



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 12:38 pm BST

PDB ID : 3BRB  
Title : Crystal structure of catalytic domain of the proto-oncogene tyrosine-protein kinase MER in complex with ADP  
Authors : Walker, J.R.; Huang, X.; Finerty Jr, P.J.; Weigelt, J.; Arrowsmith, C.H.; Edwards, A.M.; Bochkarev, A.; Dhe-Paganon, S.; Structural Genomics Consortium (SGC)  
Deposited on : 2007-12-21  
Resolution : 1.90 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](mailto: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.

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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 : 2.11  
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) : 2.11

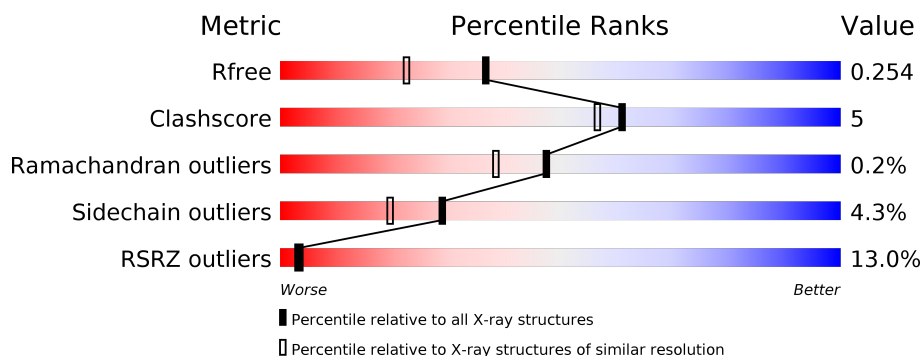
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . 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	313	<div> <div>11%</div> <div> <div></div> <div>72%</div> <div>10%</div> <div>•</div> <div>17%</div> </div> </div>
1	B	313	<div> <div>11%</div> <div> <div></div> <div>77%</div> <div>9%</div> <div>•</div> <div>13%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4502 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 Proto-oncogene tyrosine-protein kinase MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	4	0
			2069	1322	350	377	20			
1	B	271	Total	C	N	O	S	0	4	0
			2130	1359	358	392	21			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	552	MET	-	EXPRESSION TAG	UNP Q12866
A	553	GLY	-	EXPRESSION TAG	UNP Q12866
A	554	SER	-	EXPRESSION TAG	UNP Q12866
A	555	SER	-	EXPRESSION TAG	UNP Q12866
A	556	HIS	-	EXPRESSION TAG	UNP Q12866
A	557	HIS	-	EXPRESSION TAG	UNP Q12866
A	558	HIS	-	EXPRESSION TAG	UNP Q12866
A	559	HIS	-	EXPRESSION TAG	UNP Q12866
A	560	HIS	-	EXPRESSION TAG	UNP Q12866
A	561	HIS	-	EXPRESSION TAG	UNP Q12866
A	562	SER	-	EXPRESSION TAG	UNP Q12866
A	563	SER	-	EXPRESSION TAG	UNP Q12866
A	564	GLY	-	EXPRESSION TAG	UNP Q12866
A	565	LEU	-	EXPRESSION TAG	UNP Q12866
A	566	VAL	-	EXPRESSION TAG	UNP Q12866
A	567	PRO	-	EXPRESSION TAG	UNP Q12866
A	568	ARG	-	EXPRESSION TAG	UNP Q12866
A	569	GLY	-	EXPRESSION TAG	UNP Q12866
B	552	MET	-	EXPRESSION TAG	UNP Q12866
B	553	GLY	-	EXPRESSION TAG	UNP Q12866
B	554	SER	-	EXPRESSION TAG	UNP Q12866
B	555	SER	-	EXPRESSION TAG	UNP Q12866
B	556	HIS	-	EXPRESSION TAG	UNP Q12866
B	557	HIS	-	EXPRESSION TAG	UNP Q12866
B	558	HIS	-	EXPRESSION TAG	UNP Q12866

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Chain	Residue	Modelled	Actual	Comment	Reference
B	559	HIS	-	EXPRESSION TAG	UNP Q12866
B	560	HIS	-	EXPRESSION TAG	UNP Q12866
B	561	HIS	-	EXPRESSION TAG	UNP Q12866
B	562	SER	-	EXPRESSION TAG	UNP Q12866
B	563	SER	-	EXPRESSION TAG	UNP Q12866
B	564	GLY	-	EXPRESSION TAG	UNP Q12866
B	565	LEU	-	EXPRESSION TAG	UNP Q12866
B	566	VAL	-	EXPRESSION TAG	UNP Q12866
B	567	PRO	-	EXPRESSION TAG	UNP Q12866
B	568	ARG	-	EXPRESSION TAG	UNP Q12866
B	569	GLY	-	EXPRESSION TAG	UNP Q12866

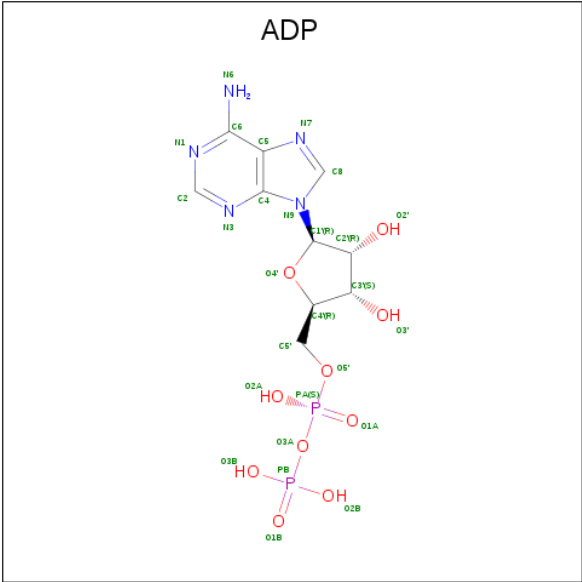
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Cl 3 3	0	0
2	A	2	Total Cl 2 2	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

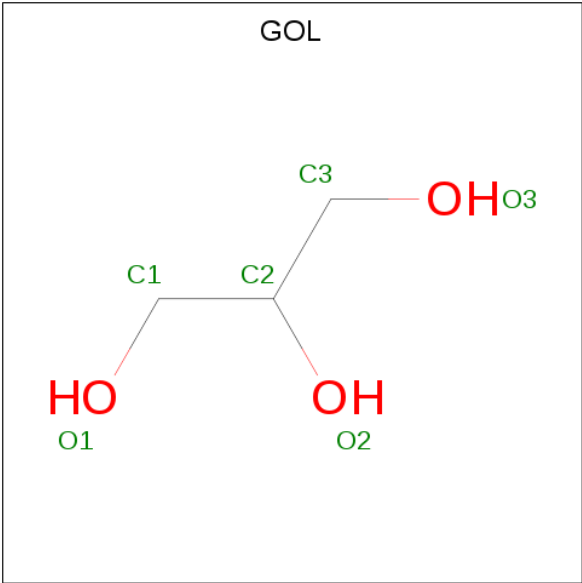
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

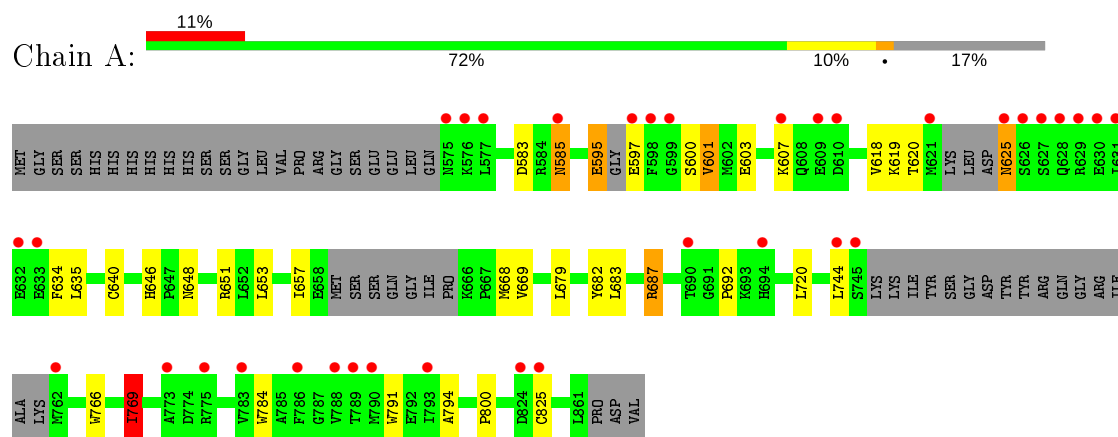
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	112	Total 114	O 114	0	2
6	B	120	Total 122	O 122	0	4

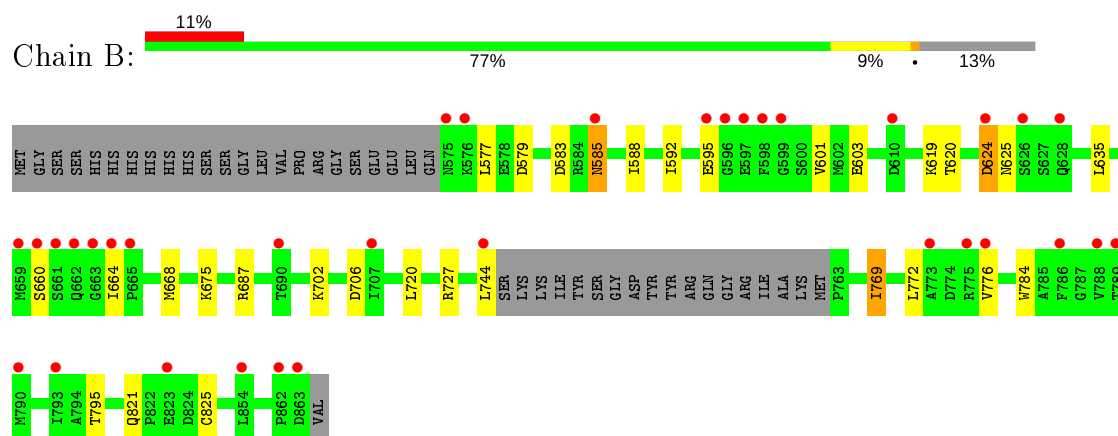
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Proto-oncogene tyrosine-protein kinase MER



- Molecule 1: Proto-oncogene tyrosine-protein kinase MER



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.38Å 89.88Å 69.54Å 90.00° 103.09° 90.00°	Depositor
Resolution (Å)	25.05 – 1.90 24.98 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.3 (25.05-1.90) 98.3 (24.98-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.192 , 0.240 0.201 , 0.254	Depositor DCC
$R_{free}$ test set	2487 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.0	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 60.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4502	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: GOL, MG, ADP, CL

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	0.65	1/2108 (0.0%)	0.72	3/2851 (0.1%)
1	B	0.62	0/2174	0.70	0/2947
All	All	0.63	1/4282 (0.0%)	0.71	3/5798 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	766	TRP	CB-CG	5.23	1.59	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	687[A]	ARG	NE-CZ-NH1	-5.33	117.64	120.30
1	A	687[B]	ARG	NE-CZ-NH1	-5.33	117.64	120.30
1	A	769	ILE	CB-CA-C	-5.08	101.44	111.60

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	2069	0	2021	23	0
1	B	2130	0	2069	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
2	B	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	27	0	12	0	0
4	B	27	0	12	0	0
5	A	6	0	8	0	0
6	A	114	0	0	1	0
6	B	122	0	0	3	0
All	All	4502	0	4122	38	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 5.

All (38) 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:646:HIS:HD2	1:A:648:ASN:H	1.25	0.81
1:A:620:THR:HG22	1:A:668:MET:HG2	1.69	0.74
1:A:646:HIS:CD2	1:A:648:ASN:H	2.09	0.69
1:B:660:SER:HB3	1:B:664:ILE:H	1.58	0.68
1:B:620:THR:HG22	1:B:668:MET:HG2	1.78	0.64
1:B:727[A]:ARG:HG2	6:B:224:HOH:O	1.98	0.62
1:B:577:LEU:O	1:B:635:LEU:HD13	1.99	0.62
1:A:687[A]:ARG:HH12	1:B:687[A]:ARG:NH2	2.00	0.58
1:B:583:ASP:OD2	1:B:585:ASN:ND2	2.37	0.56
1:B:601:VAL:HG22	1:B:619:LYS:HG2	1.90	0.54
1:B:588:ILE:HG12	6:B:85:HOH:O	2.08	0.54
1:A:634:PHE:CE1	1:A:744:LEU:HD22	2.43	0.53
1:B:702:LYS:NZ	1:B:706:ASP:OD1	2.42	0.53
1:A:646:HIS:HE1	6:A:142:HOH:O	1.91	0.52
1:A:595:GLU:O	1:A:597:GLU:N	2.43	0.52
1:A:687[A]:ARG:HH12	1:B:687[A]:ARG:CZ	2.24	0.49
1:A:769:ILE:HG13	1:A:784:TRP:CZ3	2.49	0.48
1:A:651[A]:ARG:HE	1:A:653:LEU:HD21	1.80	0.46
1:B:675:LYS:NZ	6:B:126:HOH:O	2.48	0.45
1:A:687[A]:ARG:NH1	1:B:687[A]:ARG:CZ	2.79	0.45
1:A:585:ASN:C	1:A:585:ASN:HD22	2.20	0.45
1:A:635:LEU:HD21	1:A:657:ILE:HD11	1.99	0.44
1:A:625:ASN:C	1:A:625:ASN:HD22	2.21	0.44
1:B:592:ILE:HG21	1:B:595:GLU:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:791:TRP:CZ3	1:A:800:PRO:HA	2.52	0.43
1:B:821:GLN:NE2	1:B:825[B]:CYS:O	2.46	0.43
1:B:769:ILE:HG13	1:B:784:TRP:CZ3	2.54	0.43
1:A:601:VAL:HB	1:A:619:LYS:HG2	2.00	0.43
1:A:769:ILE:HG13	1:A:784:TRP:CH2	2.54	0.42
1:A:601:VAL:HA	1:A:618:VAL:O	2.19	0.42
1:A:679:LEU:O	1:A:683:LEU:HG	2.20	0.42
1:B:624:ASP:OD1	1:B:625:ASN:ND2	2.53	0.41
1:A:794:ALA:HB1	1:A:825[A]:CYS:SG	2.59	0.41
1:A:682:TYR:CE2	1:A:692:PRO:HG3	2.56	0.41
1:A:687[B]:ARG:NH1	1:B:795:THR:O	2.54	0.40
1:B:585:ASN:HD22	1:B:585:ASN:C	2.25	0.40
1:A:583:ASP:OD2	1:A:585:ASN:ND2	2.53	0.40
1:B:702:LYS:HD2	1:B:702:LYS:HA	1.93	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	254/313 (81%)	247 (97%)	7 (3%)	0	100	100
1	B	271/313 (87%)	263 (97%)	7 (3%)	1 (0%)	34	24
All	All	525/626 (84%)	510 (97%)	14 (3%)	1 (0%)	47	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	776	VAL

### 5.3.2 Protein sidechains ⓘ

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	221/280 (79%)	210 (95%)	11 (5%)	24	15
1	B	227/280 (81%)	219 (96%)	8 (4%)	36	27
All	All	448/560 (80%)	429 (96%)	19 (4%)	29	20

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	585	ASN
1	A	595	GLU
1	A	600	SER
1	A	601	VAL
1	A	603	GLU
1	A	607	LYS
1	A	625	ASN
1	A	640	CYS
1	A	669	VAL
1	A	720	LEU
1	A	769	ILE
1	B	579	ASP
1	B	585	ASN
1	B	603	GLU
1	B	624	ASP
1	B	720	LEU
1	B	744	LEU
1	B	769	ILE
1	B	772	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	585	ASN
1	A	625	ASN
1	A	646	HIS

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Mol	Chain	Res	Type
1	B	585	ASN
1	B	694	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 7 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 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	$\# Z  > 2$
4	ADP	A	901	3	24,29,29	1.07	3 (12%)	29,45,45	1.37	2 (6%)
4	ADP	B	901	3	24,29,29	1.15	3 (12%)	29,45,45	1.41	5 (17%)
5	GOL	A	3	-	5,5,5	0.38	0	5,5,5	0.48	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	901	3	-	3/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	B	901	3	-	0/12/32/32	0/3/3/3
5	GOL	A	3	-	-	4/4/4/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	901	ADP	C5-C4	2.54	1.47	1.40
4	A	901	ADP	C2-N3	2.53	1.36	1.32
4	B	901	ADP	C4-N3	2.48	1.39	1.35
4	B	901	ADP	C2-N3	2.12	1.35	1.32
4	A	901	ADP	C5-C4	2.06	1.46	1.40
4	A	901	ADP	O4'-C1'	2.03	1.43	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	ADP	N3-C2-N1	-4.07	122.31	128.68
4	B	901	ADP	N3-C2-N1	-3.82	122.70	128.68
4	B	901	ADP	O4'-C1'-C2'	-2.53	103.22	106.93
4	B	901	ADP	C2-N1-C6	2.26	122.61	118.75
4	A	901	ADP	C2-N1-C6	2.22	122.56	118.75
4	B	901	ADP	N6-C6-N1	2.14	123.01	118.57
4	B	901	ADP	O2A-PA-O1A	2.03	122.25	112.24

There are no chirality outliers.

All (7) torsion outliers are listed below:

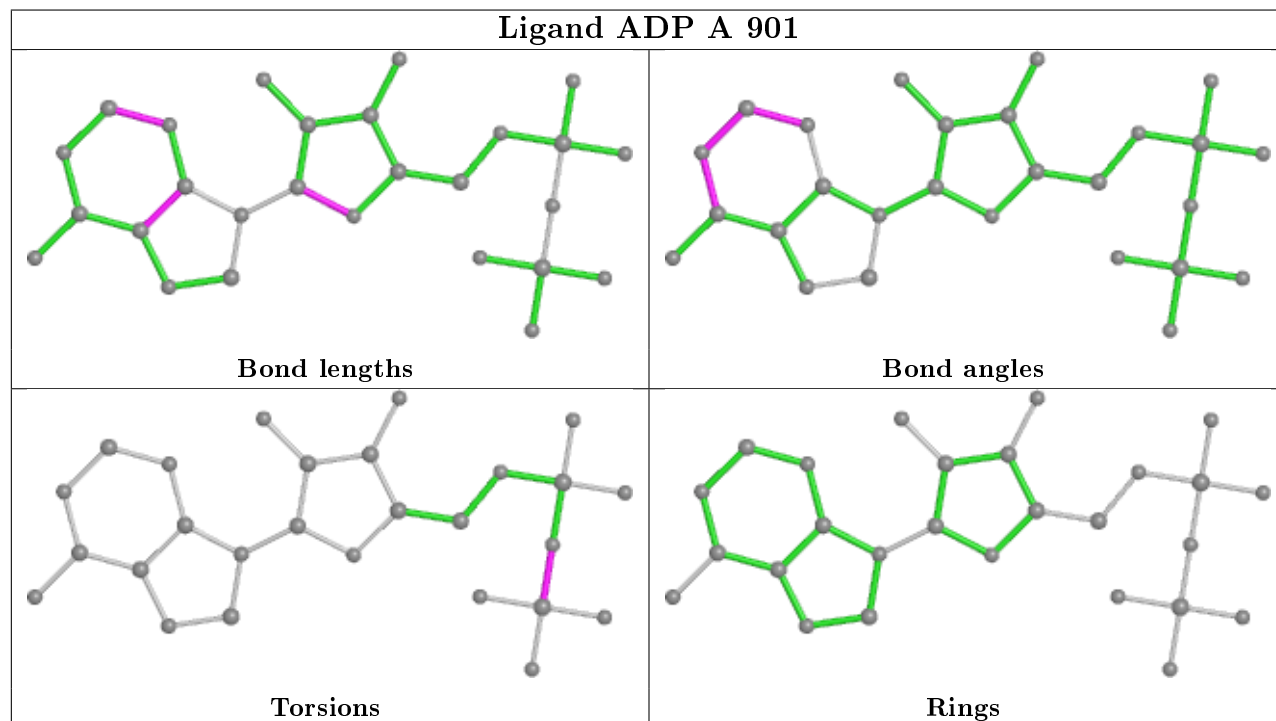
Mol	Chain	Res	Type	Atoms
4	A	901	ADP	PA-O3A-PB-O2B
5	A	3	GOL	O1-C1-C2-C3
5	A	3	GOL	C1-C2-C3-O3
5	A	3	GOL	O1-C1-C2-O2
5	A	3	GOL	O2-C2-C3-O3
4	A	901	ADP	PA-O3A-PB-O3B
4	A	901	ADP	PA-O3A-PB-O1B

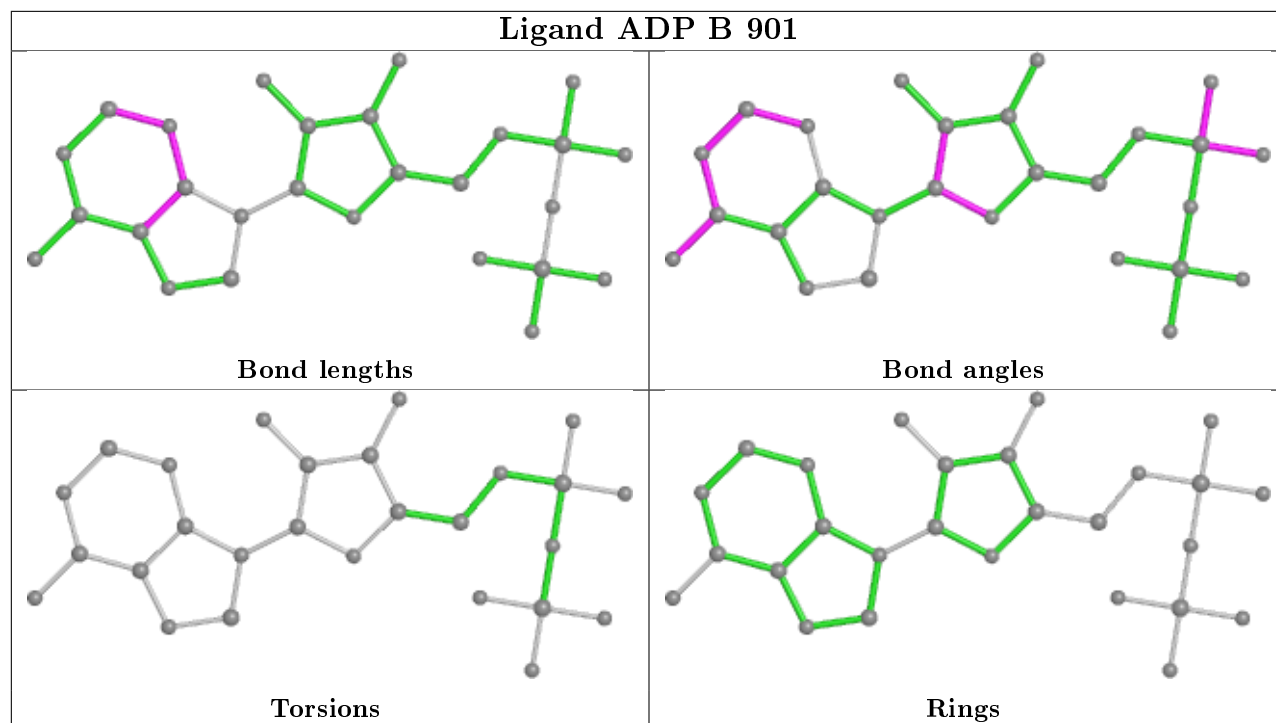
There are no ring outliers.

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 than 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 ⓘ

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	260/313 (83%)	0.66	35 (13%) 3 3	29, 45, 102, 160	0
1	B	271/313 (86%)	0.63	34 (12%) 3 4	30, 45, 85, 114	0
All	All	531/626 (84%)	0.64	69 (12%) 3 3	29, 45, 92, 160	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	598	PHE	9.1
1	A	631	ILE	8.3
1	A	629	ARG	6.4
1	A	598	PHE	6.3
1	B	661	SER	6.3
1	B	659	MET	6.0
1	A	745	SER	5.3
1	A	744	LEU	5.3
1	A	627	SER	5.2
1	A	626	SER	5.0
1	B	744	LEU	4.9
1	A	625	ASN	4.9
1	A	628	GLN	4.8
1	B	775	ARG	4.5
1	B	596	GLY	4.5
1	B	599	GLY	4.3
1	B	862	PRO	4.2
1	A	690	THR	4.2
1	B	786	PHE	4.1
1	B	597	GLU	4.0
1	B	628	GLN	3.9
1	B	863	ASP	3.7
1	A	630	GLU	3.7
1	B	575	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	597	GLU	3.5
1	B	690	THR	3.5
1	B	663	GLY	3.5
1	B	776	VAL	3.4
1	A	786	PHE	3.4
1	B	665	PRO	3.3
1	A	599	GLY	3.3
1	B	789	THR	3.3
1	A	585	ASN	3.3
1	B	576	LYS	3.3
1	B	788	VAL	3.0
1	A	633	GLU	3.0
1	A	575	ASN	3.0
1	A	610	ASP	3.0
1	A	789	THR	2.9
1	A	632	GLU	2.8
1	B	624	ASP	2.8
1	B	595	GLU	2.8
1	A	775	ARG	2.8
1	A	788	VAL	2.7
1	A	694	HIS	2.7
1	B	662	GLN	2.7
1	A	790	MET	2.7
1	B	790	MET	2.6
1	A	576	LYS	2.6
1	B	610	ASP	2.5
1	A	577	LEU	2.5
1	B	854	LEU	2.5
1	A	793	ILE	2.5
1	B	585	ASN	2.5
1	B	823	GLU	2.5
1	A	621	MET	2.4
1	A	609	GLU	2.4
1	A	607	LYS	2.4
1	B	793	ILE	2.4
1	B	660	SER	2.2
1	B	707	ILE	2.2
1	A	773	ALA	2.2
1	A	825[A]	CYS	2.2
1	A	824	ASP	2.2
1	B	773	ALA	2.2
1	B	626	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	762	MET	2.1
1	A	783	VAL	2.1
1	B	664	ILE	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

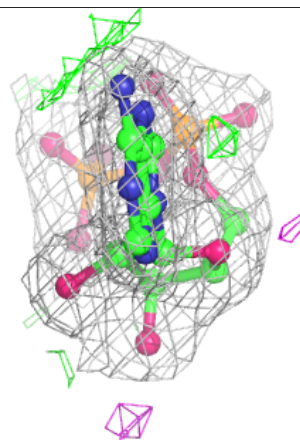
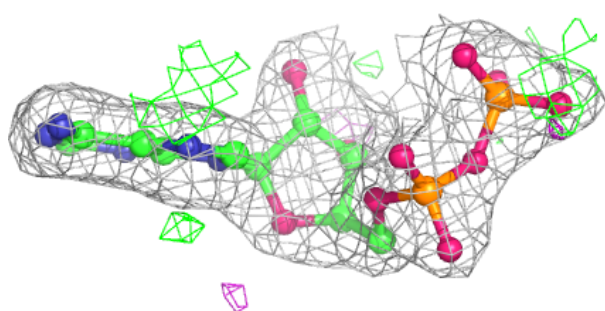
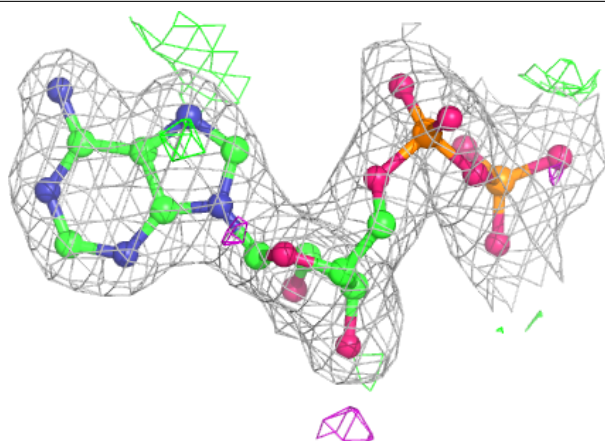
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

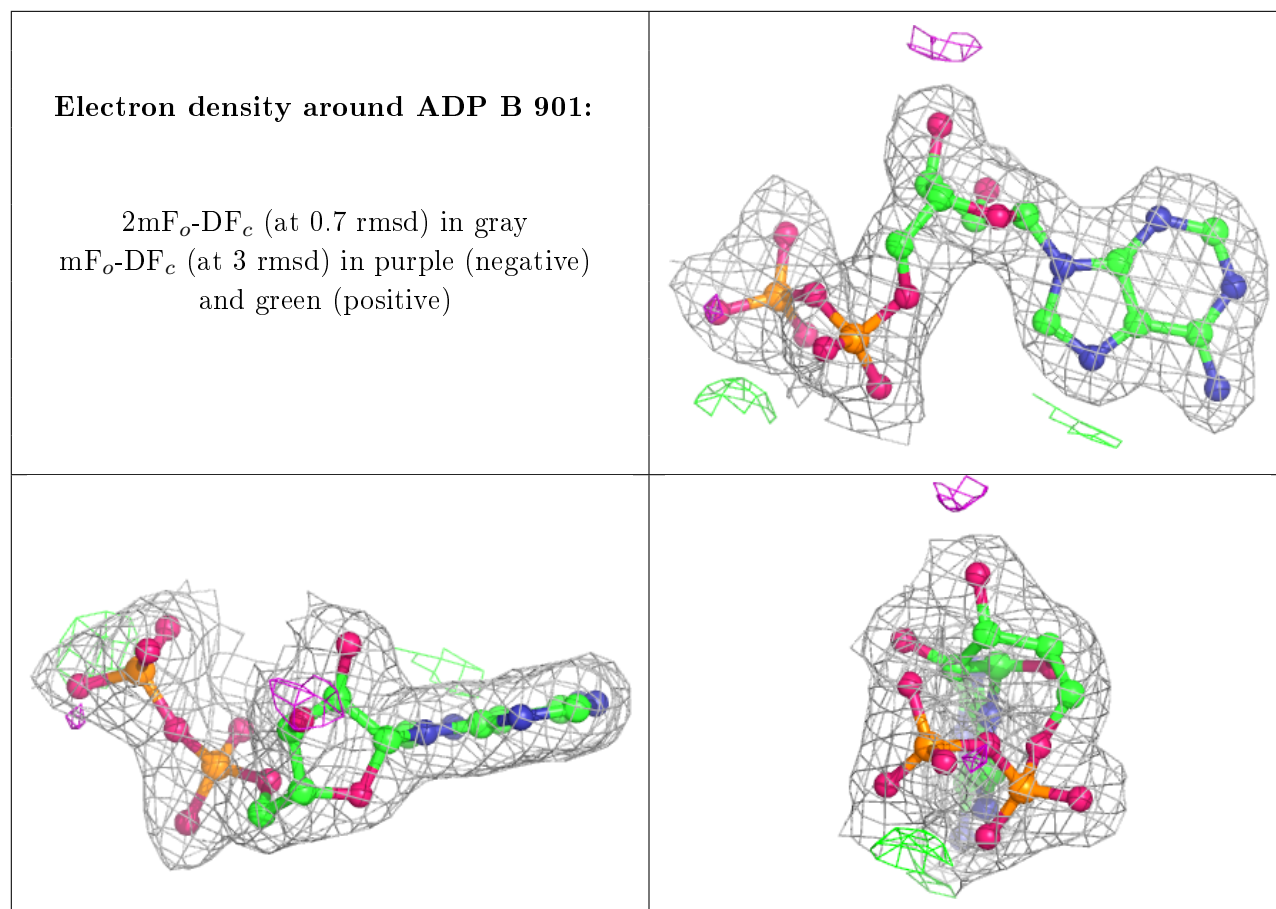
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	GOL	A	3	6/6	0.75	0.19	52,62,64,66	0
4	ADP	A	901	27/27	0.96	0.08	33,41,49,50	0
4	ADP	B	901	27/27	0.97	0.07	38,41,48,52	0
2	CL	B	8	1/1	0.98	0.06	48,48,48,48	0
2	CL	B	6	1/1	0.98	0.05	57,57,57,57	0
3	MG	B	9	1/1	0.98	0.02	41,41,41,41	0
3	MG	A	10	1/1	0.98	0.06	40,40,40,40	0
2	CL	B	7	1/1	0.99	0.14	38,38,38,38	0
2	CL	A	5	1/1	0.99	0.12	37,37,37,37	0
2	CL	A	4	1/1	0.99	0.09	42,42,42,42	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 ADP A 901:**

$2mF_o - DF_c$  (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.