Full wwPDB X-ray Structure Validation Report (i)

Feb 6, 2024 – 12:10 PM EST

PDB ID	:	2B0D
Title	:	EcoRV Restriction Endonuclease/GAATTC/Ca2+
Authors	:	Hiller, D.A.; Rodriguez, A.M.; Perona, J.J.
Deposited on	:	2005-09-13
Resolution	:	2.00 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 (i) 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 (1)) were used in the production of this report:

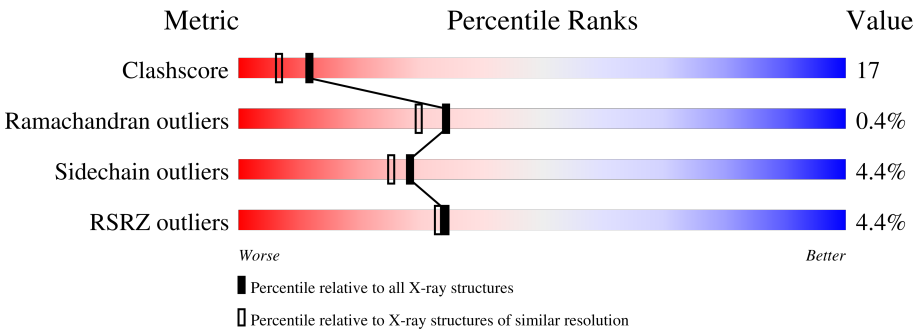
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	9%; 9%, 55%, 36%
1	D	11	9%; 9%, 73%, 9%, 9%
2	A	245	3%; 71%, 22%, • • •
2	B	245	5%; 69%, 25%, • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4488 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 5'-D(*AP*AP*AP*GP*AP*AP*TP*TP*CP*TP*T)-3'.

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

- Molecule 2 is a protein called Type II restriction enzyme EcoRV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	236	1876	1216	309	350	1	0	0	0
2	B	239	1902	1229	315	357	1	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	2	2	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	C	12	12	12	0	0
4	D	18	18	18	0	0
4	A	125	125	125	0	0
4	B	107	107	107	0	0

3 Residue-property plots (i)

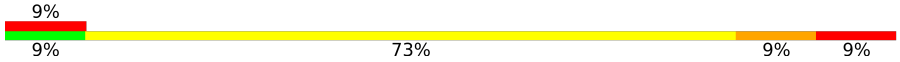
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 5'-D(*AP*AP*AP*GP*AP*AP*TP*TP*CP*TP*T)-3'

Chain C:

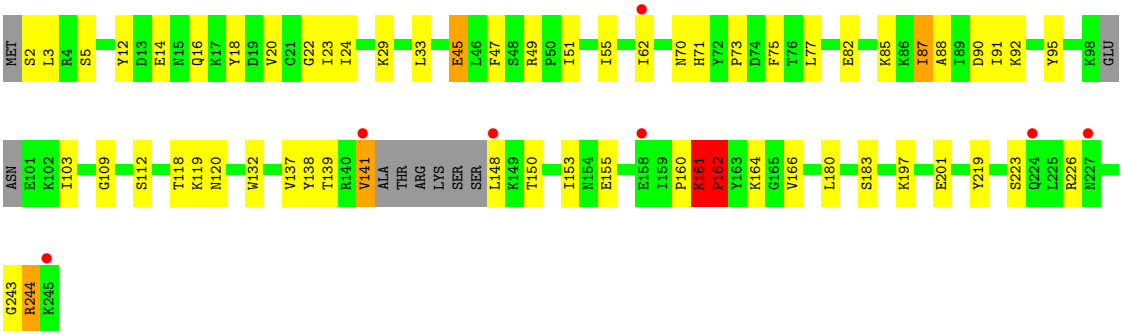
- Molecule 1: 5'-D(*AP*AP*AP*GP*AP*AP*TP*TP*CP*TP*T)-3'

Chain D:



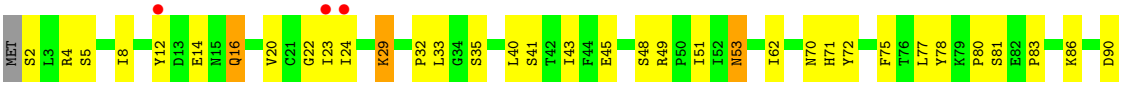
- Molecule 2: Type II restriction enzyme EcoRV

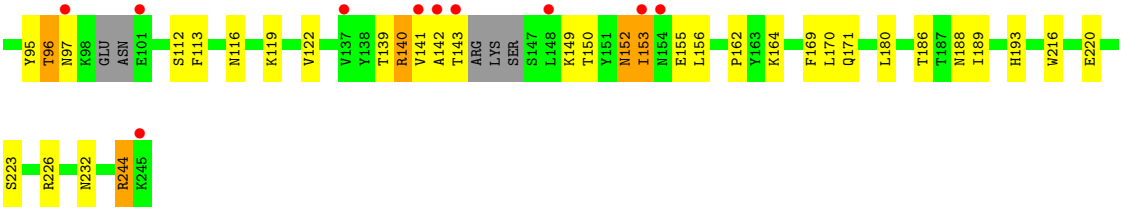
Chain A:



- Molecule 2: Type II restriction enzyme EcoRV

Chain B:




Y95
T96
N97
K98
GLU
ASN
E101
S112
F113
N116
K119
V122
V137
Y138
T139
R140
V141
A142
T143
ARG
LYS
SER
S147
L148
K149
T150
Y151
N152
I153
N154
E155
L156
P162
Y163
K164
F169
L170
Q171
L180
T186
T187
N188
I189
H193
W216
E220
S223
R226
N232
R244
K245

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	48.00Å 48.40Å 63.60Å 97.20° 109.00° 106.60°	Depositor
Resolution (Å)	6.00 – 2.00 19.68 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-2.00) 89.0 (19.68-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.62 (at 2.01Å)	Xtriage
Refinement program	X-PLOR, CNS	Depositor
R, R_{free}	0.220 , 0.302 0.202 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 90.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4488	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.35% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.59	0/250	0.92	0/384
1	D	0.72	0/250	1.24	2/384 (0.5%)
2	A	0.82	6/1925 (0.3%)	1.41	11/2619 (0.4%)
2	B	0.57	2/1951 (0.1%)	0.76	2/2653 (0.1%)
All	All	0.70	8/4376 (0.2%)	1.13	15/6040 (0.2%)

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	C	0	4
1	D	0	1
2	A	0	2
2	B	0	2
All	All	0	9

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	161	LYS	CA-C	13.44	1.88	1.52
2	A	244	ARG	C-N	13.19	1.64	1.34
2	A	161	LYS	C-O	11.58	1.45	1.23
2	B	244	ARG	C-N	9.00	1.54	1.34
2	A	244	ARG	C-O	8.22	1.39	1.23
2	A	161	LYS	CA-CB	-7.14	1.38	1.53
2	B	244	ARG	C-O	5.45	1.33	1.23
2	A	161	LYS	N-CA	-5.08	1.36	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	161	LYS	C-N-CD	-42.64	26.79	120.60
2	A	161	LYS	O-C-N	-33.21	58.00	121.10
2	A	161	LYS	CA-C-N	15.21	159.68	117.10
2	A	162	PRO	N-CD-CG	13.19	122.98	103.20
2	A	162	PRO	CA-N-CD	-11.05	96.03	111.50
2	A	244	ARG	O-C-N	9.93	138.59	122.70
2	A	161	LYS	N-CA-CB	9.01	126.81	110.60
2	A	161	LYS	CA-C-O	-6.13	107.23	120.10
2	B	244	ARG	O-C-N	6.02	132.33	122.70
2	B	244	ARG	CA-C-N	-5.62	104.84	117.20
2	A	160	PRO	C-N-CA	5.56	135.61	121.70
2	A	161	LYS	N-CA-C	-5.38	96.48	111.00
1	D	1	DA	O4'-C1'-C2'	5.37	110.20	105.90
2	A	62	ILE	CB-CG1-CD1	-5.16	99.44	113.90
1	D	8	DT	N1-C1'-C2'	5.13	122.35	112.60

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	161	LYS	Mainchain,Peptide
2	B	142	ALA	Peptide
2	B	244	ARG	Mainchain
1	C	10	DT	Sidechain
1	C	2	DA	Sidechain
1	C	4	DG	Sidechain
1	C	6	DA	Sidechain
1	D	1	DA	Sidechain

5.2 Too-close contacts (i)

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	24	0
1	D	223	0	127	22	0
2	A	1876	0	1755	53	0
2	B	1902	0	1783	60	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	125	0	0	1	0
4	B	107	0	0	5	0
4	C	12	0	0	2	0
4	D	18	0	0	0	0
All	All	4488	0	3792	138	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 17.

All (138) 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)
2:A:161:LYS:CA	2:A:162:PRO:HD2	1.28	1.58
2:A:161:LYS:CA	2:A:161:LYS:C	1.87	1.39
2:A:161:LYS:CA	2:A:162:PRO:CD	2.10	1.28
2:B:141:VAL:HB	2:B:143:THR:O	1.40	1.17
2:A:161:LYS:CB	2:A:162:PRO:HD2	1.92	0.98
2:A:49:ARG:HG2	2:A:75:PHE:HZ	1.28	0.97
1:D:1:DA:H2"	1:D:2:DA:H5'	1.49	0.92
1:C:10:DT:H2"	1:C:11:DT:H71	1.51	0.91
1:C:10:DT:C2'	1:C:11:DT:H71	2.05	0.86
2:B:141:VAL:CB	2:B:143:THR:O	2.25	0.83
2:A:49:ARG:HG2	2:A:75:PHE:CZ	2.17	0.78
2:B:4:ARG:O	2:B:8:ILE:HG13	1.84	0.78
1:C:2:DA:H3'	2:B:223:SER:OG	1.85	0.77
1:D:1:DA:H2"	1:D:2:DA:C5'	2.14	0.77
1:C:10:DT:H2"	1:C:11:DT:C7	2.15	0.77
2:A:23:ILE:HD13	2:B:23:ILE:HG22	1.67	0.76
2:B:41:SER:O	2:B:45:GLU:HG3	1.85	0.76
2:A:45:GLU:HG2	2:A:91:ILE:HD12	1.67	0.75
1:C:5:DA:H2'	1:C:6:DA:C8	2.23	0.73
1:C:10:DT:H2"	1:C:11:DT:C6	2.23	0.72
2:A:161:LYS:C	2:A:161:LYS:N	2.44	0.71
1:D:1:DA:H2'	1:D:2:DA:O4'	1.91	0.70
1:C:10:DT:H2"	1:C:11:DT:C5	2.26	0.70
2:B:112:SER:HA	2:B:119:LYS:HD3	1.74	0.69
2:B:78:TYR:HB3	2:B:86:LYS:HG2	1.75	0.68
2:B:220:GLU:HB2	2:B:226:ARG:HG2	1.74	0.68
1:D:1:DA:H5"	2:A:180:LEU:HD13	1.78	0.66
2:B:62:ILE:HD11	2:B:80:PRO:HG3	1.77	0.66
2:A:161:LYS:CA	2:A:162:PRO:HD3	2.21	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:112:SER:HA	2:A:119:LYS:HG2	1.80	0.64
1:C:10:DT:C2'	1:C:11:DT:C7	2.72	0.64
1:C:5:DA:H2'	1:C:6:DA:H8	1.64	0.63
1:D:4:DG:H2"	1:D:5:DA:H8	1.64	0.62
2:A:45:GLU:O	2:A:49:ARG:HG3	2.00	0.61
2:B:20:VAL:HG11	2:B:43:ILE:HG23	1.81	0.61
1:D:2:DA:H5"	2:A:223:SER:OG	2.01	0.60
2:B:48:SER:HA	2:B:51:ILE:HD12	1.84	0.60
1:C:9:DC:H1'	2:B:70:ASN:HD21	1.67	0.60
2:A:119:LYS:HG3	2:A:120:ASN:HD22	1.67	0.60
1:C:10:DT:H2'	1:C:11:DT:H71	1.84	0.60
2:B:116:ASN:HB3	2:B:119:LYS:HB2	1.83	0.59
1:C:6:DA:O4'	2:A:70:ASN:HA	2.04	0.58
2:A:148:LEU:HD13	2:B:53:ASN:ND2	2.17	0.58
2:B:32:PRO:HB2	4:B:351:HOH:O	2.03	0.58
1:D:10:DT:H2'	1:D:11:DT:C6	2.40	0.57
1:D:3:DA:H2"	1:D:4:DG:C5'	2.35	0.56
2:A:82:GLU:HB3	2:A:85:LYS:HB2	1.87	0.56
2:A:153:ILE:HG21	2:B:153:ILE:HG12	1.86	0.56
2:B:70:ASN:ND2	4:B:312:HOH:O	2.35	0.56
1:D:4:DG:H2"	1:D:5:DA:C8	2.41	0.55
2:B:113:PHE:HA	2:B:116:ASN:O	2.07	0.55
1:D:1:DA:C2'	1:D:2:DA:O4'	2.55	0.55
1:D:2:DA:C6	1:D:3:DA:C2	2.95	0.55
1:D:1:DA:C2'	1:D:2:DA:C5'	2.85	0.54
2:A:87:ILE:HD11	2:A:132:TRP:CE3	2.43	0.54
2:A:2:SER:N	2:A:5:SER:HG	2.06	0.53
2:B:152:ASN:OD1	2:B:155:GLU:HG3	2.08	0.53
2:A:14:GLU:HG2	2:A:51:ILE:HD11	1.91	0.53
1:D:3:DA:H2"	1:D:4:DG:O5'	2.09	0.52
2:A:20:VAL:HG12	2:A:33:LEU:HD11	1.89	0.52
2:B:20:VAL:HG11	2:B:43:ILE:CG2	2.39	0.52
2:A:77:LEU:HB2	2:A:87:ILE:HG23	1.90	0.52
2:B:97:ASN:HA	2:B:140:ARG:CG	2.40	0.52
1:C:1:DA:H5"	2:B:180:LEU:HD13	1.91	0.52
2:A:103:ILE:CD1	2:A:137:VAL:HG21	2.40	0.51
2:A:87:ILE:HD11	2:A:132:TRP:CD2	2.45	0.51
1:C:9:DC:H1'	2:B:70:ASN:ND2	2.26	0.51
2:B:2:SER:N	2:B:5:SER:HG	2.08	0.51
2:B:62:ILE:CD1	2:B:80:PRO:HG3	2.42	0.49
2:A:18:TYR:CZ	2:B:29:LYS:NZ	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:TYR:CD2	2:B:140:ARG:HG2	2.47	0.49
2:A:23:ILE:CD1	2:B:23:ILE:HG22	2.41	0.49
1:D:10:DT:H2"	1:D:11:DT:O4'	2.13	0.49
1:D:2:DA:H2"	1:D:3:DA:C5'	2.43	0.49
2:B:35:SER:HA	2:B:162:PRO:HB2	1.95	0.48
1:C:4:DG:H8	4:C:446:HOH:O	1.97	0.48
1:D:3:DA:H2"	1:D:4:DG:O4'	2.14	0.48
2:A:29:LYS:HE2	2:A:150:THR:CB	2.44	0.48
1:D:8:DT:H2"	1:D:9:DC:O5'	2.13	0.47
2:A:23:ILE:HD12	2:B:43:ILE:HD12	1.97	0.47
1:D:2:DA:C6	1:D:3:DA:N1	2.83	0.47
1:D:2:DA:H2"	1:D:3:DA:O4'	2.15	0.47
2:B:20:VAL:HG12	2:B:33:LEU:HD11	1.96	0.47
2:A:197:LYS:HG3	2:A:201:GLU:OE2	2.14	0.47
2:B:72:TYR:O	2:B:122:VAL:HG23	2.15	0.47
1:C:3:DA:H2"	4:C:446:HOH:O	2.15	0.46
2:B:81:SER:C	2:B:83:PRO:HD3	2.36	0.46
1:C:1:DA:H2"	1:C:2:DA:C8	2.50	0.46
2:A:103:ILE:HD12	2:A:137:VAL:HG21	1.98	0.46
1:C:2:DA:C3'	2:B:223:SER:OG	2.60	0.46
1:C:10:DT:H2'	1:C:11:DT:C7	2.44	0.45
2:B:40:LEU:HD23	2:B:40:LEU:HA	1.70	0.45
2:A:73:PRO:HG3	2:A:88:ALA:HB1	1.99	0.45
2:B:12:TYR:O	2:B:16:GLN:HB2	2.16	0.45
2:A:12:TYR:O	2:A:16:GLN:HG2	2.16	0.45
2:B:83:PRO:O	2:B:86:LYS:HG3	2.16	0.45
2:A:153:ILE:HD13	2:B:153:ILE:HG13	1.98	0.45
1:C:10:DT:C2'	1:C:11:DT:C5	2.99	0.45
2:A:153:ILE:C	2:A:155:GLU:H	2.21	0.45
1:C:9:DC:H2'	1:C:10:DT:H72	1.98	0.45
2:B:140:ARG:HA	4:B:332:HOH:O	2.17	0.45
2:A:119:LYS:O	2:A:120:ASN:HB2	2.17	0.44
2:A:137:VAL:O	2:A:166:VAL:HA	2.17	0.44
2:A:95:TYR:HB3	2:A:138:TYR:CZ	2.53	0.44
2:A:24:ILE:HD13	2:B:156:LEU:HD21	1.98	0.44
2:A:29:LYS:HE2	2:A:150:THR:HG21	2.00	0.44
2:A:141:VAL:HG12	2:A:162:PRO:C	2.38	0.44
2:B:232:ASN:ND2	4:B:272:HOH:O	2.50	0.44
2:A:14:GLU:HG3	2:A:47:PHE:CZ	2.52	0.44
2:A:3:LEU:HD12	2:A:55:ILE:HG22	1.99	0.43
2:B:96:THR:O	2:B:139:THR:HA	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:73:PRO:HG3	2:A:88:ALA:CB	2.48	0.43
2:B:62:ILE:O	2:B:77:LEU:HA	2.17	0.43
2:B:193:HIS:HE1	4:B:346:HOH:O	2.02	0.43
1:C:9:DC:C1'	2:B:70:ASN:HD21	2.31	0.43
2:B:139:THR:HB	2:B:164:LYS:HB3	2.00	0.43
2:B:24:ILE:HD11	2:B:153:ILE:CD1	2.48	0.42
2:B:95:TYR:HD2	2:B:140:ARG:HG2	1.82	0.42
1:D:2:DA:H2"	1:D:3:DA:H5'	2.01	0.42
2:B:189:ILE:HG23	2:B:216:TRP:CE2	2.54	0.42
1:C:1:DA:H5"	2:B:180:LEU:CD1	2.50	0.42
1:D:7:DT:O4	2:B:186:THR:HG21	2.19	0.42
2:A:139:THR:HB	2:A:164:LYS:HB3	2.02	0.41
2:B:149:LYS:HG2	2:B:150:THR:N	2.35	0.41
2:A:112:SER:CA	2:A:119:LYS:HG2	2.49	0.41
2:A:109:GLY:HA3	4:A:572:HOH:O	2.20	0.41
2:B:169:PHE:C	2:B:169:PHE:CD1	2.94	0.41
1:C:8:DT:OP2	2:A:92:LYS:HD2	2.20	0.41
2:A:22:GLY:HA2	2:A:33:LEU:HG	2.03	0.41
2:B:22:GLY:HA2	2:B:33:LEU:HG	2.01	0.41
2:B:141:VAL:CG2	2:B:143:THR:O	2.67	0.41
2:A:243:GLY:O	2:A:244:ARG:HB2	2.21	0.40
2:B:49:ARG:HG3	2:B:75:PHE:HE1	1.85	0.40
2:A:219:TYR:CZ	2:A:226:ARG:HD3	2.56	0.40
2:B:78:TYR:CB	2:B:86:LYS:HG2	2.48	0.40
2:B:170:LEU:HD23	2:B:171:GLN:N	2.37	0.40
1:D:4:DG:O6	2:A:183:SER:HB2	2.21	0.40
2:B:51:ILE:H	2:B:51:ILE:HG13	1.69	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	230/245 (94%)	214 (93%)	14 (6%)	2 (1%)	17	11
2	B	233/245 (95%)	222 (95%)	11 (5%)	0	100	100
All	All	463/490 (94%)	436 (94%)	25 (5%)	2 (0%)	34	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	162	PRO
2	A	161	LYS

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	
2	A	190/221 (86%)	184 (97%)	6 (3%)	39	38
2	B	194/221 (88%)	183 (94%)	11 (6%)	20	16
All	All	384/442 (87%)	367 (96%)	17 (4%)	28	25

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	45	GLU
2	A	71	HIS
2	A	87	ILE
2	A	90	ASP
2	A	118	THR
2	A	141	VAL
2	B	14	GLU
2	B	16	GLN
2	B	29	LYS
2	B	53	ASN
2	B	71	HIS
2	B	90	ASP
2	B	96	THR
2	B	140	ARG

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Mol	Chain	Res	Type
2	B	152	ASN
2	B	153	ILE
2	B	188	ASN

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

Mol	Chain	Res	Type
2	A	16	GLN
2	A	84	ASN
2	A	120	ASN
2	B	9	ASN
2	B	15	ASN
2	B	16	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	244:ARG	C	245:LYS	N	1.64

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	C	11/11 (100%)	0.26	1 (9%)	9	8	21, 28, 51, 57	0
1	D	11/11 (100%)	-0.07	1 (9%)	9	8	21, 26, 39, 56	0
2	A	236/245 (96%)	0.02	7 (2%)	50	49	14, 24, 39, 55	0
2	B	239/245 (97%)	0.09	13 (5%)	25	24	11, 23, 41, 68	0
All	All	497/512 (97%)	0.06	22 (4%)	34	33	11, 24, 41, 68	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	143	THR	7.8
2	A	245	LYS	6.0
2	B	245	LYS	5.8
2	B	142	ALA	4.8
2	B	141	VAL	3.7
2	A	158	GLU	3.6
2	B	97	ASN	3.1
2	A	227	ASN	3.1
1	C	1	DA	3.1
2	A	141	VAL	2.9
2	B	24	ILE	2.6
2	B	148	LEU	2.4
2	A	148	LEU	2.4
2	A	62	ILE	2.3
2	B	12	TYR	2.2
1	D	11	DT	2.2
2	B	154	ASN	2.2
2	B	101	GLU	2.1
2	B	153	ILE	2.1
2	B	23	ILE	2.1
2	B	137	VAL	2.1
2	A	224	GLN	2.0

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 monosaccharides 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	CA	A	502	1/1	0.80	0.40	81,81,81,81	0
3	CA	A	246	1/1	0.96	0.12	47,47,47,47	0

6.5 Other polymers (i)

There are no such residues in this entry.