

Full wwPDB X-ray Structure Validation Report (i)

Jan 28, 2024 – 09:23 pm GMT

PDB ID : 5LXM

Title : Crystal structure of Aurora-A bound to a hydrocarbon-stapled proteomimetic

of TPX2

Authors : McIntyre, P.J.; Bayliss, R.

Deposited on : 2016-09-22

Resolution : 2.08 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, 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)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

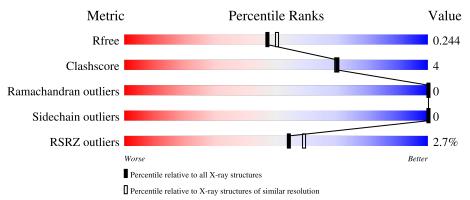
Validation Pipeline (wwPDB-VP) : 2.36

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 2.08 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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	283	87%		7	% 6%	ı
2	D	38	76%	8%		13%	I



2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 2615 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 Aurora kinase A.

Mol	Chain	Residues		A	toms	3			ZeroOcc	AltConf	Trace
1	A	267	Total 2181	C 1398	N 379	O 398	P 1	S 5	1	5	0

There are 3 discrepancies between the modelled and reference sequences:

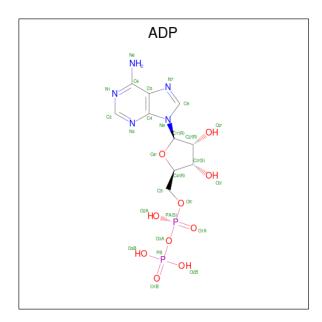
Chain	Residue	Modelled	Actual	Comment	Reference
Α	121	MET	-	initiating methionine	UNP O14965
A	290	ALA	CYS	engineered mutation	UNP O14965
A	393	ALA	CYS	engineered mutation	UNP O14965

• Molecule 2 is a protein called Targeting protein for Xklp2.

Mol	Chain	Residues		Aton	ıs		ZeroOcc	AltConf	Trace
2	D	33	Total 271	C 173	N 40	O 58	0	0	0

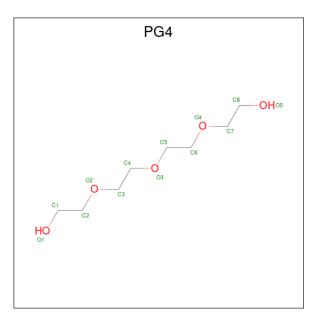
• Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).





Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
3	A	1	Total 27	C 10	_	O 10	P 2	0	0

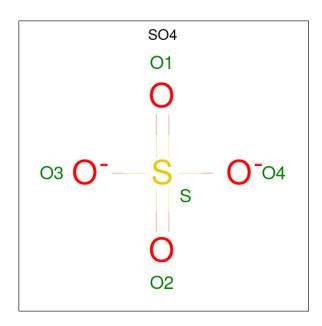
 \bullet Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $\mathrm{C_8H_{18}O_5}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 8 5	0	0

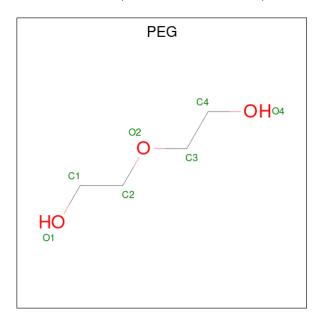
 \bullet Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$





Mol	Chain	Residues	Ato	ms		ZeroOcc	AltConf
5	A	1	Total 5	O 4	S 1	0	0

• Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).

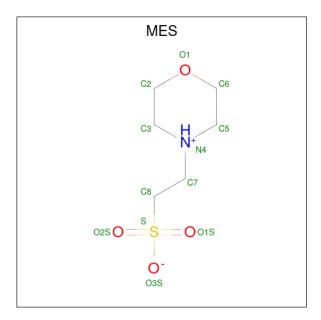


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 4 3	0	0
6	A	1	Total C O 7 4 3	0	0

 \bullet Molecule 7 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES)

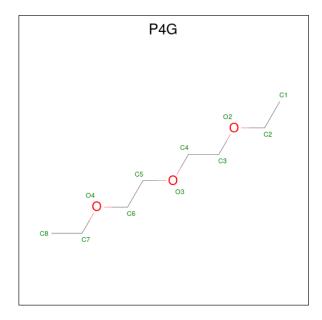


(formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
7	A	1	Total 12	C 6		O 4	S 1	0	0

 \bullet Molecule 8 is 1-ETHOXY-2-(2-ETHOXYETHOXY) ETHANE (three-letter code: P4G) (formula: $\rm C_8H_{18}O_3).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 11 8 3	0	0



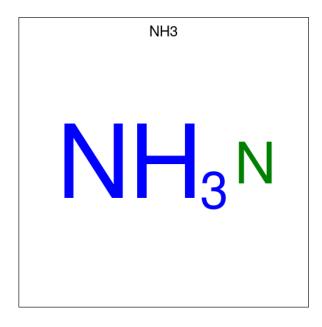
• Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total Cl 1 1	0	0

• Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	2	Total Mg 2 2	0	0

• Molecule 11 is AMMONIA (three-letter code: NH3) (formula: H₃N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	D	1	Total N 1 1	0	0

• Molecule 12 is water.

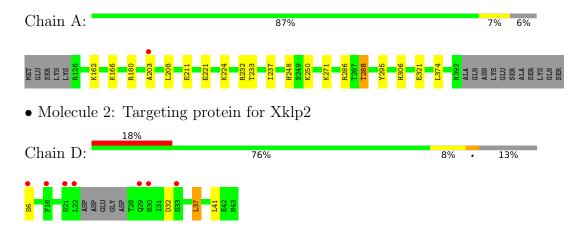
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	70	Total O 70 70	0	0
12	D	7	Total O 7 7	0	0



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: Aurora kinase A





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	79.78Å 79.78Å 140.26Å	Domositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	61.98 - 2.08	Depositor
Resolution (A)	69.09 - 2.08	EDS
% Data completeness	99.3 (61.98-2.08)	Depositor
(in resolution range)	89.4 (69.09-2.08)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.85 (at 2.08Å)	Xtriage
Refinement program	PHENIX	Depositor
D.D.	0.200 , 0.243	Depositor
R, R_{free}	0.205 , 0.244	DCC
R_{free} test set	1603 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 70.5	EDS
L-test for twinning ²	$< L >=0.44, < L^2>=0.27$	Xtriage
Estimated twinning fraction	0.059 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2615	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: NH3, TPO, PG4, ADP, MK8, P4G, MG, CL, SO4, MES, PEG

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			
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5			
1	A	0.21	0/2231	0.37	0/3025			
2	D	0.28	0/257	0.43	0/344			
All	All	0.22	0/2488	0.38	0/3369			

There are no bond length outliers.

There are no bond angle outliers.

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	2181	0	2126	15	0
2	D	271	0	234	3	0
3	A	27	0	12	1	0
4	A	13	0	18	1	0
5	A	5	0	0	0	0
6	A	14	0	20	3	0
7	A	12	0	13	1	0
8	A	11	0	18	0	0
9	A	1	0	0	0	0
10	A	2	0	0	0	0
11	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	A	70	0	0	0	0
12	D	7	0	0	1	0
All	All	2615	0	2441	18	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 (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	${\rm distance} \ (\mathring{\rm A})$	overlap (Å)	
1:A:211:GLU:OE1	1:A:271:LYS:NZ	2.33	0.62	
1:A:295:TYR:OH	1:A:321:GLU:OE1	2.17	0.59	
1:A:221[B]:GLU:OE1	1:A:232:ARG:NH2	2.32	0.59	
1:A:374:LEU:HB2	6:A:504:PEG:H21	1.87	0.56	
2:D:6:SER:N	12:D:201:HOH:O	2.39	0.55	
3:A:501:ADP:H8	3:A:501:ADP:H5'1	1.73	0.54	
1:A:250:LYS:HE3	2:D:32:ASP:HB3	1.88	0.54	
1:A:248:HIS:ND1	6:A:504:PEG:O4	2.23	0.51	
1:A:162:LYS:HB3	1:A:208:LEU:HB2	1.95	0.49	
1:A:374:LEU:H	6:A:504:PEG:H32	1.78	0.48	
1:A:224:LYS:NZ	4:A:502:PG4:H51	2.30	0.47	
1:A:180:ARG:NH1	7:A:506:MES:O3S	2.50	0.45	
1:A:286:ARG:HB2	1:A:306:HIS:CE1	2.51	0.45	
2:D:37:MK8:HB1B	2:D:37:MK8:HGA	1.77	0.44	
1:A:233:THR:O	1:A:237:ILE:HG12	2.20	0.42	
1:A:166:LYS:HZ2	1:A:203:ALA:H	1.68	0.41	
1:A:286:ARG:HB3	1:A:288:TPO:O2P	2.20	0.41	
1:A:224:LYS:HB3	1:A:224:LYS:HE2	1.86	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	Perce	ntiles
1	A	$269/283 \; (95\%)$	256 (95%)	13 (5%)	0	100	100
2	D	27/38 (71%)	26 (96%)	1 (4%)	0	100	100
All	All	$296/321 \ (92\%)$	282 (95%)	14 (5%)	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	227/248 (92%)	227 (100%)	0	100 100		
2	D	29/33 (88%)	29 (100%)	0	100 100		
All	All	256/281 (91%)	256 (100%)	0	100 100		

There are no protein residues with a non-rotameric sidechain to report.

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)

3 non-standard protein/DNA/RNA residues 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	ype Chain	$ain \mid Res \mid$	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MK8	D	41	2	5,8,9	1.48	1 (20%)	4,10,12	0.91	0
1	TPO	A	288	1	8,10,11	1.60	1 (12%)	10,14,16	1.65	1 (10%)
2	MK8	D	37	2	5,8,9	1.51	1 (20%)	4,10,12	0.83	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
2	MK8	D	41	2	-	2/6/8/11	-
1	TPO	A	288	1	-	0/9/11/13	-
2	MK8	D	37	2	-	1/6/8/11	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
1	A	288	TPO	P-O1P	3.41	1.61	1.50
2	D	37	MK8	CB-CA	-2.72	1.51	1.55
2	D	41	MK8	CB-CA	-2.70	1.52	1.55

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	288	TPO	P-OG1-CB	-4.47	109.72	123.21

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	37	MK8	CA-CB-CG-CD
2	D	41	MK8	C-CA-CB-CG
2	D	41	MK8	CB1-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	288	TPO	1	0
2	D	37	MK8	1	0



5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 3 are monoatomic and 1 is modelled with single atom - leaving 7 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	Bo	ond leng	$ ag{ths}$	Bond angles		
MIOI	Type	Chain	nes	es Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PEG	A	505	10	6,6,6	0.57	0	5,5,5	0.26	0
8	P4G	A	507	-	10,10,10	0.60	0	9,9,9	0.21	0
4	PG4	A	502	-	12,12,12	0.68	0	11,11,11	0.20	0
7	MES	A	506	-	12,12,12	1.19	2 (16%)	14,16,16	2.74	7 (50%)
6	PEG	A	504	-	6,6,6	0.56	0	5,5,5	0.33	0
5	SO4	A	503	-	4,4,4	0.15	0	6,6,6	0.06	0
3	ADP	A	501	10	24,29,29	0.97	1 (4%)	29,45,45	1.32	4 (13%)

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
6	PEG	A	505	10	-	3/4/4/4	-
8	P4G	A	507	-	-	3/8/8/8	-
4	PG4	A	502	-	-	4/10/10/10	-
7	MES	A	506	-	-	2/6/14/14	0/1/1/1
6	PEG	A	504	-	-	3/4/4/4	-
3	ADP	A	501	10	-	4/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
3	A	501	ADP	C5-C4	2.54	1.47	1.40
7	A	506	MES	O2S-S	2.20	1.51	1.45
7	A	506	MES	O1S-S	2.19	1.51	1.45

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
7	A	506	MES	C6-C5-N4	4.28	116.60	110.10
7	A	506	MES	O3S-S-O1S	-4.14	101.16	111.27
7	A	506	MES	C2-C3-N4	4.06	116.25	110.10
7	A	506	MES	C5-N4-C3	3.84	117.46	108.83
7	A	506	MES	O1S-S-C8	3.73	111.41	106.92
7	A	506	MES	O3S-S-C8	3.26	111.05	105.77
3	A	501	ADP	N3-C2-N1	-3.04	123.92	128.68
7	A	506	MES	O2S-S-C8	2.90	110.41	106.92
3	A	501	ADP	PA-O3A-PB	-2.87	122.98	132.83
3	A	501	ADP	C3'-C2'-C1'	2.63	104.94	100.98
3	A	501	ADP	C4-C5-N7	-2.50	106.79	109.40

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	ADP	C5'-O5'-PA-O1A
6	A	505	PEG	O2-C3-C4-O4
6	A	505	PEG	O1-C1-C2-O2
4	A	502	PG4	O3-C5-C6-O4
6	A	504	PEG	C1-C2-O2-C3
3	A	501	ADP	C5'-O5'-PA-O3A
8	A	507	P4G	O2-C3-C4-O3
6	A	505	PEG	C4-C3-O2-C2
8	A	507	P4G	C5-C6-O4-C7
4	A	502	PG4	O1-C1-C2-O2
6	A	504	PEG	O1-C1-C2-O2
6	A	504	PEG	C4-C3-O2-C2
4	A	502	PG4	C3-C4-O3-C5
3	A	501	ADP	O4'-C4'-C5'-O5'
7	A	506	MES	C8-C7-N4-C3
4	A	502	PG4	C8-C7-O4-C6
8	A	507	P4G	C6-C5-O3-C4
3	A	501	ADP	C5'-O5'-PA-O2A
7	A	506	MES	C7-C8-S-O1S

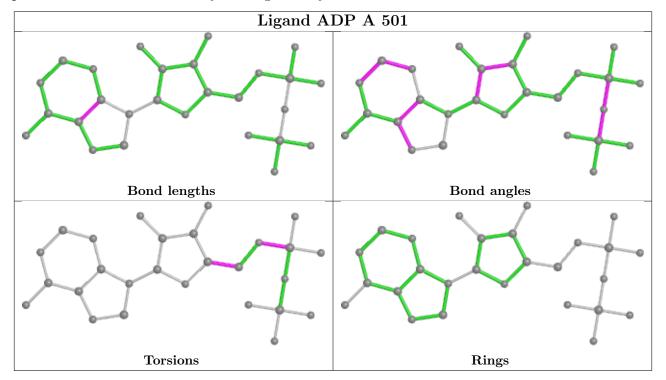


There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	PG4	1	0
7	A	506	MES	1	0
6	A	504	PEG	3	0
3	A	501	ADP	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.



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, 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	$266/283 \ (93\%)$	0.30	1 (0%) 92 93	45, 69, 102, 132	1 (0%)
2	D	31/38 (81%)	0.96	7 (22%) 0 0	54, 89, 141, 149	0
All	All	297/321 (92%)	0.37	8 (2%) 54 59	45, 70, 107, 149	1 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	21	SER	3.7
2	D	22	LEU	3.6
1	A	203	ALA	3.2
2	D	30	ASN	3.0
2	D	16	PHE	2.8
2	D	6	SER	2.2
2	D	29	GLN	2.1
2	D	33	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	MK8	D	41	9/10	0.95	0.14	51,58,60,67	0
2	MK8	D	37	9/10	0.96	0.14	63,65,74,76	0
1	TPO	A	288	11/12	0.97	0.15	48,59,62,78	0



6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

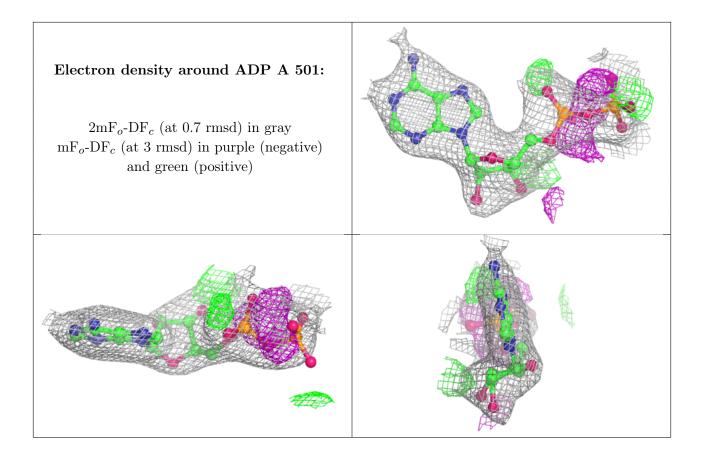
6.4 Ligands (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
10	MG	A	509	1/1	-0.10	0.12	143,143,143,143	0
9	CL	A	508	1/1	0.49	0.09	116,116,116,116	0
6	PEG	A	505	7/7	0.66	0.14	91,95,105,110	0
8	P4G	A	507	11/11	0.70	0.16	69,96,105,107	0
4	PG4	A	502	13/13	0.81	0.15	93,105,111,111	0
10	MG	A	510	1/1	0.81	0.38	144,144,144,144	0
5	SO4	A	503	5/5	0.83	0.19	142,143,145,146	0
7	MES	A	506	12/12	0.87	0.20	79,85,112,125	0
6	PEG	A	504	7/7	0.91	0.11	59,66,74,85	0
3	ADP	A	501	27/27	0.92	0.15	50,74,163,169	0
11	NH3	D	101	1/1	0.97	0.12	49,49,49,49	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.





6.5 Other polymers (i)

There are no such residues in this entry.

