



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:27 AM GMT

PDB ID : 3AV6
Title : Crystal structure of mouse DNA methyltransferase 1 with AdoMet
Authors : Takeshita, K.; Suetake, I.; Yamashita, E.; Suga, M.; Narita, H.; Nakagawa, A.; Tajima, S.
Deposited on : 2011-02-22
Resolution : 3.09 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

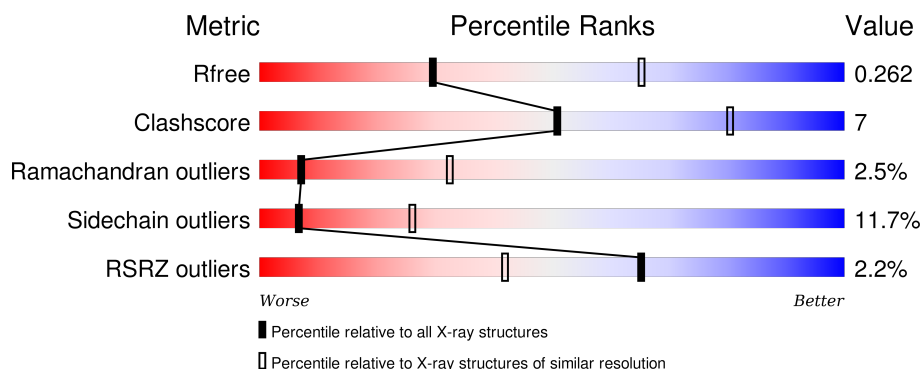
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

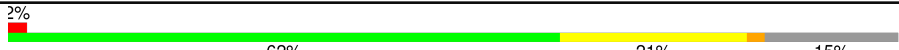
The reported resolution of this entry is 3.09 Å.

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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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	1330	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9110 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.

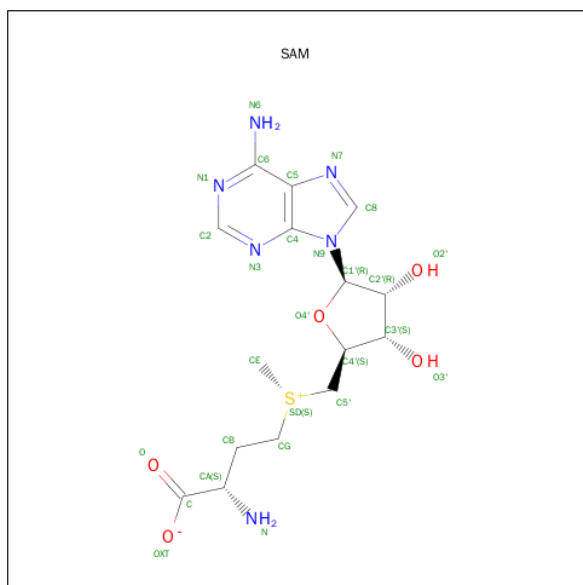
- Molecule 1 is a protein called DNA (cytosine-5)-methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1135	Total	C	N	O	S	0	0	0
			9079	5744	1579	1697	59			

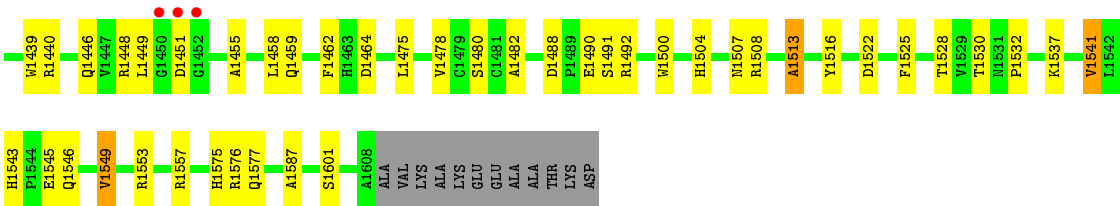
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Zn	0	0
			4	4		

- Molecule 3 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C₁₅H₂₂N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.00Å 97.14Å 130.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.14 – 3.09 43.14 – 3.09	Depositor EDS
% Data completeness (in resolution range)	(Not available) (43.14-3.09) 99.6 (43.14-3.09)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.02 (at 3.12Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.191 , 0.255 0.198 , 0.262	Depositor DCC
R_{free} test set	1626 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 64.6	EDS
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 31971 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9110	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, SAM

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	0.52	0/9299	0.79	2/12573 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1360	LEU	C-N-CA	7.21	139.73	121.70
1	A	1042	ILE	C-N-CA	6.25	137.34	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9079	0	8847	124	0
2	A	4	0	0	0	0
3	A	27	0	22	0	0
All	All	9110	0	8869	124	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 7.

All (124) 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:1543:HIS:HD2	1:A:1546:GLN:H	1.21	0.88
1:A:885:LYS:HA	1:A:886:THR:HG23	1.60	0.82
1:A:975:GLU:OE1	1:A:978:ARG:HD2	1.81	0.80
1:A:886:THR:H	1:A:887:GLN:HG2	1.50	0.77
1:A:1543:HIS:CD2	1:A:1546:GLN:H	2.02	0.76
1:A:1488:ASP:O	1:A:1491:SER:HB3	1.88	0.73
1:A:1159:HIS:HE1	1:A:1166:THR:H	1.37	0.72
1:A:1543:HIS:CD2	1:A:1545:GLU:H	2.10	0.70
1:A:1043:ASN:ND2	1:A:1085:ARG:O	2.23	0.66
1:A:1541:VAL:HG13	1:A:1549:VAL:HG22	1.78	0.65
1:A:1234:GLY:HA3	1:A:1278:ARG:HH21	1.62	0.63
1:A:783:THR:HG21	1:A:897:CYS:HB2	1.80	0.63
1:A:1023:LYS:O	1:A:1048:SER:HB3	1.99	0.62
1:A:753:VAL:HG22	1:A:761:GLU:HB3	1.81	0.62
1:A:1333:PRO:HD2	1:A:1359:ARG:HB2	1.82	0.61
1:A:1478:VAL:HG13	1:A:1500:TRP:NE1	2.17	0.60
1:A:445:ALA:O	1:A:458:GLY:HA3	2.02	0.59
1:A:929:SER:HB3	1:A:938:ARG:HG2	1.83	0.58
1:A:1157:GLY:HA3	1:A:1587:ALA:HB3	1.85	0.58
1:A:992:PRO:HD2	1:A:1336:VAL:HG22	1.86	0.58
1:A:1543:HIS:HD2	1:A:1545:GLU:H	1.53	0.57
1:A:1530:THR:O	1:A:1575:HIS:HB3	2.05	0.56
1:A:1229:CYS:O	1:A:1231:GLY:N	2.38	0.56
1:A:1413:ARG:O	1:A:1553:ARG:HD2	2.05	0.56
1:A:1374:MET:HE1	1:A:1525:PHE:HZ	1.70	0.56
1:A:1023:LYS:HE2	1:A:1052:ALA:HB2	1.87	0.54
1:A:522:LEU:HD11	1:A:587:MET:HE3	1.88	0.54
1:A:472:LEU:H	1:A:603:ALA:HB1	1.73	0.54
1:A:526:PRO:O	1:A:527:ASP:HB2	2.09	0.53
1:A:1139:LEU:HD21	1:A:1163:ILE:HG22	1.89	0.53
1:A:595:GLY:HA3	1:A:1504:HIS:CE1	2.44	0.53
1:A:380:ALA:HB1	1:A:462:LYS:HB3	1.90	0.53
1:A:955:LYS:NZ	1:A:955:LYS:H	2.07	0.53
1:A:1330:PHE:H	1:A:1356:ASN:HD21	1.57	0.52
1:A:1005:CYS:HB2	1:A:1017:ILE:HA	1.90	0.52
1:A:1385:SER:C	1:A:1416:ILE:HD11	2.30	0.52
1:A:1371:ARG:NH2	1:A:1522:ASP:OD1	2.44	0.51
1:A:774:SER:O	1:A:776:PRO:HD3	2.10	0.51
1:A:1171:GLU:O	1:A:1191:THR:HA	2.10	0.50
1:A:386:MET:HG3	1:A:459:ILE:HD13	1.93	0.50
1:A:1306:GLN:HB3	1:A:1333:PRO:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1040:THR:CG2	1:A:1366:ARG:HH22	2.24	0.50
1:A:535:ASN:O	1:A:539:THR:HB	2.12	0.50
1:A:410:MET:HG2	1:A:491:GLU:HB2	1.93	0.50
1:A:1407:HIS:HD2	1:A:1409:GLN:HE21	1.60	0.49
1:A:580:PRO:HD2	1:A:583:LEU:HD12	1.94	0.49
1:A:1143:ARG:HG2	1:A:1167:LEU:HD11	1.94	0.49
1:A:1449:LEU:HD21	1:A:1455:ALA:HB2	1.94	0.49
1:A:770:PRO:HB3	1:A:778:TYR:CE1	2.47	0.49
1:A:730:ASN:HD21	1:A:732:ASP:HB2	1.77	0.49
1:A:886:THR:OG1	1:A:887:GLN:HA	2.13	0.49
1:A:705:ASP:O	1:A:1235:MET:HB2	2.12	0.48
1:A:567:VAL:HG13	1:A:581:ILE:HG23	1.95	0.48
1:A:793:MET:HB3	1:A:828:LEU:HD12	1.95	0.48
1:A:1030:THR:HG22	1:A:1032:ARG:H	1.78	0.48
1:A:966:ASP:HB2	1:A:967:PRO:HD2	1.96	0.47
1:A:1275:VAL:HG22	1:A:1283:LEU:HD22	1.95	0.47
1:A:376:HIS:CE1	1:A:462:LYS:HB2	2.50	0.47
1:A:1027:PRO:O	1:A:1030:THR:HB	2.14	0.47
1:A:1370:VAL:O	1:A:1374:MET:HG2	2.15	0.47
1:A:1254:PHE:HD2	1:A:1268:LEU:HD12	1.80	0.46
1:A:1002:GLU:HB2	1:A:1020:ARG:HB3	1.98	0.46
1:A:783:THR:CG2	1:A:897:CYS:HB2	2.45	0.46
1:A:1302:LEU:O	1:A:1314:ARG:HA	2.16	0.46
1:A:1274:PHE:HA	1:A:1277:TYR:CD1	2.51	0.46
1:A:522:LEU:HB3	1:A:581:ILE:HG13	1.97	0.46
1:A:639:ILE:HD11	1:A:1238:PHE:HB3	1.97	0.45
1:A:1462:PHE:O	1:A:1475:LEU:HB3	2.16	0.45
1:A:1374:MET:HE1	1:A:1525:PHE:CZ	2.50	0.45
1:A:1302:LEU:HD12	1:A:1317:ILE:HD13	1.98	0.45
1:A:1275:VAL:HG11	1:A:1346:VAL:HG22	1.99	0.45
1:A:1440:ARG:NH2	1:A:1513:ALA:HA	2.31	0.45
1:A:357:PRO:HB2	1:A:366:LEU:HD22	1.98	0.45
1:A:1403:LEU:HD12	1:A:1557:ARG:HD3	1.99	0.45
1:A:472:LEU:H	1:A:603:ALA:CB	2.29	0.45
1:A:414:THR:HG22	1:A:415:SER:H	1.82	0.45
1:A:978:ARG:NH2	1:A:1507:ASN:OD1	2.50	0.45
1:A:1266:PHE:HB3	1:A:1320:ALA:HB3	1.98	0.45
1:A:392:LEU:HB3	1:A:411:HIS:CE1	2.52	0.45
1:A:780:ALA:HB2	1:A:799:TRP:CE3	2.51	0.45
1:A:533:LEU:HD22	1:A:537:ILE:HD12	1.98	0.44
1:A:737:LEU:HB2	1:A:753:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:TYR:CE2	1:A:517:ILE:HD11	2.52	0.44
1:A:914:VAL:HA	1:A:930:ILE:HG22	2.00	0.44
1:A:472:LEU:HD21	1:A:512:ILE:HG12	2.00	0.44
1:A:1464:ASP:HA	1:A:1482:ALA:HB1	1.98	0.44
1:A:735:SER:HA	1:A:793:MET:HE1	1.98	0.44
1:A:1439:TRP:HB3	1:A:1516:TYR:HB2	2.00	0.44
1:A:1420:MET:HA	1:A:1420:MET:HE2	2.00	0.44
1:A:1426:ALA:O	1:A:1430:HIS:HD2	2.01	0.44
1:A:1360:LEU:CB	1:A:1361:SER:HB2	2.47	0.43
1:A:811:THR:HG21	1:A:1284:LYS:HB3	2.01	0.43
1:A:1048:SER:OG	1:A:1050:GLU:HB2	2.18	0.43
1:A:726:LYS:HA	1:A:770:PRO:HA	2.00	0.43
1:A:371:LEU:HD11	1:A:424:HIS:CD2	2.52	0.43
1:A:776:PRO:O	1:A:777:LEU:HB2	2.19	0.43
1:A:526:PRO:O	1:A:527:ASP:CB	2.67	0.43
1:A:1330:PHE:H	1:A:1356:ASN:ND2	2.17	0.42
1:A:1246:PHE:HA	1:A:1249:SER:HB3	2.02	0.42
1:A:802:ALA:HA	1:A:817:LEU:HD12	2.00	0.42
1:A:964:LYS:O	1:A:965:LYS:HB2	2.20	0.42
1:A:980:TYR:HA	1:A:981:SER:HA	1.73	0.42
1:A:723:GLN:N	1:A:724:GLY:HA3	2.34	0.42
1:A:1143:ARG:HB2	1:A:1221:GLU:HG3	2.01	0.42
1:A:1394:GLU:HG3	1:A:1395:PRO:HD2	2.02	0.41
1:A:1360:LEU:HD22	1:A:1360:LEU:HA	1.89	0.41
1:A:413:PHE:HD2	1:A:416:PHE:HB3	1.85	0.41
1:A:594:ALA:HB1	1:A:1492:ARG:HH21	1.85	0.41
1:A:635:PHE:HD1	1:A:1243:TYR:CD2	2.39	0.41
1:A:1223:LEU:CB	1:A:1263:PRO:HG3	2.50	0.41
1:A:1144:THR:HA	1:A:1222:MET:O	2.20	0.41
1:A:955:LYS:HZ2	1:A:955:LYS:H	1.69	0.41
1:A:588:ARG:O	1:A:592:HIS:HD2	2.03	0.41
1:A:1076:GLN:HE22	1:A:1080:GLN:HG3	1.84	0.41
1:A:1173:TRP:CD1	1:A:1175:PRO:HD2	2.56	0.41
1:A:1418:LYS:HD2	1:A:1532:PRO:HD2	2.03	0.41
1:A:434:GLU:C	1:A:436:ASN:H	2.24	0.41
1:A:1151:CYS:HB3	1:A:1577:GLN:HG2	2.03	0.41
1:A:414:THR:HG21	1:A:453:PRO:O	2.21	0.41
1:A:1030:THR:C	1:A:1032:ARG:H	2.23	0.40
1:A:631:PHE:HE1	1:A:1246:PHE:CE2	2.38	0.40
1:A:381:VAL:O	1:A:461:GLY:HA2	2.22	0.40
1:A:897:CYS:HB3	1:A:900:CYS:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:GLN:O	1:A:692:ARG:HG3	2.21	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	1113/1330 (84%)	991 (89%)	94 (8%)	28 (2%)	7	32

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	465	GLY
1	A	573	ALA
1	A	772	ASP
1	A	777	LEU
1	A	896	PHE
1	A	965	LYS
1	A	1230	GLN
1	A	1233	SER
1	A	1361	SER
1	A	430	THR
1	A	476	ASP
1	A	732	ASP
1	A	1037	SER
1	A	408	SER
1	A	730	ASN
1	A	850	GLY
1	A	1229	CYS
1	A	1513	ALA
1	A	480	LYS
1	A	603	ALA

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Mol	Chain	Res	Type
1	A	921	VAL
1	A	1038	TYR
1	A	379	ASP
1	A	776	PRO
1	A	922	ASP
1	A	1362	SER
1	A	1410	PRO
1	A	409	PRO

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	1000/1162 (86%)	883 (88%)	117 (12%)	7 26

All (117) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	A	385	GLN
1	A	405	TYR
1	A	406	GLU
1	A	408	SER
1	A	410	MET
1	A	414	THR
1	A	421	SER
1	A	429	ASP
1	A	448	ILE
1	A	451	GLU
1	A	459	ILE
1	A	469	GLN
1	A	476	ASP
1	A	479	GLU
1	A	481	VAL
1	A	500	GLU
1	A	507	LEU

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Mol	Chain	Res	Type
1	A	515	SER
1	A	533	LEU
1	A	539	THR
1	A	548	VAL
1	A	549	ASN
1	A	581	ILE
1	A	590	LEU
1	A	602	ARG
1	A	639	ILE
1	A	640	GLU
1	A	654	ARG
1	A	656	CYS
1	A	666	GLU
1	A	693	ARG
1	A	697	LEU
1	A	710	ASP
1	A	719	LYS
1	A	723	GLN
1	A	725	LYS
1	A	727	LYS
1	A	728	LYS
1	A	729	GLN
1	A	749	TYR
1	A	755	ILE
1	A	758	GLU
1	A	759	MET
1	A	772	ASP
1	A	775	LYS
1	A	779	LEU
1	A	817	LEU
1	A	826	MET
1	A	844	GLU
1	A	845	ASN
1	A	865	LYS
1	A	872	TRP
1	A	876	GLU
1	A	882	SER
1	A	892	ASN
1	A	900	CYS
1	A	902	ARG
1	A	915	LEU
1	A	917	GLN

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Mol	Chain	Res	Type
1	A	920	GLU
1	A	943	VAL
1	A	951	THR
1	A	955	LYS
1	A	981	SER
1	A	990	ASP
1	A	1005	CYS
1	A	1008	LYS
1	A	1012	VAL
1	A	1040	THR
1	A	1042	ILE
1	A	1055	ASN
1	A	1062	ARG
1	A	1066	GLU
1	A	1094	SER
1	A	1095	LYS
1	A	1142	LEU
1	A	1197	LEU
1	A	1198	LEU
1	A	1199	LYS
1	A	1207	THR
1	A	1209	SER
1	A	1213	ARG
1	A	1223	LEU
1	A	1229	CYS
1	A	1232	PHE
1	A	1237	ARG
1	A	1241	ARG
1	A	1270	ASN
1	A	1271	VAL
1	A	1272	ARG
1	A	1275	VAL
1	A	1289	CYS
1	A	1292	ARG
1	A	1312	THR
1	A	1313	ARG
1	A	1317	ILE
1	A	1337	PHE
1	A	1354	VAL
1	A	1360	LEU
1	A	1361	SER
1	A	1412	LEU

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Mol	Chain	Res	Type
1	A	1416	ILE
1	A	1446	GLN
1	A	1448	ARG
1	A	1451	ASP
1	A	1458	LEU
1	A	1459	GLN
1	A	1480	SER
1	A	1490	GLU
1	A	1508	ARG
1	A	1528	THR
1	A	1537	LYS
1	A	1541	VAL
1	A	1549	VAL
1	A	1576	ARG
1	A	1601	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	376	HIS
1	A	468	ASN
1	A	469	GLN
1	A	730	ASN
1	A	892	ASN
1	A	917	GLN
1	A	953	ASN
1	A	1076	GLN
1	A	1159	HIS
1	A	1212	GLN
1	A	1239	ASN
1	A	1402	GLN
1	A	1409	GLN
1	A	1430	HIS
1	A	1446	GLN
1	A	1509	HIS
1	A	1543	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 5 ligands modelled in this entry, 4 are 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	$\# Z > 2$
3	SAM	A	1	-	21,29,29	1.06	0	17,42,42	2.76	4 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SAM	A	1	-	-	0/8/33/33	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	SAM	N3-C2-N1	-8.53	122.36	128.89
3	A	1	SAM	O3'-C3'-C4'	-4.70	96.94	111.05
3	A	1	SAM	C4-C5-N7	-3.58	106.19	109.48
3	A	1	SAM	O2'-C2'-C3'	2.91	121.29	111.83

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

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 ⓘ

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	1135/1330 (85%)	-0.11	25 (2%) 65 42	13, 52, 100, 127	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	390	GLU	4.4
1	A	408	SER	4.4
1	A	923	GLY	3.9
1	A	379	ASP	3.5
1	A	378	GLU	3.3
1	A	405	TYR	3.3
1	A	1001	LYS	3.0
1	A	1022	TYR	2.9
1	A	1452	GLY	2.9
1	A	919	GLU	2.8
1	A	547	ASN	2.7
1	A	654	ARG	2.6
1	A	636	SER	2.6
1	A	409	PRO	2.4
1	A	1451	ASP	2.4
1	A	1240	SER	2.4
1	A	653	ARG	2.3
1	A	918	ILE	2.3
1	A	1450	GLY	2.2
1	A	1007	LYS	2.2
1	A	1008	LYS	2.1
1	A	1006	GLY	2.1
1	A	662	CYS	2.1
1	A	1005	CYS	2.1
1	A	1002	GLU	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. 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
3	SAM	A	1	27/27	0.97	0.17	-0.15	42,43,50,51	0
2	ZN	A	2004	1/1	1.00	0.10	-1.08	47,47,47,47	0
2	ZN	A	2001	1/1	0.99	0.14	-1.18	55,55,55,55	0
2	ZN	A	2005	1/1	1.00	0.11	-2.21	33,33,33,33	0
2	ZN	A	2002	1/1	1.00	0.07	-2.63	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.