Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 06:39 PM GMT

PDB ID	:	1BSS
Title	:	ECORV-T93A/DNA/CA2+
Authors	:	Perona, J.J.; Horton, N.C.
Deposited on	:	1998-08-30
Resolution	:	2.15 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 (i) symbol.

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
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 (i)

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

The reported resolution of this entry is 2.15 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	Percentile Ranks	Value
Clashscore		21
Ramachandran outliers		1.6%
Sidechain outliers		5.4%

Worse *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
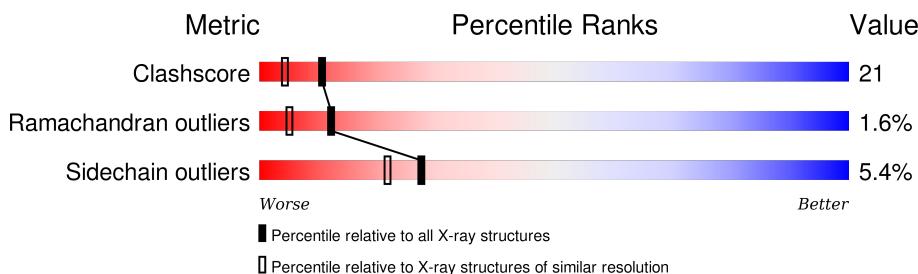
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	11	82% 18%
1	D	11	9% 73% 18%
2	A	244	61% 30% • 6%
2	B	244	59% 32% • 7%
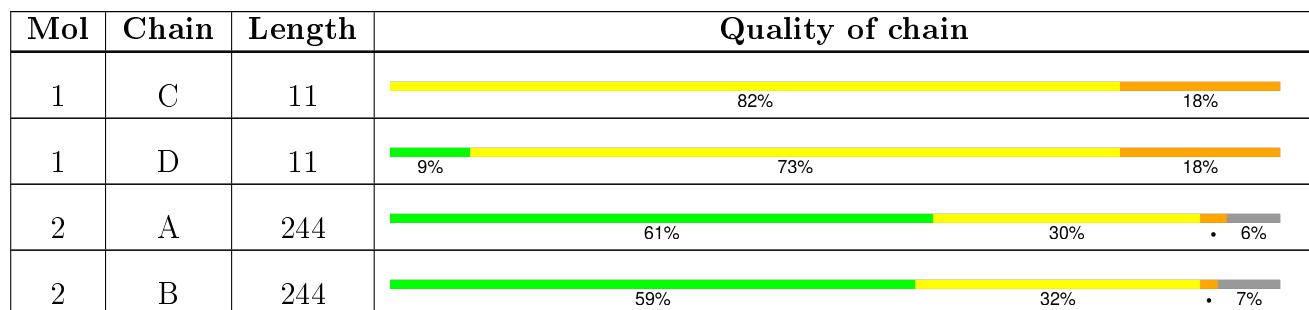
2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4186 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*TP*AP*TP*CP*TP*T)-3'.

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

- Molecule 2 is a protein called ECORV ENDONUCLEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	230	Total 1795	C 1164	N 291	O 339	S 1	0	0	0
2	B	228	Total 1777	C 1153	N 294	O 329	S 1	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93	ALA	THR	ENGINEERED	UNP P04390
B	93	ALA	THR	ENGINEERED	UNP P04390

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

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	78	Total 78	O 78	0	0
4	B	57	Total 57	O 57	0	0

Continued on next page...

Continued from previous page...

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	11	Total 11	O 11	0	0
4	D	20	Total 20	O 20	0	0

3 Residue-property plots (i)

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.

Note EDS was not executed.

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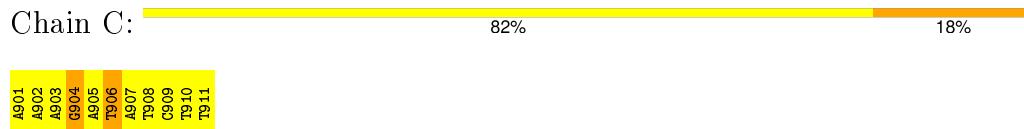
Chain C:

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

Chain D:

- Molecule 2: ECORV ENDONUCLEASE

Chain A:

- Molecule 2: ECORV ENDONUCLEASE

Chain B:

R217 N218 Y219 E220 R221 T222 L225 R226 Y230 N231 N232 E235 Y236 R237 N238 W239 I240 Y241 R242 K245
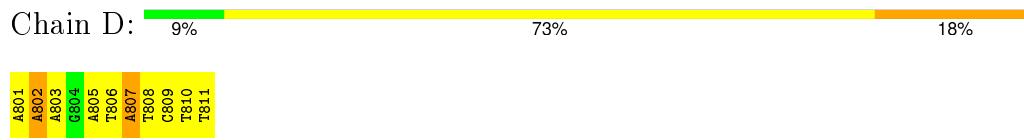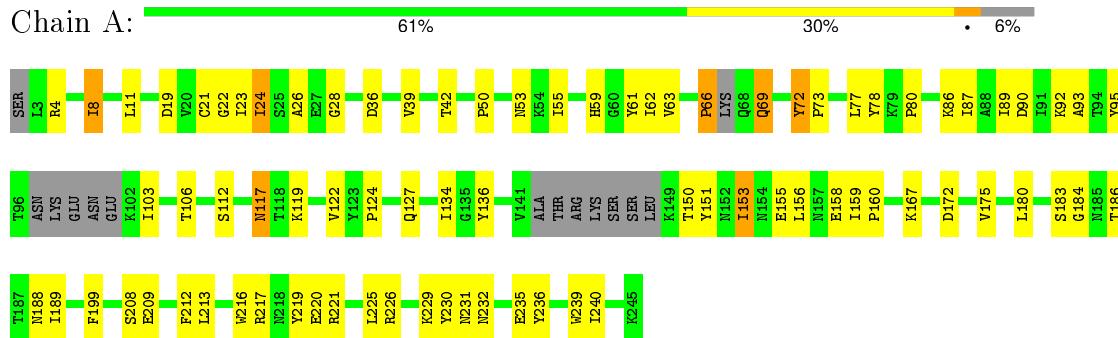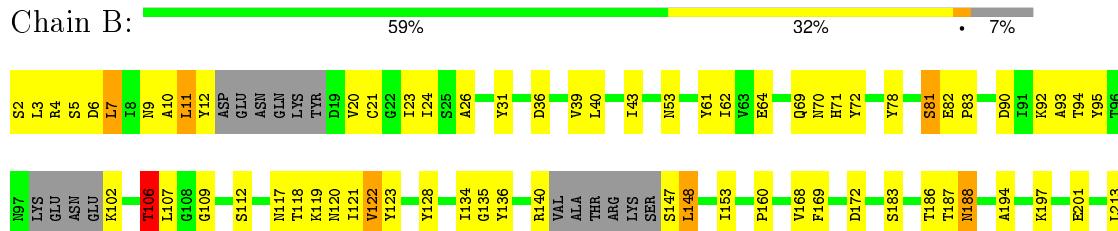
4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	50.00Å 64.40Å 49.20Å 109.20° 108.70° 95.80°	Depositor
Resolution (Å)	6.00 – 2.15	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.15)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.184 , 0.246	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4186	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

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	0.81	0/250	0.95	0/384
1	D	0.78	0/250	1.00	0/384
2	A	0.55	0/1843	0.76	2/2516 (0.1%)
2	B	0.58	0/1823	0.80	2/2482 (0.1%)
All	All	0.60	0/4166	0.81	4/5766 (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	C	0	2
1	D	0	2
2	A	0	2
All	All	0	6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	72	TYR	C-N-CD	-6.17	107.04	120.60
2	B	106	THR	N-CA-C	-5.91	95.04	111.00
2	A	72	TYR	C-N-CD	-5.10	109.38	120.60
2	A	106	THR	N-CA-C	-5.01	97.47	111.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	219	TYR	Sidechain
2	A	95	TYR	Sidechain
1	C	904	DG	Sidechain
1	C	906	DT	Sidechain
1	D	802	DA	Sidechain
1	D	807	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	23	0
2	A	1795	0	1634	63	0
2	B	1777	0	1639	73	0
3	A	2	0	0	0	0
4	A	78	0	0	5	0
4	B	57	0	0	1	0
4	C	11	0	0	1	0
4	D	20	0	0	0	0
All	All	4186	0	3527	157	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 21.

All (157) 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:D:806:DT:C2'	1:D:807:DA:H5"	1.76	1.14
1:D:806:DT:H2"	1:D:807:DA:H5"	1.19	1.11
2:A:42:THR:HG21	2:B:39:VAL:HG12	1.38	1.05
2:A:156:LEU:HD11	2:B:26:ALA:HA	1.50	0.94
1:D:807:DA:H62	2:B:186:THR:HG21	1.35	0.87
1:C:906:DT:H2"	1:C:907:DA:H5'	1.56	0.87
1:D:810:DT:H2"	1:D:811:DT:C7	2.05	0.86
1:D:809:DC:H5"	2:A:69:GLN:NE2	1.97	0.80
2:B:39:VAL:O	2:B:43:ILE:HG12	1.82	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:810:DT:H2"	1:D:811:DT:H71	1.66	0.75
1:D:806:DT:C2'	1:D:807:DA:C5'	2.62	0.75
2:A:66:PRO:HB3	2:A:122:VAL:CG2	2.18	0.74
1:D:811:DT:OP2	1:D:811:DT:H71	1.87	0.73
1:C:901:DA:H2'	1:C:902:DA:C8	2.23	0.73
1:D:801:DA:H5"	2:A:180:LEU:HD13	1.70	0.73
1:D:801:DA:H2'	1:D:802:DA:C8	2.24	0.73
1:D:801:DA:H2"	1:D:802:DA:C5'	2.19	0.72
2:A:23:ILE:HD12	2:B:20:VAL:HG21	1.71	0.72
1:C:902:DA:H2"	1:C:903:DA:OP2	1.90	0.72
2:A:42:THR:CG2	2:B:39:VAL:HG12	2.17	0.71
1:D:809:DC:H5"	2:A:69:GLN:HE22	1.55	0.71
1:C:910:DT:H2"	1:C:911:DT:C6	2.26	0.71
1:D:801:DA:H2"	1:D:802:DA:H5'	1.73	0.70
1:C:909:DC:H2"	1:C:910:DT:H5'	1.73	0.70
2:B:222:THR:OG1	2:B:225:LEU:HD13	1.91	0.69
1:C:907:DA:H62	2:A:186:THR:HG21	1.57	0.68
2:B:148:LEU:H	2:B:148:LEU:HD12	1.59	0.68
1:D:810:DT:H2"	1:D:811:DT:C5	2.28	0.67
1:C:910:DT:H2"	1:C:911:DT:C5	2.30	0.66
2:B:238:ASN:O	2:B:242:ARG:HG3	1.96	0.66
1:D:806:DT:H2'	1:D:807:DA:H5"	1.74	0.66
2:A:66:PRO:HB3	2:A:122:VAL:HG21	1.78	0.66
2:A:124:PRO:HD2	2:A:127:GLN:NE2	2.11	0.65
2:A:153:ILE:HD12	2:A:153:ILE:H	1.63	0.64
2:A:4:ARG:O	2:A:8:ILE:HG13	1.98	0.63
2:B:102:LYS:HA	2:B:194:ALA:O	2.01	0.61
2:B:93:ALA:HA	2:B:136:TYR:O	2.00	0.60
1:C:901:DA:C5	1:C:902:DA:C2	2.90	0.59
2:A:23:ILE:HG21	2:B:43:ILE:HD12	1.83	0.59
2:B:81:SER:C	2:B:83:PRO:HD3	2.23	0.59
2:B:236:TYR:O	2:B:239:TRP:HB3	2.03	0.58
2:A:183:SER:OG	2:A:188:ASN:HB2	2.04	0.58
2:B:62:ILE:HD11	2:B:78:TYR:CE2	2.39	0.58
2:B:213:LEU:O	2:B:217:ARG:HG3	2.04	0.57
2:A:220:GLU:HB2	2:A:226:ARG:HG2	1.86	0.57
2:B:3:LEU:HD12	2:B:61:TYR:CE1	2.40	0.57
2:B:121:ILE:HD11	2:B:128:TYR:CE1	2.40	0.57
2:A:112:SER:HA	2:A:119:LYS:HD3	1.87	0.56
2:B:197:LYS:O	2:B:201:GLU:HG3	2.06	0.56
2:B:95:TYR:CZ	2:B:140:ARG:NH2	2.73	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:122:VAL:HG22	2:B:123:TYR:CD2	2.42	0.55
2:B:24:ILE:HD11	2:B:153:ILE:HD11	1.89	0.55
1:C:910:DT:H5"	2:B:70:ASN:ND2	2.20	0.55
2:A:151:TYR:CG	2:A:159:ILE:HG12	2.41	0.55
2:B:183:SER:OG	2:B:188:ASN:HB2	2.05	0.55
2:B:23:ILE:CG1	2:B:31:TYR:HB2	2.36	0.55
2:B:11:LEU:HD11	2:B:134:ILE:HD13	1.88	0.54
1:C:901:DA:H2"	1:C:902:DA:O5'	2.07	0.54
2:B:112:SER:HA	2:B:119:LYS:HD3	1.90	0.54
2:A:19:ASP:HA	4:A:479:HOH:O	2.07	0.54
1:D:801:DA:H2"	1:D:802:DA:O4'	2.08	0.53
2:A:220:GLU:HB3	2:A:225:LEU:HB2	1.90	0.53
2:B:219:TYR:CE1	2:B:226:ARG:HD3	2.43	0.53
2:A:221:ARG:NH1	4:A:481:HOH:O	2.41	0.53
2:A:156:LEU:CD1	2:B:26:ALA:HA	2.32	0.53
2:B:220:GLU:HB2	2:B:226:ARG:HG2	1.91	0.52
2:A:221:ARG:NH1	4:A:507:HOH:O	2.42	0.52
2:B:147:SER:N	2:B:160:PRO:HG3	2.25	0.52
2:B:36:ASP:O	2:B:39:VAL:HG22	2.09	0.52
2:A:36:ASP:CB	2:A:39:VAL:HG23	2.39	0.51
2:A:209:GLU:O	2:A:212:PHE:HB3	2.09	0.51
2:B:62:ILE:CD1	2:B:64:GLU:HG3	2.41	0.51
2:A:78:TYR:HB3	2:A:86:LYS:HG2	1.93	0.51
1:C:901:DA:H2"	1:C:902:DA:C5'	2.41	0.50
1:D:803:DA:C8	2:A:184:GLY:HA3	2.46	0.50
2:A:220:GLU:HB2	2:A:226:ARG:CG	2.40	0.50
2:A:26:ALA:HA	2:B:21:CYS:SG	2.51	0.50
2:A:21:CYS:SG	2:B:26:ALA:HB2	2.51	0.49
2:A:117:ASN:HD21	2:A:124:PRO:HB3	1.77	0.49
2:A:208:SER:HB2	4:A:503:HOH:O	2.12	0.49
2:B:39:VAL:HG23	2:B:40:LEU:HG	1.95	0.49
1:C:904:DG:H8	4:C:330:HOH:O	1.95	0.49
2:A:93:ALA:HA	2:A:136:TYR:O	2.14	0.48
2:A:124:PRO:HD2	2:A:127:GLN:HE22	1.76	0.48
1:C:901:DA:N7	1:C:902:DA:C2	2.83	0.47
2:A:55:ILE:O	2:A:59:HIS:HD2	1.96	0.47
1:C:911:DT:H73	1:C:911:DT:OP2	2.14	0.47
2:A:221:ARG:NH2	4:A:486:HOH:O	2.48	0.47
1:C:905:DA:H2'	1:C:906:DT:C6	2.50	0.47
2:A:22:GLY:O	2:B:24:ILE:HG22	2.14	0.47
2:B:81:SER:O	2:B:83:PRO:HD3	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:910:DT:H2"	1:C:911:DT:C7	2.44	0.47
2:A:62:ILE:HG12	2:A:80:PRO:HD3	1.96	0.47
2:A:232:ASN:OD1	2:A:235:GLU:HG3	2.15	0.46
1:D:806:DT:H2'	1:D:807:DA:C5'	2.39	0.46
1:D:809:DC:H3'	2:B:95:TYR:OH	2.15	0.46
2:B:10:ALA:C	2:B:12:TYR:H	2.19	0.46
2:A:236:TYR:CE1	2:A:240:ILE:HD11	2.51	0.46
2:A:66:PRO:HB3	2:A:122:VAL:HG22	1.98	0.46
2:B:4:ARG:NH1	2:B:172:ASP:OD1	2.46	0.46
2:B:230:TYR:CD1	2:B:236:TYR:HB2	2.51	0.46
1:C:901:DA:C2'	1:C:902:DA:C8	2.97	0.45
1:D:801:DA:O5'	1:D:802:DA:N7	2.50	0.45
2:A:61:TYR:CD2	2:A:77:LEU:HB3	2.51	0.45
2:A:90:ASP:OD2	2:A:92:LYS:HE2	2.17	0.45
2:B:153:ILE:HD12	2:B:153:ILE:H	1.82	0.45
2:B:39:VAL:HG23	2:B:40:LEU:N	2.32	0.45
2:A:24:ILE:HD11	2:A:28:GLY:HA2	1.99	0.45
1:D:805:DA:H2'	1:D:806:DT:C6	2.52	0.45
2:B:62:ILE:HD11	2:B:78:TYR:CZ	2.52	0.45
2:A:172:ASP:HB2	2:A:175:VAL:HG23	1.99	0.44
2:B:135:GLY:O	2:B:168:VAL:HA	2.17	0.44
2:B:23:ILE:HG13	2:B:31:TYR:HB2	2.00	0.44
2:B:232:ASN:OD1	2:B:235:GLU:HG3	2.16	0.44
2:A:229:LYS:HE2	2:A:239:TRP:CZ2	2.52	0.44
2:A:236:TYR:O	2:A:239:TRP:HB3	2.18	0.44
1:C:906:DT:H2"	1:C:907:DA:C5'	2.39	0.43
2:B:218:ASN:HB2	2:B:230:TYR:OH	2.18	0.43
2:B:121:ILE:HG12	2:B:123:TYR:O	2.18	0.43
2:A:50:PRO:HG2	2:B:31:TYR:CE2	2.53	0.43
2:B:168:VAL:HG22	2:B:169:PHE:N	2.34	0.43
1:D:808:DT:H72	2:B:106:THR:HG21	2.01	0.43
2:B:109:GLY:HA3	4:B:280:HOH:O	2.17	0.43
2:B:6:ASP:O	2:B:9:ASN:HB2	2.19	0.43
2:A:189:ILE:HG23	2:A:216:TRP:CE2	2.54	0.43
2:B:153:ILE:HD12	2:B:153:ILE:N	2.35	0.42
2:B:10:ALA:O	2:B:12:TYR:N	2.52	0.42
2:A:230:TYR:CD1	2:A:230:TYR:O	2.72	0.42
2:B:236:TYR:CZ	2:B:240:ILE:HD11	2.54	0.42
2:A:23:ILE:HG21	2:B:43:ILE:CD1	2.49	0.42
1:C:910:DT:C2'	1:C:911:DT:H72	2.48	0.42
2:A:61:TYR:CE2	2:A:87:ILE:HD12	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:72:TYR:CD1	2:A:73:PRO:HD3	2.54	0.42
2:A:156:LEU:HD11	2:B:26:ALA:CA	2.33	0.42
1:C:908:DT:H73	2:A:188:ASN:ND2	2.35	0.41
2:B:220:GLU:HB2	2:B:226:ARG:CG	2.49	0.41
2:B:92:LYS:HE3	2:B:107:LEU:HA	2.02	0.41
1:C:906:DT:C2'	1:C:907:DA:H5'	2.39	0.41
2:B:23:ILE:HG13	2:B:23:ILE:O	2.21	0.41
2:B:82:GLU:N	2:B:83:PRO:HD3	2.35	0.41
2:A:11:LEU:HD11	2:A:134:ILE:HD13	2.02	0.41
2:A:53:ASN:OD1	2:B:148:LEU:HD22	2.21	0.41
1:C:902:DA:H2	1:D:811:DT:O2	2.03	0.41
1:C:909:DC:O3'	2:B:69:GLN:CB	2.68	0.41
2:B:119:LYS:NZ	2:B:120:ASN:OD1	2.54	0.41
1:C:910:DT:H2"	1:C:911:DT:H72	2.03	0.41
2:A:159:ILE:HA	2:A:160:PRO:HD2	1.82	0.41
2:B:2:SER:N	2:B:5:SER:OG	2.53	0.41
2:A:23:ILE:HD12	2:B:20:VAL:CG2	2.46	0.40
2:B:119:LYS:HG2	2:B:120:ASN:OD1	2.22	0.40
2:A:77:LEU:HD13	2:A:89:ILE:HD12	2.02	0.40
2:B:7:LEU:O	2:B:11:LEU:HG	2.22	0.40
2:B:90:ASP:OD2	2:B:92:LYS:HE2	2.21	0.40
2:A:213:LEU:O	2:A:217:ARG:HG3	2.21	0.40
2:B:95:TYR:N	2:B:95:TYR:CD1	2.90	0.40
2:A:86:LYS:HD2	2:A:127:GLN:HB3	2.02	0.40
2:A:103:ILE:HG13	2:A:199:PHE:CE2	2.56	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	
2	A	224/244 (92%)	207 (92%)	13 (6%)	4 (2%)	11	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	220/244 (90%)	207 (94%)	10 (4%)	3 (1%)	14	7
All	All	444/488 (91%)	414 (93%)	23 (5%)	7 (2%)	12	5

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	69	GLN
2	A	117	ASN
2	A	155	GLU
2	B	117	ASN
2	B	11	LEU
2	B	187	THR
2	A	66	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	
2	A	177/219 (81%)	169 (96%)	8 (4%)	34	30
2	B	175/219 (80%)	164 (94%)	11 (6%)	22	16
All	All	352/438 (80%)	333 (95%)	19 (5%)	27	22

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	8	ILE
2	A	24	ILE
2	A	63	VAL
2	A	150	THR
2	A	153	ILE
2	A	158	GLU
2	A	167	LYS
2	A	231	ASN
2	B	7	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	53	ASN
2	B	71	HIS
2	B	81	SER
2	B	94	THR
2	B	106	THR
2	B	118	THR
2	B	122	VAL
2	B	148	LEU
2	B	188	ASN
2	B	231	ASN

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	15	ASN
2	A	69	GLN
2	A	116	ASN
2	A	188	ASN
2	B	70	ASN
2	B	127	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)

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)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.