



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:07 AM UTC

PDB ID : 3ON5 / pdb_00003on5
Title : Crystal structure of a xanthine dehydrogenase (BH1974) from *Bacillus halodurans* at 2.80 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2010-08-27
Resolution : 2.80 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

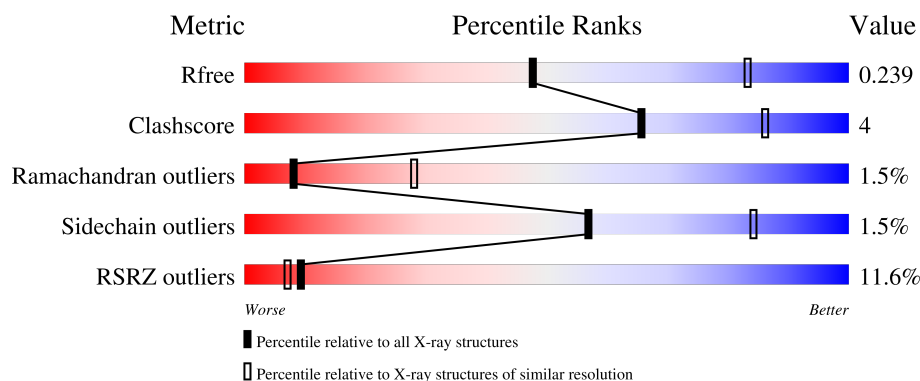
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of 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 $\leq 5\%$. 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	362	6% 77% 16% 7%
1	B	362	15% 79% 9% 11%

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
2	CL	A	345	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5218 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 BH1974 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	Se	0	5	0
			2651	1714	443	485	4	5			
1	B	323	Total	C	N	O	S	Se	0	1	0
			2514	1637	414	454	3	6			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MSE	-	expression tag	UNP Q9KBF4
A	-17	GLY	-	expression tag	UNP Q9KBF4
A	-16	SER	-	expression tag	UNP Q9KBF4
A	-15	ASP	-	expression tag	UNP Q9KBF4
A	-14	LYS	-	expression tag	UNP Q9KBF4
A	-13	ILE	-	expression tag	UNP Q9KBF4
A	-12	HIS	-	expression tag	UNP Q9KBF4
A	-11	HIS	-	expression tag	UNP Q9KBF4
A	-10	HIS	-	expression tag	UNP Q9KBF4
A	-9	HIS	-	expression tag	UNP Q9KBF4
A	-8	HIS	-	expression tag	UNP Q9KBF4
A	-7	HIS	-	expression tag	UNP Q9KBF4
A	-6	GLU	-	expression tag	UNP Q9KBF4
A	-5	ASN	-	expression tag	UNP Q9KBF4
A	-4	LEU	-	expression tag	UNP Q9KBF4
A	-3	TYR	-	expression tag	UNP Q9KBF4
A	-2	PHE	-	expression tag	UNP Q9KBF4
A	-1	GLN	-	expression tag	UNP Q9KBF4
A	0	GLY	-	expression tag	UNP Q9KBF4
B	-18	MSE	-	expression tag	UNP Q9KBF4
B	-17	GLY	-	expression tag	UNP Q9KBF4
B	-16	SER	-	expression tag	UNP Q9KBF4
B	-15	ASP	-	expression tag	UNP Q9KBF4
B	-14	LYS	-	expression tag	UNP Q9KBF4
B	-13	ILE	-	expression tag	UNP Q9KBF4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP Q9KBF4
B	-11	HIS	-	expression tag	UNP Q9KBF4
B	-10	HIS	-	expression tag	UNP Q9KBF4
B	-9	HIS	-	expression tag	UNP Q9KBF4
B	-8	HIS	-	expression tag	UNP Q9KBF4
B	-7	HIS	-	expression tag	UNP Q9KBF4
B	-6	GLU	-	expression tag	UNP Q9KBF4
B	-5	ASN	-	expression tag	UNP Q9KBF4
B	-4	LEU	-	expression tag	UNP Q9KBF4
B	-3	TYR	-	expression tag	UNP Q9KBF4
B	-2	PHE	-	expression tag	UNP Q9KBF4
B	-1	GLN	-	expression tag	UNP Q9KBF4
B	0	GLY	-	expression tag	UNP Q9KBF4

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	1	Total Cl 1 1	0	0

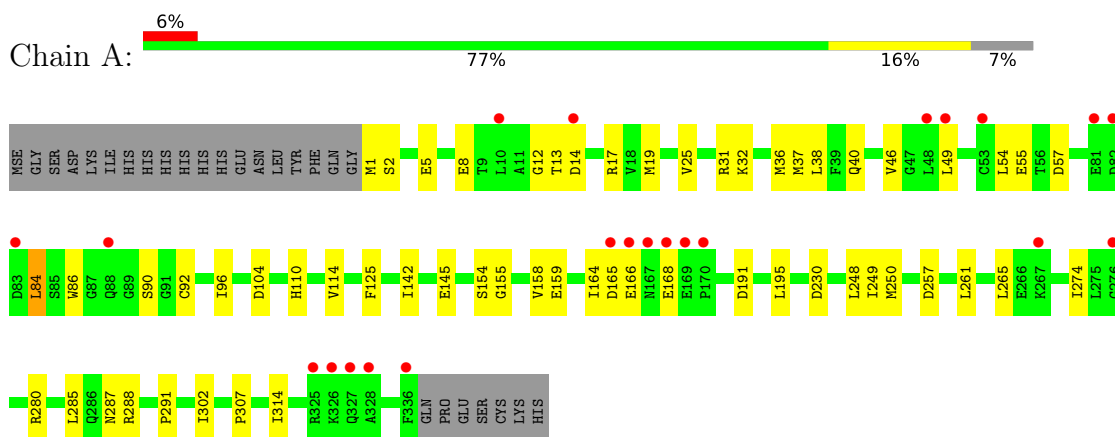
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	29	Total O 29 29	0	0
3	B	22	Total O 22 22	0	0

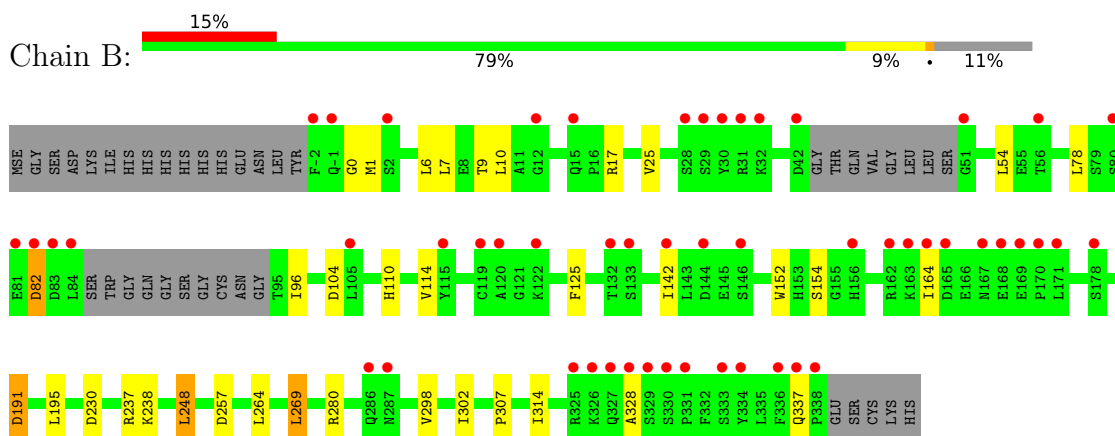
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: BH1974 protein



• Molecule 1: BH1974 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	94.24Å 94.24Å 245.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.24 – 2.80 87.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (94.24-2.80) 99.8 (87.98-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.82Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.8.0, BUSTER 2.8.0	Depositor
R, R_{free}	0.195 , 0.222 0.212 , 0.239	Depositor DCC
R_{free} test set	1418 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	63.1	Xtriage
Anisotropy	0.223	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 80.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5218	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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:
CL

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	0.87	0/2725	1.29	11/3701 (0.3%)
1	B	0.85	1/2575 (0.0%)	1.26	10/3500 (0.3%)
All	All	0.86	1/5300 (0.0%)	1.28	21/7201 (0.3%)

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	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	298	VAL	CA-C	5.16	1.58	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	ASP	CA-CB-CG	7.32	119.92	112.60
1	A	104	ASP	CA-CB-CG	6.66	119.25	112.60
1	B	104	ASP	CA-CB-CG	6.26	118.86	112.60
1	B	328	ALA	CA-C-N	6.04	131.16	122.40
1	B	328	ALA	C-N-CA	6.04	131.16	122.40
1	A	164	ILE	CA-C-N	5.82	128.88	120.79
1	A	164	ILE	C-N-CA	5.82	128.88	120.79
1	B	82	ASP	CA-C-N	5.62	130.56	122.35
1	B	82	ASP	C-N-CA	5.62	130.56	122.35
1	A	1	MSE	CA-C-N	5.61	129.22	120.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	MSE	C-N-CA	5.61	129.22	120.75
1	A	302	ILE	N-CA-C	-5.59	107.29	112.43
1	B	164	ILE	N-CA-CB	5.51	117.81	110.26
1	B	302	ILE	N-CA-C	-5.34	107.52	112.43
1	A	86	TRP	N-CA-C	-5.30	106.66	113.23
1	B	191	ASP	CA-CB-CG	5.29	117.89	112.60
1	A	8	GLU	CA-C-N	5.20	127.77	120.28
1	A	8	GLU	C-N-CA	5.20	127.77	120.28
1	A	55	GLU	CB-CG-CD	5.06	121.21	112.60
1	B	269	LEU	CA-C-N	5.04	127.03	120.28
1	B	269	LEU	C-N-CA	5.04	127.03	120.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	337	GLN	Peptide,Mainchain

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	2651	0	2564	25	0
1	B	2514	0	2382	14	0
2	A	1	0	0	2	0
2	B	1	0	0	0	0
3	A	29	0	0	0	0
3	B	22	0	0	0	0
All	All	5218	0	4946	38	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 4.

All (38) 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:195:LEU:HD21	1:A:248:LEU:HD23	1.58	0.85
1:A:287:ASN:HA	2:A:345:CL:CL	2.13	0.84
1:A:19:MSE:HE2	1:A:36:MSE:SE	2.39	0.73
1:A:57:ASP:HB2	1:A:84:LEU:HD21	1.71	0.70
1:B:257:ASP:OD2	1:B:280:ARG:NH2	2.27	0.65
1:A:195:LEU:HD21	1:A:248:LEU:CD2	2.27	0.64
1:B:248:LEU:HD21	1:B:314:ILE:HG21	1.79	0.63
1:A:19:MSE:CE	1:A:36:MSE:SE	3.02	0.57
1:A:257:ASP:OD2	1:A:280:ARG:NH2	2.37	0.57
1:A:285:LEU:O	1:A:288:ARG:HB2	2.06	0.56
1:A:191:ASP:HA	1:A:307:PRO:HB3	1.89	0.53
1:A:248:LEU:HD21	1:A:314:ILE:HG21	1.92	0.52
1:A:248:LEU:HG	1:A:250:MSE:HE3	1.92	0.52
1:A:145:GLU:HA	1:A:158:VAL:HG21	1.90	0.52
1:B:264:LEU:HD22	1:B:269:LEU:HD11	1.94	0.49
1:B:152:TRP:NE1	1:B:154:SER:O	2.45	0.49
1:A:287:ASN:CA	2:A:345:CL:CL	2.94	0.49
1:B:191:ASP:HA	1:B:307:PRO:HB3	1.94	0.49
1:A:110:HIS:O	1:A:114:VAL:HG23	2.13	0.48
1:B:9:THR:HG22	1:B:17:ARG:NH1	2.28	0.48
1:B:1:MSE:SE	1:B:6:LEU:HD12	2.64	0.47
1:B:110:HIS:O	1:B:114:VAL:HG23	2.15	0.46
1:A:265:LEU:HD23	1:A:291:PRO:HG3	1.98	0.45
1:A:25:VAL:HG22	1:A:96:ILE:HG22	1.98	0.45
1:A:38:LEU:HB2	1:A:46:VAL:HB	1.99	0.45
1:A:90:SER:O	1:B:280:ARG:NH1	2.50	0.44
1:B:7:LEU:HA	1:B:10:LEU:HD12	1.99	0.44
1:A:249:ILE:HD12	1:A:274:ILE:HG12	1.99	0.43
1:B:25:VAL:HG22	1:B:96:ILE:HG22	2.01	0.43
1:B:195:LEU:HD21	1:B:248:LEU:HD23	2.01	0.43
1:A:31[B]:ARG:NH1	1:A:32:LYS:H	2.17	0.43
1:A:37:MSE:SE	1:A:49:LEU:HG	2.70	0.42
1:A:2:SER:HB3	1:A:5:GLU:HG2	2.01	0.42
1:A:261:LEU:HD13	1:A:274:ILE:HD11	2.01	0.42
1:B:237:ARG:NH2	1:B:238:LYS:HD2	2.35	0.42
1:B:125:PHE:HB3	1:B:142:ILE:HB	2.03	0.41
1:A:125:PHE:HB3	1:A:142:ILE:HB	2.01	0.41
1:A:17:ARG:HG2	1:A:40:GLN:HG2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	339/362 (94%)	313 (92%)	17 (5%)	9 (3%)	4	15
1	B	318/362 (88%)	295 (93%)	21 (7%)	2 (1%)	21	51
All	All	657/724 (91%)	608 (92%)	38 (6%)	11 (2%)	8	25

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	THR
1	A	14[A]	ASP
1	A	14[B]	ASP
1	A	155	GLY
1	A	166	GLU
1	A	84	LEU
1	A	154	SER
1	A	168	GLU
1	A	12	GLY
1	B	0	GLY
1	B	82	ASP

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	279/316 (88%)	275 (99%)	4 (1%)	59	85
1	B	254/316 (80%)	250 (98%)	4 (2%)	55	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	533/632 (84%)	525 (98%)	8 (2%)	57 84

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	LEU
1	A	92	CYS
1	A	159	GLU
1	A	230	ASP
1	B	54	LEU
1	B	78	LEU
1	B	230	ASP
1	B	248	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	HIS
1	A	69	GLN
1	A	287	ASN
1	B	69	GLN
1	B	153	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	330/362 (91%)	0.35	22 (6%) 24 17	32, 63, 105, 135	5 (1%)
1	B	317/362 (87%)	0.70	53 (16%) 4 3	36, 78, 135, 155	1 (0%)
All	All	647/724 (89%)	0.52	75 (11%) 9 7	32, 68, 123, 155	6 (0%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	81	GLU	7.3
1	B	84	LEU	6.1
1	B	82	ASP	6.1
1	B	330	SER	5.9
1	B	28	SER	5.9
1	B	338	PRO	5.1
1	A	169	GLU	5.0
1	B	328	ALA	4.2
1	B	2	SER	4.0
1	A	326	LYS	4.0
1	A	167	ASN	4.0
1	B	327	GLN	4.0
1	A	168	GLU	3.8
1	B	329	SER	3.7
1	A	14[A]	ASP	3.7
1	B	80	SER	3.6
1	A	328	ALA	3.6
1	A	49	LEU	3.6
1	B	163	LYS	3.6
1	B	30	TYR	3.6
1	B	132	THR	3.5
1	B	146	SER	3.5
1	B	164	ILE	3.2
1	B	337	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	-1	GLN	3.1
1	B	119	CYS	3.1
1	A	82	ASP	3.0
1	B	51	GLY	3.0
1	A	165	ASP	2.9
1	A	327	GLN	2.9
1	A	166	GLU	2.9
1	B	115	TYR	2.8
1	B	29	SER	2.8
1	B	331	PRO	2.8
1	B	120	ALA	2.7
1	B	168	GLU	2.7
1	B	326	LYS	2.7
1	B	325	ARG	2.7
1	A	170	PRO	2.7
1	B	287	ASN	2.7
1	A	267[A]	LYS	2.6
1	B	336	PHE	2.6
1	A	83	ASP	2.6
1	B	32	LYS	2.6
1	B	171	LEU	2.5
1	A	88	GLN	2.5
1	B	162	ARG	2.4
1	B	165	ASP	2.4
1	A	53	CYS	2.3
1	B	105	LEU	2.3
1	B	42	ASP	2.3
1	B	56	THR	2.3
1	B	334	TYR	2.3
1	B	167	ASN	2.3
1	B	83	ASP	2.3
1	B	122	LYS	2.3
1	A	325	ARG	2.3
1	B	142	ILE	2.2
1	A	10	LEU	2.2
1	B	286	GLN	2.2
1	B	170	PRO	2.2
1	B	169	GLU	2.2
1	B	156	HIS	2.2
1	B	144	ASP	2.2
1	A	336	PHE	2.2
1	B	-2	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	48	LEU	2.2
1	B	81	GLU	2.2
1	B	133	SER	2.1
1	B	178[A]	SER	2.1
1	B	31	ARG	2.1
1	A	276	GLY	2.1
1	B	15	GLN	2.0
1	B	333	SER	2.0
1	B	12	GLY	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CL	A	345	1/1	0.86	0.13	121,121,121,121	0
2	CL	B	344	1/1	0.96	0.08	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.