



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:31 PM GMT

PDB ID : 4LUY  
Title : Crystal structure of CdALR mutant K 271 T  
Authors : Asojo, O.A.  
Deposited on : 2013-07-25  
Resolution : 2.60 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

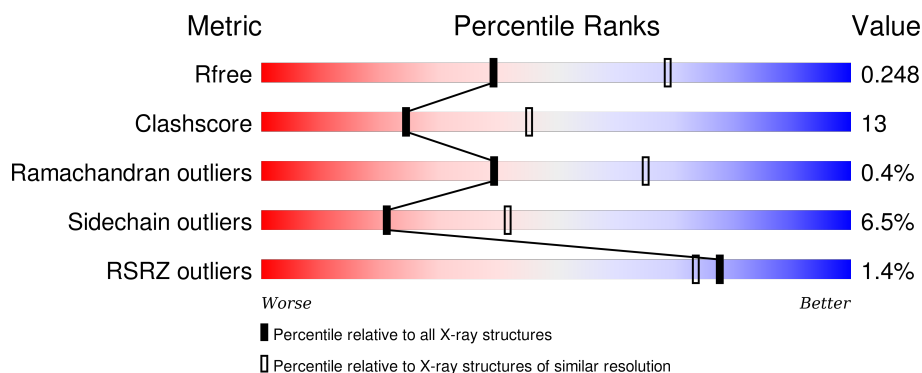
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	385	<div> <div>3%</div> <div> <div></div> <div>71%</div> <div>25%</div> <div>..</div> </div> </div>
1	B	385	<div> <div>70%</div> <div>25%</div> <div>..</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6158 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 Alanine racemase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	P	S	0	0	0
			3036	1927	505	587	1	16			
1	B	383	Total	C	N	O	P	S	0	0	0
			3036	1927	505	587	1	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	271	THR	LYS	ENGINEERED MUTATION	UNP Q180W0
B	271	THR	LYS	ENGINEERED MUTATION	UNP Q180W0

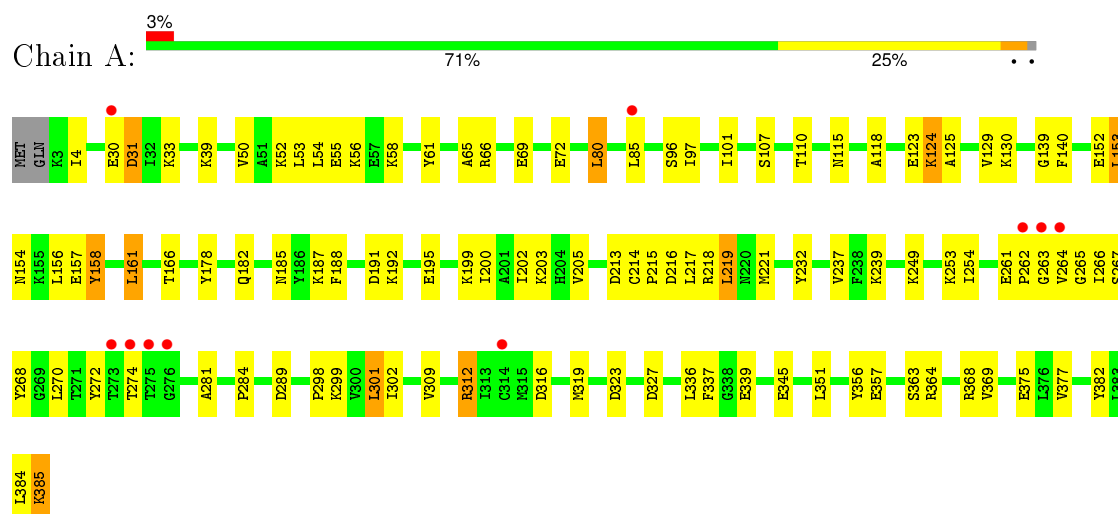
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		
2	B	42	Total	O	0	0
			42	42		

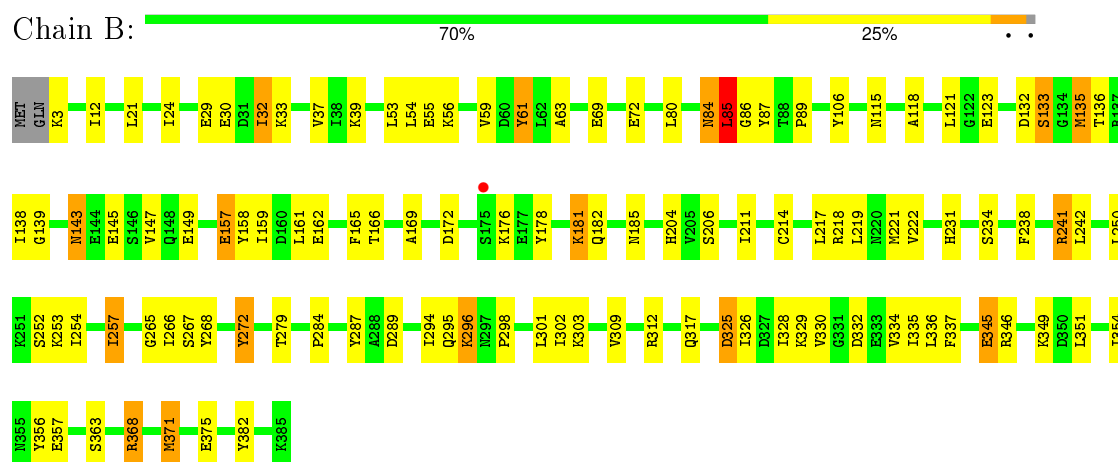
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: Alanine racemase



#### • Molecule 1: Alanine racemase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.97Å 154.33Å 55.77Å 90.00° 113.63° 90.00°	Depositor
Resolution (Å)	28.83 – 2.60 28.83 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.1 (28.83-2.60) 97.2 (28.83-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.40 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, $R_{free}$	0.181 , 0.252 0.182 , 0.248	Depositor DCC
$R_{free}$ test set	1182 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.8	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 43.4	EDS
Estimated twinning fraction	0.044 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 23092 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6158	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LLP, 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	1.69	8/3041 (0.3%)	0.92	4/4102 (0.1%)
1	B	1.72	11/3041 (0.4%)	0.90	2/4102 (0.0%)
All	All	1.71	19/6082 (0.3%)	0.91	6/8204 (0.1%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	357	GLU	CD-OE1	-6.26	1.18	1.25
1	B	69	GLU	CD-OE1	-6.09	1.19	1.25
1	B	162	GLU	CD-OE2	-5.87	1.19	1.25
1	B	72	GLU	CD-OE1	-5.79	1.19	1.25
1	B	345	GLU	CD-OE2	-5.77	1.19	1.25
1	A	357	GLU	CD-OE1	-5.69	1.19	1.25
1	A	345	GLU	CD-OE2	-5.61	1.19	1.25
1	B	72	GLU	CD-OE2	-5.55	1.19	1.25
1	B	357	GLU	CD-OE2	-5.52	1.19	1.25
1	A	72	GLU	CD-OE1	-5.50	1.19	1.25
1	A	72	GLU	CD-OE2	-5.33	1.19	1.25
1	A	382	TYR	CE1-CZ	-5.32	1.31	1.38
1	B	272	TYR	CE1-CZ	-5.28	1.31	1.38
1	B	317	GLN	C-O	-5.21	1.13	1.23
1	A	357	GLU	CD-OE2	-5.08	1.20	1.25
1	A	69	GLU	CD-OE2	-5.07	1.20	1.25
1	B	287	TYR	CE1-CZ	-5.05	1.31	1.38
1	A	364	ARG	CZ-NH2	-5.05	1.26	1.33
1	B	382	TYR	CE1-CZ	-5.01	1.32	1.38

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	TYR	N-CA-CB	-9.71	93.12	110.60
1	A	153	LEU	CA-CB-CG	6.71	130.72	115.30
1	A	158	TYR	N-CA-C	-5.33	96.60	111.00
1	B	332	ASP	CB-CG-OD1	5.24	123.01	118.30
1	A	356	TYR	CA-CB-CG	5.04	122.98	113.40
1	B	85	LEU	CA-CB-CG	5.02	126.84	115.30

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	3036	0	3084	78	0
1	B	3036	0	3085	80	0
2	A	44	0	0	2	0
2	B	42	0	0	2	0
All	All	6158	0	6169	158	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 13.

All (158) 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:115:ASN:ND2	1:B:157:GLU:O	1.83	1.10
1:A:264:VAL:H	1:A:274:THR:HG22	1.18	1.08
1:B:295:GLN:O	1:B:296:LYS:HB2	1.49	1.06
1:A:52:LYS:O	1:A:56:LYS:HD2	1.65	0.96
1:A:261:GLU:O	1:A:274:THR:HG21	1.65	0.95
1:A:52:LYS:O	1:A:56:LYS:CD	2.19	0.89
1:B:149:GLU:OE1	2:B:422:HOH:O	1.88	0.88
1:A:214:CYS:HB3	1:A:217:LEU:HD12	1.56	0.86
1:A:214:CYS:HB3	1:A:217:LEU:CD1	2.12	0.78
1:B:118:ALA:HB1	1:B:123:GLU:O	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:GLU:OE2	2:A:529:HOH:O	2.04	0.75
1:B:214:CYS:HB3	1:B:217:LEU:HD12	1.70	0.72
1:A:298:PRO:HB2	1:A:309:VAL:HB	1.71	0.72
1:A:55:GLU:HG2	1:A:80:LEU:HD22	1.72	0.72
1:A:214:CYS:CB	1:A:217:LEU:HD12	2.20	0.72
1:B:135:MET:O	1:B:136:THR:OG1	2.08	0.71
1:A:262:PRO:HA	1:A:274:THR:HG23	1.71	0.70
1:A:266:ILE:HD12	1:A:272:TYR:CD2	2.27	0.69
1:A:107:SER:OG	1:A:110:THR:HG23	1.91	0.69
1:B:61:TYR:HB2	1:B:221:MET:HE2	1.73	0.69
1:B:135:MET:HE1	1:B:169:ALA:HA	1.74	0.68
1:A:53:LEU:C	1:A:53:LEU:HD23	2.14	0.68
1:B:211:ILE:HD11	1:B:222:VAL:HB	1.75	0.68
1:A:52:LYS:O	1:A:56:LYS:HD3	1.95	0.66
1:A:312:ARG:HG2	1:A:312:ARG:HH11	1.59	0.66
1:B:133:SER:OG	1:B:166:THR:OG1	2.11	0.66
1:A:266:ILE:HD12	1:A:272:TYR:HD2	1.60	0.66
1:A:261:GLU:O	1:A:274:THR:CG2	2.43	0.65
1:A:53:LEU:O	1:A:53:LEU:HD23	1.97	0.65
1:B:61:TYR:HB2	1:B:221:MET:CE	2.26	0.65
1:B:143:ASN:OD1	1:B:145:GLU:N	2.28	0.64
1:A:264:VAL:N	1:A:274:THR:HG22	2.03	0.64
1:B:84:ASN:ND2	1:B:86:GLY:H	1.96	0.63
1:B:84:ASN:C	1:B:84:ASN:HD22	2.00	0.63
1:B:84:ASN:HD22	1:B:85:LEU:N	1.98	0.62
1:A:263:GLY:N	1:A:274:THR:O	2.26	0.62
1:A:267:SER:OG	1:A:268:TYR:N	2.29	0.62
1:B:39:LLP:H2'3	1:B:85:LEU:HG	1.81	0.62
1:B:161:LEU:O	1:B:161:LEU:HG	1.98	0.62
1:A:336:LEU:HD22	1:A:336:LEU:H	1.65	0.62
1:B:157:GLU:O	1:B:158:TYR:HB2	2.00	0.61
1:A:336:LEU:HD22	1:A:336:LEU:N	2.15	0.61
1:B:325:ASP:OD1	1:B:325:ASP:N	2.31	0.61
1:A:213:ASP:C	1:A:215:PRO:HD3	2.21	0.61
1:B:214:CYS:CB	1:B:217:LEU:HD12	2.30	0.61
1:B:61:TYR:HD2	1:B:221:MET:HE1	1.67	0.60
1:B:106:TYR:HB3	1:B:139:GLY:HA2	1.84	0.59
1:A:312:ARG:HH11	1:A:312:ARG:CG	2.17	0.58
1:A:375:GLU:O	1:A:377:VAL:HG13	2.04	0.58
1:B:55:GLU:HG2	1:B:80:LEU:HG	1.86	0.57
1:B:181:LYS:O	1:B:185:ASN:ND2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:TYR:O	1:B:182:GLN:HG3	2.05	0.56
1:A:213:ASP:O	1:A:215:PRO:HD3	2.05	0.56
1:B:371:MET:HA	1:B:375:GLU:O	2.06	0.56
1:B:295:GLN:O	1:B:296:LYS:CB	2.36	0.55
1:A:50:VAL:O	1:A:54:LEU:HG	2.07	0.55
1:B:63:ALA:HB1	1:B:85:LEU:HD22	1.89	0.54
1:B:87:TYR:CE2	1:B:89:PRO:HD3	2.43	0.54
1:B:84:ASN:C	1:B:84:ASN:ND2	2.59	0.54
1:B:298:PRO:HG2	1:B:309:VAL:HB	1.90	0.54
1:A:185:ASN:O	1:A:188:PHE:HB3	2.08	0.54
1:B:115:ASN:ND2	1:B:158:TYR:HB2	2.22	0.53
1:B:135:MET:C	1:B:136:THR:OG1	2.47	0.53
1:A:249:LYS:NZ	1:A:339:GLU:OE2	2.42	0.53
1:B:325:ASP:C	1:B:326:ILE:HG23	2.29	0.52
1:B:165:PHE:HB3	1:B:204:HIS:CE1	2.44	0.52
1:B:268:TYR:O	1:B:312:ARG:HD2	2.10	0.52
1:B:32:ILE:N	1:B:32:ILE:CD1	2.73	0.52
1:B:250:LEU:HG	1:B:336:LEU:HD23	1.91	0.52
1:A:203:LYS:HB3	1:A:219:LEU:HD23	1.90	0.52
1:A:384:LEU:O	1:A:385:LYS:HB2	2.09	0.52
1:A:30:GLU:HA	1:A:30:GLU:OE1	2.09	0.51
1:A:154:ASN:HB2	1:A:161:LEU:HD12	1.92	0.50
1:B:157:GLU:O	1:B:158:TYR:CB	2.57	0.50
1:B:115:ASN:HD22	1:B:159:ILE:HG12	1.76	0.50
1:B:267:SER:OG	1:B:268:TYR:N	2.42	0.50
1:B:257:ILE:HD11	1:B:279:THR:CG2	2.42	0.50
1:A:263:GLY:N	1:A:274:THR:CG2	2.74	0.50
1:B:30:GLU:H	1:B:30:GLU:CD	2.12	0.49
1:B:337:PHE:C	1:B:337:PHE:CD1	2.85	0.49
1:B:185:ASN:HD22	1:B:185:ASN:H	1.59	0.49
1:B:253:LYS:O	1:B:284:PRO:HD2	2.12	0.49
1:A:214:CYS:N	1:A:215:PRO:HD3	2.28	0.49
1:B:214:CYS:HB3	1:B:217:LEU:CD1	2.42	0.49
1:A:124:LYS:HE3	1:A:157:GLU:O	2.13	0.48
1:A:385:LYS:HD2	1:A:385:LYS:HA	1.66	0.48
1:B:61:TYR:CD2	1:B:221:MET:HE1	2.48	0.48
1:A:124:LYS:CE	1:A:157:GLU:O	2.61	0.48
1:A:253:LYS:O	1:A:284:PRO:HD2	2.14	0.48
1:A:4:ILE:HD11	1:A:369:VAL:HG11	1.96	0.47
1:B:294:ILE:HG22	1:B:294:ILE:O	2.14	0.47
1:B:143:ASN:O	1:B:147:VAL:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ILE:HG12	1:B:334:VAL:HG22	1.96	0.47
1:A:97:ILE:HG12	1:A:125:ALA:HB2	1.97	0.47
1:B:132:ASP:OD2	1:B:136:THR:HA	2.15	0.46
1:A:130:KCX:HE2	1:A:166:THR:HA	1.97	0.46
1:A:39:LLP:C2	1:A:85:LEU:HD13	2.45	0.46
1:A:254:ILE:HD13	1:A:281:ALA:HB1	1.97	0.46
1:B:33:LYS:HB3	1:B:221:MET:HE3	1.98	0.46
1:B:238:PHE:HB3	1:B:241:ARG:HG3	1.98	0.46
1:B:32:ILE:N	1:B:32:ILE:HD12	2.31	0.45
1:A:33:LYS:CB	1:A:221:MET:HG3	2.46	0.45
1:A:65:ALA:C	1:A:66:ARG:HG2	2.36	0.45
1:A:263:GLY:N	1:A:274:THR:HG23	2.30	0.45
1:B:39:LLP:C2'	1:B:85:LEU:HG	2.46	0.45
1:B:266:ILE:O	1:B:267:SER:HB3	2.17	0.45
1:A:96:SER:HB3	1:A:101:ILE:HB	1.96	0.45
1:A:166:THR:HG22	1:A:205:VAL:HG12	1.98	0.45
1:A:192:LYS:HD3	1:A:192:LYS:HA	1.74	0.45
1:A:337:PHE:C	1:A:337:PHE:CD1	2.90	0.45
1:B:301:LEU:HB3	1:B:335:ILE:HB	1.98	0.45
1:A:115:ASN:OD1	1:A:158:TYR:HB2	2.16	0.45
1:A:268:TYR:O	1:A:312:ARG:HD2	2.16	0.45
1:B:325:ASP:C	1:B:326:ILE:CG2	2.85	0.44
1:A:53:LEU:CD2	1:A:53:LEU:C	2.85	0.44
1:B:303:LYS:HB2	1:B:326:ILE:HD12	2.00	0.44
1:B:37:VAL:HG11	1:B:39:LLP:HE3	2.00	0.44
1:B:21:LEU:O	1:B:24:ILE:HB	2.18	0.44
1:A:312:ARG:CG	1:A:312:ARG:NH1	2.79	0.44
1:B:354:ILE:HD12	1:B:356:TYR:CD1	2.53	0.44
1:A:39:LLP:H2'3	1:A:85:LEU:HD13	2.00	0.43
1:A:266:ILE:O	1:A:267:SER:HB3	2.18	0.43
1:A:153:LEU:O	1:A:156:LEU:HD12	2.18	0.43
1:B:54:LEU:HD22	1:B:59:VAL:HG11	2.00	0.43
1:A:129:VAL:HG13	1:A:140:PHE:CE2	2.54	0.43
1:B:206:SER:HB2	1:B:222:VAL:HG12	2.00	0.42
1:A:39:LLP:C2'	1:A:85:LEU:HD13	2.49	0.42
1:B:231:HIS:HD2	1:B:345:GLU:OE2	2.01	0.42
1:A:130:KCX:HB2	1:A:139:GLY:HA2	2.01	0.42
1:B:218:ARG:NH1	2:B:411:HOH:O	2.52	0.42
1:B:3:LYS:HD2	1:B:3:LYS:HA	1.62	0.42
1:B:218:ARG:O	1:B:219:LEU:HB2	2.18	0.42
1:A:178:TYR:O	1:A:182:GLN:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:ILE:HG21	1:A:221:MET:CE	2.50	0.42
1:A:289:ASP:HA	1:A:363:SER:HB2	2.01	0.42
1:A:263:GLY:N	1:A:274:THR:HG22	2.34	0.42
1:A:263:GLY:H	1:A:274:THR:HG23	1.85	0.42
1:B:257:ILE:HD11	1:B:279:THR:HG22	2.02	0.42
1:A:301:LEU:C	1:A:302:ILE:HG13	2.40	0.42
1:A:187:LYS:NZ	1:A:191:ASP:OD2	2.46	0.41
1:A:232:TYR:CD2	1:A:239:LYS:HE2	2.55	0.41
1:A:265:GLY:HA3	1:A:270:LEU:HD22	2.02	0.41
1:B:326:ILE:HG13	1:B:328:ILE:HG23	2.01	0.41
1:A:118:ALA:HB1	1:A:123:GLU:O	2.20	0.41
1:B:12:ILE:CD1	1:B:368:ARG:HG2	2.51	0.41
1:A:80:LEU:HD12	1:A:80:LEU:HA	1.84	0.41
1:B:265:GLY:HA2	1:B:272:TYR:O	2.21	0.41
1:B:172:ASP:HB2	1:B:234:SER:HB3	2.02	0.41
1:B:29:GLU:HB2	1:B:32:ILE:HD13	2.02	0.41
1:B:53:LEU:HD23	1:B:53:LEU:C	2.41	0.41
1:B:289:ASP:HA	1:B:363:SER:OG	2.21	0.40
1:A:218:ARG:HG2	1:A:218:ARG:H	1.74	0.40
1:A:262:PRO:CA	1:A:274:THR:HG23	2.47	0.40
1:B:138:ILE:HD13	1:B:138:ILE:HG21	1.85	0.40
1:B:169:ALA:H	1:B:182:GLN:HE22	1.68	0.40
1:A:219:LEU:HD12	2:A:525:HOH:O	2.21	0.40
1:B:254:ILE:HG22	1:B:330:VAL:HA	2.04	0.40
1:A:216:ASP:N	1:A:216:ASP:OD1	2.48	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	379/385 (98%)	365 (96%)	12 (3%)	2 (0%)	34 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	379/385 (98%)	369 (97%)	9 (2%)	1 (0%)	46	72
All	All	758/770 (98%)	734 (97%)	21 (3%)	3 (0%)	39	65

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	296	LYS
1	A	200	ILE
1	A	31	ASP

### 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	330/332 (99%)	310 (94%)	20 (6%)	23	46
1	B	330/332 (99%)	307 (93%)	23 (7%)	19	37
All	All	660/664 (99%)	617 (94%)	43 (6%)	21	42

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

Mol	Chain	Res	Type
1	A	31	ASP
1	A	58	LYS
1	A	61	TYR
1	A	80	LEU
1	A	124	LYS
1	A	152	GLU
1	A	161	LEU
1	A	199	LYS
1	A	219	LEU
1	A	237	VAL
1	A	299	LYS
1	A	301	LEU
1	A	312	ARG

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Mol	Chain	Res	Type
1	A	316	ASP
1	A	319	MET
1	A	323	ASP
1	A	327	ASP
1	A	351	LEU
1	A	368	ARG
1	A	385	LYS
1	B	32	ILE
1	B	56	LYS
1	B	61	TYR
1	B	84	ASN
1	B	85	LEU
1	B	121	LEU
1	B	133	SER
1	B	135	MET
1	B	143	ASN
1	B	157	GLU
1	B	176	LYS
1	B	181	LYS
1	B	241	ARG
1	B	242	LEU
1	B	252	SER
1	B	257	ILE
1	B	325	ASP
1	B	329	LYS
1	B	346	ARG
1	B	349	LYS
1	B	351	LEU
1	B	368	ARG
1	B	371	MET

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

Mol	Chain	Res	Type
1	B	84	ASN
1	B	141	GLN
1	B	182	GLN
1	B	185	ASN
1	B	231	HIS
1	B	259	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	A	130	1	7,11,12	1.61	1 (14%)	7,12,14	1.06	0
1	LLP	A	39	1	23,24,25	2.83	10 (43%)	28,32,34	1.57	5 (17%)
1	KCX	B	130	1	7,11,12	0.78	0	7,12,14	1.98	2 (28%)
1	LLP	B	39	1	23,24,25	3.24	11 (47%)	28,32,34	1.79	7 (25%)

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	A	130	1	-	0/6/10/12	0/0/0/0
1	LLP	A	39	1	-	1/15/17/19	0/1/1/1
1	KCX	B	130	1	-	0/6/10/12	0/0/0/0
1	LLP	B	39	1	-	1/15/17/19	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	LLP	P-OP2	-4.69	1.37	1.54
1	A	39	LLP	P-OP3	-4.67	1.37	1.54
1	B	39	LLP	P-OP1	-4.16	1.37	1.51
1	A	39	LLP	P-OP1	-4.10	1.37	1.51
1	B	39	LLP	P-OP3	-3.73	1.41	1.54
1	B	39	LLP	P-OP2	-3.62	1.41	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	KCX	CB-CA	-3.57	1.50	1.53
1	B	39	LLP	CB-CA	-3.09	1.50	1.53
1	A	39	LLP	CB-CA	-3.04	1.50	1.53
1	A	39	LLP	P-OP4	-2.84	1.50	1.60
1	A	39	LLP	O3-C3	-2.44	1.31	1.37
1	B	39	LLP	P-OP4	-2.09	1.53	1.60
1	B	39	LLP	C6-N1	-2.04	1.30	1.34
1	A	39	LLP	C3-C2	2.38	1.42	1.40
1	B	39	LLP	C4-C4'	2.50	1.51	1.46
1	A	39	LLP	C4-C5	4.17	1.47	1.42
1	A	39	LLP	C4-C3	4.45	1.46	1.40
1	B	39	LLP	C4-C5	4.98	1.48	1.42
1	B	39	LLP	C4-C3	5.20	1.47	1.40
1	B	39	LLP	C4'-NZ	6.08	1.45	1.27
1	A	39	LLP	C4'-NZ	6.40	1.46	1.27
1	B	39	LLP	C3-C2	8.44	1.46	1.40

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	39	LLP	OP4-P-OP1	-4.15	96.58	107.14
1	A	39	LLP	O-C-CA	-3.17	117.22	125.49
1	A	39	LLP	C4-C4'-NZ	-2.92	108.81	125.06
1	B	130	KCX	O-C-CA	-2.76	118.31	125.49
1	B	39	LLP	C4-C4'-NZ	-2.70	110.03	125.06
1	A	39	LLP	OP4-P-OP1	2.28	112.96	107.14
1	B	39	LLP	C6-N1-C2	2.31	123.98	119.28
1	B	39	LLP	O3-C3-C2	2.45	121.93	117.66
1	A	39	LLP	C6-N1-C2	2.68	124.74	119.28
1	B	39	LLP	OP3-P-OP2	2.70	117.66	107.38
1	A	39	LLP	OP3-P-OP2	2.85	118.23	107.38
1	B	39	LLP	OP4-C5'-C5	3.20	114.28	108.99
1	B	130	KCX	CE-NZ-CX	4.24	128.29	123.49
1	B	39	LLP	CD-CE-NZ	4.53	118.40	110.98

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	39	LLP	C4-C4'-NZ-CE
1	B	39	LLP	C4-C4'-NZ-CE

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	130	KCX	2	0
1	A	39	LLP	3	0
1	B	39	LLP	3	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	381/385 (98%)	-0.13	10 (2%) 59 53	26, 39, 58, 79	0
1	B	381/385 (98%)	-0.28	1 (0%) 94 93	23, 39, 59, 67	0
All	All	762/770 (98%)	-0.21	11 (1%) 78 74	23, 39, 59, 79	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	LEU	3.6
1	A	30	GLU	3.1
1	A	276	GLY	2.9
1	A	275	THR	2.8
1	A	262	PRO	2.8
1	A	273	THR	2.7
1	B	175	SER	2.4
1	A	274	THR	2.3
1	A	263	GLY	2.2
1	A	264	VAL	2.1
1	A	314	CYS	2.1

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	KCX	A	130	12/13	0.96	0.25	-	29,31,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	LLP	A	39	24/25	0.98	0.28	-	29,33,37,42	0
1	LLP	B	39	24/25	0.97	0.24	-	30,35,38,38	0
1	KCX	B	130	12/13	0.93	0.23	-	42,47,57,61	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.