



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 02:05 PM EDT

PDB ID : 5OJO / pdb_00005ojo
Title : Sirtuin 5 from Danio rerio in complex with 3-hydroxy-3-methylglutaryl-CPS1 peptide
Authors : Pannek, M.; Steegborn, C.
Deposited on : 2017-07-22
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

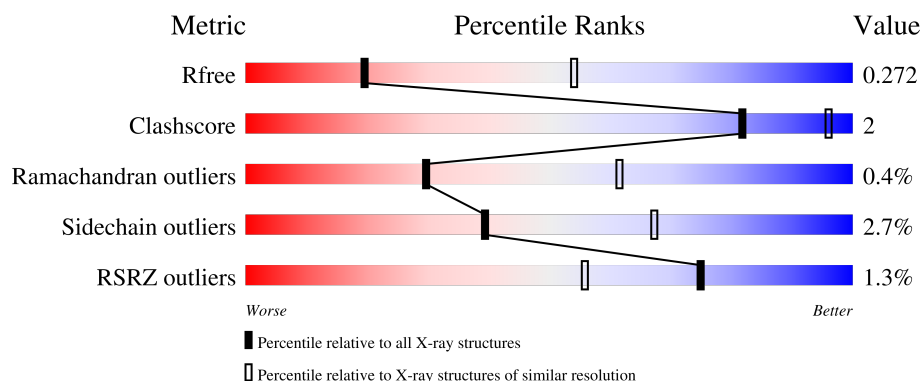
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	275	
1	B	275	
2	C	9	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 4320 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 NAD-dependent protein deacylase sirtuin-5, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	2	0
			2072	1308	374	375	15			
1	B	265	Total	C	N	O	S	0	1	0
			2066	1304	373	374	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	expression tag	UNP Q6DHI5
A	25	ILE	-	expression tag	UNP Q6DHI5
A	26	ASP	-	expression tag	UNP Q6DHI5
A	27	PRO	-	expression tag	UNP Q6DHI5
A	28	PHE	-	expression tag	UNP Q6DHI5
A	29	THR	-	expression tag	UNP Q6DHI5
B	24	GLY	-	expression tag	UNP Q6DHI5
B	25	ILE	-	expression tag	UNP Q6DHI5
B	26	ASP	-	expression tag	UNP Q6DHI5
B	27	PRO	-	expression tag	UNP Q6DHI5
B	28	PHE	-	expression tag	UNP Q6DHI5
B	29	THR	-	expression tag	UNP Q6DHI5

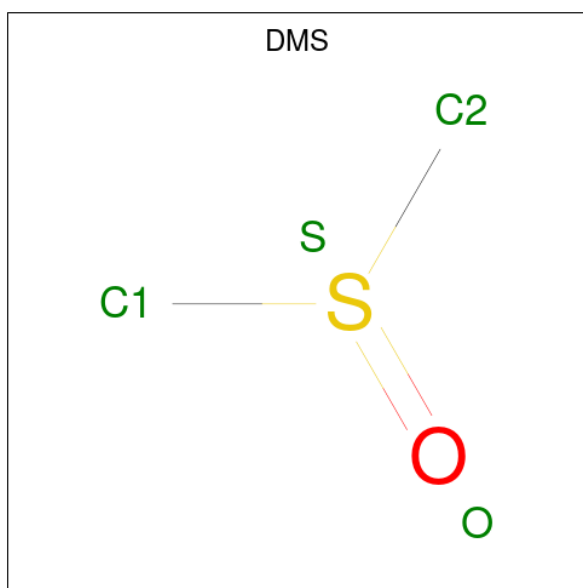
- Molecule 2 is a protein called Carbamoyl-phosphate synthase [ammonia], mitochondrial.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	0	1	0
			97	65	11	21			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	4	HLV	LYS	microheterogeneity	UNP P31327

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

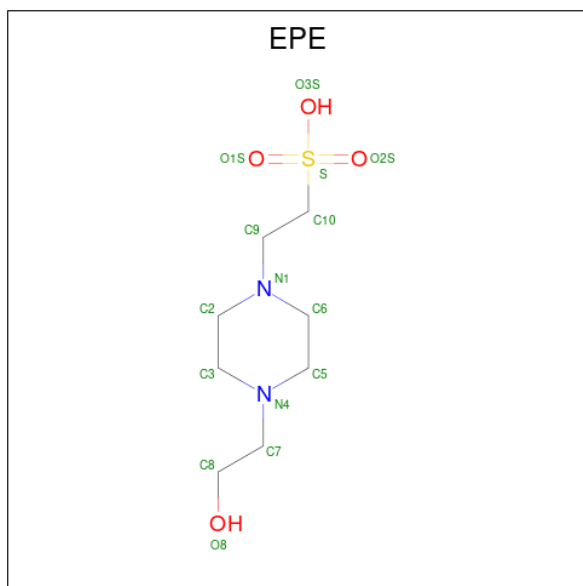
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total 1	Na 1	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	35	Total 35	O 35	0	0
8	B	22	Total 22	O 22	0	0
8	C	2	Total 2	O 2	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	87.54Å 87.54Å 316.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.67 – 3.10 48.67 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.67-3.10) 99.9 (48.67-3.10)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.196 , 0.266 0.206 , 0.272	Depositor DCC
R_{free} test set	713 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	70.8	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.8	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	4320	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 3.54% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, EPE, DMS, ZN, EDO, GZB, HLY, SKH

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	0.72	0/2134	0.94	2/2893 (0.1%)
1	B	0.71	0/2125	0.95	4/2881 (0.1%)
2	C	0.29	0/46	0.69	0/60
All	All	0.71	0/4305	0.94	6/5834 (0.1%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	CYS	N-CA-C	7.69	120.56	111.71
1	B	65	THR	N-CA-C	-6.35	99.29	109.96
1	B	189	ASN	CB-CA-C	-5.77	101.82	110.88
1	A	294	PRO	N-CA-C	5.77	117.73	110.70
1	B	294	PRO	N-CA-C	5.36	117.24	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2072	0	2038	12	1
1	B	2066	0	2030	10	1
2	C	97	0	46	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	4	0	6	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	4	0	6	0	0
6	B	15	0	18	0	0
7	B	1	0	0	0	0
8	A	35	0	0	0	0
8	B	22	0	0	1	0
8	C	2	0	0	0	0
All	All	4320	0	4144	19	1

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 2.

The worst 5 of 19 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)
2:C:4[A]:HLY:OAP	2:C:4[A]:HLY:OAR	1.99	0.75
1:A:235:LEU:HD13	1:A:256:PHE:HB3	1.77	0.66
1:A:277:ALA:O	1:A:280:ARG:NH2	2.32	0.62
1:A:109:MET:HE2	1:B:116:ALA:N	2.16	0.60
1:A:185:ALA:HB3	1:A:190:THR:HG21	1.87	0.57

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	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:CYS:SG	1:B:274:CYS:CB[12_554]	1.80	0.40

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	265/275 (96%)	254 (96%)	10 (4%)	1 (0%)	30	61
1	B	264/275 (96%)	251 (95%)	12 (4%)	1 (0%)	30	61
2	C	5/9 (56%)	3 (60%)	2 (40%)	0	100	100
All	All	534/559 (96%)	508 (95%)	24 (4%)	2 (0%)	30	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	ASP
1	B	278	THR

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	222/229 (97%)	216 (97%)	6 (3%)	39	67
1	B	221/229 (96%)	216 (98%)	5 (2%)	44	70
2	C	5/5 (100%)	4 (80%)	1 (20%)	1	6
All	All	448/463 (97%)	436 (97%)	12 (3%)	39	67

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	156	SER
1	B	173	LYS
2	C	3	LEU
1	B	238	CYS
1	A	238	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	ASN

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Mol	Chain	Res	Type
1	A	209	ASN
1	B	42	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are 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	SKH	C	4[B]	2	17,18,19	1.09	2 (11%)	15,23,25	2.17	6 (40%)
2	HLY	C	4[A]	2	17,18,19	1.10	1 (5%)	15,23,25	1.63	4 (26%)
2	GZB	C	1	2	12,12,13	1.54	1 (8%)	13,14,16	1.10	1 (7%)

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	SKH	C	4[B]	2	-	10/19/20/22	-
2	HLY	C	4[A]	2	-	10/19/20/22	-
2	GZB	C	1	2	-	0/7/8/9	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	GZB	CAG-CAE	-4.98	1.39	1.50
2	C	4[B]	SKH	CAN-CAM	-2.63	1.52	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4[A]	HLY	CAN-CAM	-2.47	1.52	1.54
2	C	4[B]	SKH	CAL-CAM	-2.26	1.52	1.54

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4[B]	SKH	CAR-CAM-CAN	-4.12	106.26	111.30
2	C	4[B]	SKH	CAR-CAM-CAL	-3.43	107.11	111.30
2	C	4[B]	SKH	CD-CG-CB	-2.94	102.54	113.62
2	C	4[B]	SKH	CG-CD-CE	-2.89	100.22	113.56
2	C	4[A]	HLY	CG-CD-CE	-2.88	100.28	113.56

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	4[A]	HLY	C-CA-CB-CG
2	C	4[A]	HLY	N-CA-CB-CG
2	C	4[A]	HLY	CAK-CAL-CAM-OAR
2	C	4[B]	SKH	C-CA-CB-CG
2	C	4[B]	SKH	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	4[A]	HLY	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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
5	EDO	A	303	-	3,3,3	0.53	0	2,2,2	0.14	0
3	DMS	A	301	-	3,3,3	0.58	0	3,3,3	0.53	0
6	EPE	B	301	-	15,15,15	2.03	1 (6%)	19,20,20	1.37	4 (21%)

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
5	EDO	A	303	-	-	1/1/1/1	-
6	EPE	B	301	-	-	3/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	301	EPE	C10-S	-7.53	1.67	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	301	EPE	O1S-S-C10	3.24	111.63	106.73
6	B	301	EPE	C5-C6-N1	-2.47	105.68	110.65
6	B	301	EPE	C2-C3-N4	2.39	115.47	110.65
6	B	301	EPE	C5-N4-C3	2.08	113.32	108.84

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	301	EPE	C10-C9-N1-C6
5	A	303	EDO	O1-C1-C2-O2
6	B	301	EPE	N4-C7-C8-O8
6	B	301	EPE	C10-C9-N1-C2

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 [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	265/275 (96%)	-0.31	1 (0%) 88 76	25, 61, 105, 124	2 (0%)
1	B	265/275 (96%)	-0.14	0 100 100	37, 73, 133, 164	1 (0%)
2	C	6/9 (66%)	6.94	6 (100%) 0 0	31, 36, 42, 48	6 (100%)
All	All	536/559 (95%)	-0.14	7 (1%) 75 56	25, 64, 120, 164	9 (1%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	8	VAL	9.4
2	C	7	GLY	7.9
2	C	6	TYR	7.2
2	C	5	GLU	6.0
2	C	3	LEU	5.6

6.2 Non-standard residues in protein, DNA, RNA chains [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	GZB	C	1	12/13	0.93	0.42	68,72,74,74	12
2	HLY	C	4[A]	19/20	0.95	0.33	60,69,74,75	19
2	SKH	C	4[B]	19/20	-	-	69,76,81,82	19

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
7	NA	B	303	1/1	0.16	0.33	116,116,116,116	1
5	EDO	A	303	4/4	0.87	0.22	62,66,67,67	0
6	EPE	B	301	15/15	0.90	0.15	71,76,90,93	0
3	DMS	A	301	4/4	0.91	0.17	71,72,73,74	0
4	ZN	B	302	1/1	0.94	0.08	100,100,100,100	0
4	ZN	A	302	1/1	1.00	0.03	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.