

# Full wwPDB X-ray Structure Validation Report (i)

### Jun 21, 2021 – 12:03 PM BST

PDB ID	:	6TLE
$\operatorname{Title}$	:	Human Eg5 motor domain mutant E344K
Authors	:	Garcia-Saez, I.; Skoufias, D.A.
Deposited on		
$\operatorname{Resolution}$	:	1.75  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 following versions of software and data (see references (1)) were used in the production of this report:

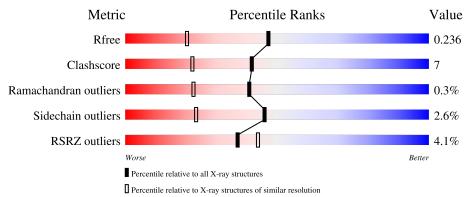
5	:	4.02b-467
Mogul	:	1.8.5 (274361),  CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.20
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry $(proteins)$	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.20

# 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 1.75 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
$R_{free}$	130704	$2340 \ (1.76-1.76)$
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437(1.76-1.76)
Sidechain outliers	138945	2437(1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	А	367	78%	13%	• 8%
1	В	367	<sup>3%</sup> 75%	11% •	13%



#### 6TLE

# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5890 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 Kinesin-like protein KIF11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	338	Total 2656	C 1662	N 467	0 517	S 10	0	0	0
1	В	320	Total 2526	C 1587	N 439	O 490	S 10	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

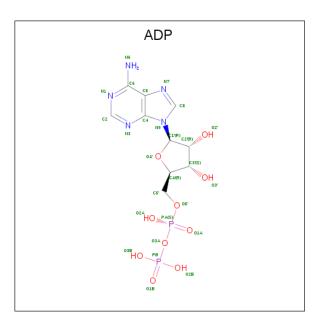
Chain	Residue	Modelled	Actual Comment		Reference
А	344	LYS	GLU	engineered mutation	UNP P52732
В	344	LYS	GLU	engineered mutation	UNP P52732

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Mg 1 1	0	0
2	В	1	Total Mg 1 1	0	0

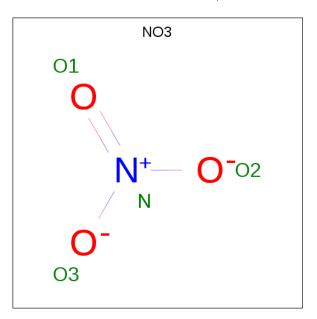
• Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	Δ	1	Total	С	Ν	Ο	Р	0	0
0	A	T	27	10	5	10	2	0	0
9	D	1	Total	С	Ν	Ο	Р	0	0
0	D	L	27	10	5	10	2	0	0

• Molecule 4 is NITRATE ION (three-letter code: NO3) (formula:  $NO_3$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
4	В	1	Total 4	N 1	O 3	0	0

• Molecule 5 is water.

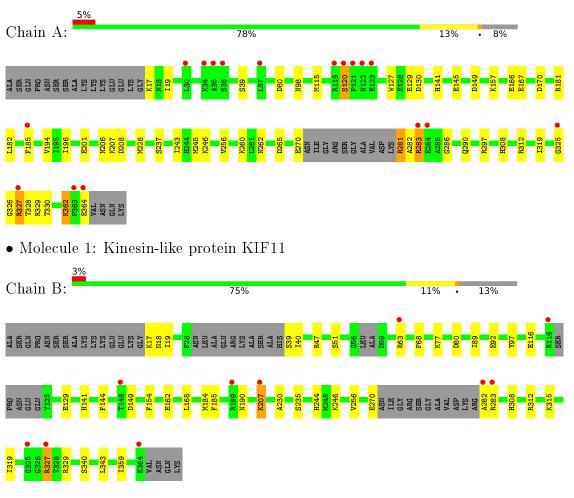


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	345	Total O 345 345	0	0
5	В	303	Total O 303 303	0	0



# 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: Kinesin-like protein KIF11



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	46.93Å 47.15Å 85.50Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$93.91^{\circ}$ $101.17^{\circ}$ $109.23^{\circ}$	Depositor
Resolution (Å)	44.07 - 1.75	Depositor
Resolution (A)	44.06 - 1.75	EDS
% Data completeness	91.5 (44.07-1.75)	Depositor
(in resolution range)	91.5(44.06-1.75)	EDS
R <sub>merge</sub>	0.04	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.91 (at 1.75 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D.	0.201 , $0.235$	Depositor
$R, R_{free}$	0.203 , $0.236$	DCC
$R_{free}$ test set	3047 reflections $(4.88%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	22.8	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , $48.7$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5890	wwPDB-VP
Average B, all atoms $(Å^2)$	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.10% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities 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: NO3, ADP, MG  $\,$ 

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
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.30	0/2695	0.54	0/3641
1	В	0.28	0/2566	0.49	0/3461
All	All	0.29	0/5261	0.51	0/7102

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	А	2656	0	2689	38	0
1	В	2526	0	2569	39	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	27	0	12	0	0
3	В	27	0	12	0	0
4	В	4	0	0	0	0
5	А	345	0	0	14	2
5	В	303	0	0	18	2
All	All	5890	0	5282	74	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 (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A tom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:281:ARG:HD3	1:A:282:ALA:H	1.35	0.89
1:A:17:LYS:N	5:A:501:HOH:O	2.05	0.89
1:B:312:ARG:NH1	5:B:504:HOH:O	2.15	0.80
1:B:19:ILE:HG12	1:B:327:ARG:HH22	1.48	0.78
1:A:196:ILE:HD11	1:A:319:ILE:HD12	1.72	0.70
1:B:51:SER:HB2	1:B:63:ARG:NE	2.08	0.69
1:A:149:ASP:O	5:A:502:HOH:O	2.10	0.68
1:B:77:LYS:NZ	5:B:509:HOH:O	2.22	0.68
1:A:327:ARG:N	5:A:507:HOH:O	2.21	0.67
1:B:246:LYS:NZ	5:B:507:HOH:O	2.21	0.67
1:A:201:GLU:OE2	5:A:503:HOH:O	2.13	0.67
1:A:297:ARG:NH1	5:A:509:HOH:O	2.23	0.67
1:B:80:ASP:OD2	5:B:501:HOH:O	2.13	0.67
1:B:270:GLU:O	5:B:502:HOH:O	2.13	0.67
1:B:129:GLU:OE2	1:B:141:HIS:ND1	2.29	0.66
1:A:120:SER:N	1:A:130:ASP:OD2	2.31	0.64
1:A:129:GLU:OE1	1:A:207:LYS:HE3	1.97	0.64
1:A:157:LYS:NZ	5:A:516:HOH:O	2.32	0.61
1:B:312:ARG:CZ	5:B:504:HOH:O	2.45	0.61
1:A:228:MET:HE1	5:A:780:HOH:O	2.00	0.61
1:A:185:PHE:CZ	1:B:308:HIS:HB2	2.36	0.60
1:B:246:LYS:HG2	1:B:256:VAL:HG12	1.83	0.60
1:A:170:ASP:HB2	1:A:182:LEU:HD11	1.84	0.59
1:B:168:LEU:HD21	1:B:319:ILE:HD11	1.86	0.58
1:A:19:ILE:HD13	1:A:330:THR:HB	1.87	0.57
1:B:47:ARG:NH2	5:B:523:HOH:O	2.37	0.57
1:A:185:PHE:CE2	1:B:308:HIS:HB2	2.40	0.57
1:B:282:ALA:N	5:B:522:HOH:O	2.37	0.57
1:B:149:ASP:CG	5:B:512:HOH:O	2.44	0.56
1:A:312:ARG:NH1	5:B:504:HOH:O	2.39	0.55
1:B:39:SER:N	5:B:527:HOH:O	2.39	0.55
1:A:129:GLU:OE1	1:A:207:LYS:CE	2.55	0.55
1:A:141:HIS:ND1	1:A:207:LYS:HD2	2.22	0.55
1:B:19:ILE:HD11	1:B:327:ARG:HH12	1.72	0.54
1:A:327:ARG:O	1:A:327:ARG:HG3	2.09	0.53
1:A:127:TRP:HZ2	5:A:709:HOH:O	1.91	0.53
1:A:308:HIS:HB2	1:B:185:PHE:CZ	2.44	0.53
1:A:270:GLU:O	5:A:504:HOH:O	2.19	0.52

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Continued from prev	l average and a second se	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:B:116:GLU:OE2	5:B:506:HOH:O	2.19	0.51	
1:B:230:ALA:O	5:B:505:HOH:O	2.18	0.50	
1:B:18:ASN:HB3	1:B:329:ARG:HA	1.92	0.50	
1:B:144:PHE:CB	1:B:207[A]:LYS:HD2	2.42	0.50	
1:A:194:VAL:HG21	1:A:319:ILE:HD13	1.96	0.48	
1:A:39:SER:OG	5:A:505:HOH:O	2.20	0.48	
1:B:39:SER:N	5:B:535:HOH:O	2.47	0.48	
1:A:167:GLU:HG2	5:A:531:HOH:O	2.14	0.47	
1:A:286:GLY:O	1:A:290:GLN:HG2	2.14	0.47	
1:B:184:MET:SD	1:B:315:LYS:HD3	2.54	0.47	
1:A:326:GLY:N	5:A:507:HOH:O	2.47	0.47	
1:A:17:LYS:HB3	1:A:19:ILE:H	1.81	0.46	
1:A:98:ASN:O	1:A:328:THR:HG21	2.15	0.46	
1:A:328:THR:OG1	5:A:506:HOH:O	2.21	0.46	
1:B:92:GLU:HG2	1:B:97:TYR:HB2	1.98	0.46	
1:B:154:PHE:HA	1:B:244:HIS:O	2.16	0.46	
1:B:141:HIS:ND1	1:B:207[B]:LYS:HD2	2.30	0.45	
1:B:40:ILE:HD12	1:B:343:LEU:HD13	1.99	0.45	
1:A:237:SER:HB3	1:A:265:ASP:HB3	1.98	0.45	
1:B:68:PHE:HA	1:B:359:ILE:HD12	1.98	0.45	
1:B:244:HIS:HB2	5:B:631:HOH:O	2.17	0.45	
1:B:89:ILE:HG12	1:B:329:ARG:HB3	2.01	0.43	
1:B:144:PHE:HB3	1:B:207[A]:LYS:HD2	2.01	0.43	
1:A:246:LYS:HG2	1:A:256:VAL:HG22	2.01	0.42	
1:A:260:LYS:HE2	1:A:262:ASN:OD1	2.20	0.42	
1:B:63:ARG:NH1	5:B:513:HOH:O	2.28	0.42	
1:A:181:ARG:NH1	1:A:228:MET:HE3	2.35	0.41	
1:B:40:ILE:HD13	1:B:340:SER:HA	2.02	0.41	
1:B:162:GLU:HG3	1:B:235:SER:HB2	2.01	0.41	
1:A:283:ARG:H	1:A:286:GLY:H	1.67	0.41	
1:A:243:ILE:HG22	1:A:245:MET:HG3	2.02	0.41	
1:A:362:LYS:H	1:A:362:LYS:NZ	2.18	0.41	
1:A:80:ASP:OD2	5:A:508:HOH:O	2.22	0.40	
1:B:190:ASN:HA	5:B:690:HOH:O	2.21	0.40	
1:B:312:ARG:HD2	5:B:504:HOH:O	2.20	0.40	

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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)
5:A:812:HOH:O	5:B:783:HOH:O[1_556]	1.85	0.35
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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:829:HOH:O	5:B:794:HOH:O[1_455]	1.94	0.26

## 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	lysed Favoured Allowed		Outliers	Perce	$\mathbf{ntiles}$
1	А	334/367~(91%)	327~(98%)	5(2%)	2(1%)	25	10
1	В	312/367~(85%)	312~(100%)	0	0	100	100
All	All	646/734~(88%)	639~(99%)	5 (1%)	2~(0%)	41	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	325	GLY
1	А	283	ARG

#### 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	А	298/321~(93%)	287~(96%)	11 (4%)	34 12
1	В	286/321~(89%)	281 (98%)	5(2%)	60 42
All	All	584/642~(91%)	568~(97%)	16 (3%)	46 22

All (16) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	115	MET
1	А	120	SER
1	А	145	GLU
1	А	166	GLU
1	А	206	ASN
1	А	208	ASP
1	А	281	ARG
1	А	327	ARG
1	А	329	ARG
1	А	362	LYS
1	А	364	GLU
1	В	17	LYS
1	В	207[A]	LYS
1	В	207[B]	LYS
1	В	283	ARG
1	В	327	ARG

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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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



Mol Type Ch		Chain	Chain Res	Link	Bo	ond leng	ths	B	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NO3	В	403	-	$1,\!3,\!3$	0.63	0	0,3,3	0.00	-
3	ADP	А	402	2	24,29,29	0.91	1 (4%)	29,45,45	1.28	4 (13%)
3	ADP	В	402	2	24, 29, 29	0.96	1 (4%)	29,45,45	1.32	3(10%)

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).

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
3	ADP	А	402	2	-	2/12/32/32	0/3/3/3
3	ADP	В	402	2	-	2/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
3	В	402	ADP	C5-C4	2.44	1.47	1.40
3	А	402	ADP	C5-C4	2.26	1.46	1.40

Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
3	А	402	ADP	N3-C2-N1	-3.24	123.61	128.68
3	В	402	ADP	N3-C2-N1	-3.09	123.85	128.68
3	В	402	ADP	C4-C5-N7	-2.63	106.66	109.40
3	В	402	ADP	PA-O3A-PB	-2.57	123.99	132.83
3	А	402	ADP	C4-C5-N7	-2.55	106.74	109.40
3	А	402	ADP	PA-O3A-PB	-2.12	125.55	132.83
3	А	402	ADP	O3B-PB-O2B	2.01	115.31	107.64

All (7) bond angle outliers are listed below:

There are no chirality outliers.

All (4) torsion outliers are listed below:

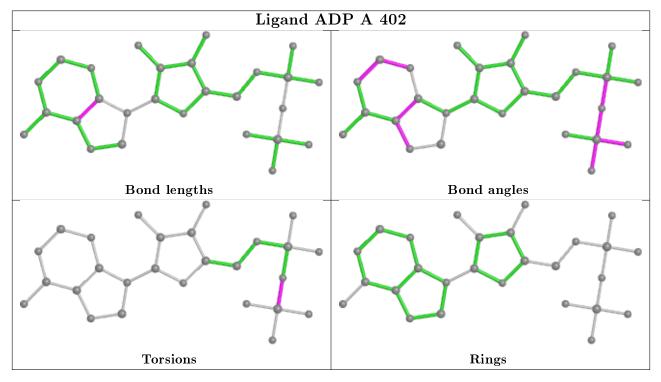
Mol	Chain	Res	Type	Atoms
3	А	402	ADP	PA-O3A-PB-O2B
3	А	402	ADP	PA-O3A-PB-O3B
3	В	402	ADP	PA-O3A-PB-O1B
3	В	402	ADP	PA-O3A-PB-O3B



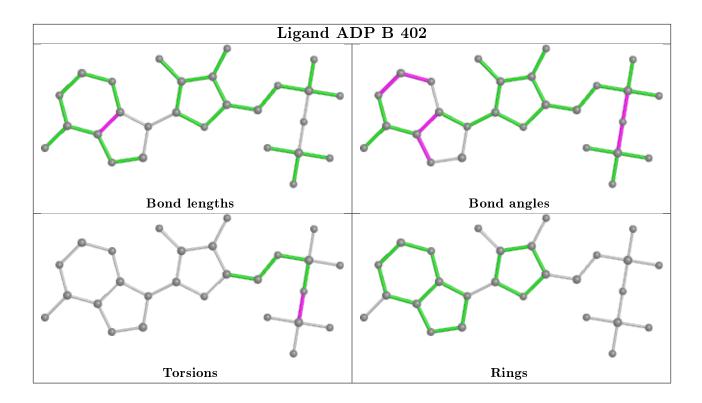
There are no ring outliers.

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.







## 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 $>$	RZ> #RSRZ>2		$\mathbf{OWAB}(\mathrm{\AA}^2)$	$\mathbf{Q}{<}0.9$
1	А	338/367~(92%)	0.18	17 (5%) 28	34	12, 24, 49, 73	0
1	В	320/367~(87%)	0.12	10 (3%) 49	55	13, 26, 46, 68	0
All	All	658/734~(89%)	0.15	27 (4%) 37	44	12, 25, 47, 73	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	120	SER	7.2
1	А	121	PRO	5.4
1	А	283	ARG	5.0
1	А	364	GLU	4.8
1	А	35	ALA	3.4
1	А	36	SER	3.3
1	А	325	GLY	3.3
1	В	282	ALA	2.9
1	А	122	ASN	2.9
1	В	325	GLY	2.8
1	В	189	ARG	2.8
1	В	119	ARG	2.6
1	А	34	LYS	2.6
1	В	327	ARG	2.5
1	В	207[A]	LYS	2.5
1	А	119	ARG	2.5
1	А	57	LEU	2.4
1	В	364	GLU	2.4
1	А	284	GLU	2.3
1	А	327	ARG	2.3
1	А	123	GLU	2.3
1	В	63	ARG	2.2
1	В	148	THR	2.2
1	А	363	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	А	185	PHE	2.1
1	В	283	ARG	2.0
1	А	30	LEU	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.

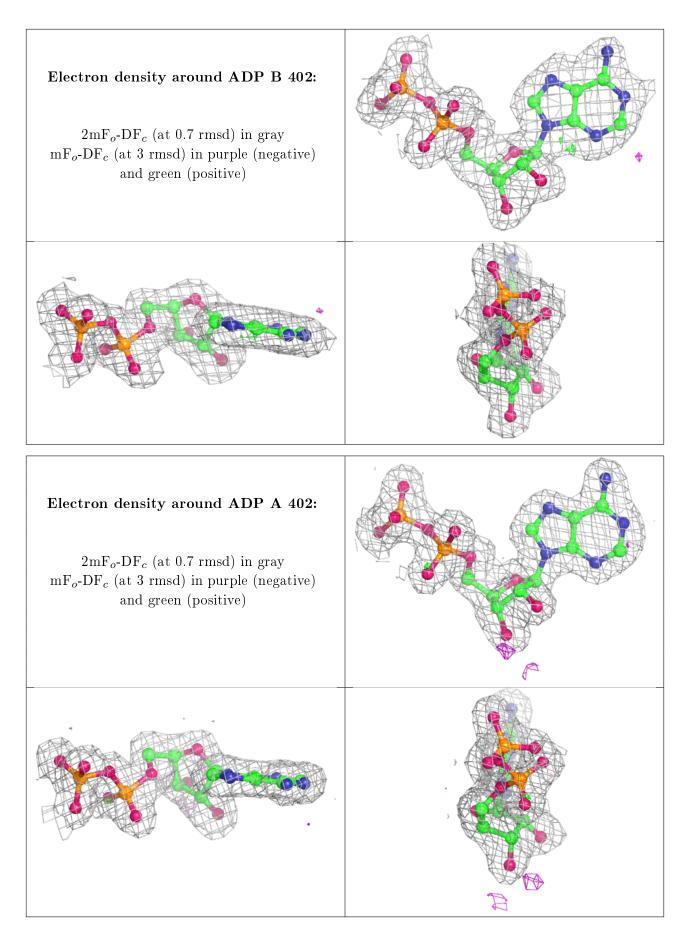
## 6.4 Ligands (i)

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	${f B} ext{-factors}({ m \AA}^2)$	Q<0.9
4	NO3	В	403	4/4	0.94	0.16	$39,\!39,\!40,\!41$	0
3	ADP	В	402	27/27	0.97	0.08	17,23,30,35	0
3	ADP	А	402	27/27	0.97	0.08	$14,\!17,\!28,\!39$	0
2	MG	В	401	1/1	0.99	0.04	20,20,20,20	0
2	MG	А	401	1/1	0.99	0.08	17,17,17,17	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.

