



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 03:08 PM GMT

PDB ID : 3S1S
Title : Characterization and crystal structure of the type IIG restriction endonuclease BpuSI
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Deposited on : 2011-05-16
Resolution : 2.35 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

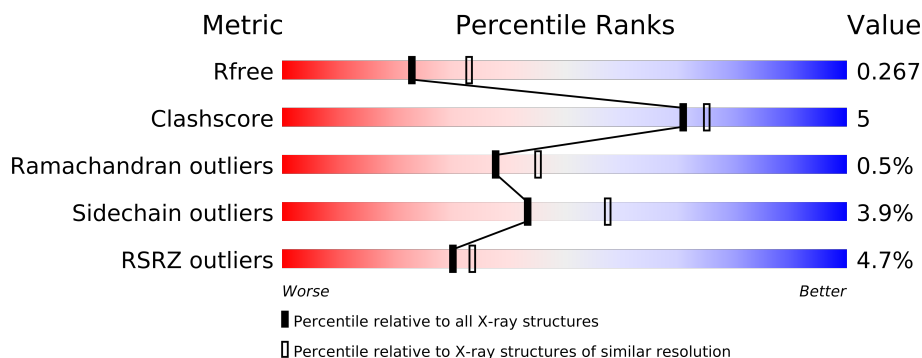
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.35 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}	66092	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	878	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	EDO	A	905	-	X
3	EDO	A	909	-	X
3	EDO	A	913	-	X
3	EDO	A	915	-	X
3	EDO	A	917	-	X
3	EDO	A	921	-	X

2 Entry composition i

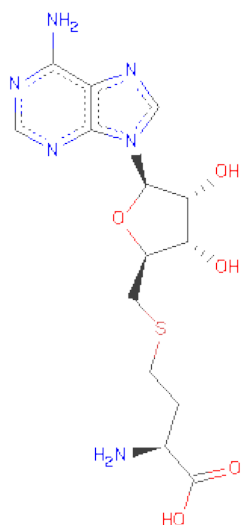
There are 6 unique types of molecules in this entry. The entry contains 7588 atoms, of which 0 are hydrogen and 0 are deuterium.

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 restriction endonuclease BpuSI.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	870	7127	4527	1205	1378	9	8	0	30	0

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mn 1 1	0	0

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	38	Total I 38 38	0	0

- Molecule 6 is water.

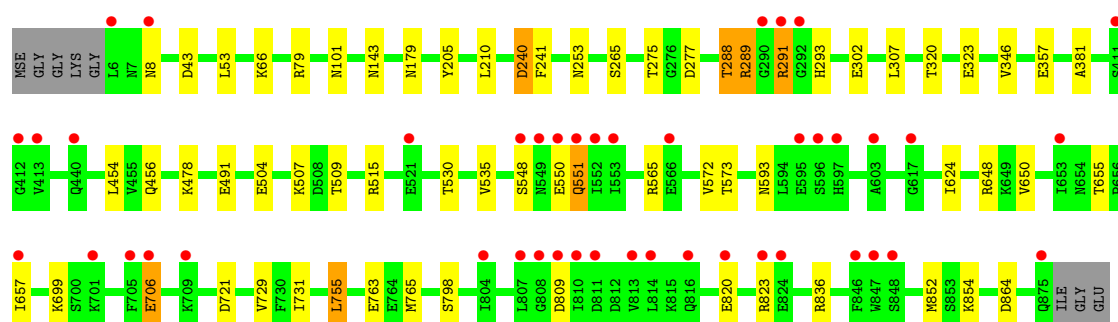
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	316	Total O 316 316	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: restriction endonuclease BpuSI

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	213.47Å 215.73Å 73.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.35 50.04 – 2.18	Depositor EDS
% Data completeness (in resolution range)	92.8 (30.00-2.35) 79.2 (50.04-2.18)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.212 , 0.268 0.214 , 0.267	Depositor DCC
R_{free} test set	3569 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.329	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.9	EDS
Estimated twinning fraction	0.016 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 70448 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7588	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, IOD, EDO, MN

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	0.51	0/7344	0.61	0/9942

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7127	0	0	29	0
2	A	26	0	0	1	0
3	A	80	0	0	0	0
4	A	1	0	0	0	0
5	A	38	0	0	7	1
6	A	316	0	0	8	1
All	All	7588	0	0	33	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (33) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:A:952:IOD:I	6:A:1248:HOH:O	2.36	1.11
1:A:240:ASP:CG	1:A:241:PHE:N	2.11	1.01
5:A:939:IOD:I	6:A:1106:HOH:O	2.69	0.80
1:A:288:THR:CG2	1:A:288:THR:O	2.38	0.71
2:A:900:SAH:N6	6:A:1235:HOH:O	2.23	0.71
1:A:763[B]:GLU:OE2	1:A:763[B]:GLU:CA	2.38	0.70
1:A:820:GLU:OE1	1:A:823:ARG:NH2	2.28	0.65
5:A:947:IOD:I	6:A:1250:HOH:O	2.85	0.64
1:A:143[B]:ASN:ND2	6:A:1246:HOH:O	2.30	0.62
1:A:699:LYS:NZ	5:A:940:IOD:I	3.02	0.62
1:A:240:ASP:OD2	1:A:241:PHE:N	2.33	0.60
1:A:79:ARG:NH2	1:A:535:VAL:O	2.38	0.57
1:A:289:ARG:NE	1:A:289:ARG:O	2.39	0.55
1:A:504:GLU:O	5:A:963:IOD:I	2.96	0.54
1:A:550:GLU:N	1:A:550:GLU:OE1	2.39	0.54
1:A:275:THR:CG2	1:A:277:ASP:OD2	2.57	0.53
1:A:8:ASN:ND2	6:A:1253:HOH:O	2.44	0.50
1:A:491:GLU:OE2	1:A:515:ARG:CZ	2.61	0.49
1:A:240:ASP:OD1	1:A:381:ALA:CB	2.61	0.49
1:A:240:ASP:OD1	6:A:1038:HOH:O	2.20	0.48
1:A:293:HIS:CE1	1:A:357:GLU:OE1	2.66	0.48
1:A:798:SER:OG	5:A:936:IOD:I	3.02	0.48
1:A:550:GLU:CG	1:A:551:GLN:N	2.77	0.47
1:A:706:GLU:N	1:A:706:GLU:CD	2.69	0.46
1:A:179[A]:ASN:ND2	5:A:935:IOD:I	3.19	0.46
1:A:205:TYR:OH	1:A:275:THR:O	2.34	0.45
1:A:648:ARG:NH1	6:A:1131:HOH:O	2.51	0.43
1:A:43:ASP:O	1:A:66:LYS:NZ	2.52	0.42
1:A:507:LYS:NZ	1:A:864:ASP:OD2	2.53	0.42
1:A:593:ASN:OD1	1:A:854:LYS:CE	2.68	0.42
1:A:302:GLU:CA	1:A:302:GLU:OE1	2.68	0.41
1:A:320:THR:N	1:A:323:GLU:OE2	2.53	0.41
1:A:731:ILE:O	1:A:755:LEU:N	2.53	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:A:959:IOD:I	6:A:1176:HOH:O[6_554]	1.91	0.29

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	898/878 (102%)	861 (96%)	33 (4%)	4 (0%)	43 52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	ASP
1	A	548	SER
1	A	101	ASN
1	A	291	ARG

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	809/774 (104%)	778 (96%)	31 (4%)	44 59

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	LEU
1	A	210	LEU
1	A	253	ASN
1	A	265	SER
1	A	288	THR
1	A	289	ARG
1	A	291	ARG
1	A	307	LEU
1	A	346	VAL
1	A	454	LEU

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Mol	Chain	Res	Type
1	A	456	GLN
1	A	478	LYS
1	A	509[A]	THR
1	A	509[B]	THR
1	A	530	THR
1	A	551	GLN
1	A	565	ARG
1	A	572	VAL
1	A	573	THR
1	A	624	ILE
1	A	650	VAL
1	A	655	THR
1	A	657	ILE
1	A	706	GLU
1	A	721	ASP
1	A	729	VAL
1	A	755	LEU
1	A	765	MSE
1	A	809	ASP
1	A	836	ARG
1	A	852	MSE

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 chains 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 60 ligands modelled in this entry, 39 are monoatomic - leaving 21 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	$\# Z > 2$
2	SAH	A	900	-	28,28,28	1.37	5 (17%)	40,40,40	2.58	16 (40%)
3	EDO	A	901	-	3,3,3	0.54	0	2,2,2	0.35	0
3	EDO	A	903	-	3,3,3	0.80	0	2,2,2	0.12	0
3	EDO	A	904	-	3,3,3	0.62	0	2,2,2	0.29	0
3	EDO	A	905	-	3,3,3	0.57	0	2,2,2	0.52	0
3	EDO	A	906	-	3,3,3	0.70	0	2,2,2	0.50	0
3	EDO	A	907	-	3,3,3	0.50	0	2,2,2	0.50	0
3	EDO	A	908	-	3,3,3	0.50	0	2,2,2	0.45	0
3	EDO	A	909	-	3,3,3	0.48	0	2,2,2	0.50	0
3	EDO	A	910	-	3,3,3	0.46	0	2,2,2	0.38	0
3	EDO	A	911	-	3,3,3	0.58	0	2,2,2	0.28	0
3	EDO	A	912	-	3,3,3	0.46	0	2,2,2	0.55	0
3	EDO	A	913	-	3,3,3	0.53	0	2,2,2	0.38	0
3	EDO	A	914	-	3,3,3	0.63	0	2,2,2	0.27	0
3	EDO	A	915	-	3,3,3	0.62	0	2,2,2	0.32	0
3	EDO	A	916	-	3,3,3	0.55	0	2,2,2	0.49	0
3	EDO	A	917	-	3,3,3	0.43	0	2,2,2	0.47	0
3	EDO	A	918	-	3,3,3	0.56	0	2,2,2	0.46	0
3	EDO	A	919	-	3,3,3	0.58	0	2,2,2	0.36	0
3	EDO	A	920	-	3,3,3	0.64	0	2,2,2	0.16	0
3	EDO	A	921	-	3,3,3	0.67	0	2,2,2	0.08	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SAH	A	900	-	-	0/15/31/31	0/1/3/3
3	EDO	A	901	-	-	0/1/1/1	0/0/0/0
3	EDO	A	903	-	-	0/1/1/1	0/0/0/0
3	EDO	A	904	-	-	0/1/1/1	0/0/0/0
3	EDO	A	905	-	-	0/1/1/1	0/0/0/0
3	EDO	A	906	-	-	0/1/1/1	0/0/0/0
3	EDO	A	907	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	908	-	-	0/1/1/1	0/0/0/0
3	EDO	A	909	-	-	0/1/1/1	0/0/0/0
3	EDO	A	910	-	-	0/1/1/1	0/0/0/0
3	EDO	A	911	-	-	0/1/1/1	0/0/0/0
3	EDO	A	912	-	-	0/1/1/1	0/0/0/0
3	EDO	A	913	-	-	0/1/1/1	0/0/0/0
3	EDO	A	914	-	-	0/1/1/1	0/0/0/0
3	EDO	A	915	-	-	0/1/1/1	0/0/0/0
3	EDO	A	916	-	-	0/1/1/1	0/0/0/0
3	EDO	A	917	-	-	0/1/1/1	0/0/0/0
3	EDO	A	918	-	-	0/1/1/1	0/0/0/0
3	EDO	A	919	-	-	0/1/1/1	0/0/0/0
3	EDO	A	920	-	-	0/1/1/1	0/0/0/0
3	EDO	A	921	-	-	0/1/1/1	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	SAH	C5-C4	3.65	1.48	1.40
2	A	900	SAH	C2-N3	2.61	1.37	1.32
2	A	900	SAH	C5'-SD	-2.25	1.76	1.81
2	A	900	SAH	OXT-C	-2.07	1.22	1.30
2	A	900	SAH	C4-N9	-2.01	1.34	1.37

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	SAH	N3-C4-N9	7.48	138.94	125.43
2	A	900	SAH	CB-CG-SD	-5.78	102.43	113.57
2	A	900	SAH	N3-C2-N1	-5.62	124.01	128.71
2	A	900	SAH	C5-C4-N3	-3.78	117.47	125.70
2	A	900	SAH	N6-C6-N1	3.62	126.48	119.36
2	A	900	SAH	C8-N9-C4	3.61	109.65	106.90
2	A	900	SAH	O4'-C1'-C2'	-3.35	101.64	106.77
2	A	900	SAH	OXT-C-O	-3.34	116.51	124.07
2	A	900	SAH	OXT-C-CA	3.09	123.81	116.88
2	A	900	SAH	C4'-O4'-C1'	-3.03	106.46	109.75
2	A	900	SAH	C8-N9-C1'	-2.97	120.53	126.38
2	A	900	SAH	O4'-C1'-N9	2.74	110.99	108.44
2	A	900	SAH	C5-C6-N6	-2.74	114.53	120.72
2	A	900	SAH	C-CA-N	2.67	113.79	109.36
2	A	900	SAH	C5-C4-N9	-2.48	103.59	107.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	SAH	C2-N3-C4	2.36	120.74	114.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	870/878 (99%)	0.23	44 (5%)	27 30	24, 41, 64, 76	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	6	LEU	6.5
1	A	848	SER	5.4
1	A	552	ILE	5.4
1	A	290	GLY	5.1
1	A	548	SER	5.1
1	A	292	GLY	5.0
1	A	413	VAL	4.6
1	A	807	LEU	4.6
1	A	657	ILE	4.5
1	A	814	LEU	4.4
1	A	440[A]	GLN	4.4
1	A	847	TRP	4.2
1	A	705	PHE	4.2
1	A	810	ILE	4.0
1	A	412	GLY	3.9
1	A	551	GLN	3.8
1	A	596	SER	3.8
1	A	809	ASP	3.8
1	A	549	ASN	3.7
1	A	553	ILE	3.5
1	A	8	ASN	3.2
1	A	550	GLU	3.2
1	A	824	GLU	3.2
1	A	291	ARG	3.2
1	A	813	VAL	3.2
1	A	701	LYS	3.1
1	A	811[A]	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	597	HIS	3.0
1	A	566[A]	GLU	2.7
1	A	706	GLU	2.7
1	A	709	LYS	2.7
1	A	823	ARG	2.7
1	A	617	GLY	2.6
1	A	521[A]	GLU	2.6
1	A	820	GLU	2.6
1	A	816	GLN	2.5
1	A	653	ILE	2.4
1	A	603	ALA	2.3
1	A	411	SER	2.3
1	A	804	ILE	2.3
1	A	875	GLN	2.2
1	A	595	GLU	2.2
1	A	846	PHE	2.1
1	A	808	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	EDO	A	905	4/4	0.40	9.19	39,40,40,41	0
3	EDO	A	921	4/4	0.40	7.10	60,61,61,63	0
3	EDO	A	909	4/4	0.18	6.19	32,32,32,32	0
3	EDO	A	913	4/4	0.20	5.09	45,45,45,46	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	EDO	A	915	4/4	0.17	3.96	55,56,56,56	0
3	EDO	A	917	4/4	0.28	2.52	39,39,41,44	0
3	EDO	A	904	4/4	0.17	1.89	46,48,49,49	0
3	EDO	A	920	4/4	0.16	1.78	55,55,55,56	0
3	EDO	A	903	4/4	0.20	1.74	41,43,44,45	0
3	EDO	A	906	4/4	0.20	0.98	40,41,41,41	0
3	EDO	A	914	4/4	0.16	0.96	60,61,62,62	0
3	EDO	A	907	4/4	0.15	0.45	43,45,45,46	0
5	IOD	A	931	1/1	0.18	-0.07	168,168,168,168	0
2	SAH	A	900	26/26	0.13	-0.15	35,39,42,44	0
3	EDO	A	916	4/4	0.11	-0.48	48,48,49,49	0
5	IOD	A	955	1/1	0.08	-0.53	40,40,40,40	0
3	EDO	A	901	4/4	0.14	-0.64	50,50,50,52	0
5	IOD	A	942	1/1	0.10	-0.64	138,138,138,138	0
3	EDO	A	919	4/4	0.12	-0.68	70,70,70,71	0
3	EDO	A	908	4/4	0.11	-0.70	53,55,57,58	0
5	IOD	A	937	1/1	0.09	-0.78	132,132,132,132	0
5	IOD	A	959	1/1	0.11	-1.10	54,54,54,54	0
4	MN	A	930	1/1	0.14	-1.19	27,27,27,27	0
3	EDO	A	911	4/4	0.10	-1.23	51,51,52,53	0
5	IOD	A	936	1/1	0.08	-1.31	125,125,125,125	0
3	EDO	A	910	4/4	0.10	-1.37	32,33,33,35	0
5	IOD	A	961	1/1	0.04	-1.70	125,125,125,125	0
5	IOD	A	951	1/1	0.06	-1.87	154,154,154,154	0
5	IOD	A	957	1/1	0.09	-1.99	120,120,120,120	0
3	EDO	A	918	4/4	0.11	-2.02	57,58,58,59	0
5	IOD	A	939	1/1	0.02	-2.27	90,90,90,90	0
5	IOD	A	948	1/1	0.05	-2.36	143,143,143,143	0
5	IOD	A	933	1/1	0.03	-2.46	87,87,87,87	0
5	IOD	A	947	1/1	0.13	-2.46	158,158,158,158	0
3	EDO	A	912	4/4	0.10	-2.49	44,44,45,45	0
5	IOD	A	934	1/1	0.05	-2.66	117,117,117,117	0
5	IOD	A	953	1/1	0.03	-2.72	119,119,119,119	0
5	IOD	A	963	1/1	0.07	-2.77	139,139,139,139	0
5	IOD	A	950	1/1	0.03	-2.79	118,118,118,118	0
5	IOD	A	946	1/1	0.04	-2.95	121,121,121,121	0
5	IOD	A	967	1/1	0.04	-3.02	65,65,65,65	0
5	IOD	A	943	1/1	0.03	-3.05	138,138,138,138	0
5	IOD	A	956	1/1	0.05	-3.18	74,74,74,74	0
5	IOD	A	932	1/1	0.03	-3.24	66,66,66,66	0
5	IOD	A	944	1/1	0.04	-3.50	136,136,136,136	0
5	IOD	A	960	1/1	0.03	-3.51	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	IOD	A	935	1/1	0.07	-3.57	51,51,51,51	0
5	IOD	A	966	1/1	0.02	-3.60	78,78,78,78	0
5	IOD	A	958	1/1	0.02	-3.77	82,82,82,82	0
5	IOD	A	938	1/1	0.05	-3.87	108,108,108,108	0
5	IOD	A	952	1/1	0.03	-3.90	104,104,104,104	0
5	IOD	A	968	1/1	0.02	-3.93	65,65,65,65	0
5	IOD	A	940	1/1	0.10	-4.08	166,166,166,166	0
5	IOD	A	949	1/1	0.07	-4.08	173,173,173,173	0
5	IOD	A	965	1/1	0.03	-4.10	72,72,72,72	0
5	IOD	A	962	1/1	0.04	-4.33	81,81,81,81	0
5	IOD	A	945	1/1	0.05	-4.62	155,155,155,155	0
5	IOD	A	954	1/1	0.02	-5.04	83,83,83,83	0
5	IOD	A	964	1/1	0.09	-17.08	79,79,79,79	1
5	IOD	A	941	1/1	0.08	-105.00	121,121,121,121	0

6.5 Other polymers ⓘ

There are no such residues in this entry.