



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 07:17 PM GMT

PDB ID : 4RDR  
Title : Structure of the bacterial Zn-transporter ZnuD from *Neisseria meningitidis*  
(locked conformation bound to zinc and cadmium ions)  
Authors : Calmettes, C.; Moraes, T.F.  
Deposited on : 2014-09-19  
Resolution : 2.47 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

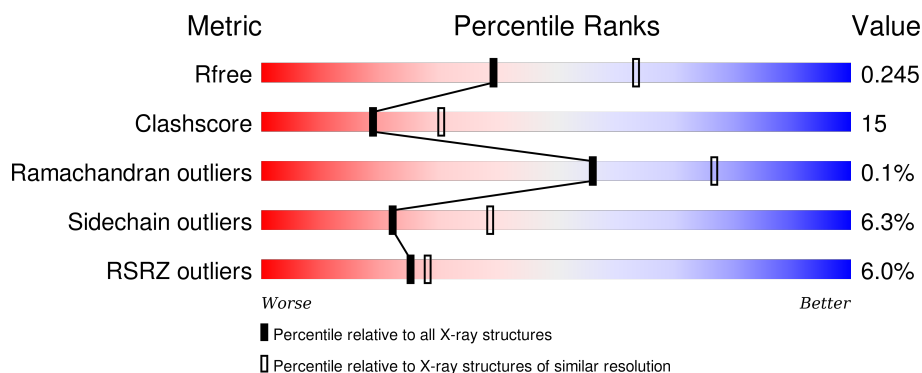
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.47 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	4309 (2.50-2.46)
Clashscore	102246	5050 (2.50-2.46)
Ramachandran outliers	100387	4961 (2.50-2.46)
Sidechain outliers	100360	4963 (2.50-2.46)
RSRZ outliers	91569	4319 (2.50-2.46)

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  $\geq 3$ , 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	748	<div> <div>6%</div> <div>65%</div> <div>27%</div> <div>6%</div> </div>

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	C8E	A	805	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	C8E	A	806	-	-	-	X
4	C8E	A	807	-	-	-	X
5	SO4	A	810	-	-	X	-
5	SO4	A	812	-	-	X	-
5	SO4	A	814	-	-	-	X
5	SO4	A	815	-	-	-	X
5	SO4	A	816	-	-	-	X
5	SO4	A	819	-	-	-	X
5	SO4	A	820	-	-	X	X
5	SO4	A	823	-	-	-	X
5	SO4	A	827	-	-	-	X
5	SO4	A	828	-	-	-	X
5	SO4	A	829	-	-	-	X
7	EDO	A	834	-	-	-	X
7	EDO	A	835	-	-	-	X
7	EDO	A	836	-	-	-	X
7	EDO	A	838	-	-	X	-

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5985 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 ZnuD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	706	Total	C	N	O	S	Se	0	1	0
			5633	3528	1039	1057	2	7			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MSE	-	EXPRESSION TAG	UNP Q9JZN9
A	-12	ALA	-	EXPRESSION TAG	UNP Q9JZN9
A	-11	HIS	-	EXPRESSION TAG	UNP Q9JZN9
A	-10	HIS	-	EXPRESSION TAG	UNP Q9JZN9
A	-9	HIS	-	EXPRESSION TAG	UNP Q9JZN9
A	-8	HIS	-	EXPRESSION TAG	UNP Q9JZN9
A	-7	HIS	-	EXPRESSION TAG	UNP Q9JZN9
A	-6	HIS	-	EXPRESSION TAG	UNP Q9JZN9
A	-5	LEU	-	EXPRESSION TAG	UNP Q9JZN9
A	-4	VAL	-	EXPRESSION TAG	UNP Q9JZN9
A	-3	PRO	-	EXPRESSION TAG	UNP Q9JZN9
A	-2	ARG	-	EXPRESSION TAG	UNP Q9JZN9
A	-1	GLY	-	EXPRESSION TAG	UNP Q9JZN9
A	0	SER	-	EXPRESSION TAG	UNP Q9JZN9

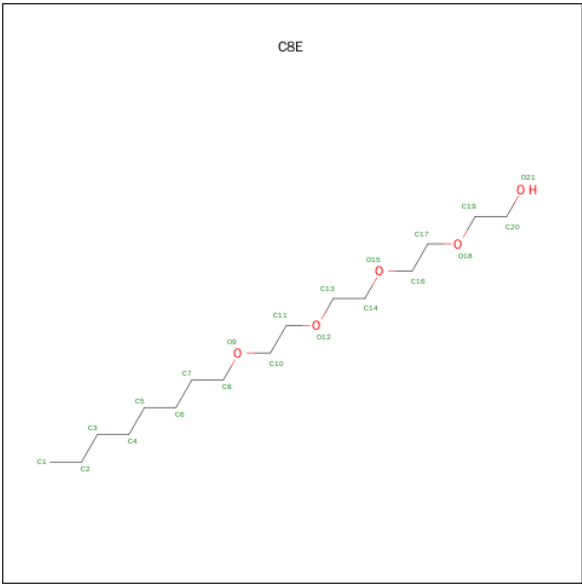
- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cd	0	0
			2	2		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

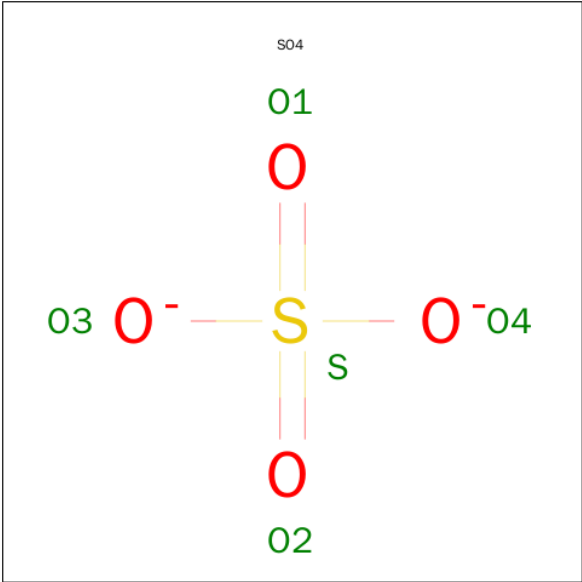
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: C<sub>16</sub>H<sub>34</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			21	16	5		
4	A	1	Total	C	O	0	0
			21	16	5		
4	A	1	Total	C	O	0	0
			21	16	5		
4	A	1	Total	C	O	0	0
			21	16	5		
4	A	1	Total	C	O	0	0
			21	16	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

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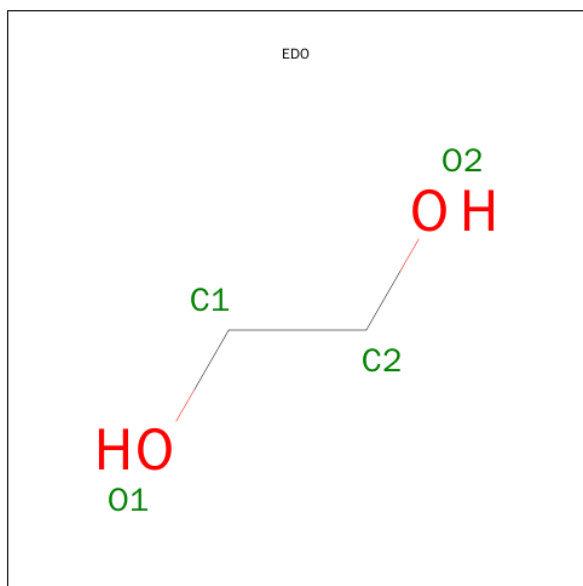
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 8 is water.

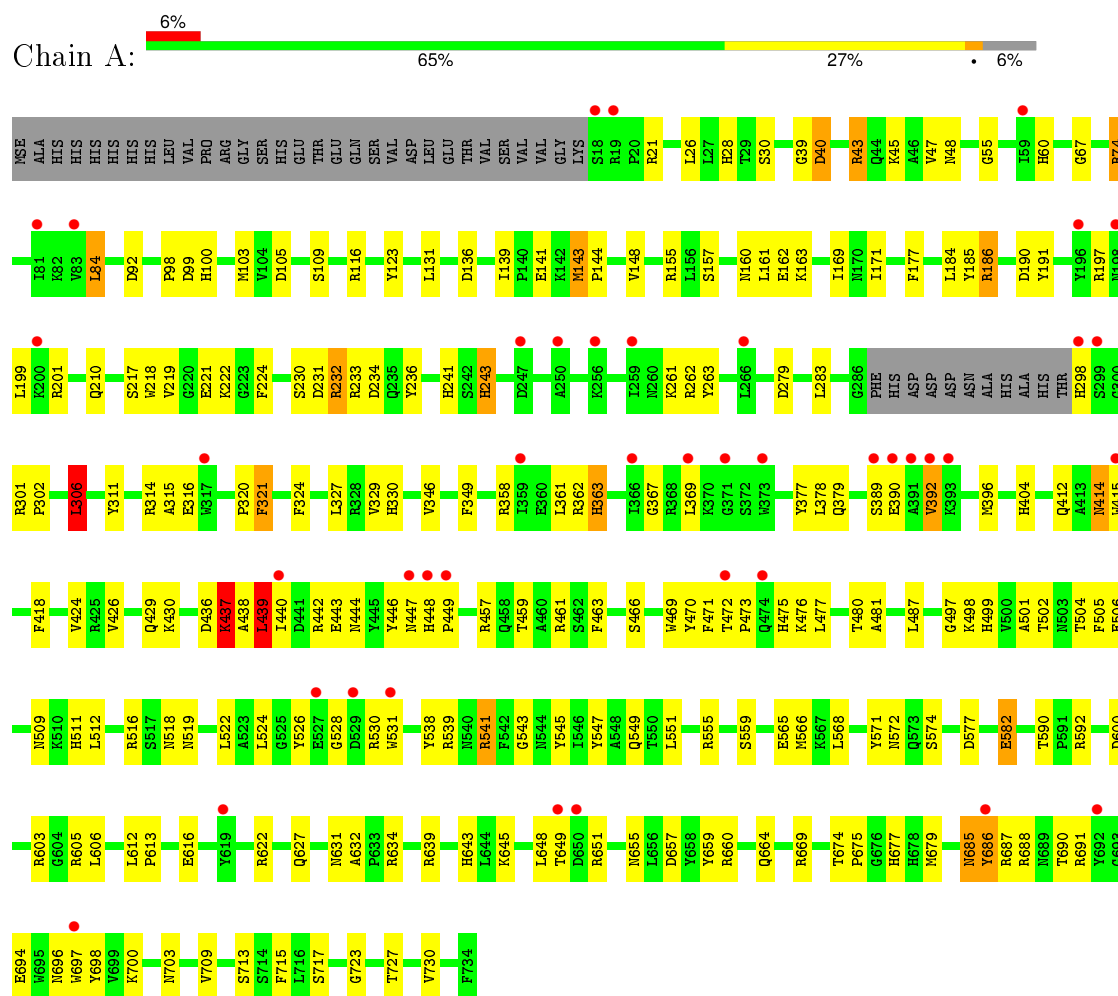
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	95	Total	O	0	0
			95	95		



### 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 ( $\text{RSRZ} > 2$ ). 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: ZnuD



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.07Å 155.82Å 159.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.98 – 2.47 39.98 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.98-2.47) 92.9 (39.98-2.47)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.218 , 0.248 0.216 , 0.245	Depositor DCC
$R_{free}$ test set	3846 reflections (4.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.2	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 65.7	EDS
Estimated twinning fraction	0.019 for -h,-l,-k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 45375 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5985	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, EDO, CD, C8E, 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	0.33	0/5767	0.58	2/7793 (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	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	439	LEU	CA-CB-CG	6.94	131.25	115.30
1	A	306	LEU	CA-CB-CG	5.92	128.91	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	437	LYS	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	5633	0	5433	174	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	105	0	170	11	0
5	A	105	0	0	10	0
6	A	24	0	32	1	0
7	A	20	0	30	10	0
8	A	95	0	0	17	0
All	All	5985	0	5665	177	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 15.

All (177) 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:516:ARG:HH21	7:A:838:EDO:H11	0.97	1.07
1:A:516:ARG:NH2	7:A:838:EDO:H11	1.71	1.06
1:A:516:ARG:HH21	7:A:838:EDO:C1	1.70	1.04
1:A:263:TYR:HB3	1:A:440:ILE:HD11	1.53	0.89
1:A:143:MSE:HE3	1:A:144:PRO:HD2	1.59	0.82
1:A:664:GLN:NE2	5:A:814:SO4:O2	2.22	0.73
1:A:362:ARG:NH2	5:A:820:SO4:O3	2.21	0.73
1:A:243:HIS:CE1	1:A:298:HIS:O	2.42	0.72
1:A:234:ASP:HB2	1:A:306:LEU:HG	1.72	0.72
1:A:414:ASN:ND2	8:A:935:HOH:O	2.23	0.71
1:A:590:THR:HG22	1:A:592:ARG:H	1.56	0.71
1:A:687:ARG:NH2	1:A:694:GLU:OE1	2.23	0.71
1:A:241:HIS:ND1	8:A:994:HOH:O	2.24	0.71
1:A:603:ARG:NH2	5:A:810:SO4:O4	2.24	0.70
1:A:457:ARG:NH1	5:A:812:SO4:S	2.63	0.70
1:A:518:ASN:ND2	7:A:838:EDO:O2	2.24	0.70
1:A:162:GLU:OE2	1:A:186:ARG:NH2	2.25	0.70
1:A:530:ARG:HG3	1:A:531:TRP:CD1	2.27	0.70
1:A:645:LYS:NZ	8:A:968:HOH:O	2.24	0.69
1:A:315:ALA:HB3	1:A:329:VAL:HG22	1.74	0.69
1:A:457:ARG:NH1	5:A:812:SO4:O1	2.26	0.69
1:A:84:LEU:HD22	1:A:131:LEU:HD11	1.75	0.68
1:A:160:ASN:HB3	1:A:162:GLU:H	1.58	0.68
1:A:45:LYS:O	1:A:155:ARG:NH2	2.26	0.67
1:A:592:ARG:NH1	8:A:971:HOH:O	2.26	0.67
1:A:516:ARG:O	1:A:543:GLY:HA3	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:ARG:NH1	5:A:812:SO4:O2	2.22	0.65
1:A:320:PRO:HB2	1:A:321:PHE:HD1	1.61	0.65
1:A:116:ARG:NH2	8:A:905:HOH:O	2.25	0.64
1:A:185:TYR:HD1	1:A:210:GLN:HB3	1.61	0.63
1:A:516:ARG:HH21	7:A:838:EDO:C2	2.11	0.63
1:A:262:ARG:NH1	1:A:443:GLU:OE2	2.33	0.62
1:A:43:ARG:NH2	1:A:109:SER:O	2.32	0.62
1:A:463:PHE:HB2	4:A:808:C8E:H11	1.82	0.61
1:A:415:TRP:HD1	1:A:418:PHE:HD2	1.47	0.61
1:A:555:ARG:NH2	1:A:613:PRO:O	2.33	0.61
1:A:613:PRO:HB2	1:A:622:ARG:HD3	1.81	0.61
1:A:518:ASN:HD22	4:A:808:C8E:H201	1.65	0.61
1:A:686:TYR:HB3	1:A:697[B]:TRP:HB2	1.83	0.60
1:A:459:THR:HB	6:A:830:GOL:H2	1.83	0.60
1:A:233:ARG:HD3	4:A:804:C8E:H202	1.82	0.60
1:A:471:PHE:O	1:A:475:HIS:HB3	2.02	0.60
1:A:389:SER:N	1:A:390:GLU:HA	2.17	0.59
1:A:279:ASP:OD1	1:A:622:ARG:NH2	2.27	0.59
1:A:685:ASN:OD1	1:A:685:ASN:N	2.35	0.59
1:A:634:ARG:HB2	1:A:713:SER:HA	1.85	0.58
1:A:424:VAL:HG12	1:A:463:PHE:HD1	1.68	0.58
1:A:136:ASP:OD1	1:A:314:ARG:NH1	2.34	0.58
1:A:603:ARG:HH12	1:A:631:ASN:ND2	2.01	0.57
1:A:105:ASP:OD2	7:A:836:EDO:O1	2.22	0.57
1:A:232:ARG:NH1	1:A:234:ASP:OD2	2.37	0.57
1:A:690:THR:OG1	1:A:691:ARG:N	2.39	0.56
1:A:221:GLU:HB3	1:A:222:LYS:HA	1.87	0.56
1:A:330:HIS:HB3	1:A:358:ARG:HG3	1.87	0.56
1:A:139:ILE:HG23	1:A:217:SER:HB3	1.89	0.55
1:A:660:ARG:NH1	8:A:972:HOH:O	2.38	0.55
1:A:686:TYR:HB3	1:A:697[A]:TRP:HB2	1.88	0.55
1:A:98:PRO:HG3	1:A:715:PHE:CD1	2.41	0.55
1:A:48:ASN:ND2	8:A:907:HOH:O	2.37	0.55
1:A:547:TYR:OH	1:A:549:GLN:NE2	2.40	0.55
1:A:530:ARG:HG3	1:A:531:TRP:HD1	1.70	0.55
1:A:530:ARG:NH1	8:A:977:HOH:O	2.40	0.54
1:A:163:LYS:HD2	4:A:807:C8E:H112	1.89	0.54
1:A:659:TYR:HB2	1:A:679:MSE:HB3	1.89	0.54
1:A:160:ASN:HB3	1:A:162:GLU:N	2.22	0.54
1:A:418:PHE:CE1	4:A:806:C8E:H72	2.43	0.53
1:A:74:ARG:HB3	1:A:538:TYR:CZ	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:PHE:HE1	4:A:806:C8E:H31	1.73	0.53
1:A:509:ASN:HB3	1:A:512:LEU:HG	1.89	0.53
1:A:378:LEU:HB3	1:A:404:HIS:HB2	1.89	0.53
1:A:677:HIS:CE1	1:A:709:VAL:HG13	2.43	0.53
1:A:157:SER:HB2	1:A:162:GLU:HB3	1.89	0.53
1:A:469:TRP:CE3	4:A:806:C8E:H52	2.44	0.53
1:A:505:PHE:HB3	1:A:568:LEU:HD13	1.92	0.52
1:A:155:ARG:NH1	8:A:939:HOH:O	2.43	0.52
1:A:141:GLU:HG2	1:A:224:PHE:CE1	2.44	0.52
1:A:136:ASP:CG	1:A:314:ARG:HH22	2.14	0.51
1:A:367:GLY:H	1:A:369:LEU:HD23	1.75	0.51
1:A:703:ASN:ND2	1:A:723:GLY:O	2.44	0.51
1:A:446:TYR:HB3	1:A:447:ASN:OD1	2.11	0.50
1:A:549:GLN:HE22	1:A:627:GLN:HE22	1.59	0.50
1:A:55:GLY:HA2	1:A:639:ARG:HH12	1.75	0.50
1:A:74:ARG:HD2	1:A:538:TYR:CE1	2.46	0.50
1:A:43:ARG:HB3	7:A:834:EDO:H12	1.92	0.50
1:A:84:LEU:HD21	1:A:123:TYR:CD1	2.47	0.49
1:A:505:PHE:HB2	1:A:566:MSE:HE3	1.93	0.49
1:A:697[B]:TRP:CD1	1:A:730:VAL:HG13	2.48	0.49
1:A:67:GLY:HA3	1:A:236:TYR:CD2	2.48	0.48
1:A:39:GLY:O	1:A:43:ARG:HG2	2.13	0.48
1:A:436:ASP:OD2	1:A:439:LEU:HB3	2.14	0.48
1:A:55:GLY:HA2	1:A:639:ARG:NH1	2.29	0.48
1:A:60:HIS:ND1	5:A:827:SO4:O4	2.40	0.48
1:A:505:PHE:HB2	1:A:566:MSE:CE	2.43	0.48
1:A:426:VAL:HG22	1:A:461:ARG:HG2	1.95	0.48
1:A:21:ARG:NH2	5:A:820:SO4:O2	2.38	0.47
1:A:616:GLU:HB2	1:A:622:ARG:NH2	2.28	0.47
1:A:687:ARG:HD3	1:A:696:ASN:OD1	2.15	0.47
1:A:316:GLU:HA	1:A:327:LEU:O	2.14	0.47
1:A:99:ASP:HB3	1:A:100:HIS:CD2	2.49	0.47
1:A:603:ARG:NH2	5:A:810:SO4:S	2.87	0.47
1:A:498:LYS:HG3	1:A:566:MSE:HE1	1.96	0.46
1:A:549:GLN:NE2	1:A:627:GLN:HE22	2.14	0.46
1:A:698:TYR:OH	7:A:834:EDO:O2	2.32	0.46
1:A:477:LEU:HD12	1:A:524:LEU:HD13	1.97	0.46
1:A:539:ARG:HD2	1:A:541:ARG:CZ	2.45	0.46
1:A:148:VAL:HG12	1:A:171:ILE:HG12	1.98	0.45
1:A:60:HIS:CE1	1:A:639:ARG:HE	2.35	0.45
1:A:559:SER:OG	8:A:906:HOH:O	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:LYS:HB3	1:A:263:TYR:CZ	2.52	0.45
1:A:472:THR:O	1:A:475:HIS:HB2	2.16	0.45
1:A:473:PRO:HA	1:A:475:HIS:N	2.32	0.45
1:A:643:HIS:ND1	1:A:657:ASP:OD1	2.37	0.45
1:A:92:ASP:HB3	1:A:103:MSE:HG2	1.99	0.45
1:A:528:GLY:O	1:A:530:ARG:N	2.45	0.44
1:A:526:TYR:OH	8:A:977:HOH:O	2.20	0.44
1:A:470:TYR:CE2	1:A:476:LYS:HE2	2.52	0.44
1:A:243:HIS:HE1	1:A:298:HIS:O	1.94	0.44
1:A:649:THR:C	1:A:651:ARG:H	2.21	0.44
1:A:549:GLN:CD	1:A:612:LEU:HD11	2.37	0.44
1:A:466:SER:HB2	1:A:480:THR:HG23	1.99	0.44
1:A:461:ARG:NE	8:A:942:HOH:O	2.48	0.44
1:A:232:ARG:HD3	1:A:234:ASP:OD1	2.17	0.44
1:A:700:LYS:HB3	1:A:727:THR:HB	2.00	0.44
1:A:448:HIS:HA	1:A:449:PRO:HD3	1.88	0.43
1:A:424:VAL:HG12	1:A:463:PHE:CD1	2.52	0.43
1:A:197:ARG:C	1:A:199:LEU:H	2.21	0.43
1:A:396:MSE:HA	1:A:497:GLY:HA3	2.01	0.43
1:A:697[B]:TRP:HD1	1:A:730:VAL:HG13	1.83	0.43
1:A:473:PRO:HA	1:A:475:HIS:H	1.83	0.43
1:A:436:ASP:C	1:A:438:ALA:HB3	2.39	0.43
1:A:674:THR:HG22	1:A:675:PRO:O	2.18	0.43
4:A:806:C8E:H102	4:A:806:C8E:H71	1.75	0.43
1:A:92:ASP:HB2	8:A:958:HOH:O	2.19	0.43
1:A:516:ARG:HH21	7:A:838:EDO:H22	1.83	0.43
1:A:283:LEU:HD21	1:A:566:MSE:HE2	2.00	0.43
1:A:565:GLU:OE1	8:A:908:HOH:O	2.21	0.43
1:A:551:LEU:O	1:A:555:ARG:HD2	2.19	0.43
1:A:47:VAL:HG21	1:A:186:ARG:HD3	2.01	0.42
1:A:346:VAL:HG11	1:A:349:PHE:CE1	2.54	0.42
1:A:415:TRP:CD1	1:A:418:PHE:HD2	2.33	0.42
1:A:74:ARG:NH2	1:A:582:GLU:OE2	2.40	0.42
1:A:603:ARG:HH12	1:A:631:ASN:HD21	1.67	0.42
1:A:686:TYR:CE1	1:A:688:ARG:HB2	2.53	0.42
1:A:390:GLU:HG3	1:A:392:VAL:N	2.34	0.42
1:A:377:TYR:OH	1:A:379:GLN:NE2	2.51	0.42
1:A:530:ARG:CZ	8:A:977:HOH:O	2.67	0.42
1:A:190:ASP:O	1:A:201:ARG:HD3	2.20	0.42
1:A:437:LYS:HA	1:A:440:ILE:HG22	2.01	0.42
1:A:649:THR:O	1:A:651:ARG:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:808:C8E:H111	4:A:808:C8E:H142	1.84	0.42
1:A:430:LYS:HE2	5:A:812:SO4:O2	2.20	0.42
1:A:301:ARG:HA	1:A:302:PRO:HD3	1.82	0.42
1:A:28:HIS:CE1	1:A:30:SER:HB2	2.55	0.42
1:A:538:TYR:OH	8:A:918:HOH:O	2.21	0.42
1:A:40:ASP:N	1:A:40:ASP:OD1	2.53	0.42
1:A:437:LYS:O	1:A:440:ILE:HG22	2.19	0.41
4:A:808:C8E:H81	4:A:808:C8E:H52	1.62	0.41
1:A:143:MSE:HG2	1:A:219:VAL:HG21	2.02	0.41
1:A:606:LEU:HD23	1:A:632:ALA:HA	2.03	0.41
1:A:499:HIS:CE1	1:A:501:ALA:HB3	2.56	0.41
1:A:545:TYR:N	1:A:574:SER:O	2.52	0.41
1:A:60:HIS:CE1	1:A:639:ARG:HH21	2.39	0.41
1:A:506:GLU:OE2	1:A:571:TYR:OH	2.31	0.41
1:A:324:PHE:HA	1:A:363:HIS:HA	2.03	0.41
1:A:191:TYR:OH	7:A:835:EDO:O2	2.34	0.41
1:A:687:ARG:CZ	1:A:696:ASN:HD21	2.33	0.41
1:A:541:ARG:HD2	1:A:577:ASP:OD1	2.21	0.41
1:A:429:GLN:HB2	1:A:487:LEU:HD13	2.02	0.41
1:A:502:THR:O	1:A:504:THR:HG23	2.21	0.41
1:A:160:ASN:H	1:A:161:LEU:HA	1.87	0.40
1:A:231:ASP:OD2	8:A:945:HOH:O	2.21	0.40
1:A:162:GLU:OE2	1:A:186:ARG:HD2	2.21	0.40
1:A:197:ARG:HD3	1:A:197:ARG:HA	1.90	0.40
1:A:143:MSE:HA	1:A:144:PRO:HD3	1.98	0.40
1:A:655:ASN:HD21	1:A:700:LYS:NZ	2.20	0.40
1:A:518:ASN:HD22	4:A:808:C8E:C20	2.33	0.40
1:A:481:ALA:HA	1:A:519:ASN:O	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	703/748 (94%)	655 (93%)	47 (7%)	1 (0%)	56 77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	392	VAL

### 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	589/617 (96%)	552 (94%)	37 (6%)	22 39

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	40	ASP
1	A	43	ARG
1	A	74	ARG
1	A	84	LEU
1	A	143	MSE
1	A	169	ILE
1	A	177	PHE
1	A	184	LEU
1	A	186	ARG
1	A	218	TRP
1	A	230	SER
1	A	232	ARG
1	A	243	HIS
1	A	306	LEU
1	A	311	TYR
1	A	321	PHE
1	A	361	LEU
1	A	363	HIS
1	A	412	GLN

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Mol	Chain	Res	Type
1	A	414	ASN
1	A	437	LYS
1	A	439	LEU
1	A	442	ARG
1	A	444	ASN
1	A	511	HIS
1	A	522	LEU
1	A	541	ARG
1	A	572	ASN
1	A	582	GLU
1	A	600	ASP
1	A	605	ARG
1	A	648	LEU
1	A	669	ARG
1	A	685	ASN
1	A	686	TYR
1	A	717	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	HIS
1	A	210	GLN
1	A	241	HIS
1	A	243	HIS
1	A	308	ASN
1	A	334	ASN
1	A	379	GLN
1	A	400	ASN
1	A	404	HIS
1	A	412	GLN
1	A	429	GLN
1	A	456	HIS
1	A	483	HIS
1	A	518	ASN
1	A	549	GLN
1	A	631	ASN
1	A	655	ASN
1	A	677	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 38 ligands modelled in this entry, 3 are monoatomic - leaving 35 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	$\# Z  > 2$
4	C8E	A	804	-	20,20,20	0.93	0	19,19,19	0.87	0
4	C8E	A	805	-	20,20,20	0.78	0	19,19,19	0.91	0
4	C8E	A	806	-	20,20,20	0.84	0	19,19,19	0.82	0
4	C8E	A	807	-	20,20,20	0.66	0	19,19,19	0.80	0
4	C8E	A	808	-	20,20,20	0.76	0	19,19,19	0.86	0
5	SO4	A	809	-	4,4,4	0.82	0	6,6,6	0.12	0
5	SO4	A	810	-	4,4,4	0.74	0	6,6,6	0.16	0
5	SO4	A	811	-	4,4,4	0.57	0	6,6,6	0.15	0
5	SO4	A	812	-	4,4,4	0.63	0	6,6,6	0.11	0
5	SO4	A	813	-	4,4,4	0.61	0	6,6,6	0.21	0
5	SO4	A	814	-	4,4,4	0.65	0	6,6,6	0.21	0
5	SO4	A	815	-	4,4,4	0.53	0	6,6,6	0.31	0
5	SO4	A	816	-	4,4,4	0.47	0	6,6,6	0.13	0
5	SO4	A	817	-	4,4,4	0.54	0	6,6,6	0.32	0
5	SO4	A	818	-	4,4,4	0.60	0	6,6,6	0.16	0
5	SO4	A	819	-	4,4,4	0.57	0	6,6,6	0.26	0
5	SO4	A	820	-	4,4,4	0.47	0	6,6,6	0.30	0
5	SO4	A	821	-	4,4,4	0.45	0	6,6,6	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	A	822	-	4,4,4	0.42	0	6,6,6	0.15	0
5	SO4	A	823	-	4,4,4	0.48	0	6,6,6	0.21	0
5	SO4	A	824	-	4,4,4	0.48	0	6,6,6	0.17	0
5	SO4	A	825	-	4,4,4	0.40	0	6,6,6	0.20	0
5	SO4	A	826	-	4,4,4	0.47	0	6,6,6	0.14	0
5	SO4	A	827	-	4,4,4	0.52	0	6,6,6	0.12	0
5	SO4	A	828	-	4,4,4	0.41	0	6,6,6	0.11	0
5	SO4	A	829	-	4,4,4	0.56	0	6,6,6	0.12	0
6	GOL	A	830	-	5,5,5	0.43	0	5,5,5	0.29	0
6	GOL	A	831	-	5,5,5	0.57	0	5,5,5	0.37	0
6	GOL	A	832	-	5,5,5	0.13	0	5,5,5	0.27	0
6	GOL	A	833	-	5,5,5	0.47	0	5,5,5	0.24	0
7	EDO	A	834	-	3,3,3	0.36	0	2,2,2	0.43	0
7	EDO	A	835	-	3,3,3	0.32	0	2,2,2	0.61	0
7	EDO	A	836	-	3,3,3	0.31	0	2,2,2	0.57	0
7	EDO	A	837	-	3,3,3	0.37	0	2,2,2	0.34	0
7	EDO	A	838	-	3,3,3	0.36	0	2,2,2	0.35	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
4	C8E	A	804	-	-	0/18/18/18	0/0/0/0
4	C8E	A	805	-	-	0/18/18/18	0/0/0/0
4	C8E	A	806	-	-	0/18/18/18	0/0/0/0
4	C8E	A	807	-	-	0/18/18/18	0/0/0/0
4	C8E	A	808	-	-	0/18/18/18	0/0/0/0
5	SO4	A	809	-	-	0/0/0/0	0/0/0/0
5	SO4	A	810	-	-	0/0/0/0	0/0/0/0
5	SO4	A	811	-	-	0/0/0/0	0/0/0/0
5	SO4	A	812	-	-	0/0/0/0	0/0/0/0
5	SO4	A	813	-	-	0/0/0/0	0/0/0/0
5	SO4	A	814	-	-	0/0/0/0	0/0/0/0
5	SO4	A	815	-	-	0/0/0/0	0/0/0/0
5	SO4	A	816	-	-	0/0/0/0	0/0/0/0
5	SO4	A	817	-	-	0/0/0/0	0/0/0/0
5	SO4	A	818	-	-	0/0/0/0	0/0/0/0
5	SO4	A	819	-	-	0/0/0/0	0/0/0/0
5	SO4	A	820	-	-	0/0/0/0	0/0/0/0
5	SO4	A	821	-	-	0/0/0/0	0/0/0/0
5	SO4	A	822	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SO4	A	823	-	-	0/0/0/0	0/0/0/0
5	SO4	A	824	-	-	0/0/0/0	0/0/0/0
5	SO4	A	825	-	-	0/0/0/0	0/0/0/0
5	SO4	A	826	-	-	0/0/0/0	0/0/0/0
5	SO4	A	827	-	-	0/0/0/0	0/0/0/0
5	SO4	A	828	-	-	0/0/0/0	0/0/0/0
5	SO4	A	829	-	-	0/0/0/0	0/0/0/0
6	GOL	A	830	-	-	0/4/4/4	0/0/0/0
6	GOL	A	831	-	-	0/4/4/4	0/0/0/0
6	GOL	A	832	-	-	0/4/4/4	0/0/0/0
6	GOL	A	833	-	-	0/4/4/4	0/0/0/0
7	EDO	A	834	-	-	0/1/1/1	0/0/0/0
7	EDO	A	835	-	-	0/1/1/1	0/0/0/0
7	EDO	A	836	-	-	0/1/1/1	0/0/0/0
7	EDO	A	837	-	-	0/1/1/1	0/0/0/0
7	EDO	A	838	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	804	C8E	1	0
4	A	806	C8E	4	0
4	A	807	C8E	1	0
4	A	808	C8E	5	0
5	A	810	SO4	2	0
5	A	812	SO4	4	0
5	A	814	SO4	1	0
5	A	820	SO4	2	0
5	A	827	SO4	1	0
6	A	830	GOL	1	0
7	A	834	EDO	2	0
7	A	835	EDO	1	0
7	A	836	EDO	1	0
7	A	838	EDO	6	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	699/748 (93%)	0.35	42 (6%) 25 28	55, 84, 136, 189	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	392	VAL	6.7
1	A	389	SER	5.3
1	A	18	SER	5.2
1	A	447	ASN	4.9
1	A	19	ARG	4.9
1	A	391	ALA	4.7
1	A	200	LYS	4.5
1	A	366	ILE	4.4
1	A	390	GLU	4.3
1	A	317	TRP	3.4
1	A	619	TYR	3.3
1	A	692	TYR	3.3
1	A	369	LEU	3.2
1	A	299	SER	3.2
1	A	449	PRO	3.1
1	A	371	GLY	3.1
1	A	196	TYR	2.9
1	A	256	LYS	2.8
1	A	527	GLU	2.8
1	A	259	ILE	2.8
1	A	415	TRP	2.7
1	A	247	ASP	2.5
1	A	472	THR	2.5
1	A	474	GLN	2.4
1	A	266	LEU	2.4
1	A	83	VAL	2.4
1	A	531	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	529	ASP	2.3
1	A	440	ILE	2.3
1	A	298	HIS	2.2
1	A	448	HIS	2.2
1	A	697[A]	TRP	2.2
1	A	198	ASN	2.1
1	A	649	THR	2.1
1	A	59	ILE	2.1
1	A	359	ILE	2.1
1	A	650	ASP	2.1
1	A	250	ALA	2.1
1	A	81	ILE	2.1
1	A	393	LYS	2.1
1	A	373	TRP	2.0
1	A	686	TYR	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
7	EDO	A	836	4/4	0.72	0.86	17.93	127,128,132,132	0
5	SO4	A	828	5/5	0.17	0.78	14.09	148,151,153,156	5
5	SO4	A	819	5/5	0.71	0.59	11.22	75,82,87,89	5
7	EDO	A	835	4/4	0.78	0.35	11.17	101,109,114,118	0
5	SO4	A	827	5/5	0.71	0.56	8.42	145,146,148,150	5
5	SO4	A	829	5/5	0.86	0.63	7.29	137,137,139,140	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	C8E	A	805	21/21	0.70	0.38	6.12	90,103,114,119	0
5	SO4	A	820	5/5	0.84	0.40	6.11	132,132,133,134	5
5	SO4	A	814	5/5	0.73	0.34	5.86	74,85,101,104	5
5	SO4	A	815	5/5	0.84	0.27	5.19	95,102,108,116	5
4	C8E	A	806	21/21	0.77	0.38	5.11	73,98,116,122	0
5	SO4	A	816	5/5	0.80	0.35	4.74	117,118,118,118	5
7	EDO	A	834	4/4	0.87	0.25	2.31	101,106,107,115	0
5	SO4	A	823	5/5	0.80	0.31	2.14	158,160,160,161	5
4	C8E	A	807	21/21	0.53	0.34	2.03	127,140,146,147	0
7	EDO	A	837	4/4	0.85	0.27	1.63	103,105,109,112	0
4	C8E	A	808	21/21	0.80	0.27	1.53	97,111,141,143	0
5	SO4	A	824	5/5	0.77	0.28	1.41	133,134,136,136	5
5	SO4	A	818	5/5	0.79	0.30	1.08	98,116,119,125	5
4	C8E	A	804	21/21	0.89	0.23	0.63	68,92,109,119	0
3	ZN	A	803	1/1	0.99	0.18	-0.03	58,58,58,58	0
5	SO4	A	809	5/5	0.97	0.10	-1.94	79,85,91,92	5
5	SO4	A	822	5/5	0.62	0.28	-	141,143,148,149	5
2	CD	A	802	1/1	0.93	0.07	-	113,113,113,113	0
6	GOL	A	833	6/6	0.43	0.34	-	107,117,122,128	0
6	GOL	A	830	6/6	0.43	0.27	-	117,124,127,130	0
5	SO4	A	810	5/5	0.91	0.11	-	78,79,84,97	5
7	EDO	A	838	4/4	0.63	0.40	-	109,109,111,113	0
6	GOL	A	831	6/6	0.77	0.23	-	106,112,119,122	0
2	CD	A	801	1/1	0.97	0.14	-	92,92,92,92	0
5	SO4	A	817	5/5	0.85	0.16	-	115,118,123,127	5
5	SO4	A	825	5/5	0.68	0.32	-	137,139,141,145	5
5	SO4	A	821	5/5	0.69	0.38	-	148,152,153,158	5
5	SO4	A	826	5/5	0.81	0.26	-	129,130,134,138	5
5	SO4	A	811	5/5	0.90	0.13	-	92,96,99,99	5
5	SO4	A	813	5/5	0.84	0.23	-	82,97,107,109	5
5	SO4	A	812	5/5	0.90	0.10	-	99,100,102,103	5
6	GOL	A	832	6/6	0.34	0.32	-	99,111,119,123	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.