



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 30, 2020 – 10:35 AM BST

PDB ID : 3HBR
Title : Crystal structure of OXA-48 beta-lactamase
Authors : Calderone, V.; Mangani, S.; Benvenuti, M.; Rossolini, G.M.; Docquier, J.D.
Deposited on : 2009-05-05
Resolution : 1.90 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
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) : 2.13

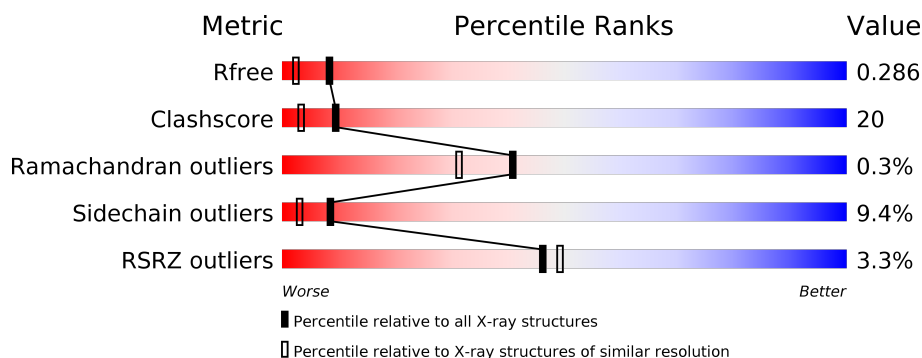
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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	265	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 61%, yellow 23%, orange 6%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 61% 23% 6% 9% </div> </div>
1	B	265	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 60%, yellow 26%, orange 1%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 60% 26% • 9% </div> </div>
1	C	265	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, green 55%, yellow 29%, orange 5%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 55% 29% 5% 9% </div> </div>
1	D	265	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 7%, green 56%, yellow 31%, orange 1%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 7% 56% 31% • 10% </div> </div>

2 Entry composition [i](#)

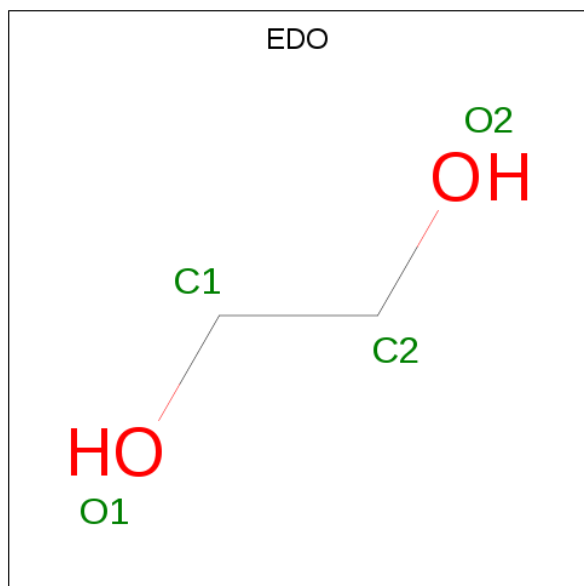
There are 3 unique types of molecules in this entry. The entry contains 8635 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 OXA-48.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	0
			1965	1253	345	360	7			
1	B	241	Total	C	N	O	S	0	0	0
			1974	1257	348	362	7			
1	C	240	Total	C	N	O	S	0	0	0
			1967	1253	347	360	7			
1	D	239	Total	C	N	O	S	0	0	0
			1951	1244	341	359	7			

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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

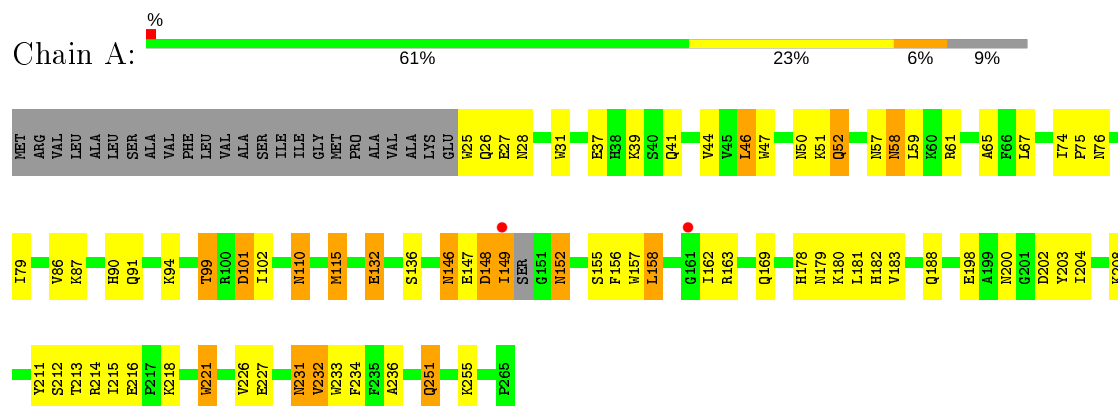
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	234	Total	O	0	0
			234	234		
3	B	209	Total	O	0	0
			209	209		
3	C	160	Total	O	0	0
			160	160		
3	D	159	Total	O	0	0
			159	159		

3 Residue-property plots

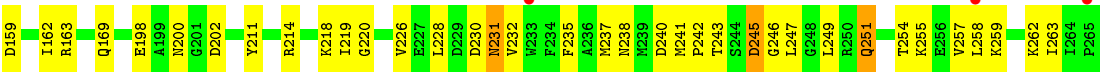
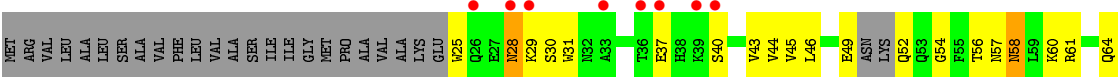
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: OXA-48





● Molecule 1: OXA-48



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.70Å 107.19Å 80.79Å 90.00° 111.04° 90.00°	Depositor
Resolution (Å)	30.51 – 1.90 30.51 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.51-1.90) 88.6 (30.51-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.27 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.217 , 0.286 0.217 , 0.286	Depositor DCC
R_{free} test set	7101 reflections (9.00%)	wwPDB-VP
Wilson B-factor (Å ²)	14.4	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.35$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	0.165 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8635	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, KCX

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	0.78	0/2000	0.82	1/2703 (0.0%)
1	B	0.78	0/2010	0.83	2/2718 (0.1%)
1	C	0.68	0/2002	0.74	1/2705 (0.0%)
1	D	0.68	0/1986	0.73	1/2686 (0.0%)
All	All	0.73	0/7998	0.78	5/10812 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	158	LEU	CA-CB-CG	6.52	130.29	115.30
1	A	115	MET	CG-SD-CE	-6.19	90.30	100.20
1	B	96	ASP	CB-CG-OD1	6.05	123.75	118.30
1	B	115	MET	CG-SD-CE	-5.89	90.77	100.20
1	C	158	LEU	CA-CB-CG	5.59	128.15	115.30

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	1965	0	1915	70	0
1	B	1974	0	1926	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1967	0	1918	83	0
1	D	1951	0	1895	75	0
2	A	4	0	6	0	0
2	B	8	0	12	4	0
2	C	4	0	6	1	0
3	A	234	0	0	19	0
3	B	209	0	0	22	0
3	C	160	0	0	18	0
3	D	159	0	0	23	0
All	All	8635	0	7678	304	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 (304) 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:74:ILE:HD11	3:A:364:HOH:O	1.40	1.18
1:C:170:ILE:HG23	3:C:386:HOH:O	1.47	1.11
1:C:67:LEU:O	1:C:221:TRP:HZ3	1.35	1.09
1:A:236:ALA:HB2	3:A:456:HOH:O	1.53	1.08
2:B:267:EDO:H21	3:B:399:HOH:O	1.54	1.07
1:A:67:LEU:HD11	1:A:215:ILE:HD12	1.37	1.06
1:D:228:LEU:HD12	3:D:408:HOH:O	1.63	0.98
1:A:52:GLN:HG3	1:A:52:GLN:O	1.65	0.93
1:D:230:ASP:HB3	3:D:386:HOH:O	1.67	0.92
1:B:85:VAL:HG21	3:B:442:HOH:O	1.68	0.92
1:C:67:LEU:O	1:C:221:TRP:CZ3	2.25	0.89
1:A:155:SER:HA	3:A:460:HOH:O	1.74	0.86
1:B:178:HIS:HB2	1:B:180:LYS:HE3	1.59	0.85
1:D:243:THR:HB	3:D:424:HOH:O	1.76	0.85
1:C:52:GLN:HG3	1:C:52:GLN:O	1.76	0.85
1:C:87:LYS:H	1:C:91:GLN:HE22	1.22	0.84
1:B:94:LYS:NZ	1:B:94:LYS:HB3	1.93	0.83
1:A:251:GLN:HE21	1:A:251:GLN:H	1.25	0.83
1:C:104:THR:CG2	1:C:117:TYR:HB3	2.08	0.82
1:B:175:LYS:HG2	1:B:180:LYS:HZ2	1.43	0.82
1:D:251:GLN:H	1:D:251:GLN:HE21	1.24	0.82
1:A:67:LEU:O	1:A:221:TRP:HZ3	1.62	0.81
1:C:152:ASN:HB2	1:C:155:SER:OG	1.80	0.81
1:B:100:ARG:H	1:B:106:ASN:HD21	1.27	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:31:TRP:HB2	1:D:57:ASN:HB3	1.64	0.79
1:C:93:PHE:O	3:C:425:HOH:O	1.99	0.79
1:A:146:ASN:HD21	1:A:162:ILE:HA	1.49	0.78
1:A:226:VAL:HG13	1:A:233:TRP:HB2	1.65	0.78
1:A:87:LYS:H	1:A:91:GLN:NE2	1.82	0.77
1:B:174:ARG:NH2	3:B:421:HOH:O	2.19	0.75
1:A:208:LYS:HB3	3:A:364:HOH:O	1.87	0.75
1:A:236:ALA:HB1	3:A:481:HOH:O	1.87	0.74
1:A:146:ASN:HB2	3:A:463:HOH:O	1.87	0.74
1:A:87:LYS:H	1:A:91:GLN:HE22	1.35	0.73
1:D:200:ASN:HB3	1:D:202:ASP:H	1.53	0.73
1:B:255:LYS:HE3	3:B:351:HOH:O	1.89	0.73
1:B:130:ILE:HG13	3:B:442:HOH:O	1.88	0.72
1:C:200:ASN:HB3	1:C:202:ASP:H	1.56	0.71
1:A:208:LYS:CB	3:A:364:HOH:O	2.39	0.71
1:C:110:ASN:ND2	1:C:113:THR:H	1.88	0.71
1:B:50:ASN:H	1:B:231:ASN:HD21	1.39	0.71
1:A:50:ASN:H	1:A:231:ASN:HD21	1.40	0.70
1:C:104:THR:HG21	1:C:117:TYR:HB3	1.71	0.70
1:D:129:GLN:O	1:D:134:ARG:NH1	2.25	0.70
1:D:157:TRP:CD1	1:D:158:LEU:HD13	2.27	0.70
1:A:200:ASN:HB3	1:A:202:ASP:H	1.56	0.69
1:C:143:ASP:O	2:C:266:EDO:H21	1.92	0.68
1:B:34:HIS:O	1:B:38:HIS:HD2	1.76	0.68
1:A:149:ILE:HD13	1:A:149:ILE:H	1.59	0.68
1:C:26:GLN:HE21	1:C:28:ASN:HD21	1.42	0.68
1:C:87:LYS:H	1:C:91:GLN:NE2	1.90	0.68
1:C:52:GLN:HB2	3:C:269:HOH:O	1.95	0.67
1:B:175:LYS:HG2	1:B:180:LYS:NZ	2.08	0.67
1:C:110:ASN:C	1:C:110:ASN:HD22	1.98	0.67
1:D:100:ARG:H	1:D:106:ASN:HD21	1.42	0.67
1:D:251:GLN:NE2	1:D:251:GLN:H	1.93	0.67
1:C:251:GLN:O	1:C:255:LYS:HG3	1.94	0.66
1:C:29:LYS:O	1:C:32:ASN:HB2	1.96	0.66
1:C:215:ILE:O	3:C:333:HOH:O	2.12	0.66
1:B:175:LYS:HA	1:B:180:LYS:HZ2	1.60	0.65
1:B:25:TRP:N	2:B:267:EDO:HO2	1.95	0.65
1:C:66:PHE:HB2	1:C:221:TRP:CH2	2.32	0.65
1:D:87:LYS:HE2	3:D:410:HOH:O	1.98	0.64
1:B:146:ASN:HD21	1:B:162:ILE:HA	1.61	0.64
1:B:158:LEU:HB2	3:B:431:HOH:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:218:LYS:HE3	1:D:242:PRO:HA	1.78	0.63
1:D:52:GLN:OE1	3:D:425:HOH:O	2.15	0.63
1:D:243:THR:HG23	1:D:245:ASP:HB2	1.80	0.63
1:B:80:ALA:HB1	1:B:85:VAL:HG22	1.81	0.63
1:A:90:HIS:HE1	3:B:376:HOH:O	1.83	0.62
1:A:146:ASN:C	1:A:146:ASN:HD22	2.02	0.62
1:C:41:GLN:HG3	1:C:240:ASP:OD2	2.00	0.62
1:A:152:ASN:HB3	1:A:156:PHE:HB3	1.80	0.62
1:C:50:ASN:H	1:C:231:ASN:HD21	1.48	0.62
1:C:264:ILE:CD1	3:C:274:HOH:O	2.48	0.61
1:C:52:GLN:CG	1:C:52:GLN:O	2.47	0.61
1:C:251:GLN:HE21	1:C:251:GLN:H	1.48	0.60
1:B:218:LYS:HG2	3:B:417:HOH:O	2.02	0.60
1:A:149:ILE:CD1	1:A:149:ILE:H	2.15	0.60
1:C:102:ILE:HG22	1:C:104:THR:HB	1.84	0.60
1:A:101:ASP:OD1	1:A:101:ASP:N	2.35	0.60
1:D:159:ASP:OD2	1:D:214:ARG:NH1	2.32	0.59
1:B:251:GLN:HE21	1:B:251:GLN:H	1.48	0.59
1:D:198:GLU:OE2	3:D:415:HOH:O	2.17	0.59
1:D:251:GLN:N	1:D:251:GLN:HE21	1.97	0.59
1:A:67:LEU:HD11	1:A:215:ILE:CD1	2.25	0.59
3:A:273:HOH:O	1:C:262:LYS:HE3	2.02	0.59
1:B:56:THR:CG2	1:B:59:LEU:HD23	2.32	0.59
1:A:67:LEU:O	1:A:221:TRP:CZ3	2.52	0.59
1:A:146:ASN:HD22	1:A:147:GLU:N	2.00	0.58
1:D:101:ASP:HB2	3:D:391:HOH:O	2.03	0.58
1:A:216:GLU:OE1	1:A:218:LYS:NZ	2.32	0.58
1:A:226:VAL:CG1	1:A:233:TRP:HB2	2.32	0.58
1:D:98:GLN:HG2	3:D:385:HOH:O	2.04	0.58
1:B:251:GLN:HG2	2:B:266:EDO:H11	1.85	0.58
1:C:106:ASN:N	1:C:106:ASN:HD22	2.02	0.57
1:C:124:GLN:HB3	1:C:154:ASP:HB2	1.86	0.57
1:D:58:ASN:HD22	1:D:58:ASN:C	2.05	0.57
1:C:58:ASN:C	1:C:58:ASN:HD22	2.07	0.57
1:B:221:TRP:CD1	1:B:237:MET:O	2.57	0.57
1:C:264:ILE:HD11	3:C:274:HOH:O	2.04	0.57
1:D:246:GLY:O	1:D:249:LEU:HG	2.04	0.57
1:D:87:LYS:H	1:D:91:GLN:NE2	2.03	0.57
1:D:103:ALA:HB3	3:D:326:HOH:O	2.04	0.57
1:C:175:LYS:HA	1:C:180:LYS:HE2	1.85	0.56
1:A:213:THR:HA	1:A:218:LYS:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:GLY:O	1:B:238:ASN:HA	2.05	0.56
1:C:133:ALA:O	1:C:137:LYS:HG2	2.05	0.56
1:A:204:ILE:HB	1:A:227:GLU:HB2	1.88	0.56
1:B:175:LYS:CG	1:B:180:LYS:HZ2	2.15	0.56
1:D:31:TRP:CZ3	1:D:56:THR:HA	2.41	0.55
1:B:31:TRP:HB2	1:B:57:ASN:HB3	1.88	0.55
1:B:58:ASN:ND2	1:B:61:ARG:H	2.05	0.55
1:C:26:GLN:NE2	1:C:28:ASN:HD21	2.04	0.55
1:D:44:VAL:HG11	1:D:257:VAL:HG21	1.89	0.55
1:B:58:ASN:C	1:B:58:ASN:HD22	2.09	0.55
1:D:219:ILE:HG22	3:D:388:HOH:O	2.05	0.55
1:A:148:ASP:H	1:A:162:ILE:HG13	1.72	0.54
1:B:255:LYS:CG	3:B:351:HOH:O	2.55	0.54
1:C:146:ASN:ND2	1:C:162:ILE:HD12	2.22	0.54
1:A:178:HIS:HB2	1:A:180:LYS:HE3	1.88	0.54
1:A:99:THR:CG2	3:A:350:HOH:O	2.56	0.54
1:B:28:ASN:HD22	1:B:28:ASN:C	2.10	0.54
1:B:124:GLN:O	1:B:128:ARG:HG3	2.07	0.54
1:B:94:LYS:HZ2	1:B:94:LYS:HB3	1.69	0.54
1:C:205:ILE:HD11	3:C:366:HOH:O	2.06	0.54
1:C:33:ALA:HA	1:C:36:THR:HB	1.89	0.54
1:C:134:ARG:HG3	3:C:313:HOH:O	2.08	0.54
1:D:146:ASN:HD21	1:D:162:ILE:HA	1.73	0.54
1:A:31:TRP:HB2	1:A:57:ASN:HB3	1.88	0.54
1:D:100:ARG:HD3	1:D:105:TRP:HE3	1.72	0.53
1:D:87:LYS:HG2	3:D:358:HOH:O	2.07	0.53
1:D:132:GLU:HG3	1:D:149:ILE:HD11	1.89	0.53
1:B:61:ARG:NH2	3:B:387:HOH:O	2.31	0.53
1:D:240:ASP:HB3	3:D:378:HOH:O	2.08	0.53
1:B:100:ARG:H	1:B:106:ASN:ND2	2.00	0.53
1:D:231:ASN:HB3	3:D:408:HOH:O	2.08	0.53
1:C:49:GLU:HB2	1:C:232:VAL:HG13	1.91	0.53
1:D:43:VAL:HB	1:D:61:ARG:HG2	1.91	0.53
1:C:110:ASN:HD21	1:C:113:THR:H	1.57	0.52
1:C:49:GLU:CB	1:C:232:VAL:HG13	2.39	0.52
1:C:26:GLN:HE21	1:C:28:ASN:ND2	2.06	0.52
1:B:181:LEU:H	1:B:188:GLN:HE22	1.55	0.52
1:B:94:LYS:HB3	1:B:94:LYS:HZ1	1.75	0.52
1:D:143:ASP:HA	1:D:147:GLU:OE2	2.10	0.52
1:A:251:GLN:H	1:A:251:GLN:NE2	2.02	0.52
1:B:104:THR:HB	3:B:348:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:THR:HG22	1:B:245:ASP:H	1.75	0.52
1:C:25:TRP:HZ3	1:C:45:VAL:CG1	2.23	0.52
1:D:211:TYR:CE2	1:D:241:MET:HG2	2.45	0.52
1:A:58:ASN:ND2	1:A:61:ARG:H	2.08	0.51
1:D:103:ALA:HA	3:D:288:HOH:O	2.10	0.51
1:D:110:ASN:C	1:D:110:ASN:HD22	2.13	0.51
1:B:64:GLN:NE2	3:B:305:HOH:O	2.43	0.51
1:C:31:TRP:CH2	1:C:46:LEU:HD22	2.46	0.51
1:B:127:ALA:HB1	1:B:153:VAL:O	2.10	0.51
1:B:28:ASN:HD22	1:B:30:SER:H	1.59	0.51
1:C:104:THR:HG22	1:C:105:TRP:CD1	2.46	0.51
1:B:240:ASP:CG	3:B:387:HOH:O	2.50	0.51
1:D:137:LYS:NZ	3:D:418:HOH:O	2.43	0.50
1:C:240:ASP:HB2	3:C:315:HOH:O	2.09	0.50
1:C:231:ASN:ND2	1:C:232:VAL:H	2.09	0.50
1:C:234:PHE:HB2	3:C:386:HOH:O	2.11	0.50
1:D:211:TYR:CE2	1:D:241:MET:CG	2.94	0.50
1:A:99:THR:HG23	3:A:350:HOH:O	2.11	0.50
1:C:179:ASN:HA	1:C:188:GLN:NE2	2.27	0.50
1:C:70:SER:HB2	1:C:210:GLY:HA2	1.92	0.50
1:A:74:ILE:HB	1:A:75:PRO:CD	2.42	0.50
1:C:146:ASN:HD21	1:C:162:ILE:HA	1.77	0.50
1:D:146:ASN:HD22	1:D:146:ASN:C	2.14	0.50
1:B:115:MET:HG3	1:B:208:LYS:HE2	1.93	0.50
1:C:92:VAL:HG12	3:C:319:HOH:O	2.11	0.49
1:B:104:THR:CG2	1:B:117:TYR:HB3	2.41	0.49
1:A:149:ILE:N	1:A:149:ILE:HD13	2.26	0.49
1:B:116:LYS:HE2	1:B:117:TYR:CZ	2.46	0.49
1:B:255:LYS:CE	3:B:351:HOH:O	2.52	0.49
1:C:83:LEU:HD12	1:C:130:ILE:HG12	1.95	0.49
1:B:140:HIS:HB2	3:B:402:HOH:O	2.12	0.49
1:B:128:ARG:NH2	3:B:440:HOH:O	2.45	0.48
1:B:164:ILE:O	1:B:221:TRP:HH2	1.96	0.48
1:C:237:MET:HG2	1:C:254:THR:OG1	2.13	0.48
1:A:146:ASN:C	1:A:146:ASN:ND2	2.66	0.48
1:B:175:LYS:HA	1:B:180:LYS:NZ	2.26	0.48
1:D:262:LYS:HA	3:D:371:HOH:O	2.13	0.48
1:B:60:LYS:HG2	3:B:359:HOH:O	2.13	0.48
1:D:254:THR:O	1:D:258:LEU:HG	2.14	0.48
1:A:198:GLU:OE2	1:A:203:TYR:OH	2.23	0.48
1:B:48:ASN:HB2	1:B:233:TRP:CH2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:SER:OG	1:B:208:LYS:NZ	2.38	0.48
1:B:67:LEU:O	1:B:221:TRP:HZ3	1.96	0.48
1:C:124:GLN:NE2	3:C:330:HOH:O	2.46	0.48
1:D:220:GLY:O	1:D:238:ASN:HA	2.13	0.48
1:B:197:THR:HG22	2:B:266:EDO:H21	1.95	0.48
1:B:231:ASN:ND2	1:B:232:VAL:H	2.12	0.47
1:B:38:HIS:HB3	1:B:249:LEU:HD22	1.97	0.47
1:C:218:LYS:HG2	3:C:333:HOH:O	2.14	0.47
1:A:181:LEU:H	1:A:188:GLN:HE22	1.62	0.47
1:A:39:LYS:HG3	1:A:39:LYS:O	2.15	0.47
1:B:237:MET:HB3	3:B:407:HOH:O	2.15	0.47
1:C:96:ASP:OD1	1:C:100:ARG:NH1	2.49	0.46
1:A:47:TRP:HB3	1:A:234:PHE:HB2	1.97	0.46
1:A:212:SER:O	1:A:218:LYS:HA	2.16	0.46
1:D:211:TYR:CG	1:D:247:LEU:HD21	2.50	0.46
1:A:110:ASN:C	1:A:110:ASN:HD22	2.19	0.46
1:D:228:LEU:HD11	1:D:263:ILE:O	2.15	0.46
1:D:45:VAL:O	1:D:235:PHE:HA	2.15	0.46
1:B:211:TYR:CE2	1:B:241:MET:HG2	2.51	0.46
1:A:26:GLN:HG2	3:A:414:HOH:O	2.15	0.46
1:D:100:ARG:HD3	1:D:105:TRP:CE3	2.51	0.45
1:D:251:GLN:N	1:D:251:GLN:NE2	2.60	0.45
1:D:58:ASN:ND2	1:D:61:ARG:H	2.14	0.45
1:A:157:TRP:CD1	1:A:158:LEU:HD13	2.52	0.45
1:B:148:ASP:O	1:B:162:ILE:HB	2.16	0.45
1:C:92:VAL:CG2	1:C:108:ASP:HB3	2.47	0.45
1:D:243:THR:CG2	1:D:245:ASP:HB2	2.46	0.45
1:D:94:LYS:HG2	1:D:108:ASP:OD1	2.16	0.45
1:A:162:ILE:HG12	3:A:436:HOH:O	2.16	0.45
1:A:87:LYS:N	1:A:91:GLN:NE2	2.59	0.45
1:C:226:VAL:HG13	1:C:233:TRP:HB2	1.97	0.45
1:A:255:LYS:NZ	3:A:374:HOH:O	2.22	0.45
1:A:75:PRO:O	1:A:79:ILE:HG13	2.16	0.45
1:B:221:TRP:CD1	1:B:223:VAL:CG1	3.00	0.45
1:D:124:GLN:HG2	1:D:154:ASP:O	2.17	0.45
1:A:94:LYS:HB3	3:A:464:HOH:O	2.17	0.44
1:C:104:THR:HG22	1:C:105:TRP:HD1	1.82	0.44
1:A:251:GLN:N	1:A:251:GLN:HE21	2.02	0.44
1:B:251:GLN:NE2	1:B:251:GLN:H	2.14	0.44
1:C:265:PRO:OXT	3:C:378:HOH:O	2.21	0.44
1:D:37:GLU:HG2	3:D:421:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:110:ASN:ND2	1:D:113:THR:H	2.15	0.44
1:C:249:LEU:HA	1:C:252:ALA:HB3	2.00	0.44
1:A:31:TRP:CH2	1:A:46:LEU:HD22	2.53	0.44
1:D:73:KCX:HE2	1:D:123:TYR:CD1	2.52	0.44
1:B:85:VAL:HG11	3:B:442:HOH:O	2.17	0.44
1:C:157:TRP:CD1	1:C:158:LEU:HD13	2.53	0.44
1:C:214:ARG:O	1:C:215:ILE:HD12	2.17	0.44
1:D:100:ARG:CD	1:D:105:TRP:HE3	2.31	0.44
1:C:25:TRP:HZ3	1:C:45:VAL:HG13	1.82	0.43
1:D:99:THR:HB	3:D:377:HOH:O	2.17	0.43
1:C:230:ASP:HB3	3:C:323:HOH:O	2.18	0.43
1:D:255:LYS:O	1:D:259:LYS:N	2.48	0.43
1:B:28:ASN:ND2	1:B:30:SER:H	2.17	0.43
1:C:92:VAL:HG22	1:C:108:ASP:HB3	2.00	0.43
1:D:46:LEU:O	1:D:54:GLY:HA2	2.18	0.43
1:A:44:VAL:HG12	1:A:46:LEU:HD13	2.00	0.43
1:B:29:LYS:HD2	3:B:477:HOH:O	2.18	0.43
1:D:139:LEU:HD12	1:D:149:ILE:CG2	2.49	0.43
1:C:110:ASN:C	1:C:110:ASN:ND2	2.70	0.43
1:A:155:SER:CA	3:A:460:HOH:O	2.50	0.42
1:C:255:LYS:O	1:C:259:LYS:HG3	2.18	0.42
1:D:214:ARG:NE	3:D:416:HOH:O	2.50	0.42
1:A:214:ARG:HB2	3:A:395:HOH:O	2.20	0.42
1:C:247:LEU:HD22	1:C:250:ARG:CZ	2.49	0.42
1:D:83:LEU:HD23	1:D:83:LEU:HA	1.85	0.42
1:B:226:VAL:HG13	1:B:233:TRP:HB2	2.00	0.42
1:B:198:GLU:OE2	1:B:203:TYR:OH	2.25	0.42
1:C:230:ASP:N	1:C:230:ASP:OD1	2.52	0.42
1:A:183:VAL:HG23	1:A:188:GLN:HG3	2.02	0.42
1:C:96:ASP:CG	1:C:100:ARG:HH12	2.23	0.42
1:C:79:ILE:HG23	1:C:138:MET:SD	2.60	0.42
1:D:25:TRP:CE3	1:D:54:GLY:HA3	2.55	0.42
1:C:146:ASN:ND2	1:C:163:ARG:H	2.18	0.42
1:D:120:VAL:HB	1:D:121:PRO:HD3	2.02	0.42
1:B:104:THR:HG21	3:B:438:HOH:O	2.19	0.42
1:C:218:LYS:HA	3:C:333:HOH:O	2.20	0.41
1:D:237:MET:HG2	1:D:254:THR:OG1	2.20	0.41
1:A:132:GLU:HG3	3:A:352:HOH:O	2.19	0.41
1:A:179:ASN:HA	1:A:188:GLN:NE2	2.35	0.41
1:A:231:ASN:ND2	1:A:232:VAL:H	2.18	0.41
1:B:178:HIS:HB2	1:B:180:LYS:CE	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:HIS:O	1:B:38:HIS:CD2	2.65	0.41
1:C:27:GLU:HB2	1:C:59:LEU:HG	2.02	0.41
1:D:64:GLN:HB3	3:D:420:HOH:O	2.21	0.41
1:A:25:TRP:N	3:A:292:HOH:O	2.52	0.41
1:A:86:VAL:HA	1:A:91:GLN:HE22	1.86	0.41
1:D:49:GLU:HB3	3:D:330:HOH:O	2.20	0.41
1:D:58:ASN:HD21	1:D:60:LYS:HB3	1.86	0.41
1:A:211:TYR:OH	3:A:275:HOH:O	2.18	0.41
1:B:110:ASN:C	1:B:110:ASN:HD22	2.23	0.41
1:C:25:TRP:O	1:C:26:GLN:C	2.59	0.41
1:A:87:LYS:N	1:A:91:GLN:HE22	2.11	0.41
1:B:104:THR:HG21	1:B:117:TYR:CD1	2.55	0.41
1:B:36:THR:HA	3:B:386:HOH:O	2.20	0.41
1:C:106:ASN:N	1:C:106:ASN:ND2	2.67	0.41
1:D:231:ASN:ND2	1:D:232:VAL:H	2.19	0.41
1:A:65:ALA:HB1	1:A:163:ARG:HB3	2.03	0.41
1:B:34:HIS:NE2	1:B:260:GLN:NE2	2.64	0.41
1:A:50:ASN:H	1:A:231:ASN:ND2	2.12	0.41
1:D:100:ARG:HG2	3:D:344:HOH:O	2.21	0.41
1:B:47:TRP:HB3	1:B:234:PHE:HB2	2.03	0.41
1:D:65:ALA:HB1	1:D:163:ARG:HB3	2.02	0.41
1:D:28:ASN:HB2	3:D:374:HOH:O	2.20	0.41
1:C:140:HIS:CD2	1:C:147:GLU:OE1	2.74	0.41
1:C:174:ARG:NH2	3:C:374:HOH:O	2.54	0.41
1:B:56:THR:HG21	1:B:59:LEU:HD23	2.03	0.40
1:D:28:ASN:ND2	1:D:30:SER:OG	2.54	0.40
1:A:27:GLU:HB2	1:A:59:LEU:HD11	2.02	0.40
1:A:136:SER:HB2	1:A:149:ILE:HG13	2.04	0.40
1:C:200:ASN:CB	1:C:202:ASP:H	2.31	0.40
1:D:58:ASN:ND2	1:D:58:ASN:C	2.74	0.40
1:D:87:LYS:H	1:D:91:GLN:HE21	1.70	0.40
1:B:86:VAL:HG13	1:B:93:PHE:HZ	1.87	0.40
1:C:104:THR:HG23	1:C:117:TYR:HB3	1.98	0.40
1:C:255:LYS:CG	3:C:274:HOH:O	2.69	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	235/265 (89%)	230 (98%)	5 (2%)	0	100	100
1	B	238/265 (90%)	232 (98%)	6 (2%)	0	100	100
1	C	235/265 (89%)	226 (96%)	8 (3%)	1 (0%)	34	24
1	D	234/265 (88%)	218 (93%)	14 (6%)	2 (1%)	17	7
All	All	942/1060 (89%)	906 (96%)	33 (4%)	3 (0%)	41	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	39	LYS
1	D	29	LYS
1	D	107	ARG

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	207/227 (91%)	182 (88%)	25 (12%)	5	1
1	B	209/227 (92%)	191 (91%)	18 (9%)	10	4
1	C	208/227 (92%)	188 (90%)	20 (10%)	8	3
1	D	206/227 (91%)	191 (93%)	15 (7%)	14	6
All	All	830/908 (91%)	752 (91%)	78 (9%)	8	3

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	37	GLU
1	A	41	GLN
1	A	46	LEU
1	A	51	LYS
1	A	52	GLN
1	A	58	ASN
1	A	76	ASN
1	A	99	THR
1	A	101	ASP
1	A	102	ILE
1	A	110	ASN
1	A	115	MET
1	A	132	GLU
1	A	146	ASN
1	A	148	ASP
1	A	149	ILE
1	A	152	ASN
1	A	158	LEU
1	A	169	GLN
1	A	182	HIS
1	A	221	TRP
1	A	231	ASN
1	A	232	VAL
1	A	251	GLN
1	B	28	ASN
1	B	46	LEU
1	B	51	LYS
1	B	58	ASN
1	B	76	ASN
1	B	85	VAL
1	B	92	VAL
1	B	94	LYS
1	B	101	ASP
1	B	104	THR
1	B	110	ASN
1	B	115	MET
1	B	146	ASN
1	B	158	LEU
1	B	169	GLN
1	B	221	TRP
1	B	231	ASN
1	B	251	GLN

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Mol	Chain	Res	Type
1	C	44	VAL
1	C	46	LEU
1	C	51	LYS
1	C	52	GLN
1	C	58	ASN
1	C	76	ASN
1	C	87	LYS
1	C	92	VAL
1	C	106	ASN
1	C	110	ASN
1	C	118	SER
1	C	146	ASN
1	C	158	LEU
1	C	169	GLN
1	C	215	ILE
1	C	218	LYS
1	C	221	TRP
1	C	230	ASP
1	C	231	ASN
1	C	251	GLN
1	D	28	ASN
1	D	40	SER
1	D	58	ASN
1	D	76	ASN
1	D	92	VAL
1	D	94	LYS
1	D	99	THR
1	D	110	ASN
1	D	146	ASN
1	D	158	LEU
1	D	169	GLN
1	D	226	VAL
1	D	231	ASN
1	D	245	ASP
1	D	251	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	28	ASN
1	A	53	GLN

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Mol	Chain	Res	Type
1	A	58	ASN
1	A	63	ASN
1	A	76	ASN
1	A	90	HIS
1	A	91	GLN
1	A	110	ASN
1	A	124	GLN
1	A	140	HIS
1	A	146	ASN
1	A	169	GLN
1	A	188	GLN
1	A	193	GLN
1	A	231	ASN
1	A	251	GLN
1	A	260	GLN
1	B	26	GLN
1	B	28	ASN
1	B	38	HIS
1	B	58	ASN
1	B	63	ASN
1	B	106	ASN
1	B	110	ASN
1	B	124	GLN
1	B	140	HIS
1	B	146	ASN
1	B	169	GLN
1	B	188	GLN
1	B	231	ASN
1	B	251	GLN
1	B	260	GLN
1	C	26	GLN
1	C	34	HIS
1	C	38	HIS
1	C	58	ASN
1	C	63	ASN
1	C	64	GLN
1	C	76	ASN
1	C	91	GLN
1	C	106	ASN
1	C	110	ASN
1	C	124	GLN
1	C	140	HIS

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Mol	Chain	Res	Type
1	C	146	ASN
1	C	169	GLN
1	C	188	GLN
1	C	193	GLN
1	C	231	ASN
1	C	251	GLN
1	C	260	GLN
1	D	28	ASN
1	D	58	ASN
1	D	63	ASN
1	D	64	GLN
1	D	76	ASN
1	D	90	HIS
1	D	91	GLN
1	D	106	ASN
1	D	110	ASN
1	D	124	GLN
1	D	146	ASN
1	D	169	GLN
1	D	188	GLN
1	D	193	GLN
1	D	231	ASN
1	D	251	GLN
1	D	260	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	KCX	C	73	1	7,11,12	1.38	1 (14%)	4,12,14	1.35	1 (25%)
1	KCX	B	73	1	7,11,12	1.23	1 (14%)	4,12,14	1.32	1 (25%)
1	KCX	D	73	1	7,11,12	0.76	0	4,12,14	0.69	0
1	KCX	A	73	1	7,11,12	0.80	0	4,12,14	0.46	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
1	KCX	C	73	1	-	1/7/10/12	-
1	KCX	B	73	1	-	0/7/10/12	-
1	KCX	D	73	1	-	0/7/10/12	-
1	KCX	A	73	1	-	0/7/10/12	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	73	KCX	CE-NZ	3.45	1.53	1.45
1	B	73	KCX	CB-CA	2.19	1.56	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	73	KCX	CE-NZ-CX	2.24	126.73	122.95
1	B	73	KCX	CE-NZ-CX	2.19	126.65	122.95

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	73	KCX	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	73	KCX	1	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

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	EDO	B	266	-	3,3,3	0.37	0	2,2,2	0.31	0
2	EDO	A	266	-	3,3,3	0.52	0	2,2,2	0.25	0
2	EDO	B	267	-	3,3,3	0.68	0	2,2,2	0.18	0
2	EDO	C	266	-	3,3,3	0.44	0	2,2,2	0.33	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
2	EDO	B	266	-	-	0/1/1/1	-
2	EDO	A	266	-	-	1/1/1/1	-
2	EDO	B	267	-	-	1/1/1/1	-
2	EDO	C	266	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	266	EDO	O1-C1-C2-O2
2	B	267	EDO	O1-C1-C2-O2
2	C	266	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	266	EDO	2	0
2	B	267	EDO	2	0
2	C	266	EDO	1	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	239/265 (90%)	-0.13	2 (0%) 86 87	3, 11, 23, 38	0
1	B	240/265 (90%)	-0.17	0 100 100	4, 11, 20, 25	0
1	C	239/265 (90%)	0.47	11 (4%) 32 35	4, 20, 39, 46	0
1	D	238/265 (89%)	0.50	19 (7%) 12 13	6, 20, 39, 45	0
All	All	956/1060 (90%)	0.17	32 (3%) 46 49	3, 14, 34, 46	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	103	ALA	5.9
1	C	97	GLY	5.1
1	A	149	ILE	4.7
1	D	102	ILE	4.5
1	D	33	ALA	4.4
1	C	95	TRP	4.2
1	C	25	TRP	4.0
1	C	104	THR	3.9
1	D	95	TRP	3.4
1	C	245	ASP	3.3
1	C	102	ILE	3.3
1	D	233	TRP	3.3
1	C	105	TRP	3.0
1	D	36	THR	2.7
1	D	103	ALA	2.7
1	D	37	GLU	2.7
1	C	106	ASN	2.6
1	D	98	GLN	2.5
1	D	101	ASP	2.5
1	A	161	GLY	2.5
1	C	51	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	99	THR	2.4
1	D	96	ASP	2.4
1	D	28	ASN	2.4
1	D	39	LYS	2.3
1	D	40	SER	2.3
1	D	105	TRP	2.3
1	D	26	GLN	2.3
1	C	127	ALA	2.2
1	D	258	LEU	2.1
1	D	265	PRO	2.1
1	D	29	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	KCX	D	73	12/13	0.91	0.10	9,10,13,13	0
1	KCX	C	73	12/13	0.95	0.10	11,13,18,18	0
1	KCX	A	73	12/13	0.95	0.09	6,7,16,19	0
1	KCX	B	73	12/13	0.96	0.09	4,6,14,15	0

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(Å ²)	Q<0.9
2	EDO	B	267	4/4	0.78	0.17	21,22,23,23	0
2	EDO	A	266	4/4	0.83	0.14	18,24,24,26	0
2	EDO	B	266	4/4	0.92	0.12	18,18,19,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	C	266	4/4	0.95	0.16	15,17,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.