



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:32 PM GMT

PDB ID : 1B96
Title : ANALYSIS OF A MUTATIONAL HOT-SPOT IN THE ECORV RESTRICTION ENDONUCLEASE: A CATALYTIC ROLE FOR A MAIN CHAIN CARBONYL GROUP
Authors : Thomas, M.P.; Halford, S.E.; Brady, R.L.
Deposited on : 1999-02-19
Resolution : 2.30 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
<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

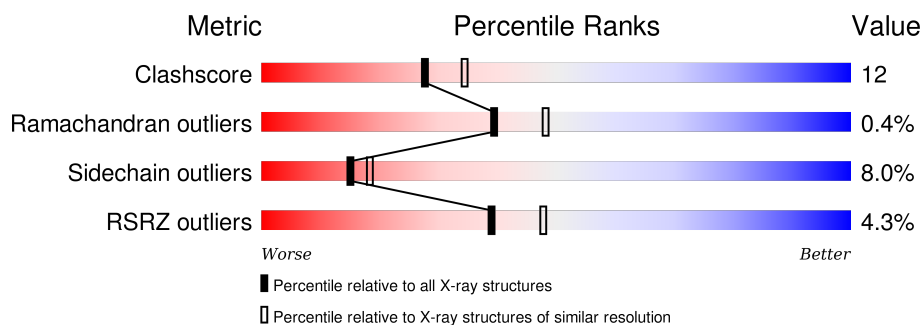
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	C	11	
1	D	11	
2	A	244	
2	B	244	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4779 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 DNA chain called DNA (5'-D(*AP*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	11	Total	C	N	O	P	0	0	0
			223	109	41	63	10			
1	D	11	Total	C	N	O	P	0	0	0
			223	109	41	63	10			

- Molecule 2 is a protein called RESTRICTION ENDONUCLEASE ECORV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	244	Total	C	N	O	S	0	2	0
			2031	1306	342	382	1			
2	B	244	Total	C	N	O	S	0	0	0
			2023	1300	340	382	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	GLU	GLN	ENGINEERED	UNP P04390
B	69	GLU	GLN	ENGINEERED	UNP P04390

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	144	Total	O	0	0
			144	144		
3	B	103	Total	O	0	0
			103	103		
3	C	12	Total	O	0	0
			12	12		
3	D	20	Total	O	0	0
			20	20		

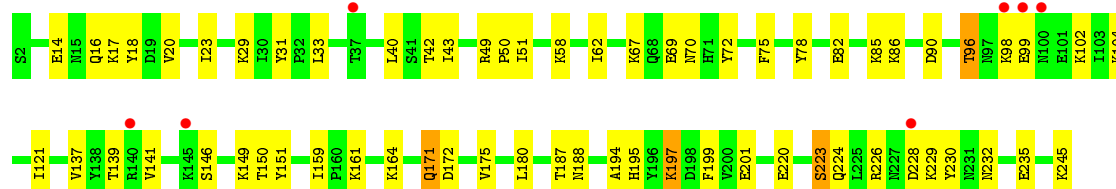
- Molecule 1: DNA (5'-D(*AP*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3')



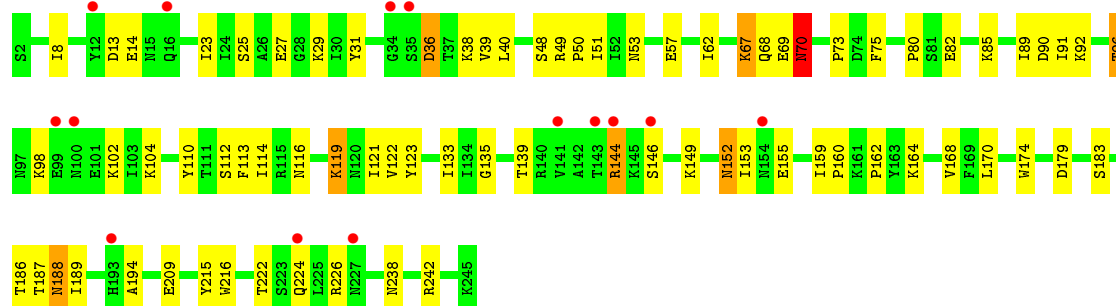
- Chain D:  9% 18% 27% 55%



- Chain A: 



- Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	48.35Å 48.78Å 63.64Å 96.61° 108.94° 107.44°	Depositor
Resolution (Å)	12.50 – 2.30 12.46 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (12.50-2.30) 88.5 (12.46-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.30Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.189 , 0.282 0.193 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 59.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 21703 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4779	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.79% 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

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	C	1.08	0/250	2.31	16/384 (4.2%)
1	D	1.03	0/250	2.15	12/384 (3.1%)
2	A	0.36	0/2092	0.96	0/2826
2	B	0.36	0/2074	0.97	3/2804 (0.1%)
All	All	0.48	0/4666	1.19	31/6398 (0.5%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2	DA	P-O3'-C3'	12.54	134.75	119.70
1	D	8	DT	P-O3'-C3'	10.59	132.41	119.70
1	D	3	DA	P-O3'-C3'	10.00	131.70	119.70
1	C	8	DT	P-O3'-C3'	9.71	131.36	119.70
1	C	1	DA	O4'-C4'-C3'	-9.02	100.59	106.00
1	D	10	DT	P-O3'-C3'	8.43	129.82	119.70
1	C	1	DA	C4'-C3'-C2'	-7.90	95.99	103.10
1	C	6	DT	O4'-C4'-C3'	-7.60	101.44	106.00
1	C	3	DA	P-O3'-C3'	7.54	128.75	119.70
1	D	7	DA	P-O3'-C3'	7.53	128.73	119.70
1	C	7	DA	P-O3'-C3'	7.03	128.13	119.70
1	D	1	DA	O4'-C4'-C3'	-6.95	101.72	104.50
1	C	10	DT	P-O3'-C3'	6.77	127.82	119.70
1	D	1	DA	P-O3'-C3'	6.68	127.71	119.70
1	C	4	DG	O4'-C1'-N9	6.30	112.41	108.00
1	C	10	DT	C5-C6-N1	-6.29	119.93	123.70
2	B	36	ASP	CB-CG-OD1	6.21	123.89	118.30
1	C	8	DT	C5-C6-N1	-6.18	119.99	123.70
1	D	10	DT	C5'-C4'-C3'	6.12	125.11	114.10
2	B	70	ASN	CA-CB-CG	6.11	126.84	113.40
1	D	2	DA	O4'-C1'-N9	-6.05	103.76	108.00
1	D	1	DA	C4'-C3'-C2'	-6.03	97.67	103.10
1	D	2	DA	P-O3'-C3'	6.00	126.89	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	6	DT	C5-C6-N1	-5.70	120.28	123.70
1	C	1	DA	P-O3'-C3'	5.60	126.42	119.70
1	C	6	DT	C4-C5-C6	5.58	121.35	118.00
1	C	10	DT	O4'-C1'-N1	-5.52	104.14	108.00
1	D	10	DT	O4'-C1'-N1	-5.35	104.25	108.00
1	D	6	DT	C4-C5-C6	5.13	121.08	118.00
2	B	96	THR	N-CA-CB	5.04	119.87	110.30
1	C	10	DT	C4-C5-C6	5.01	121.01	118.00

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	C	223	0	127	7	0
1	D	223	0	127	14	0
2	A	2031	0	2003	42	0
2	B	2023	0	1985	56	0
3	A	144	0	0	0	0
3	B	103	0	0	2	0
3	C	12	0	0	0	0
3	D	20	0	0	0	0
All	All	4779	0	4242	102	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 (102) 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:1:DA:O5'	1:C:1:DA:H2'	1.51	1.09
2:A:67[A]:LYS:HG2	2:B:144:ARG:NE	1.81	0.96
1:D:9:DC:H2''	1:D:10:DT:H5'	1.52	0.92
2:A:67[A]:LYS:HG2	2:B:144:ARG:CD	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:67[A]:LYS:HG2	2:B:144:ARG:HD2	1.60	0.82
2:B:14:GLU:HG2	2:B:51:ILE:HD11	1.67	0.76
1:C:1:DA:O5'	1:C:1:DA:C2'	2.27	0.75
1:C:2:DA:H61	1:D:11:DT:H3	1.33	0.74
2:B:67:LYS:HE2	2:B:68:GLN:H	1.53	0.73
1:C:1:DA:HO5'	1:C:1:DA:H2'	1.51	0.73
2:B:49:ARG:HG2	2:B:75:PHE:HZ	1.54	0.71
2:B:49:ARG:HB2	2:B:50:PRO:HD3	1.76	0.67
2:A:42:THR:HG23	2:B:39:VAL:HG22	1.78	0.66
1:D:1:DA:H5'	1:D:1:DA:N3	2.12	0.65
2:B:62:ILE:HD11	2:B:80:PRO:HG3	1.78	0.64
1:C:1:DA:H2''	1:C:2:DA:C8	2.32	0.63
2:A:67[A]:LYS:CG	2:B:144:ARG:HD2	2.30	0.62
2:A:23:ILE:HG13	2:A:31:TYR:HB2	1.82	0.62
1:C:2:DA:N6	1:D:11:DT:H3	1.98	0.61
2:B:112:SER:HA	2:B:119:LYS:HD2	1.84	0.59
1:D:1:DA:H2''	1:D:2:DA:C8	2.38	0.58
1:D:1:DA:O5'	1:D:1:DA:H2'	2.05	0.57
2:B:82:GLU:HB3	2:B:85:LYS:HG2	1.88	0.55
2:A:102:LYS:HD3	2:A:194:ALA:HA	1.87	0.55
2:A:14:GLU:HG2	2:A:51:ILE:HD11	1.89	0.54
1:D:1:DA:H3'	2:A:180:LEU:HD13	1.90	0.54
2:B:25:SER:HB2	2:B:27:GLU:OE1	2.08	0.54
2:A:228:ASP:OD1	2:A:229:LYS:N	2.42	0.53
2:A:18:TYR:CZ	2:B:29:LYS:HE3	2.45	0.52
1:D:1:DA:N3	1:D:1:DA:C5'	2.72	0.52
1:D:1:DA:N3	1:D:1:DA:H2'	2.23	0.52
2:B:67:LYS:NZ	2:B:122:VAL:HG22	2.24	0.52
2:A:62:ILE:HD12	2:A:78:TYR:CE2	2.44	0.52
2:B:48:SER:HA	2:B:51:ILE:HD12	1.91	0.52
2:B:67:LYS:CD	2:B:67:LYS:H	2.22	0.52
2:B:114:ILE:HG23	3:B:263:HOH:O	2.10	0.51
2:A:69:GLU:O	2:A:70:ASN:HB2	2.11	0.51
2:B:92:LYS:HG2	2:B:133:ILE:HG23	1.94	0.49
2:B:91:ILE:N	2:B:91:ILE:HD12	2.28	0.49
2:A:20:VAL:HG21	2:A:43:ILE:HG23	1.94	0.49
2:B:67:LYS:HE2	2:B:68:GLN:N	2.25	0.48
2:A:49:ARG:HB2	2:A:50:PRO:HD3	1.96	0.47
2:A:49:ARG:HG2	2:A:75:PHE:CZ	2.49	0.47
2:A:67[B]:LYS:HB3	2:B:144:ARG:HD2	1.97	0.47
2:A:96:THR:HG22	2:A:139:THR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:ARG:HG2	2:B:75:PHE:CZ	2.42	0.47
2:B:135:GLY:O	2:B:168:VAL:HA	2.14	0.47
2:B:174:TRP:CD1	2:B:209:GLU:HB2	2.50	0.46
2:A:171:GLN:HG2	2:A:199:PHE:O	2.14	0.46
2:B:121:ILE:HG12	2:B:123:TYR:O	2.15	0.46
2:A:82:GLU:HB3	2:A:85:LYS:HB2	1.96	0.46
1:D:3:DA:P	2:A:223:SER:HB2	2.55	0.46
2:A:146:SER:HB2	2:A:151:TYR:OH	2.17	0.45
1:D:7:DA:H62	2:B:186:THR:HG21	1.80	0.45
2:A:18:TYR:HD1	2:B:27:GLU:HB2	1.81	0.45
2:A:220:GLU:HB2	2:A:226:ARG:HG2	1.99	0.45
2:B:152:ASN:ND2	2:B:155:GLU:HG3	2.31	0.45
2:A:72:TYR:O	2:A:121:ILE:HA	2.16	0.45
2:B:238:ASN:O	2:B:242:ARG:HG3	2.17	0.45
2:B:102:LYS:HD3	2:B:194:ALA:HA	1.99	0.45
2:B:67:LYS:CE	2:B:67:LYS:H	2.30	0.45
2:A:197:LYS:O	2:A:201:GLU:HG3	2.16	0.45
2:B:67:LYS:HD3	2:B:67:LYS:H	1.82	0.44
2:A:20:VAL:HG12	2:A:33:LEU:HD11	1.99	0.44
1:D:7:DA:N6	2:B:186:THR:HG21	2.33	0.44
2:A:49:ARG:HG2	2:A:75:PHE:HZ	1.83	0.44
2:B:8:ILE:HG12	2:B:170:LEU:HB3	2.00	0.44
2:A:172:ASP:HB2	2:A:175:VAL:HG23	2.00	0.44
2:B:40:LEU:HD21	2:B:162:PRO:HG2	2.00	0.44
2:B:112:SER:CA	2:B:119:LYS:HD2	2.48	0.43
2:A:151:TYR:CG	2:A:159:ILE:HG12	2.53	0.43
2:B:179:ASP:HB2	2:B:215:TYR:OH	2.17	0.43
2:A:172:ASP:HB2	2:A:175:VAL:CG2	2.48	0.43
2:A:78:TYR:HB3	2:A:86:LYS:HG2	2.00	0.43
1:D:6:DT:H4'	2:B:70:ASN:HA	2.00	0.43
2:B:96:THR:O	2:B:139:THR:HA	2.19	0.43
2:B:82:GLU:HB3	2:B:85:LYS:CG	2.47	0.42
2:A:229:LYS:HB3	2:A:230:TYR:H	1.73	0.42
2:A:40:LEU:HA	2:A:40:LEU:HD23	1.88	0.42
2:B:113:PHE:HA	2:B:116:ASN:O	2.18	0.42
2:A:102:LYS:HE3	2:A:195:HIS:CD2	2.54	0.42
2:B:67:LYS:HG2	2:B:68:GLN:HG3	2.01	0.42
2:A:23:ILE:CG1	2:A:31:TYR:HB2	2.49	0.42
1:C:1:DA:H1'	1:C:2:DA:H5'	2.01	0.42
2:B:73:PRO:HD2	3:B:280:HOH:O	2.19	0.42
2:B:110:TYR:HB3	2:B:189:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:149:LYS:HE2	2:A:150:THR:O	2.19	0.42
2:B:183:SER:OG	2:B:188:ASN:HB2	2.21	0.41
2:A:49:ARG:HB2	2:A:50:PRO:CD	2.49	0.41
2:B:75:PHE:HB2	2:B:89:ILE:HB	2.01	0.41
2:A:232:ASN:OD1	2:A:235:GLU:HG3	2.21	0.41
2:B:222:THR:O	2:B:226:ARG:HG3	2.21	0.41
1:D:6:DT:O4'	2:B:70:ASN:HB2	2.21	0.41
2:A:62:ILE:HG13	2:A:78:TYR:O	2.20	0.41
2:A:141:VAL:CG2	2:A:164:LYS:HD3	2.51	0.41
2:B:159:ILE:HA	2:B:160:PRO:HD2	1.90	0.41
2:B:189:ILE:HG12	2:B:216:TRP:CD2	2.56	0.41
2:B:62:ILE:CD1	2:B:80:PRO:HG3	2.48	0.41
2:B:53:ASN:O	2:B:57:GLU:HG3	2.20	0.41
2:B:170:LEU:HD23	2:B:170:LEU:C	2.41	0.40
2:A:18:TYR:CE2	2:B:29:LYS:HE3	2.56	0.40
2:B:23:ILE:CG1	2:B:31:TYR:HB2	2.51	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	
2	A	244/244 (100%)	233 (96%)	10 (4%)	1 (0%)	39	48
2	B	242/244 (99%)	232 (96%)	9 (4%)	1 (0%)	39	48
All	All	486/488 (100%)	465 (96%)	19 (4%)	2 (0%)	39	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	187	THR
2	B	187	THR

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	
2	A	222/220 (101%)	205 (92%)	17 (8%)	16	20
2	B	220/220 (100%)	202 (92%)	18 (8%)	14	17
All	All	442/440 (100%)	407 (92%)	35 (8%)	15	19

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	16	GLN
2	A	17	LYS
2	A	29	LYS
2	A	58	LYS
2	A	90	ASP
2	A	96	THR
2	A	98	LYS
2	A	99	GLU
2	A	104	LYS
2	A	137	VAL
2	A	161	LYS
2	A	171	GLN
2	A	188	ASN
2	A	197	LYS
2	A	223	SER
2	A	224	GLN
2	A	245	LYS
2	B	13	ASP
2	B	36	ASP
2	B	38	LYS
2	B	67	LYS
2	B	69	GLU
2	B	70	ASN
2	B	90	ASP
2	B	98	LYS
2	B	104	LYS
2	B	119	LYS

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Mol	Chain	Res	Type
2	B	144	ARG
2	B	146	SER
2	B	149	LYS
2	B	152	ASN
2	B	153	ILE
2	B	164	LYS
2	B	188	ASN
2	B	224	GLN

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

Mol	Chain	Res	Type
2	A	68	GLN
2	A	195	HIS
2	A	224	GLN
2	A	231	ASN
2	B	100	ASN
2	B	224	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	C	11/11 (100%)	-0.46	0 100 100	21, 24, 42, 49	0
1	D	11/11 (100%)	-0.19	1 (9%) 11 17	20, 25, 39, 53	0
2	A	244/244 (100%)	-0.08	7 (2%) 55 64	16, 26, 46, 55	0
2	B	244/244 (100%)	0.02	14 (5%) 27 36	14, 27, 45, 67	0
All	All	510/510 (100%)	-0.05	22 (4%) 39 48	14, 26, 46, 67	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	100	ASN	7.0
2	B	143	THR	5.6
2	B	99	GLU	4.5
2	B	144	ARG	4.0
2	A	228	ASP	3.4
2	A	37	THR	3.0
2	B	224	GLN	2.9
2	B	146	SER	2.9
2	A	100	ASN	2.8
2	A	98	LYS	2.8
1	D	11	DT	2.8
2	B	16	GLN	2.7
2	B	193	HIS	2.6
2	B	227	ASN	2.6
2	A	145[A]	LYS	2.4
2	B	141	VAL	2.3
2	A	140	ARG	2.2
2	B	154	ASN	2.2
2	B	34	GLY	2.1
2	A	99	GLU	2.1
2	B	12	TYR	2.1
2	B	35	SER	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.