



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:35 am GMT

PDB ID : 4E8T
Title : Structure of *Oceanobacillus iheyensis* group II intron in the presence of K⁺,
Ca²⁺ and an oligonucleotide fragment substrate (low energy dataset)
Authors : Marcia, M.; Pyle, A.M.
Deposited on : 2012-03-20
Resolution : 3.34 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

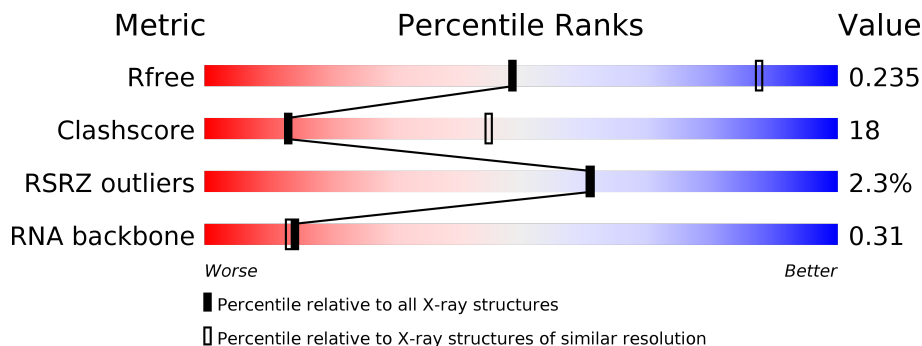
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

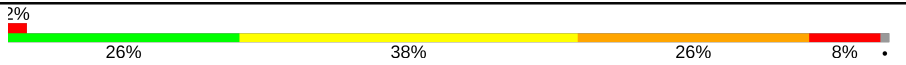

The reported resolution of this entry is 3.34 Å.

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}	100719	1167 (3.40-3.28)
Clashscore	112137	1239 (3.40-3.28)
RSRZ outliers	101464	1176 (3.40-3.28)
RNA backbone	2435	1121 (3.88-2.80)

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	393	
2	B	8	

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	CA	A	408	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CA	A	413	-	-	-	X
4	K	A	426	-	-	-	X
4	K	A	431	-	-	-	X
5	SPM	A	440	-	-	-	X
5	SPM	A	441	-	-	-	X
6	EPE	A	442	-	-	-	X
6	EPE	A	444	-	-	-	X
6	EPE	A	445	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8640 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 RNA chain called Group IIC intron.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	P	0	0	0
			8326	3715	1547	2676	388			

- Molecule 2 is a RNA chain called 5'-R(*AP*UP*UP*UP*AP*UP*UP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	8	Total	C	N	O	P	0	0	0
			163	75	25	56	7			

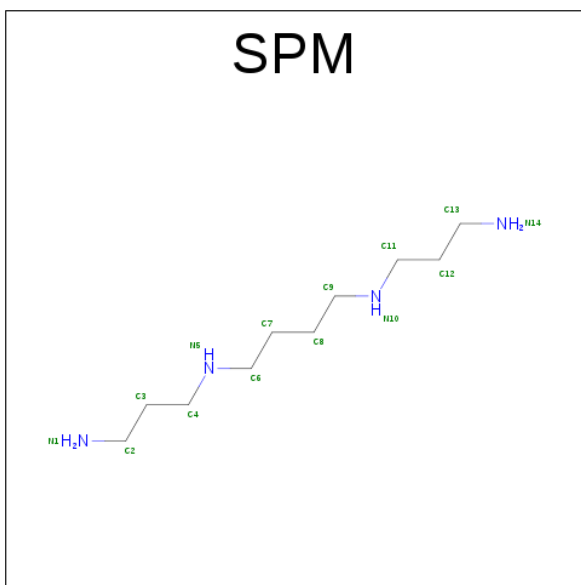
- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total	Ca	0	0
			25	25		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

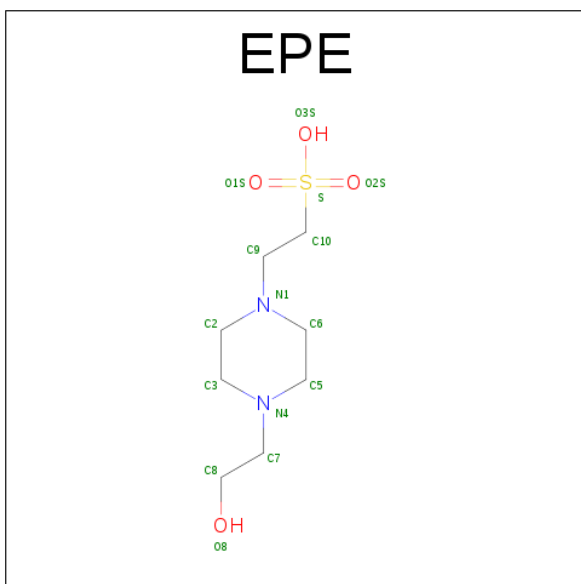
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total	K	0	0
			14	14		

- Molecule 5 is SPERMINE (three-letter code: SPM) (formula: C₁₀H₂₆N₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			14	10	4		
5	A	1	Total	C	N	0	0
			14	10	4		

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			12	6	2	3	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 4 3 1	0	0
6	A	1	Total C N O S 12 6 2 3 1	0	0
6	A	1	Total C O S 5 1 3 1	0	0
6	A	1	Total C O S 5 1 3 1	0	0
6	A	1	Total C O S 6 2 3 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	38	Total O 38 38	0	0
7	B	2	Total O 2 2	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.46Å 95.77Å 225.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.61 – 3.34 48.61 – 3.34	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.61-3.34) 99.9 (48.61-3.34)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.189 , 0.235 0.187 , 0.235	Depositor DCC
R_{free} test set	1444 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	122.4	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 71.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8640	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, EPE, CA, SPM

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	0.47	0/9331	1.25	157/14556 (1.1%)
2	B	0.56	0/181	1.36	3/279 (1.1%)
All	All	0.47	0/9512	1.25	160/14835 (1.1%)

There are no bond length outliers.

All (160) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	U	O5'-P-OP2	13.62	127.04	110.70
1	A	245	A	P-O3'-C3'	-12.43	104.78	119.70
1	A	356	A	P-O3'-C3'	-12.11	105.16	119.70
1	A	65	U	O5'-P-OP1	-11.94	94.95	105.70
1	A	232	G	P-O3'-C3'	-11.64	105.73	119.70
1	A	206	A	P-O3'-C3'	11.64	133.67	119.70
1	A	331	G	P-O3'-C3'	-11.58	105.80	119.70
1	A	118	G	P-O3'-C3'	-10.61	106.97	119.70
2	B	1	A	P-O3'-C3'	10.54	132.34	119.70
1	A	115	A	O3'-P-O5'	-10.51	84.04	104.00
1	A	271	U	P-O3'-C3'	-10.43	107.18	119.70
1	A	55	G	O3'-P-O5'	-10.12	84.77	104.00
1	A	291	G	P-O3'-C3'	9.97	131.66	119.70
1	A	119	C	P-O3'-C3'	-9.87	107.86	119.70
1	A	135	G	O5'-P-OP2	-9.80	96.88	105.70
1	A	168	U	P-O3'-C3'	9.67	131.30	119.70
1	A	224	A	P-O3'-C3'	9.51	131.12	119.70
1	A	37	U	P-O3'-C3'	-9.39	108.43	119.70
1	A	108	G	P-O3'-C3'	9.31	130.88	119.70
1	A	341	C	P-O3'-C3'	9.17	130.71	119.70
1	A	188	A	P-O3'-C3'	-8.92	109.00	119.70
1	A	6	C	O5'-P-OP1	-8.90	97.69	105.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	U	P-O3'-C3'	8.74	130.18	119.70
1	A	16	G	O5'-P-OP1	8.50	120.90	110.70
1	A	176	U	P-O3'-C3'	-8.45	109.56	119.70
1	A	34	G	OP2-P-O3'	8.36	123.60	105.20
1	A	52	G	P-O3'-C3'	-8.27	109.77	119.70
1	A	225	U	O5'-P-OP1	-8.22	98.30	105.70
1	A	330	A	P-O3'-C3'	-8.18	109.89	119.70
1	A	340	U	P-O3'-C3'	8.14	129.47	119.70
1	A	16	G	O5'-P-OP2	-8.10	98.41	105.70
1	A	137	A	P-O3'-C3'	8.06	129.37	119.70
1	A	123	C	P-O3'-C3'	-7.98	110.13	119.70
1	A	281	G	P-O3'-C3'	-7.90	110.22	119.70
1	A	266	G	O5'-P-OP1	-7.86	98.63	105.70
1	A	265	G	OP1-P-O3'	7.72	122.18	105.20
1	A	261	C	P-O3'-C3'	7.68	128.92	119.70
1	A	48	G	O5'-P-OP2	-7.55	98.90	105.70
1	A	336	G	P-O3'-C3'	-7.52	110.68	119.70
1	A	107	G	P-O3'-C3'	-7.49	110.71	119.70
1	A	22	U	P-O3'-C3'	-7.46	110.75	119.70
1	A	292	A	N9-C1'-C2'	-7.40	103.86	112.00
1	A	373	G	P-O3'-C3'	7.28	128.43	119.70
1	A	195	U	P-O3'-C3'	-7.00	111.30	119.70
1	A	139	C	P-O3'-C3'	6.97	128.06	119.70
1	A	210	U	P-O3'-C3'	-6.86	111.46	119.70
1	A	287	A	O3'-P-O5'	-6.85	90.99	104.00
1	A	54	A	O3'-P-O5'	-6.78	91.11	104.00
1	A	171	A	O5'-P-OP1	-6.70	99.67	105.70
1	A	58	G	O3'-P-O5'	-6.67	91.33	104.00
1	A	239	G	P-O3'-C3'	6.65	127.68	119.70
1	A	329	A	P-O3'-C3'	-6.57	111.82	119.70
1	A	127	C	O3'-P-O5'	-6.55	91.56	104.00
1	A	181	A	P-O3'-C3'	-6.55	111.84	119.70
1	A	148	C	P-O3'-C3'	-6.54	111.85	119.70
1	A	93	A	OP2-P-O3'	6.49	119.48	105.20
1	A	353	U	P-O3'-C3'	-6.48	111.93	119.70
1	A	96	U	P-O3'-C3'	-6.45	111.97	119.70
1	A	113	G	P-O3'-C3'	-6.43	111.98	119.70
1	A	29	G	P-O3'-C3'	-6.41	112.01	119.70
1	A	297	A	O3'-P-O5'	6.39	116.14	104.00
1	A	127	C	P-O3'-C3'	-6.31	112.13	119.70
1	A	280	A	P-O3'-C3'	-6.31	112.13	119.70
1	A	105	A	OP2-P-O3'	6.28	119.01	105.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	G	P-O3'-C3'	-6.27	112.17	119.70
1	A	197	C	P-O3'-C3'	6.26	127.21	119.70
1	A	170	G	O5'-P-OP1	6.25	118.19	110.70
1	A	126	U	P-O3'-C3'	-6.24	112.21	119.70
1	A	57	A	O5'-P-OP2	6.22	118.16	110.70
1	A	265	G	P-O3'-C3'	-6.20	112.26	119.70
1	A	121	A	P-O3'-C3'	6.19	127.12	119.70
1	A	268	A	O3'-P-O5'	-6.17	92.28	104.00
1	A	354	G	P-O3'-C3'	6.16	127.09	119.70
1	A	58	G	OP2-P-O3'	6.11	118.64	105.20
1	A	52	G	OP1-P-O3'	6.10	118.62	105.20
2	B	3	U	P-O3'-C3'	-6.09	112.39	119.70
1	A	195	U	OP2-P-O3'	6.07	118.55	105.20
1	A	240	A	OP2-P-O3'	6.05	118.51	105.20
1	A	91	C	P-O3'-C3'	-6.04	112.45	119.70
1	A	199	U	O5'-P-OP1	-6.03	100.27	105.70
1	A	156	G	P-O3'-C3'	6.00	126.90	119.70
1	A	84	U	P-O3'-C3'	5.99	126.88	119.70
1	A	238	U	OP1-P-O3'	5.98	118.37	105.20
1	A	56	A	O3'-P-O5'	-5.97	92.66	104.00
1	A	299	A	P-O3'-C3'	5.95	126.83	119.70
1	A	377	C	P-O3'-C3'	-5.93	112.58	119.70
1	A	249	A	OP1-P-O3'	-5.87	92.28	105.20
1	A	229	G	P-O3'-C3'	-5.86	112.67	119.70
1	A	62	C	O5'-P-OP1	-5.83	100.45	105.70
1	A	119	C	O5'-P-OP2	-5.83	100.45	105.70
2	B	4	U	P-O3'-C3'	5.80	126.67	119.70
1	A	207	A	P-O3'-C3'	-5.80	112.74	119.70
1	A	344	G	P-O3'-C3'	-5.80	112.74	119.70
1	A	17	U	P-O3'-C3'	5.80	126.66	119.70
1	A	333	A	C4'-C3'-O3'	-5.79	97.23	109.40
1	A	221	U	O3'-P-O5'	5.79	115.00	104.00
1	A	278	A	P-O3'-C3'	-5.75	112.80	119.70
1	A	310	C	P-O3'-C3'	5.75	126.60	119.70
1	A	74	C	OP2-P-O3'	5.74	117.82	105.20
1	A	171	A	OP1-P-O3'	-5.74	92.58	105.20
1	A	234	U	P-O3'-C3'	-5.72	112.83	119.70
1	A	86	C	O3'-P-O5'	-5.72	93.13	104.00
1	A	88	U	O3'-P-O5'	5.71	114.86	104.00
1	A	133	G	OP2-P-O3'	5.71	117.75	105.20
1	A	24	U	P-O3'-C3'	-5.70	112.86	119.70
1	A	58	G	O5'-P-OP2	-5.70	100.57	105.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	A	OP1-P-O3'	-5.69	92.67	105.20
1	A	36	G	OP1-P-O3'	5.68	117.70	105.20
1	A	201	C	P-O3'-C3'	-5.68	112.88	119.70
1	A	119	C	O4'-C4'-C3'	-5.65	98.35	104.00
1	A	34	G	P-O3'-C3'	5.64	126.47	119.70
1	A	131	C	O5'-P-OP2	-5.63	100.63	105.70
1	A	110	A	P-O3'-C3'	5.61	126.43	119.70
1	A	63	A	O5'-P-OP2	-5.59	100.67	105.70
1	A	88	U	P-O3'-C3'	-5.59	112.99	119.70
1	A	221	U	P-O3'-C3'	5.58	126.40	119.70
1	A	8	C	P-O3'-C3'	-5.58	113.01	119.70
1	A	51	G	OP1-P-O3'	5.58	117.47	105.20
1	A	80	G	O5'-P-OP1	-5.57	100.69	105.70
1	A	134	A	O5'-P-OP1	-5.57	100.69	105.70
1	A	265	G	O3'-P-O5'	-5.56	93.44	104.00
1	A	190	C	OP2-P-O3'	5.54	117.39	105.20
1	A	375	U	P-O3'-C3'	5.53	126.34	119.70
1	A	139	C	O5'-P-OP2	5.52	117.33	110.70
1	A	120	A	O3'-P-O5'	-5.51	93.53	104.00
1	A	97	G	P-O3'-C3'	-5.49	113.11	119.70
1	A	28	G	P-O3'-C3'	-5.48	113.12	119.70
1	A	134	A	O3'-P-O5'	5.47	114.40	104.00
1	A	9	G	P-O3'-C3'	-5.47	113.13	119.70
1	A	201	C	O3'-P-O5'	-5.45	93.64	104.00
1	A	297	A	P-O3'-C3'	5.44	126.23	119.70
1	A	159	A	P-O3'-C3'	-5.41	113.20	119.70
1	A	174	A	O5'-P-OP1	5.40	117.18	110.70
1	A	274	G	OP1-P-O3'	-5.38	93.36	105.20
1	A	383	G	P-O3'-C3'	-5.37	113.26	119.70
1	A	186	A	P-O3'-C3'	-5.34	113.29	119.70
1	A	55	G	OP1-P-O3'	5.33	116.93	105.20
1	A	193	A	O5'-P-OP1	5.33	117.10	110.70
1	A	56	A	O5'-P-OP2	5.31	117.08	110.70
1	A	253	C	P-O3'-C3'	-5.31	113.33	119.70
1	A	337	C	P-O3'-C3'	-5.30	113.33	119.70
1	A	197	C	O5'-P-OP1	-5.29	100.94	105.70
1	A	93	A	OP1-P-O3'	-5.27	93.61	105.20
1	A	47	U	OP2-P-O3'	5.24	116.73	105.20
1	A	40	C	O5'-P-OP2	5.24	116.98	110.70
1	A	185	C	P-O3'-C3'	-5.24	113.42	119.70
1	A	326	A	P-O3'-C3'	5.22	125.96	119.70
1	A	99	A	C2'-C3'-O3'	5.21	122.04	113.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	359	G	OP2-P-O3'	5.15	116.53	105.20
1	A	51	G	O5'-P-OP1	-5.14	101.07	105.70
1	A	15	G	OP2-P-O3'	5.14	116.50	105.20
1	A	336	G	O3'-P-O5'	-5.11	94.30	104.00
1	A	378	G	O5'-P-OP2	-5.06	101.14	105.70
1	A	319	A	C4'-C3'-O3'	-5.06	98.78	109.40
1	A	368	C	OP2-P-O3'	5.05	116.32	105.20
1	A	382	G	P-O3'-C3'	-5.05	113.64	119.70
1	A	287	A	C5'-C4'-O4'	5.05	115.16	109.10
1	A	276	A	OP2-P-O3'	5.04	116.29	105.20
1	A	242	G	O5'-P-OP1	5.04	116.75	110.70
1	A	320	G	O5'-P-OP1	-5.02	101.18	105.70

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	8326	0	4178	221	0
2	B	163	0	85	9	0
3	A	25	0	0	0	0
4	A	14	0	0	0	0
5	A	28	0	52	3	0
6	A	44	0	31	6	0
7	A	38	0	0	3	0
7	B	2	0	0	1	0
All	All	8640	0	4346	235	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 18.

All (235) 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:287:A:H4'	1:A:288:G:OP1	1.41	1.13
1:A:287:A:H5'	7:A:910:HOH:O	1.53	1.09
1:A:40:C:H6	1:A:40:C:H5'	1.22	1.03
1:A:195:U:H6	1:A:195:U:H5''	1.24	1.02
1:A:321:G:H2'	1:A:322:A:C8	1.96	1.00
1:A:238:U:H6	1:A:238:U:H5'	1.27	0.99
1:A:387:U:H2'	1:A:388:G:H5'	1.41	0.99
1:A:117:G:O6	6:A:446:EPE:O3S	1.80	0.96
1:A:351:C:H2'	1:A:352:U:H5'	1.51	0.90
1:A:309:U:O2	1:A:309:U:H2'	1.71	0.90
1:A:40:C:C6	1:A:40:C:H5'	2.06	0.89
1:A:321:G:H2'	1:A:322:A:H8	1.35	0.88
1:A:361:C:H2'	1:A:362:G:H8	1.36	0.88
2:B:5:A:H2'	2:B:6:U:C6	2.09	0.87
1:A:340:U:H2'	1:A:340:U:O2	1.72	0.87
1:A:83:G:H2'	1:A:83:G:N3	1.93	0.84
2:B:5:A:H2'	2:B:6:U:H6	1.42	0.84
1:A:351:C:C2'	1:A:352:U:H5'	2.09	0.82
1:A:66:U:H2'	1:A:67:A:C8	2.14	0.82
1:A:296:C:H2'	1:A:297:A:C8	2.18	0.79
1:A:387:U:C2'	1:A:388:G:H5'	2.12	0.79
1:A:361:C:H2'	1:A:362:G:C8	2.19	0.78
1:A:238:U:C6	1:A:238:U:H5'	2.16	0.77
1:A:238:U:H6	1:A:238:U:C5'	1.96	0.77
1:A:40:C:H6	1:A:40:C:C5'	1.97	0.77
1:A:65:U:H5''	1:A:66:U:O5'	1.86	0.76
1:A:5:G:H4'	1:A:6:C:OP2	1.84	0.76
1:A:287:A:C4'	1:A:288:G:OP1	2.31	0.75
1:A:137:A:O2'	1:A:138:A:OP2	2.04	0.75
1:A:206:A:O2'	1:A:207:A:H5''	1.86	0.75
1:A:195:U:C6	1:A:195:U:H5''	2.16	0.75
1:A:287:A:O2'	1:A:288:G:O5'	2.04	0.74
1:A:287:A:OP1	1:A:287:A:O4'	2.06	0.73
1:A:329:A:H2'	1:A:330:A:H8	1.54	0.72
1:A:38:C:H2'	1:A:39:C:H6	1.52	0.72
6:A:442:EPE:H21	6:A:442:EPE:O2S	1.89	0.71
1:A:154:A:OP2	7:A:917:HOH:O	2.09	0.70
1:A:83:G:OP1	1:A:83:G:H3'	1.91	0.70
1:A:43:A:H61	1:A:65:U:H3	1.37	0.70
1:A:309:U:O2	1:A:309:U:C2'	2.40	0.69
1:A:131:C:H2'	1:A:132:U:H6	1.58	0.69
1:A:347:U:H2'	1:A:348:A:H5'	1.75	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:C:H4'	1:A:311:G:O5'	1.92	0.69
1:A:195:U:H6	1:A:195:U:C5'	2.05	0.68
1:A:292:A:O2'	1:A:293:A:O5'	2.12	0.68
1:A:267:G:H1'	1:A:285:U:O4	1.94	0.68
1:A:19:C:H42	1:A:252:G:H1	1.41	0.67
1:A:295:U:H5'	1:A:296:C:OP2	1.95	0.67
1:A:38:C:H2'	1:A:39:C:C6	2.31	0.66
1:A:287:A:O2'	1:A:288:G:C5'	2.44	0.66
1:A:39:C:C2'	1:A:40:C:H5''	2.27	0.64
5:A:441:SPM:H131	5:A:441:SPM:H92	1.80	0.64
1:A:138:A:OP1	1:A:139:C:C5	2.50	0.64
1:A:209:G:H2'	1:A:210:U:C6	2.32	0.64
1:A:39:C:H2'	1:A:40:C:H5''	1.81	0.63
1:A:22:U:C4	1:A:23:C:C5	2.88	0.62
1:A:5:G:C8	1:A:376:A:N6	2.68	0.62
1:A:108:G:C8	1:A:108:G:H5'	2.34	0.62
1:A:108:G:O2'	1:A:109:A:OP2	2.18	0.62
1:A:318:A:O2'	1:A:319:A:H5'	1.99	0.62
1:A:76:C:H2'	1:A:77:A:O4'	2.00	0.62
1:A:340:U:C2'	1:A:340:U:O2	2.46	0.61
1:A:52:G:H2'	1:A:53:C:C6	2.35	0.61
1:A:63:A:H2'	1:A:64:G:H8	1.64	0.61
1:A:161:G:H1	1:A:216:C:H42	1.47	0.60
1:A:292:A:HO2'	1:A:293:A:H8	1.50	0.60
1:A:61:A:H2'	1:A:62:C:H6	1.67	0.60
1:A:117:G:N7	6:A:446:EPE:O1S	2.33	0.60
1:A:117:G:O5'	1:A:117:G:H8	1.84	0.60
1:A:388:G:O2'	1:A:389:U:C5	2.55	0.59
1:A:212:G:H2'	1:A:213:G:C8	2.38	0.59
1:A:32:G:N2	1:A:34:G:H3'	2.17	0.59
1:A:39:C:C3'	1:A:40:C:H5''	2.32	0.59
2:B:1:A:H1'	2:B:2:U:P	2.43	0.58
1:A:60:A:O2'	1:A:61:A:H5'	2.03	0.58
1:A:63:A:H2'	1:A:64:G:C8	2.38	0.58
1:A:287:A:OP1	1:A:287:A:H8	1.86	0.58
1:A:154:A:H3'	1:A:155:G:H8	1.69	0.58
1:A:290:A:C2	1:A:291:G:O6	2.57	0.57
1:A:311:G:H2'	1:A:311:G:N3	2.17	0.57
1:A:108:G:O4'	1:A:110:A:H1'	2.04	0.57
1:A:290:A:H62	1:A:354:G:H3'	1.70	0.57
1:A:73:A:H2'	1:A:74:C:O4'	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:A:O2'	1:A:293:A:P	2.63	0.56
1:A:119:C:O3'	1:A:237:A:H2'	2.05	0.56
1:A:100:A:H2'	1:A:101:U:O4'	2.06	0.56
1:A:19:C:N4	1:A:252:G:H1	2.03	0.55
1:A:40:C:H2'	1:A:41:G:O4'	2.06	0.55
1:A:338:G:N2	1:A:344:G:C4	2.74	0.55
6:A:442:EPE:S	6:A:442:EPE:H21	2.45	0.55
1:A:66:U:OP1	1:A:66:U:H4'	2.05	0.55
1:A:329:A:H2'	1:A:330:A:C8	2.40	0.55
1:A:250:C:H2'	1:A:251:U:H6	1.72	0.55
1:A:355:A:N6	1:A:388:G:H1'	2.22	0.55
1:A:7:C:H2'	1:A:8:C:H6	1.72	0.55
1:A:70:C:H5''	1:A:70:C:H6	1.70	0.55
1:A:250:C:H2'	1:A:251:U:C6	2.42	0.54
2:B:1:A:O2'	2:B:2:U:O4'	2.26	0.54
1:A:152:U:O2'	1:A:153:G:OP1	2.21	0.53
1:A:212:G:H2'	1:A:213:G:H8	1.71	0.53
1:A:336:G:N2	1:A:346:C:C2	2.76	0.53
1:A:95:A:C5	1:A:96:U:C5	2.95	0.53
2:B:7:U:H5'	7:B:101:HOH:O	2.08	0.53
1:A:64:G:H5''	1:A:65:U:OP2	2.08	0.53
1:A:121:A:N7	1:A:248:G:H1'	2.23	0.53
1:A:336:G:C2	1:A:346:C:C2	2.96	0.53
1:A:59:U:H2'	1:A:59:U:O2	2.08	0.53
1:A:121:A:C8	1:A:248:G:H1'	2.43	0.53
1:A:238:U:C2'	1:A:239:G:H5'	2.39	0.53
1:A:52:G:H2'	1:A:53:C:H6	1.70	0.53
1:A:347:U:C2'	1:A:348:A:H5'	2.38	0.52
1:A:162:U:OP1	1:A:162:U:H4'	2.09	0.52
1:A:114:G:C6	1:A:115:A:C2	2.97	0.52
1:A:300:G:N2	1:A:318:A:OP2	2.27	0.52
1:A:66:U:H2'	1:A:67:A:H8	1.70	0.52
1:A:291:G:O2'	1:A:292:A:OP2	2.22	0.52
1:A:60:A:C2'	1:A:61:A:H5'	2.40	0.52
1:A:35:A:O2'	1:A:37:U:OP2	2.28	0.51
1:A:287:A:O2'	1:A:288:G:H5'	2.09	0.51
1:A:324:G:C6	1:A:325:G:N1	2.79	0.51
1:A:343:C:H5''	1:A:343:C:H6	1.76	0.51
1:A:293:A:H2'	1:A:294:G:O4'	2.10	0.51
1:A:72:A:H2'	1:A:73:A:C8	2.45	0.51
1:A:137:A:HO2'	1:A:138:A:P	2.32	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:G:H8	1:A:218:G:H5''	1.76	0.51
1:A:296:C:H2'	1:A:297:A:H8	1.67	0.51
1:A:251:U:H2'	1:A:252:G:C8	2.46	0.51
1:A:276:A:H8	1:A:276:A:OP1	1.92	0.51
1:A:292:A:H61	1:A:325:G:C2'	2.24	0.51
1:A:331:G:C6	1:A:332:U:C4	2.99	0.51
1:A:161:G:H1	1:A:216:C:N4	2.09	0.50
1:A:221:U:O2	1:A:221:U:H2'	2.11	0.50
1:A:22:U:H2'	1:A:23:C:O5'	2.12	0.50
1:A:39:C:H2'	1:A:39:C:O2	2.10	0.50
1:A:19:C:O2'	1:A:20:A:H5'	2.11	0.50
1:A:339:U:H3'	1:A:341:C:H41	1.77	0.50
1:A:61:A:H2'	1:A:62:C:C6	2.47	0.49
1:A:137:A:O2'	1:A:138:A:P	2.70	0.49
1:A:169:G:C6	1:A:170:G:C5	3.01	0.49
1:A:19:C:C2'	1:A:20:A:H5'	2.43	0.49
1:A:206:A:HO2'	1:A:208:A:H8	1.59	0.49
1:A:194:G:H1'	1:A:240:A:O2'	2.12	0.48
1:A:40:C:C6	1:A:40:C:C5'	2.84	0.48
1:A:336:G:C2	1:A:346:C:N3	2.81	0.48
1:A:305:C:H42	1:A:314:G:H1	1.59	0.48
1:A:36:G:O6	7:A:925:HOH:O	2.19	0.48
2:B:8:A:OP2	2:B:8:A:H4'	2.14	0.48
1:A:383:G:H2'	1:A:384:U:H6	1.79	0.48
1:A:238:U:H2'	1:A:239:G:H5'	1.95	0.47
1:A:134:A:H2'	1:A:135:G:H5'	1.96	0.47
1:A:39:C:C2'	1:A:39:C:O2	2.62	0.47
1:A:56:A:C2	1:A:201:C:C2	3.02	0.47
1:A:205:C:H2'	1:A:206:A:OP1	2.14	0.47
1:A:4:U:C4	1:A:5:G:C6	3.02	0.47
1:A:83:G:N3	1:A:83:G:C2'	2.73	0.47
1:A:238:U:C5'	1:A:238:U:C6	2.86	0.47
1:A:123:C:H42	1:A:243:G:H1	1.61	0.47
1:A:336:G:N1	1:A:346:C:C4	2.83	0.47
1:A:27:A:H2'	1:A:28:G:O4'	2.14	0.47
5:A:441:SPM:H131	5:A:441:SPM:C9	2.43	0.47
1:A:151:A:H4'	1:A:153:G:C8	2.50	0.46
1:A:123:C:H2'	1:A:123:C:O2	2.14	0.46
1:A:333:A:N3	1:A:334:U:O2'	2.45	0.46
1:A:114:G:O6	6:A:445:EPE:O3S	2.27	0.46
1:A:134:A:C2'	1:A:135:G:H5'	2.45	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:G:H2'	1:A:157:C:C6	2.51	0.46
1:A:60:A:H2'	1:A:61:A:O4'	2.15	0.46
1:A:57:A:C2	1:A:200:U:C2	3.03	0.46
1:A:335:G:C2	1:A:347:U:O2	2.69	0.46
1:A:383:G:O2'	1:A:384:U:H5'	2.16	0.46
1:A:67:A:C2	1:A:249:A:O4'	2.68	0.46
1:A:73:A:O5'	1:A:73:A:H8	1.99	0.46
1:A:147:U:OP2	1:A:147:U:H6	1.99	0.45
1:A:362:G:H2'	1:A:363:U:C6	2.51	0.45
1:A:204:C:H3'	1:A:204:C:C6	2.52	0.45
1:A:317:G:O2'	1:A:318:A:H5''	2.16	0.45
1:A:95:A:C6	1:A:96:U:C4	3.04	0.45
1:A:206:A:O2'	1:A:208:A:H8	2.00	0.45
1:A:287:A:OP1	1:A:287:A:C8	2.67	0.45
1:A:306:U:H2'	1:A:306:U:O2	2.15	0.45
1:A:62:C:H2'	1:A:63:A:H8	1.82	0.44
1:A:146:U:H2'	1:A:147:U:C6	2.52	0.44
1:A:174:A:H1'	1:A:239:G:O4'	2.17	0.44
1:A:51:G:C2	1:A:52:G:C8	3.05	0.44
1:A:5:G:N9	1:A:376:A:N6	2.65	0.44
1:A:107:G:H2'	1:A:107:G:N3	2.32	0.44
1:A:161:G:H2'	1:A:162:U:O4'	2.17	0.44
1:A:324:G:H8	1:A:324:G:O5'	2.00	0.44
1:A:5:G:C4	1:A:376:A:N6	2.86	0.44
1:A:122:A:O4'	1:A:247:A:H4'	2.18	0.44
1:A:85:C:H5''	1:A:86:C:OP2	2.18	0.44
1:A:157:C:H2'	1:A:158:U:C6	2.52	0.43
1:A:375:U:OP1	2:B:6:U:H4'	2.17	0.43
1:A:132:U:O2'	1:A:133:G:H5'	2.17	0.43
6:A:442:EPE:H102	6:A:442:EPE:H22	1.46	0.43
1:A:355:A:H61	1:A:388:G:H1'	1.83	0.43
1:A:133:G:C6	1:A:145:C:N4	2.86	0.43
1:A:343:C:H2'	1:A:344:G:C8	2.54	0.43
1:A:139:C:H2'	1:A:140:A:O5'	2.19	0.43
1:A:92:G:H1'	1:A:273:U:O2'	2.18	0.43
1:A:151:A:N3	1:A:151:A:H2'	2.34	0.43
1:A:292:A:O2'	1:A:293:A:H8	2.01	0.43
1:A:296:C:N4	1:A:297:A:N6	2.67	0.43
1:A:140:A:H3'	1:A:141:C:H6	1.83	0.42
1:A:62:C:H2'	1:A:63:A:C8	2.54	0.42
1:A:335:G:C6	1:A:336:G:C5	3.08	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:7:U:O2	2:B:7:U:H2'	2.19	0.42
1:A:361:C:O2'	1:A:362:G:H5'	2.19	0.42
1:A:209:G:H2'	1:A:210:U:H6	1.82	0.42
1:A:23:C:H2'	1:A:23:C:O2	2.19	0.42
1:A:174:A:H4'	1:A:238:U:O2'	2.20	0.42
1:A:342:G:H2'	1:A:343:C:O4'	2.20	0.42
1:A:117:G:C8	1:A:117:G:O5'	2.69	0.41
1:A:131:C:H2'	1:A:132:U:C6	2.47	0.41
1:A:206:A:O2'	1:A:208:A:C8	2.69	0.41
1:A:154:A:OP2	1:A:155:G:N7	2.54	0.41
1:A:12:A:O2'	1:A:13:U:H3'	2.20	0.41
1:A:374:G:H8	1:A:374:G:H5''	1.86	0.41
5:A:441:SPM:HN0	5:A:441:SPM:H62	1.85	0.41
1:A:148:C:O2	1:A:148:C:H2'	2.21	0.41
1:A:7:C:C2	1:A:8:C:C5	3.09	0.41
1:A:3:G:C2	1:A:4:U:H1'	2.56	0.41
1:A:83:G:H4'	1:A:84:U:OP1	2.18	0.41
1:A:134:A:H2'	1:A:135:G:O4'	2.21	0.40
1:A:218:G:H5''	1:A:218:G:C8	2.55	0.40
2:B:5:A:C4	2:B:6:U:C5	3.09	0.40
1:A:25:A:O2'	1:A:26:U:P	2.79	0.40
1:A:72:A:H2'	1:A:73:A:H8	1.85	0.40
1:A:324:G:H5''	1:A:325:G:OP2	2.22	0.40
1:A:35:A:C2	1:A:245:A:C4	3.09	0.40
1:A:176:U:H2'	1:A:177:U:C6	2.56	0.40
1:A:389:U:OP2	1:A:389:U:H6	2.05	0.40
1:A:290:A:C2	1:A:291:G:C6	3.10	0.40
1:A:292:A:C8	1:A:326:A:C6	3.09	0.40
1:A:318:A:O2'	1:A:319:A:C5'	2.68	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	386/393 (98%)	137 (35%)	0
2	B	7/8 (87%)	6 (85%)	0
All	All	393/401 (98%)	143 (36%)	0

All (143) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	12	A
1	A	16	G
1	A	20	A
1	A	23	C
1	A	25	A
1	A	28	G
1	A	33	A
1	A	35	A
1	A	36	G
1	A	39	C
1	A	40	C
1	A	41	G
1	A	49	A
1	A	50	A
1	A	51	G
1	A	60	A
1	A	64	G
1	A	65	U
1	A	66	U
1	A	67	A
1	A	68	G
1	A	70	C
1	A	83	G
1	A	84	U
1	A	85	C
1	A	86	C
1	A	89	G
1	A	91	C
1	A	101	U
1	A	108	G
1	A	109	A
1	A	110	A
1	A	111	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	113	G
1	A	116	C
1	A	119	C
1	A	124	C
1	A	125	U
1	A	126	U
1	A	134	A
1	A	137	A
1	A	138	A
1	A	139	C
1	A	140	A
1	A	145	C
1	A	147	U
1	A	148	C
1	A	151	A
1	A	152	U
1	A	153	G
1	A	157	C
1	A	160	G
1	A	162	U
1	A	163	A
1	A	164	U
1	A	165	C
1	A	166	A
1	A	167	A
1	A	169	G
1	A	174	A
1	A	180	C
1	A	188	A
1	A	190	C
1	A	195	U
1	A	206	A
1	A	207	A
1	A	208	A
1	A	217	A
1	A	218	G
1	A	221	U
1	A	222	A
1	A	223	A
1	A	224	A
1	A	228	A
1	A	235	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	236	G
1	A	237	A
1	A	238	U
1	A	239	G
1	A	245	A
1	A	246	A
1	A	247	A
1	A	255	U
1	A	259	U
1	A	260	A
1	A	265	G
1	A	269	G
1	A	278	A
1	A	285	U
1	A	287	A
1	A	288	G
1	A	289	C
1	A	291	G
1	A	292	A
1	A	293	A
1	A	295	U
1	A	296	C
1	A	298	U
1	A	300	G
1	A	307	G
1	A	308	U
1	A	309	U
1	A	310	C
1	A	311	G
1	A	312	C
1	A	313	A
1	A	318	A
1	A	320	G
1	A	321	G
1	A	325	G
1	A	327	A
1	A	333	A
1	A	334	U
1	A	337	C
1	A	340	U
1	A	341	C
1	A	342	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	348	A
1	A	352	U
1	A	353	U
1	A	354	G
1	A	355	A
1	A	356	A
1	A	357	C
1	A	359	G
1	A	365	U
1	A	369	G
1	A	370	A
1	A	374	G
1	A	377	C
1	A	381	C
1	A	382	G
1	A	383	G
1	A	387	U
1	A	388	G
1	A	389	U
2	B	2	U
2	B	3	U
2	B	4	U
2	B	5	A
2	B	6	U
2	B	8	A

There are no RNA pucker outliers to report.

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](#)

Of 47 ligands modelled in this entry, 39 are monoatomic - leaving 8 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$
5	SPM	A	440	-	13,13,13	0.48	0	12,12,12	1.35	2 (16%)
5	SPM	A	441	-	13,13,13	0.39	0	12,12,12	1.25	2 (16%)
6	EPE	A	442	-	12,12,15	2.61	2 (16%)	14,16,20	1.60	2 (14%)
6	EPE	A	443	-	0,3,15	0.00	-	0,3,20	0.00	-
6	EPE	A	444	-	12,12,15	2.51	2 (16%)	14,16,20	1.76	2 (14%)
6	EPE	A	445	-	2,4,15	2.30	1 (50%)	1,6,20	3.96	1 (100%)
6	EPE	A	446	-	2,4,15	1.89	1 (50%)	1,6,20	0.56	0
6	EPE	A	447	-	5,5,15	2.48	2 (40%)	7,7,20	3.38	3 (42%)

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
5	SPM	A	440	-	-	0/11/11/11	0/0/0/0
5	SPM	A	441	-	-	0/11/11/11	0/0/0/0
6	EPE	A	442	-	-	0/6/14/19	0/1/1/1
6	EPE	A	443	-	-	0/0/0/19	0/0/0/1
6	EPE	A	444	-	-	0/6/14/19	0/1/1/1
6	EPE	A	445	-	-	0/0/0/19	0/0/0/1
6	EPE	A	446	-	-	0/0/0/19	0/0/0/1
6	EPE	A	447	-	-	0/3/3/19	0/0/0/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	442	EPE	C10-S	-7.44	1.66	1.77
6	A	444	EPE	C10-S	-6.97	1.67	1.77
6	A	447	EPE	C10-S	-2.12	1.68	1.77
6	A	446	EPE	O3S-S	2.29	1.62	1.47
6	A	445	EPE	O3S-S	2.96	1.66	1.47
6	A	442	EPE	O3S-S	5.05	1.64	1.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	447	EPE	O3S-S	5.05	1.64	1.47
6	A	444	EPE	O3S-S	5.14	1.64	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	445	EPE	O2S-S-O1S	-3.96	107.02	117.93
6	A	447	EPE	O3S-S-O2S	-2.10	106.55	111.37
5	A	440	SPM	C3-C4-N5	2.20	117.67	112.06
5	A	441	SPM	C11-N10-C9	2.27	121.59	113.33
6	A	442	EPE	O2S-S-C10	2.55	108.98	106.79
5	A	440	SPM	C11-N10-C9	2.58	122.73	113.33
5	A	441	SPM	C6-N5-C4	2.81	123.55	113.33
6	A	444	EPE	O2S-S-C10	3.92	110.16	106.79
6	A	444	EPE	O1S-S-C10	3.95	110.18	106.79
6	A	442	EPE	O3S-S-C10	4.10	111.10	106.06
6	A	447	EPE	O1S-S-C10	4.73	110.85	106.79
6	A	447	EPE	O3S-S-C10	6.87	114.51	106.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	441	SPM	3	0
6	A	442	EPE	3	0
6	A	445	EPE	1	0
6	A	446	EPE	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 [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	388/393 (98%)	-0.08	8 (2%) 64 64	65, 105, 227, 332	0
2	B	8/8 (100%)	1.10	1 (12%) 4 4	92, 122, 190, 205	1 (12%)
All	All	396/401 (98%)	-0.06	9 (2%) 61 61	65, 106, 227, 332	1 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	390	G	16.1
2	B	8	A	7.0
1	A	311	G	2.8
1	A	3	G	2.5
1	A	190	C	2.4
1	A	289	C	2.3
1	A	181	A	2.2
1	A	378	G	2.2
1	A	175	G	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(Å ²)	Q<0.9
5	SPM	A	441	14/14	0.52	1.53	116.15	43,58,68,72	14
6	EPE	A	444	12/15	0.56	0.95	41.57	67,78,122,125	12
5	SPM	A	440	14/14	0.57	0.95	28.28	61,83,98,106	14
6	EPE	A	442	12/15	0.81	0.46	19.28	92,94,123,131	12
6	EPE	A	445	5/15	0.90	0.40	11.82	56,56,72,76	5
4	K	A	426	1/1	0.90	0.24	9.18	129,129,129,129	0
3	CA	A	413	1/1	0.96	0.67	6.28	102,102,102,102	0
3	CA	A	408	1/1	0.98	0.36	4.35	92,92,92,92	0
4	K	A	431	1/1	0.85	0.33	3.19	103,103,103,103	0
3	CA	A	402	1/1	0.96	0.14	-2.02	84,84,84,84	0
3	CA	A	401	1/1	0.99	0.12	-2.63	92,92,92,92	0
4	K	A	433	1/1	0.99	0.07	-2.65	79,79,79,79	0
4	K	A	429	1/1	0.85	0.16	-4.54	81,81,81,81	0
3	CA	A	420	1/1	0.92	0.66	-	125,125,125,125	0
3	CA	A	407	1/1	0.64	0.94	-	109,109,109,109	0
3	CA	A	421	1/1	0.80	0.34	-	143,143,143,143	0
6	EPE	A	446	5/15	0.93	0.62	-	67,68,79,79	5
4	K	A	427	1/1	0.89	0.50	-	116,116,116,116	0
4	K	A	435	1/1	0.85	0.39	-	96,96,96,96	0
3	CA	A	425	1/1	0.69	0.45	-	140,140,140,140	0
3	CA	A	403	1/1	0.94	0.42	-	100,100,100,100	0
4	K	A	438	1/1	0.79	0.57	-	107,107,107,107	0
3	CA	A	414	1/1	0.84	0.46	-	106,106,106,106	0
3	CA	A	410	1/1	0.89	0.86	-	167,167,167,167	0
3	CA	A	422	1/1	0.76	0.22	-	111,111,111,111	0
3	CA	A	418	1/1	0.89	0.31	-	108,108,108,108	0
3	CA	A	416	1/1	0.96	0.18	-	85,85,85,85	0
3	CA	A	409	1/1	0.93	0.62	-	119,119,119,119	0
3	CA	A	405	1/1	0.93	0.40	-	121,121,121,121	0
4	K	A	430	1/1	0.92	0.25	-	140,140,140,140	0
4	K	A	428	1/1	0.72	0.27	-	109,109,109,109	0
3	CA	A	406	1/1	0.90	0.40	-	85,85,85,85	0
4	K	A	434	1/1	0.97	0.18	-	79,79,79,79	0
3	CA	A	415	1/1	0.92	0.72	-	104,104,104,104	0
3	CA	A	424	1/1	0.88	0.40	-	123,123,123,123	0
4	K	A	432	1/1	0.79	0.35	-	145,145,145,145	0
3	CA	A	417	1/1	0.91	0.11	-	137,137,137,137	0
3	CA	A	423	1/1	0.87	0.21	-	129,129,129,129	0
4	K	A	437	1/1	0.87	0.49	-	114,114,114,114	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	EPE	A	443	4/15	0.77	0.81	-	101,105,113,114	4
6	EPE	A	447	6/15	0.92	0.58	-	72,99,101,105	6
3	CA	A	419	1/1	0.97	0.05	-	103,103,103,103	0
4	K	A	436	1/1	0.98	0.62	-	99,99,99,99	0
3	CA	A	412	1/1	0.94	0.70	-	117,117,117,117	0
4	K	A	439	1/1	0.94	0.57	-	113,113,113,113	0
3	CA	A	404	1/1	0.79	0.28	-	119,119,119,119	0
3	CA	A	411	1/1	0.87	0.43	-	114,114,114,114	0

6.5 Other polymers [i](#)

There are no such residues in this entry.