



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:30 AM UTC

PDB ID : 5J43 / pdb_00005j43
Title : CdiA-CT from uropathogenic Escherichia coli in complex with CysK
Authors : Morse, R.P.; Goulding, C.W.; Johnson, P.M.
Deposited on : 2016-03-31
Resolution : 2.70 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
Mogul : 2022.3.0, CSD as543be (2022)
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

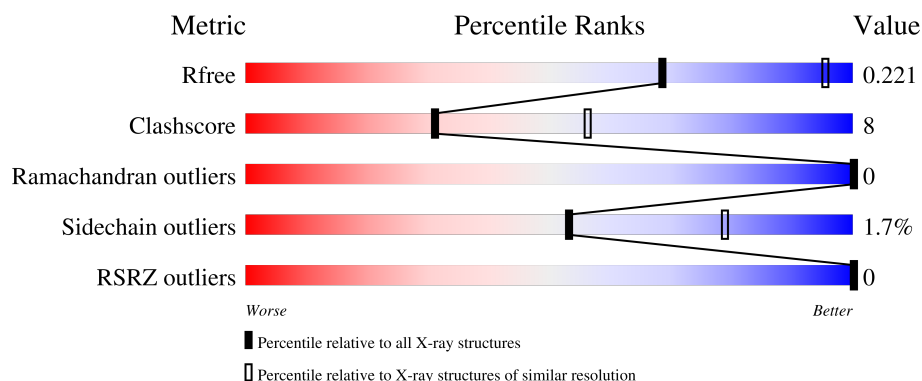
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	323	80% 17% ..
1	E	323	76% 20% ..
2	B	239	33% 8% 58%
2	F	239	35% 7% 58%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6328 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 Cysteine synthase A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	E	314	Total	C	N	O	P	S	0	0	0
			2351	1483	405	456	1	6			
1	A	313	Total	C	N	O	P	S	0	0	0
			2346	1480	404	455	1	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	2	GLY	SER	conflict	UNP P0ABK6
A	2	GLY	SER	conflict	UNP P0ABK6

- Molecule 2 is a protein called tRNA nuclease CdiA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	101	Total	C	N	O	S	0	0	0
			765	469	141	152	3			
2	B	101	Total	C	N	O	S	0	0	0
			756	461	140	152	3			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	MET	-	initiating methionine	UNP Q0T963
F	-10	ALA	-	expression tag	UNP Q0T963
F	-9	LYS	-	expression tag	UNP Q0T963
F	-8	SER	-	expression tag	UNP Q0T963
F	-7	HIS	-	expression tag	UNP Q0T963
F	-6	HIS	-	expression tag	UNP Q0T963
F	-5	HIS	-	expression tag	UNP Q0T963
F	-4	HIS	-	expression tag	UNP Q0T963
F	-3	HIS	-	expression tag	UNP Q0T963
F	-2	HIS	-	expression tag	UNP Q0T963

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	THR	-	expression tag	UNP Q0T963
F	0	SER	-	expression tag	UNP Q0T963
F	178	ALA	HIS	engineered mutation	UNP Q0T963
B	-11	MET	-	initiating methionine	UNP Q0T963
B	-10	ALA	-	expression tag	UNP Q0T963
B	-9	LYS	-	expression tag	UNP Q0T963
B	-8	SER	-	expression tag	UNP Q0T963
B	-7	HIS	-	expression tag	UNP Q0T963
B	-6	HIS	-	expression tag	UNP Q0T963
B	-5	HIS	-	expression tag	UNP Q0T963
B	-4	HIS	-	expression tag	UNP Q0T963
B	-3	HIS	-	expression tag	UNP Q0T963
B	-2	HIS	-	expression tag	UNP Q0T963
B	-1	THR	-	expression tag	UNP Q0T963
B	0	SER	-	expression tag	UNP Q0T963
B	178	ALA	HIS	engineered mutation	UNP Q0T963

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	40	Total O 40 40	0	0
3	F	9	Total O 9 9	0	0
3	A	48	Total O 48 48	0	0
3	B	13	Total O 13 13	0	0

SER	GLY	THR	GLY	THR	PRO	PRO	PRO	SER	GLU	ASN	ASP	PRO	LYS	GLN	GLN	ASN	GLU	K127	L132	N133	Q134	K135	Q136	I140	K141	K142	T146	N149	A150	L151	K166	P167	V168	P169	K170	E171	D177	A178	M179	Q183	N201	P202	T212	I218	E219	I227						
ASP	ARG	MET	THR	SER	THR	ASP	GLU	LEU	HIS	HIS	THR	SER	ILE	THR	LEU	GLN	MET	ASN	ASP	GLY	ASN	ASP	GLU	ILE	THR	LYS	TYR	SER	GLY	GLY	ALA	ALA	SER	ASN	ASN	ASN	ILE	GLY	LYS	ASP	LEU	THR	ASP	ALA	GLU	LYS	VAL	GLU	LEU	GLY	SER	GLY
MET	LYS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	THR	SER	SER	VAL	GLU	VAL	ASN	ASN	LEU	LEU	VAL	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	LYS	ALA	GLY	MET	GLY	LEU	LEU	ALA	ALA	ALA	ALA	VAL	LYS	ASP	MET

4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	64.01Å 64.01Å 365.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.92 – 2.70 44.92 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (44.92-2.70) 99.3 (44.92-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.43 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.200 , 0.224 (Not available) , 0.221	Depositor DCC
R_{free} test set	1990 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	47.5	Xtriage
Anisotropy	0.717	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.499 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6328	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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: LLP

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	0/2354	0.90	4/3185 (0.1%)
1	E	0.58	0/2359	0.93	3/3192 (0.1%)
2	B	0.59	0/762	0.93	3/1022 (0.3%)
2	F	0.53	0/773	0.90	1/1038 (0.1%)
All	All	0.56	0/6248	0.92	11/8437 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	149	ASN	CA-C-N	-7.10	111.66	119.19
1	E	149	ASN	C-N-CA	-7.10	111.66	119.19
2	B	168	VAL	CA-C-N	6.53	126.49	120.03
2	B	168	VAL	C-N-CA	6.53	126.49	120.03
2	F	172	ASN	N-CA-C	-6.45	104.99	112.92
1	E	152	ILE	CB-CA-C	-6.42	101.86	112.26
1	A	149	ASN	CA-C-N	-6.37	112.44	119.19
1	A	149	ASN	C-N-CA	-6.37	112.44	119.19
2	B	149	ASN	N-CA-C	5.79	118.81	111.69
1	A	146	ASN	CA-C-N	5.77	125.87	119.87
1	A	146	ASN	C-N-CA	5.77	125.87	119.87

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	2346	0	2412	38	0
1	E	2351	0	2414	49	0
2	B	756	0	749	15	0
2	F	765	0	757	10	0
3	A	48	0	0	2	0
3	B	13	0	0	0	0
3	E	40	0	0	0	0
3	F	9	0	0	0	0
All	All	6328	0	6332	103	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 8.

All (103) 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:E:48:ASN:HD22	1:E:152:ILE:HG22	1.56	0.70
2:F:167:PRO:HD2	2:F:169:PRO:HD3	1.74	0.69
1:E:65:LEU:HD22	1:E:141:LEU:HD21	1.76	0.67
1:A:65:LEU:HD22	1:A:141:LEU:HD21	1.78	0.66
1:E:152:ILE:HG12	1:E:153:HIS:N	2.11	0.65
1:E:256:ILE:HG12	1:E:272:ILE:HD12	1.80	0.64
1:E:260:ARG:HH22	1:E:313:ALA:HB3	1.63	0.62
2:B:177:ASP:OD1	2:B:177:ASP:N	2.24	0.61
1:A:228:GLN:HB3	3:A:429:HOH:O	2.03	0.59
1:A:114:THR:HG21	1:A:123:ALA:HA	1.83	0.59
2:F:151:LEU:HD21	2:F:218:ILE:HD11	1.84	0.58
1:E:45:ILE:HG22	1:E:152:ILE:HD11	1.85	0.58
2:B:142:LYS:O	2:B:146:THR:HG23	2.04	0.58
1:E:114:THR:HG21	1:E:123:ALA:HA	1.85	0.58
1:E:44:ARG:HB3	1:E:152:ILE:HG13	1.86	0.57
1:E:45:ILE:O	1:E:49:MET:HB2	2.04	0.57
1:E:164:ASP:HA	1:A:2:GLY:HA3	1.87	0.57
1:A:256:ILE:HG12	1:A:272:ILE:HD12	1.87	0.56
1:A:308:SER:OG	2:B:166:LYS:HE3	2.05	0.55
1:E:38:SER:HB2	1:E:75:ILE:HG22	1.90	0.54
2:F:142:LYS:O	2:F:146:THR:HG23	2.09	0.53
1:A:190:LYS:NZ	1:A:243:LEU:O	2.42	0.53
1:E:252:ASN:HD21	2:F:179:MET:HE1	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:162:TRP:NE1	1:E:193:LYS:HE2	2.24	0.53
1:E:263:MET:HG2	1:E:269:LEU:HA	1.90	0.53
1:E:155:LYS:O	1:E:159:PRO:HG2	2.09	0.52
1:E:2:GLY:HA3	1:A:164:ASP:HA	1.92	0.52
1:A:45:ILE:O	1:A:49:MET:HB2	2.09	0.52
1:E:48:ASN:HD22	1:E:152:ILE:CG2	2.21	0.52
1:A:252:ASN:HD21	2:B:179:MET:HE1	1.75	0.52
1:E:152:ILE:O	1:E:156:THR:N	2.38	0.51
1:E:190:LYS:NZ	1:E:243:LEU:O	2.44	0.50
1:E:171:VAL:HB	1:E:295:ILE:HG12	1.94	0.50
1:A:307:LEU:HA	1:A:312:PHE:CE1	2.47	0.49
1:A:38:SER:HB2	1:A:75:ILE:HG22	1.95	0.49
1:A:263:MET:HG2	1:A:269:LEU:HA	1.95	0.48
1:E:270:ALA:HB1	1:E:274:SER:HB2	1.95	0.48
1:A:257:SER:O	1:A:261:ARG:HG3	2.14	0.48
1:E:49:MET:HG2	1:E:141:LEU:HD12	1.96	0.48
1:E:257:SER:O	1:E:261:ARG:HG3	2.14	0.48
1:E:44:ARG:HH22	1:E:160:GLU:CD	2.22	0.47
1:E:157:THR:O	1:E:161:ILE:HG13	2.14	0.47
1:A:252:ASN:ND2	2:B:179:MET:HE1	2.30	0.47
1:E:30:ALA:HB1	1:E:299:LEU:HD22	1.98	0.46
1:A:36:ASN:HB3	1:A:43:CYS:SG	2.56	0.46
1:E:252:ASN:ND2	2:F:179:MET:HE1	2.30	0.46
1:A:45:ILE:HB	1:A:49:MET:HE3	1.98	0.46
2:B:179:MET:HE3	2:B:183:GLN:NE2	2.31	0.46
1:A:222:PRO:HD2	2:B:219:GLU:OE2	2.15	0.46
1:E:209:PRO:O	1:E:213:GLN:HG3	2.15	0.46
1:E:153:HIS:CG	1:E:181:THR:HA	2.51	0.45
1:E:175:GLY:HA2	1:E:203:VAL:HB	1.98	0.45
1:E:45:ILE:HG22	1:E:152:ILE:CD1	2.45	0.45
1:E:45:ILE:HB	1:E:49:MET:HE3	1.97	0.45
1:E:190:LYS:HA	1:E:195:LYS:O	2.17	0.45
1:A:155:LYS:O	1:A:159:PRO:HG2	2.16	0.45
1:A:33:GLU:OE2	1:A:44:ARG:NH1	2.50	0.45
2:B:136:GLN:O	2:B:140:ILE:HG13	2.16	0.45
1:A:171:VAL:HB	1:A:295:ILE:HG12	1.98	0.45
1:E:48:ASN:HA	1:E:51:TRP:HB2	1.99	0.45
1:A:146:ASN:HA	1:A:147:PRO:HD2	1.80	0.45
2:B:151:LEU:HD21	2:B:218:ILE:HD11	1.98	0.45
1:E:222:PRO:HD2	2:F:219:GLU:OE2	2.17	0.44
1:A:153:HIS:CG	1:A:181:THR:HA	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:272:ILE:HD13	1:E:311:LEU:HD13	2.00	0.44
1:A:44:ARG:HH22	1:A:160:GLU:CD	2.26	0.44
1:A:42:LLP:OP3	1:A:42:LLP:H4'1	2.18	0.44
1:E:156:THR:OG1	1:E:157:THR:N	2.51	0.44
1:A:126:LYS:O	1:A:130:ILE:HG13	2.18	0.44
1:A:49:MET:HG2	1:A:141:LEU:HD12	2.00	0.43
2:F:147:ILE:O	2:F:151:LEU:HB2	2.18	0.43
1:A:79:TYR:CE2	1:A:80:VAL:HG23	2.54	0.43
1:E:92:MET:HE1	1:E:111:LEU:HB3	2.01	0.43
2:F:165:GLY:C	2:F:167:PRO:HD3	2.44	0.43
1:A:156:THR:OG1	1:A:157:THR:N	2.52	0.42
1:E:272:ILE:H	1:E:272:ILE:HG12	1.63	0.42
1:A:209:PRO:O	1:A:213:GLN:HG3	2.18	0.42
1:A:30:ALA:HB1	1:A:299:LEU:HD22	2.00	0.42
1:E:63:VAL:HA	1:E:137:LYS:O	2.20	0.42
2:B:201:ASN:HA	2:B:202:PRO:HD3	1.88	0.42
1:E:42:LLP:HE3	1:E:73:THR:OG1	2.19	0.42
1:E:45:ILE:HB	1:E:49:MET:CE	2.50	0.42
1:E:146:ASN:HA	1:E:147:PRO:HD2	1.82	0.42
2:B:170:LYS:HA	2:B:171:GLU:HA	1.76	0.42
1:E:307:LEU:HA	1:E:312:PHE:CE1	2.55	0.42
2:F:133:ASN:OD1	2:F:136:GLN:HG3	2.20	0.41
1:E:288:GLU:HA	1:E:291:THR:OG1	2.19	0.41
1:A:256:ILE:HG12	1:A:272:ILE:CD1	2.49	0.41
1:A:15:THR:HG22	1:A:35:ARG:O	2.20	0.41
2:B:133:ASN:ND2	2:B:135:LYS:HB3	2.35	0.41
1:A:42:LLP:H4'1	1:A:42:LLP:OP4	2.21	0.41
1:E:120:MET:O	1:E:124:ILE:HG13	2.21	0.41
1:A:35:ARG:HB3	3:A:430:HOH:O	2.21	0.41
1:A:162:TRP:NE1	1:A:193:LYS:HE2	2.36	0.41
2:B:179:MET:HE2	2:B:179:MET:HB3	1.94	0.41
2:F:201:ASN:HA	2:F:202:PRO:HD3	1.92	0.41
1:E:44:ARG:C	1:E:152:ILE:HD12	2.46	0.40
1:E:256:ILE:HG12	1:E:272:ILE:CD1	2.48	0.40
1:E:60:LYS:HB2	1:E:61:PRO:HD2	2.03	0.40
1:A:60:LYS:HB2	1:A:61:PRO:HD2	2.03	0.40
1:A:228:GLN:H	1:A:228:GLN:HG3	1.72	0.40
2:B:132:LEU:HD21	2:B:201:ASN:HB3	2.04	0.40
2:B:151:LEU:HD23	2:B:151:LEU:HA	1.87	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	310/323 (96%)	300 (97%)	10 (3%)	0	100	100
1	E	311/323 (96%)	300 (96%)	11 (4%)	0	100	100
2	B	99/239 (41%)	98 (99%)	1 (1%)	0	100	100
2	F	99/239 (41%)	97 (98%)	2 (2%)	0	100	100
All	All	819/1124 (73%)	795 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	246/257 (96%)	245 (100%)	1 (0%)	84	93
1	E	246/257 (96%)	241 (98%)	5 (2%)	48	76
2	B	77/190 (40%)	74 (96%)	3 (4%)	28	57
2	F	78/190 (41%)	76 (97%)	2 (3%)	40	70
All	All	647/894 (72%)	636 (98%)	11 (2%)	53	79

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	60	LYS
1	E	87	LYS

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Mol	Chain	Res	Type
1	E	92	MET
1	E	110	ASN
1	E	152	ILE
2	F	212	THR
2	F	222	LEU
1	A	110	ASN
2	B	166	LYS
2	B	177	ASP
2	B	212	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	48	ASN
1	E	228	GLN
1	E	285	GLN
2	F	180	GLN
2	F	183	GLN
1	A	21	ASN
1	A	72	ASN
1	A	252	ASN
1	A	285	GLN
2	B	149	ASN
2	B	180	GLN
2	B	183	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	LLP	E	42	1	23,24,25	1.76	4 (17%)	25,32,34	2.39	4 (16%)
1	LLP	A	42	1	23,24,25	1.82	4 (17%)	25,32,34	2.27	4 (16%)

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	LLP	E	42	1	-	3/16/17/19	0/1/1/1
1	LLP	A	42	1	-	5/16/17/19	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	42	LLP	O3-C3	-5.58	1.24	1.36
1	E	42	LLP	O3-C3	-5.32	1.24	1.36
1	A	42	LLP	C2-N1	3.09	1.39	1.33
1	E	42	LLP	C2-N1	3.05	1.39	1.33
1	A	42	LLP	C4-C4'	2.71	1.52	1.46
1	E	42	LLP	C4-C4'	2.59	1.52	1.46
1	A	42	LLP	C6-N1	2.46	1.39	1.34
1	E	42	LLP	C6-N1	2.39	1.39	1.34

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	42	LLP	OP4-C5'-C5	7.64	123.68	109.36
1	A	42	LLP	OP4-C5'-C5	7.19	122.83	109.36
1	E	42	LLP	C5-C4-C4'	-5.58	112.86	121.47
1	A	42	LLP	C5-C4-C4'	-5.44	113.08	121.47
1	A	42	LLP	C3-C4-C4'	3.99	127.61	120.40
1	E	42	LLP	CE-NZ-C4'	-3.99	105.94	118.72
1	E	42	LLP	C3-C4-C4'	3.95	127.54	120.40
1	A	42	LLP	CE-NZ-C4'	-3.46	107.62	118.72

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	42	LLP	C4-C4'-NZ-CE
1	E	42	LLP	CD-CE-NZ-C4'
1	E	42	LLP	CE-CD-CG-CB
1	A	42	LLP	CE-CD-CG-CB
1	A	42	LLP	CA-CB-CG-CD
1	E	42	LLP	CG-CD-CE-NZ
1	A	42	LLP	CG-CD-CE-NZ
1	A	42	LLP	CD-CE-NZ-C4'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	42	LLP	1	0
1	A	42	LLP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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, 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	312/323 (96%)	-1.58	0 100 100	28, 38, 59, 74	0
1	E	313/323 (96%)	-1.57	0 100 100	28, 39, 60, 73	0
2	B	101/239 (42%)	-1.44	0 100 100	33, 45, 98, 128	0
2	F	101/239 (42%)	-1.42	0 100 100	30, 44, 96, 125	0
All	All	827/1124 (73%)	-1.54	0 100 100	28, 40, 62, 128	0

There are no RSRZ outliers to report.

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	LLP	E	42	24/25	1.00	0.03	28,35,42,44	0
1	LLP	A	42	24/25	1.00	0.03	29,36,42,45	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.