50,50	1.39	3 (9%)
2	J4G	A	901[B]	-	31,34,34	4.25	10 (32%)	32,50,50	1.39	3 (9%)

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	J4G	A	901[A]	-	-	8/19/39/39	0/3/3/3
2	J4G	A	901[B]	-	-	2/19/39/39	0/3/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901[B]	J4G	O21-C22	15.51	1.62	1.41
2	A	901[A]	J4G	O21-C22	15.51	1.62	1.41
2	A	901[A]	J4G	C02-C22	-12.48	1.34	1.53
2	A	901[B]	J4G	C02-C22	-12.41	1.34	1.53
2	A	901[B]	J4G	O21-C14	-7.43	1.28	1.45
2	A	901[A]	J4G	O21-C14	-7.42	1.28	1.45
2	A	901[B]	J4G	C05-N04	6.75	1.48	1.34
2	A	901[A]	J4G	C05-N04	6.75	1.48	1.34
2	A	901[B]	J4G	C14-C03	4.05	1.60	1.52
2	A	901[A]	J4G	C14-C03	4.01	1.60	1.52
2	A	901[A]	J4G	C03-N04	-2.94	1.41	1.45
2	A	901[B]	J4G	C03-N04	-2.93	1.41	1.45
2	A	901[A]	J4G	P17-O16	2.68	1.68	1.60
2	A	901[B]	J4G	P17-O16	2.67	1.68	1.60
2	A	901[A]	J4G	O01-C02	2.49	1.48	1.43
2	A	901[B]	J4G	O01-C02	2.47	1.48	1.43
2	A	901[A]	J4G	C28-N29	2.46	1.43	1.34
2	A	901[B]	J4G	C28-N29	2.44	1.42	1.34
2	A	901[A]	J4G	C02-C03	-2.13	1.50	1.53
2	A	901[B]	J4G	C02-C03	-2.11	1.50	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	901[A]	J4G	N25-C26-N27	-4.85	121.11	128.68
2	A	901[B]	J4G	N25-C26-N27	-4.82	121.14	128.68
2	A	901[A]	J4G	C06-C05-N04	2.73	119.94	116.15
2	A	901[B]	J4G	C06-C05-N04	2.71	119.91	116.15
2	A	901[A]	J4G	C24-C30-N31	-2.39	106.91	109.40
2	A	901[B]	J4G	C24-C30-N31	-2.37	106.93	109.40

There are no chirality outliers.

All (10) torsion outliers are listed below:

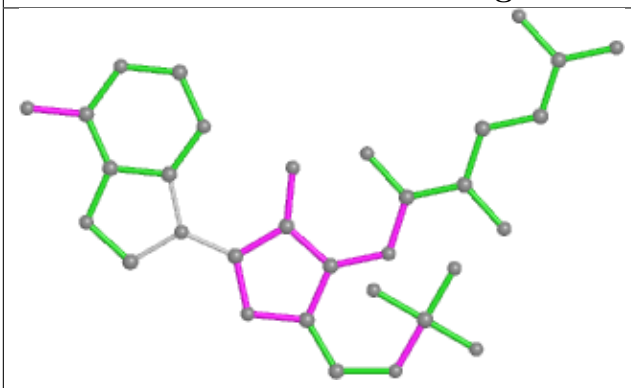
Mol	Chain	Res	Type	Atoms
2	A	901[A]	J4G	N12-C06-C07-C08
2	A	901[A]	J4G	C15-O16-P17-O18
2	A	901[A]	J4G	C15-O16-P17-O20
2	A	901[B]	J4G	C15-O16-P17-O18
2	A	901[A]	J4G	C05-C06-C07-C08
2	A	901[B]	J4G	C15-O16-P17-O20
2	A	901[A]	J4G	C14-C15-O16-P17
2	A	901[A]	J4G	C15-O16-P17-O19
2	A	901[A]	J4G	C07-C08-C09-O10
2	A	901[A]	J4G	C07-C08-C09-O11

There are no ring outliers.

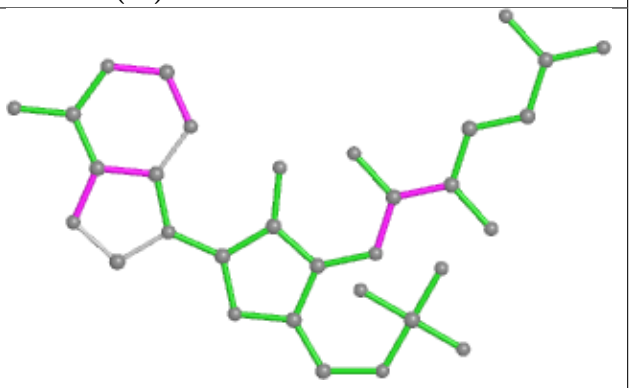
No monomer is involved in short contacts.

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.

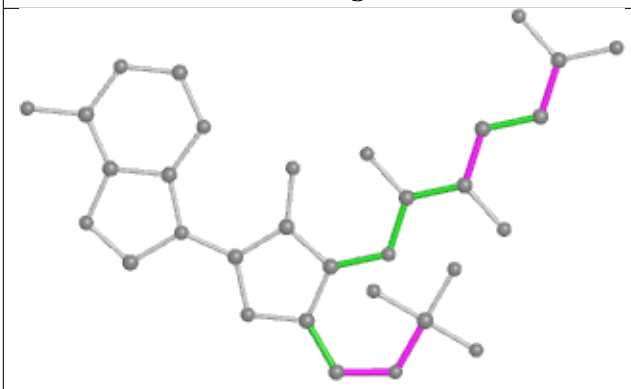
Ligand J4G A 901 (A)



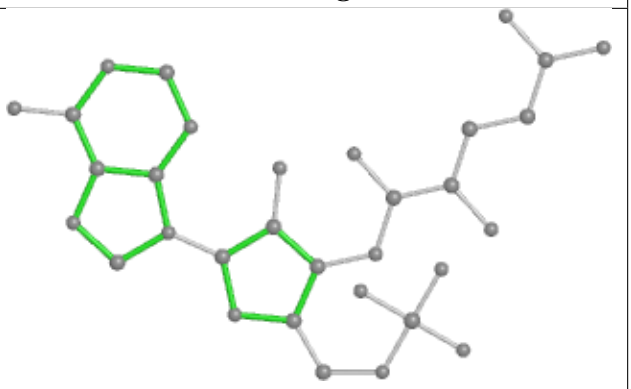
Bond lengths



Bond angles

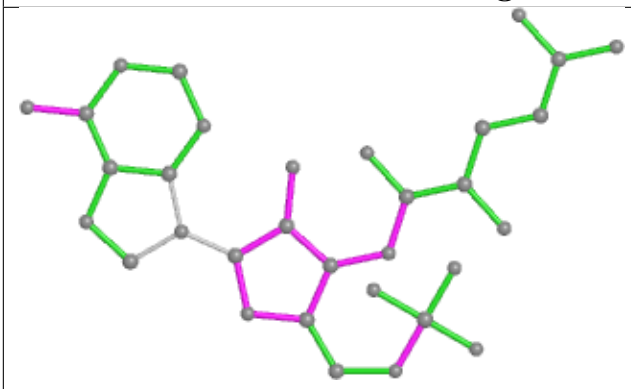


Torsions

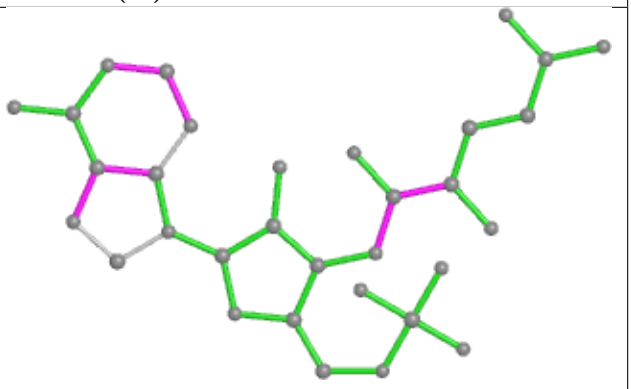


Rings

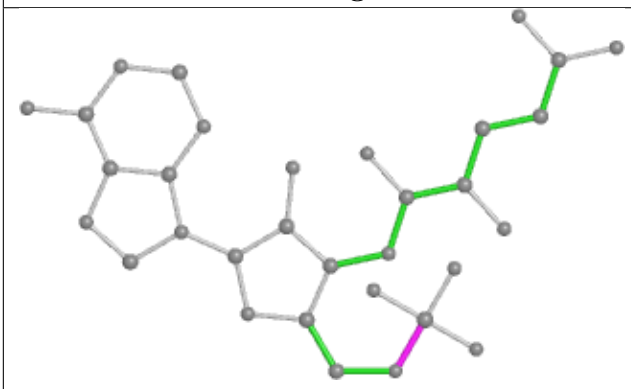
Ligand J4G A 901 (B)



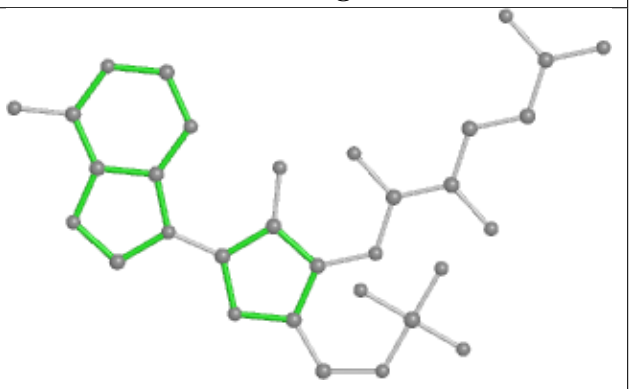
Bond lengths



Bond angles



Torsions



Rings

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	803/861 (93%)	0.28	31 (3%) 39 47	26, 45, 82, 167	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	502	ALA	21.6
1	A	499	ALA	15.5
1	A	501	TRP	15.1
1	A	331	ALA	11.5
1	A	72	GLY	10.8
1	A	357	ALA	10.6
1	A	500	ILE	9.3
1	A	360	PRO	7.3
1	A	405	THR	4.9
1	A	205	TYR	4.4
1	A	276	ALA	4.1
1	A	218	ASN	3.9
1	A	330	PRO	3.5
1	A	319	MET	3.1
1	A	630	VAL	3.0
1	A	219	GLY	2.9
1	A	507	HIS	2.9
1	A	373	ARG	2.9
1	A	497	SER	2.9
1	A	361	GLU	2.8
1	A	750	ALA	2.6
1	A	503	PRO	2.5
1	A	403	ASP	2.4
1	A	313	ASP	2.3
1	A	362	THR	2.2
1	A	287	ARG	2.2
1	A	359	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	645	ASP	2.1
1	A	498	ALA	2.0
1	A	397	MET	2.0
1	A	356	ARG	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 monosaccharides in this entry.

6.4 Ligands (i)

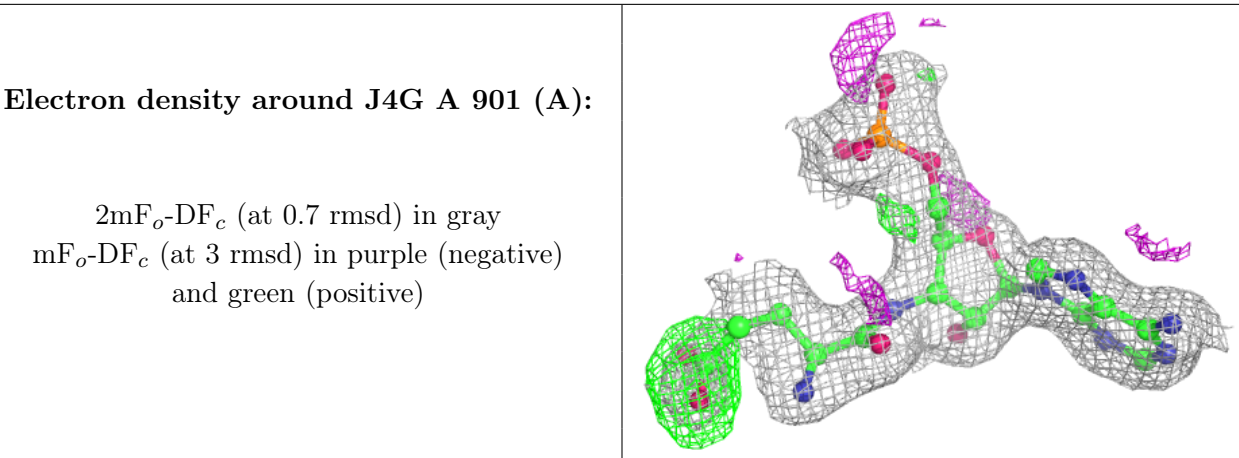
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

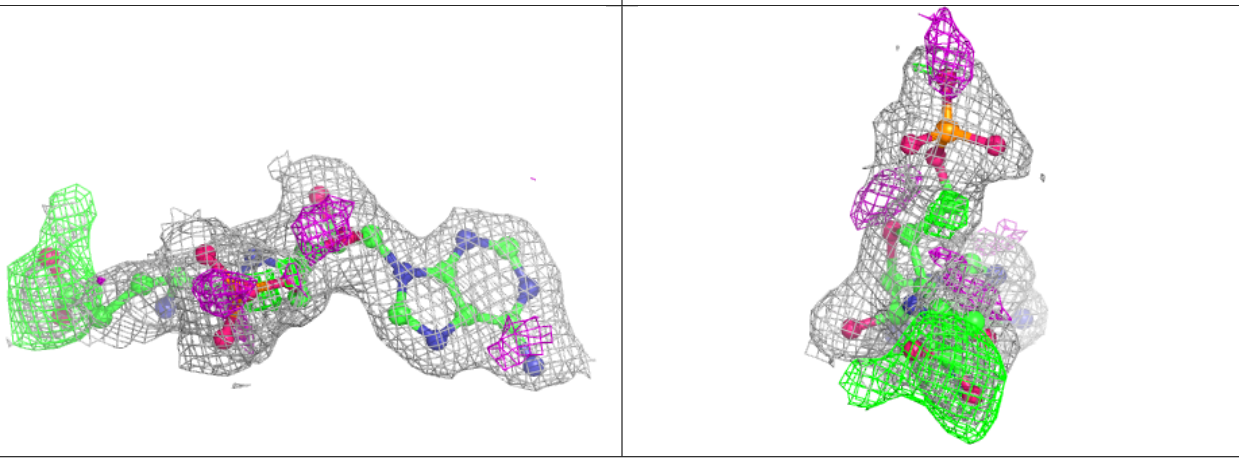
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	J4G	A	901[A]	32/32	0.90	0.16	27,32,61,80	32
2	J4G	A	901[B]	32/32	0.90	0.16	27,32,61,80	28

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 J4G A 901 (A):

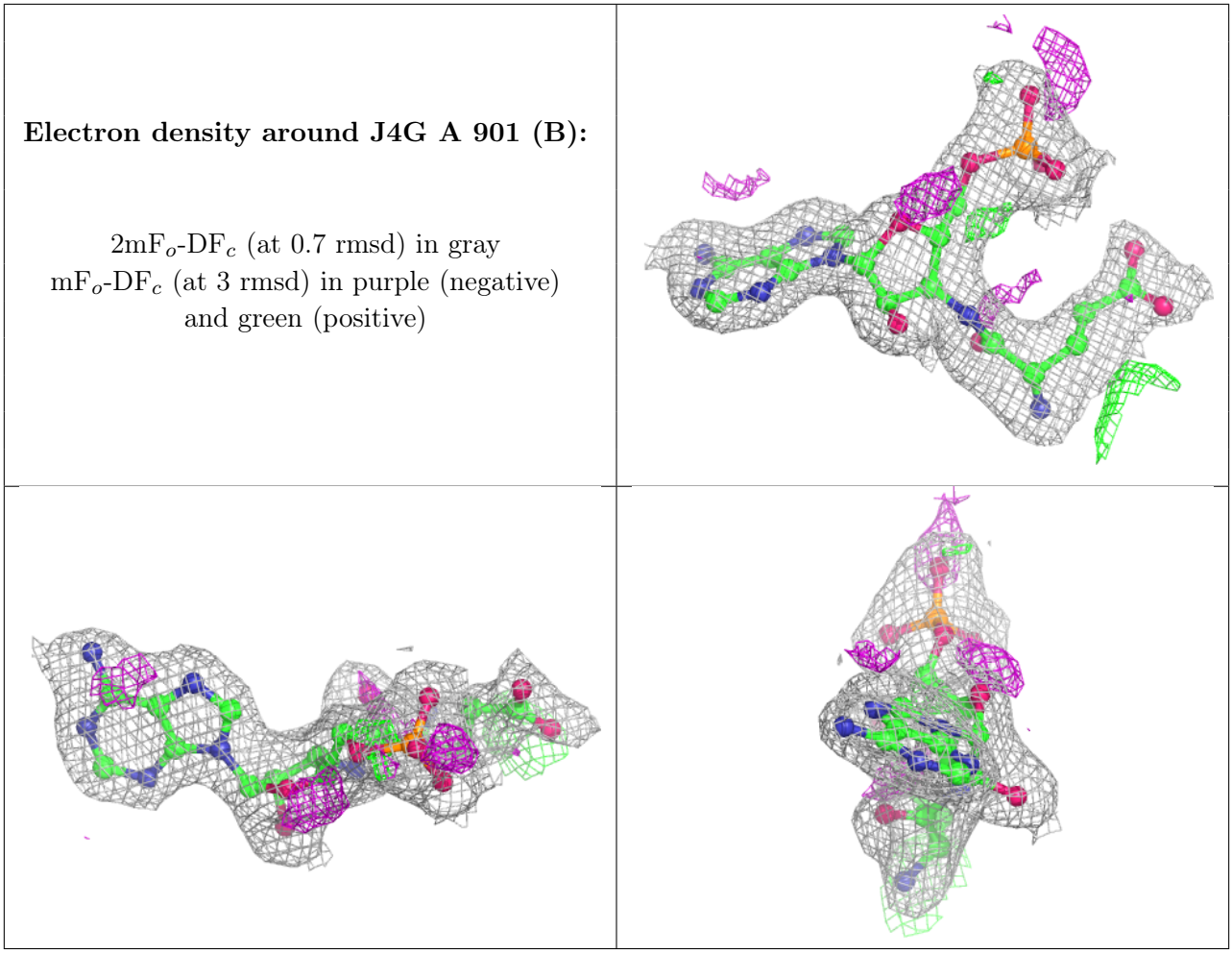
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around J4G A 901 (B):

$2mF_o$-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

There are no such residues in this entry.