



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:15 AM UTC

PDB ID : 3G0Q / pdb_00003g0q
Title : Crystal Structure of MutY bound to its inhibitor DNA
Authors : Lee, S.; Verdine, G.L.
Deposited on : 2009-01-28
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 ⓘ 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
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

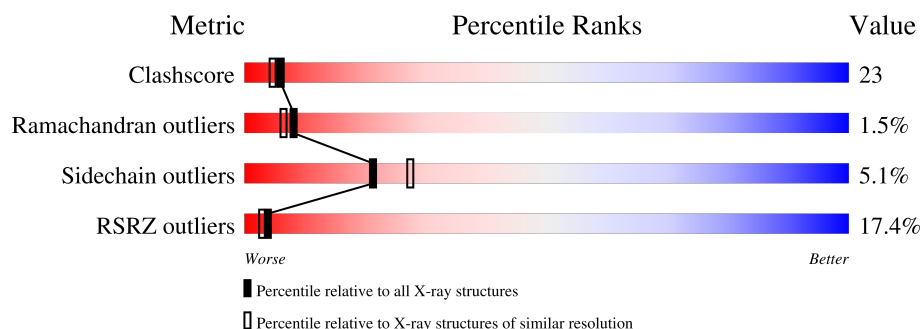
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 $\leq 5\%$. 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	352	18% 57% 36% 5%
2	B	11	55% 45%
3	C	11	9% 45% 45% 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	A5L	C	18	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3239 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 A/G-specific adenine glycosylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2760	1768	473	508	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	144	ASP	ASN	engineered mutation	UNP P83847
A	164	CYS	PRO	engineered mutation	UNP P83847

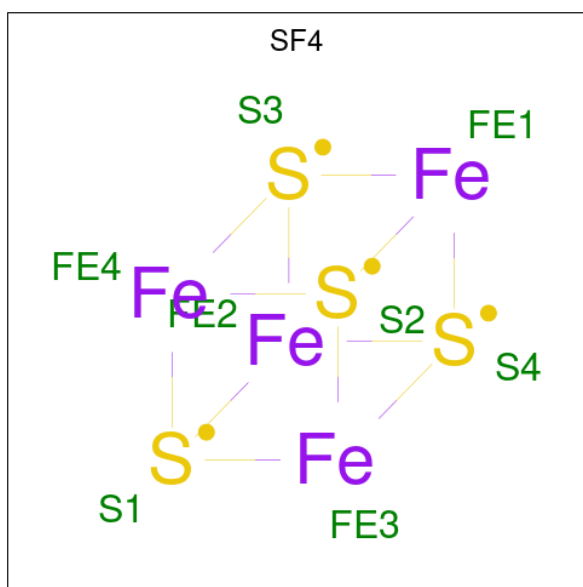
- Molecule 2 is a DNA chain called 5'-D(*AP*AP*GP*AP*CP*(8OG)P*GP*GP*GP*AP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	P	0	0	0
			230	108	51	61	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	P	0	0	0
			198	96	33	60	9			

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

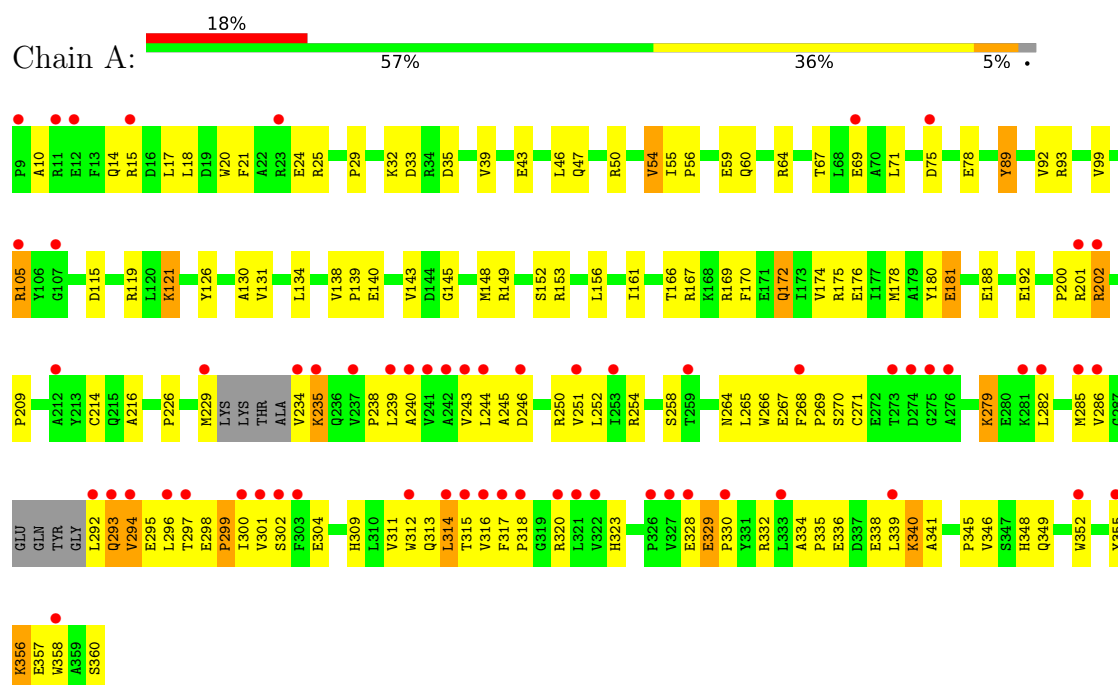
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	26	Total	O	0	0
			26	26		
6	B	9	Total	O	0	0
			9	9		
6	C	7	Total	O	0	0
			7	7		

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.

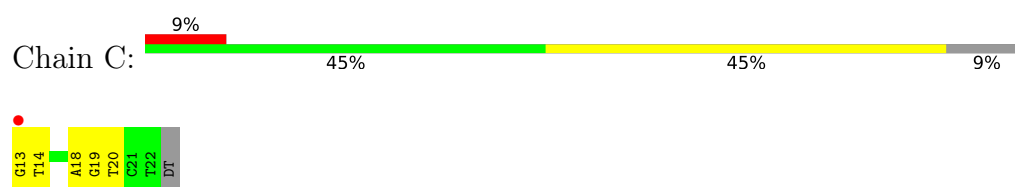
- Molecule 1: A/G-specific adenine glycosylase



- Molecule 2: 5'-D(*AP*AP*GP*AP*CP*(8OG)P*GP*GP*GP*AP*C)-3'



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	37.70Å 85.90Å 142.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.6 (50.00-2.20) 97.1 (50.00-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.11 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.246 , 0.277 0.241 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3239	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, SF4, 8OG, A5L

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	0.41	0/2828	0.89	7/3841 (0.2%)
2	B	0.27	0/233	0.60	0/356
3	C	0.27	0/195	0.70	0/296
All	All	0.39	0/3256	0.86	7/4493 (0.2%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	214	CYS	N-CA-C	7.45	120.41	108.41
1	A	131	VAL	N-CA-C	6.92	117.06	110.42
1	A	54	VAL	N-CA-C	6.49	116.63	110.53
1	A	357	GLU	N-CA-C	-6.11	105.66	113.23
1	A	143	VAL	N-CA-C	5.55	115.78	107.51
1	A	89	TYR	N-CA-C	5.40	118.96	112.38
1	A	24	GLU	N-CA-C	5.24	119.67	113.28

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	2760	0	2715	136	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	230	0	123	6	0
3	C	198	0	113	11	0
4	A	8	0	0	0	0
5	A	1	0	0	0	0
6	A	26	0	0	2	0
6	B	9	0	0	0	0
6	C	7	0	0	2	0
All	All	3239	0	2951	140	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 23.

All (140) 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:245:ALA:HB3	1:A:320:ARG:HH21	1.29	0.94
1:A:10:ALA:O	1:A:14:GLN:HG3	1.69	0.91
1:A:21:PHE:HE1	1:A:192:GLU:HG3	1.41	0.85
1:A:314:LEU:H	1:A:314:LEU:HD23	1.39	0.85
1:A:167:ARG:HB3	1:A:167:ARG:NH1	1.92	0.84
1:A:328:GLU:HG3	1:A:329:GLU:H	1.44	0.82
1:A:167:ARG:HB3	1:A:167:ARG:HH11	1.42	0.82
1:A:188:GLU:HG2	6:A:376:HOH:O	1.78	0.80
1:A:202:ARG:HB2	1:A:202:ARG:NH1	1.98	0.79
1:A:235:LYS:HD2	1:A:235:LYS:H	1.48	0.78
1:A:105:ARG:NH2	1:A:105:ARG:HB2	1.98	0.76
1:A:200:PRO:HB2	1:A:201:ARG:HD3	1.68	0.74
1:A:245:ALA:HB3	1:A:320:ARG:NH2	2.03	0.72
1:A:294:VAL:HG21	1:A:320:ARG:O	1.90	0.71
1:A:149:ARG:HG3	1:A:226:PRO:HD3	1.72	0.70
1:A:294:VAL:HG22	1:A:295:GLU:H	1.55	0.70
1:A:294:VAL:HG22	1:A:295:GLU:N	2.07	0.70
1:A:329:GLU:HB3	1:A:330:PRO:CD	2.22	0.69
1:A:169:ARG:HH21	1:A:169:ARG:HG2	1.60	0.67
1:A:345:PRO:O	1:A:349:GLN:HG3	1.96	0.66
1:A:300:ILE:HD11	1:A:358:TRP:NE1	2.11	0.66
1:A:279:LYS:HB2	1:A:279:LYS:HZ2	1.61	0.66
1:A:202:ARG:HB2	1:A:202:ARG:HH11	1.60	0.65
1:A:201:ARG:NH2	2:B:11:DC:H5'	2.12	0.65
1:A:201:ARG:HH22	2:B:11:DC:H5'	1.60	0.65
1:A:254:ARG:NH2	1:A:270:SER:H	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:PHE:CE1	1:A:192:GLU:HG3	2.30	0.64
1:A:239:LEU:O	1:A:314:LEU:HA	1.99	0.62
1:A:64:ARG:HA	1:A:64:ARG:HE	1.66	0.61
1:A:299:PRO:HG3	1:A:317:PHE:CE1	2.36	0.61
1:A:302:SER:OG	1:A:315:THR:HG22	2.00	0.60
1:A:267:GLU:HB2	1:A:348:HIS:CE1	2.37	0.60
1:A:279:LYS:HB2	1:A:279:LYS:NZ	2.17	0.60
1:A:258:SER:HA	1:A:264:ASN:OD1	2.02	0.59
1:A:279:LYS:HD2	1:A:297:THR:O	2.01	0.59
1:A:235:LYS:HB3	1:A:235:LYS:NZ	2.18	0.58
1:A:130:ALA:O	1:A:134:LEU:HG	2.05	0.56
1:A:64:ARG:HD3	1:A:78:GLU:OE1	2.05	0.56
1:A:105:ARG:HB2	1:A:105:ARG:HH21	1.66	0.56
1:A:358:TRP:C	1:A:360:SER:H	2.13	0.56
1:A:201:ARG:HD3	1:A:201:ARG:N	2.21	0.56
1:A:346:VAL:HG21	2:B:7:DG:H3'	1.87	0.55
1:A:29:PRO:O	1:A:32:LYS:HG3	2.07	0.55
1:A:15:ARG:HH22	1:A:18:LEU:HD12	1.71	0.55
1:A:43:GLU:OE2	3:C:18:A5L:H8	2.07	0.55
1:A:304:GLU:OE1	1:A:311:VAL:HG11	2.07	0.54
1:A:239:LEU:HD12	1:A:271:CYS:C	2.33	0.54
3:C:13:DG:H2'	3:C:14:DT:H71	1.87	0.54
3:C:18:A5L:H4'	6:C:28:HOH:O	2.07	0.54
1:A:47:GLN:HG2	3:C:19:DG:H4'	1.90	0.53
1:A:329:GLU:HB3	1:A:330:PRO:HD2	1.89	0.53
1:A:93:ARG:HH11	1:A:93:ARG:HG2	1.74	0.53
1:A:55:ILE:HB	1:A:56:PRO:HD3	1.88	0.53
1:A:339:LEU:C	1:A:341:ALA:H	2.16	0.53
1:A:316:VAL:HG12	1:A:317:PHE:N	2.25	0.52
1:A:20:TRP:CG	1:A:209:PRO:HG3	2.44	0.52
1:A:126:TYR:OH	3:C:18:A5L:C8	2.57	0.52
1:A:340:LYS:HD3	1:A:340:LYS:C	2.35	0.51
1:A:126:TYR:OH	3:C:18:A5L:H8	2.10	0.51
1:A:172:GLN:O	1:A:176:GLU:HG3	2.11	0.51
1:A:254:ARG:NH2	1:A:270:SER:O	2.43	0.51
1:A:238:PRO:HA	1:A:313:GLN:HB2	1.92	0.50
1:A:174:VAL:HG12	1:A:178:MET:HE2	1.93	0.50
1:A:300:ILE:HD11	1:A:358:TRP:CE2	2.47	0.50
1:A:167:ARG:HH11	1:A:167:ARG:CB	2.19	0.50
1:A:314:LEU:H	1:A:314:LEU:CD2	2.19	0.50
1:A:35:ASP:OD1	1:A:35:ASP:C	2.55	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:LYS:HZ2	1:A:296:LEU:HB2	1.78	0.49
1:A:105:ARG:HB2	1:A:105:ARG:CZ	2.42	0.49
1:A:115:ASP:O	1:A:119:ARG:HG3	2.12	0.49
1:A:46:LEU:HD23	1:A:54:VAL:HG21	1.94	0.49
1:A:169:ARG:HH21	1:A:169:ARG:CG	2.27	0.48
1:A:251:VAL:HG12	1:A:252:LEU:N	2.28	0.48
1:A:181:GLU:H	1:A:181:GLU:CD	2.21	0.48
1:A:294:VAL:CG2	1:A:295:GLU:H	2.25	0.48
1:A:71:LEU:HD23	1:A:99:VAL:HG21	1.96	0.47
1:A:265:LEU:HD13	1:A:345:PRO:HG3	1.96	0.47
1:A:294:VAL:CG2	1:A:295:GLU:N	2.77	0.47
1:A:15:ARG:HH22	1:A:18:LEU:CD1	2.28	0.47
1:A:293:GLN:NE2	1:A:293:GLN:N	2.62	0.47
1:A:161:ILE:HA	1:A:166:THR:HG21	1.96	0.47
1:A:239:LEU:HD12	1:A:271:CYS:O	2.15	0.46
1:A:43:GLU:OE2	3:C:18:A5L:C8	2.63	0.46
1:A:175:ARG:O	1:A:180:TYR:OH	2.30	0.46
1:A:50:ARG:HH22	2:B:8:DG:H21	1.62	0.46
1:A:75:ASP:OD1	1:A:78:GLU:N	2.46	0.46
1:A:64:ARG:HA	1:A:64:ARG:NE	2.30	0.46
1:A:296:LEU:HD13	1:A:317:PHE:HB3	1.98	0.46
1:A:15:ARG:NH2	1:A:18:LEU:HD12	2.31	0.46
1:A:21:PHE:O	1:A:25:ARG:HB3	2.16	0.45
1:A:240:ALA:HB1	1:A:282:LEU:HD11	1.98	0.45
1:A:46:LEU:O	3:C:18:A5L:H3'	2.16	0.45
1:A:138:VAL:HA	1:A:139:PRO:HD3	1.79	0.45
1:A:234:VAL:CG2	1:A:311:VAL:HG23	2.46	0.45
1:A:356:LYS:O	1:A:360:SER:HB2	2.17	0.45
1:A:244:LEU:HD22	1:A:244:LEU:N	2.32	0.45
1:A:46:LEU:O	3:C:18:A5L:H5'	2.16	0.44
1:A:328:GLU:HG3	1:A:329:GLU:N	2.24	0.44
1:A:35:ASP:O	1:A:39:VAL:HG23	2.17	0.44
1:A:320:ARG:HA	1:A:320:ARG:NE	2.33	0.44
1:A:334:ALA:HA	1:A:335:PRO:HD3	1.87	0.44
1:A:67:THR:OG1	1:A:69:GLU:HG3	2.18	0.44
1:A:148:MET:HG2	1:A:170:PHE:CD1	2.53	0.44
1:A:286:VAL:HG13	1:A:292:LEU:O	2.17	0.44
1:A:246:ASP:OD1	1:A:323:HIS:NE2	2.49	0.44
1:A:266:TRP:CH2	1:A:332:ARG:HD3	2.53	0.43
1:A:293:GLN:O	1:A:294:VAL:HB	2.18	0.43
1:A:250:ARG:HH21	1:A:323:HIS:HE2	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:PRO:HD2	1:A:338:GLU:CD	2.44	0.43
3:C:18:A5L:H2	6:C:50:HOH:O	2.18	0.43
1:A:33:ASP:OD1	1:A:33:ASP:C	2.61	0.43
1:A:318:PRO:HD3	6:A:369:HOH:O	2.18	0.43
1:A:201:ARG:O	1:A:202:ARG:HG3	2.18	0.43
1:A:268:PHE:O	1:A:269:PRO:C	2.60	0.43
1:A:202:ARG:HD3	1:A:202:ARG:O	2.19	0.42
1:A:336:GLU:HG3	1:A:352:TRP:CZ2	2.54	0.42
1:A:169:ARG:CG	1:A:169:ARG:NH2	2.82	0.42
1:A:15:ARG:CZ	1:A:15:ARG:HA	2.49	0.42
2:B:8:DG:H2''	2:B:9:DG:C8	2.54	0.42
1:A:39:VAL:O	1:A:43:GLU:HG2	2.19	0.42
1:A:121:LYS:N	1:A:121:LYS:HD3	2.34	0.41
1:A:202:ARG:HB2	1:A:202:ARG:CZ	2.48	0.41
1:A:145:GLY:HA2	1:A:148:MET:HE3	2.02	0.41
1:A:126:TYR:HB3	3:C:20:DT:P	2.61	0.41
1:A:138:VAL:HG12	1:A:140:GLU:HG2	2.01	0.41
1:A:358:TRP:C	1:A:360:SER:N	2.78	0.41
1:A:229:MET:HE3	1:A:229:MET:C	2.46	0.41
1:A:339:LEU:C	1:A:341:ALA:N	2.77	0.41
1:A:243:VAL:HG21	1:A:355:TYR:HD2	1.86	0.41
1:A:89:TYR:O	1:A:92:VAL:HG12	2.20	0.41
1:A:169:ARG:HG2	1:A:169:ARG:NH2	2.33	0.41
1:A:229:MET:C	1:A:229:MET:SD	3.04	0.41
1:A:235:LYS:HD3	1:A:309:HIS:O	2.21	0.41
1:A:298:GLU:O	1:A:299:PRO:O	2.39	0.41
1:A:15:ARG:HA	1:A:15:ARG:NE	2.36	0.40
1:A:312:TRP:HB3	1:A:314:LEU:HD22	2.04	0.40
1:A:153:ARG:O	1:A:216:ALA:HB2	2.21	0.40
1:A:201:ARG:CZ	2:B:11:DC:H5'	2.52	0.40
1:A:148:MET:O	1:A:152:SER:HB3	2.21	0.40
1:A:201:ARG:C	1:A:202:ARG:HG3	2.46	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	338/352 (96%)	306 (90%)	27 (8%)	5 (2%)	8 6

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	VAL
1	A	299	PRO
1	A	329	GLU
1	A	285	MET
1	A	301	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	293/300 (98%)	278 (95%)	15 (5%)	21 27

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	59	GLU
1	A	60	GLN
1	A	105	ARG
1	A	121	LYS
1	A	156	LEU
1	A	172	GLN
1	A	181	GLU
1	A	202	ARG
1	A	235	LYS
1	A	279	LYS
1	A	293	GLN

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Mol	Chain	Res	Type
1	A	314	LEU
1	A	340	LYS
1	A	356	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	60	GLN
1	A	94	ASN
1	A	172	GLN
1	A	182	ASN
1	A	293	GLN
1	A	313	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	8OG	B	6	2	22,25,26	1.05	2 (9%)	26,37,40	1.77	4 (15%)
3	A5L	C	18	3	20,23,25	0.20	0	28,33,38	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	8OG	B	6	2	-	1/7/21/22	0/3/3/3
3	A5L	C	18	3	-	3/7/21/26	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	6	8OG	C8-N7	-3.55	1.31	1.38
2	B	6	8OG	C5-C4	2.22	1.40	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6	8OG	N7-C8-N9	6.54	113.88	106.61
2	B	6	8OG	C5-N7-C8	-4.26	103.60	109.47
2	B	6	8OG	C4-C5-N7	2.82	111.23	106.06
2	B	6	8OG	O8-C8-N7	-2.13	122.48	126.47

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	18	A5L	O4'-C1'-N9-C4
3	C	18	A5L	C4'-C5'-O5'-P
3	C	18	A5L	O4'-C1'-N9-C8
2	B	6	8OG	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	18	A5L	8	0

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	SF4	A	400	1	0,12,12	-	-	-		

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	SF4	A	400	1	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	344/352 (97%)	0.98	62 (18%) 3 2	27, 54, 109, 129	0
2	B	10/11 (90%)	0.53	0 100 100	43, 54, 86, 102	0
3	C	9/11 (81%)	0.51	1 (11%) 10 8	36, 50, 76, 84	0
All	All	363/374 (97%)	0.96	63 (17%) 4 3	27, 54, 108, 129	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	292	LEU	6.2
1	A	358	TRP	4.8
1	A	286	VAL	4.8
1	A	316	VAL	4.5
1	A	355	TYR	4.2
1	A	12	GLU	4.1
1	A	69	GLU	4.1
1	A	300	ILE	4.0
1	A	244	LEU	4.0
1	A	296	LEU	4.0
1	A	317	PHE	3.9
1	A	282	LEU	3.7
1	A	326	PRO	3.6
1	A	234	VAL	3.4
1	A	327	VAL	3.4
1	A	320	ARG	3.4
1	A	352	TRP	3.3
1	A	314	LEU	3.2
1	A	241	VAL	3.2
1	A	229	MET	3.1
1	A	274	ASP	3.1
1	A	9	PRO	3.1
1	A	303	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	322	VAL	3.0
1	A	15	ARG	3.0
1	A	273	THR	3.0
1	A	201	ARG	2.8
1	A	333	LEU	2.8
1	A	285	MET	2.8
1	A	318	PRO	2.7
1	A	239	LEU	2.7
1	A	243	VAL	2.7
1	A	275	GLY	2.7
1	A	23	ARG	2.7
1	A	301	VAL	2.7
1	A	294	VAL	2.6
1	A	339	LEU	2.6
1	A	315	THR	2.6
1	A	321	LEU	2.6
1	A	240	ALA	2.6
1	A	297	THR	2.6
1	A	251	VAL	2.6
1	A	75	ASP	2.5
1	A	330	PRO	2.5
1	A	302	SER	2.5
1	A	202	ARG	2.4
1	A	242	ALA	2.4
1	A	328	GLU	2.4
1	A	312	TRP	2.4
1	A	105	ARG	2.3
1	A	293	GLN	2.3
1	A	276	ALA	2.3
1	A	237	VAL	2.2
1	A	11	ARG	2.2
1	A	259	THR	2.2
1	A	281	LYS	2.1
1	A	268	PHE	2.1
1	A	212	ALA	2.1
3	C	13	DG	2.1
1	A	246	ASP	2.1
1	A	107	GLY	2.1
1	A	235	LYS	2.0
1	A	253	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
3	A5L	C	18	21/23	0.82	0.17	48,56,70,71	0
2	8OG	B	6	23/24	0.95	0.07	29,38,41,45	0

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	CA	A	1	1/1	0.89	0.20	66,66,66,66	0
4	SF4	A	400	8/8	0.99	0.03	34,36,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.