



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:25 PM GMT

PDB ID : 1AQI
Title : STRUCTURE OF ADENINE-N6-DNA-METHYLTRANSFERASE TAQI
Authors : Schluckebier, G.; Saenger, W.
Deposited on : 1996-07-25
Resolution : 2.60 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

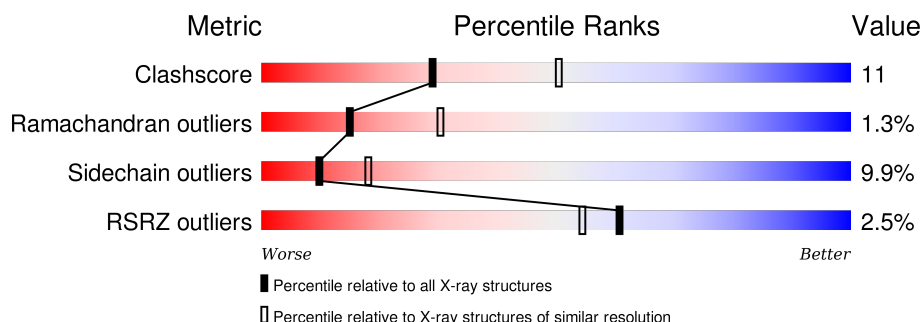
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	421	
1	B	421	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6322 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.

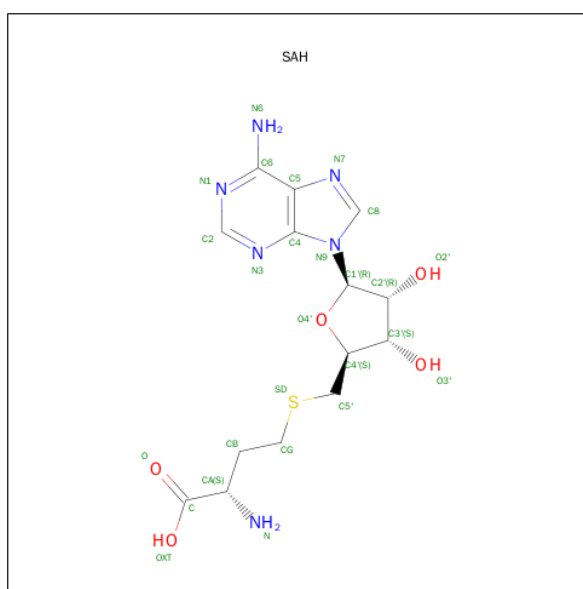
- Molecule 1 is a protein called ADENINE-N6-DNA-METHYLTRANSFERASE TAQI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	0
			3101	2028	534	533	6			
1	B	382	Total	C	N	O	S	0	0	0
			3101	2028	534	533	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	370	THR	SER	CONFLICT	UNP P14385
B	370	THR	SER	CONFLICT	UNP P14385

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

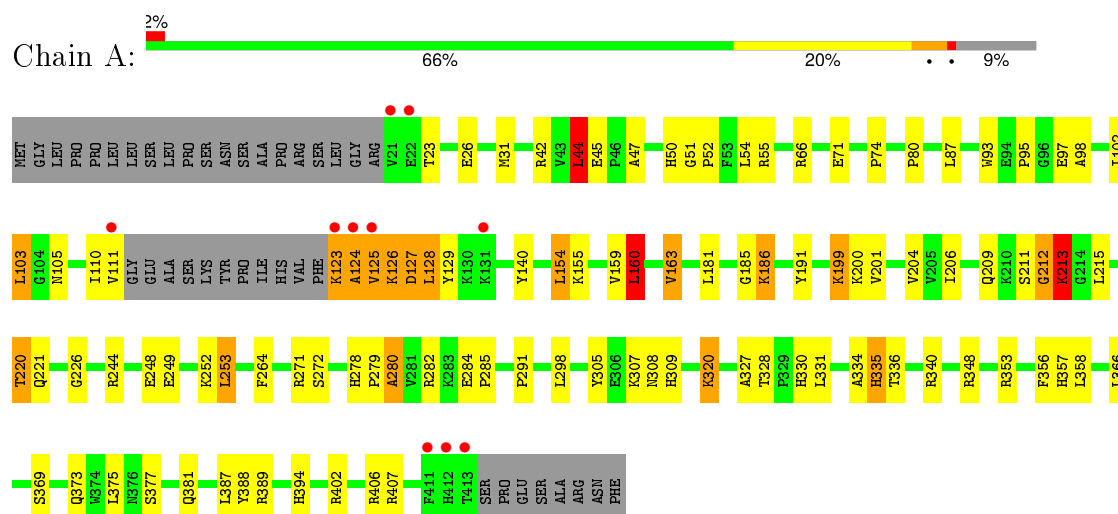
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total	O	0	0
			36	36		
3	B	32	Total	O	0	0
			32	32		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: ADENINE-N6-DNA-METHYLTRANSFERASE TAQI



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.08 Å 144.06 Å 53.44 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60 19.96 – 2.62	Depositor EDS
% Data completeness (in resolution range)	96.0 (10.00-2.60) 96.5 (19.96-2.62)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.29 (at 2.63 Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.219 , 0.281 0.208 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 75.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 30278 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6322	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.40 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.8616e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: SAH

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	0.43	0/3200	0.71	6/4347 (0.1%)
1	B	0.44	0/3200	0.71	6/4347 (0.1%)
All	All	0.43	0/6400	0.71	12/8694 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	LEU	CA-CB-CG	7.08	131.58	115.30
1	B	215	LEU	CA-CB-CG	6.80	130.95	115.30
1	A	160	LEU	CA-CB-CG	6.28	129.75	115.30
1	B	160	LEU	CA-CB-CG	6.07	129.27	115.30
1	A	125	VAL	N-CA-C	-5.69	95.64	111.00
1	B	125	VAL	N-CA-C	-5.63	95.79	111.00
1	B	199	LYS	N-CA-C	5.53	125.92	111.00
1	A	44	LEU	CA-CB-CG	5.39	127.69	115.30
1	A	199	LYS	N-CA-C	5.39	125.54	111.00
1	B	44	LEU	CA-CB-CG	5.12	127.08	115.30
1	A	103	LEU	CA-CB-CG	5.06	126.93	115.30
1	B	48	CYS	N-CA-C	5.01	124.53	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	123	LYS	Mainchain

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	3101	0	3099	75	0
1	B	3101	0	3099	67	0
2	A	26	0	19	1	0
2	B	26	0	19	4	0
3	A	36	0	0	3	0
3	B	32	0	0	0	0
All	All	6322	0	6236	142	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 11.

All (142) 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:186:LYS:HD3	1:A:209:GLN:HB3	1.43	0.99
1:B:186:LYS:HD3	1:B:209:GLN:HB3	1.42	0.97
1:B:123:LYS:N	1:B:126:LYS:HB3	1.91	0.85
1:B:31:MET:SD	1:B:163:VAL:HG22	2.18	0.84
1:A:31:MET:SD	1:A:163:VAL:HG22	2.19	0.82
1:A:124:ALA:O	1:A:128:LEU:HB2	1.78	0.81
1:A:95:PRO:HB2	1:A:97:GLU:HG2	1.64	0.79
1:B:42:ARG:HG2	1:B:66:ARG:HD3	1.66	0.78
1:B:124:ALA:O	1:B:128:LEU:HB2	1.83	0.78
1:A:123:LYS:HG3	1:A:123:LYS:O	1.82	0.78
1:B:95:PRO:HB2	1:B:97:GLU:HG2	1.63	0.77
1:A:42:ARG:HG2	1:A:66:ARG:HD3	1.67	0.75
1:B:330:HIS:HE1	1:B:357:HIS:HD2	1.36	0.73
1:A:328:THR:O	1:A:330:HIS:HD2	1.73	0.71
1:A:330:HIS:HE1	1:A:357:HIS:HD2	1.37	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:THR:O	1:B:330:HIS:HD2	1.75	0.70
1:B:105:ASN:ND2	2:B:500:SAH:HN1	1.91	0.68
1:B:330:HIS:HE1	1:B:357:HIS:CD2	2.12	0.68
1:A:123:LYS:O	1:A:124:ALA:HB3	1.93	0.68
1:A:330:HIS:HE1	1:A:357:HIS:CD2	2.10	0.67
1:A:186:LYS:HE3	1:A:211:SER:HB2	1.79	0.65
1:B:186:LYS:HE3	1:B:211:SER:HB2	1.79	0.64
1:B:93:TRP:CZ2	1:B:95:PRO:HB3	2.34	0.62
1:A:331:LEU:HD23	1:A:358:LEU:HD22	1.81	0.62
1:A:93:TRP:CZ2	1:A:95:PRO:HB3	2.35	0.62
1:A:50:HIS:CE1	1:A:52:PRO:HG3	2.35	0.61
1:B:105:ASN:HD21	2:B:500:SAH:HN1	1.49	0.61
1:A:123:LYS:N	1:A:126:LYS:HB3	2.16	0.60
1:A:244:ARG:HE	1:A:387:LEU:HD22	1.69	0.58
1:B:74:PRO:HB3	1:B:87:LEU:HD11	1.86	0.58
1:B:244:ARG:HH12	1:B:402:ARG:CZ	2.16	0.58
1:B:124:ALA:HA	1:B:127:ASP:HB2	1.84	0.58
1:A:123:LYS:O	1:A:124:ALA:CB	2.52	0.57
1:A:74:PRO:HB3	1:A:87:LEU:HD11	1.86	0.57
1:B:185:GLY:HA2	1:B:212:GLY:N	2.19	0.56
1:B:42:ARG:HD3	1:B:66:ARG:NH1	2.22	0.55
1:A:47:ALA:HB1	2:A:500:SAH:O4'	2.07	0.55
1:B:331:LEU:HD23	1:B:358:LEU:HD22	1.88	0.55
1:A:244:ARG:HH12	1:A:402:ARG:CZ	2.19	0.54
1:A:309:HIS:HE1	3:A:529:HOH:O	1.90	0.54
1:B:50:HIS:CE1	1:B:52:PRO:HG3	2.42	0.54
1:B:55:ARG:NH2	1:B:80:PRO:HD3	2.23	0.54
1:A:185:GLY:HA2	1:A:212:GLY:N	2.23	0.54
1:A:42:ARG:HD3	1:A:66:ARG:NH1	2.23	0.53
1:A:320:LYS:HB3	1:A:327:ALA:HB2	1.90	0.53
1:B:244:ARG:HE	1:B:387:LEU:HD22	1.73	0.53
1:B:284:GLU:HG2	1:B:285:PRO:HD2	1.90	0.53
1:B:320:LYS:HB3	1:B:327:ALA:HB2	1.89	0.53
1:B:21:VAL:HG22	2:B:500:SAH:HN2	1.74	0.53
1:A:124:ALA:HA	1:A:127:ASP:HB2	1.90	0.52
1:B:279:PRO:O	1:B:280:ALA:CB	2.58	0.52
1:B:366:LEU:H	1:B:366:LEU:HD23	1.73	0.52
1:B:366:LEU:N	1:B:366:LEU:HD23	2.25	0.52
1:B:244:ARG:NH1	1:B:402:ARG:NH1	2.59	0.51
1:A:244:ARG:NH1	1:A:402:ARG:NH1	2.58	0.51
1:B:71:GLU:O	1:B:87:LEU:HA	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:GLU:O	1:A:87:LEU:HA	2.10	0.51
1:B:298:LEU:HD23	1:B:334:ALA:HB2	1.92	0.51
1:A:272:SER:OG	1:A:353:ARG:HD2	2.10	0.51
1:A:284:GLU:HG2	1:A:285:PRO:HD2	1.93	0.50
1:A:213:LYS:HE2	1:A:213:LYS:HA	1.92	0.50
1:A:124:ALA:H	1:A:127:ASP:H	1.59	0.50
1:B:305:TYR:CE2	1:B:348:ARG:HD3	2.47	0.50
1:A:305:TYR:CE2	1:A:348:ARG:HD3	2.47	0.50
1:B:272:SER:OG	1:B:353:ARG:HD2	2.12	0.50
1:A:55:ARG:NH2	1:A:80:PRO:HD3	2.27	0.49
1:B:278:HIS:CD2	1:B:279:PRO:O	2.65	0.49
1:A:279:PRO:O	1:A:280:ALA:CB	2.60	0.49
1:A:191:TYR:O	1:A:220:THR:HB	2.12	0.49
1:A:42:ARG:HD3	1:A:66:ARG:HH11	1.76	0.49
1:B:213:LYS:HA	1:B:213:LYS:HE2	1.94	0.48
1:B:51:GLY:N	1:B:52:PRO:HD3	2.28	0.48
1:B:42:ARG:HD3	1:B:66:ARG:HH11	1.77	0.48
1:A:366:LEU:HD23	1:A:366:LEU:H	1.78	0.48
1:A:278:HIS:CD2	1:A:279:PRO:O	2.67	0.48
1:A:126:LYS:O	1:A:129:TYR:HB2	2.13	0.47
1:B:279:PRO:O	1:B:280:ALA:HB3	2.14	0.47
1:B:335:HIS:HB3	1:B:356:PHE:CE2	2.49	0.47
1:B:44:LEU:HD22	1:B:45:GLU:N	2.29	0.47
1:A:335:HIS:O	1:A:394:HIS:HB2	2.15	0.47
1:B:50:HIS:CD2	1:B:50:HIS:H	2.32	0.47
1:A:366:LEU:HD23	1:A:366:LEU:N	2.30	0.46
1:B:249:GLU:HA	1:B:252:LYS:HE3	1.96	0.46
1:A:298:LEU:HD23	1:A:334:ALA:HB2	1.96	0.46
1:B:126:LYS:O	1:B:129:TYR:HB2	2.16	0.46
1:B:21:VAL:CG2	2:B:500:SAH:HN2	2.29	0.46
1:A:50:HIS:H	1:A:50:HIS:CD2	2.34	0.46
1:A:291:PRO:HB3	1:A:308:ASN:HD22	1.80	0.46
1:B:191:TYR:O	1:B:220:THR:HB	2.16	0.46
1:A:305:TYR:CZ	1:A:348:ARG:HD3	2.51	0.46
1:A:51:GLY:N	1:A:52:PRO:HD3	2.31	0.45
1:B:45:GLU:HB2	1:B:54:LEU:HD13	1.97	0.45
1:B:123:LYS:O	1:B:124:ALA:HB3	2.17	0.45
1:A:279:PRO:O	1:A:280:ALA:HB3	2.16	0.45
1:B:377:SER:O	1:B:381:GLN:HG2	2.17	0.45
1:B:335:HIS:O	1:B:394:HIS:HB2	2.17	0.45
1:A:102:ILE:HD12	1:A:154:LEU:HD13	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:ARG:HA	1:B:282:ARG:HE	1.83	0.44
1:B:244:ARG:NH1	1:B:402:ARG:CZ	2.80	0.44
1:A:26:GLU:CD	1:A:26:GLU:H	2.21	0.44
1:A:282:ARG:HA	1:A:282:ARG:HE	1.82	0.44
1:B:102:ILE:HD12	1:B:154:LEU:HD13	2.00	0.44
1:A:249:GLU:HA	1:A:252:LYS:HE3	1.99	0.43
1:A:110:ILE:HG22	1:A:111:VAL:H	1.82	0.43
1:A:124:ALA:CA	1:A:127:ASP:HB2	2.48	0.43
1:B:284:GLU:CG	1:B:285:PRO:HD2	2.49	0.43
1:A:44:LEU:HD22	1:A:45:GLU:N	2.33	0.43
1:A:123:LYS:O	1:A:123:LYS:CG	2.60	0.43
1:A:126:LYS:O	1:A:129:TYR:N	2.51	0.43
1:A:98:ALA:CB	1:A:155:LYS:HG3	2.48	0.43
1:A:377:SER:O	1:A:381:GLN:HG2	2.19	0.43
1:A:406:ARG:HH11	1:A:406:ARG:HG3	1.84	0.43
1:A:244:ARG:NH1	1:A:402:ARG:CZ	2.81	0.43
1:A:335:HIS:HB3	1:A:356:PHE:CE2	2.54	0.43
1:A:200:LYS:HE3	1:A:200:LYS:HB2	1.84	0.43
1:B:358:LEU:N	1:B:358:LEU:HD12	2.34	0.42
1:B:110:ILE:HG22	1:B:111:VAL:H	1.83	0.42
1:B:160:LEU:C	1:B:160:LEU:HD23	2.40	0.42
1:A:185:GLY:HA2	1:A:212:GLY:HA2	2.02	0.42
1:B:388:TYR:O	1:B:389:ARG:C	2.57	0.42
1:B:26:GLU:CD	1:B:26:GLU:H	2.23	0.42
1:A:307:LYS:HB3	1:A:309:HIS:CE1	2.55	0.42
1:B:264:PHE:CZ	1:B:366:LEU:HD13	2.55	0.42
1:B:186:LYS:H	1:B:186:LYS:HD2	1.85	0.42
1:B:323:ARG:HB2	1:B:326:TYR:CD2	2.54	0.42
1:B:253:LEU:HD23	1:B:253:LEU:HA	1.84	0.41
1:A:335:HIS:HD2	1:A:336:THR:HG23	1.85	0.41
1:A:406:ARG:HG3	1:A:406:ARG:NH1	2.36	0.41
1:A:264:PHE:CZ	1:A:366:LEU:HD13	2.55	0.41
1:A:264:PHE:HZ	1:A:366:LEU:HD13	1.85	0.41
1:A:124:ALA:H	1:A:127:ASP:HB2	1.85	0.41
1:A:388:TYR:O	1:A:389:ARG:C	2.59	0.41
1:A:160:LEU:HD23	1:A:160:LEU:C	2.41	0.41
1:B:44:LEU:HD22	1:B:45:GLU:H	1.85	0.41
1:B:53:PHE:HB3	1:B:103:LEU:HD13	2.03	0.41
1:B:406:ARG:HH11	1:B:406:ARG:HG3	1.86	0.41
1:A:253:LEU:HA	1:A:253:LEU:HD23	1.87	0.41
1:A:199:LYS:HA	1:A:199:LYS:HD3	1.97	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:GLY:HA3	3:A:528:HOH:O	2.20	0.41
1:A:309:HIS:CE1	3:A:529:HOH:O	2.70	0.40
1:B:264:PHE:HZ	1:B:366:LEU:HD13	1.86	0.40
1:B:185:GLY:HA2	1:B:212:GLY:HA2	2.03	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	378/421 (90%)	356 (94%)	17 (4%)	5 (1%)	15	30
1	B	378/421 (90%)	356 (94%)	17 (4%)	5 (1%)	15	30
All	All	756/842 (90%)	712 (94%)	34 (4%)	10 (1%)	15	30

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	GLY
1	A	213	LYS
1	A	280	ALA
1	A	407	ARG
1	B	124	ALA
1	B	212	GLY
1	B	280	ALA
1	B	407	ARG
1	A	124	ALA
1	B	213	LYS

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	323/356 (91%)	291 (90%)	32 (10%)	10	18
1	B	323/356 (91%)	291 (90%)	32 (10%)	10	18
All	All	646/712 (91%)	582 (90%)	64 (10%)	10	18

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	THR
1	A	44	LEU
1	A	54	LEU
1	A	103	LEU
1	A	105	ASN
1	A	123	LYS
1	A	125	VAL
1	A	126	LYS
1	A	127	ASP
1	A	128	LEU
1	A	140	TYR
1	A	154	LEU
1	A	159	VAL
1	A	160	LEU
1	A	163	VAL
1	A	181	LEU
1	A	186	LYS
1	A	201	VAL
1	A	204	VAL
1	A	206	ILE
1	A	213	LYS
1	A	220	THR
1	A	221	GLN
1	A	248	GLU
1	A	253	LEU
1	A	271	ARG
1	A	320	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	335	HIS
1	A	340	ARG
1	A	369	SER
1	A	373	GLN
1	A	375	LEU
1	B	23	THR
1	B	44	LEU
1	B	54	LEU
1	B	103	LEU
1	B	105	ASN
1	B	123	LYS
1	B	125	VAL
1	B	126	LYS
1	B	127	ASP
1	B	128	LEU
1	B	140	TYR
1	B	154	LEU
1	B	159	VAL
1	B	160	LEU
1	B	163	VAL
1	B	181	LEU
1	B	186	LYS
1	B	201	VAL
1	B	204	VAL
1	B	206	ILE
1	B	213	LYS
1	B	220	THR
1	B	221	GLN
1	B	248	GLU
1	B	253	LEU
1	B	271	ARG
1	B	320	LYS
1	B	335	HIS
1	B	340	ARG
1	B	369	SER
1	B	373	GLN
1	B	375	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	105	ASN
1	A	278	HIS
1	A	309	HIS
1	A	330	HIS
1	A	335	HIS
1	A	357	HIS
1	B	50	HIS
1	B	105	ASN
1	B	278	HIS
1	B	309	HIS
1	B	330	HIS
1	B	335	HIS
1	B	357	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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	SAH	A	500	-	20,28,28	1.00	2 (10%)	19,40,40	1.14	2 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAH	B	500	-	20,28,28	0.86	2 (10%)	19,40,40	0.93	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	SAH	A	500	-	-	0/7/31/31	0/3/3/3
2	SAH	B	500	-	-	0/7/31/31	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	SAH	C8-N7	-2.78	1.29	1.34
2	B	500	SAH	C8-N7	-2.46	1.29	1.34
2	B	500	SAH	O4'-C1'	2.23	1.44	1.41
2	A	500	SAH	O4'-C1'	2.97	1.45	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	SAH	C2'-C1'-N9	-2.33	110.73	114.29
2	A	500	SAH	C5'-SD-CG	3.13	111.81	102.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	SAH	1	0
2	B	500	SAH	4	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	382/421 (90%)	-0.52	10 (2%) 59 53	4, 20, 56, 130	0
1	B	382/421 (90%)	-0.50	9 (2%) 62 56	4, 21, 59, 128	0
All	All	764/842 (90%)	-0.51	19 (2%) 61 54	4, 21, 59, 130	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	ALA	6.7
1	B	413	THR	5.6
1	A	123	LYS	4.9
1	A	413	THR	4.9
1	B	123	LYS	4.0
1	A	412	HIS	3.9
1	A	125	VAL	3.5
1	B	22	GLU	3.3
1	B	21	VAL	3.2
1	A	131	LYS	3.1
1	A	111	VAL	3.0
1	B	139	LYS	2.8
1	A	411	PHE	2.7
1	A	21	VAL	2.5
1	B	224	GLU	2.5
1	B	111	VAL	2.4
1	B	124	ALA	2.3
1	B	126	LYS	2.3
1	A	22	GLU	2.1

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SAH	A	500	26/26	0.94	0.13	-0.12	19,24,33,36	0
2	SAH	B	500	26/26	0.96	0.12	-0.21	10,20,31,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.