



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 11:39 AM EDT

PDB ID : 4UU7 / pdb_00004uu7
Title : Crystal structure of zebrafish Sirtuin 5 in complex with 3-methyl- succinylated CPS1-peptide
Authors : Pannek, M.; Gertz, M.; Steegborn, C.
Deposited on : 2014-07-24
Resolution : 3.00 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

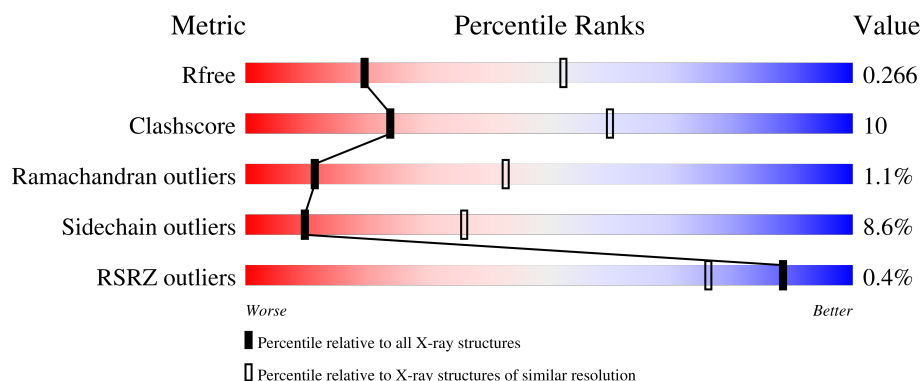
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	70% 24% • 5%
1	B	275	74% 20% • •
2	D	9	11% 22% 44% 22% 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
9	SUH	D	1010[B]	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 4342 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	262	Total	C	N	O	S	0	1	0
			2038	1286	367	370	15			
1	B	266	Total	C	N	O	S	0	1	0
			2073	1307	375	376	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 CARBAMOYLPHOSPHATE SYNTHETASE I.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	9	Total	C	N	O	0	9	0
			136	94	18	24			

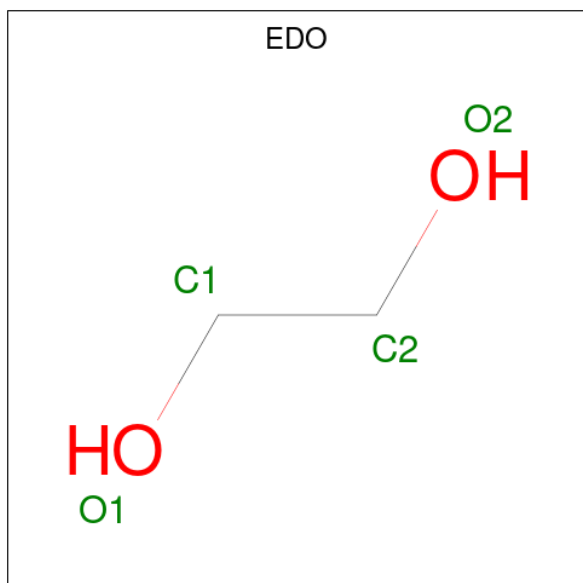
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	BEZ	-	modified residue	UNP Q5R209

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

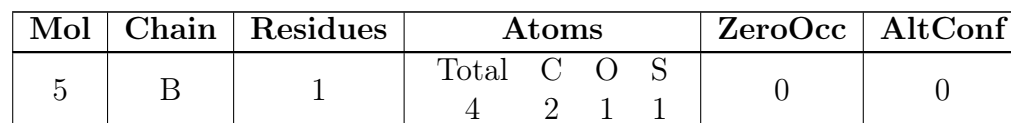
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



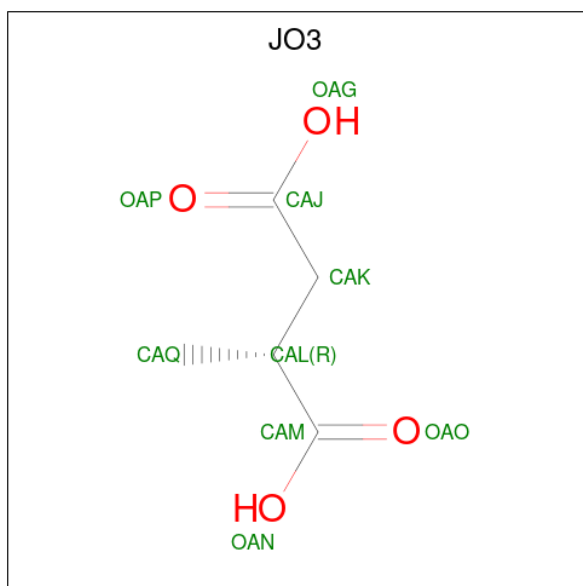
-
- The chemical structure of EPE (1,4-bis(2-hydroxyethyl)piperazine) is shown. The molecule consists of a central piperazine ring with two nitrogen atoms (N1 and N4) and four carbon atoms (C2, C3, C5, C6). Each nitrogen atom is substituted with a 2-hydroxyethyl group. The atoms are labeled as follows: N1 and N4 are the nitrogen atoms in the ring; C2, C3, C5, and C6 are the carbon atoms in the ring; C7 and C8 are the carbon atoms of the hydroxyethyl group attached to N4; C9 and C10 are the carbon atoms of the hydroxyethyl group attached to N1. The hydroxyl groups are labeled O8 and O3S. The sulfur atom is labeled S. The oxygen atoms are labeled O1S and O2S. The chemical formula is $C_{10}H_{20}N_2O_4$.

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

- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

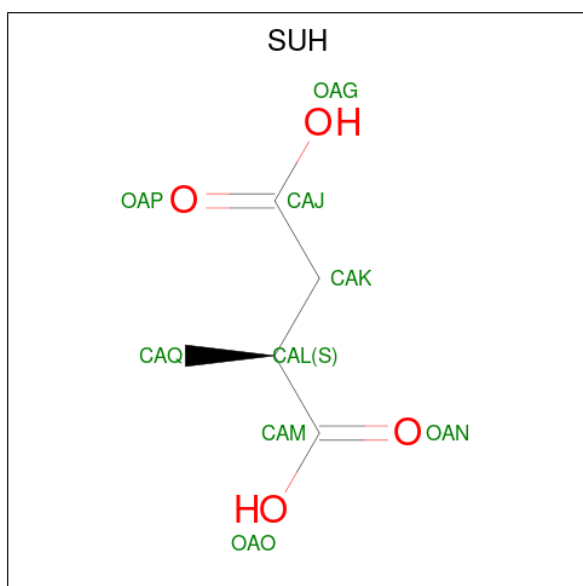
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Na 1 1	0	0

- Molecule 8 is (2R)-2-methylbutanedioic acid (CCD ID: JO3) (formula: $C_5H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total	C	O	0	1
			8	5	3		

- Molecule 9 is (2S)-2-methylbutanedioic acid (CCD ID: SUH) (formula: $C_5H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	D	1	Total	C	O	0	1
			8	5	3		

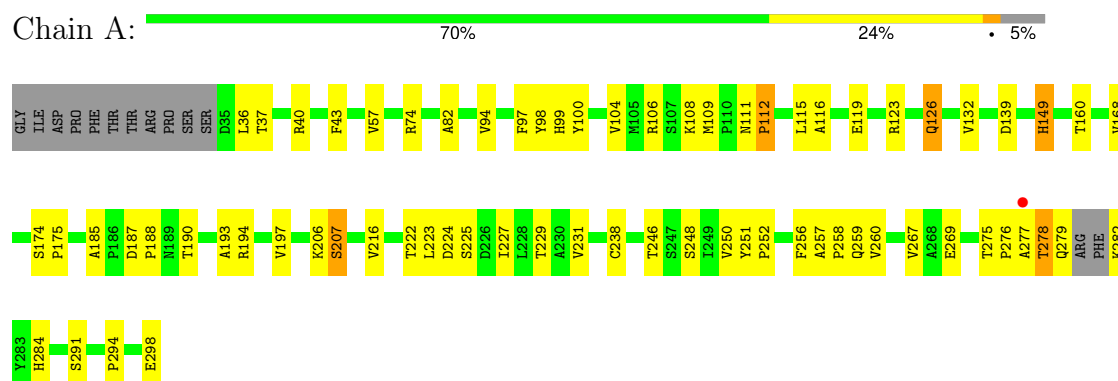
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	26	Total	O	0	0
			26	26		
10	B	15	Total	O	0	0
			15	15		

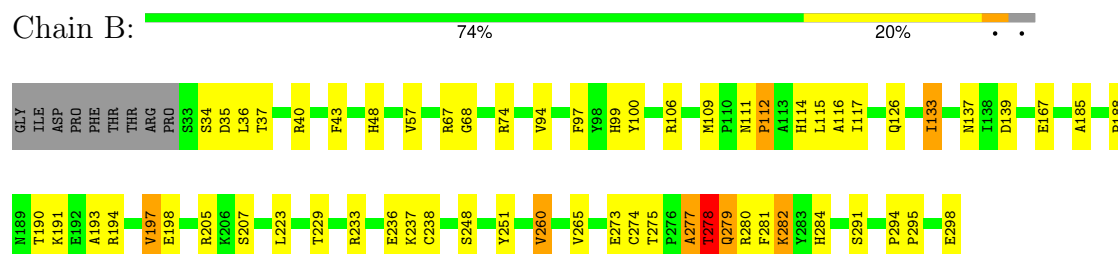
3 Residue-property plots [i](#)

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.

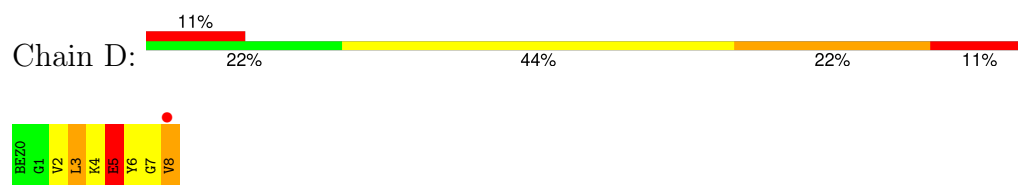
• Molecule 1: NAD-DEPENDENT PROTEIN DEACYLASE SIRTUIN-5, MITOCHONDRIAL



• Molecule 1: NAD-DEPENDENT PROTEIN DEACYLASE SIRTUIN-5, MITOCHONDRIAL



• Molecule 2: CARBAMOYLPHOSPHATE SYNTHETASE I



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	87.51Å 87.51Å 314.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.39 – 3.00 48.39 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.39-3.00) 99.8 (48.39-3.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.199 , 0.270 0.204 , 0.266	Depositor DCC
R_{free} test set	740 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	65.6	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4342	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: JO3, DMS, EPE, BEZ, NA, EDO, ZN, SUH

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	1.00	1/2095 (0.0%)	1.08	3/2840 (0.1%)
1	B	0.97	1/2131 (0.0%)	1.08	1/2888 (0.0%)
2	D	0.75	0/120	0.86	0/158
All	All	0.98	2/4346 (0.0%)	1.07	4/5886 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	THR	CA-C	5.26	1.57	1.52
1	B	278	THR	CA-CB	5.14	1.58	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	275	THR	CB-CA-C	6.70	119.41	109.22
1	A	119	GLU	N-CA-C	-5.26	105.61	112.23
1	B	251	TYR	N-CA-C	-5.24	103.43	109.93
1	A	294	PRO	N-CA-C	5.19	117.03	110.70

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	2038	0	2002	44	0
1	B	2073	0	2041	33	0
2	D	136	0	132	19	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	12	0	18	0	0
4	B	4	0	6	1	0
5	B	4	0	6	0	0
6	B	15	0	18	0	0
7	B	1	0	0	0	0
8	D	8	0	6	3	0
9	D	8	0	6	4	0
10	A	26	0	0	0	0
10	B	15	0	0	0	0
All	All	4342	0	4235	86	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 10.

The worst 5 of 86 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:D:5[B]:GLU:HB3	2:D:8[B]:VAL:HB	1.35	1.09
2:D:4[B]:LYS:HD2	9:D:1010[B]:SUH:OAG	1.50	1.03
1:A:298:GLU:OXT	1:B:106:ARG:NH2	2.04	0.88
1:A:278:THR:O	1:A:279:GLN:HG3	1.74	0.88
1:B:278:THR:O	1:B:279:GLN:HG3	1.79	0.81

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	259/275 (94%)	242 (93%)	17 (7%)	0	100	100
1	B	265/275 (96%)	239 (90%)	21 (8%)	5 (2%)	6	30
2	D	14/9 (156%)	8 (57%)	4 (29%)	2 (14%)	0	1
All	All	538/559 (96%)	489 (91%)	42 (8%)	7 (1%)	11	38

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	282	LYS
1	B	279	GLN
1	B	35	ASP
1	B	277	ALA
2	D	5[A]	GLU

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	218/229 (95%)	200 (92%)	18 (8%)	10	37
1	B	222/229 (97%)	204 (92%)	18 (8%)	11	38
2	D	12/6 (200%)	6 (50%)	6 (50%)	0	0
All	All	452/464 (97%)	410 (91%)	42 (9%)	10	32

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	229	THR
1	B	291	SER
1	B	238	CYS
1	B	273	GLU
2	D	3[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	ASN
1	B	136	GLN
1	B	284	HIS
1	A	142	HIS
1	A	42	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 11 ligands modelled in this entry, 3 are monoatomic - leaving 8 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$
8	JO3	D	1009[A]	2	7,7,8	1.23	0	7,8,10	0.89	0
5	DMS	B	1300	-	3,3,3	0.59	0	3,3,3	1.04	0
4	EDO	B	1302	-	3,3,3	0.63	0	2,2,2	0.38	0
9	SUH	D	1010[B]	2	7,7,8	1.68	1 (14%)	8,8,10	2.76	2 (25%)
4	EDO	A	1300	-	3,3,3	0.57	0	2,2,2	0.15	0
6	EPE	B	1303	-	15,15,15	1.93	1 (6%)	19,20,20	2.37	6 (31%)
4	EDO	A	1302	-	3,3,3	0.54	0	2,2,2	0.62	0
4	EDO	A	1301	-	3,3,3	0.49	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
8	JO3	D	1009[A]	2	-	5/7/7/8	-
4	EDO	B	1302	-	-	1/1/1/1	-
9	SUH	D	1010[B]	2	-	1/7/7/8	-
4	EDO	A	1300	-	-	0/1/1/1	-
6	EPE	B	1303	-	-	2/9/19/19	0/1/1/1
4	EDO	A	1302	-	-	1/1/1/1	-
4	EDO	A	1301	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	1303	EPE	C10-S	-7.24	1.67	1.77
9	D	1010[B]	SUH	OAG-CAJ	-3.61	1.23	1.42

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D	1010[B]	SUH	CAJ-CAK-CAL	-7.04	103.91	112.76
6	B	1303	EPE	O1S-S-C10	5.07	114.39	106.73
6	B	1303	EPE	O2S-S-O1S	-4.33	99.76	113.82
6	B	1303	EPE	C3-C2-N1	-4.19	102.19	110.65
6	B	1303	EPE	C5-C6-N1	3.18	117.05	110.65

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	D	1009[A]	JO3	CAK-CAL-CAM-OAN
8	D	1009[A]	JO3	CAJ-CAK-CAL-CAM
4	B	1302	EDO	O1-C1-C2-O2
9	D	1010[B]	SUH	OAG-CAJ-CAK-CAL
6	B	1303	EPE	C10-C9-N1-C6

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	D	1009[A]	JO3	3	0
4	B	1302	EDO	1	0
9	D	1010[B]	SUH	4	0

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	262/275 (95%)	-0.43	1 (0%) 88 76	19, 53, 84, 118	1 (0%)
1	B	266/275 (96%)	-0.15	0 100 100	27, 66, 114, 138	1 (0%)
2	D	8/9 (88%)	0.18	1 (12%) 8 5	23, 28, 30, 32	8 (100%)
All	All	536/559 (95%)	-0.28	2 (0%) 88 76	19, 58, 107, 138	10 (1%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	8[A]	VAL	2.8
1	A	277	ALA	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
4	EDO	A	1301	4/4	0.76	0.26	82,87,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	NA	B	1301	1/1	0.77	0.13	78,78,78,78	1
4	EDO	A	1302	4/4	0.87	0.11	57,57,58,60	0
4	EDO	B	1302	4/4	0.88	0.13	42,46,47,47	0
6	EPE	B	1303	15/15	0.92	0.12	56,67,74,74	0
4	EDO	A	1300	4/4	0.95	0.08	42,43,44,46	0
5	DMS	B	1300	4/4	0.95	0.11	49,51,54,58	0
8	JO3	D	1009[A]	8/9	0.96	0.13	55,66,72,74	8
9	SUH	D	1010[B]	8/9	0.96	0.12	42,51,54,54	8
3	ZN	B	1299	1/1	0.98	0.04	93,93,93,93	0
3	ZN	A	1299	1/1	1.00	0.02	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.