



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:16 PM GMT

PDB ID : 4L5B
Title : Human dCK C4S-S74E mutant in complex with UDP and the DI-43 inhibitor
Authors : Nomme, J.; Lavie, A.
Deposited on : 2013-06-10
Resolution : 1.94 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
<http://wwpdb.org/validation/2016/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 : 1.7 (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

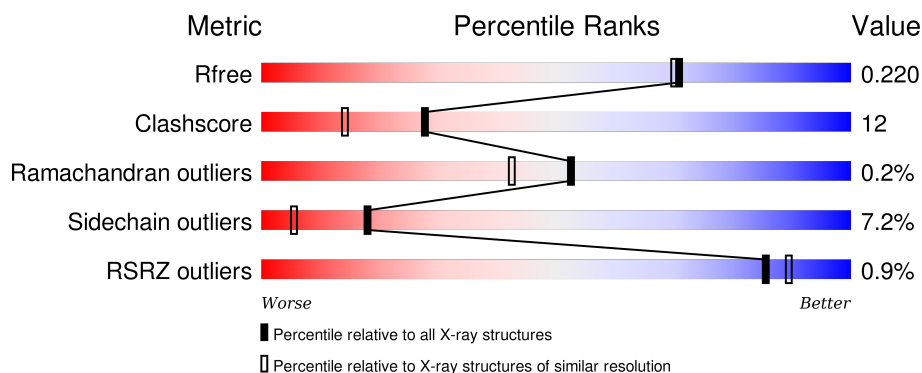
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	2910 (1.96-1.92)
Clashscore	102246	3095 (1.96-1.92)
Ramachandran outliers	100387	3062 (1.96-1.92)
Sidechain outliers	100360	3062 (1.96-1.92)
RSRZ outliers	91569	2915 (1.96-1.92)

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. 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	280	
1	B	280	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4046 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 Deoxycytidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	3	0
			1932	1240	319	365	8			
1	B	230	Total	C	N	O	S	0	3	0
			1925	1237	317	363	8			

There are 50 discrepancies between the modelled and reference sequences:

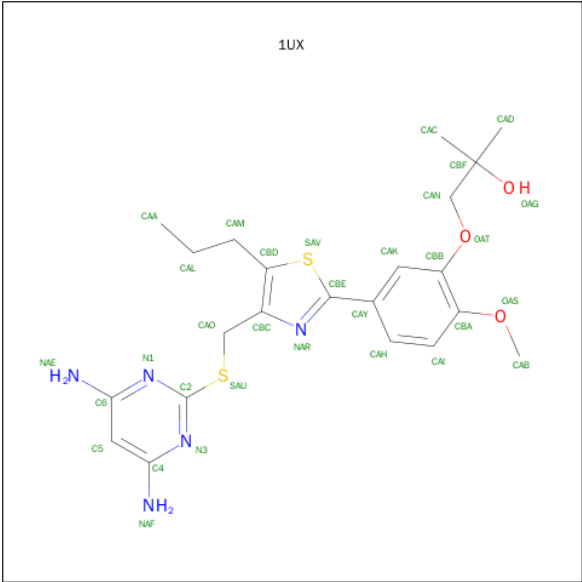
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	INITIATING METHIONINE	UNP P27707
A	-18	GLY	-	EXPRESSION TAG	UNP P27707
A	-17	SER	-	EXPRESSION TAG	UNP P27707
A	-16	SER	-	EXPRESSION TAG	UNP P27707
A	-15	HIS	-	EXPRESSION TAG	UNP P27707
A	-14	HIS	-	EXPRESSION TAG	UNP P27707
A	-13	HIS	-	EXPRESSION TAG	UNP P27707
A	-12	HIS	-	EXPRESSION TAG	UNP P27707
A	-11	HIS	-	EXPRESSION TAG	UNP P27707
A	-10	HIS	-	EXPRESSION TAG	UNP P27707
A	-9	SER	-	EXPRESSION TAG	UNP P27707
A	-8	SER	-	EXPRESSION TAG	UNP P27707
A	-7	GLY	-	EXPRESSION TAG	UNP P27707
A	-6	LEU	-	EXPRESSION TAG	UNP P27707
A	-5	VAL	-	EXPRESSION TAG	UNP P27707
A	-4	PRO	-	EXPRESSION TAG	UNP P27707
A	-3	ARG	-	EXPRESSION TAG	UNP P27707
A	-2	GLY	-	EXPRESSION TAG	UNP P27707
A	-1	SER	-	EXPRESSION TAG	UNP P27707
A	0	HIS	-	EXPRESSION TAG	UNP P27707
A	9	SER	CYS	ENGINEERED MUTATION	UNP P27707
A	45	SER	CYS	ENGINEERED MUTATION	UNP P27707
A	59	SER	CYS	ENGINEERED MUTATION	UNP P27707
A	74	GLU	SER	ENGINEERED MUTATION	UNP P27707
A	146	SER	CYS	ENGINEERED MUTATION	UNP P27707

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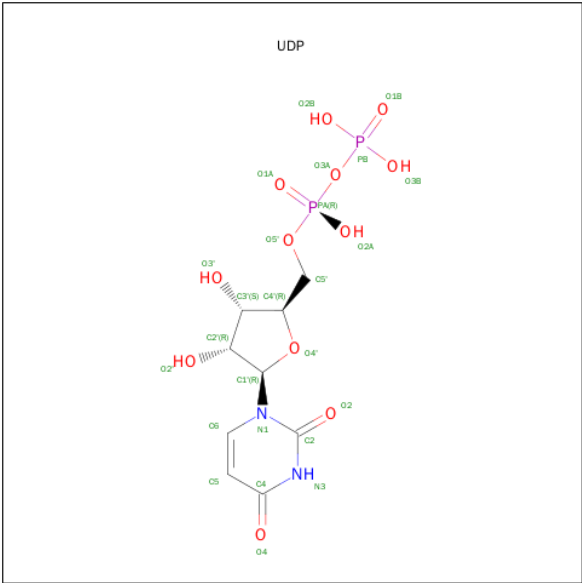
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	INITIATING METHIONINE	UNP P27707
B	-18	GLY	-	EXPRESSION TAG	UNP P27707
B	-17	SER	-	EXPRESSION TAG	UNP P27707
B	-16	SER	-	EXPRESSION TAG	UNP P27707
B	-15	HIS	-	EXPRESSION TAG	UNP P27707
B	-14	HIS	-	EXPRESSION TAG	UNP P27707
B	-13	HIS	-	EXPRESSION TAG	UNP P27707
B	-12	HIS	-	EXPRESSION TAG	UNP P27707
B	-11	HIS	-	EXPRESSION TAG	UNP P27707
B	-10	HIS	-	EXPRESSION TAG	UNP P27707
B	-9	SER	-	EXPRESSION TAG	UNP P27707
B	-8	SER	-	EXPRESSION TAG	UNP P27707
B	-7	GLY	-	EXPRESSION TAG	UNP P27707
B	-6	LEU	-	EXPRESSION TAG	UNP P27707
B	-5	VAL	-	EXPRESSION TAG	UNP P27707
B	-4	PRO	-	EXPRESSION TAG	UNP P27707
B	-3	ARG	-	EXPRESSION TAG	UNP P27707
B	-2	GLY	-	EXPRESSION TAG	UNP P27707
B	-1	SER	-	EXPRESSION TAG	UNP P27707
B	0	HIS	-	EXPRESSION TAG	UNP P27707
B	9	SER	CYS	ENGINEERED MUTATION	UNP P27707
B	45	SER	CYS	ENGINEERED MUTATION	UNP P27707
B	59	SER	CYS	ENGINEERED MUTATION	UNP P27707
B	74	GLU	SER	ENGINEERED MUTATION	UNP P27707
B	146	SER	CYS	ENGINEERED MUTATION	UNP P27707

- Molecule 2 is 1-[5-(4-{|(4,6-DIAMINOPYRIMIDIN-2-YL)SULFANYL|METHYL}-5-PROPYL-1,3-THIAZOL-2-YL)-2-METHOXYPHENOXY]-2-METHYLPROPAN-2-OL (three-letter code: 1UX) (formula: C₂₂H₂₉N₅O₃S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			32	22	5	3	2		
2	B	1	Total	C	N	O	S	0	0
			32	22	5	3	2		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

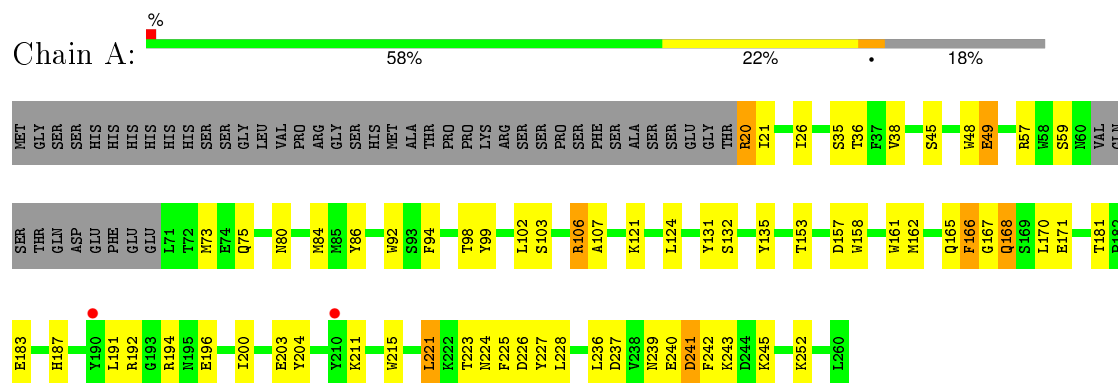
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	40	Total 40	O 40	0	0
4	B	35	Total 35	O 35	0	0

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: Deoxycytidine kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	68.67Å 68.67Å 120.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.94 27.49 – 1.94	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-1.94) 97.4 (27.49-1.94)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 1.93Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.188 , 0.233 0.189 , 0.220	Depositor DCC
R_{free} test set	2011 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.7	EDS
Estimated twinning fraction	0.511 for H, K, L 0.489 for -H, K, -L 0.477 for h,-k,-l	Xtriage
Reported twinning fraction	0.511 for H, K, L 0.489 for -H, K, -L	Depositor
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 40963 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4046	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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, 0.375 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: 1UX, UDP

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	0.55	0/1987	0.72	0/2686
1	B	0.58	0/1980	0.75	0/2676
All	All	0.57	0/3967	0.74	0/5362

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	1932	0	1878	48	0
1	B	1925	0	1874	53	0
2	A	32	0	29	1	0
2	B	32	0	29	1	0
3	A	25	0	11	2	0
3	B	25	0	11	2	0
4	A	40	0	0	3	0
4	B	35	0	0	3	0
All	All	4046	0	3832	92	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 12.

All (92) 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:192:ARG:NH2	3:B:302:UDP:O2B	2.01	0.93
1:B:49:GLU:HG2	1:B:115:LYS:HD3	1.58	0.84
1:A:168:GLN:HE21	1:A:168:GLN:HA	1.42	0.83
1:A:102:LEU:HD12	1:B:158:TRP:HD1	1.52	0.74
1:B:48:TRP:O	4:B:425:HOH:O	2.05	0.73
1:B:120:GLU:CD	1:B:120:GLU:H	1.96	0.69
1:A:102:LEU:HD12	1:B:158:TRP:CD1	2.34	0.62
1:A:102:LEU:CD1	1:B:158:TRP:HD1	2.13	0.61
1:A:94:PHE:O	1:A:98:THR:HG23	2.02	0.59
1:A:183:GLU:N	1:A:183:GLU:OE2	2.30	0.59
1:A:20:ARG:HG3	1:A:21:ILE:N	2.17	0.59
1:A:45:SER:O	4:A:430:HOH:O	2.17	0.58
1:B:232:PRO:HG2	1:B:260:LEU:HD21	1.85	0.58
1:B:232:PRO:CG	1:B:260:LEU:HD21	2.34	0.57
1:A:48:TRP:O	4:A:430:HOH:O	2.18	0.57
1:A:158:TRP:O	1:A:162:MET:HB2	2.04	0.57
1:B:45:SER:HB3	1:B:48:TRP:CG	2.41	0.55
1:A:103:SER:HA	1:A:106:ARG:HG2	1.88	0.55
1:A:194:ARG:HB2	4:A:439:HOH:O	2.06	0.55
1:A:181:THR:HB	1:A:183:GLU:OE2	2.08	0.54
1:A:204:TYR:CE1	2:A:301:1UX:H3	2.43	0.54
1:B:49:GLU:HG3	1:B:50:VAL:N	2.23	0.53
1:B:166:PHE:HB3	1:B:169:SER:OG	2.09	0.53
1:B:120:GLU:N	1:B:120:GLU:CD	2.61	0.53
1:B:178:LEU:HB3	1:B:238:VAL:HG21	1.91	0.53
1:A:106:ARG:HG3	1:A:107:ALA:N	2.24	0.52
1:A:187:HIS:O	1:A:191:LEU:HG	2.09	0.52
1:B:42:LYS:NZ	1:B:42:LYS:HB3	2.24	0.52
1:B:106:ARG:CG	4:B:429:HOH:O	2.58	0.52
1:B:184:THR:OG1	1:B:239:ASN:OD1	2.10	0.52
1:A:135:TYR:HB3	1:A:221:LEU:HD21	1.91	0.51
1:A:187:HIS:CE1	1:A:191:LEU:HD21	2.46	0.51
1:A:102:LEU:CD1	1:B:158:TRP:CD1	2.93	0.51
1:B:83:GLN:HG3	1:B:196:GLU:OE2	2.10	0.51
1:B:129:SER:O	1:B:132:SER:HB3	2.11	0.50
1:B:186:LEU:HD22	1:B:202:LEU:HD13	1.92	0.50
1:B:128:ARG:HD3	1:B:132:SER:OG	2.12	0.50
1:A:168:GLN:NE2	1:A:168:GLN:HA	2.18	0.50
1:A:166:PHE:CZ	1:B:162:MET:HG3	2.47	0.50
1:A:161:TRP:CZ2	1:A:165:GLN:HG3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:ARG:O	1:B:108:GLN:HG3	2.12	0.49
1:A:215:TRP:HB2	1:A:221:LEU:HD22	1.95	0.49
1:B:81:VAL:HA	1:B:84[A]:MET:HE2	1.93	0.49
1:B:192:ARG:HB2	3:B:302:UDP:H4'	1.95	0.48
1:A:192:ARG:NH1	3:A:302:UDP:O1A	2.47	0.48
1:B:119:ALA:HB3	1:B:122:PRO:HB3	1.95	0.48
1:B:109:LEU:HD11	1:B:166:PHE:CE2	2.49	0.48
1:B:228:LEU:HD23	1:B:231:VAL:HG21	1.96	0.47
1:B:47:ASP:HB3	1:B:121:LYS:O	2.14	0.47
1:B:255:GLU:O	1:B:259:THR:HG23	2.14	0.47
1:A:35[B]:SER:HA	1:A:38:VAL:HG22	1.97	0.46
1:B:213:GLU:OE2	1:B:217:LEU:HD13	2.15	0.46
1:B:49:GLU:HG3	1:B:50:VAL:H	1.81	0.46
1:B:89:PRO:HD3	2:B:301:IUX:H12	1.98	0.46
1:B:183:GLU:CD	1:B:183:GLU:H	2.19	0.46
1:B:202:LEU:O	1:B:206:GLU:HG3	2.16	0.46
1:A:166:PHE:HZ	1:B:162:MET:HG3	1.81	0.46
1:A:237:ASP:OD2	1:A:239:ASN:HB2	2.16	0.45
1:B:42:LYS:HD2	1:B:49:GLU:OE1	2.16	0.45
1:A:99:TYR:CD1	1:B:154:ILE:HG23	2.52	0.45
1:A:237:ASP:OD2	1:A:239:ASN:ND2	2.48	0.45
1:A:84[B]:MET:HB3	1:A:92:TRP:CD1	2.52	0.44
1:B:38:VAL:HG13	1:B:50:VAL:HG21	1.99	0.44
1:A:153:THR:HG22	1:B:77:ASN:HD21	1.82	0.44
1:B:20:ARG:HB2	1:B:20:ARG:HH11	1.83	0.44
1:B:161:TRP:O	1:B:165:GLN:HG2	2.18	0.44
1:A:157:ASP:OD1	1:B:106:ARG:NH2	2.51	0.44
1:B:260:LEU:HD23	1:B:260:LEU:HA	1.56	0.44
1:A:225:PHE:HB2	1:A:228:LEU:HD12	1.99	0.43
1:A:36:THR:HG22	1:A:242:PHE:CE1	2.53	0.43
1:A:103:SER:O	1:A:106:ARG:HG2	2.18	0.43
1:B:59:SER:HB3	1:B:194:ARG:NH1	2.35	0.42
1:A:80:ASN:O	1:A:84[A]:MET:HG3	2.20	0.42
1:A:168:GLN:C	1:A:170:LEU:H	2.23	0.42
1:B:81:VAL:HG13	1:B:96:PHE:HD1	1.85	0.42
1:B:82:LEU:O	1:B:86:TYR:HD1	2.03	0.41
1:A:167:GLY:O	1:A:170:LEU:HB2	2.20	0.41
1:A:86:TYR:OH	1:A:200:ILE:HD11	2.19	0.41
1:A:171:GLU:HA	1:A:227:TYR:OH	2.20	0.41
1:A:240:GLU:HG2	1:A:241:ASP:O	2.20	0.41
1:A:49:GLU:C	1:A:124:LEU:HD12	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:LYS:HB3	1:A:121:LYS:HE2	1.95	0.41
1:B:192:ARG:HD3	1:B:194:ARG:NE	2.36	0.41
1:B:232:PRO:HG3	1:B:260:LEU:HD21	2.02	0.41
1:A:131:TYR:CD2	1:A:228:LEU:HD11	2.56	0.41
1:B:106:ARG:HG3	4:B:429:HOH:O	2.20	0.41
1:A:243:LYS:HD2	3:A:302:UDP:C2	2.56	0.41
1:A:57:ARG:HH21	1:A:75:GLN:NE2	2.19	0.41
1:B:21:ILE:HA	1:B:122:PRO:HG2	2.03	0.40
1:A:240:GLU:OE2	1:A:245:LYS:NZ	2.38	0.40
1:A:236:LEU:CD2	1:A:252:LYS:HD2	2.51	0.40
1:B:228:LEU:HA	1:B:231:VAL:HG23	2.03	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	230/280 (82%)	213 (93%)	17 (7%)	0	100	100
1	B	229/280 (82%)	216 (94%)	12 (5%)	1 (0%)	39	26
All	All	459/560 (82%)	429 (94%)	29 (6%)	1 (0%)	52	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	167	GLY

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	212/256 (83%)	195 (92%)	17 (8%)	15	4
1	B	211/256 (82%)	198 (94%)	13 (6%)	23	8
All	All	423/512 (83%)	393 (93%)	30 (7%)	18	6

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

Mol	Chain	Res	Type
1	A	20	ARG
1	A	26	ILE
1	A	49	GLU
1	A	59	SER
1	A	73	MET
1	A	106	ARG
1	A	132	SER
1	A	166	PHE
1	A	168	GLN
1	A	196	GLU
1	A	203	GLU
1	A	211	LYS
1	A	221	LEU
1	A	223	THR
1	A	224	ASN
1	A	226	ASP
1	A	241	ASP
1	B	20	ARG
1	B	38	VAL
1	B	40	ILE
1	B	57	ARG
1	B	88	LYS
1	B	90	GLU
1	B	120	GLU
1	B	195	ASN
1	B	203	GLU
1	B	214	SER
1	B	217	LEU
1	B	221	LEU
1	B	230	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	GLN
1	A	168	GLN
1	A	218	HIS
1	A	229	GLN
1	B	75	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	1UX	A	301	-	31,34,34	1.37	4 (12%)	35,48,48	2.03	6 (17%)
3	UDP	A	302	-	18,26,26	0.66	0	26,40,40	1.75	3 (11%)
2	1UX	B	301	-	31,34,34	1.99	5 (16%)	35,48,48	1.92	6 (17%)
3	UDP	B	302	-	18,26,26	0.83	1 (5%)	26,40,40	1.46	1 (3%)

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	1UX	A	301	-	-	0/17/20/20	0/3/3/3
3	UDP	A	302	-	-	0/12/32/32	0/2/2/2
2	1UX	B	301	-	-	0/17/20/20	0/3/3/3
3	UDP	B	302	-	-	0/12/32/32	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	1UX	CBD-SAV	-6.50	1.62	1.74
2	B	301	1UX	CBD-CBC	-4.63	1.33	1.42
2	A	301	1UX	CBD-SAV	-4.31	1.66	1.74
2	A	301	1UX	CBD-CBC	-4.14	1.34	1.42
2	A	301	1UX	CBE-SAV	-2.53	1.70	1.73
3	B	302	UDP	O4'-C1'	2.11	1.43	1.41
2	B	301	1UX	CAN-CBF	2.68	1.56	1.51
2	B	301	1UX	CAO-CBC	2.69	1.53	1.50
2	A	301	1UX	CAO-CBC	2.72	1.53	1.50
2	B	301	1UX	C2-SAU	5.61	1.85	1.75

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	1UX	CAB-OAS-CBA	-5.19	109.67	117.54
2	B	301	1UX	N1-C2-N3	-3.74	119.63	126.75
3	A	302	UDP	O3A-PA-O5'	-3.59	93.41	102.94
2	B	301	1UX	CAM-CBD-CBC	-3.54	124.39	127.56
2	A	301	1UX	N1-C2-N3	-3.12	120.81	126.75
2	A	301	1UX	CAM-CBD-CBC	-3.11	124.77	127.56
2	B	301	1UX	CAC-CBF-CAD	-2.22	105.39	110.24
3	A	302	UDP	O3B-PB-O1B	2.85	119.76	110.58
2	A	301	1UX	CAM-CBD-SAV	3.76	125.50	120.24
2	A	301	1UX	C2-N1-C6	4.08	119.95	115.97
2	B	301	1UX	CAM-CBD-SAV	4.74	126.87	120.24
2	B	301	1UX	C2-N1-C6	4.80	120.65	115.97
2	B	301	1UX	C2-N3-C4	6.20	122.01	115.97
3	B	302	UDP	C4-N3-C2	6.22	120.31	114.14
3	A	302	UDP	C4-N3-C2	6.73	120.81	114.14
2	A	301	1UX	C2-N3-C4	6.78	122.58	115.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	1UX	1	0
3	A	302	UDP	2	0
2	B	301	1UX	1	0
3	B	302	UDP	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	231/280 (82%)	0.21	2 (0%) 85 89	35, 45, 62, 67	0
1	B	230/280 (82%)	0.28	2 (0%) 85 89	33, 46, 62, 72	0
All	All	461/560 (82%)	0.25	4 (0%) 85 89	33, 46, 62, 72	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	167	GLY	2.9
1	A	210	TYR	2.9
1	B	210	TYR	2.3
1	A	190	TYR	2.1

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 carbohydrates 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. 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	1UX	A	301	32/32	0.98	0.12	0.11	34,45,50,53	0
2	1UX	B	301	32/32	0.97	0.12	0.05	37,43,47,48	0
3	UDP	A	302	25/25	0.97	0.11	-0.51	38,46,55,58	0
3	UDP	B	302	25/25	0.98	0.10	-1.03	35,44,51,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.