



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2024 – 08:14 pm BST

PDB ID : 2XGX
Title : Crystal structure of transcription factor NtcA from *Synechococcus elongatus* (mercury derivative)
Authors : Llacer, J.L.; Castells, M.A.; Rubio, V.
Deposited on : 2010-06-08
Resolution : 2.85 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

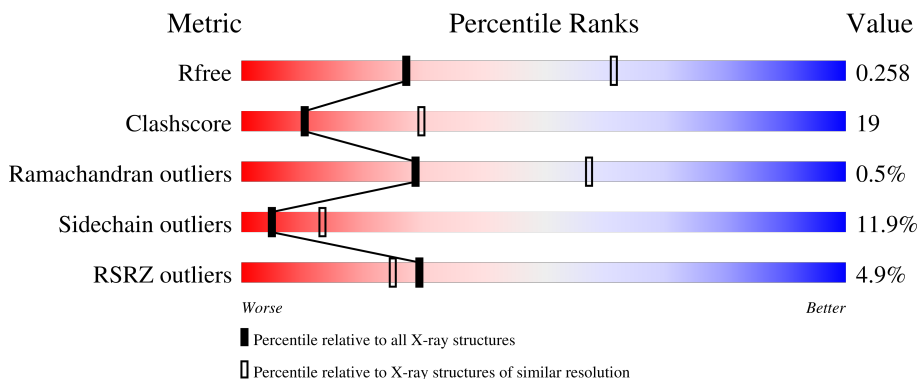
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	130704	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	222	
1	B	222	

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
2	AKG	B	519	-	-	X	-

2 Entry composition [i](#)

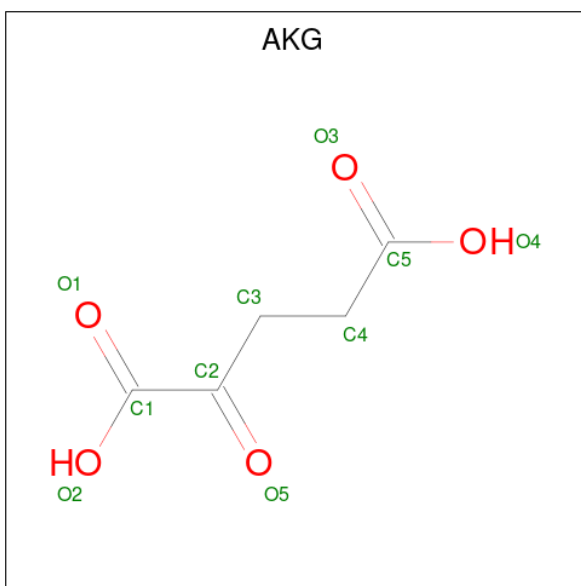
There are 5 unique types of molecules in this entry. The entry contains 3362 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLOBAL NITROGEN REGULATOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	212	Total 1661	C 1068	N 285	O 302	S 6	0	1	0
1	B	213	Total 1656	C 1064	N 288	O 298	S 6	0	1	0

- Molecule 2 is 2-OXOGLUTARIC ACID (three-letter code: AKG) (formula: C₅H₆O₅).

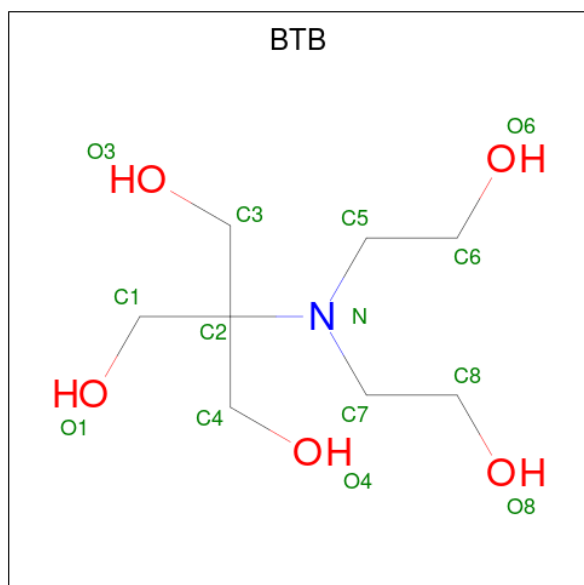


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 10	C 5	O 5	0	0
2	B	1	Total 10	C 5	O 5	0	0

- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

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

- Molecule 4 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 14 8 1 5	0	0

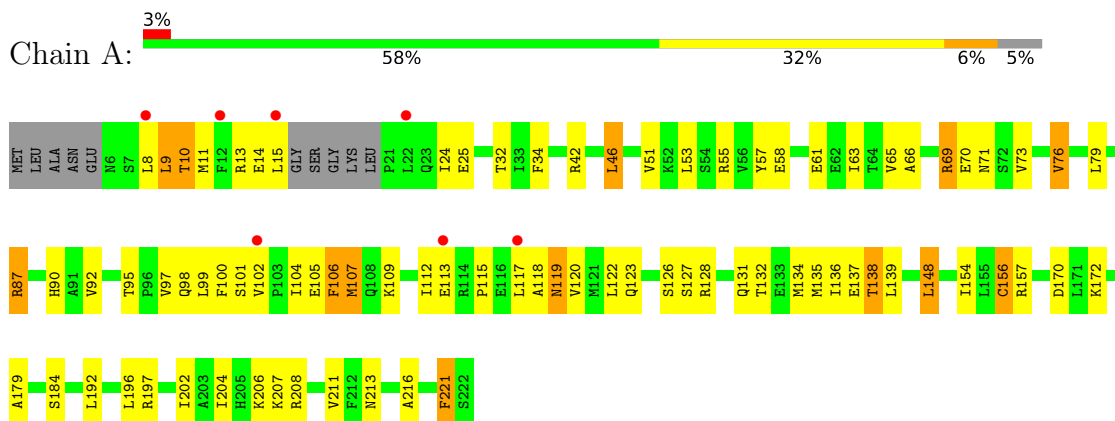
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	7	Total O 7 7	0	0
5	B	2	Total O 2 2	0	0

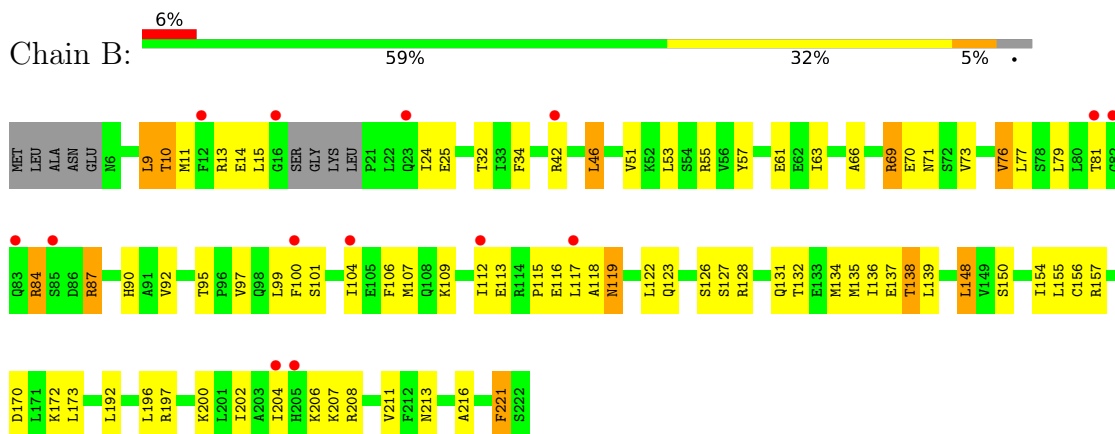
3 Residue-property plots [i](#)

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: GLOBAL NITROGEN REGULATOR



• Molecule 1: GLOBAL NITROGEN REGULATOR



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.39Å 69.97Å 149.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.85 61.40 – 2.85	Depositor EDS
% Data completeness (in resolution range)	97.1 (50.00-2.85) 97.1 (61.40-2.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.211 , 0.245 0.230 , 0.258	Depositor DCC
R_{free} test set	837 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	63.5	Xtrriage
Anisotropy	0.484	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 67.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.031 for k,h,-l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3362	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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: AKG, HG, BTB

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	0.51	0/1691	0.68	0/2286
1	B	0.47	0/1687	0.64	0/2280
All	All	0.49	0/3378	0.66	0/4566

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

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	1661	0	1709	71	0
1	B	1656	0	1695	66	0
2	A	10	0	4	3	0
2	B	10	0	4	5	0
3	A	1	0	0	1	0
3	B	1	0	0	0	0
4	A	14	0	19	2	0
5	A	7	0	0	1	0
5	B	2	0	0	0	0
All	All	3362	0	3431	126	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 19.

All (126) 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:B:79:LEU:HD23	1:B:104:ILE:HD11	1.44	0.99
1:A:79:LEU:HD23	1:A:104:ILE:HD11	1.43	0.98
1:A:46:LEU:HD12	1:A:51:VAL:HG23	1.46	0.94
1:A:122:LEU:HD23	1:B:122:LEU:HD23	1.47	0.93
1:B:46:LEU:HD12	1:B:51:VAL:HG23	1.50	0.91
1:A:11:MET:CB	1:A:117:LEU:HD13	2.10	0.81
1:B:11:MET:CB	1:B:117:LEU:HD13	2.10	0.80
1:A:15:LEU:HD12	1:A:102:VAL:HG21	1.66	0.76
1:A:128:ARG:HH11	1:A:128:ARG:HG2	1.52	0.75
1:B:128:ARG:HG2	1:B:128:ARG:HH11	1.52	0.73
1:B:127:SER:O	1:B:131:GLN:HG3	1.89	0.72
1:B:77:LEU:HB3	2:B:519:AKG:O1	1.90	0.71
1:A:156:CYS:SG	3:A:801:HG:HG	2.11	0.69
1:B:53:LEU:HD13	2:B:519:AKG:H41	1.75	0.69
1:B:79:LEU:HD23	1:B:104:ILE:CD1	2.21	0.68
1:A:122:LEU:CD2	1:B:122:LEU:HD23	2.22	0.68
2:A:519:AKG:O2	5:A:2007:HOH:O	2.12	0.67
1:B:46:LEU:CD2	1:B:70:GLU:HA	2.25	0.67
1:A:79:LEU:HD23	1:A:104:ILE:CD1	2.21	0.67
1:A:53:LEU:HD13	2:A:519:AKG:H41	1.76	0.67
1:A:90:HIS:CE1	1:A:92:VAL:CG2	2.82	0.63
1:A:55:ARG:HD2	1:B:137:GLU:OE1	1.98	0.63
1:A:46:LEU:CD2	1:A:70:GLU:HA	2.29	0.63
1:A:46:LEU:HD12	1:A:51:VAL:CG2	2.27	0.60
1:A:127:SER:O	1:A:131:GLN:HG3	2.02	0.59
1:A:99:LEU:C	1:A:99:LEU:HD12	2.23	0.59
1:B:42:ARG:NH1	1:B:101:SER:OG	2.35	0.58
1:A:136:ILE:HD11	1:B:135:MET:HB3	1.84	0.58
1:A:42:ARG:NH1	1:A:101:SER:OG	2.34	0.58
1:A:34:PHE:CD1	1:A:87:ARG:HG2	2.39	0.58
1:A:122:LEU:HD23	1:B:122:LEU:CD2	2.29	0.58
1:A:137:GLU:OE1	1:B:55:ARG:HD2	2.05	0.57
1:A:138:THR:HG21	1:A:154:ILE:HD12	1.88	0.55
1:B:34:PHE:CD1	1:B:87:ARG:HG2	2.41	0.55
1:A:197:ARG:CZ	1:A:204:ILE:HD12	2.37	0.55
1:B:57:TYR:CE2	1:B:63:ILE:HD12	2.42	0.54
1:B:115:PRO:O	1:B:118:ALA:N	2.40	0.54
1:B:46:LEU:HD23	1:B:46:LEU:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:LEU:HD12	1:A:13:ARG:HH21	1.73	0.53
1:A:135:MET:HB3	1:B:136:ILE:HD11	1.90	0.53
1:A:148:LEU:HD12	1:A:192:LEU:HB3	1.91	0.53
1:A:24:ILE:HD12	1:A:100:PHE:CZ	2.44	0.52
1:A:115:PRO:O	1:A:118:ALA:N	2.41	0.52
1:A:15:LEU:CD1	1:A:102:VAL:HG21	2.39	0.52
1:B:99:LEU:HD12	1:B:99:LEU:C	2.29	0.52
1:A:76:VAL:HG13	1:B:126:SER:HB3	1.92	0.51
1:B:197:ARG:CZ	1:B:204:ILE:HD12	2.40	0.51
1:B:128:ARG:NH2	2:B:519:AKG:O3	2.44	0.51
1:B:46:LEU:HD12	1:B:51:VAL:CG2	2.31	0.50
1:A:170:ASP:OD1	1:A:208:ARG:NH1	2.44	0.50
1:A:126:SER:HB3	1:B:76:VAL:HG13	1.94	0.49
1:A:132:THR:HG22	1:B:132:THR:HG22	1.94	0.49
1:B:9:LEU:HD12	1:B:13:ARG:HH21	1.77	0.49
4:A:1223:BTB:H52	4:A:1223:BTB:O3	2.12	0.49
1:A:57:TYR:CE2	1:A:63:ILE:HD12	2.47	0.49
1:B:81:THR:HG22	1:B:84:ARG:HE	1.77	0.49
1:A:172:LYS:HG3	1:A:207:LYS:HB3	1.94	0.49
1:B:172:LYS:HG3	1:B:207:LYS:HB3	1.94	0.48
1:B:170:ASP:OD1	1:B:208:ARG:NH1	2.47	0.48
1:B:76:VAL:N	2:B:519:AKG:O5	2.47	0.48
1:B:119:ASN:O	1:B:123:GLN:HG3	2.13	0.47
1:A:122:LEU:CD2	1:B:122:LEU:CD2	2.92	0.47
1:B:24:ILE:HD12	1:B:100:PHE:CZ	2.49	0.47
1:A:14:GLU:OE1	1:A:14:GLU:N	2.48	0.47
1:A:53:LEU:CD1	2:A:519:AKG:H41	2.44	0.47
1:B:109:LYS:HA	1:B:112:ILE:HD12	1.97	0.47
1:B:134:MET:O	1:B:138:THR:HG23	2.15	0.47
1:A:46:LEU:HD23	1:A:46:LEU:O	2.14	0.46
1:B:14:GLU:N	1:B:14:GLU:OE1	2.48	0.46
1:B:148:LEU:HD12	1:B:192:LEU:HB3	1.98	0.46
1:B:173:LEU:O	1:B:207:LYS:HG3	2.15	0.46
1:A:25:GLU:OE2	1:A:101:SER:HB3	2.14	0.46
1:B:46:LEU:HD23	1:B:46:LEU:C	2.36	0.46
1:A:95:THR:O	1:A:97:VAL:HG23	2.15	0.46
1:A:196:LEU:HB3	1:A:202:ILE:HG12	1.97	0.46
1:A:138:THR:HG21	1:A:154:ILE:CD1	2.45	0.45
1:B:90:HIS:CE1	1:B:92:VAL:CG2	2.99	0.45
1:B:113:GLU:O	1:B:115:PRO:HD3	2.17	0.45
1:A:53:LEU:HD12	1:A:66:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:THR:O	1:A:14:GLU:OE1	2.35	0.45
1:B:10:THR:O	1:B:14:GLU:OE1	2.35	0.45
1:B:196:LEU:HB3	1:B:202:ILE:HG12	1.99	0.45
1:A:128:ARG:HH11	1:A:128:ARG:CG	2.26	0.44
1:B:138:THR:HB	1:B:150:SER:OG	2.16	0.44
1:A:99:LEU:HD12	1:A:99:LEU:O	2.17	0.44
1:B:213:ASN:ND2	1:B:216:ALA:HB2	2.32	0.44
1:A:135:MET:HB3	1:B:136:ILE:CD1	2.48	0.43
1:A:46:LEU:HD21	1:A:70:GLU:HA	2.00	0.43
1:A:104:ILE:O	1:A:107:MET:N	2.52	0.43
1:A:119:ASN:O	1:A:123:GLN:HG3	2.19	0.43
1:B:69:ARG:HG2	1:B:70:GLU:N	2.32	0.43
1:A:104:ILE:HG23	1:A:105:GLU:N	2.33	0.43
1:A:102:VAL:CG1	1:A:106:PHE:HB3	2.49	0.43
1:B:138:THR:HG21	1:B:154:ILE:HD12	2.00	0.43
1:B:155:LEU:HD13	1:B:173:LEU:HD11	2.01	0.43
1:A:90:HIS:CE1	1:A:92:VAL:HG22	2.53	0.42
1:A:221:PHE:CD2	1:A:221:PHE:N	2.86	0.42
1:A:109:LYS:HA	1:A:112:ILE:HD12	2.00	0.42
1:B:46:LEU:HD21	1:B:70:GLU:HA	1.98	0.42
1:B:53:LEU:HD12	1:B:66:ALA:HB3	2.02	0.42
1:A:8:LEU:CD2	1:A:120:VAL:HG12	2.49	0.42
1:A:126:SER:CB	1:B:76:VAL:HG13	2.50	0.42
1:A:69:ARG:HG2	1:A:70:GLU:N	2.34	0.42
1:B:73:VAL:O	1:B:128:ARG:CD	2.68	0.42
1:B:119:ASN:C	1:B:119:ASN:HD22	2.23	0.42
1:A:46:LEU:HD23	1:A:46:LEU:C	2.40	0.42
1:A:179:ALA:HB1	1:A:184:SER:O	2.20	0.42
1:A:213:ASN:ND2	1:A:216:ALA:HB2	2.35	0.42
1:B:221:PHE:N	1:B:221:PHE:CD2	2.88	0.42
1:B:115:PRO:O	1:B:116:GLU:C	2.58	0.41
1:A:136:ILE:CD1	1:B:135:MET:HB3	2.49	0.41
1:B:95:THR:O	1:B:97:VAL:HG23	2.20	0.41
1:A:8:LEU:HD23	1:A:120:VAL:HG12	2.03	0.41
1:A:128:ARG:HG2	1:A:128:ARG:NH1	2.29	0.41
1:B:25:GLU:OE2	1:B:101:SER:HB3	2.19	0.41
1:A:69:ARG:O	1:A:70:GLU:C	2.59	0.41
1:B:113:GLU:C	1:B:115:PRO:HD3	2.40	0.41
1:A:25:GLU:O	1:A:98:GLN:HA	2.20	0.41
4:A:1223:BTB:O4	4:A:1223:BTB:H81	2.21	0.41
1:B:128:ARG:HH11	1:B:128:ARG:CG	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:THR:HG21	1:B:154:ILE:CD1	2.51	0.41
1:A:73:VAL:O	1:A:128:ARG:CD	2.68	0.40
1:B:128:ARG:HH21	2:B:519:AKG:C5	2.33	0.40
1:A:134:MET:O	1:A:138:THR:HG23	2.21	0.40
1:A:15:LEU:HD12	1:A:102:VAL:CG2	2.44	0.40
1:A:113:GLU:O	1:A:115:PRO:HD3	2.21	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	209/222 (94%)	197 (94%)	12 (6%)	0	100	100
1	B	210/222 (95%)	195 (93%)	13 (6%)	2 (1%)	15	40
All	All	419/444 (94%)	392 (94%)	25 (6%)	2 (0%)	29	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	84	ARG
1	B	15	LEU

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	183/194 (94%)	161 (88%)	22 (12%)	5	13
1	B	180/194 (93%)	159 (88%)	21 (12%)	5	14
All	All	363/388 (94%)	320 (88%)	43 (12%)	5	14

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	10	THR
1	A	32	THR
1	A	46	LEU
1	A	58	GLU
1	A	61	GLU
1	A	65	VAL
1	A	69	ARG
1	A	71	ASN
1	A	76	VAL
1	A	87	ARG
1	A	106	PHE
1	A	107	MET
1	A	119	ASN
1	A	138	THR
1	A	139	LEU
1	A	148	LEU
1	A	156	CYS
1	A	157	ARG
1	A	206	LYS
1	A	211	VAL
1	A	221	PHE
1	B	9	LEU
1	B	10	THR
1	B	32	THR
1	B	46	LEU
1	B	61	GLU
1	B	69	ARG
1	B	71	ASN
1	B	76	VAL
1	B	87	ARG
1	B	106	PHE
1	B	107	MET
1	B	119	ASN
1	B	138	THR

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Mol	Chain	Res	Type
1	B	139	LEU
1	B	148	LEU
1	B	156	CYS
1	B	157	ARG
1	B	200	LYS
1	B	206	LYS
1	B	211	VAL
1	B	221	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	HIS
1	A	119	ASN
1	A	123	GLN
1	A	220	GLN
1	B	90	HIS
1	B	119	ASN
1	B	123	GLN
1	B	220	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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
2	AKG	B	519	-	9,9,9	1.35	1 (11%)	11,11,11	2.71	5 (45%)
2	AKG	A	519	-	9,9,9	1.19	1 (11%)	11,11,11	2.30	3 (27%)
4	BTB	A	1223	-	13,13,13	1.17	2 (15%)	7,16,16	1.36	1 (14%)

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
2	AKG	B	519	-	-	5/9/9/9	-
2	AKG	A	519	-	-	4/9/9/9	-
4	BTB	A	1223	-	-	5/21/21/21	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1223	BTB	C5-N	2.58	1.51	1.48
2	B	519	AKG	C2-C1	-2.56	1.50	1.53
4	A	1223	BTB	C7-N	2.35	1.51	1.48
2	A	519	AKG	C2-C1	-2.23	1.50	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	519	AKG	C4-C3-C2	-5.36	102.94	113.03
2	B	519	AKG	O1-C1-C2	-5.11	114.89	121.72
2	A	519	AKG	O1-C1-C2	-4.47	115.75	121.72
2	A	519	AKG	C4-C3-C2	-4.16	105.19	113.03
2	B	519	AKG	C3-C2-C1	3.16	121.83	115.97
2	A	519	AKG	C3-C4-C5	-2.89	107.38	113.60
4	A	1223	BTB	C8-C7-N	2.53	121.45	111.59
2	B	519	AKG	O3-C5-C4	-2.26	115.82	123.08
2	B	519	AKG	O2-C1-C2	2.04	119.55	113.97

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	519	AKG	C1-C2-C3-C4
2	B	519	AKG	C1-C2-C3-C4
4	A	1223	BTB	C6-C5-N-C7
4	A	1223	BTB	C8-C7-N-C2
2	A	519	AKG	C2-C3-C4-C5
4	A	1223	BTB	O1-C1-C2-N
4	A	1223	BTB	N-C5-C6-O6
2	A	519	AKG	C3-C4-C5-O3
2	A	519	AKG	C3-C4-C5-O4
2	B	519	AKG	C3-C4-C5-O4
2	B	519	AKG	C3-C4-C5-O3
2	B	519	AKG	O5-C2-C3-C4
2	B	519	AKG	C2-C3-C4-C5
4	A	1223	BTB	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	519	AKG	5	0
2	A	519	AKG	3	0
4	A	1223	BTB	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 [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	212/222 (95%)	0.33	7 (3%) 46 41	34, 54, 100, 123	0
1	B	213/222 (95%)	0.68	14 (6%) 18 14	40, 69, 107, 126	0
All	All	425/444 (95%)	0.51	21 (4%) 29 25	34, 60, 103, 126	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	82	GLY	5.8
1	B	83	GLN	5.7
1	B	81	THR	5.6
1	B	204	ILE	4.3
1	B	112	ILE	4.1
1	B	12	PHE	3.8
1	B	85	SER	3.5
1	A	8	LEU	3.5
1	B	205[A]	HIS	3.3
1	B	117	LEU	3.3
1	B	23	GLN	3.3
1	A	15	LEU	3.0
1	A	102	VAL	2.9
1	B	16	GLY	2.8
1	B	104	ILE	2.7
1	B	100	PHE	2.7
1	A	117	LEU	2.6
1	A	113	GLU	2.4
1	A	12	PHE	2.1
1	B	42	ARG	2.0
1	A	22	LEU	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 monosaccharides 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(\AA^2)	Q<0.9
2	AKG	A	519	10/10	0.91	0.23	39,42,43,45	0
4	BTB	A	1223	14/14	0.91	0.24	85,86,87,87	0
2	AKG	B	519	10/10	0.93	0.25	56,58,61,62	0
3	HG	A	801	1/1	0.95	0.24	89,89,89,89	1
3	HG	B	801	1/1	0.99	0.31	91,91,91,91	1

6.5 Other polymers [i](#)

There are no such residues in this entry.