



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:21 PM UTC

PDB ID : 5APP / pdb_00005app
Title : Actinobacillus actinomycetemcomitans OMP100 residues 133-198 fused to GCN4 adaptors
Authors : Hartmann, M.D.; Ridderbusch, O.; Lupas, A.N.; Hernandez Alvarez, B.
Deposited on : 2015-09-17
Resolution : 2.30 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
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

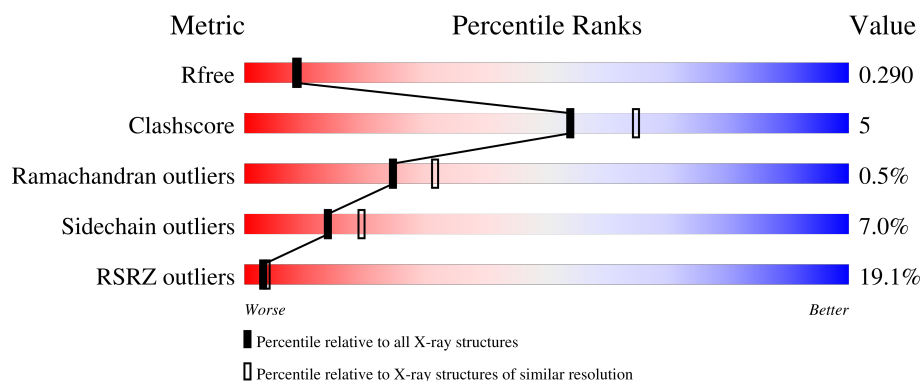
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	133	
1	B	133	
1	C	133	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2975 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 General control protein GCN4, GENERAL CONTROL PROTEIN GCN4, OUTER MEMBRANE PROTEIN 100, General control protein GCN4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	0	0
			972	603	174	194	1			
1	B	128	Total	C	N	O	S	0	0	0
			979	612	174	192	1			
1	C	128	Total	C	N	O	S	0	0	0
			984	611	177	194	2			

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	ILE	LEU	engineered mutation	UNP P03069
A	111	ILE	VAL	engineered mutation	UNP P03069
A	114	ILE	LEU	engineered mutation	UNP P03069
A	118	ILE	ASN	engineered mutation	UNP P03069
A	121	ILE	LEU	engineered mutation	UNP P03069
A	125	ILE	VAL	engineered mutation	UNP P03069
A	128	ILE	LEU	engineered mutation	UNP P03069
A	203	ILE	LEU	engineered mutation	UNP P03069
A	207	ILE	VAL	engineered mutation	UNP P03069
A	210	ILE	LEU	engineered mutation	UNP P03069
A	214	ILE	ASN	engineered mutation	UNP P03069
A	217	ILE	LEU	engineered mutation	UNP P03069
A	221	ILE	VAL	engineered mutation	UNP P03069
A	224	ILE	LEU	engineered mutation	UNP P03069
A	228	ILE	-	expression tag	UNP P03069
A	229	LYS	-	expression tag	UNP P03069
A	230	LEU	-	expression tag	UNP P03069
A	231	HIS	-	expression tag	UNP P03069
A	232	HIS	-	expression tag	UNP P03069
A	233	HIS	-	expression tag	UNP P03069
A	234	HIS	-	expression tag	UNP P03069
A	235	HIS	-	expression tag	UNP P03069

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Chain	Residue	Modelled	Actual	Comment	Reference
A	236	HIS	-	expression tag	UNP P03069
B	107	ILE	LEU	engineered mutation	UNP P03069
B	111	ILE	VAL	engineered mutation	UNP P03069
B	114	ILE	LEU	engineered mutation	UNP P03069
B	118	ILE	ASN	engineered mutation	UNP P03069
B	121	ILE	LEU	engineered mutation	UNP P03069
B	125	ILE	VAL	engineered mutation	UNP P03069
B	128	ILE	LEU	engineered mutation	UNP P03069
B	203	ILE	LEU	engineered mutation	UNP P03069
B	207	ILE	VAL	engineered mutation	UNP P03069
B	210	ILE	LEU	engineered mutation	UNP P03069
B	214	ILE	ASN	engineered mutation	UNP P03069
B	217	ILE	LEU	engineered mutation	UNP P03069
B	221	ILE	VAL	engineered mutation	UNP P03069
B	224	ILE	LEU	engineered mutation	UNP P03069
B	228	ILE	-	expression tag	UNP P03069
B	229	LYS	-	expression tag	UNP P03069
B	230	LEU	-	expression tag	UNP P03069
B	231	HIS	-	expression tag	UNP P03069
B	232	HIS	-	expression tag	UNP P03069
B	233	HIS	-	expression tag	UNP P03069
B	234	HIS	-	expression tag	UNP P03069
B	235	HIS	-	expression tag	UNP P03069
B	236	HIS	-	expression tag	UNP P03069
C	107	ILE	LEU	engineered mutation	UNP P03069
C	111	ILE	VAL	engineered mutation	UNP P03069
C	114	ILE	LEU	engineered mutation	UNP P03069
C	118	ILE	ASN	engineered mutation	UNP P03069
C	121	ILE	LEU	engineered mutation	UNP P03069
C	125	ILE	VAL	engineered mutation	UNP P03069
C	128	ILE	LEU	engineered mutation	UNP P03069
C	203	ILE	LEU	engineered mutation	UNP P03069
C	207	ILE	VAL	engineered mutation	UNP P03069
C	210	ILE	LEU	engineered mutation	UNP P03069
C	214	ILE	ASN	engineered mutation	UNP P03069
C	217	ILE	LEU	engineered mutation	UNP P03069
C	221	ILE	VAL	engineered mutation	UNP P03069
C	224	ILE	LEU	engineered mutation	UNP P03069
C	228	ILE	-	expression tag	UNP P03069
C	229	LYS	-	expression tag	UNP P03069
C	230	LEU	-	expression tag	UNP P03069
C	231	HIS	-	expression tag	UNP P03069

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Chain	Residue	Modelled	Actual	Comment	Reference
C	232	HIS	-	expression tag	UNP P03069
C	233	HIS	-	expression tag	UNP P03069
C	234	HIS	-	expression tag	UNP P03069
C	235	HIS	-	expression tag	UNP P03069
C	236	HIS	-	expression tag	UNP P03069

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

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

- Molecule 3 is water.

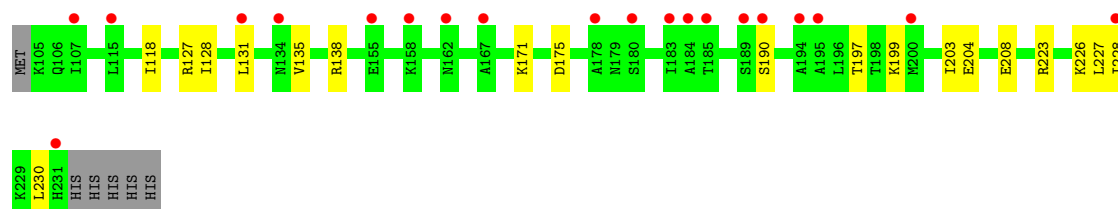
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	9	Total O 9 9	0	0
3	B	12	Total O 12 12	0	0
3	C	14	Total O 14 14	0	0

3 Residue-property plots

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.

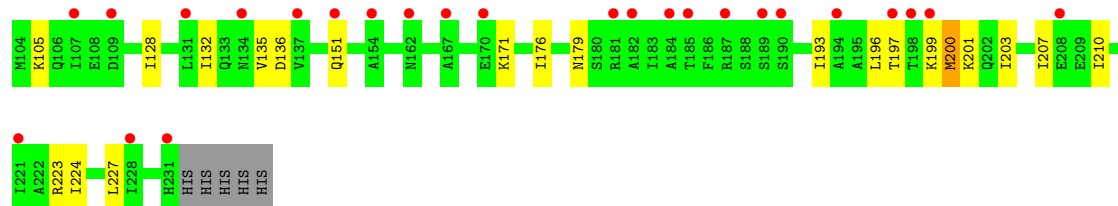
- Molecule 1: General control protein GCN4, GENERAL CONTROL PROTEIN GCN4, OUTER MEMBRANE PROTEIN 100, General control protein GCN4

Chain A: 



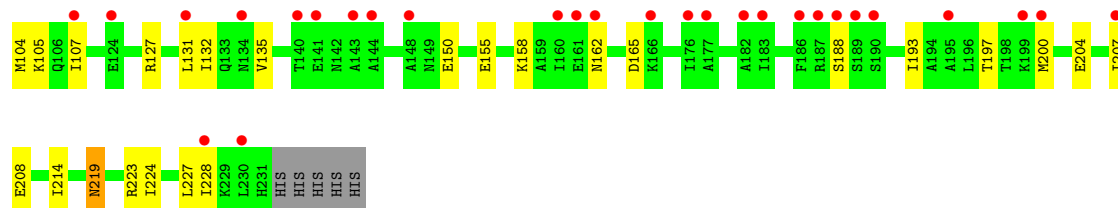
- Molecule 1: General control protein GCN4, GENERAL CONTROL PROTEIN GCN4, OUTER MEMBRANE PROTEIN 100, General control protein GCN4

Chain B: 



- Molecule 1: General control protein GCN4, GENERAL CONTROL PROTEIN GCN4, OUTER MEMBRANE PROTEIN 100, General control protein GCN4

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	62.13Å 35.86Å 198.51Å 90.00° 96.02° 90.00°	Depositor
Resolution (Å)	32.90 – 2.30 32.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.2 (32.90-2.30) 98.3 (32.90-2.30)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.225 , 0.254 0.256 , 0.290	Depositor DCC
R_{free} test set	1020 reflections (5.23%)	wwPDB-VP
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 26.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.130 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-l$ 0.126 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-l$	Xtriage
Reported twinning fraction	0.315 for H, K, L 0.343 for $1/2H-3/2K, -1/2H-1/2K, -1/2H+1/2K-L$ 0.342 for $1/2H+3/2K, 1/2H-1/2K, -1/2H-1/2K-L$	Depositor
Outliers	2 of 19496 reflections (0.010%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2975	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.73% 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	0.55	0/976	0.86	0/1313
1	B	0.53	0/983	0.85	0/1319
1	C	0.54	0/988	0.85	0/1326
All	All	0.54	0/2947	0.85	0/3958

There are no bond length outliers.

There are no bond angle outliers.

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	972	0	973	13	0
1	B	979	0	995	18	0
1	C	984	0	995	16	0
2	A	2	0	0	0	0
2	B	1	0	0	1	0
2	C	2	0	0	0	0
3	A	9	0	0	0	0
3	B	12	0	0	1	0
3	C	14	0	0	0	0
All	All	2975	0	2963	29	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 5.

All (29) 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:B:196:LEU:HD21	1:C:197:THR:HG22	1.56	0.86
1:A:228:ILE:HD11	1:C:228:ILE:HD11	1.81	0.62
1:B:193:ILE:HD11	1:C:193:ILE:CD1	2.32	0.60
1:C:193:ILE:O	1:C:197:THR:HG23	2.01	0.59
1:A:138:ARG:NH2	1:B:136:ASP:OD1	2.38	0.57
1:A:135:VAL:HG12	1:C:135:VAL:HG11	1.87	0.56
1:C:219:ASN:C	1:C:219:ASN:OD1	2.51	0.52
1:B:203:ILE:HD11	1:C:204:GLU:HG3	1.92	0.52
1:B:223:ARG:O	1:B:227:LEU:HD13	2.12	0.50
1:C:127:ARG:O	1:C:131:LEU:HD13	2.12	0.49
1:A:175:ASP:HB3	1:B:176:ILE:HG21	1.95	0.49
1:A:199:LYS:CB	1:B:200:MET:HE1	2.42	0.49
1:B:151:GLN:NE2	3:B:2007:HOH:O	2.47	0.48
1:A:203:ILE:HG23	1:B:207:ILE:HD11	1.97	0.46
1:B:210:ILE:HG23	1:C:214:ILE:HD11	1.99	0.45
1:A:228:ILE:CD1	1:C:224:ILE:HG23	2.46	0.45
1:B:203:ILE:HG23	1:C:207:ILE:CD1	2.46	0.45
1:A:127:ARG:O	1:A:131:LEU:HD13	2.16	0.45
1:B:179:ASN:ND2	2:B:1232:CL:CL	2.87	0.44
1:B:193:ILE:HD11	1:C:193:ILE:HD12	1.99	0.43
1:A:226:LYS:O	1:A:230:LEU:HG	2.19	0.43
1:A:203:ILE:O	1:A:204:GLU:C	2.62	0.42
1:B:224:ILE:HG23	1:C:228:ILE:CD1	2.49	0.42
1:C:193:ILE:N	1:C:193:ILE:HD13	2.34	0.42
1:A:135:VAL:HG11	1:B:135:VAL:HG12	2.01	0.42
1:A:128:ILE:HG23	1:B:132:ILE:HD11	2.02	0.42
1:A:223:ARG:O	1:A:227:LEU:HD13	2.20	0.42
1:B:199:LYS:C	1:C:200:MET:HE1	2.46	0.41
1:B:128:ILE:HG23	1:C:132:ILE:HD11	2.03	0.41

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	125/133 (94%)	120 (96%)	4 (3%)	1 (1%)	16	20
1	B	126/133 (95%)	120 (95%)	6 (5%)	0	100	100
1	C	126/133 (95%)	123 (98%)	2 (2%)	1 (1%)	16	20
All	All	377/399 (94%)	363 (96%)	12 (3%)	2 (0%)	24	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	162	ASN
1	A	190	SER

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	99/117 (85%)	95 (96%)	4 (4%)	28	42
1	B	99/117 (85%)	94 (95%)	5 (5%)	21	32
1	C	100/117 (86%)	88 (88%)	12 (12%)	5	5
All	All	298/351 (85%)	277 (93%)	21 (7%)	14	19

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	118	ILE

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Mol	Chain	Res	Type
1	A	171	LYS
1	A	197	THR
1	A	208	GLU
1	B	105	LYS
1	B	171	LYS
1	B	197	THR
1	B	200	MET
1	B	201	LYS
1	C	104	MET
1	C	105	LYS
1	C	107	ILE
1	C	150	GLU
1	C	155	GLU
1	C	158	LYS
1	C	165	ASP
1	C	188	SER
1	C	208	GLU
1	C	219	ASN
1	C	223	ARG
1	C	227	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	216	HIS
1	C	231	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

Of 5 ligands modelled in this entry, 5 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

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	127/133 (95%)	1.20	20 (15%) 5 6	44, 58, 83, 88	0
1	B	128/133 (96%)	1.20	25 (19%) 3 3	44, 58, 80, 89	0
1	C	128/133 (96%)	1.37	28 (21%) 2 2	43, 58, 78, 85	0
All	All	383/399 (95%)	1.26	73 (19%) 3 4	43, 58, 82, 89	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	148	ALA	5.1
1	C	195	ALA	4.5
1	A	107	ILE	4.4
1	B	190	SER	4.4
1	C	188	SER	4.2
1	C	144	ALA	4.1
1	A	183	ILE	3.9
1	A	134	ASN	3.5
1	C	187	ARG	3.5
1	A	195	ALA	3.5
1	C	131	LEU	3.4
1	B	131	LEU	3.3
1	C	143	ALA	3.2
1	C	189	SER	3.2
1	A	155	GLU	3.1
1	B	231	HIS	2.9
1	A	131	LEU	2.9
1	C	207	ILE	2.9
1	B	107	ILE	2.9
1	B	189	SER	2.8
1	C	183	ILE	2.8
1	B	109	ASP	2.8
1	B	208	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	182	ALA	2.8
1	C	177	ALA	2.7
1	B	185	THR	2.7
1	A	190	SER	2.7
1	C	141	GLU	2.7
1	B	182	ALA	2.6
1	C	199	LYS	2.6
1	B	137	VAL	2.6
1	C	230	LEU	2.6
1	B	167	ALA	2.6
1	B	194	ALA	2.6
1	A	162	ASN	2.6
1	B	162	ASN	2.6
1	A	158	LYS	2.6
1	C	107	ILE	2.5
1	A	185	THR	2.5
1	B	134	ASN	2.5
1	A	200	MET	2.4
1	C	200	MET	2.4
1	A	231	HIS	2.4
1	B	197	THR	2.4
1	C	166	LYS	2.4
1	C	162	ASN	2.4
1	C	176	ILE	2.4
1	B	199	LYS	2.3
1	C	140	THR	2.3
1	B	181	ARG	2.3
1	A	167	ALA	2.3
1	B	184	ALA	2.3
1	B	198	THR	2.3
1	B	187	ARG	2.3
1	B	154	ALA	2.3
1	C	134	ASN	2.2
1	A	184	ALA	2.2
1	A	189	SER	2.2
1	C	190	SER	2.2
1	C	161	GLU	2.2
1	A	228	ILE	2.1
1	C	228	ILE	2.1
1	A	178	ALA	2.1
1	A	180	SER	2.1
1	B	170	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	221	ILE	2.1
1	B	228	ILE	2.1
1	C	186	PHE	2.1
1	A	194	ALA	2.0
1	A	115	LEU	2.0
1	C	160	ILE	2.0
1	C	124	GLU	2.0
1	B	151	GLN	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	B	1232	1/1	0.96	0.10	60,60,60,60	0
2	CL	C	1233	1/1	0.98	0.04	61,61,61,61	0
2	CL	C	1232	1/1	0.99	0.03	44,44,44,44	0
2	CL	A	1232	1/1	0.99	0.03	44,44,44,44	0
2	CL	A	1233	1/1	1.00	0.02	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.