



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:32 PM GMT

PDB ID : 5C3P
Title : Crystal structure of the full-length *Neurospora crassa* T7H in complex with alpha-KG
Authors : Li, W.; Zhang, T.; Ding, J.
Deposited on : 2015-06-17
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

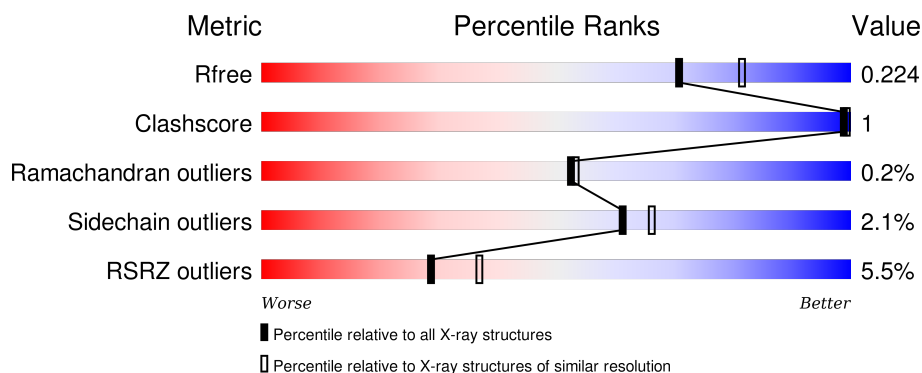
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>3%</div> <div>92%</div> <div>• • •</div> </div>
1	B	343	<div> <div>6%</div> <div>93%</div> <div>• 5%</div> </div>
1	C	343	<div> <div>3%</div> <div>93%</div> <div>• 5%</div> </div>
1	D	343	<div> <div>9%</div> <div>86%</div> <div>• 12%</div> </div>

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
3	AKG	A	402	-	-	-	X
3	AKG	B	402	-	-	-	X
4	EDO	A	404	-	-	-	X
4	EDO	A	405	-	-	-	X
4	EDO	A	408	-	-	-	X
4	EDO	B	403	-	-	-	X
4	EDO	C	403	-	-	-	X
4	EDO	C	404	-	-	-	X
4	EDO	C	405	-	-	-	X
4	EDO	D	406	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10737 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	329	Total	C	N	O	S	0	0	0
			2604	1661	440	497	6			
1	B	325	Total	C	N	O	S	0	0	0
			2568	1637	438	487	6			
1	C	325	Total	C	N	O	S	0	0	0
			2566	1634	438	488	6			
1	D	303	Total	C	N	O	S	0	1	0
			2400	1535	410	449	6			

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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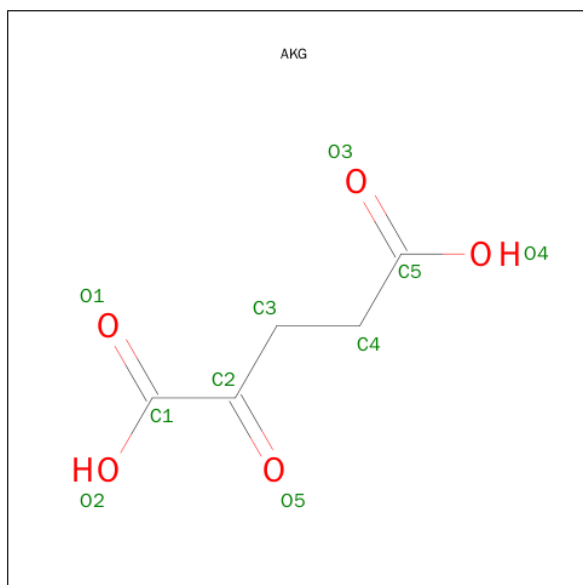
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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	expression tag	UNP Q7RYZ9
C	334	LEU	-	expression tag	UNP Q7RYZ9
C	335	GLU	-	expression tag	UNP Q7RYZ9
C	336	HIS	-	expression tag	UNP Q7RYZ9
C	337	HIS	-	expression tag	UNP Q7RYZ9
C	338	HIS	-	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 (three-letter code: NI) (formula: Ni).

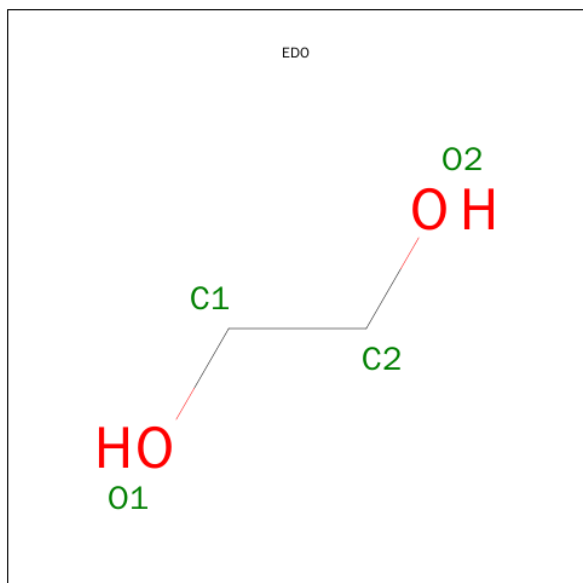
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ni 1 1	0	0
2	A	1	Total Ni 1 1	0	0
2	D	1	Total Ni 1 1	0	0
2	C	1	Total Ni 1 1	0	0

- Molecule 3 is 2-OXOGLUTARIC ACID (three-letter code: 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 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

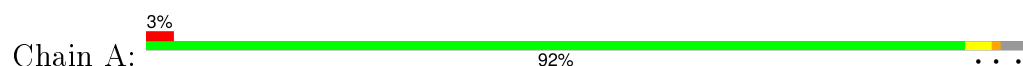
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	155	Total O 155 155	0	0
5	B	119	Total O 119 119	0	0
5	C	133	Total O 133 133	0	0
5	D	88	Total O 88 88	0	0

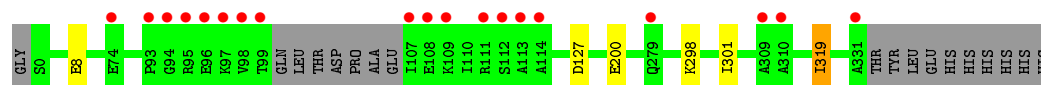
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: Thymine dioxygenase



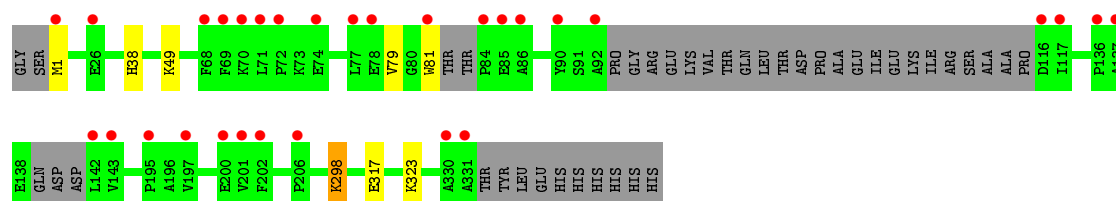
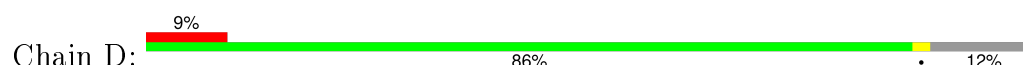
- Molecule 1: Thymine dioxygenase



- Molecule 1: Thymine dioxygenase



- Molecule 1: Thymine dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.19Å 154.73Å 75.43Å 90.00° 90.60° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 45.80 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.0 (50.00-2.10) 99.0 (45.80-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.25 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.222 0.189 , 0.224	Depositor DCC
R_{free} test set	3731 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	36.6	Xtriage
Anisotropy	0.341	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.3	EDS
Estimated twinning fraction	0.047 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 75332 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10737	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NI, AKG, EDO

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	0.38	0/2669	0.56	0/3621
1	B	0.33	0/2631	0.53	0/3566
1	C	0.35	0/2627	0.54	0/3559
1	D	0.32	0/2462	0.51	0/3332
All	All	0.35	0/10389	0.53	0/14078

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 [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	2604	0	2544	7	0
1	B	2568	0	2519	2	0
1	C	2566	0	2520	1	0
1	D	2400	0	2342	6	0
2	A	1	0	0	0	0
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	4	0	0
3	C	10	0	4	0	0
3	D	10	0	4	0	0
4	A	24	0	36	1	0
4	B	8	0	12	0	0
4	C	12	0	18	0	0
4	D	16	0	24	2	0
5	A	155	0	0	1	0
5	B	119	0	0	0	0
5	C	133	0	0	0	0
5	D	88	0	0	1	0
All	All	10737	0	10031	16	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.

All (16) 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:D:38:HIS:ND1	5:D:501:HOH:O	2.26	0.68
1:D:317:GLU:H	4:D:406:EDO:H12	1.65	0.62
1:A:206:PRO:HG2	1:A:207:GLY:H	1.68	0.57
1:A:206:PRO:CG	1:A:207:GLY:H	2.18	0.56
1:A:103:ASP:OD1	1:A:106:GLU:HG3	2.08	0.53
1:D:317:GLU:H	4:D:406:EDO:C1	2.22	0.53
1:A:205:ASN:N	1:A:205:ASN:OD1	2.44	0.51
1:D:298:LYS:CE	1:D:298:LYS:H	2.24	0.50
1:D:298:LYS:HE2	1:D:298:LYS:H	1.78	0.48
1:B:127:ASP:OD1	1:B:127:ASP:N	2.48	0.46
1:B:301:ILE:HB	1:B:319:ILE:HD12	1.98	0.45
1:A:58:ARG:HD2	4:A:408:EDO:H21	1.99	0.43
1:A:1:MET:HE3	5:A:560:HOH:O	2.18	0.43
1:D:298:LYS:N	1:D:298:LYS:HE2	2.35	0.41
1:C:68:PHE:O	1:C:71:LEU:HB2	2.21	0.41
1:A:68:PHE:O	1:A:71:LEU:HB2	2.21	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	325/343 (95%)	311 (96%)	13 (4%)	1 (0%)	46	45
1	B	321/343 (94%)	309 (96%)	12 (4%)	0	100	100
1	C	321/343 (94%)	305 (95%)	15 (5%)	1 (0%)	46	45
1	D	296/343 (86%)	285 (96%)	10 (3%)	1 (0%)	46	45
All	All	1263/1372 (92%)	1210 (96%)	50 (4%)	3 (0%)	52	53

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	141	ASP
1	A	206	PRO
1	D	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	280/292 (96%)	270 (96%)	10 (4%)	42	43
1	B	276/292 (94%)	272 (99%)	4 (1%)	74	80
1	C	276/292 (94%)	272 (99%)	4 (1%)	74	80
1	D	255/292 (87%)	250 (98%)	5 (2%)	63	68
All	All	1087/1168 (93%)	1064 (98%)	23 (2%)	61	66

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	71	LEU
1	A	88	ARG
1	A	93	PRO
1	A	103	ASP
1	A	108	GLU
1	A	205	ASN
1	A	279	GLN
1	A	311	GLU
1	A	315	LYS
1	B	8	GLU
1	B	200	GLU
1	B	298	LYS
1	B	319	ILE
1	C	74	GLU
1	C	103	ASP
1	C	281	ASP
1	C	329	LEU
1	D	1	MET
1	D	49	LYS
1	D	81	TRP
1	D	298	LYS
1	D	323	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 23 ligands modelled in this entry, 4 are monoatomic - leaving 19 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	$\# Z > 2$
3	AKG	A	402	2	3,9,9	0.55	0	4,11,11	0.56	0
4	EDO	A	403	-	3,3,3	0.49	0	2,2,2	0.19	0
4	EDO	A	404	-	3,3,3	0.71	0	2,2,2	0.56	0
4	EDO	A	405	-	3,3,3	0.48	0	2,2,2	0.33	0
4	EDO	A	406	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	A	407	-	3,3,3	0.44	0	2,2,2	0.29	0
4	EDO	A	408	-	3,3,3	0.36	0	2,2,2	0.42	0
3	AKG	B	402	2	3,9,9	0.57	0	4,11,11	0.67	0
4	EDO	B	403	-	3,3,3	0.45	0	2,2,2	0.36	0
4	EDO	B	404	-	3,3,3	0.57	0	2,2,2	0.08	0
3	AKG	C	402	2	3,9,9	0.63	0	4,11,11	0.73	0
4	EDO	C	403	-	3,3,3	0.40	0	2,2,2	0.33	0
4	EDO	C	404	-	3,3,3	0.48	0	2,2,2	0.14	0
4	EDO	C	405	-	3,3,3	0.44	0	2,2,2	0.24	0
3	AKG	D	402	2	3,9,9	0.54	0	4,11,11	0.66	0
4	EDO	D	403	-	3,3,3	0.46	0	2,2,2	0.22	0
4	EDO	D	404	-	3,3,3	0.43	0	2,2,2	0.42	0
4	EDO	D	405	-	3,3,3	0.55	0	2,2,2	0.11	0
4	EDO	D	406	-	3,3,3	0.52	0	2,2,2	0.09	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
3	AKG	A	402	2	-	0/3/9/9	0/0/0/0
4	EDO	A	403	-	-	0/1/1/1	0/0/0/0
4	EDO	A	404	-	-	0/1/1/1	0/0/0/0
4	EDO	A	405	-	-	0/1/1/1	0/0/0/0
4	EDO	A	406	-	-	0/1/1/1	0/0/0/0
4	EDO	A	407	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	408	-	-	0/1/1/1	0/0/0/0
3	AKG	B	402	2	-	0/3/9/9	0/0/0/0
4	EDO	B	403	-	-	0/1/1/1	0/0/0/0
4	EDO	B	404	-	-	0/1/1/1	0/0/0/0
3	AKG	C	402	2	-	0/3/9/9	0/0/0/0
4	EDO	C	403	-	-	0/1/1/1	0/0/0/0
4	EDO	C	404	-	-	0/1/1/1	0/0/0/0
4	EDO	C	405	-	-	0/1/1/1	0/0/0/0
3	AKG	D	402	2	-	0/3/9/9	0/0/0/0
4	EDO	D	403	-	-	0/1/1/1	0/0/0/0
4	EDO	D	404	-	-	0/1/1/1	0/0/0/0
4	EDO	D	405	-	-	0/1/1/1	0/0/0/0
4	EDO	D	406	-	-	0/1/1/1	0/0/0/0

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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	408	EDO	1	0
4	D	406	EDO	2	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 ⓘ

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	329/343 (95%)	-0.05	11 (3%) 50 59	26, 37, 70, 98	0
1	B	325/343 (94%)	0.12	19 (5%) 26 34	30, 44, 76, 100	0
1	C	325/343 (94%)	0.01	10 (3%) 52 61	27, 41, 69, 82	0
1	D	303/343 (88%)	0.37	30 (9%) 9 13	30, 50, 81, 107	0
All	All	1282/1372 (93%)	0.11	70 (5%) 29 37	26, 43, 76, 107	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	95	ARG	6.2
1	B	108	GLU	6.0
1	B	107	ILE	5.9
1	D	86	ALA	5.7
1	D	331	ALA	5.7
1	B	95	ARG	5.1
1	B	309	ALA	4.9
1	D	71	LEU	4.8
1	B	113	ALA	4.7
1	B	99	THR	4.6
1	D	206	PRO	4.5
1	C	206	PRO	4.4
1	D	116	ASP	4.3
1	D	70	LYS	4.2
1	D	137	ALA	4.2
1	D	74	GLU	4.2
1	B	112	SER	4.2
1	D	117	ILE	3.8
1	D	85	GLU	3.8
1	D	69	PHE	3.6
1	D	197	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	330	ALA	3.5
1	B	96	GLU	3.4
1	A	114	ALA	3.4
1	D	195	PRO	3.2
1	B	97	LYS	3.1
1	D	84	PRO	3.1
1	A	96	GLU	3.1
1	B	114	ALA	3.0
1	B	98	VAL	3.0
1	D	77	LEU	3.0
1	D	1	MET	2.9
1	D	78	GLU	2.9
1	D	136	PRO	2.9
1	C	77	LEU	2.9
1	B	310	ALA	2.9
1	D	143	VAL	2.9
1	A	100	GLN	2.9
1	A	130	GLY	2.8
1	A	333	TYR	2.8
1	B	93	PRO	2.8
1	B	109	LYS	2.8
1	C	141	ASP	2.8
1	B	94	GLY	2.7
1	C	96	GLU	2.7
1	A	93	PRO	2.7
1	D	90	TYR	2.7
1	A	129	PRO	2.7
1	B	111	ARG	2.6
1	D	92	ALA	2.6
1	D	142	LEU	2.6
1	A	1	MET	2.5
1	D	68	PHE	2.5
1	A	206	PRO	2.5
1	A	205	ASN	2.5
1	C	282	VAL	2.5
1	D	200	GLU	2.4
1	D	202	PHE	2.4
1	C	87	ASN	2.3
1	C	140	ASP	2.3
1	D	81	TRP	2.3
1	D	72	PRO	2.2
1	C	116	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	74	GLU	2.2
1	B	279	GLN	2.1
1	D	201	VAL	2.1
1	C	113	ALA	2.1
1	D	26	GLU	2.1
1	B	331	ALA	2.1
1	C	74	GLU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	EDO	A	408	4/4	0.79	0.36	13.18	70,71,72,75	0
4	EDO	C	404	4/4	0.88	0.26	6.11	59,61,63,67	0
4	EDO	B	403	4/4	0.91	0.30	4.54	76,77,78,80	0
4	EDO	C	405	4/4	0.87	0.18	4.25	58,63,65,71	0
4	EDO	A	404	4/4	0.88	0.24	3.19	44,45,46,46	0
3	AKG	A	402	10/10	0.96	0.15	3.14	39,42,43,44	0
4	EDO	A	405	4/4	0.87	0.18	3.04	59,63,64,65	0
4	EDO	C	403	4/4	0.98	0.18	2.45	46,50,52,54	0
3	AKG	B	402	10/10	0.94	0.14	2.11	41,48,51,52	0
4	EDO	D	406	4/4	0.75	0.18	2.08	63,65,66,68	0
4	EDO	B	404	4/4	0.91	0.19	1.85	45,49,49,49	0
4	EDO	D	405	4/4	0.95	0.17	1.66	44,45,45,45	0
4	EDO	A	407	4/4	0.91	0.17	1.27	64,66,67,68	0
3	AKG	D	402	10/10	0.95	0.15	0.79	55,59,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	AKG	C	402	10/10	0.97	0.12	0.65	44,46,48,48	0
4	EDO	A	406	4/4	0.70	0.15	0.48	82,86,86,87	0
4	EDO	D	404	4/4	0.93	0.12	-0.50	67,68,68,69	0
4	EDO	A	403	4/4	0.73	0.22	-	66,71,71,72	0
2	NI	B	401	1/1	1.00	0.21	-	43,43,43,43	0
2	NI	D	401	1/1	0.99	0.19	-	47,47,47,47	0
2	NI	A	401	1/1	1.00	0.22	-	39,39,39,39	0
4	EDO	D	403	4/4	0.81	0.27	-	62,69,71,75	0
2	NI	C	401	1/1	0.99	0.20	-	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.