



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:34 AM UTC

PDB ID : 5C3R / pdb_00005c3r
Title : Crystal structure of the full-length *Neurospora crassa* T7H in complex with alpha-KG and 5-hydroxymethyluracil (5hmU)
Authors : Li, W.; Zhang, T.; Ding, J.
Deposited on : 2015-06-17
Resolution : 2.35 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

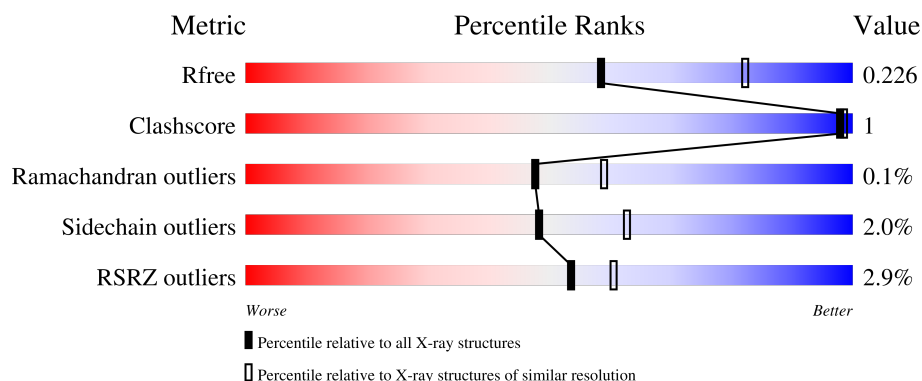
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	343	95%
1	B	343	87% 10%
1	C	343	2% 85% 5% 10%
1	D	343	6% 93%

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
4	HMU	A	403	-	X	-	-
4	HMU	B	403	-	X	-	-
4	HMU	C	403	-	X	-	-
4	HMU	D	403	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10833 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 Thymine dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2634	1679	447	502	6			
1	B	310	Total	C	N	O	S	0	0	0
			2454	1567	415	466	6			
1	C	310	Total	C	N	O	S	0	0	0
			2454	1567	415	466	6			
1	D	329	Total	C	N	O	S	0	0	0
			2598	1656	443	494	5			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q7RYZ9
A	0	SER	-	expression tag	UNP Q7RYZ9
A	334	LEU	-	expression tag	UNP Q7RYZ9
A	335	GLU	-	expression tag	UNP Q7RYZ9
A	336	HIS	-	expression tag	UNP Q7RYZ9
A	337	HIS	-	expression tag	UNP Q7RYZ9
A	338	HIS	-	expression tag	UNP Q7RYZ9
A	339	HIS	-	expression tag	UNP Q7RYZ9
A	340	HIS	-	expression tag	UNP Q7RYZ9
A	341	HIS	-	expression tag	UNP Q7RYZ9
B	-1	GLY	-	expression tag	UNP Q7RYZ9
B	0	SER	-	expression tag	UNP Q7RYZ9
B	334	LEU	-	expression tag	UNP Q7RYZ9
B	335	GLU	-	expression tag	UNP Q7RYZ9
B	336	HIS	-	expression tag	UNP Q7RYZ9
B	337	HIS	-	expression tag	UNP Q7RYZ9
B	338	HIS	-	expression tag	UNP Q7RYZ9
B	339	HIS	-	expression tag	UNP Q7RYZ9
B	340	HIS	-	expression tag	UNP Q7RYZ9
B	341	HIS	-	expression tag	UNP Q7RYZ9
C	-1	GLY	-	expression tag	UNP Q7RYZ9

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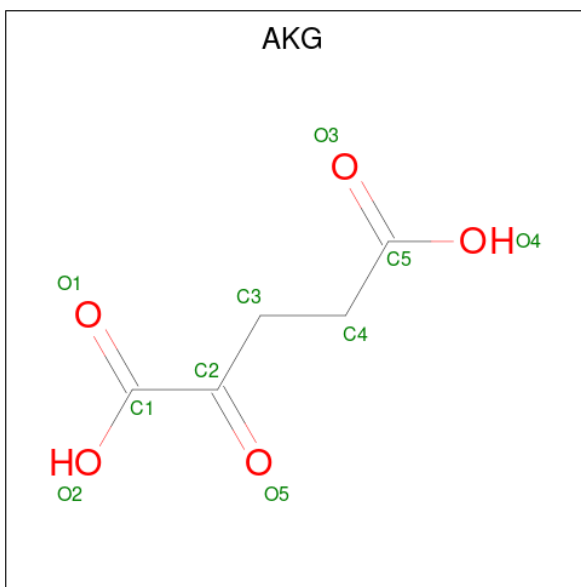
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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	expression tag	UNP Q7RYZ9
C	334	LEU	-	expression tag	UNP Q7RYZ9
C	335	GLU	-	expression tag	UNP Q7RYZ9
C	336	HIS	-	expression tag	UNP Q7RYZ9
C	337	HIS	-	expression tag	UNP Q7RYZ9
C	338	HIS	-	expression tag	UNP Q7RYZ9
C	339	HIS	-	expression tag	UNP Q7RYZ9
C	340	HIS	-	expression tag	UNP Q7RYZ9
C	341	HIS	-	expression tag	UNP Q7RYZ9
D	-1	GLY	-	expression tag	UNP Q7RYZ9
D	0	SER	-	expression tag	UNP Q7RYZ9
D	334	LEU	-	expression tag	UNP Q7RYZ9
D	335	GLU	-	expression tag	UNP Q7RYZ9
D	336	HIS	-	expression tag	UNP Q7RYZ9
D	337	HIS	-	expression tag	UNP Q7RYZ9
D	338	HIS	-	expression tag	UNP Q7RYZ9
D	339	HIS	-	expression tag	UNP Q7RYZ9
D	340	HIS	-	expression tag	UNP Q7RYZ9
D	341	HIS	-	expression tag	UNP Q7RYZ9

- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

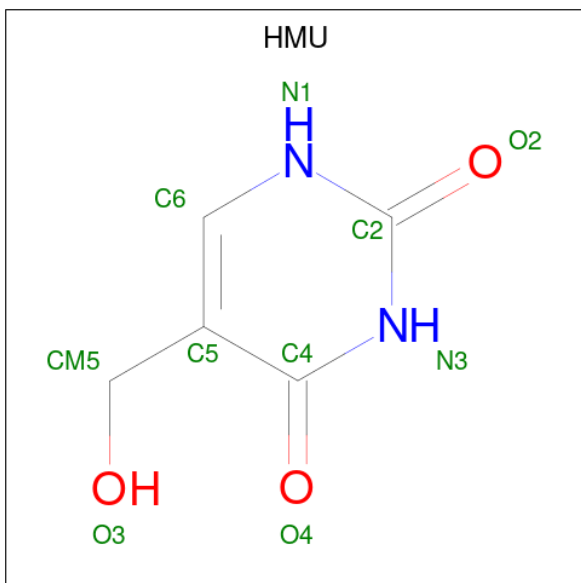
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ni 1 1	0	0
2	B	1	Total Ni 1 1	0	0
2	C	1	Total Ni 1 1	0	0
2	D	1	Total Ni 1 1	0	0

- Molecule 3 is 2-OXOGLUTARIC ACID (CCD ID: AKG) (formula: C₅H₆O₅).



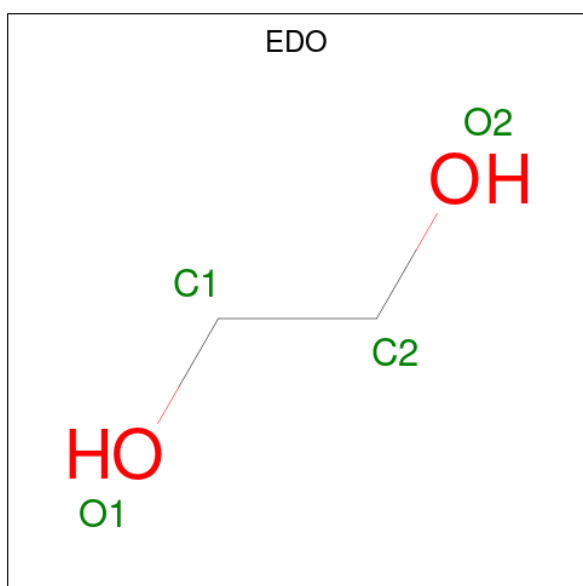
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	5	5		
3	B	1	Total	C	O	0	0
			10	5	5		
3	C	1	Total	C	O	0	0
			10	5	5		
3	D	1	Total	C	O	0	0
			10	5	5		

- Molecule 4 is 5-HYDROXYMETHYL URACIL (CCD ID: HMU) (formula: $C_5H_6N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	5	2	3		
4	B	1	Total	C	N	O	0	0
			10	5	2	3		
4	C	1	Total	C	N	O	0	0
			10	5	2	3		
4	D	1	Total	C	N	O	0	0
			10	5	2	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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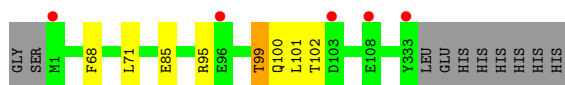
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 4 2 2	0	0
5	C	1	Total C O 4 2 2	0	0
5	D	1	Total C O 4 2 2	0	0
5	D	1	Total C O 4 2 2	0	0
5	D	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	172	Total O 172 172	0	0
6	B	134	Total O 134 134	0	0
6	C	134	Total O 134 134	0	0
6	D	117	Total O 117 117	0	0

i

- Molecule 1: Thymine dioxygenase



Position	Amino Acid	Information Content (bits)
1	GLY	0.00
2	SER	0.00
3	M1	0.35
4	F68	0.32
5	L71	0.31
6	E85	0.30
7	P93	0.38
8	GLY	0.00
9	ARG	0.00
10	GLU	0.00
11	LYS	0.00
12	VAL	0.00
13	THR	0.00
14	GLN	0.00
15	LEU	0.00
16	THR	0.00
17	ASP	0.00
18	PRO	0.00
19	ALA	0.00
20	GLU	0.00
21	ILE	0.00
22	GLU	0.00
23	LYS	0.00
24	ILE	0.00
25	ARG	0.00
26	SER	0.00
27	ALA	0.00
28	ALA	0.00
29	PRO	0.00
30	D116	0.00
31	H160	0.00
32	K203	0.28
33	L204	0.27
34	N205	0.26
35	P206	0.25
36	V209	0.24
37	S219	0.23
38	L258	0.22
39	C293	0.21
40	I319	0.20
41	T332	0.19
42	THR	0.00
43	LEU	0.00
44	GLU	0.00
45	HIS	0.00
46	HIS	0.00
47	HIS	0.00
48	HIS	0.00

Sequence logo for the 100th position. The y-axis represents information content in bits (0 to 1.3). The x-axis lists amino acids. The most prominent peak is for Glycine (GLY) at position 100, with an information content of approximately 1.2 bits. Other residues with significant information content include Arginine (ARG) and Glutamine (GLN) at positions 101 and 102, and Glutamic acid (GLU) at position 103.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.82Å 155.78Å 75.99Å 90.00° 91.65° 90.00°	Depositor
Resolution (Å)	50.00 – 2.35 50.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.2 (50.00-2.35) 98.2 (50.00-2.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.54 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.180 , 0.225 0.185 , 0.226	Depositor DCC
R_{free} test set	2689 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	25.2	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10833	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% 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: HMU, NI, EDO, AKG

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	0.45	0/2700	0.70	0/3664
1	B	0.43	0/2516	0.70	0/3413
1	C	0.44	0/2516	0.69	0/3413
1	D	0.43	0/2663	0.69	2/3614 (0.1%)
All	All	0.44	0/10395	0.69	2/14104 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	54	GLN	CA-C-N	5.44	124.90	119.24
1	D	54	GLN	C-N-CA	5.44	124.90	119.24

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	2634	0	2579	3	0
1	B	2454	0	2394	3	0
1	C	2454	0	2394	6	0
1	D	2598	0	2545	4	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	10	0	4	0	0
3	B	10	0	4	0	0
3	C	10	0	4	0	0
3	D	10	0	4	0	0
4	A	10	0	6	0	0
4	B	10	0	6	0	0
4	C	10	0	6	0	0
4	D	10	0	6	0	0
5	A	24	0	36	0	0
5	B	8	0	12	0	0
5	C	8	0	12	0	0
5	D	12	0	18	0	0
6	A	172	0	0	0	0
6	B	134	0	0	0	0
6	C	134	0	0	1	0
6	D	117	0	0	0	0
All	All	10833	0	10030	15	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 1.

The worst 5 of 15 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:C:92:ALA:HB1	1:C:93:PRO:HD2	1.82	0.61
1:B:68:PHE:O	1:B:71:LEU:HB2	2.07	0.54
1:A:99:THR:HG22	1:A:102:THR:HG23	1.92	0.52
1:D:319:ILE:HD12	1:D:324:TYR:HB2	1.92	0.51
1:D:209:VAL:HG22	1:D:274:VAL:HG12	1.92	0.50

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	331/343 (96%)	318 (96%)	13 (4%)	0	100	100
1	B	306/343 (89%)	295 (96%)	11 (4%)	0	100	100
1	C	306/343 (89%)	295 (96%)	10 (3%)	1 (0%)	36	43
1	D	327/343 (95%)	311 (95%)	16 (5%)	0	100	100
All	All	1270/1372 (93%)	1219 (96%)	50 (4%)	1 (0%)	48	59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	79	VAL

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	283/292 (97%)	279 (99%)	4 (1%)	59	73
1	B	264/292 (90%)	258 (98%)	6 (2%)	44	58
1	C	264/292 (90%)	256 (97%)	8 (3%)	36	48
1	D	279/292 (96%)	275 (99%)	4 (1%)	59	73
All	All	1090/1168 (93%)	1068 (98%)	22 (2%)	48	63

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	200	GLU
1	C	323	LYS
1	C	247	GLU
1	D	71	LEU
1	B	203	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	248	ASN
1	B	294	ASN
1	D	54	GLN
1	C	131	HIS
1	B	155	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](#)

Of 25 ligands modelled in this entry, 4 are monoatomic - leaving 21 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	404	-	3,3,3	0.42	0	2,2,2	0.26	0
5	EDO	D	405	-	3,3,3	0.41	0	2,2,2	0.30	0
5	EDO	A	407	-	3,3,3	0.51	0	2,2,2	0.05	0
3	AKG	C	402	2	9,9,9	1.62	1 (11%)	11,11,11	1.30	1 (9%)
5	EDO	D	404	-	3,3,3	0.50	0	2,2,2	0.19	0
5	EDO	D	406	-	3,3,3	0.49	0	2,2,2	0.20	0
3	AKG	D	402	2	9,9,9	1.68	1 (11%)	11,11,11	1.52	3 (27%)
5	EDO	A	409	-	3,3,3	0.41	0	2,2,2	0.39	0
5	EDO	A	406	-	3,3,3	0.51	0	2,2,2	0.12	0
5	EDO	C	404	-	3,3,3	0.51	0	2,2,2	0.23	0
4	HMU	B	403	-	10,10,10	4.07	5 (50%)	11,13,13	2.50	6 (54%)
5	EDO	B	404	-	3,3,3	0.43	0	2,2,2	0.27	0
5	EDO	B	405	-	3,3,3	0.46	0	2,2,2	0.30	0
5	EDO	A	405	-	3,3,3	0.43	0	2,2,2	0.30	0
5	EDO	C	405	-	3,3,3	0.48	0	2,2,2	0.25	0
3	AKG	B	402	2	9,9,9	1.75	1 (11%)	11,11,11	1.32	1 (9%)
5	EDO	A	408	-	3,3,3	0.35	0	2,2,2	0.46	0
4	HMU	D	403	-	10,10,10	4.20	5 (50%)	11,13,13	2.45	6 (54%)
4	HMU	A	403	-	10,10,10	3.99	5 (50%)	11,13,13	2.48	6 (54%)
3	AKG	A	402	2	9,9,9	1.67	1 (11%)	11,11,11	1.53	3 (27%)
4	HMU	C	403	-	10,10,10	4.18	5 (50%)	11,13,13	2.49	6 (54%)

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	404	-	-	0/1/1/1	-
5	EDO	D	405	-	-	0/1/1/1	-
5	EDO	A	407	-	-	1/1/1/1	-
3	AKG	C	402	2	-	0/9/9/9	-
5	EDO	D	404	-	-	0/1/1/1	-
5	EDO	D	406	-	-	1/1/1/1	-
3	AKG	D	402	2	-	0/9/9/9	-
5	EDO	A	409	-	-	0/1/1/1	-
5	EDO	A	406	-	-	1/1/1/1	-
5	EDO	C	404	-	-	0/1/1/1	-
4	HMU	B	403	-	-	2/2/2/2	0/1/1/1
5	EDO	B	404	-	-	0/1/1/1	-
5	EDO	B	405	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	405	-	-	0/1/1/1	-
5	EDO	C	405	-	-	0/1/1/1	-
3	AKG	B	402	2	-	0/9/9/9	-
5	EDO	A	408	-	-	1/1/1/1	-
4	HMU	D	403	-	-	2/2/2/2	0/1/1/1
4	HMU	A	403	-	-	2/2/2/2	0/1/1/1
3	AKG	A	402	2	-	0/9/9/9	-
4	HMU	C	403	-	-	2/2/2/2	0/1/1/1

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	403	HMU	C2-N1	8.35	1.47	1.36
4	C	403	HMU	C2-N1	8.33	1.47	1.36
4	A	403	HMU	C2-N1	8.06	1.47	1.36
4	B	403	HMU	C2-N1	8.00	1.47	1.36
4	C	403	HMU	C6-C5	6.85	1.46	1.36

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	403	HMU	C4-N3-C2	-4.84	119.70	126.37
4	B	403	HMU	C4-N3-C2	-4.55	120.11	126.37
4	C	403	HMU	C4-N3-C2	-4.50	120.17	126.37
4	D	403	HMU	C4-N3-C2	-4.47	120.22	126.37
4	C	403	HMU	N1-C2-N3	4.02	119.41	115.17

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	HMU	C4-C5-CM5-O3
4	A	403	HMU	C6-C5-CM5-O3
4	C	403	HMU	C4-C5-CM5-O3
4	C	403	HMU	C6-C5-CM5-O3
4	D	403	HMU	C4-C5-CM5-O3

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	333/343 (97%)	-0.08	5 (1%) 72 77	11, 23, 49, 66	0
1	B	310/343 (90%)	0.01	4 (1%) 75 79	14, 28, 50, 61	0
1	C	310/343 (90%)	0.10	7 (2%) 61 66	11, 29, 57, 78	0
1	D	329/343 (95%)	0.26	21 (6%) 25 28	13, 31, 70, 77	0
All	All	1282/1372 (93%)	0.07	37 (2%) 53 60	11, 27, 60, 78	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	86	ALA	4.8
1	B	206	PRO	3.9
1	A	333	TYR	3.9
1	D	206	PRO	3.8
1	D	201	VAL	3.3

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($\text{\AA}^2$)	Q<0.9
5	EDO	A	406	4/4	0.63	0.21	63,63,63,63	0
5	EDO	D	406	4/4	0.69	0.21	45,47,48,49	0
4	HMU	D	403	10/10	0.70	0.20	50,54,56,57	0
5	EDO	B	405	4/4	0.80	0.16	54,56,57,60	0
5	EDO	A	408	4/4	0.84	0.13	52,53,53,54	0
5	EDO	A	409	4/4	0.84	0.18	34,34,35,36	0
5	EDO	D	405	4/4	0.85	0.19	49,50,50,51	0
5	EDO	A	407	4/4	0.86	0.16	35,36,36,36	0
5	EDO	C	405	4/4	0.86	0.13	43,44,45,47	0
5	EDO	A	405	4/4	0.90	0.13	40,41,42,43	0
3	AKG	D	402	10/10	0.93	0.08	31,32,35,35	0
4	HMU	B	403	10/10	0.93	0.09	38,38,39,39	0
4	HMU	C	403	10/10	0.94	0.11	35,37,38,39	0
5	EDO	D	404	4/4	0.95	0.10	24,24,24,25	0
5	EDO	C	404	4/4	0.95	0.07	22,22,23,23	0
3	AKG	B	402	10/10	0.95	0.07	27,28,29,30	0
5	EDO	A	404	4/4	0.96	0.08	27,28,28,29	0
3	AKG	A	402	10/10	0.96	0.07	18,19,19,20	0
4	HMU	A	403	10/10	0.97	0.07	27,27,28,28	0
5	EDO	B	404	4/4	0.97	0.06	31,31,31,31	0
2	NI	B	401	1/1	0.99	0.06	23,23,23,23	0
3	AKG	C	402	10/10	0.99	0.05	22,22,23,23	0
2	NI	D	401	1/1	0.99	0.06	26,26,26,26	0
2	NI	A	401	1/1	0.99	0.09	18,18,18,18	0
2	NI	C	401	1/1	1.00	0.06	20,20,20,20	0

6.5 Other polymers

There are no such residues in this entry.