Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 12:06 pm BST

PDB ID	:	3ILK
Title	:	The structure of a probable methylase family protein from Haemophilus influenzae Rd KW20
Authors	:	Tan, K.; Li, H.; Buck, K.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2009-08-07
Resolution	:	2.01 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:

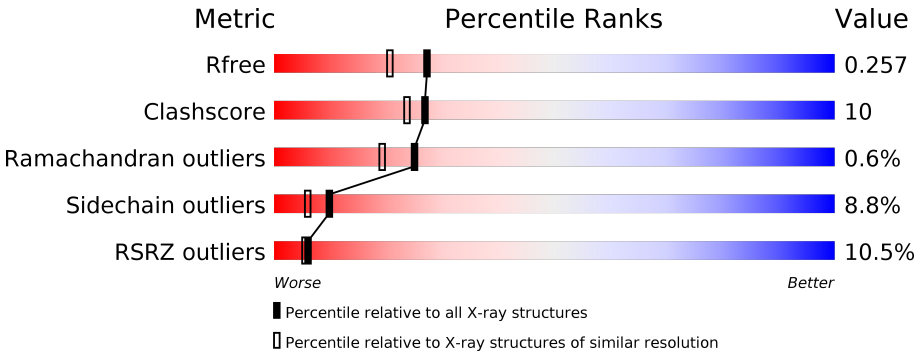
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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 <=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	244	9% 75% 20%
1	B	244	10% 70% 23% 5%

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
4	SO4	B	246	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3903 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.

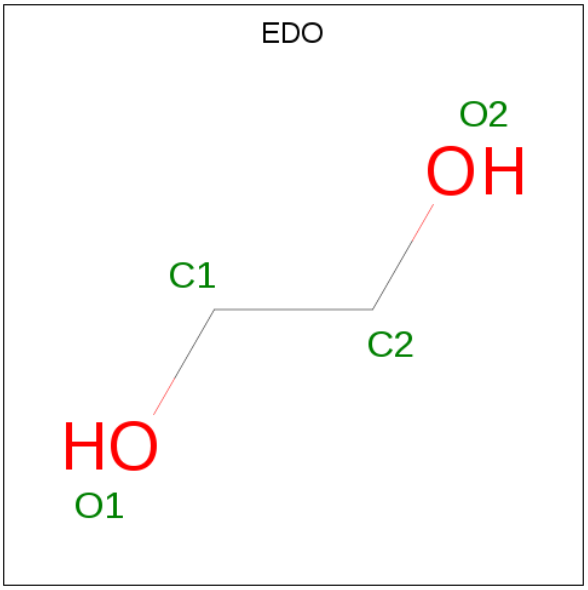
- Molecule 1 is a protein called Uncharacterized tRNA/rRNA methyltransferase HI0380.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	Se	0	4	0
			1897	1199	336	352	4	6			
1	B	233	Total	C	N	O	S	Se	0	4	0
			1853	1167	327	348	4	7			

There are 6 discrepancies between the modelled and reference sequences:

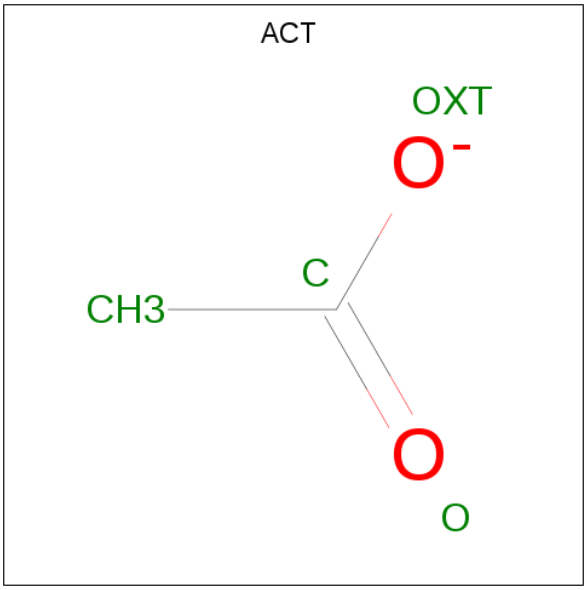
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP P44676
A	-1	ASN	-	expression tag	UNP P44676
A	0	ALA	-	expression tag	UNP P44676
B	-2	SER	-	expression tag	UNP P44676
B	-1	ASN	-	expression tag	UNP P44676
B	0	ALA	-	expression tag	UNP P44676

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



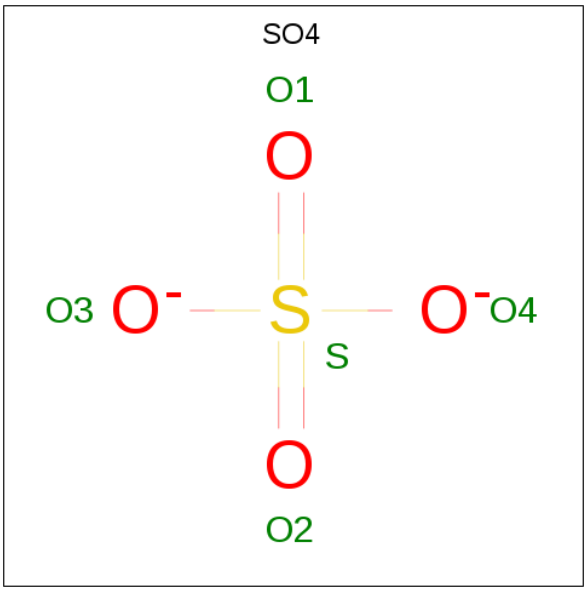
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 4 2 2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0

- Molecule 5 is water.

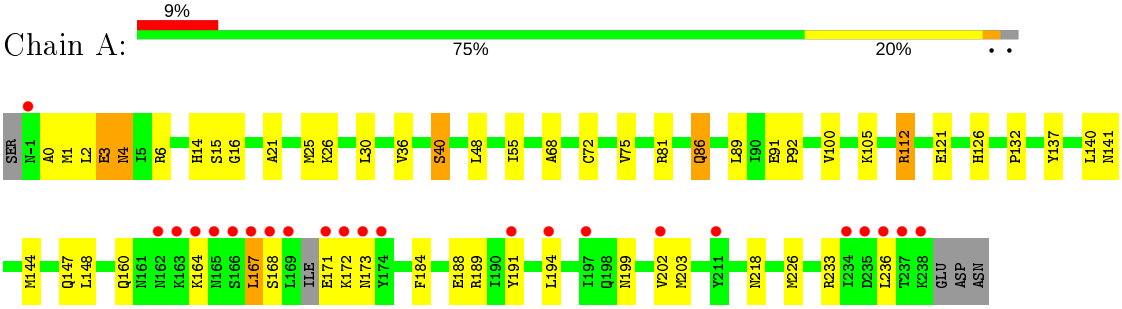
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	77	Total O 77 77	0	0
5	B	42	Total O 42 42	0	0

3 Residue-property plots (i)

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.

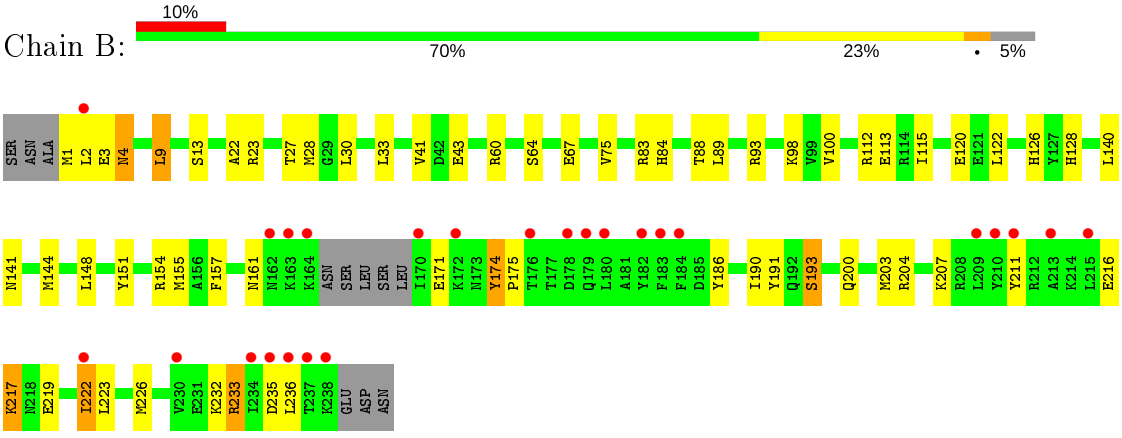
- Molecule 1: Uncharacterized tRNA/rRNA methyltransferase HI0380

Chain A:



- Molecule 1: Uncharacterized tRNA/rRNA methyltransferase HI0380

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	48.17Å 94.39Å 124.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.56 – 2.01 40.55 – 2.01	Depositor EDS
% Data completeness (in resolution range)	96.2 (40.56-2.01) 96.2 (40.55-2.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.88 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.5.0054	Depositor
R, R_{free}	0.205 , 0.246 0.219 , 0.257	Depositor DCC
R_{free} test set	1839 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	40.9	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 60.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3903	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ACT, EDO, SO4

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	0.83	0/1927	0.81	0/2586
1	B	0.77	1/1881 (0.1%)	0.80	2/2523 (0.1%)
All	All	0.80	1/3808 (0.0%)	0.80	2/5109 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	22	ALA	CA-CB	5.25	1.63	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	112	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	B	175	PRO	N-CA-CB	5.27	109.62	103.30

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	1897	0	1941	39	0
1	B	1853	0	1887	50	0
2	A	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	12	0	18	2	0
3	B	4	0	3	0	0
4	B	10	0	0	2	0
5	A	77	0	0	2	0
5	B	42	0	0	0	0
All	All	3903	0	3861	78	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 10.

All (78) 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:28:MSE:HE2	1:B:151:TYR:HA	1.11	1.08
1:B:28:MSE:HE3	1:B:154:ARG:HB3	1.36	1.06
1:A:148:LEU:HD23	1:B:148:LEU:HD23	1.45	0.99
1:B:28:MSE:HE2	1:B:151:TYR:CA	2.00	0.90
1:B:28:MSE:CE	1:B:151:TYR:HA	2.02	0.87
1:B:233:ARG:CG	1:B:233:ARG:HH11	1.97	0.78
1:A:184:PHE:O	1:A:188:GLU:HG3	1.83	0.78
1:B:4:ASN:HD22	1:B:4:ASN:H	1.31	0.78
1:B:28:MSE:CE	1:B:154:ARG:HB3	2.13	0.77
1:A:148:LEU:CD2	1:B:148:LEU:HD23	2.16	0.76
1:A:132:PRO:HB2	1:B:155:MSE:HE1	1.67	0.75
1:B:233:ARG:HG2	1:B:233:ARG:HH11	1.51	0.74
1:B:75:VAL:H	1:B:126:HIS:HD2	1.33	0.74
1:A:72:CYS:SG	1:A:105[B]:LYS:HG2	2.29	0.72
1:B:217:LYS:HD2	1:B:217:LYS:N	2.04	0.72
1:B:28:MSE:HE3	1:B:154:ARG:CB	2.18	0.72
1:A:1:MSE:O	1:A:4:ASN:ND2	2.24	0.70
1:B:223:LEU:HA	1:B:226:MSE:CE	2.21	0.70
1:B:222:ILE:O	1:B:226:MSE:HG3	1.92	0.69
1:A:147:GLN:HG2	1:B:144:MSE:HB3	1.75	0.69
1:B:75:VAL:H	1:B:126:HIS:CD2	2.13	0.67
1:B:64:SER:OG	1:B:67:GLU:HG3	1.94	0.66
1:B:174:TYR:HA	1:B:217:LYS:HE3	1.77	0.66
1:A:189:ARG:NH1	5:A:316:HOH:O	2.30	0.63
1:B:141:ASN:ND2	4:B:246:SO4:O3	2.31	0.63
1:B:223:LEU:HA	1:B:226:MSE:HE3	1.82	0.61
1:A:188:GLU:HG2	1:A:203:MSE:SE	2.52	0.59
1:A:0:ALA:HB3	1:A:3:GLU:OE2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:ARG:HH11	2:B:243:EDO:H22	1.67	0.59
1:B:217:LYS:HD2	1:B:217:LYS:H	1.70	0.56
1:A:6:ARG:HB2	1:A:105[B]:LYS:HE2	1.88	0.56
1:A:226:MSE:HB3	1:B:191:TYR:CE1	2.41	0.56
1:B:2:LEU:HB3	1:B:30:LEU:HD23	1.87	0.55
1:A:167:LEU:HD23	1:A:168:SER:H	1.72	0.55
1:A:112:ARG:NH1	1:A:121:GLU:OE1	2.40	0.55
1:A:171:GLU:O	1:A:173:ASN:N	2.39	0.55
1:B:223:LEU:HA	1:B:226:MSE:HE2	1.89	0.55
1:B:223:LEU:HD23	1:B:226:MSE:HE3	1.89	0.54
1:A:16:GLY:HA3	1:A:48:LEU:HD22	1.89	0.54
1:A:144:MSE:HE1	1:B:23:ARG:HB3	1.91	0.52
1:A:141:ASN:OD1	1:A:141:ASN:C	2.48	0.52
1:B:233:ARG:CG	1:B:233:ARG:NH1	2.64	0.52
1:B:190:ILE:O	1:B:193:SER:HB2	2.11	0.51
1:B:4:ASN:HD22	1:B:4:ASN:N	2.05	0.51
1:A:188:GLU:HG2	1:A:203:MSE:HG3	1.92	0.51
1:A:160:GLN:O	1:A:164:LYS:HG3	2.11	0.51
1:A:202:VAL:HG23	1:B:222:ILE:HD13	1.92	0.50
1:A:75:VAL:H	1:A:126:HIS:HD2	1.60	0.50
1:B:157:PHE:CE2	1:B:161:ASN:ND2	2.80	0.49
1:A:171:GLU:C	1:A:173:ASN:H	2.16	0.49
1:A:137:TYR:OH	1:B:23:ARG:HG3	2.11	0.49
1:B:88:THR:HG1	1:B:128:HIS:CE1	2.26	0.49
1:B:84:HIS:HD2	2:B:243:EDO:O1	1.96	0.48
1:A:14[B]:HIS:CD2	1:A:16:GLY:H	2.32	0.48
1:A:148:LEU:HD23	1:B:148:LEU:CD2	2.31	0.48
1:B:203:MSE:O	1:B:207:LYS:HG3	2.13	0.48
1:A:26:LYS:HB2	1:A:55:ILE:HD12	1.96	0.46
1:B:222:ILE:HG13	1:B:226:MSE:HE2	1.97	0.46
1:A:86:GLN:HA	1:A:89:LEU:HD12	1.98	0.46
1:A:105[B]:LYS:NZ	5:A:320:HOH:O	2.48	0.45
1:A:16:GLY:CA	1:A:48:LEU:HD22	2.46	0.45
1:A:81:ARG:HG2	1:A:81:ARG:HH11	1.81	0.44
1:A:91:GLU:HB3	1:A:92:PRO:CD	2.47	0.44
1:B:207:LYS:O	1:B:211:TYR:CD2	2.70	0.44
1:B:1:MSE:HB3	1:B:3:GLU:HB2	1.99	0.44
1:A:15:SER:HB3	1:A:40:SER:OG	2.17	0.44
1:A:202:VAL:HG23	1:B:222:ILE:CD1	2.47	0.44
1:A:14[B]:HIS:CE1	1:A:16:GLY:HA3	2.53	0.43
1:B:216[A]:GLU:HB2	1:B:219:GLU:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:TYR:CE1	1:B:226:MSE:HB3	2.54	0.43
1:A:21:ALA:O	1:A:25:MSE:HG3	2.19	0.43
1:B:9:LEU:HD22	1:B:33:LEU:HD11	2.01	0.42
1:A:36:VAL:HG22	1:A:68:ALA:HB2	2.02	0.42
1:B:113:GLU:HG2	4:B:246:SO4:O4	2.20	0.42
1:A:2:LEU:HB3	1:A:30[A]:LEU:HD23	2.01	0.41
1:B:232:LYS:O	1:B:236:LEU:HB2	2.20	0.41
1:B:98:LYS:HE2	1:B:98:LYS:HB2	1.87	0.41
1:B:217:LYS:CD	1:B:217:LYS:H	2.33	0.41

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	239/244 (98%)	228 (95%)	10 (4%)	1 (0%)	34	30
1	B	233/244 (96%)	223 (96%)	8 (3%)	2 (1%)	17	11
All	All	472/488 (97%)	451 (96%)	18 (4%)	3 (1%)	25	19

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	LYS
1	B	174	TYR
1	B	171	GLU

5.3.2 Protein sidechains (i)

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	206/206 (100%)	193 (94%)	13 (6%)	18 13
1	B	201/206 (98%)	178 (89%)	23 (11%)	5 3
All	All	407/412 (99%)	371 (91%)	36 (9%)	10 6

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	4	ASN
1	A	40	SER
1	A	86	GLN
1	A	100	VAL
1	A	112	ARG
1	A	140	LEU
1	A	167	LEU
1	A	194	LEU
1	A	199	ASN
1	A	218	ASN
1	A	233	ARG
1	A	236	LEU
1	B	4	ASN
1	B	9	LEU
1	B	13	SER
1	B	27	THR
1	B	41	VAL
1	B	43[A]	GLU
1	B	43[B]	GLU
1	B	60	ARG
1	B	89	LEU
1	B	93	ARG
1	B	100	VAL
1	B	115	ILE
1	B	120	GLU
1	B	122	LEU
1	B	140	LEU
1	B	186	TYR
1	B	193	SER
1	B	200	GLN
1	B	204	ARG
1	B	217	LYS

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Mol	Chain	Res	Type
1	B	222	ILE
1	B	233	ARG
1	B	235	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	126	HIS
1	A	147	GLN
1	B	4	ASN
1	B	84	HIS
1	B	86	GLN
1	B	87	ASN
1	B	126	HIS
1	B	147	GLN
1	B	192	GLN
1	B	200	GLN
1	B	218	ASN

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

8 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	$\#\|Z\| > 2$
4	SO4	B	246	-	4,4,4	0.23	0	6,6,6	0.21	0
2	EDO	A	243	-	3,3,3	0.51	0	2,2,2	0.46	0
3	ACT	B	245	-	1,3,3	1.14	0	0,3,3	0.00	-
2	EDO	B	242	-	3,3,3	0.71	0	2,2,2	0.16	0
2	EDO	A	242	-	3,3,3	0.66	0	2,2,2	0.14	0
2	EDO	B	243	-	3,3,3	0.49	0	2,2,2	0.55	0
4	SO4	B	247	-	4,4,4	0.09	0	6,6,6	0.31	0
2	EDO	B	244	-	3,3,3	0.80	0	2,2,2	0.24	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	EDO	A	243	-	-	1/1/1/1	-
2	EDO	B	242	-	-	1/1/1/1	-
2	EDO	A	242	-	-	1/1/1/1	-
2	EDO	B	244	-	-	0/1/1/1	-
2	EDO	B	243	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	243	EDO	O1-C1-C2-O2
2	A	243	EDO	O1-C1-C2-O2
2	B	242	EDO	O1-C1-C2-O2
2	A	242	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	246	SO4	2	0
2	B	243	EDO	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, 95^{th} 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	232/244 (95%)	0.70	23 (9%)	7	6	10, 25, 46, 60	0
1	B	226/244 (92%)	0.68	25 (11%)	5	4	7, 25, 35, 52	0
All	All	458/488 (93%)	0.69	48 (10%)	6	5	7, 25, 38, 60	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	237	THR	8.8
1	A	167	LEU	7.5
1	A	238	LYS	6.8
1	B	236	LEU	5.9
1	B	238	LYS	5.2
1	A	194	LEU	5.0
1	A	169	LEU	4.7
1	A	168	SER	4.7
1	B	213	ALA	4.7
1	A	237	THR	4.7
1	A	171	GLU	4.6
1	A	-1	ASN	4.3
1	B	234	ILE	4.1
1	B	211	TYR	3.9
1	A	235	ASP	3.7
1	A	166	SER	3.6
1	B	235	ASP	3.6
1	A	174	TYR	3.5
1	A	197	ILE	3.5
1	A	236	LEU	3.4
1	A	163	LYS	3.3
1	B	162	ASN	3.2
1	B	210	TYR	3.2
1	B	180	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	170	ILE	3.2
1	B	222	ILE	2.9
1	B	182	TYR	2.9
1	B	164	LYS	2.9
1	A	191	TYR	2.8
1	A	173	ASN	2.8
1	B	163	LYS	2.8
1	B	2	LEU	2.8
1	B	230	VAL	2.7
1	A	165	ASN	2.7
1	A	162	ASN	2.7
1	A	234	ILE	2.6
1	B	215	LEU	2.6
1	A	172	LYS	2.6
1	A	164	LYS	2.5
1	B	178	ASP	2.5
1	B	184	PHE	2.5
1	B	179	GLN	2.4
1	A	211	TYR	2.4
1	B	183	PHE	2.3
1	B	209	LEU	2.3
1	A	202	VAL	2.3
1	B	172	LYS	2.1
1	B	176	THR	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. The B-factors column lists the minimum, median, 95^{th} 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(Å^2)	Q<0.9
2	EDO	A	243	4/4	0.81	0.20	58,62,65,68	0
3	ACT	B	245	4/4	0.81	0.17	54,54,54,55	0
2	EDO	B	243	4/4	0.81	0.28	59,65,66,67	0
2	EDO	B	244	4/4	0.83	0.14	56,58,58,59	0
4	SO4	B	247	5/5	0.85	0.24	56,56,57,59	5
2	EDO	A	242	4/4	0.85	0.18	55,57,58,60	0
2	EDO	B	242	4/4	0.89	0.20	51,52,55,57	0
4	SO4	B	246	5/5	0.96	0.17	55,56,57,57	5

6.5 Other polymers (i)

There are no such residues in this entry.