



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 05:45 PM UTC

PDB ID : 2GP5 / pdb_00002gp5
Title : Crystal structure of catalytic core domain of jmjd2A complexed with alpha-Ketoglutarate
Authors : Chen, Z.; Zang, J.; Whetstine, J.; Hong, X.; Davrazou, F.; Kutateladze, T.G.; Simpson, M.; Dai, S.; Hagman, J.; Shi, Y.; Zhang, G.
Deposited on : 2006-04-16
Resolution : 2.28 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

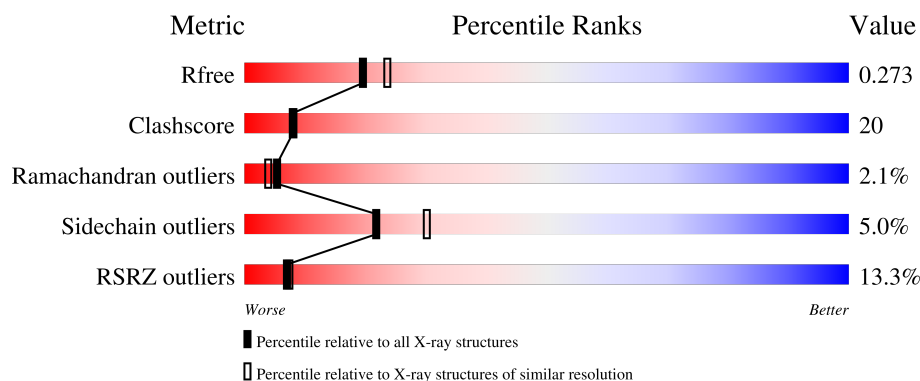
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	349	12% 62% 33% ..
1	B	349	14% 62% 31% ...

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5773 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 Jumonji domain-containing protein 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	0	0
			2848	1838	480	515	15			
1	B	337	Total	C	N	O	S	0	0	0
			2776	1796	469	496	15			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is FE (II) ION (CCD ID: FE2) (formula: Fe).

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

- Molecule 4 is 2-OXOGLUTARIC ACID (CCD ID: AKG) (formula: C₅H₆O₅).



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

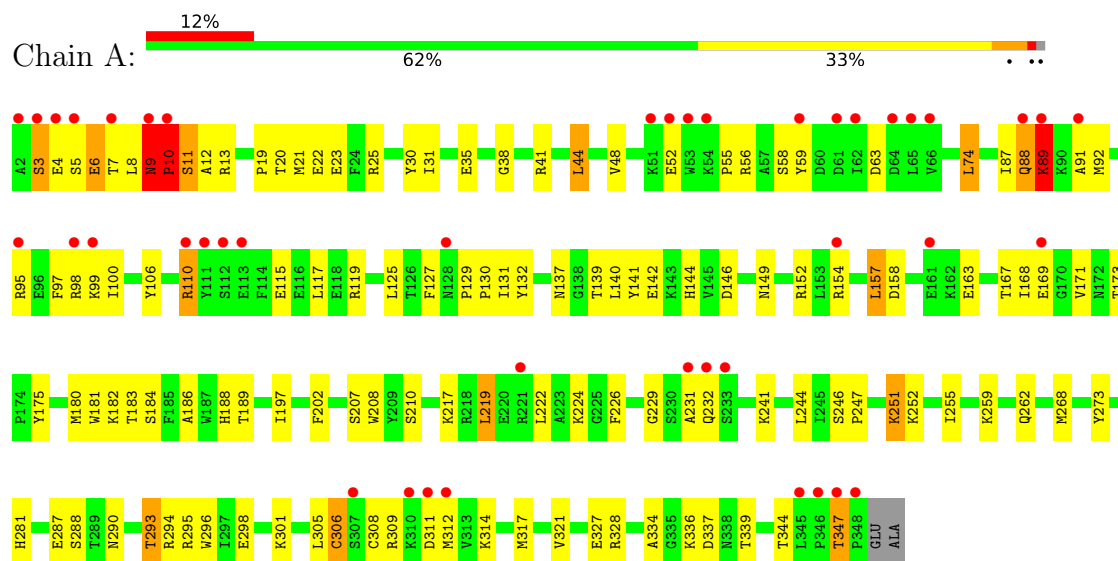
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	64	Total	O	0	0
			64	64		
5	B	61	Total	O	0	0
			61	61		

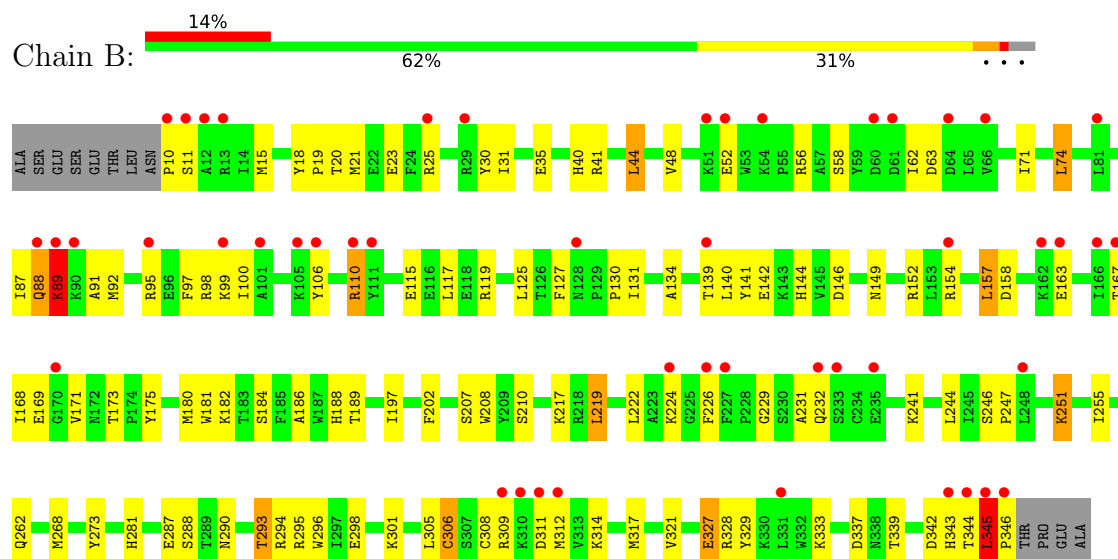
3 Residue-property plots

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: Jumonji domain-containing protein 2A



• Molecule 1: Jumonji domain-containing protein 2A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.11Å 149.52Å 57.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.67 – 2.28 49.67 – 2.28	Depositor EDS
% Data completeness (in resolution range)	80.9 (49.67-2.28) 81.0 (49.67-2.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.236 , 0.285 0.224 , 0.273	Depositor DCC
R_{free} test set	1177 reflections (3.48%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5773	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.02% 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: ZN, AKG, FE2

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	0/2934	0.96	9/3972 (0.2%)
1	B	0.44	0/2861	0.95	8/3870 (0.2%)
All	All	0.45	0/5795	0.95	17/7842 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	345	LEU	N-CA-C	10.73	133.52	109.81
1	A	9	ASN	CA-C-N	7.15	128.78	119.84
1	A	9	ASN	C-N-CA	7.15	128.78	119.84
1	A	11	SER	N-CA-C	-7.11	104.64	113.38
1	A	89	LYS	N-CA-C	-6.96	95.98	110.80
1	B	89	LYS	N-CA-C	-6.84	96.24	110.80
1	B	157	LEU	N-CA-C	-6.76	104.29	112.54
1	A	157	LEU	N-CA-C	-6.38	104.60	112.38
1	A	189	THR	N-CA-C	-6.29	100.90	110.14
1	B	184	SER	N-CA-C	6.13	118.50	109.24
1	B	189	THR	N-CA-C	-6.05	100.55	109.81
1	B	163	GLU	N-CA-C	5.83	117.44	111.14
1	A	184	SER	N-CA-C	5.68	117.60	109.14
1	A	163	GLU	N-CA-C	5.67	117.26	111.14
1	A	183	THR	N-CA-C	-5.46	101.57	110.20
1	B	71	ILE	N-CA-C	5.20	115.60	108.12
1	B	134	ALA	N-CA-C	5.06	118.02	110.52

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	2848	0	2774	118	0
1	B	2776	0	2710	104	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	10	0	4	1	0
4	B	10	0	4	0	0
5	A	64	0	0	3	0
5	B	61	0	0	0	0
All	All	5773	0	5492	218	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 20.

All (218) 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:A:139:THR:HG22	1:A:141:TYR:H	1.25	1.01
1:B:139:THR:HG22	1:B:141:TYR:H	1.26	0.98
1:A:252:LYS:HD3	1:B:15:MET:HE3	1.46	0.97
1:A:9:ASN:O	1:A:11:SER:N	2.11	0.83
1:B:329:TYR:CE2	1:B:333:LYS:HD2	2.16	0.80
1:B:229:GLY:HA2	1:B:232:GLN:HE21	1.47	0.80
1:B:293:THR:HG22	1:B:295:ARG:H	1.47	0.79
1:A:293:THR:HG22	1:A:295:ARG:H	1.50	0.77
1:A:229:GLY:HA2	1:A:232:GLN:HE21	1.51	0.74
1:B:95:ARG:O	1:B:99:LYS:HG2	1.87	0.74
1:B:171:VAL:HA	1:B:290:ASN:HD22	1.53	0.74
1:A:317:MET:HE2	1:A:317:MET:HA	1.69	0.73
1:B:317:MET:HE2	1:B:317:MET:HA	1.71	0.73
1:B:41:ARG:NE	1:B:344:THR:HG23	2.04	0.72
1:A:95:ARG:O	1:A:99:LYS:HG2	1.89	0.71
1:B:40:HIS:NE2	1:B:346:PRO:HD2	2.05	0.71
1:B:342:ASP:HB3	1:B:345:LEU:HD12	1.71	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:MET:HE1	1:A:100:ILE:HD12	1.73	0.71
1:B:328:ARG:NH2	1:B:339:THR:OG1	2.25	0.70
1:A:44:LEU:HD22	1:A:268:MET:HE3	1.74	0.69
1:A:110:ARG:CD	1:A:110:ARG:H	2.05	0.69
1:B:41:ARG:CD	1:B:344:THR:HG23	2.22	0.69
1:B:344:THR:O	1:B:344:THR:HG22	1.93	0.69
1:B:110:ARG:CD	1:B:110:ARG:H	2.05	0.68
1:A:305:LEU:HD22	1:A:312:MET:HE1	1.75	0.68
1:A:139:THR:HG23	1:A:287:GLU:OE1	1.94	0.68
1:B:20:THR:OG1	1:B:23:GLU:HG3	1.94	0.67
1:A:8:LEU:HD11	1:A:13:ARG:O	1.94	0.67
1:B:251:LYS:HB2	1:B:251:LYS:NZ	2.10	0.67
1:A:171:VAL:HA	1:A:290:ASN:HD22	1.60	0.66
1:A:251:LYS:HB2	1:A:251:LYS:NZ	2.10	0.66
1:A:188:HIS:CD2	1:A:241:LYS:HE2	2.30	0.66
1:B:63:ASP:HB3	1:B:95:ARG:HB2	1.77	0.66
1:B:293:THR:HG22	1:B:295:ARG:N	2.11	0.66
1:B:74:LEU:HD12	1:B:87:ILE:HD12	1.78	0.65
1:B:305:LEU:HD22	1:B:312:MET:HE1	1.78	0.65
1:B:139:THR:HG23	1:B:287:GLU:OE1	1.96	0.65
1:B:19:PRO:HB3	1:B:30:TYR:CZ	2.32	0.65
1:A:20:THR:OG1	1:A:23:GLU:HG3	1.96	0.65
1:B:92:MET:HE2	1:B:97:PHE:HA	1.78	0.64
1:A:63:ASP:HB3	1:A:95:ARG:HB2	1.78	0.64
1:B:224:LYS:HG3	1:B:231:ALA:HB1	1.80	0.64
1:A:19:PRO:HB3	1:A:30:TYR:CZ	2.34	0.63
1:B:44:LEU:HD22	1:B:268:MET:HE3	1.79	0.63
1:B:92:MET:HE2	1:B:97:PHE:CA	2.27	0.63
1:B:41:ARG:HD3	1:B:344:THR:HG23	1.81	0.63
1:B:127:PHE:O	1:B:182:LYS:NZ	2.32	0.62
1:A:5:SER:HB2	1:A:344:THR:HG21	1.82	0.62
1:B:40:HIS:CE1	1:B:346:PRO:HG2	2.33	0.62
1:B:92:MET:HE1	1:B:100:ILE:HD12	1.82	0.62
1:A:224:LYS:HG3	1:A:231:ALA:HB1	1.81	0.61
1:A:130:PRO:CB	1:A:180:MET:HE2	2.30	0.61
1:A:293:THR:HG22	1:A:295:ARG:N	2.16	0.61
1:B:110:ARG:H	1:B:110:ARG:NE	1.97	0.61
1:A:110:ARG:H	1:A:110:ARG:NE	1.99	0.61
1:A:127:PHE:O	1:A:182:LYS:NZ	2.34	0.61
1:B:342:ASP:HB3	1:B:345:LEU:CD1	2.31	0.60
1:A:8:LEU:O	1:A:9:ASN:C	2.44	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:TRP:HH2	1:B:317:MET:HE1	1.66	0.60
1:A:41:ARG:HD3	1:A:344:THR:HG23	1.84	0.59
1:A:296:TRP:HH2	1:A:317:MET:HE1	1.67	0.59
1:A:328:ARG:HH21	1:A:337:ASP:CG	2.10	0.59
1:B:130:PRO:CB	1:B:180:MET:HE2	2.31	0.59
1:A:130:PRO:C	1:A:131:ILE:HD12	2.26	0.59
1:A:181:TRP:CE2	1:A:182:LYS:HG3	2.37	0.59
1:B:188:HIS:CD2	1:B:241:LYS:HE2	2.38	0.59
1:A:5:SER:HB2	1:A:344:THR:CG2	2.33	0.59
1:A:74:LEU:HD12	1:A:87:ILE:HD12	1.85	0.59
1:B:181:TRP:CE2	1:B:182:LYS:HG3	2.37	0.59
1:A:251:LYS:HB2	1:A:251:LYS:HZ2	1.68	0.58
1:A:44:LEU:CD2	1:A:268:MET:HE3	2.33	0.58
1:A:92:MET:HE2	1:A:97:PHE:HA	1.85	0.58
1:A:222:LEU:HD11	1:A:226:PHE:CE1	2.39	0.57
1:B:222:LEU:HD11	1:B:226:PHE:CE1	2.39	0.57
1:B:130:PRO:C	1:B:131:ILE:HD12	2.29	0.57
1:B:329:TYR:CZ	1:B:333:LYS:HD2	2.39	0.57
1:A:110:ARG:H	1:A:110:ARG:HD2	1.70	0.57
1:B:110:ARG:H	1:B:110:ARG:HD2	1.71	0.56
1:B:224:LYS:HG3	1:B:231:ALA:CB	2.35	0.56
1:B:328:ARG:HH21	1:B:337:ASP:CG	2.14	0.56
1:B:169:GLU:HA	1:B:173:THR:OG1	2.04	0.56
1:A:224:LYS:HG3	1:A:231:ALA:CB	2.36	0.56
1:B:106:TYR:HB3	1:B:180:MET:HE3	1.88	0.56
1:A:106:TYR:HB3	1:A:180:MET:CE	2.35	0.55
1:B:171:VAL:HA	1:B:290:ASN:ND2	2.21	0.55
1:A:106:TYR:HB3	1:A:180:MET:HE3	1.87	0.55
1:B:44:LEU:CD2	1:B:268:MET:HE3	2.36	0.55
1:B:251:LYS:HB2	1:B:251:LYS:HZ2	1.72	0.54
1:B:56:ARG:HD3	1:B:58:SER:O	2.07	0.54
1:A:19:PRO:HD2	1:A:48:VAL:O	2.09	0.53
1:A:171:VAL:HA	1:A:290:ASN:ND2	2.23	0.53
1:A:301:LYS:HD3	1:A:321:VAL:HG22	1.91	0.53
1:A:8:LEU:HD13	1:A:12:ALA:HA	1.90	0.53
1:B:19:PRO:HD2	1:B:48:VAL:O	2.08	0.53
1:A:131:ILE:HD12	1:A:131:ILE:N	2.24	0.52
1:A:222:LEU:CD2	1:A:255:ILE:HD12	2.39	0.52
1:B:106:TYR:HB3	1:B:180:MET:CE	2.39	0.52
1:A:328:ARG:NH2	1:A:339:THR:OG1	2.42	0.52
1:B:139:THR:HG22	1:B:140:LEU:N	2.25	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:CYS:HB3	1:A:312:MET:SD	2.50	0.52
1:B:168:ILE:HB	1:B:171:VAL:HB	1.92	0.52
1:A:106:TYR:CG	1:A:180:MET:HE1	2.46	0.52
1:A:186:ALA:HA	1:A:244:LEU:HD23	1.91	0.52
1:A:169:GLU:HA	1:A:173:THR:OG1	2.10	0.51
1:A:252:LYS:HD3	1:B:15:MET:CE	2.32	0.51
1:B:301:LYS:HD3	1:B:321:VAL:HG22	1.93	0.51
1:A:217:LYS:HD2	1:A:273:TYR:OH	2.10	0.51
1:A:11:SER:O	1:A:12:ALA:C	2.53	0.51
1:B:56:ARG:HA	1:B:142:GLU:HG3	1.92	0.51
1:A:295:ARG:HB2	1:A:347:THR:OG1	2.10	0.50
1:B:293:THR:CG2	1:B:294:ARG:N	2.73	0.50
1:A:139:THR:HG22	1:A:140:LEU:N	2.25	0.50
1:A:293:THR:CG2	1:A:294:ARG:N	2.73	0.50
1:B:306:CYS:HB3	1:B:312:MET:SD	2.51	0.50
1:A:229:GLY:O	1:A:232:GLN:HG2	2.12	0.50
1:A:252:LYS:CD	1:B:15:MET:HE3	2.32	0.50
1:A:334:ALA:CB	1:A:336:LYS:HE2	2.42	0.50
1:B:106:TYR:CG	1:B:180:MET:HE1	2.47	0.50
1:A:8:LEU:HD13	1:A:41:ARG:HB2	1.93	0.50
1:B:74:LEU:HD12	1:B:87:ILE:CD1	2.42	0.49
1:B:92:MET:CE	1:B:97:PHE:HA	2.42	0.49
1:A:92:MET:HE2	1:A:97:PHE:CA	2.42	0.49
1:B:40:HIS:HE2	1:B:346:PRO:HD2	1.74	0.49
1:B:217:LYS:HD2	1:B:273:TYR:OH	2.12	0.49
1:B:229:GLY:O	1:B:232:GLN:HG2	2.12	0.49
1:A:56:ARG:HA	1:A:142:GLU:HG3	1.95	0.48
1:B:131:ILE:HD12	1:B:131:ILE:N	2.28	0.48
1:B:186:ALA:HA	1:B:244:LEU:HD23	1.94	0.48
1:B:197:ILE:O	1:B:288:SER:HB2	2.14	0.48
1:A:41:ARG:CD	1:A:344:THR:HG23	2.43	0.48
1:A:334:ALA:HB3	1:A:336:LYS:HE2	1.96	0.47
1:B:125:LEU:HA	1:B:182:LYS:HD2	1.95	0.47
1:A:5:SER:OG	1:A:6:GLU:N	2.47	0.47
1:A:308:CYS:SG	1:A:309:ARG:N	2.87	0.47
1:A:219:LEU:HA	1:A:255:ILE:HD13	1.97	0.47
1:B:222:LEU:CD2	1:B:255:ILE:HD12	2.44	0.47
1:A:125:LEU:HA	1:A:182:LYS:HD2	1.96	0.47
1:A:9:ASN:C	1:A:11:SER:H	2.22	0.47
1:B:95:ARG:CZ	1:B:95:ARG:HB3	2.45	0.47
1:B:142:GLU:HB2	1:B:144:HIS:CE1	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:SER:OG	1:A:281:HIS:HE1	1.98	0.46
1:A:21:MET:HG3	1:A:25:ARG:HH21	1.79	0.46
1:A:56:ARG:HD3	1:A:58:SER:O	2.14	0.46
1:A:44:LEU:HD12	1:A:210:SER:HB2	1.97	0.46
1:A:197:ILE:O	1:A:288:SER:HB2	2.15	0.46
1:A:259:LYS:HB2	5:A:552:HOH:O	2.15	0.46
1:B:298:GLU:OE2	1:B:301:LYS:HE2	2.15	0.46
1:A:95:ARG:CZ	1:A:95:ARG:HB3	2.46	0.46
1:A:222:LEU:HD23	1:A:255:ILE:HD12	1.97	0.46
1:B:40:HIS:CE1	1:B:346:PRO:CG	2.99	0.46
1:B:208:TRP:HE1	1:B:262:GLN:HE21	1.64	0.45
1:A:88:GLN:C	1:A:89:LYS:O	2.59	0.45
1:A:56:ARG:HD2	1:A:59:TYR:CD2	2.51	0.45
1:A:182:LYS:HB2	1:A:182:LYS:HE3	1.87	0.45
1:B:21:MET:HG3	1:B:25:ARG:HH21	1.82	0.45
1:B:35:GLU:HB3	1:B:346:PRO:HG3	1.99	0.45
1:B:115:GLU:HG2	1:B:119:ARG:NH1	2.32	0.45
1:A:141:TYR:CE2	1:A:149:ASN:HA	2.51	0.45
1:B:88:GLN:C	1:B:89:LYS:O	2.59	0.45
1:B:146:ASP:OD1	1:B:152:ARG:NH2	2.44	0.45
1:B:63:ASP:OD2	1:B:98:ARG:NH1	2.50	0.45
1:B:329:TYR:CE2	1:B:333:LYS:CD	2.95	0.45
1:A:202:PHE:CD1	1:A:202:PHE:C	2.94	0.44
1:B:305:LEU:CD1	1:B:314:LYS:HG2	2.47	0.44
1:A:3:SER:O	1:A:5:SER:N	2.51	0.44
1:A:7:THR:HG22	5:A:546:HOH:O	2.18	0.44
1:A:106:TYR:CD2	1:A:180:MET:HE1	2.52	0.44
1:A:154:ARG:HA	1:A:158:ASP:OD2	2.17	0.44
1:B:141:TYR:CE2	1:B:149:ASN:HA	2.52	0.44
1:B:44:LEU:HD12	1:B:210:SER:HB2	1.99	0.44
1:A:208:TRP:HE1	1:A:262:GLN:NE2	2.15	0.44
1:B:31:ILE:O	1:B:35:GLU:HG3	2.17	0.44
1:B:92:MET:HE2	1:B:97:PHE:N	2.33	0.44
1:A:130:PRO:HB3	1:A:180:MET:HE2	1.98	0.44
1:B:219:LEU:HA	1:B:255:ILE:HD13	1.99	0.43
1:A:168:ILE:HB	1:A:171:VAL:HB	2.00	0.43
1:A:31:ILE:O	1:A:35:GLU:HG3	2.18	0.43
1:B:344:THR:O	1:B:344:THR:CG2	2.63	0.43
1:A:298:GLU:OE2	1:A:301:LYS:HE2	2.18	0.43
1:A:115:GLU:HG2	1:A:119:ARG:NH1	2.34	0.43
1:B:208:TRP:HE1	1:B:262:GLN:NE2	2.15	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:LEU:HD12	1:A:87:ILE:CD1	2.47	0.43
1:B:74:LEU:CD1	1:B:87:ILE:HD12	2.48	0.43
1:A:142:GLU:HB2	1:A:144:HIS:CE1	2.54	0.43
1:A:305:LEU:CD1	1:A:314:LYS:HG2	2.49	0.43
1:A:63:ASP:OD2	1:A:98:ARG:NH1	2.52	0.42
1:B:106:TYR:CD2	1:B:180:MET:HE1	2.54	0.42
1:B:296:TRP:CH2	1:B:317:MET:HE1	2.50	0.42
1:A:9:ASN:C	1:A:11:SER:N	2.77	0.42
1:B:10:PRO:HB2	1:B:11:SER:H	1.55	0.42
1:B:154:ARG:HA	1:B:158:ASP:OD2	2.20	0.42
1:A:246:SER:HB2	1:A:247:PRO:HD2	2.02	0.42
1:B:207:SER:OG	1:B:281:HIS:HE1	2.02	0.42
1:B:262:GLN:CD	1:B:268:MET:HG2	2.45	0.42
1:A:8:LEU:HD21	1:A:13:ARG:H	1.84	0.42
1:A:296:TRP:CH2	1:A:317:MET:HE1	2.53	0.42
1:B:308:CYS:SG	1:B:309:ARG:N	2.93	0.42
1:A:9:ASN:HA	1:A:10:PRO:HD2	1.87	0.42
1:A:20:THR:C	1:A:22:GLU:N	2.77	0.42
1:A:132:TYR:OH	4:A:403:AKG:O4	2.37	0.42
1:A:222:LEU:HD22	1:A:255:ILE:HD12	2.02	0.42
1:A:208:TRP:HE1	1:A:262:GLN:HE21	1.65	0.41
1:A:328:ARG:NH2	1:A:337:ASP:OD2	2.48	0.41
1:A:251:LYS:HG2	1:B:18:TYR:CE1	2.55	0.41
1:A:55:PRO:O	1:A:142:GLU:HG3	2.20	0.41
1:B:327:GLU:CD	1:B:327:GLU:H	2.26	0.41
1:A:137:ASN:HD21	1:A:169:GLU:CD	2.29	0.41
1:B:246:SER:HB2	1:B:247:PRO:HD2	2.02	0.41
1:A:8:LEU:O	1:A:10:PRO:N	2.53	0.41
1:A:146:ASP:OD1	1:A:152:ARG:NH2	2.46	0.41
1:A:3:SER:C	1:A:5:SER:N	2.78	0.41
1:A:8:LEU:HD12	1:A:38:GLY:O	2.20	0.41
1:B:202:PHE:CD1	1:B:202:PHE:C	2.98	0.41
1:A:139:THR:CG2	1:A:141:TYR:HB2	2.51	0.41
1:A:317:MET:HE2	1:A:317:MET:CA	2.46	0.41
1:B:222:LEU:HD23	1:B:255:ILE:HD12	2.03	0.41
1:A:129:PRO:HG3	5:A:526:HOH:O	2.22	0.40
1:B:74:LEU:CD1	1:B:87:ILE:CD1	2.99	0.40

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	345/349 (99%)	315 (91%)	21 (6%)	9 (3%)	4	2
1	B	335/349 (96%)	309 (92%)	21 (6%)	5 (2%)	8	7
All	All	680/698 (97%)	624 (92%)	42 (6%)	14 (2%)	5	4

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	PRO
1	A	91	ALA
1	B	91	ALA
1	B	343	HIS
1	A	3	SER
1	A	4	GLU
1	A	6	GLU
1	A	311	ASP
1	B	311	ASP
1	A	9	ASN
1	A	89	LYS
1	B	89	LYS
1	A	347	THR
1	B	62	ILE

5.3.2 Protein sidechains [i](#)

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	305/306 (100%)	290 (95%)	15 (5%)	22	31
1	B	296/306 (97%)	281 (95%)	15 (5%)	21	29
All	All	601/612 (98%)	571 (95%)	30 (5%)	22	30

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	PRO
1	A	44	LEU
1	A	52	GLU
1	A	74	LEU
1	A	88	GLN
1	A	110	ARG
1	A	117	LEU
1	A	157	LEU
1	A	167	THR
1	A	175	TYR
1	A	219	LEU
1	A	251	LYS
1	A	293	THR
1	A	306	CYS
1	A	327	GLU
1	B	44	LEU
1	B	52	GLU
1	B	74	LEU
1	B	88	GLN
1	B	110	ARG
1	B	117	LEU
1	B	157	LEU
1	B	167	THR
1	B	175	TYR
1	B	219	LEU
1	B	251	LYS
1	B	293	THR
1	B	306	CYS
1	B	327	GLU
1	B	345	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	ASN
1	A	128	ASN
1	A	232	GLN
1	A	262	GLN
1	A	281	HIS
1	A	290	ASN
1	B	88	GLN
1	B	124	ASN
1	B	128	ASN
1	B	215	HIS
1	B	232	GLN
1	B	262	GLN
1	B	281	HIS
1	B	290	ASN

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 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	$\# Z > 2$
4	AKG	B	403	3	9,9,9	1.35	1 (11%)	11,11,11	1.25	2 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	AKG	A	403	3	9,9,9	1.16	1 (11%)	11,11,11	1.39	2 (18%)

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
4	AKG	B	403	3	-	0/9/9/9	-
4	AKG	A	403	3	-	0/9/9/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	403	AKG	C2-C1	-3.26	1.48	1.53
4	A	403	AKG	C2-C1	-2.56	1.49	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	403	AKG	C3-C2-C1	2.35	119.85	115.86
4	A	403	AKG	O2-C1-C2	2.13	119.48	113.59
4	B	403	AKG	C3-C2-C1	2.08	119.39	115.86
4	B	403	AKG	O2-C1-C2	2.06	119.30	113.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	403	AKG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	347/349 (99%)	0.70	43 (12%) 8 8	21, 43, 99, 152	0
1	B	337/349 (96%)	0.71	48 (14%) 6 6	21, 44, 95, 116	0
All	All	684/698 (97%)	0.70	91 (13%) 7 7	21, 44, 96, 152	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	348	PRO	6.6
1	B	10	PRO	6.5
1	A	347	THR	6.0
1	B	312	MET	5.2
1	A	2	ALA	5.1
1	B	11	SER	5.1
1	B	346	PRO	4.7
1	A	9	ASN	4.2
1	A	312	MET	4.1
1	B	106	TYR	4.0
1	A	10	PRO	4.0
1	B	345	LEU	3.9
1	B	310	LYS	3.7
1	A	112	SER	3.7
1	A	95	ARG	3.6
1	A	310	LYS	3.5
1	A	62	ILE	3.5
1	A	311	ASP	3.4
1	B	110	ARG	3.4
1	B	311	ASP	3.4
1	A	3	SER	3.4
1	B	128	ASN	3.4
1	B	89	LYS	3.4
1	B	166	ILE	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	227	PHE	3.3
1	A	91	ALA	3.3
1	B	111	TYR	3.3
1	A	54	LYS	3.2
1	B	61	ASP	3.2
1	B	95	ARG	3.1
1	A	89	LYS	3.1
1	A	345	LEU	3.1
1	A	7	THR	3.1
1	A	52	GLU	3.0
1	B	163	GLU	3.0
1	A	110	ARG	3.0
1	B	331	LEU	3.0
1	A	98	ARG	3.0
1	B	90	LYS	3.0
1	B	60	ASP	3.0
1	A	51	LYS	2.9
1	A	232	GLN	2.9
1	A	307	SER	2.9
1	A	65	LEU	2.9
1	A	5	SER	2.8
1	A	66	VAL	2.8
1	A	99	LYS	2.7
1	B	235	GLU	2.7
1	B	248	LEU	2.6
1	B	51	LYS	2.6
1	B	139	THR	2.6
1	B	233	SER	2.6
1	A	221	ARG	2.6
1	A	346	PRO	2.6
1	A	233	SER	2.6
1	B	226	PHE	2.6
1	B	99	LYS	2.5
1	B	88	GLN	2.5
1	B	154	ARG	2.5
1	A	61	ASP	2.5
1	B	170	GLY	2.5
1	B	343	HIS	2.5
1	B	162	LYS	2.5
1	B	81	LEU	2.4
1	B	66	VAL	2.4
1	A	161	GLU	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	101	ALA	2.4
1	B	167	THR	2.4
1	A	88	GLN	2.4
1	A	59	TYR	2.3
1	A	231	ALA	2.3
1	B	12	ALA	2.3
1	B	13	ARG	2.3
1	B	224	LYS	2.3
1	B	344	THR	2.3
1	B	64	ASP	2.2
1	B	54	LYS	2.2
1	A	53	TRP	2.2
1	A	128	ASN	2.2
1	B	309	ARG	2.1
1	A	4	GLU	2.1
1	B	232	GLN	2.1
1	A	154	ARG	2.1
1	B	105	LYS	2.1
1	A	64	ASP	2.1
1	B	52	GLU	2.1
1	B	25	ARG	2.1
1	A	111	TYR	2.1
1	A	113	GLU	2.0
1	B	29	ARG	2.0
1	A	169	GLU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
4	AKG	A	403	10/10	0.76	0.22	22,22,22,23	10
4	AKG	B	403	10/10	0.78	0.16	22,22,22,22	10
2	ZN	B	401	1/1	0.98	0.03	39,39,39,39	1
3	FE2	B	402	1/1	0.99	0.07	33,33,33,33	0
2	ZN	A	401	1/1	0.99	0.05	40,40,40,40	1
3	FE2	A	402	1/1	0.99	0.07	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.