

Full wwPDB X-ray Structure Validation Report (i)

Apr 21, 2024 - 05:47 am BST

PDB ID	:	4ANB
Title	:	Crystal structures of human MEK1 with carboxamide-based allosteric inhibitor
		XL518 (GDC-0973), or related analogs.
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		Kennedy, A.R.; Kim, A.I.; Koltun, E.S.; Lougheed, J.C.; Manalo, J.C.L.;
		Martini, J.F.; Nuss, J.M.; Peto, C.J.; Tsang, T.H.; Yu, P.; Johnston, S.
Deposited on	:	2012-03-16
Resolution	:	2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

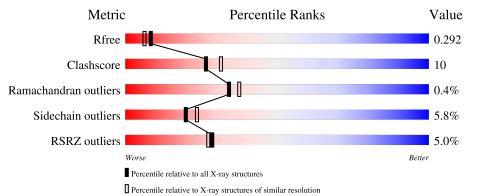
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	٨	201	5%		
1	A	301	72%	19%	• 6%

Ideal geometry (DNA, RNA) : Parkinson et al. (1996) Validation Pipeline (wwPDB-VP) : 2.36.2

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2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2324 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 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1.

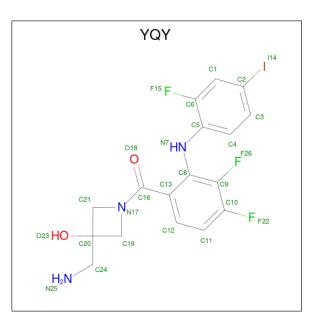
Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	282	Total 2209	C 1412	N 376	0 405	S 16	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	58	MET	-	expression tag	UNP Q02750
А	59	ALA	-	expression tag	UNP Q02750
А	60	LEU	-	expression tag	UNP Q02750
А	393	GLU	-	expression tag	UNP Q02750
А	394	GLY	-	expression tag	UNP Q02750
А	395	HIS	-	expression tag	UNP Q02750
А	396	HIS	-	expression tag	UNP Q02750
А	397	HIS	-	expression tag	UNP Q02750
А	398	HIS	-	expression tag	UNP Q02750
А	399	HIS	-	expression tag	UNP Q02750
А	400	HIS	-	expression tag	UNP Q02750
А	218	GLU	SER	engineered mutation	UNP Q02750
А	222	GLU	SER	engineered mutation	UNP Q02750
А	328	ALA	GLY	engineered mutation	UNP Q02750

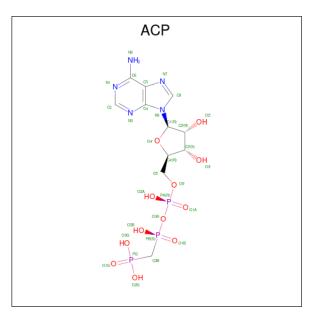
• Molecule 2 is [3-(AMINOMETHYL)-3-OXIDANYL-AZETIDIN-1-YL]-[3,4-BIS(FLUOR ANYL)-2-[(2-FLUORANYL-4-IODANYL-PHENYL)AMINO]PHENYL]METHANONE (three-letter code: YQY) (formula: C₁₇H₁₅F₃IN₃O₂).





Mol	Chain	Residues		Α	ton	ıs		ZeroOcc	AltConf
2	А	1	Total 26				N 3	0	0

• Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
3	А	1	Total	C	1		Р	0	0
			31	11	5	12	3		

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Mg 1 1	0	0

• Molecule 5 is water.

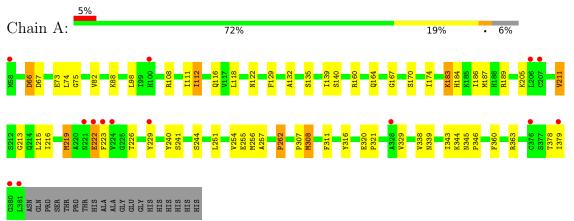
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	57	$\begin{array}{cc} \text{Total} & \text{O} \\ 57 & 57 \end{array}$	0	0



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: DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants	109.00Å 109.00Å 48.08Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	-
Resolution (Å)	94.49 - 2.20	Depositor
	35.68 - 2.20	EDS
% Data completeness	99.4 (94.49-2.20)	Depositor
(in resolution range)	99.5 (35.68 - 2.20)	EDS
R _{merge}	0.05	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.04 (at 2.20 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.226 , 0.296	Depositor
R, R_{free}	0.223 , 0.292	DCC
R_{free} test set	858 reflections (5.15%)	wwPDB-VP
Wilson B-factor $(Å^2)$	56.8	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 49.0	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.039 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2324	wwPDB-VP
Average B, all atoms $(Å^2)$	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: MG, ACP, YQY

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).

Mal	Chain	Bo	nd lengths	Bond angles		
Mol Chair		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.93	1/2254~(0.0%)	0.91	3/3038~(0.1%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	262	PRO	C-N	13.59	1.65	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	98	LEU	CA-CB-CG	6.85	131.04	115.30
1	А	256	MET	CG-SD-CE	6.40	110.44	100.20
1	А	262	PRO	O-C-N	-6.32	112.59	122.70

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	2209	0	2237	43	0
2	А	26	0	15	3	0
3	А	31	0	14	0	0
4	А	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	А	57	0	0	5	2
All	All	2324	0	2266	46	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 10.

All (46) 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:67:ASP:O	1:A:88:LYS:HE2	1.70	0.89
1:A:170:SER:O	1:A:174:ILE:HG12	1.79	0.81
1:A:311:PHE:CD2	5:A:612:HOH:O	2.35	0.80
1:A:183:LYS:HB3	1:A:184:HIS:CD2	2.23	0.72
1:A:229:TYR:OH	1:A:255:GLU:OE1	2.09	0.70
1:A:316:TYR:CE1	1:A:320:GLU:HG3	2.29	0.67
1:A:183:LYS:HD3	1:A:184:HIS:NE2	2.12	0.64
1:A:108:ARG:O	1:A:112:ILE:HG13	1.97	0.64
1:A:186:ILE:HD13	1:A:211:VAL:HG13	1.81	0.62
1:A:215:LEU:O	1:A:219:MET:HB2	2.01	0.61
1:A:378:THR:HG22	1:A:379:ILE:HG23	1.84	0.60
1:A:320:GLU:O	1:A:344:LYS:NZ	2.28	0.60
1:A:187:MET:HE3	1:A:240:TYR:CD1	2.37	0.58
1:A:160:ARG:HG2	1:A:257:ALA:O	2.03	0.57
1:A:187:MET:CE	1:A:240:TYR:HD1	2.18	0.57
1:A:339:ASN:O	1:A:343:ILE:HD13	2.05	0.57
1:A:187:MET:HE3	1:A:240:TYR:HD1	1.72	0.55
1:A:363:ARG:NH2	5:A:602:HOH:O	2.30	0.54
1:A:189:ARG:HA	1:A:240:TYR:CZ	2.44	0.52
1:A:111:ILE:HG21	1:A:139:ILE:HD13	1.91	0.52
1:A:307:PRO:O	1:A:308:MET:HB3	2.09	0.52
1:A:255:GLU:HB2	1:A:262:PRO:HD3	1.93	0.51
1:A:187:MET:HE1	1:A:240:TYR:HB3	1.93	0.50
1:A:343:ILE:HG22	1:A:345:ASN:H	1.76	0.50
1:A:254:VAL:HG12	1:A:262:PRO:HB3	1.94	0.49
2:A:501:YQY:H211	2:A:501:YQY:H12	1.95	0.49
1:A:73:GLU:HG2	1:A:75:GLY:H	1.78	0.49
2:A:501:YQY:H12	2:A:501:YQY:C21	2.42	0.48
1:A:222:GLU:HG2	1:A:223:PHE:CZ	2.49	0.48
1:A:241:SER:HB2	5:A:646:HOH:O	2.13	0.47
1:A:205:LYS:NZ	5:A:605:HOH:O	2.38	0.46
1:A:213:GLY:HA2	1:A:216:ILE:HD12	1.96	0.46

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Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:A:112:ILE:HG22	1:A:116:GLN:NE2	2.32	0.44
1:A:118:LEU:HB2	1:A:129:PHE:CD2	2.52	0.43
1:A:66:ASP:O	1:A:88:LYS:NZ	2.23	0.43
1:A:67:ASP:C	1:A:88:LYS:HE2	2.37	0.43
1:A:132:ALA:HA	1:A:140:SER:O	2.19	0.43
1:A:343:ILE:HD13	1:A:343:ILE:N	2.34	0.43
1:A:229:TYR:CD1	1:A:251:LEU:HD23	2.54	0.42
2:A:501:YQY:C21	2:A:501:YQY:C12	2.97	0.42
1:A:74:LEU:HD12	1:A:82:VAL:HG12	2.01	0.42
1:A:320:GLU:HB3	1:A:321:PRO:CD	2.50	0.41
1:A:88:LYS:HE3	1:A:88:LYS:HB2	1.86	0.41
1:A:167:GLY:HA2	1:A:360:PHE:CE2	2.56	0.41
1:A:187:MET:CE	1:A:240:TYR:CD1	2.99	0.40
1:A:186:ILE:HA	5:A:611: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:655:HOH:O	5:A:657:HOH:O[5_554]	2.11	0.09
5:A:633:HOH:O	5:A:657:HOH:O[5_554]	2.16	0.04

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	А	280/301~(93%)	266~(95%)	13~(5%)	1 (0%)	34 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	308	MET



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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	243/258~(94%)	229~(94%)	14 (6%)	20 23

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	66	ASP
1	А	112	ILE
1	А	122	ASN
1	А	135	SER
1	А	164	GLN
1	А	183	LYS
1	А	211	VAL
1	А	219	MET
1	А	222	GLU
1	А	226	THR
1	А	244	SER
1	А	329	VAL
1	А	338	VAL
1	А	346	PRO

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

Mol	Chain	Res	Type
1	А	122	ASN
1	А	164	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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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).

Mal	Type Chain		Chain Res	Link	Bond lengths			Bond angles		
	Type	Unann	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	ACP	А	502	4	27,33,33	1.48	4 (14%)	32,52,52	1.62	6 (18%)
2	YQY	А	501	-	26,28,28	1.48	4 (15%)	29,42,42	2.00	9 (31%)

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	ACP	А	502	4	-	1/15/38/38	0/3/3/3
2	YQY	А	501	-	-	0/12/25/25	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
3	А	502	ACP	PB-O3A	4.48	1.63	1.58
2	А	501	YQY	C24-C20	-4.17	1.52	1.56
2	А	501	YQY	C2-I14	2.80	2.17	2.10
3	А	502	ACP	C2-N3	2.56	1.36	1.32
2	А	501	YQY	C3-C4	2.41	1.43	1.38
2	А	501	YQY	F26-C9	-2.35	1.31	1.35
3	А	502	ACP	PG-O3G	-2.28	1.49	1.54
3	А	502	ACP	C6-C5	2.24	1.51	1.43

All (15) bond angle outliers are listed below:



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Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	501	YQY	C3-C2-I14	3.73	125.31	119.68
2	А	501	YQY	C4-C3-C2	3.68	124.39	119.56
3	А	502	ACP	O2B-PB-C3B	3.53	121.04	106.58
3	А	502	ACP	N3-C2-N1	-3.46	123.27	128.68
2	А	501	YQY	C3-C2-C1	-3.43	117.05	121.09
2	А	501	YQY	F22-C10-C9	-3.31	113.65	118.30
2	А	501	YQY	C4-C5-N7	3.03	127.64	121.39
2	А	501	YQY	C19-N17-C21	2.95	98.29	95.19
3	А	502	ACP	O1G-PG-C3B	-2.88	105.04	111.24
3	А	502	ACP	C4-C5-N7	-2.76	106.53	109.40
2	А	501	YQY	O18-C16-N17	-2.64	117.97	122.34
2	А	501	YQY	F22-C10-C11	2.63	124.46	118.59
2	А	501	YQY	C1-C6-C5	2.50	125.88	123.50
3	А	502	ACP	O3'-C3'-C2'	-2.38	104.11	111.82
3	А	502	ACP	O4'-C1'-C2'	-2.22	103.68	106.93

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	502	ACP	PB-C3B-PG-O1G

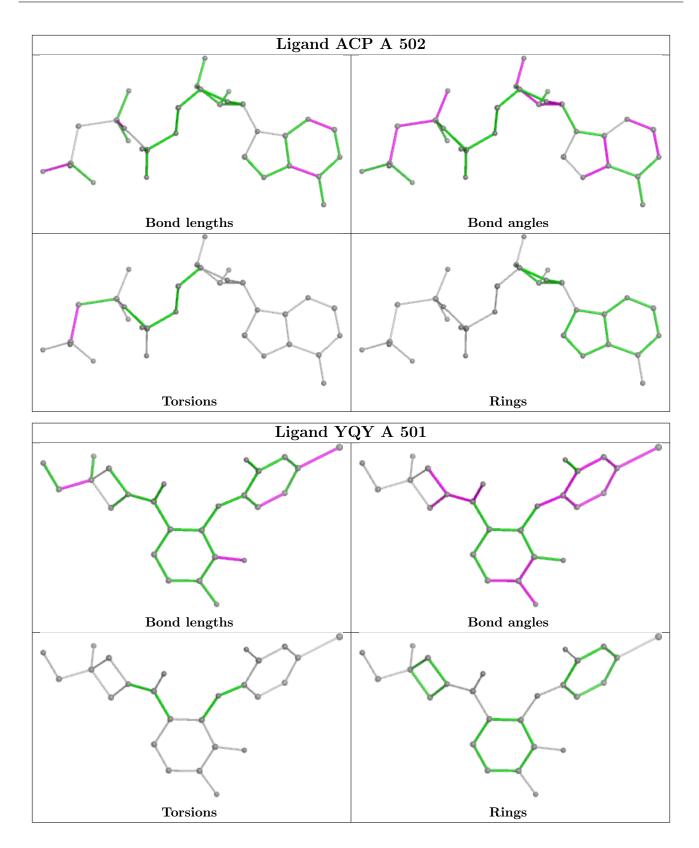
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	\mathbf{Res}	Type	Clashes	Symm-Clashes
2	А	501	YQY	3	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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	А	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	262:PRO	С	305:ARG	Ν	1.65



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 $>$	#RS	\mathbf{RZ} >	-2	$OWAB(Å^2)$	Q<0.9
1	А	282/301~(93%)	0.12	14 (4%)	28	27	40, 58, 80, 96	8 (2%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	224	VAL	4.6
1	А	379	ILE	4.3
1	А	381	LEU	4.2
1	А	380	GLY	4.0
1	А	221	ASN	3.5
1	А	223	PHE	2.5
1	А	222	GLU	2.5
1	А	206	LEU	2.3
1	А	207	CYS	2.3
1	А	376	CYS	2.2
1	А	328	ALA	2.1
1	А	100	HIS	2.1
1	А	229	TYR	2.1
1	А	58	MET	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.

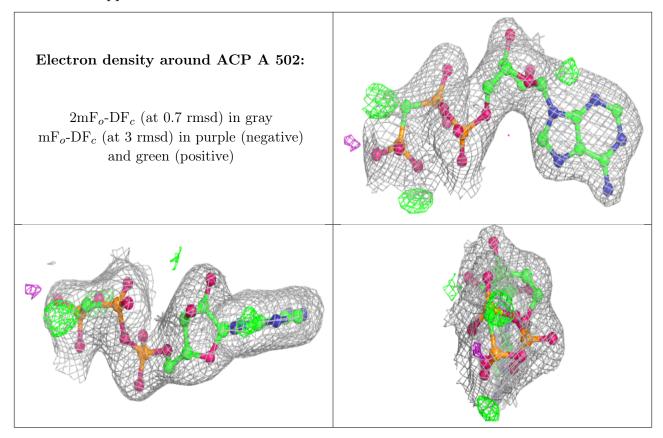


6.4 Ligands (i)

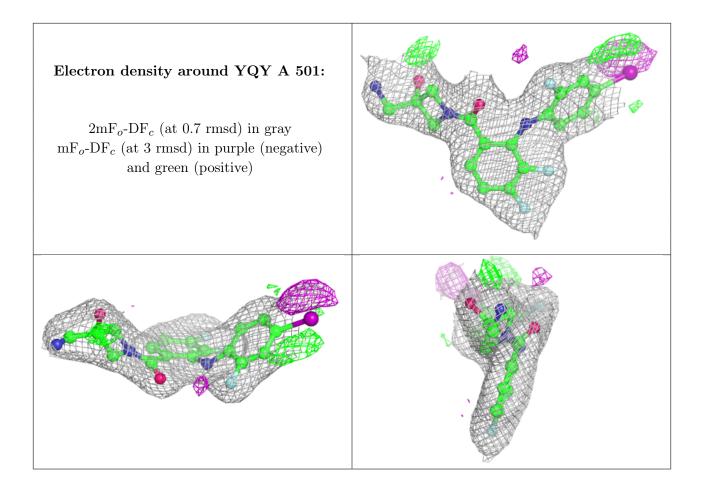
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
4	MG	А	503	1/1	0.69	0.15	58, 58, 58, 58	0
3	ACP	А	502	31/31	0.97	0.13	45,52,62,63	0
2	YQY	А	501	26/26	0.99	0.15	40,45,51,55	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.

