



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2018 – 01:53 pm GMT

PDB ID : 1VQ1
Title : Crystal structure of N5-glutamine methyltransferase, HemK(EC 2.1.1.-)
(TM0488) from Thermotoga maritima at 2.80 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2004-12-02
Resolution : 2.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

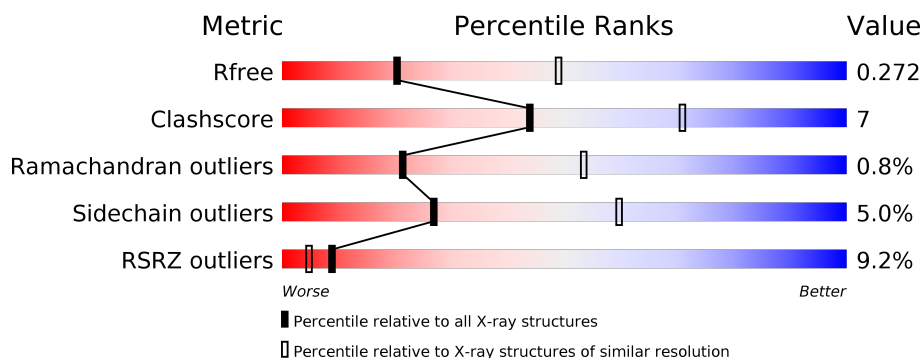
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

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	294	<div> <div>7%</div> <div> <div></div> <div>73%</div> <div>17%</div> <div>•</div> <div>10%</div> </div> </div>
1	B	294	<div> <div>10%</div> <div> <div></div> <div>70%</div> <div>18%</div> <div>•</div> <div>10%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4177 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 N5-glutamine methyltransferase, HemK.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	Se	0	0	0
			2075	1337	344	390	1	3			
1	B	264	Total	C	N	O	S	Se	0	0	0
			2041	1315	336	386	1	3			

There are 32 discrepancies between the modelled and reference sequences:

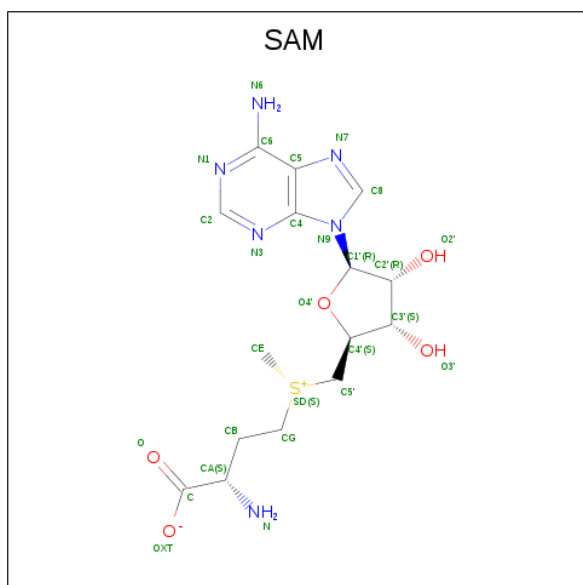
Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MSE	-	LEADER SEQUENCE	UNP Q9WYV8
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYV8
A	-9	SER	-	LEADER SEQUENCE	UNP Q9WYV8
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYV8
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYV8
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYV8
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
A	0	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
A	89	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
A	193	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
A	245	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
B	-11	MSE	-	LEADER SEQUENCE	UNP Q9WYV8
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYV8
B	-9	SER	-	LEADER SEQUENCE	UNP Q9WYV8
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYV8
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYV8
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYV8
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYV8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
B	0	HIS	-	LEADER SEQUENCE	UNP Q9WYV8
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
B	89	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
B	193	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8
B	245	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV8

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



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

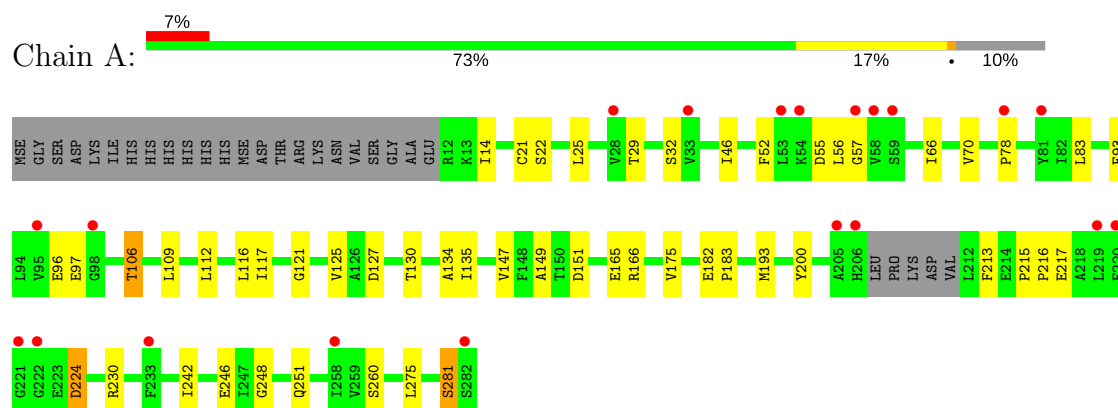
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	O	0	0
			2	2		
3	B	5	Total	O	0	0
			5	5		

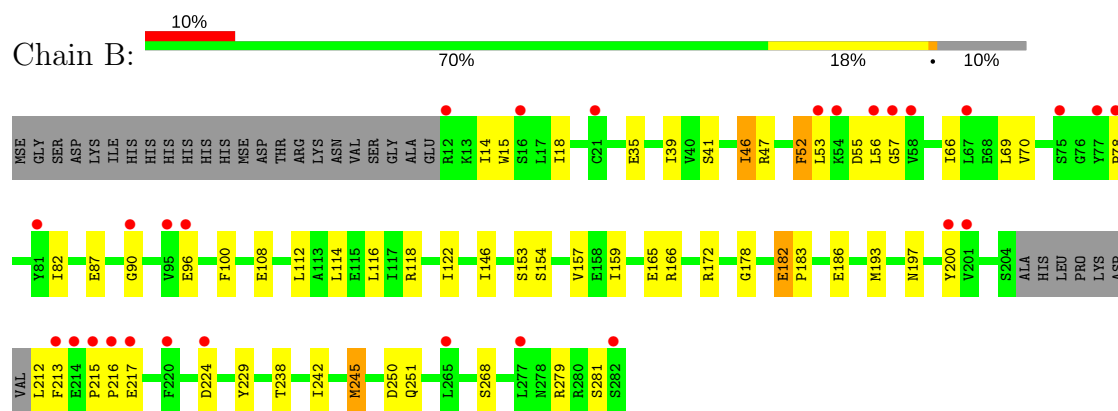
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: N5-glutamine methyltransferase, HemK



- Molecule 1: N5-glutamine methyltransferase, HemK



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.97Å 58.61Å 85.67Å 90.00° 109.46° 90.00°	Depositor
Resolution (Å)	36.09 – 2.80 36.09 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.9 (36.09-2.80) 96.0 (36.09-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.208 , 0.273 0.212 , 0.272	Depositor DCC
R_{free} test set	801 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	68.0	Xtriage
Anisotropy	0.727	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 92.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4177	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.69% 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: 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	0.75	0/2109	0.78	1/2836 (0.0%)
1	B	0.65	0/2073	0.71	0/2790
All	All	0.70	0/4182	0.75	1/5626 (0.0%)

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	A	0	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	127	ASP	CB-CG-OD2	-5.11	113.70	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	281	SER	Peptide
1	A	52	PHE	Peptide
1	B	281	SER	Peptide
1	B	52	PHE	Peptide

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	2075	0	2077	28	0
1	B	2041	0	2034	32	0
2	A	27	0	22	1	0
2	B	27	0	22	2	0
3	A	2	0	0	0	0
3	B	5	0	0	0	0
All	All	4177	0	4155	60	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 (60) 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:B:116:LEU:HB3	1:B:193:MSE:HE1	1.60	0.83
1:A:116:LEU:HD13	1:A:193:MSE:HE1	1.67	0.77
1:A:151:ASP:OD1	2:A:301:SAM:O2'	2.05	0.72
1:B:108:GLU:OE2	1:B:268:SER:OG	2.09	0.68
1:B:193:MSE:HE2	1:B:242:ILE:HG21	1.78	0.64
1:A:200:TYR:HB2	1:A:251:GLN:HE22	1.66	0.61
1:A:14:ILE:HG22	1:A:56:LEU:HA	1.84	0.60
1:B:229:TYR:CD2	1:B:245:MSE:HE3	2.39	0.58
1:A:116:LEU:HD13	1:A:193:MSE:CE	2.33	0.57
1:B:14:ILE:HG22	1:B:56:LEU:HA	1.85	0.57
1:A:275:LEU:C	1:A:275:LEU:HD12	2.26	0.56
1:B:153:SER:O	1:B:157:VAL:HG23	2.07	0.55
1:A:109:LEU:C	1:A:109:LEU:HD23	2.26	0.55
1:B:197:ASN:O	2:B:301:SAM:HE2	2.05	0.54
1:A:66:ILE:O	1:A:70:VAL:HG23	2.08	0.53
1:B:100:PHE:CD2	2:B:301:SAM:HG2	2.44	0.52
1:B:78:PRO:HD3	1:B:213:PHE:CB	2.39	0.52
1:B:122:ILE:CD1	1:B:193:MSE:HE3	2.40	0.52
1:B:165:GLU:OE1	1:B:165:GLU:HA	2.10	0.51
1:A:200:TYR:OH	1:A:246:GLU:OE2	2.26	0.50
1:A:78:PRO:HD3	1:A:213:PHE:CB	2.41	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:GLY:N	1:A:251:GLN:OE1	2.43	0.50
1:B:15:TRP:HA	1:B:18:ILE:HD12	1.94	0.49
1:B:182:GLU:N	1:B:183:PRO:CD	2.75	0.49
1:B:69:LEU:HD22	1:B:82:ILE:HG23	1.95	0.48
1:B:52:PHE:O	1:B:53:LEU:HD22	2.13	0.48
1:A:125:VAL:O	1:A:147:VAL:HA	2.13	0.47
1:B:46:ILE:HG23	1:B:47:ARG:N	2.30	0.47
1:B:193:MSE:HE2	1:B:242:ILE:CG2	2.45	0.46
1:B:114:LEU:O	1:B:118:ARG:HG3	2.15	0.46
1:A:165:GLU:OE1	1:A:165:GLU:HA	2.16	0.46
1:A:93:PHE:CZ	1:A:134:ALA:HA	2.50	0.45
1:B:200:TYR:O	1:B:251:GLN:NE2	2.49	0.45
1:B:46:ILE:CG2	1:B:47:ARG:N	2.80	0.45
1:B:166:ARG:O	1:B:166:ARG:CG	2.64	0.45
1:A:25:LEU:HD21	1:A:70:VAL:HG13	1.99	0.44
1:B:35:GLU:O	1:B:39:ILE:HG13	2.18	0.43
1:A:106:THR:HG21	1:A:135:ILE:HD11	1.99	0.43
1:A:149:ALA:O	1:A:175:VAL:HA	2.18	0.43
1:A:78:PRO:HD3	1:A:213:PHE:HB3	2.00	0.43
1:B:178:GLY:HA3	1:B:183:PRO:HG3	2.01	0.43
1:B:66:ILE:O	1:B:70:VAL:HG23	2.19	0.42
1:A:106:THR:CG2	1:A:135:ILE:HD11	2.49	0.42
1:A:166:ARG:O	1:A:166:ARG:HG2	2.20	0.41
1:A:224:ASP:OD2	1:A:230:ARG:NH2	2.53	0.41
1:B:215:PRO:HA	1:B:216:PRO:HD2	1.89	0.41
1:B:229:TYR:CE2	1:B:245:MSE:HE3	2.56	0.41
1:A:117:ILE:O	1:A:121:GLY:N	2.53	0.41
1:A:215:PRO:HA	1:A:216:PRO:HD2	1.87	0.41
1:B:212:LEU:HD13	1:B:216:PRO:HG3	2.02	0.41
1:A:21:CYS:O	1:A:22:SER:C	2.59	0.41
1:A:193:MSE:CE	1:A:242:ILE:HG21	2.50	0.41
1:B:200:TYR:HB2	1:B:251:GLN:HE22	1.86	0.41
1:B:87:GLU:OE1	1:B:90:GLY:HA2	2.21	0.41
1:A:130:THR:HB	1:A:149:ALA:HB1	2.04	0.40
1:A:182:GLU:N	1:A:183:PRO:CD	2.84	0.40
1:A:96:GLU:O	1:A:97:GLU:C	2.59	0.40
1:B:146:ILE:HG22	1:B:172:ARG:HG2	2.03	0.40
1:B:166:ARG:HG2	1:B:166:ARG:O	2.21	0.40
1:B:238:THR:OG1	1:B:279:ARG:NH1	2.54	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	262/294 (89%)	241 (92%)	19 (7%)	2 (1%)	21	53
1	B	260/294 (88%)	242 (93%)	16 (6%)	2 (1%)	21	53
All	All	522/588 (89%)	483 (92%)	35 (7%)	4 (1%)	21	53

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	55	ASP
1	A	55	ASP
1	A	57	GLY
1	B	57	GLY

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	221/250 (88%)	211 (96%)	10 (4%)	30	64
1	B	216/250 (86%)	204 (94%)	12 (6%)	23	54
All	All	437/500 (87%)	415 (95%)	22 (5%)	27	60

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	THR
1	A	32	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	46	ILE
1	A	83	LEU
1	A	106	THR
1	A	112	LEU
1	A	217	GLU
1	A	224	ASP
1	A	260	SER
1	A	281	SER
1	B	41	SER
1	B	46	ILE
1	B	96	GLU
1	B	112	LEU
1	B	154	SER
1	B	159	ILE
1	B	182	GLU
1	B	186	GLU
1	B	217	GLU
1	B	224	ASP
1	B	245	MSE
1	B	250	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

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	SAM	A	301	-	21,29,29	1.18	2 (9%)	16,42,42	3.36	4 (25%)
2	SAM	B	301	-	21,29,29	1.18	2 (9%)	16,42,42	3.02	3 (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
2	SAM	A	301	-	-	0/8/33/33	0/3/3/3
2	SAM	B	301	-	-	0/8/33/33	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	SAM	C2-N1	2.23	1.38	1.33
2	A	301	SAM	C2-N1	2.44	1.38	1.33
2	A	301	SAM	C2-N3	3.61	1.38	1.32
2	B	301	SAM	C2-N3	3.76	1.38	1.32

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	SAM	N3-C2-N1	-11.59	118.94	128.86
2	B	301	SAM	N3-C2-N1	-10.95	119.49	128.86
2	A	301	SAM	C4-C5-N7	-2.67	106.83	109.41
2	A	301	SAM	C1'-N9-C4	-2.22	122.80	126.64
2	B	301	SAM	C2'-C3'-C4'	2.01	106.48	102.62
2	B	301	SAM	C4'-O4'-C1'	2.75	112.69	109.83
2	A	301	SAM	C4'-O4'-C1'	4.67	114.70	109.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	SAM	1	0
2	B	301	SAM	2	0

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	263/294 (89%)	0.45	20 (7%) 14 7	81, 88, 92, 107	0
1	B	261/294 (88%)	0.57	28 (10%) 6 3	84, 88, 91, 94	0
All	All	524/588 (89%)	0.51	48 (9%) 9 5	81, 88, 91, 107	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	206	HIS	8.1
1	B	78	PRO	8.0
1	A	54	LYS	6.1
1	A	58	VAL	5.3
1	B	58	VAL	5.1
1	A	220	PHE	4.9
1	B	81	TYR	4.6
1	B	90	GLY	4.1
1	B	57	GLY	3.5
1	A	53	LEU	3.5
1	B	21	CYS	3.5
1	B	201	VAL	3.3
1	B	53	LEU	3.1
1	B	215	PRO	3.0
1	B	220	PHE	2.9
1	B	216	PRO	2.9
1	B	54	LYS	2.9
1	B	214	GLU	2.9
1	B	282	SER	2.8
1	A	57	GLY	2.8
1	A	59	SER	2.8
1	A	98	GLY	2.7
1	B	16	SER	2.7
1	B	96	GLU	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	258	ILE	2.6
1	B	67	LEU	2.5
1	B	265	LEU	2.5
1	A	205	ALA	2.5
1	B	200	TYR	2.4
1	A	78	PRO	2.3
1	B	224	ASP	2.3
1	A	282	SER	2.3
1	A	219	LEU	2.3
1	A	222	GLY	2.3
1	B	75	SER	2.2
1	B	95	VAL	2.2
1	A	28	VAL	2.2
1	A	221	GLY	2.2
1	B	213	PHE	2.2
1	A	95	VAL	2.2
1	B	217	GLU	2.2
1	A	81	TYR	2.2
1	B	77	TYR	2.2
1	B	277	LEU	2.2
1	A	33	VAL	2.2
1	B	12	ARG	2.1
1	A	233	PHE	2.1
1	B	56	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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(\AA^2)	Q<0.9
2	SAM	B	301	27/27	0.81	0.32	80,96,103,103	1
2	SAM	A	301	27/27	0.83	0.29	80,89,94,95	1

6.5 Other polymers [i](#)

There are no such residues in this entry.