



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:27 AM UTC

PDB ID : 1WB9 / pdb_00001wb9
Title : Crystal Structure of E. coli DNA Mismatch Repair enzyme MutS, E38T mutant, in complex with a G.T mismatch
Authors : Natrajan, G.; Georgijevic, D.; Lebbink, J.H.G.; Winterwerp, H.H.K.; de Wind, N.; Sixma, T.K.
Deposited on : 2004-10-31
Resolution : 2.10 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

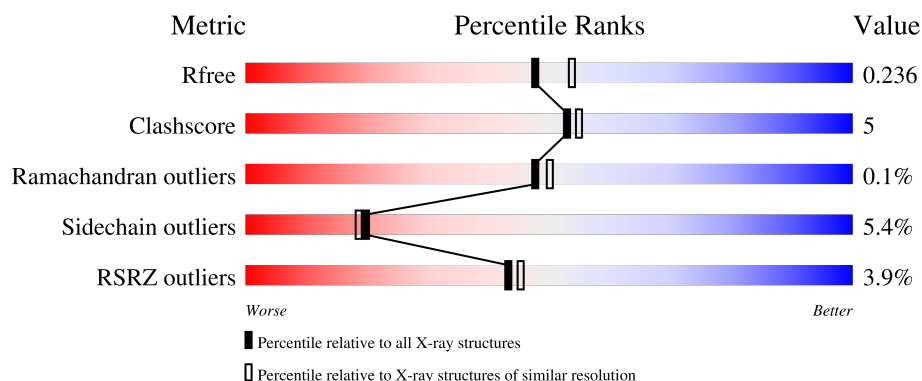
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 $\leq 5\%$. 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	800	3% 86% 10% • •
1	B	800	4% 80% 13% • 6%
2	E	18	6% 89% 6% 6%
3	F	17	6% 82% 18%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13862 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 DNA MISMATCH REPAIR PROTEIN MUTS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	788	Total	C	N	O	S	0	0	0
			6204	3904	1103	1168	29			
1	B	754	Total	C	N	O	S	0	0	0
			5961	3755	1060	1118	28			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	38	THR	GLU	engineered mutation	UNP P23909
B	38	THR	GLU	engineered mutation	UNP P23909

- Molecule 2 is a DNA chain called 5'-D(*AP*GP*CP*TP*GP*CP*CP*AP*GP*GP *CP*A P*CP*CP*AP*GP*TP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	18	Total	C	N	O	P	0	0	0
			367	174	72	104	17			

- Molecule 3 is a DNA chain called 5'-D(*AP*CP*TP*GP*GP*TP*GP*CP*TP*TP *GP*G P*CP*AP*GP*CP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	17	Total	C	N	O	P	0	0	0
			347	166	62	103	16			

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

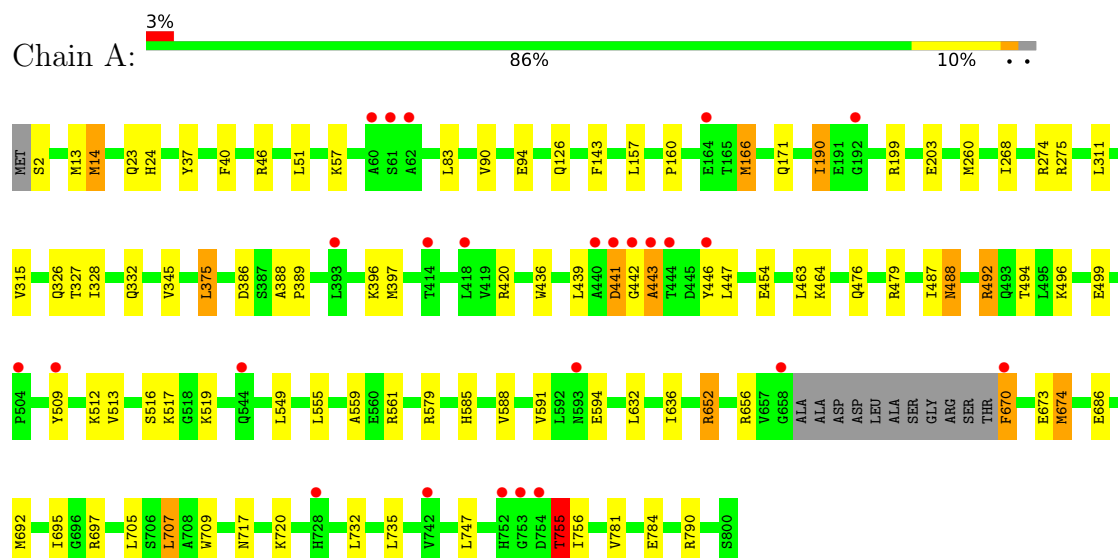
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	492	Total O 492 492	0	0
6	B	423	Total O 423 423	0	0
6	E	23	Total O 23 23	0	0
6	F	17	Total O 17 17	0	0

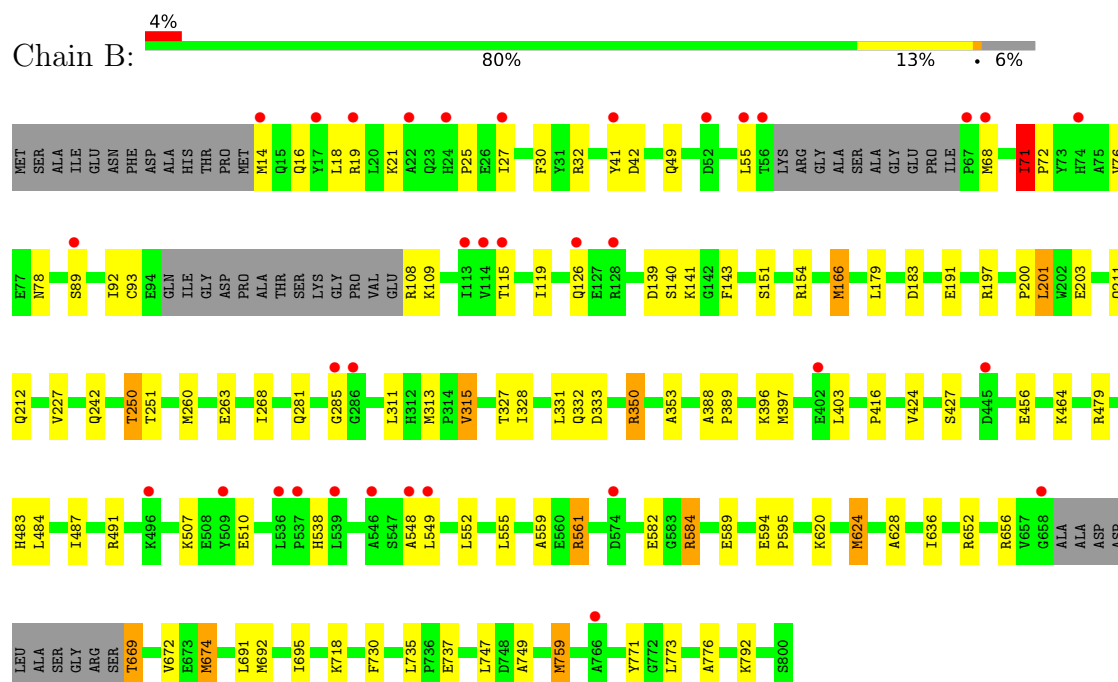
3 Residue-property plots [i](#)

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: DNA MISMATCH REPAIR PROTEIN MUTS

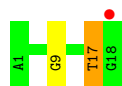


• Molecule 1: DNA MISMATCH REPAIR PROTEIN MUTS



- Molecule 2: 5'-D(*AP*GP*CP*TP*GP*CP*CP*AP*GP*GP *CP*AP*CP*CP*AP*GP*TP*G)-3'

Chain E:  6% 89% 6% 6%



- Molecule 3: 5'-D(*AP*CP*TP*GP*GP*TP*GP*CP*TP*TP *GP*GP*CP*AP*GP*CP*T)-3',

Chain F:  6% 82% 18%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.65Å 92.12Å 260.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	91.7 (20.00-2.10) 91.3 (20.00-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.189 , 0.234 0.200 , 0.236	Depositor DCC
R_{free} test set	2306 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13862	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ADP

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	0.85	2/6310 (0.0%)	0.93	5/8542 (0.1%)
1	B	0.83	4/6059 (0.1%)	0.92	1/8197 (0.0%)
2	E	0.47	0/412	1.13	2/634 (0.3%)
3	F	0.52	0/388	1.28	1/598 (0.2%)
All	All	0.82	6/13169 (0.0%)	0.95	9/17971 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	166	MET	SD-CE	-21.18	1.26	1.79
1	B	166	MET	SD-CE	-11.15	1.51	1.79
1	B	624	MET	SD-CE	-9.78	1.55	1.79
1	B	674	MET	SD-CE	-8.17	1.59	1.79
1	A	14	MET	SD-CE	-6.57	1.63	1.79
1	B	71	ILE	CA-CB	5.27	1.58	1.54

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	487	ILE	CA-C-N	5.88	128.97	120.38
1	A	487	ILE	C-N-CA	5.88	128.97	120.38
3	F	23	DT	O4'-C1'-N1	-5.66	99.92	108.40
2	E	17	DT	O4'-C1'-N1	5.35	116.43	108.40
1	A	190	ILE	CB-CA-C	5.31	115.62	110.63
2	E	9	DG	O3'-P-O5'	-5.18	96.23	104.00
1	A	755	THR	N-CA-C	5.15	117.69	109.81
1	A	442	GLY	N-CA-C	-5.13	106.49	113.37
1	B	191	GLU	N-CA-C	5.03	116.76	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	6204	0	6252	67	0
1	B	5961	0	6019	67	0
2	E	367	0	202	1	0
3	F	347	0	194	1	0
4	A	27	0	12	0	0
5	A	1	0	0	0	0
6	A	492	0	0	11	0
6	B	423	0	0	14	0
6	E	23	0	0	1	0
6	F	17	0	0	0	0
All	All	13862	0	12679	129	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 (129) 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:674:MET:SD	6:B:2404:HOH:O	2.35	0.84
1:A:143:PHE:CB	1:A:166:MET:HE3	2.09	0.83
1:B:584:ARG:HD2	1:B:589:GLU:OE1	1.81	0.80
1:A:13:MET:HE3	1:A:14:MET:HE2	1.67	0.76
1:B:350:ARG:NH1	6:B:2198:HOH:O	2.21	0.73
1:A:707:LEU:HD23	1:B:773:LEU:CD2	2.20	0.71
1:B:692:MET:HE2	1:B:695:ILE:HD13	1.72	0.70
1:B:108:ARG:N	6:B:2054:HOH:O	2.24	0.70
1:B:350:ARG:HH11	1:B:350:ARG:HG2	1.57	0.69
1:A:454:GLU:OE2	6:A:2299:HOH:O	2.11	0.69
1:B:350:ARG:HH11	1:B:350:ARG:CG	2.06	0.68
1:B:250:THR:HG22	1:B:251:THR:O	1.92	0.68
1:A:13:MET:HE3	1:A:14:MET:CE	2.24	0.67
1:B:143:PHE:HB3	1:B:166:MET:CE	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:THR:HG21	1:B:555:LEU:HD13	1.78	0.66
1:A:327:THR:HG21	1:A:555:LEU:HD13	1.78	0.65
1:A:143:PHE:HB3	1:A:166:MET:HE3	1.80	0.64
1:B:594:GLU:HG3	1:B:595:PRO:HD2	1.80	0.62
1:B:759:MET:HA	1:B:759:MET:HE2	1.80	0.62
1:B:328:ILE:HG23	1:B:559:ALA:HA	1.82	0.62
1:B:263:GLU:HG3	1:B:268:ILE:HD11	1.86	0.58
1:A:397:MET:HE3	1:A:549:LEU:HD21	1.86	0.57
1:A:14:MET:HE1	1:A:40:PHE:CE2	2.40	0.56
1:A:692:MET:HE3	1:A:695:ILE:HD13	1.87	0.56
1:A:143:PHE:CG	1:A:166:MET:HE3	2.40	0.56
1:A:784:GLU:HG3	6:B:2363:HOH:O	2.05	0.55
1:A:328:ILE:HG23	1:A:559:ALA:HA	1.87	0.55
1:B:151:SER:O	1:B:353:ALA:HB2	2.06	0.55
1:A:160:PRO:HB2	1:A:166:MET:HE2	1.88	0.55
1:B:281:GLN:HE21	1:B:285:GLY:HA2	1.72	0.55
1:A:707:LEU:HD23	1:B:773:LEU:HD23	1.89	0.55
1:A:443:ALA:HB1	1:A:509:TYR:OH	2.08	0.54
1:A:709:TRP:CE3	1:A:732:LEU:HD23	2.42	0.54
1:B:584:ARG:CD	1:B:589:GLU:OE1	2.52	0.53
1:A:707:LEU:HD23	1:B:773:LEU:HD22	1.91	0.53
1:A:674:MET:CG	1:B:776:ALA:HA	2.39	0.53
1:A:199:ARG:HD3	1:A:203:GLU:OE1	2.08	0.53
1:B:139:ASP:HB3	1:B:141:LYS:H	1.74	0.52
1:B:315:VAL:HG23	6:B:2150:HOH:O	2.09	0.52
1:B:624:MET:HE1	1:B:692:MET:O	2.09	0.52
1:B:730:PHE:HD1	6:B:2399:HOH:O	1.93	0.52
1:A:171:GLN:OE1	1:A:274:ARG:HD2	2.10	0.52
1:A:717:ASN:O	1:A:720:LYS:NZ	2.43	0.51
1:B:71:ILE:HD12	1:B:72:PRO:O	2.10	0.51
1:B:396:LYS:HD3	1:B:548:ALA:HB2	1.91	0.51
1:B:143:PHE:HB3	1:B:166:MET:HE3	1.92	0.51
1:B:212:GLN:OE1	1:B:242:GLN:NE2	2.44	0.51
1:A:674:MET:HG2	1:B:776:ALA:HA	1.93	0.51
1:B:154:ARG:HD2	6:B:2096:HOH:O	2.10	0.50
1:B:538:HIS:HE1	6:B:2267:HOH:O	1.93	0.50
1:A:396:LYS:NZ	6:A:2271:HOH:O	2.44	0.50
1:B:628:ALA:HB2	1:B:691:LEU:HD11	1.94	0.50
1:B:427:SER:HB3	6:B:2243:HOH:O	2.12	0.50
3:F:28:DG:C5	3:F:29:DC:C4	3.00	0.50
1:B:397:MET:HG3	1:B:549:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:670:PHE:HD2	6:A:2400:HOH:O	1.95	0.49
1:B:179:LEU:HD23	1:B:197:ARG:HB2	1.94	0.49
1:B:332:GLN:NE2	1:B:333:ASP:OD1	2.42	0.49
1:A:585:HIS:CD2	1:A:588:VAL:H	2.32	0.48
1:A:37:TYR:OH	1:A:94:GLU:OE2	2.23	0.48
1:B:143:PHE:CB	1:B:166:MET:CE	2.92	0.48
1:A:143:PHE:CB	1:A:166:MET:CE	2.88	0.47
1:A:436:TRP:CZ2	1:A:519:LYS:HD2	2.49	0.47
1:A:375:LEU:HD12	1:A:397:MET:CE	2.44	0.47
1:B:416:PRO:HD2	1:B:424:VAL:HG22	1.96	0.47
1:B:227:VAL:HG12	1:B:260:MET:HB2	1.97	0.47
1:B:27:ILE:HG12	1:B:89:SER:HB2	1.96	0.47
1:B:311:LEU:HD23	1:B:636:ILE:HD13	1.96	0.47
1:A:585:HIS:HD2	1:A:588:VAL:H	1.64	0.46
1:B:507:LYS:NZ	1:B:510:GLU:OE1	2.48	0.46
1:A:83:LEU:HD13	1:A:90:VAL:HG21	1.97	0.45
1:A:585:HIS:CE1	6:A:2360:HOH:O	2.68	0.45
1:A:143:PHE:HB2	1:A:166:MET:HE3	1.93	0.45
1:B:483:HIS:CE1	1:B:484:LEU:HG	2.51	0.45
1:A:463:LEU:HA	1:A:476:GLN:O	2.16	0.45
1:A:397:MET:CE	1:A:549:LEU:HD21	2.47	0.45
1:B:594:GLU:HG3	1:B:595:PRO:CD	2.46	0.45
1:A:83:LEU:HD13	1:A:90:VAL:CG2	2.47	0.45
1:A:160:PRO:HG2	1:A:166:MET:CE	2.47	0.45
1:B:268:ILE:HB	1:B:652:ARG:HG2	1.98	0.45
1:A:326:GLN:HB3	6:A:2266:HOH:O	2.16	0.45
1:B:350:ARG:NH1	1:B:350:ARG:CG	2.76	0.45
2:E:17:DT:H73	6:E:2022:HOH:O	2.17	0.45
1:A:585:HIS:HE1	6:A:2360:HOH:O	2.00	0.45
1:B:620:LYS:HG3	1:B:747:LEU:HD12	1.98	0.45
1:A:143:PHE:HB2	1:A:166:MET:CE	2.47	0.44
1:B:327:THR:HG22	1:B:331:LEU:HD12	1.99	0.44
1:B:792:LYS:NZ	6:B:2415:HOH:O	2.49	0.44
1:A:585:HIS:CD2	1:A:588:VAL:HG23	2.52	0.44
1:A:686:GLU:HG2	1:A:720:LYS:HB2	1.98	0.44
1:B:718:LYS:HD2	6:B:2363:HOH:O	2.15	0.44
1:A:446:TYR:CD2	1:A:446:TYR:C	2.92	0.44
1:B:108:ARG:HA	6:B:2054:HOH:O	2.18	0.44
1:A:199:ARG:CD	1:A:203:GLU:OE1	2.66	0.44
1:A:345:VAL:HG11	1:A:549:LEU:HD13	2.00	0.43
1:A:388:ALA:HB3	1:A:389:PRO:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:ASP:OD1	1:B:201:LEU:HD11	2.19	0.43
1:A:488:ASN:ND2	6:A:2309:HOH:O	2.51	0.43
1:A:670:PHE:N	6:A:2400:HOH:O	2.51	0.43
1:A:755:THR:HG23	1:A:756:ILE:N	2.33	0.43
1:A:509:TYR:CZ	1:A:513:VAL:HG21	2.53	0.43
1:A:157:LEU:HD12	1:A:260:MET:HG3	2.01	0.43
1:B:582:GLU:HG3	6:B:2302:HOH:O	2.18	0.42
1:B:759:MET:HA	1:B:759:MET:CE	2.49	0.42
1:B:669:THR:CG2	1:B:672:VAL:H	2.32	0.42
1:B:749:ALA:HB3	1:B:771:TYR:CE1	2.54	0.42
1:A:511:LEU:HD21	1:A:83:LEU:HG	2.01	0.42
1:A:268:ILE:HB	1:A:652:ARG:HG2	2.02	0.42
1:A:579:ARG:HD3	6:A:2369:HOH:O	2.18	0.42
1:A:632:LEU:C	1:A:632:LEU:HD23	2.45	0.42
1:B:41:TYR:HB3	1:B:42:ASP:H	1.78	0.42
1:B:30:PHE:HB2	1:B:92:ILE:HD13	2.02	0.41
1:A:652:ARG:HH11	1:A:652:ARG:HB3	1.86	0.41
1:A:674:MET:HG3	1:B:776:ALA:HA	2.02	0.41
1:A:311:LEU:HD23	1:A:636:ILE:HD13	2.02	0.41
1:A:492:ARG:HG2	6:A:2313:HOH:O	2.19	0.41
1:A:496:LYS:HE2	6:A:2314:HOH:O	2.19	0.41
1:B:388:ALA:HB3	1:B:389:PRO:HD3	2.03	0.41
1:A:781:VAL:HG21	1:B:674:MET:CE	2.51	0.41
1:B:718:LYS:CD	6:B:2363:HOH:O	2.68	0.41
1:B:669:THR:HG23	1:B:672:VAL:H	1.86	0.41
1:B:200:PRO:HG2	1:B:203:GLU:HG3	2.03	0.41
1:B:561:ARG:HA	1:B:561:ARG:HD2	1.72	0.41
1:A:447:LEU:HD21	1:A:509:TYR:CE2	2.55	0.40
1:A:494:THR:OG1	1:A:499:GLU:OE2	2.20	0.40
1:B:71:ILE:HD11	1:B:76:VAL:HA	2.03	0.40
1:B:21:LYS:HE3	1:B:25:PRO:HA	2.04	0.40
1:A:23:GLN:HB3	1:A:24:HIS:CD2	2.56	0.40
1:A:561:ARG:HA	1:A:561:ARG:HD2	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	784/800 (98%)	762 (97%)	20 (3%)	2 (0%)	36	36
1	B	746/800 (93%)	733 (98%)	13 (2%)	0	100	100
All	All	1530/1600 (96%)	1495 (98%)	33 (2%)	2 (0%)	48	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	443	ALA
1	A	441	ASP

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	656/664 (99%)	622 (95%)	34 (5%)	21	20
1	B	631/664 (95%)	595 (94%)	36 (6%)	18	17
All	All	1287/1328 (97%)	1217 (95%)	70 (5%)	20	18

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	46	ARG
1	A	57	LYS
1	A	126	GLN

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Mol	Chain	Res	Type
1	A	190	ILE
1	A	275	ARG
1	A	315	VAL
1	A	332	GLN
1	A	375	LEU
1	A	386	ASP
1	A	420	ARG
1	A	439	LEU
1	A	441	ASP
1	A	464	LYS
1	A	479	ARG
1	A	488	ASN
1	A	492	ARG
1	A	512	LYS
1	A	516	SER
1	A	517	LYS
1	A	591	VAL
1	A	594	GLU
1	A	652	ARG
1	A	656	ARG
1	A	670	PHE
1	A	673	GLU
1	A	674	MET
1	A	697	ARG
1	A	705	LEU
1	A	707	LEU
1	A	735	LEU
1	A	747	LEU
1	A	755	THR
1	A	790	ARG
1	B	14	MET
1	B	16	GLN
1	B	18	LEU
1	B	19	ARG
1	B	32	ARG
1	B	49	GLN
1	B	55	LEU
1	B	68	MET
1	B	71	ILE
1	B	78	ASN
1	B	93	CYS
1	B	109	LYS

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Mol	Chain	Res	Type
1	B	115	THR
1	B	119	ILE
1	B	126	GLN
1	B	140	SER
1	B	201	LEU
1	B	211	GLN
1	B	250	THR
1	B	313	MET
1	B	315	VAL
1	B	350	ARG
1	B	403	LEU
1	B	456	GLU
1	B	464	LYS
1	B	479	ARG
1	B	487	ILE
1	B	491	ARG
1	B	552	LEU
1	B	561	ARG
1	B	584	ARG
1	B	656	ARG
1	B	669	THR
1	B	735	LEU
1	B	737	GLU
1	B	759	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	248	GLN
1	A	497	ASN
1	A	538	HIS
1	A	585	HIS
1	A	590	GLN
1	A	616	ASN
1	A	679	ASN
1	A	714	ASN
1	A	734	GLN
1	B	131	ASN
1	B	138	GLN
1	B	242	GLN
1	B	248	GLN

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Mol	Chain	Res	Type
1	B	281	GLN
1	B	391	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	1801	5	28,29,29	1.20	3 (10%)	43,45,45	1.70	8 (18%)

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	1801	5	-	0/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1801	ADP	C2-N3	3.00	1.39	1.33
4	A	1801	ADP	C2-N1	2.30	1.38	1.33
4	A	1801	ADP	C8-N7	2.19	1.35	1.31

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1801	ADP	N3-C2-N1	-5.55	120.18	128.58
4	A	1801	ADP	C5-C4-N3	-3.94	121.29	126.72
4	A	1801	ADP	N9-C8-N7	-3.29	109.27	113.94
4	A	1801	ADP	C2-N3-C4	3.14	119.51	111.83
4	A	1801	ADP	C5-N7-C8	3.00	108.16	103.45
4	A	1801	ADP	N3-C4-N9	2.44	131.32	127.17
4	A	1801	ADP	C3'-C2'-C1'	2.26	105.75	101.46
4	A	1801	ADP	C4-C5-N7	-2.23	108.03	110.58

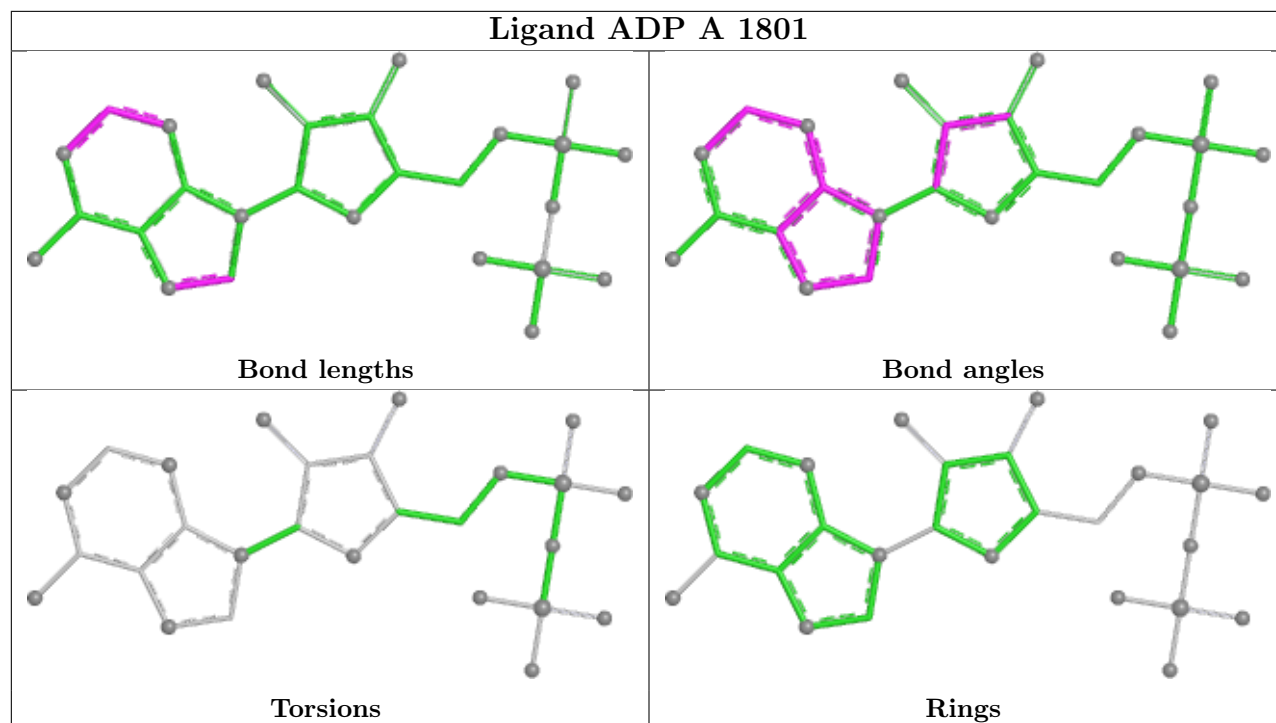
There are no chirality outliers.

There are no torsion outliers.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	788/800 (98%)	-0.03	25 (3%) 50 53	4, 18, 27, 38	0
1	B	754/800 (94%)	0.14	34 (4%) 38 40	9, 18, 26, 38	0
2	E	18/18 (100%)	-0.02	1 (5%) 30 32	10, 17, 37, 45	0
3	F	17/17 (100%)	0.06	1 (5%) 28 30	12, 20, 39, 40	0
All	All	1577/1635 (96%)	0.05	61 (3%) 43 45	4, 18, 27, 45	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	115	THR	5.6
1	B	445	ASP	4.8
1	B	41	TYR	4.6
1	B	89	SER	4.2
1	A	418	LEU	4.1
1	A	62	ALA	4.1
1	A	440	ALA	3.9
1	A	742	VAL	3.6
1	B	114	VAL	3.6
1	A	444	THR	3.6
1	B	68	MET	3.3
1	B	658	GLY	3.2
1	B	509	TYR	3.2
1	B	549	LEU	3.2
1	A	393	LEU	3.2
1	B	539	LEU	3.1
1	B	113	ILE	3.1
1	B	52	ASP	3.1
1	A	658	GLY	2.9
2	E	18	DG	2.9
1	A	61	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	74	HIS	2.8
1	A	504	PRO	2.8
1	B	14	MET	2.8
1	B	548	ALA	2.8
1	B	766	ALA	2.8
1	B	536	LEU	2.7
1	A	509	TYR	2.7
1	A	752	HIS	2.7
1	A	441	ASP	2.7
1	B	27	ILE	2.6
1	A	192	GLY	2.5
1	B	496	LYS	2.5
1	B	574	ASP	2.5
1	A	414	THR	2.5
1	B	56	THR	2.5
1	A	60	ALA	2.5
1	B	24	HIS	2.5
3	F	14	DA	2.4
1	A	443	ALA	2.4
1	B	546	ALA	2.4
1	A	753	GLY	2.4
1	B	19	ARG	2.4
1	B	67	PRO	2.4
1	B	126	GLN	2.3
1	A	544	GLN	2.3
1	A	446	TYR	2.3
1	A	442	GLY	2.3
1	A	670	PHE	2.3
1	A	754	ASP	2.3
1	B	17	TYR	2.2
1	B	537	PRO	2.1
1	A	164	GLU	2.1
1	A	728	HIS	2.1
1	B	286	GLY	2.1
1	B	55	LEU	2.0
1	A	593	ASN	2.0
1	B	285	GLY	2.0
1	B	402	GLU	2.0
1	B	22	ALA	2.0
1	B	128	ARG	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](#)

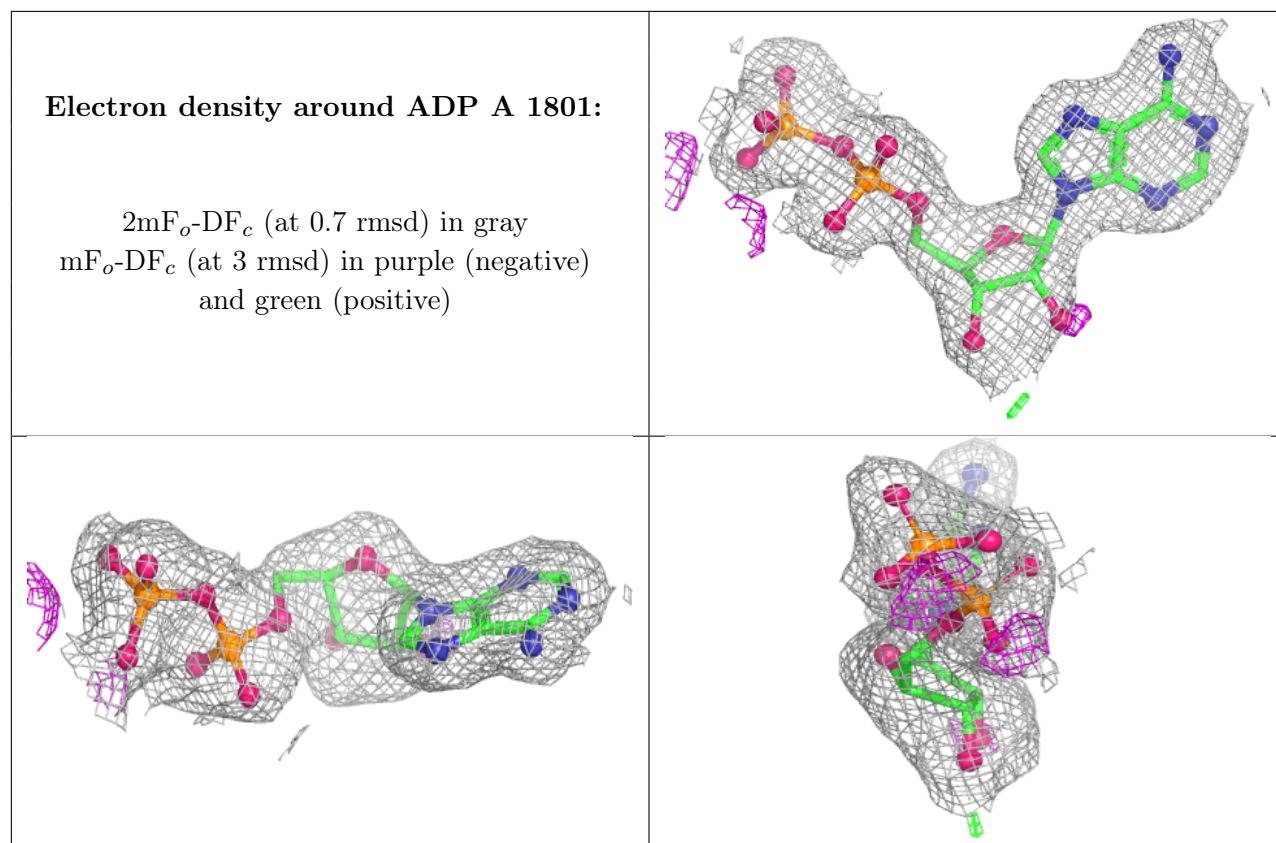
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	MG	A	1802	1/1	0.96	0.06	17,17,17,17	0
4	ADP	A	1801	27/27	0.97	0.06	13,19,21,26	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 ⓘ

There are no such residues in this entry.