



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:19 AM UTC

PDB ID : 2VDD / pdb_00002vdd
Title : Crystal Structure of the Open State of TolC Outer Membrane Component of Mutlidrug Efflux Pumps
Authors : Bavro, V.N.; Pietras, Z.; Furnham, N.; Perez-Cano, L.; Fernandez-Recio, J.; Pei, X.Y.; Truer, R.; Misra, R.; Luisi, B.
Deposited on : 2007-10-04
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

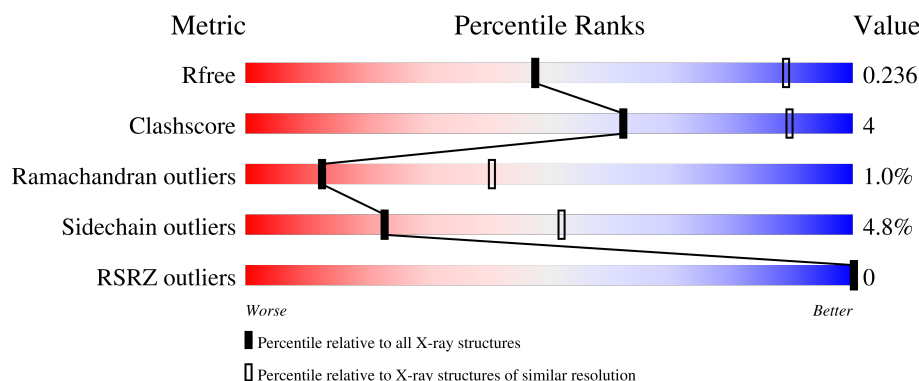
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	460	
1	B	460	
1	C	460	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9915 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 OUTER MEMBRANE PROTEIN TOLC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	12	0	1
			3303	2037	584	677	5			
1	B	429	Total	C	N	O	S	31	0	1
			3302	2036	584	677	5			
1	C	429	Total	C	N	O	S	5	0	1
			3303	2037	584	677	5			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ARG	LYS	conflict	UNP P02930
B	2	ARG	LYS	conflict	UNP P02930
C	2	ARG	LYS	conflict	UNP P02930
A	191	LEU	VAL	engineered mutation	UNP P02930
A	384	PHE	TYR	engineered mutation	UNP P02930
A	389	GLU	ARG	engineered mutation	UNP P02930
B	191	LEU	VAL	engineered mutation	UNP P02930
B	384	PHE	TYR	engineered mutation	UNP P02930
B	389	GLU	ARG	engineered mutation	UNP P02930
C	191	LEU	VAL	engineered mutation	UNP P02930
C	384	PHE	TYR	engineered mutation	UNP P02930
C	389	GLU	ARG	engineered mutation	UNP P02930

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	K	0	0
			2	2		
3	C	1	Total	K	0	0
			1	1		

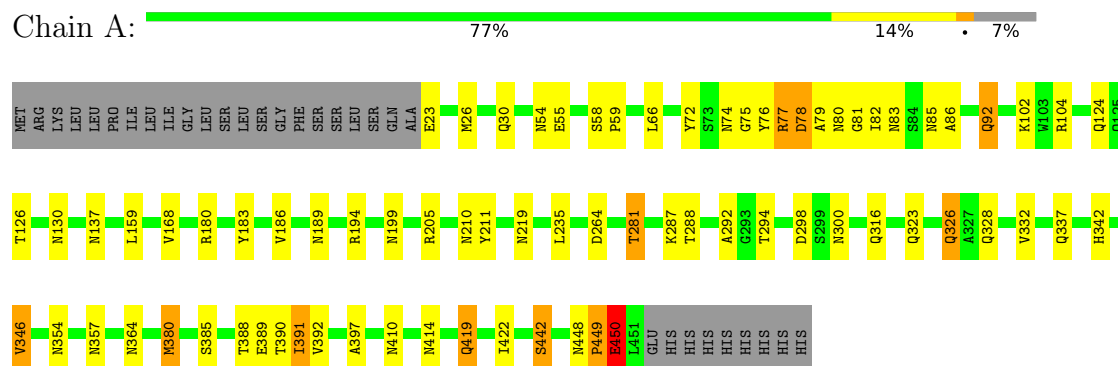
- Molecule 4 is water.

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

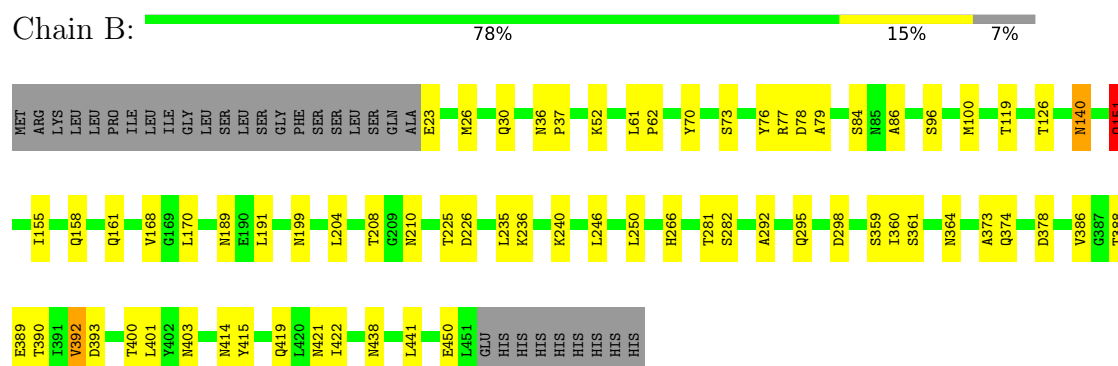
3 Residue-property plots

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.

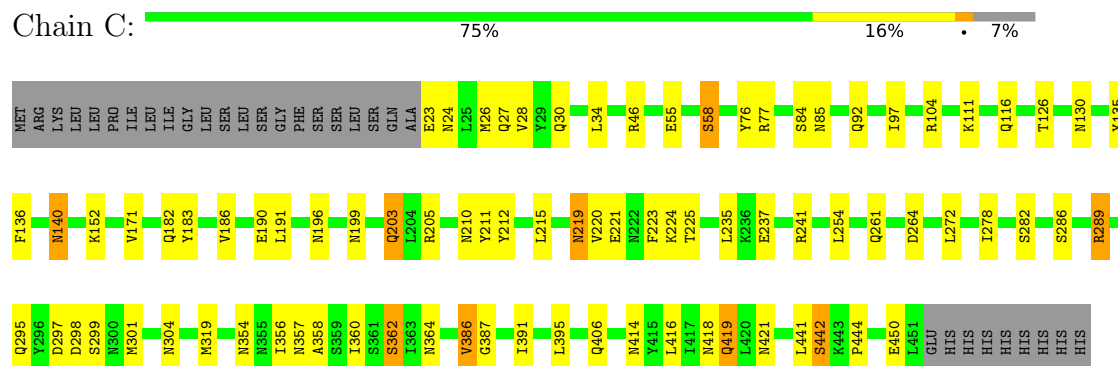
• Molecule 1: OUTER MEMBRANE PROTEIN TOLC



• Molecule 1: OUTER MEMBRANE PROTEIN TOLC



• Molecule 1: OUTER MEMBRANE PROTEIN TOLC



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.48Å 70.97Å 219.95Å 90.00° 100.61° 90.00°	Depositor
Resolution (Å)	29.80 – 3.30 29.80 – 3.30	Depositor EDS
% Data completeness (in resolution range)	97.2 (29.80-3.30) 97.1 (29.80-3.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 3.24Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.236 , 0.295 (Not available) , 0.236	Depositor DCC
R_{free} test set	1410 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 4.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.427 for $1/2^*h+3/2^*k, 1/2^*h-1/2^*k, -1/2^*h-1/2^*k-l$ 0.429 for $1/2^*h-3/2^*k, -1/2^*h-1/2^*k, -1/2^*h+1/2^*k-l$	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9915	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.18% 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: K, CL

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	0.71	18/3344 (0.5%)	0.89	3/4543 (0.1%)
1	B	0.70	16/3343 (0.5%)	0.91	4/4541 (0.1%)
1	C	0.72	20/3344 (0.6%)	0.91	2/4543 (0.0%)
All	All	0.71	54/10031 (0.5%)	0.90	9/13627 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	392	VAL	CA-CB	7.48	1.65	1.54
1	B	450	GLU	C-N	-6.86	1.23	1.33
1	C	450	GLU	C-N	-6.72	1.24	1.33
1	A	450	GLU	C-N	-6.62	1.24	1.33
1	C	224	LYS	CA-CB	-6.20	1.45	1.53
1	B	393	ASP	CA-CB	5.78	1.62	1.53
1	B	199	ASN	CG-OD1	5.48	1.33	1.23
1	A	357	ASN	CG-OD1	5.46	1.33	1.23
1	C	406	GLN	CD-OE1	5.44	1.33	1.23
1	A	130	ASN	CG-OD1	5.42	1.33	1.23
1	B	414	ASN	CG-OD1	5.41	1.33	1.23
1	A	414	ASN	CG-OD1	5.38	1.33	1.23
1	A	124	GLN	CD-OE1	5.37	1.33	1.23
1	A	354	ASN	CG-OD1	5.36	1.33	1.23
1	B	266	HIS	ND1-CE1	5.36	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	414	ASN	CG-OD1	5.36	1.33	1.23
1	B	438	ASN	CG-OD1	5.35	1.33	1.23
1	B	295	GLN	CD-OE1	5.34	1.33	1.23
1	C	295	GLN	CD-OE1	5.33	1.33	1.23
1	C	364	ASN	CG-OD1	5.33	1.33	1.23
1	A	199	ASN	CG-OD1	5.33	1.33	1.23
1	A	137	ASN	CG-OD1	5.31	1.33	1.23
1	C	354	ASN	CG-OD1	5.29	1.33	1.23
1	C	85	ASN	CG-OD1	5.27	1.33	1.23
1	C	140	ASN	CG-OD1	5.26	1.33	1.23
1	A	326	GLN	CD-OE1	5.26	1.33	1.23
1	A	364	ASN	CG-OD1	5.25	1.33	1.23
1	C	196	ASN	CG-OD1	5.24	1.33	1.23
1	A	323	GLN	CD-OE1	5.24	1.33	1.23
1	A	92	GLN	CD-OE1	5.23	1.33	1.23
1	C	219	ASN	CG-OD1	5.22	1.33	1.23
1	B	158	GLN	CD-OE1	5.21	1.33	1.23
1	A	342	HIS	ND1-CE1	5.21	1.37	1.32
1	B	140	ASN	CG-OD1	5.20	1.33	1.23
1	B	403	ASN	CG-OD1	5.18	1.33	1.23
1	C	130	ASN	CG-OD1	5.18	1.33	1.23
1	B	364	ASN	CG-OD1	5.17	1.33	1.23
1	C	203	GLN	CD-OE1	5.16	1.33	1.23
1	C	92	GLN	CD-OE1	5.16	1.33	1.23
1	B	421	ASN	CG-OD1	5.14	1.33	1.23
1	A	316	GLN	CD-OE1	5.14	1.33	1.23
1	C	182	GLN	CD-OE1	5.13	1.33	1.23
1	A	410	ASN	CG-OD1	5.11	1.33	1.23
1	B	374	GLN	CD-OE1	5.10	1.33	1.23
1	B	151	GLN	CD-OE1	5.09	1.33	1.23
1	C	357	ASN	CG-OD1	5.09	1.33	1.23
1	A	419	GLN	CD-OE1	5.08	1.33	1.23
1	B	161	GLN	CD-OE1	5.07	1.33	1.23
1	C	421	ASN	CG-OD1	5.05	1.33	1.23
1	C	418	ASN	CG-OD1	5.05	1.33	1.23
1	A	189	ASN	CG-OD1	5.04	1.33	1.23
1	A	54	ASN	CG-ND2	-5.04	1.22	1.33
1	C	419	GLN	CD-OE1	5.03	1.33	1.23
1	C	304	ASN	CG-OD1	5.01	1.33	1.23

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	224	LYS	CB-CA-C	12.78	132.20	111.24
1	B	226	ASP	CA-CB-CG	-10.28	102.32	112.60
1	C	224	LYS	CA-CB-CG	7.32	128.74	114.10
1	B	392	VAL	CB-CA-C	-6.76	101.68	112.16
1	A	342	HIS	CB-CG-CD2	-6.65	122.55	131.20
1	B	266	HIS	CB-CG-CD2	-6.51	122.73	131.20
1	A	342	HIS	CB-CG-ND1	5.63	131.14	122.70
1	B	266	HIS	CB-CG-ND1	5.58	131.06	122.70
1	A	385	SER	N-CA-C	-5.42	106.73	113.55

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	292	ALA	Peptide
1	B	79	ALA	Peptide

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	3303	0	3246	30	0
1	B	3302	0	3242	22	0
1	C	3303	0	3246	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	2	0	0	0	0
3	C	1	0	0	0	0
4	C	1	0	0	0	0
All	All	9915	0	9734	79	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 4.

All (79) 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:C:205:ARG:HH21	1:C:211:TYR:HB2	1.43	0.84
1:A:380:MET:HE3	1:A:397:ALA:HB2	1.63	0.80
1:A:104:ARG:HG3	1:A:264:ASP:OD2	1.88	0.72
1:C:104:ARG:HG3	1:C:264:ASP:OD2	1.93	0.69
1:C:26:MET:O	1:C:30:GLN:HG2	1.94	0.67
1:B:204:LEU:O	1:B:208:THR:HG22	1.95	0.67
1:C:299:SER:HB2	1:C:301:MET:HE3	1.76	0.67
1:C:261:GLN:HA	1:C:264:ASP:OD2	1.96	0.66
1:B:208:THR:HG23	1:B:210:ASN:H	1.59	0.66
1:B:281:THR:O	1:B:298:ASP:HB2	1.96	0.65
1:C:76:TYR:CD1	1:C:77:ARG:HG2	2.31	0.65
1:A:75:GLY:H	1:A:83:ASN:HB3	1.63	0.64
1:A:26:MET:O	1:A:30:GLN:HG2	1.97	0.63
1:C:97:ILE:HD11	1:C:272:LEU:HB2	1.81	0.62
1:C:55:GLU:O	1:C:58:SER:HB3	2.02	0.60
1:C:76:TYR:HD1	1:C:77:ARG:HG2	1.64	0.59
1:A:82:ILE:HG22	1:A:288:THR:HB	1.86	0.57
1:A:194:ARG:HG3	1:A:449:PRO:HB3	1.86	0.57
1:A:86:ALA:HB2	1:A:281:THR:HG23	1.87	0.56
1:A:77:ARG:C	1:A:79:ALA:H	2.12	0.56
1:A:235:LEU:HD11	1:A:346:VAL:HG23	1.88	0.56
1:A:219:ASN:HD22	1:A:442:SER:HB2	1.71	0.55
1:A:77:ARG:CZ	1:A:77:ARG:HB3	2.37	0.55
1:C:152:LYS:HD3	1:C:190:GLU:OE1	2.07	0.54
1:B:168:VAL:HG13	1:B:170:LEU:HD23	1.89	0.54
1:C:441:LEU:O	1:C:442:SER:HB3	2.07	0.53
1:A:58:SER:OG	1:C:319:MET:HB2	2.09	0.53
1:A:76:TYR:HA	1:A:80:ASN:HA	1.91	0.52
1:B:360:ILE:HG13	1:B:361:SER:N	2.25	0.52
1:C:223:PHE:HD2	1:C:225:THR:H	1.56	0.51
1:A:74:ASN:HA	1:A:83:ASN:HB2	1.93	0.50
1:C:199:ASN:O	1:C:203:GLN:HG2	2.11	0.50
1:C:356:ILE:HD11	1:C:419:GLN:HG2	1.92	0.50
1:A:55:GLU:O	1:A:58:SER:HB3	2.11	0.50
1:B:419:GLN:O	1:B:422:ILE:HG22	2.12	0.50
1:B:84:SER:HA	1:B:282:SER:O	2.12	0.49
1:B:388:THR:HG22	1:B:389:GLU:HG3	1.96	0.48
1:B:26:MET:O	1:B:30:GLN:HG2	2.14	0.48
1:A:82:ILE:HG13	1:A:82:ILE:O	2.13	0.48
1:C:183:TYR:O	1:C:186:VAL:HG12	2.13	0.48
1:A:448:ASN:C	1:A:450:GLU:H	2.21	0.47
1:C:46:ARG:HA	1:C:116:GLN:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:135:TYR:CE1	1:C:215:LEU:HD22	2.49	0.47
1:B:360:ILE:HG13	1:B:361:SER:H	1.78	0.47
1:C:23:GLU:OE2	1:C:444:PRO:HB3	2.15	0.46
1:C:358:ALA:O	1:C:362:SER:HB2	2.16	0.46
1:A:72:TYR:HD1	1:A:85:ASN:HB3	1.80	0.46
1:C:136:PHE:O	1:C:140:ASN:HB2	2.16	0.45
1:A:300:ASN:O	1:B:78:ASP:HB3	2.16	0.45
1:B:236:LYS:O	1:B:240:LYS:HE3	2.17	0.45
1:C:225:THR:HG23	1:C:360:ILE:HG12	1.98	0.45
1:B:151:GLN:O	1:B:155:ILE:HG12	2.16	0.44
1:C:441:LEU:O	1:C:442:SER:CB	2.65	0.44
1:B:246:LEU:O	1:B:250:LEU:HG	2.17	0.43
1:B:390:THR:HG22	1:B:392:VAL:H	1.84	0.43
1:C:84:SER:HA	1:C:282:SER:O	2.19	0.43
1:A:183:TYR:O	1:A:186:VAL:HG12	2.18	0.43
1:A:205:ARG:NH1	1:A:211:TYR:HB2	2.34	0.43
1:A:328:GLN:O	1:A:332:VAL:HG23	2.19	0.43
1:C:111:LYS:HB3	1:C:254:LEU:HD23	2.00	0.43
1:A:59:PRO:HB2	1:A:102:LYS:HD3	1.99	0.43
1:C:205:ARG:NH2	1:C:211:TYR:HB2	2.24	0.42
1:B:373:ALA:HB1	1:B:401:LEU:HA	2.01	0.42
1:A:326:GLN:OE1	1:B:52:LYS:HD3	2.19	0.42
1:B:70:TYR:HA	1:B:86:ALA:O	2.18	0.42
1:A:77:ARG:O	1:A:79:ALA:N	2.44	0.42
1:B:61:LEU:HB3	1:B:62:PRO:CD	2.49	0.42
1:A:77:ARG:HB3	1:A:77:ARG:NH2	2.35	0.42
1:C:219:ASN:C	1:C:221:GLU:H	2.28	0.42
1:C:237:GLU:OE2	1:C:241:ARG:NH1	2.53	0.42
1:A:159:LEU:HD21	1:A:180:ARG:HH11	1.84	0.42
1:B:359:SER:HB3	1:B:415:TYR:HB2	2.03	0.41
1:A:419:GLN:O	1:A:422:ILE:HG22	2.20	0.41
1:A:77:ARG:C	1:A:79:ALA:N	2.78	0.41
1:A:81:GLY:HA3	1:A:287:LYS:H	1.86	0.41
1:B:36:ASN:HA	1:B:37:PRO:HD3	1.83	0.41
1:C:24:ASN:HB3	1:C:27:GLN:HB2	2.03	0.41
1:B:61:LEU:HB3	1:B:62:PRO:HD2	2.03	0.40
1:C:28:VAL:HG22	1:C:212:TYR:CE2	2.56	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	427/460 (93%)	397 (93%)	24 (6%)	6 (1%)	9	33
1	B	427/460 (93%)	414 (97%)	12 (3%)	1 (0%)	43	71
1	C	427/460 (93%)	395 (92%)	26 (6%)	6 (1%)	9	33
All	All	1281/1380 (93%)	1206 (94%)	62 (5%)	13 (1%)	12	40

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	78	ASP
1	C	289	ARG
1	C	386	VAL
1	C	442	SER
1	A	292	ALA
1	B	77	ARG
1	C	286	SER
1	A	391	ILE
1	A	450	GLU
1	A	442	SER
1	C	220	VAL
1	C	387	GLY
1	A	449	PRO

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	358/387 (92%)	339 (95%)	19 (5%)	20	49
1	B	358/387 (92%)	341 (95%)	17 (5%)	23	52
1	C	358/387 (92%)	342 (96%)	16 (4%)	24	53
All	All	1074/1161 (92%)	1022 (95%)	52 (5%)	23	52

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLU
1	A	66	LEU
1	A	77	ARG
1	A	78	ASP
1	A	92	GLN
1	A	126	THR
1	A	168	VAL
1	A	210	ASN
1	A	281	THR
1	A	294	THR
1	A	298	ASP
1	A	337	GLN
1	A	346	VAL
1	A	380	MET
1	A	388	THR
1	A	389	GLU
1	A	390	THR
1	A	391	ILE
1	A	392	VAL
1	B	23	GLU
1	B	73	SER
1	B	76	TYR
1	B	96	SER
1	B	100	MET
1	B	119	THR
1	B	126	THR
1	B	140	ASN
1	B	151	GLN
1	B	189	ASN
1	B	191	LEU
1	B	225	THR
1	B	235	LEU
1	B	378	ASP
1	B	386	VAL

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Mol	Chain	Res	Type
1	B	400	THR
1	B	441	LEU
1	C	34	LEU
1	C	58	SER
1	C	126	THR
1	C	171	VAL
1	C	191	LEU
1	C	210	ASN
1	C	235	LEU
1	C	278	ILE
1	C	289	ARG
1	C	297	ASP
1	C	298	ASP
1	C	362	SER
1	C	386	VAL
1	C	391	ILE
1	C	395	LEU
1	C	416	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	116	GLN
1	A	304	ASN
1	A	374	GLN
1	A	438	ASN
1	B	121	GLN
1	B	124	GLN
1	B	219	ASN
1	B	266	HIS
1	C	24	ASN
1	C	31	GLN
1	C	74	ASN
1	C	85	ASN
1	C	109	GLN
1	C	124	GLN
1	C	161	GLN
1	C	182	GLN
1	C	206	GLN
1	C	210	ASN
1	C	219	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	429/460 (93%)	-1.50	0 100 100	20, 47, 85, 93	2 (0%)
1	B	428/460 (93%)	-1.48	0 100 100	14, 47, 79, 90	7 (1%)
1	C	429/460 (93%)	-1.49	0 100 100	18, 48, 85, 97	1 (0%)
All	All	1286/1380 (93%)	-1.49	0 100 100	14, 47, 84, 97	10 (0%)

There are no RSRZ outliers to report.

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 oligosaccharides 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
3	K	A	1456	1/1	0.98	0.05	68,68,68,68	0
3	K	C	1455	1/1	0.98	0.06	79,79,79,79	0
3	K	A	1455	1/1	0.99	0.04	66,66,66,66	0
2	CL	A	1454	1/1	0.99	0.05	51,51,51,51	0
2	CL	B	1454	1/1	0.99	0.02	31,31,31,31	0
2	CL	C	1454	1/1	1.00	0.04	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.