



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 02:38 AM UTC

PDB ID : 9PRB / pdb_00009prb
Title : Crystal structure of the N-terminal domain of the A subunit of the *Bacillus cereus* GerI germinant receptor
Authors : Li, Y.; Hao, B.
Deposited on : 2025-07-23
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

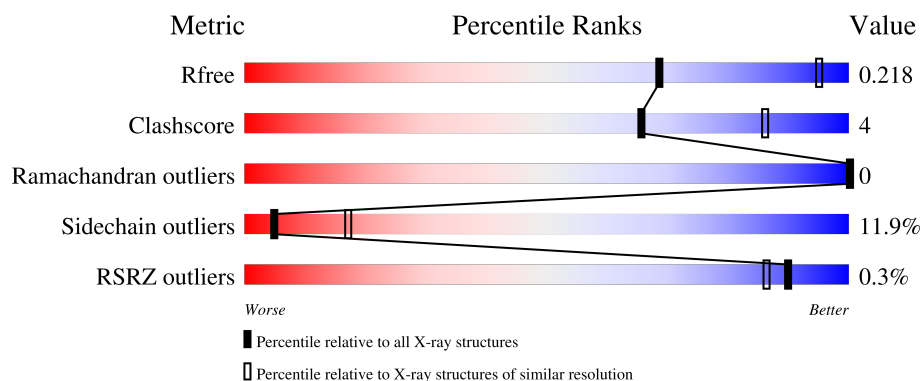
1 Overall quality at a glance

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	260	 71% 17% • 8%
1	B	260	 75% 15% • 8%
1	C	260	 76% 14% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5964 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 Spore germination protein GerIA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	238	Total	C	N	O	S	Se	0	0	0
			1930	1232	311	377	1	9			
1	B	239	Total	C	N	O	S	Se	0	0	0
			1930	1233	309	378	1	9			
1	C	240	Total	C	N	O	S	Se	0	0	0
			1938	1237	311	380	1	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	GLY	-	expression tag	UNP O85467
A	242	GLY	-	expression tag	UNP O85467
A	243	GLY	-	expression tag	UNP O85467
A	244	ARG	-	expression tag	UNP O85467
B	241	GLY	-	expression tag	UNP O85467
B	242	GLY	-	expression tag	UNP O85467
B	243	GLY	-	expression tag	UNP O85467
B	244	ARG	-	expression tag	UNP O85467
C	241	GLY	-	expression tag	UNP O85467
C	242	GLY	-	expression tag	UNP O85467
C	243	GLY	-	expression tag	UNP O85467
C	244	ARG	-	expression tag	UNP O85467

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

- Molecule 3 is water.

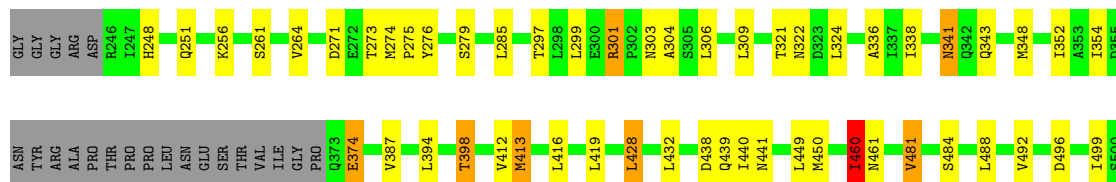
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	60	Total	O	0	0
			60	60		
3	B	71	Total	O	0	0
			71	71		
3	C	31	Total	O	0	0
			31	31		

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.

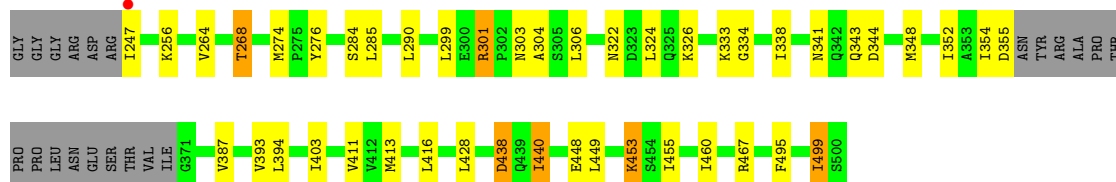
- Molecule 1: Spore germination protein GerIA

Chain A: 




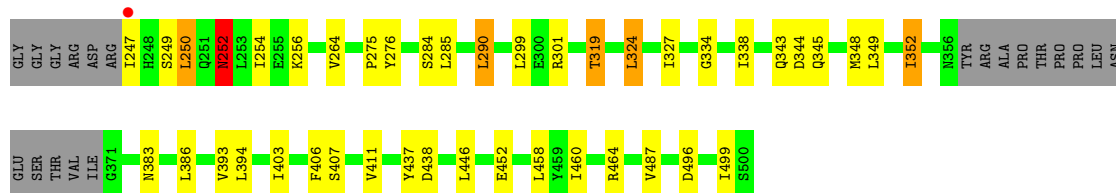
- Molecule 1: Spore germination protein GerIA

Chain B: 



- Molecule 1: Spore germination protein GerIA

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	82.15Å 122.85Å 212.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.30 – 2.80 38.30 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (38.30-2.80) 94.5 (38.30-2.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.199 , 0.229 0.187 , 0.218	Depositor DCC
R_{free} test set	2000 reflections (7.43%)	wwPDB-VP
Wilson B-factor (Å ²)	61.6	Xtriage
Anisotropy	0.802	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 60.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5964	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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: ACT

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	0.88	2/1953 (0.1%)	1.33	11/2623 (0.4%)
1	B	0.82	0/1954	1.26	6/2626 (0.2%)
1	C	0.84	0/1962	1.30	8/2637 (0.3%)
All	All	0.84	2/5869 (0.0%)	1.30	25/7886 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	413	MSE	SE-CE	-9.63	1.66	1.95
1	A	450	MSE	SE-CE	5.62	2.12	1.95

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	441	ASN	CA-C-N	6.94	129.47	120.44
1	A	441	ASN	C-N-CA	6.94	129.47	120.44
1	C	437	TYR	CA-C-N	6.65	129.09	120.44
1	C	437	TYR	C-N-CA	6.65	129.09	120.44
1	C	438	ASP	CA-CB-CG	5.96	118.56	112.60
1	C	499	ILE	CA-C-N	5.85	132.23	121.70
1	C	499	ILE	C-N-CA	5.85	132.23	121.70
1	A	499	ILE	CA-C-N	5.82	132.18	121.70
1	A	499	ILE	C-N-CA	5.82	132.18	121.70
1	A	374	GLU	CA-C-N	5.76	128.41	121.38
1	A	374	GLU	C-N-CA	5.76	128.41	121.38
1	B	499	ILE	CA-C-N	5.62	131.81	121.70
1	B	499	ILE	C-N-CA	5.62	131.81	121.70
1	C	496	ASP	CA-CB-CG	5.57	118.17	112.60
1	A	496	ASP	CA-CB-CG	5.47	118.07	112.60
1	A	439	GLN	CA-C-N	5.27	130.38	122.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	439	GLN	C-N-CA	5.27	130.38	122.58
1	B	416	LEU	CA-C-N	5.23	127.54	120.38
1	B	416	LEU	C-N-CA	5.23	127.54	120.38
1	A	460	ILE	N-CA-CB	5.20	120.44	111.39
1	C	252	ASN	CA-C-N	5.16	127.46	120.44
1	C	252	ASN	C-N-CA	5.16	127.46	120.44
1	A	341	ASN	CA-CB-CG	5.07	117.67	112.60
1	B	453	LYS	CA-C-N	5.07	127.96	120.82
1	B	453	LYS	C-N-CA	5.07	127.96	120.82

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	1930	0	1937	18	0
1	B	1930	0	1934	12	0
1	C	1938	0	1940	15	0
2	C	4	0	3	0	0
3	A	60	0	0	0	0
3	B	71	0	0	0	0
3	C	31	0	0	0	0
All	All	5964	0	5814	44	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 (44) 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:413:MSE:HE2	1:A:432:LEU:HD12	1.52	0.92
1:A:413:MSE:CE	1:A:432:LEU:HD12	2.09	0.81
1:C:338:ILE:HD13	1:C:348:MSE:HE2	1.72	0.72
1:A:271:ASP:OD2	1:A:274:MSE:HG2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:ILE:HG23	1:A:492:VAL:HG21	1.82	0.61
1:C:250:LEU:HD22	1:C:324:LEU:HD23	1.81	0.61
1:C:284:SER:HB3	1:C:334:GLY:HA2	1.84	0.60
1:A:261:SER:OG	1:A:398:THR:HG22	2.02	0.60
1:C:319:THR:HG23	1:C:349:LEU:HB2	1.86	0.57
1:A:413:MSE:HE1	1:A:428:LEU:C	2.30	0.57
1:C:338:ILE:HB	1:C:348:MSE:HG3	1.86	0.56
1:A:306:LEU:HD22	1:A:348:MSE:HB2	1.90	0.54
1:A:275:PRO:HB2	1:A:276:TYR:CD2	2.45	0.52
1:A:285:LEU:HD21	1:A:336:ALA:HB2	1.93	0.51
1:B:301:ARG:HB2	1:B:304:ALA:HB2	1.92	0.51
1:B:284:SER:HB3	1:B:334:GLY:HA2	1.93	0.50
1:C:383:ASN:HA	1:C:386:LEU:HD12	1.93	0.50
1:A:413:MSE:HE1	1:A:428:LEU:HB3	1.94	0.50
1:B:499:ILE:HD11	1:C:403:ILE:HG22	1.93	0.49
1:B:341:ASN:ND2	1:B:343:GLN:HG2	2.29	0.47
1:A:338:ILE:HD13	1:A:348:MSE:HE2	1.97	0.47
1:C:406:PHE:HE2	1:C:446:LEU:HD11	1.79	0.47
1:B:438:ASP:HB3	1:B:440:ILE:HD12	1.97	0.46
1:A:398:THR:HG23	1:A:412:VAL:HG13	1.97	0.45
1:B:306:LEU:HD22	1:B:348:MSE:HB2	1.99	0.45
1:C:250:LEU:HD21	1:C:327:ILE:CD1	2.47	0.45
1:B:274:MSE:HE1	1:B:303:ASN:HB2	1.99	0.45
1:C:249:SER:HB3	1:C:252:ASN:HB2	1.99	0.44
1:A:274:MSE:HE1	1:A:303:ASN:HB2	1.99	0.44
1:B:268:THR:HB	1:B:276:TYR:H	1.84	0.43
1:B:341:ASN:HD22	1:B:343:GLN:HG2	1.83	0.43
1:C:275:PRO:HB2	1:C:276:TYR:CD2	2.54	0.43
1:C:403:ILE:HD12	1:C:411:VAL:HG21	2.00	0.43
1:B:338:ILE:HB	1:B:348:MSE:HB3	2.00	0.42
1:A:481:VAL:HG22	1:A:484:SER:HB3	2.01	0.42
1:C:250:LEU:O	1:C:254:ILE:HG12	2.20	0.42
1:B:495:PHE:HA	1:B:499:ILE:HD12	2.01	0.42
1:A:416:LEU:HD13	1:A:419:LEU:HD22	2.02	0.41
1:C:290:LEU:HD12	1:C:352:ILE:HD13	2.03	0.41
1:C:458:LEU:HD12	1:C:458:LEU:HA	1.86	0.41
1:A:276:TYR:CE2	1:A:309:LEU:HD11	2.56	0.41
1:A:301:ARG:HB2	1:A:304:ALA:HB2	2.02	0.41
1:B:403:ILE:HD12	1:B:411:VAL:HG21	2.02	0.41
1:A:413:MSE:CE	1:A:428:LEU:HB3	2.50	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	234/260 (90%)	228 (97%)	6 (3%)	0	100	100
1	B	235/260 (90%)	226 (96%)	9 (4%)	0	100	100
1	C	236/260 (91%)	223 (94%)	13 (6%)	0	100	100
All	All	705/780 (90%)	677 (96%)	28 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	221/229 (96%)	193 (87%)	28 (13%)	4	15
1	B	221/229 (96%)	192 (87%)	29 (13%)	4	14
1	C	222/229 (97%)	200 (90%)	22 (10%)	7	24
All	All	664/687 (97%)	585 (88%)	79 (12%)	5	17

All (79) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	248	HIS
1	A	251	GLN
1	A	256	LYS
1	A	264	VAL
1	A	273	THR

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Mol	Chain	Res	Type
1	A	279	SER
1	A	297	THR
1	A	299	LEU
1	A	301	ARG
1	A	321	THR
1	A	322	ASN
1	A	324	LEU
1	A	341	ASN
1	A	343	GLN
1	A	352	ILE
1	A	354	ILE
1	A	374	GLU
1	A	387	VAL
1	A	394	LEU
1	A	398	THR
1	A	428	LEU
1	A	438	ASP
1	A	440	ILE
1	A	449	LEU
1	A	460	ILE
1	A	461	ASN
1	A	481	VAL
1	A	488	LEU
1	B	247	ILE
1	B	256	LYS
1	B	264	VAL
1	B	268	THR
1	B	285	LEU
1	B	290	LEU
1	B	299	LEU
1	B	301	ARG
1	B	322	ASN
1	B	324	LEU
1	B	326	LYS
1	B	333	LYS
1	B	344	ASP
1	B	352	ILE
1	B	354	ILE
1	B	355	ASP
1	B	387	VAL
1	B	393	VAL
1	B	394	LEU

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Mol	Chain	Res	Type
1	B	413	MSE
1	B	428	LEU
1	B	438	ASP
1	B	440	ILE
1	B	448	GLU
1	B	449	LEU
1	B	453	LYS
1	B	455	ILE
1	B	460	ILE
1	B	467	ARG
1	C	247	ILE
1	C	250	LEU
1	C	252	ASN
1	C	256	LYS
1	C	264	VAL
1	C	285	LEU
1	C	290	LEU
1	C	299	LEU
1	C	301	ARG
1	C	319	THR
1	C	324	LEU
1	C	343	GLN
1	C	344	ASP
1	C	345	GLN
1	C	352	ILE
1	C	393	VAL
1	C	394	LEU
1	C	407	SER
1	C	452	GLU
1	C	460	ILE
1	C	464	ARG
1	C	487	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	252	ASN
1	A	335	HIS
1	A	373	GLN
1	B	251	GLN
1	B	252	ASN
1	B	335	HIS

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Mol	Chain	Res	Type
1	B	341	ASN
1	B	343	GLN
1	B	424	ASN
1	B	447	GLN
1	B	461	ASN
1	C	248	HIS
1	C	251	GLN
1	C	252	ASN
1	C	339	GLN

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACT	C	601	-	3,3,3	1.04	0	3,3,3	0.83	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.

No monomer is involved in short contacts.

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 [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	229/260 (88%)	-0.42	0	100 100	53, 76, 108, 143	0
1	B	230/260 (88%)	-0.38	1 (0%)	88 84	50, 78, 115, 133	0
1	C	231/260 (88%)	-0.10	1 (0%)	88 84	56, 94, 163, 182	0
All	All	690/780 (88%)	-0.30	2 (0%)	90 86	50, 81, 146, 182	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	247	ILE	2.3
1	C	247	ILE	2.3

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	ACT	C	601	4/4	0.83	0.21	105,105,106,108	0

6.5 Other polymers [i](#)

There are no such residues in this entry.