Full wwPDB X-ray Structure Validation Report (i)

Jun 22, 2024 – 05:32 PM EDT

PDB ID	:	6G2Z
Title	:	Crystal structure of the p97 D2 domain in a helical split-washer conformation
Authors	:	Stach, L.; Morgan, R.M.L.; Freemont, P.S.
Deposited on	:	2018-03-23
Resolution	:	1.92 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:

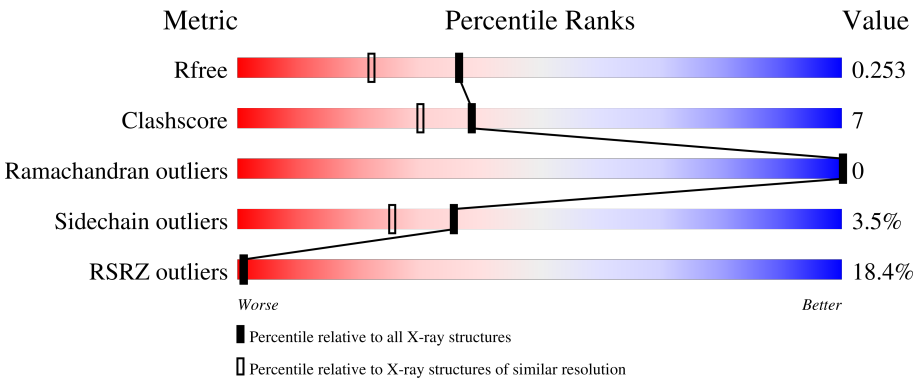
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.92 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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 <=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	306	16% 72% 14% • 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NA	A	808	-	-	-	X

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 2242 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.

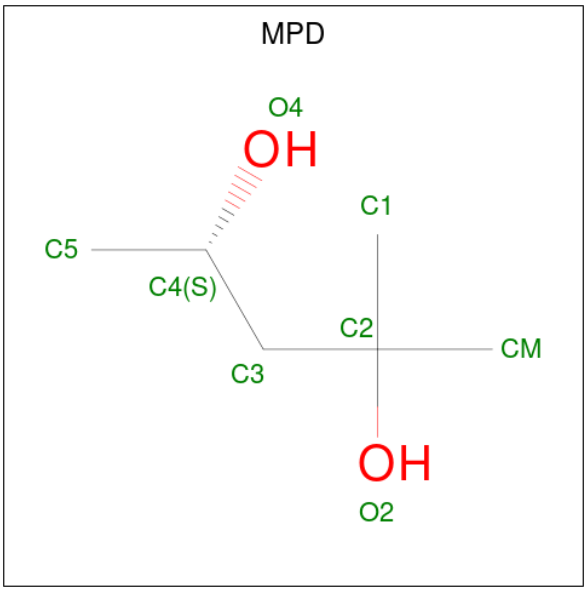
- Molecule 1 is a protein called Transitional endoplasmic reticulum ATPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	266	2112	1336	369	396	11	0	1	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	459	GLY	-	expression tag	UNP P55072
A	460	PRO	-	expression tag	UNP P55072
A	461	GLY	-	expression tag	UNP P55072

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



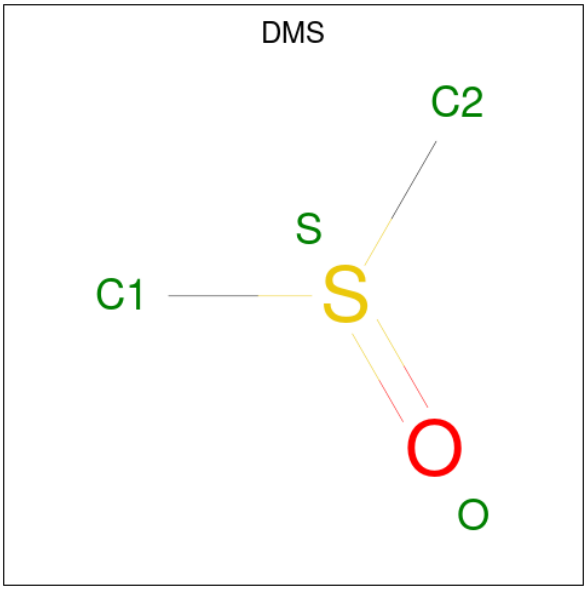
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	8	6	2	0	0

Continued on next page...

Continued from previous page...

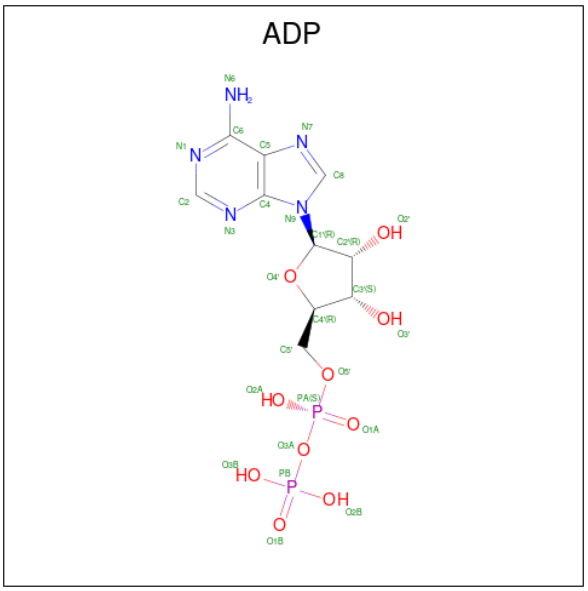
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
2	A	1	8	6	2		0	0
			Total	C	O			
2	A	1	8	6	2		0	0
			Total	C	O			
2	A	1	8	6	2		0	0

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
3	A	1	4	2	1	1	0	0
			Total	C	O	S		
3	A	1	4	2	1	1	0	0

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

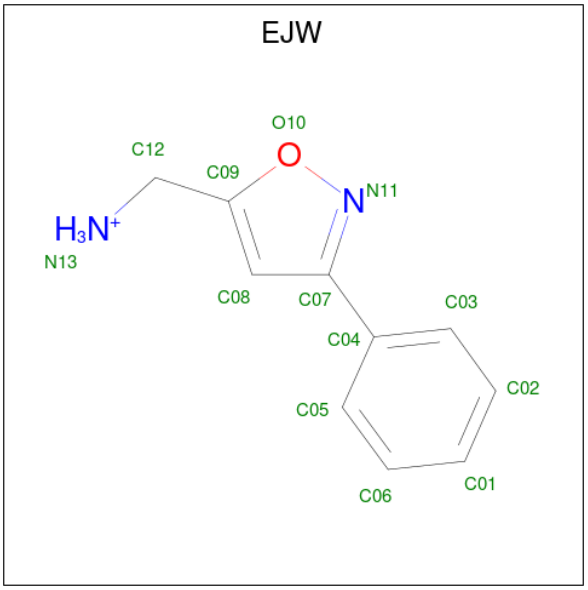


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	27	10	5	10	2	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
5	A	1	1	1	0	0

- Molecule 6 is (3-phenyl-1,2-oxazol-5-yl)methylazanium (three-letter code: EJW) (formula: $C_{10}H_{11}N_2O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	A	1	13	10	2	1	0	0

- Molecule 7 is water.

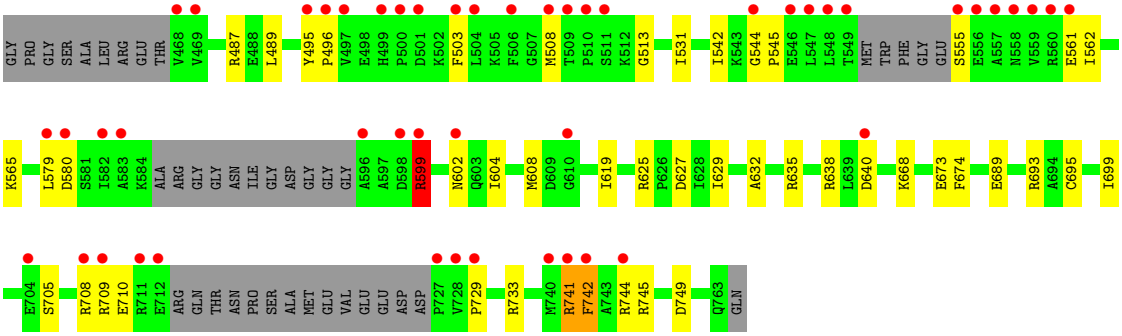
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	49	49	49	0	0

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: Transitional endoplasmic reticulum ATPase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	92.39Å 92.39Å 65.99Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.01 – 1.92 50.91 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.4 (40.01-1.92) 99.9 (50.91-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 1.92Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.223 , 0.247 0.227 , 0.253	Depositor DCC
R_{free} test set	1087 reflections (4.44%)	wwPDB-VP
Wilson B-factor (Å^2)	38.3	Xtriage
Anisotropy	0.616	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 68.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.048 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	2242	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, DMS, ADP, MPD, EJW

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	0.33	0/2148	0.55	0/2893

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	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	599	ARG	Peptide
1	A	741	ARG	Peptide

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	2112	0	2145	33	2

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	32	0	56	6	0
3	A	8	0	12	0	0
4	A	27	0	12	0	0
5	A	1	0	0	0	0
6	A	13	0	0	0	0
7	A	49	0	0	1	0
All	All	2242	0	2225	33	2

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 (33) 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:599:ARG:HB2	1:A:602:ASN:HB2	1.61	0.82
1:A:599:ARG:HB2	1:A:602:ASN:CB	2.13	0.78
1:A:625:ARG:NH2	1:A:627:ASP:OD2	2.14	0.78
1:A:629:ILE:HA	2:A:802:MPD:H11	1.66	0.78
1:A:495:TYR:HB3	1:A:503:PHE:CZ	2.21	0.76
1:A:745:ARG:NH2	1:A:749:ASP:OD1	2.21	0.67
1:A:495:TYR:HB3	1:A:503:PHE:HZ	1.58	0.66
1:A:604:ILE:O	1:A:608:MET:HG3	1.97	0.65
1:A:729:PRO:HD2	2:A:801:MPD:HM1	1.84	0.60
1:A:579:LEU:HB3	2:A:802:MPD:O2	2.05	0.56
1:A:729:PRO:O	2:A:801:MPD:HM3	2.07	0.55
1:A:555:SER:O	1:A:555:SER:OG	2.27	0.52
1:A:561:GLU:O	1:A:565:LYS:HG2	2.11	0.51
1:A:632:ALA:O	1:A:635:ARG:HG3	2.10	0.50
1:A:673:GLU:OE1	1:A:673:GLU:N	2.42	0.50
1:A:674:PHE:HD2	2:A:803:MPD:H31	1.78	0.49
1:A:513:GLY:O	1:A:640:ASP:N	2.43	0.48
1:A:489:LEU:HD22	1:A:531:ILE:HD11	1.96	0.47
1:A:508:MET:N	7:A:904:HOH:O	2.49	0.46
1:A:627:ASP:OD1	1:A:627:ASP:N	2.40	0.46
1:A:689:GLU:HB3	1:A:693:ARG:NH1	2.32	0.45
1:A:542:ILE:HD12	1:A:562:ILE:HG21	1.97	0.45
1:A:695:CYS:O	1:A:699:ILE:HG12	2.16	0.44
1:A:544:GLY:N	1:A:545:PRO:HD2	2.33	0.44
1:A:599:ARG:HB2	1:A:602:ASN:HB3	1.98	0.43
1:A:693:ARG:NH2	1:A:742:PHE:CE2	2.87	0.43
1:A:744:ARG:NE	1:A:745:ARG:O	2.43	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:MET:HE2	1:A:638:ARG:HA	2.01	0.42
1:A:513:GLY:HA2	1:A:619:ILE:O	2.18	0.42
1:A:496:PRO:HA	1:A:503:PHE:CD1	2.55	0.42
1:A:599:ARG:HA	1:A:602:ASN:H	1.85	0.42
1:A:733:ARG:HG3	2:A:803:MPD:H13	2.02	0.41
1:A:742:PHE:CD1	1:A:742:PHE:C	2.93	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:LYS:NZ	1:A:710:GLU:O[6_645]	1.68	0.52
1:A:668:LYS:NZ	1:A:710:GLU:C[6_645]	2.08	0.12

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	259/306 (85%)	251 (97%)	8 (3%)	0	100 100

There are no Ramachandran outliers to report.

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	231/258 (90%)	223 (96%)	8 (4%)	36 25

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	487	ARG
1	A	580	ASP
1	A	599	ARG
1	A	705	SER
1	A	708	ARG
1	A	709	ARG
1	A	741	ARG
1	A	742	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	641	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)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	DMS	A	806	-	3,3,3	0.66	0	3,3,3	0.42	0
3	DMS	A	805	-	3,3,3	0.67	0	3,3,3	0.50	0
4	ADP	A	807	5	24,29,29	0.97	2 (8%)	29,45,45	1.06	2 (6%)
2	MPD	A	804	-	7,7,7	0.29	0	9,10,10	0.47	0
2	MPD	A	803	-	7,7,7	0.31	0	9,10,10	0.26	0
6	EJW	A	809	-	12,14,14	1.97	1 (8%)	14,18,18	1.54	3 (21%)
2	MPD	A	801	-	7,7,7	0.33	0	9,10,10	0.56	0
2	MPD	A	802	-	7,7,7	0.29	0	9,10,10	0.54	0

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
4	ADP	A	807	5	-	3/12/32/32	0/3/3/3
2	MPD	A	804	-	-	4/5/5/5	-
2	MPD	A	803	-	-	5/5/5/5	-
6	EJW	A	809	-	-	0/4/6/6	0/2/2/2
2	MPD	A	801	-	-	4/5/5/5	-
2	MPD	A	802	-	-	0/5/5/5	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	809	EJW	C04-C07	-6.63	1.38	1.49
4	A	807	ADP	PA-O3A	2.33	1.62	1.59
4	A	807	ADP	O4'-C1'	2.02	1.43	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	807	ADP	N3-C2-N1	-3.60	123.79	128.67
6	A	809	EJW	C04-C07-N11	3.36	126.32	120.96
6	A	809	EJW	C08-C07-C04	-2.95	125.34	129.44
6	A	809	EJW	C12-C09-C08	-2.73	125.89	129.52
4	A	807	ADP	C4-C5-N7	-2.33	106.87	109.34

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	MPD	C2-C3-C4-C5
2	A	803	MPD	C2-C3-C4-O4
2	A	803	MPD	C2-C3-C4-C5
2	A	801	MPD	C2-C3-C4-O4
2	A	801	MPD	C1-C2-C3-C4
2	A	803	MPD	C1-C2-C3-C4
2	A	803	MPD	CM-C2-C3-C4
2	A	804	MPD	C1-C2-C3-C4
2	A	804	MPD	CM-C2-C3-C4
4	A	807	ADP	PA-O3A-PB-O1B
4	A	807	ADP	PA-O3A-PB-O2B
4	A	807	ADP	PA-O3A-PB-O3B
2	A	803	MPD	O2-C2-C3-C4
2	A	804	MPD	O2-C2-C3-C4
2	A	804	MPD	C2-C3-C4-O4
2	A	801	MPD	CM-C2-C3-C4

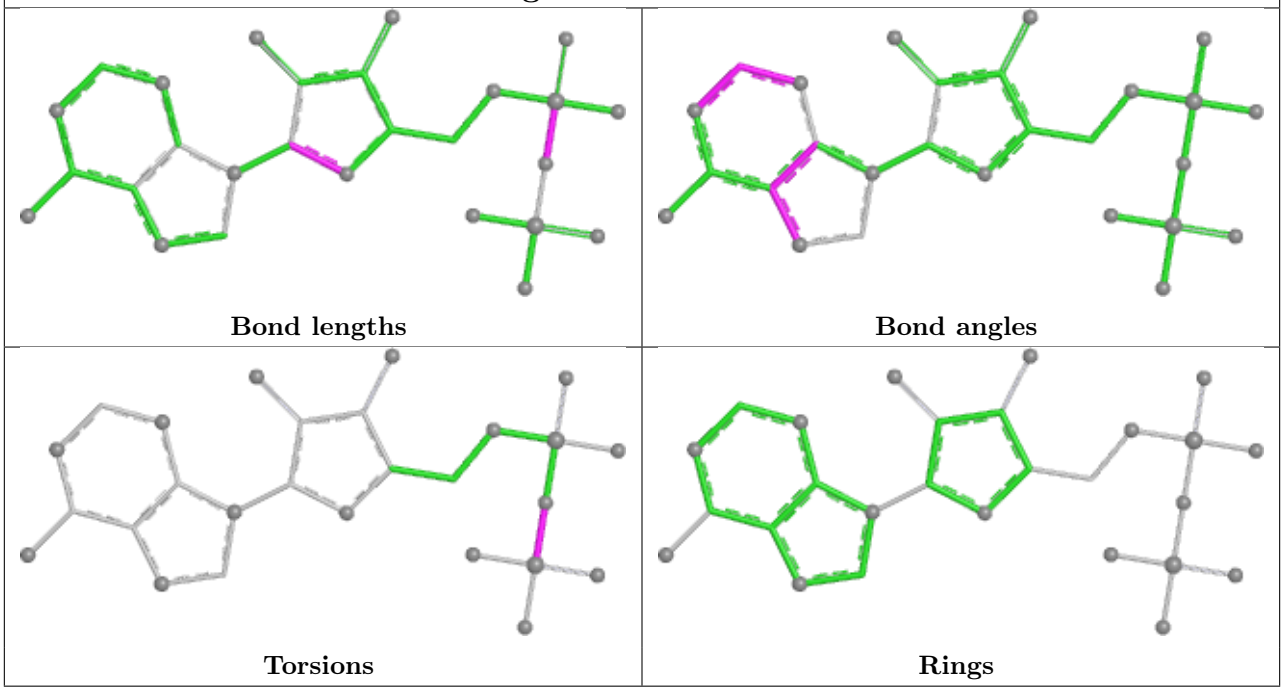
There are no ring outliers.

3 monomers are involved in 6 short contacts:

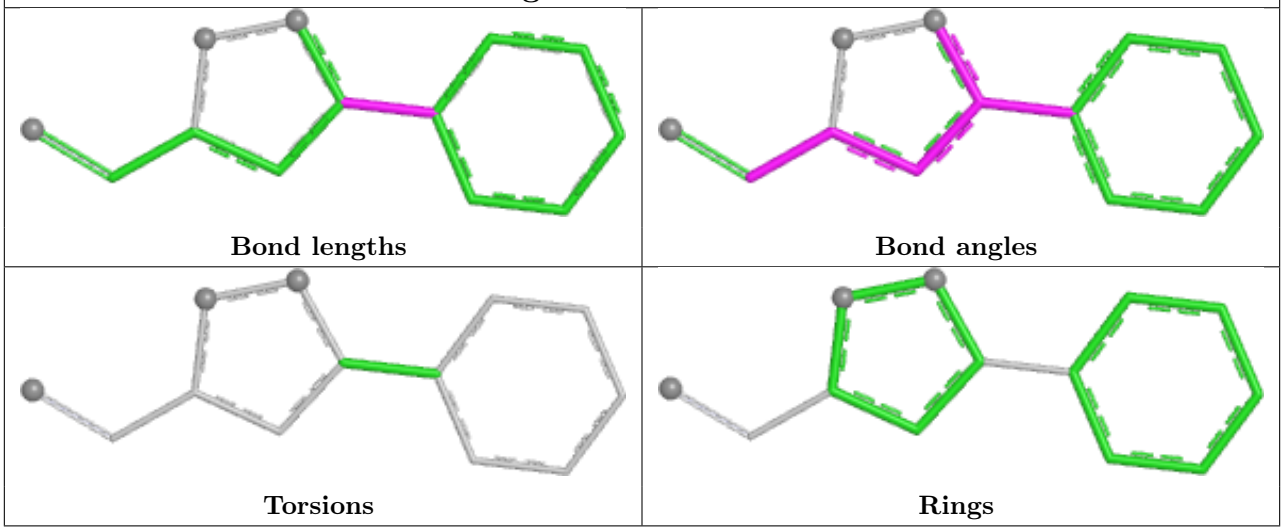
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	803	MPD	2	0
2	A	801	MPD	2	0
2	A	802	MPD	2	0

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 ADP A 807



Ligand EJW A 809



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	266/306 (86%)	1.15	49 (18%) 1 1	34, 54, 94, 121	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	742	PHE	14.2
1	A	549	THR	13.0
1	A	500	PRO	10.9
1	A	510	PRO	9.6
1	A	499	HIS	7.6
1	A	495	TYR	5.9
1	A	508	MET	5.7
1	A	501	ASP	5.4
1	A	497	VAL	5.4
1	A	511	SER	5.3
1	A	503	PHE	5.0
1	A	496	PRO	4.7
1	A	506	PHE	4.7
1	A	582	ILE	4.5
1	A	548	LEU	4.3
1	A	556	GLU	4.2
1	A	557	ALA	4.0
1	A	509	THR	4.0
1	A	728	VAL	3.9
1	A	579	LEU	3.9
1	A	468	VAL	3.9
1	A	560	ARG	3.8
1	A	711	ARG	3.8
1	A	599	ARG	3.6
1	A	504	LEU	3.5
1	A	544	GLY	3.4
1	A	744	ARG	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	555	SER	3.2
1	A	558	ASN	3.1
1	A	598	ASP	2.9
1	A	740	MET	2.8
1	A	559	VAL	2.8
1	A	741	ARG	2.7
1	A	729	PRO	2.6
1	A	561	GLU	2.5
1	A	596	ALA	2.5
1	A	708	ARG	2.4
1	A	547	LEU	2.3
1	A	727	PRO	2.3
1	A	580	ASP	2.3
1	A	640	ASP	2.2
1	A	583	ALA	2.2
1	A	546	GLU	2.2
1	A	709	ARG	2.2
1	A	602	ASN	2.2
1	A	704	GLU	2.1
1	A	610	GLY	2.1
1	A	712	GLU	2.0
1	A	469	VAL	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, 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	MPD	A	801	8/8	0.56	0.30	68,79,90,94	0

Continued on next page...

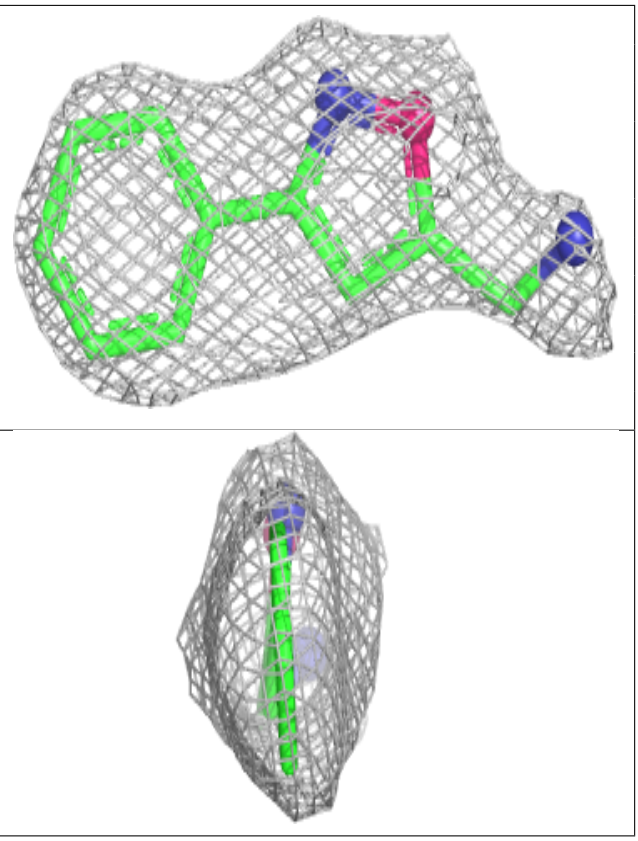
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NA	A	808	1/1	0.73	0.50	72,72,72,72	0
2	MPD	A	804	8/8	0.75	0.23	53,67,76,82	0
2	MPD	A	803	8/8	0.81	0.30	52,58,77,81	0
2	MPD	A	802	8/8	0.85	0.30	47,59,66,79	0
3	DMS	A	805	4/4	0.87	0.18	78,81,84,105	0
6	EJW	A	809	13/13	0.89	0.21	50,60,77,85	0
3	DMS	A	806	4/4	0.92	0.17	63,65,83,100	0
4	ADP	A	807	27/27	0.97	0.13	32,36,42,45	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.

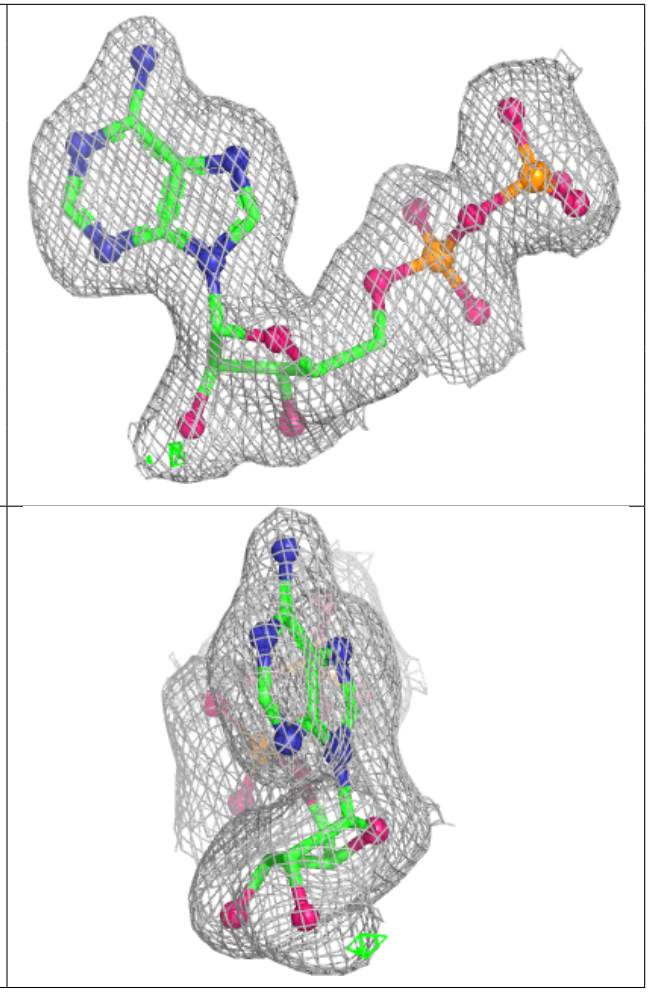
Electron density around EJW A 809:

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 ADP A 807:

$2mF_o$-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.