



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:19 PM UTC

PDB ID : 5EPA / pdb_00005epa
Title : Crystal structure of non-heme alpha ketoglutarate dependent carbocyclase
SnoK from nogalamycin biosynthesis
Authors : Selvaraj, B.; Lindqvist, Y.; Siitonen, V.; Niiranen, L.; Metsa-Ketela, M.;
Schneider, G.
Deposited on : 2015-11-11
Resolution : 2.24 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
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

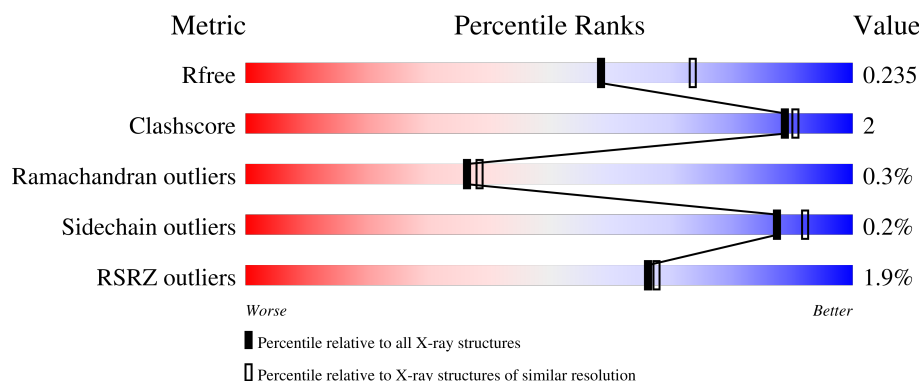
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	279	
1	B	279	
1	C	279	
1	D	279	
1	E	279	

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Mol	Chain	Length	Quality of chain
1	F	279	3% 87% • • 9%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13238 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 SnoK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			2030	1277	362	383	8			
1	B	258	Total	C	N	O	S	0	1	0
			2038	1282	365	383	8			
1	C	258	Total	C	N	O	S	0	1	0
			2038	1282	365	383	8			
1	D	258	Total	C	N	O	S	0	0	0
			2030	1277	362	383	8			
1	E	258	Total	C	N	O	S	0	2	0
			2046	1287	368	383	8			
1	F	253	Total	C	N	O	S	0	0	0
			1988	1248	357	375	8			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP Q9RN60
A	-10	ALA	-	expression tag	UNP Q9RN60
A	-9	HIS	-	expression tag	UNP Q9RN60
A	-8	HIS	-	expression tag	UNP Q9RN60
A	-7	HIS	-	expression tag	UNP Q9RN60
A	-6	HIS	-	expression tag	UNP Q9RN60
A	-5	HIS	-	expression tag	UNP Q9RN60
A	-4	HIS	-	expression tag	UNP Q9RN60
A	-3	HIS	-	expression tag	UNP Q9RN60
A	-2	ARG	-	expression tag	UNP Q9RN60
A	-1	SER	-	expression tag	UNP Q9RN60
A	0	ALA	-	expression tag	UNP Q9RN60
A	1	ASP	-	expression tag	UNP Q9RN60
B	-11	MET	-	initiating methionine	UNP Q9RN60
B	-10	ALA	-	expression tag	UNP Q9RN60
B	-9	HIS	-	expression tag	UNP Q9RN60
B	-8	HIS	-	expression tag	UNP Q9RN60

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	HIS	-	expression tag	UNP Q9RN60
B	-6	HIS	-	expression tag	UNP Q9RN60
B	-5	HIS	-	expression tag	UNP Q9RN60
B	-4	HIS	-	expression tag	UNP Q9RN60
B	-3	HIS	-	expression tag	UNP Q9RN60
B	-2	ARG	-	expression tag	UNP Q9RN60
B	-1	SER	-	expression tag	UNP Q9RN60
B	0	ALA	-	expression tag	UNP Q9RN60
B	1	ASP	-	expression tag	UNP Q9RN60
C	-11	MET	-	initiating methionine	UNP Q9RN60
C	-10	ALA	-	expression tag	UNP Q9RN60
C	-9	HIS	-	expression tag	UNP Q9RN60
C	-8	HIS	-	expression tag	UNP Q9RN60
C	-7	HIS	-	expression tag	UNP Q9RN60
C	-6	HIS	-	expression tag	UNP Q9RN60
C	-5	HIS	-	expression tag	UNP Q9RN60
C	-4	HIS	-	expression tag	UNP Q9RN60
C	-3	HIS	-	expression tag	UNP Q9RN60
C	-2	ARG	-	expression tag	UNP Q9RN60
C	-1	SER	-	expression tag	UNP Q9RN60
C	0	ALA	-	expression tag	UNP Q9RN60
C	1	ASP	-	expression tag	UNP Q9RN60
D	-11	MET	-	initiating methionine	UNP Q9RN60
D	-10	ALA	-	expression tag	UNP Q9RN60
D	-9	HIS	-	expression tag	UNP Q9RN60
D	-8	HIS	-	expression tag	UNP Q9RN60
D	-7	HIS	-	expression tag	UNP Q9RN60
D	-6	HIS	-	expression tag	UNP Q9RN60
D	-5	HIS	-	expression tag	UNP Q9RN60
D	-4	HIS	-	expression tag	UNP Q9RN60
D	-3	HIS	-	expression tag	UNP Q9RN60
D	-2	ARG	-	expression tag	UNP Q9RN60
D	-1	SER	-	expression tag	UNP Q9RN60
D	0	ALA	-	expression tag	UNP Q9RN60
D	1	ASP	-	expression tag	UNP Q9RN60
E	-11	MET	-	initiating methionine	UNP Q9RN60
E	-10	ALA	-	expression tag	UNP Q9RN60
E	-9	HIS	-	expression tag	UNP Q9RN60
E	-8	HIS	-	expression tag	UNP Q9RN60
E	-7	HIS	-	expression tag	UNP Q9RN60
E	-6	HIS	-	expression tag	UNP Q9RN60
E	-5	HIS	-	expression tag	UNP Q9RN60

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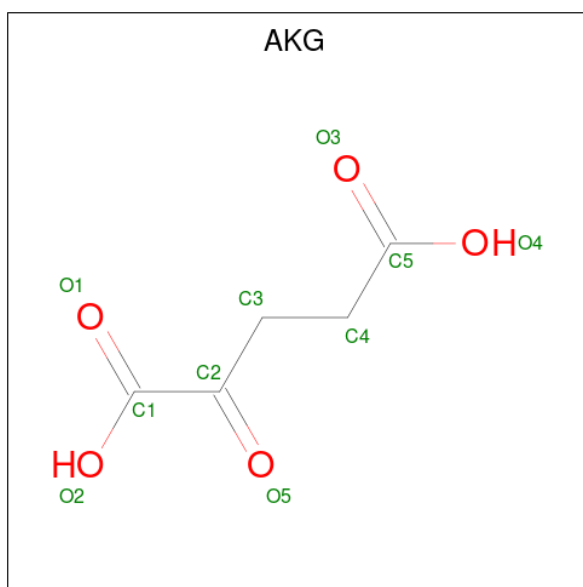
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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	expression tag	UNP Q9RN60
E	-3	HIS	-	expression tag	UNP Q9RN60
E	-2	ARG	-	expression tag	UNP Q9RN60
E	-1	SER	-	expression tag	UNP Q9RN60
E	0	ALA	-	expression tag	UNP Q9RN60
E	1	ASP	-	expression tag	UNP Q9RN60
F	-11	MET	-	initiating methionine	UNP Q9RN60
F	-10	ALA	-	expression tag	UNP Q9RN60
F	-9	HIS	-	expression tag	UNP Q9RN60
F	-8	HIS	-	expression tag	UNP Q9RN60
F	-7	HIS	-	expression tag	UNP Q9RN60
F	-6	HIS	-	expression tag	UNP Q9RN60
F	-5	HIS	-	expression tag	UNP Q9RN60
F	-4	HIS	-	expression tag	UNP Q9RN60
F	-3	HIS	-	expression tag	UNP Q9RN60
F	-2	ARG	-	expression tag	UNP Q9RN60
F	-1	SER	-	expression tag	UNP Q9RN60
F	0	ALA	-	expression tag	UNP Q9RN60
F	1	ASP	-	expression tag	UNP Q9RN60

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	D	2	Total	Mg	0	0
			2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	201	Total	O	0	0
			201	201		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	124	Total 124	O 124	0	0
5	C	181	Total 181	O 181	0	0
5	D	191	Total 191	O 191	0	0
5	E	206	Total 206	O 206	0	0
5	F	96	Total 96	O 96	0	0

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: SnoK

Chain A: 



- Molecule 1: SnoK

Chain B: 



- Molecule 1: SnoK

Chain C: 



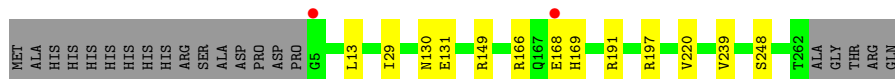
- Molecule 1: SnoK

Chain D: 

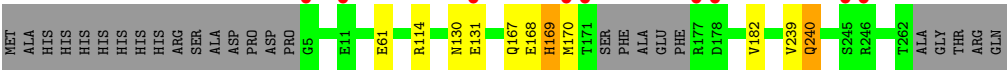
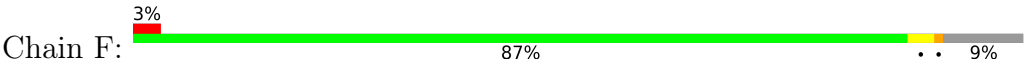


- Molecule 1: SnoK

Chain E: 



- Molecule 1: SnoK



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.01Å 83.15Å 271.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.70 – 2.24 47.70 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.0 (47.70-2.24) 92.0 (47.70-2.24)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.193 , 0.228 0.199 , 0.235	Depositor DCC
R_{free} test set	4146 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.7	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	0.94	EDS
Total number of atoms	13238	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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: MG, FE, 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	0.93	0/2083	0.94	4/2842 (0.1%)
1	B	0.91	1/2094 (0.0%)	0.92	3/2856 (0.1%)
1	C	0.92	0/2094	0.93	3/2856 (0.1%)
1	D	0.91	0/2083	0.93	1/2842 (0.0%)
1	E	0.95	0/2105	0.96	5/2870 (0.2%)
1	F	0.86	0/2038	0.88	1/2780 (0.0%)
All	All	0.91	1/12497 (0.0%)	0.92	17/17046 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	201	VAL	C-O	-5.06	1.19	1.24

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	239	VAL	N-CA-C	-12.42	96.17	110.21
1	B	239	VAL	N-CA-C	-11.85	96.82	110.21
1	A	239	VAL	N-CA-C	-11.81	96.86	110.21
1	C	239	VAL	N-CA-C	8.06	123.49	111.89
1	D	239	VAL	N-CA-C	7.94	122.84	112.76
1	F	239	VAL	N-CA-C	7.75	123.05	111.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	169	HIS	N-CA-C	-6.81	96.30	110.80
1	C	168	GLU	CB-CA-C	6.05	119.76	109.53
1	E	191	ARG	CB-CA-C	-5.83	100.81	110.14
1	A	132	LEU	N-CA-CB	5.56	119.24	110.23
1	C	191	ARG	CB-CA-C	-5.33	101.61	110.14
1	A	240	GLN	N-CA-C	5.27	118.98	112.24
1	B	29	ILE	CA-C-N	-5.12	115.08	120.66
1	B	29	ILE	C-N-CA	-5.12	115.08	120.66
1	E	29	ILE	CA-C-N	-5.09	115.11	120.66
1	E	29	ILE	C-N-CA	-5.09	115.11	120.66
1	A	168	GLU	N-CA-C	5.08	121.61	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	170	MET	Peptide

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	2030	0	1967	6	0
1	B	2038	0	1980	7	0
1	C	2038	0	1980	6	0
1	D	2030	0	1967	15	1
1	E	2046	0	1993	6	0
1	F	1988	0	1932	10	1
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
2	E	1	0	0	0	0
2	F	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	10	0	4	0	0
3	E	10	0	4	0	0
3	F	10	0	4	0	0
4	B	1	0	0	0	0
4	D	2	0	0	0	0
5	A	201	0	0	5	0
5	B	124	0	0	1	0
5	C	181	0	0	1	0
5	D	191	0	0	8	0
5	E	206	0	0	5	0
5	F	96	0	0	0	0
All	All	13238	0	11843	46	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.

All (46) 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:F:131:GLU:O	1:F:131:GLU:HG2	1.77	0.85
1:B:131:GLU:O	1:B:131:GLU:HG2	1.76	0.82
1:C:262:THR:C	5:C:461:HOH:O	2.22	0.81
1:A:262:THR:O	5:A:401:HOH:O	2.13	0.67
1:D:177:ARG:NE	5:D:403:HOH:O	2.31	0.63
1:B:131:GLU:O	1:B:131:GLU:CG	2.48	0.62
1:D:177:ARG:HE	1:D:182:VAL:HG22	1.65	0.60
1:D:177:ARG:CD	5:D:403:HOH:O	2.50	0.60
1:E:166:ARG:NH2	5:E:405:HOH:O	2.37	0.58
1:A:114:ARG:HD2	5:A:574:HOH:O	2.05	0.57
1:D:177:ARG:HD2	5:D:403:HOH:O	2.04	0.57
1:F:131:GLU:O	1:F:131:GLU:CG	2.48	0.56
1:A:46:GLU:HG2	5:A:588:HOH:O	2.06	0.55
1:A:131:GLU:N	5:A:403:HOH:O	2.27	0.55
1:F:167:GLN:HG3	1:F:182:VAL:HG11	1.90	0.54
1:E:149[A]:ARG:NH2	1:E:220:VAL:O	2.36	0.54
1:B:188:TRP:CD1	1:D:197:ARG:NH1	2.76	0.53
1:C:168:GLU:O	1:C:169:HIS:C	2.56	0.49
1:D:220:VAL:O	5:D:401:HOH:O	2.20	0.48
1:E:130:ASN:O	1:E:131:GLU:C	2.57	0.48
1:C:130:ASN:O	1:C:131:GLU:C	2.56	0.48
1:F:167:GLN:CG	1:F:182:VAL:HG21	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ARG:HH11	1:F:114:ARG:NH1	2.11	0.48
1:A:19:ARG:NH1	5:A:414:HOH:O	2.44	0.48
1:C:114:ARG:NH1	1:F:114:ARG:NH1	2.62	0.47
1:D:114:ARG:HD2	5:D:543:HOH:O	2.14	0.47
1:E:13:LEU:O	5:E:401:HOH:O	2.20	0.47
1:D:15:LYS:HE2	5:E:421:HOH:O	2.14	0.47
1:D:169:HIS:CE1	5:D:482:HOH:O	2.68	0.45
1:E:197[A]:ARG:HD2	5:E:493:HOH:O	2.15	0.45
1:D:130:ASN:O	1:D:131:GLU:C	2.59	0.45
1:F:240:GLN:HE21	1:F:240:GLN:HA	1.82	0.45
1:D:149:ARG:NH1	5:D:401:HOH:O	2.48	0.45
1:F:168:GLU:O	1:F:169:HIS:C	2.60	0.44
1:D:15:LYS:CE	5:E:421:HOH:O	2.66	0.44
1:B:130:ASN:O	1:B:131:GLU:C	2.59	0.44
1:B:168:GLU:O	1:B:169:HIS:C	2.59	0.43
1:F:130:ASN:O	1:F:131:GLU:C	2.62	0.42
1:C:167:GLN:HG2	1:C:168:GLU:O	2.20	0.42
1:B:63:GLU:HG2	5:B:505:HOH:O	2.21	0.41
1:D:15:LYS:NZ	1:E:248:SER:OG	2.42	0.41
1:A:149:ARG:HG2	1:A:149:ARG:O	2.21	0.41
1:D:5:GLY:HA3	1:D:31:ARG:NH2	2.35	0.40
1:D:256:GLU:HG3	5:D:561:HOH:O	2.20	0.40
1:B:149:ARG:HG2	1:B:149:ARG:O	2.22	0.40
1:F:167:GLN:HG3	1:F:182:VAL:HG21	2.03	0.40

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:D:50:GLU:OE1	1:F:61:GLU:OE2[1_565]	2.11	0.09

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	256/279 (92%)	250 (98%)	6 (2%)	0	100	100
1	B	257/279 (92%)	252 (98%)	4 (2%)	1 (0%)	30	30
1	C	257/279 (92%)	251 (98%)	5 (2%)	1 (0%)	30	30
1	D	256/279 (92%)	250 (98%)	6 (2%)	0	100	100
1	E	258/279 (92%)	251 (97%)	6 (2%)	1 (0%)	30	30
1	F	249/279 (89%)	244 (98%)	4 (2%)	1 (0%)	30	30
All	All	1533/1674 (92%)	1498 (98%)	31 (2%)	4 (0%)	36	38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	169	HIS
1	B	169	HIS
1	F	169	HIS
1	E	168	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	217/234 (93%)	217 (100%)	0	100	100
1	B	218/234 (93%)	217 (100%)	1 (0%)	81	86
1	C	218/234 (93%)	218 (100%)	0	100	100
1	D	217/234 (93%)	217 (100%)	0	100	100
1	E	219/234 (94%)	219 (100%)	0	100	100
1	F	213/234 (91%)	212 (100%)	1 (0%)	81	86
All	All	1302/1404 (93%)	1300 (100%)	2 (0%)	87	92

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	16	GLU
1	F	240	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	130	ASN
1	C	189	GLN
1	D	130	ASN
1	E	130	ASN
1	F	130	ASN
1	F	240	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 15 ligands modelled in this entry, 9 are monoatomic - leaving 6 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	E	301	2	9,9,9	1.75	2 (22%)	11,11,11	2.87	4 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AKG	D	302	2	9,9,9	1.98	2 (22%)	11,11,11	2.07	4 (36%)
3	AKG	B	302	2	9,9,9	1.71	3 (33%)	11,11,11	2.73	3 (27%)
3	AKG	A	301	2	9,9,9	2.01	2 (22%)	11,11,11	2.02	2 (18%)
3	AKG	F	301	2	9,9,9	1.71	1 (11%)	11,11,11	2.94	4 (36%)
3	AKG	C	301	2	9,9,9	1.71	2 (22%)	11,11,11	2.20	5 (45%)

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	E	301	2	-	0/9/9/9	-
3	AKG	D	302	2	-	0/9/9/9	-
3	AKG	B	302	2	-	2/9/9/9	-
3	AKG	A	301	2	-	0/9/9/9	-
3	AKG	F	301	2	-	0/9/9/9	-
3	AKG	C	301	2	-	0/9/9/9	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	AKG	C2-C1	-4.64	1.46	1.53
3	D	302	AKG	C2-C1	-4.02	1.47	1.53
3	E	301	AKG	C2-C1	-3.86	1.47	1.53
3	C	301	AKG	C2-C1	-3.59	1.48	1.53
3	F	301	AKG	C2-C1	-3.49	1.48	1.53
3	B	302	AKG	O1-C1	3.26	1.30	1.22
3	D	302	AKG	C3-C2	2.81	1.54	1.51
3	C	301	AKG	O1-C1	2.65	1.29	1.22
3	E	301	AKG	O1-C1	2.26	1.28	1.22
3	B	302	AKG	C2-C1	-2.21	1.50	1.53
3	A	301	AKG	O4-C5	-2.11	1.23	1.30
3	B	302	AKG	C3-C2	2.04	1.53	1.51

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	301	AKG	O1-C1-C2	-7.32	112.70	121.81
3	E	301	AKG	O1-C1-C2	-7.20	112.85	121.81
3	B	302	AKG	O1-C1-C2	-7.18	112.87	121.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	302	AKG	O5-C2-C1	-4.42	113.35	119.67
3	A	301	AKG	O5-C2-C1	-3.92	114.07	119.67
3	C	301	AKG	O1-C1-C2	-3.91	116.95	121.81
3	F	301	AKG	C3-C2-C1	3.89	122.46	115.86
3	F	301	AKG	O5-C2-C1	-3.71	114.36	119.67
3	E	301	AKG	O5-C2-C1	-3.55	114.60	119.67
3	A	301	AKG	C3-C2-C1	3.24	121.37	115.86
3	C	301	AKG	O5-C2-C1	-3.11	115.22	119.67
3	C	301	AKG	C3-C2-C1	2.86	120.72	115.86
3	F	301	AKG	O2-C1-C2	2.75	121.22	113.59
3	B	302	AKG	O5-C2-C1	-2.69	115.82	119.67
3	D	302	AKG	O5-C2-C3	2.61	126.77	121.17
3	C	301	AKG	O2-C1-O1	2.56	129.99	123.90
3	B	302	AKG	C3-C2-C1	2.51	120.12	115.86
3	D	302	AKG	O1-C1-C2	-2.45	118.76	121.81
3	D	302	AKG	C3-C2-C1	2.36	119.88	115.86
3	E	301	AKG	O5-C2-C3	2.36	126.23	121.17
3	E	301	AKG	O4-C5-C4	2.17	120.86	114.00
3	C	301	AKG	C4-C3-C2	2.08	116.81	112.91

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	AKG	C3-C4-C5-O3
3	B	302	AKG	C3-C4-C5-O4

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

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	258/279 (92%)	-0.22	1 (0%) 88 90	22, 30, 45, 62	0
1	B	258/279 (92%)	0.08	12 (4%) 36 35	15, 34, 64, 92	1 (0%)
1	C	258/279 (92%)	-0.17	3 (1%) 76 78	16, 32, 48, 71	1 (0%)
1	D	258/279 (92%)	-0.20	2 (0%) 82 84	22, 31, 46, 57	0
1	E	258/279 (92%)	-0.31	2 (0%) 82 84	15, 27, 42, 65	2 (0%)
1	F	253/279 (90%)	0.29	9 (3%) 46 46	27, 42, 67, 87	0
All	All	1543/1674 (92%)	-0.09	29 (1%) 66 68	15, 32, 56, 92	4 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	174	ALA	4.8
1	A	5	GLY	3.9
1	B	173	PHE	3.7
1	B	176	PHE	3.7
1	F	5	GLY	3.3
1	B	5	GLY	3.2
1	C	168	GLU	3.1
1	F	246	ARG	3.1
1	C	5	GLY	3.1
1	E	168	GLU	3.0
1	B	131	GLU	2.9
1	B	172	SER	2.9
1	B	175	GLU	2.8
1	B	168	GLU	2.8
1	F	170	MET	2.8
1	F	171	THR	2.7
1	B	132	LEU	2.7
1	E	5	GLY	2.6
1	F	131	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	177	ARG	2.5
1	B	171	THR	2.5
1	F	178	ASP	2.5
1	B	170	MET	2.3
1	C	15	LYS	2.3
1	D	5	GLY	2.2
1	B	240	GLN	2.1
1	F	11	GLU	2.1
1	F	245	SER	2.0
1	D	262	THR	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
4	MG	D	303	1/1	0.93	0.03	36,36,36,36	0
3	AKG	A	301	10/10	0.94	0.09	12,13,14,16	0
4	MG	D	304	1/1	0.94	0.08	41,41,41,41	0
2	FE	D	301	1/1	0.95	0.20	27,27,27,27	0
3	AKG	C	301	10/10	0.96	0.09	10,12,14,14	0
3	AKG	D	302	10/10	0.96	0.07	10,14,18,18	0
4	MG	B	303	1/1	0.97	0.03	30,30,30,30	0
3	AKG	B	302	10/10	0.97	0.10	11,12,14,14	0
3	AKG	F	301	10/10	0.97	0.12	13,14,15,15	0
2	FE	C	300	1/1	0.98	0.18	25,25,25,25	0
3	AKG	E	301	10/10	0.98	0.08	11,12,14,15	0
2	FE	B	301	1/1	0.99	0.18	22,22,22,22	0
2	FE	E	300	1/1	0.99	0.16	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FE	F	300	1/1	0.99	0.23	21,21,21,21	0
2	FE	A	300	1/1	0.99	0.18	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.