Full wwPDB X-ray Structure Validation Report (i)

Oct 18, 2023 – 10:39 PM EDT

PDB ID	:	2I06
Title	:	Escherichia Coli Replication Terminator Protein (Tus) Complexed With DNA-Locked form
Authors	:	Oakley, A.J.; Mulcair, M.D.; Schaeffer, P.M.; Dixon, N.E.
Deposited on	:	2006-08-10
Resolution	:	2.20 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:

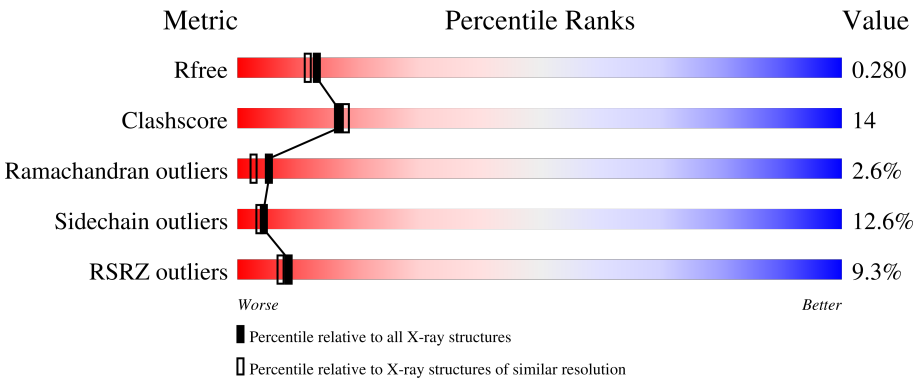
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	B	16	12%; 12%, 50%, 31%, 6%
2	C	16	19%; 25%, 44%, 19%, 12%
3	A	309	8%; 65%, 26%, 7% ••

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	IOD	A	1003	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3106 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(*T*TP*AP*GP*TP*TP*AP*CP*AP*AP*CP*AP*TP*AP*CP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	B	15	286	137	52	83	14	0	0	0

- Molecule 2 is a DNA chain called 5'-D(*TP*G*AP*TP*AP*TP*GP*TP*TP*GP*TP*AP*AP*CP*TP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	14	251	119	40	79	13	0	0	1

- Molecule 3 is a protein called DNA replication terminus site-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	305	2495	1584	469	439	3	0	0	0

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	I		
4	A	3	3	3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	B	5	5	5	0	0
5	C	9	9	9	0	0
5	A	57	57	57	0	0

3 Residue-property plots (i)

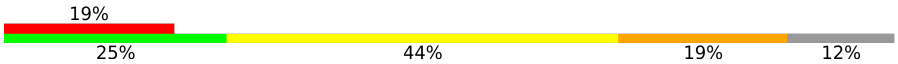
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

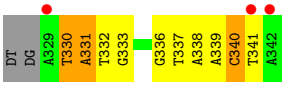
• Molecule 1: 5'-D(*T*TP*AP*GP*TP*TP*AP*CP*AP*AP*CP*AP*TP*AP*CP*T)-3'

Chain B:

• Molecule 2: 5'-D(*TP*G*AP*TP*AP*TP*GP*TP*TP*GP*TP*AP*AP*CP*TP*A)-3'

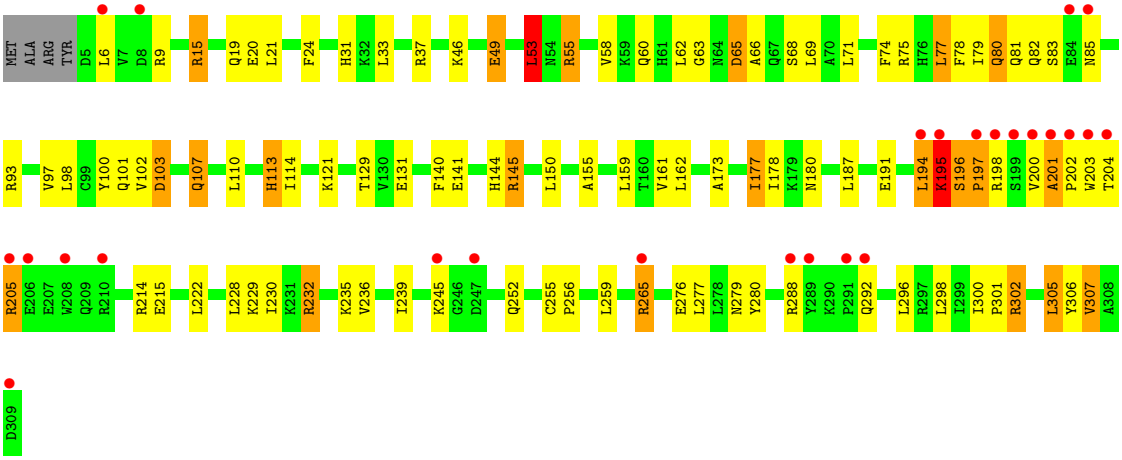
Chain C:





• Molecule 3: DNA replication terminus site-binding protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	62.83Å 62.83Å 252.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 43.76 – 2.20	Depositor EDS
% Data completeness (in resolution range)	64.8 (50.00-2.20) 64.6 (43.76-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	4.29 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.218 , 0.280 0.223 , 0.280	Depositor DCC
R_{free} test set	878 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	32.6	Xtriage
Anisotropy	0.556	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 51.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3106	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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: IOD

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	B	1.47	1/320 (0.3%)	2.80	31/492 (6.3%)
2	C	1.45	1/279 (0.4%)	2.43	18/431 (4.2%)
3	A	0.75	0/2553	0.85	2/3465 (0.1%)
All	All	0.93	2/3152 (0.1%)	1.43	51/4388 (1.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	338	DA	N3-C4	6.37	1.38	1.34
1	B	323	DA	N3-C4	5.46	1.38	1.34

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	318	DA	O4'-C1'-N9	18.57	121.00	108.00
1	B	320	DC	O4'-C4'-C3'	-15.26	96.84	106.00
2	C	338	DA	O4'-C1'-N9	12.90	117.03	108.00
2	C	337	DT	C4-C5-C7	12.77	126.66	119.00
2	C	337	DT	C6-C5-C7	-12.11	115.64	122.90
1	B	315	DT	O4'-C4'-C3'	-11.04	99.37	106.00
1	B	317	DC	O4'-C4'-C3'	-10.66	99.61	106.00
2	C	340	DC	O4'-C1'-N1	10.29	115.20	108.00
1	B	315	DT	C4-C5-C7	9.53	124.72	119.00
1	B	313	DG	O4'-C1'-N9	9.24	114.47	108.00
1	B	317	DC	C1'-O4'-C4'	-9.13	100.97	110.10
1	B	323	DA	O4'-C1'-N9	-8.94	101.74	108.00
1	B	319	DA	O4'-C1'-N9	8.49	113.94	108.00
2	C	330	DT	O4'-C1'-N1	7.76	113.43	108.00
2	C	331	DA	O4'-C1'-N9	7.73	113.41	108.00
1	B	311	DT	C6-C5-C7	-7.71	118.28	122.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	318	DA	C3'-C2'-C1'	-7.51	93.49	102.50
1	B	316	DA	O4'-C1'-N9	7.10	112.97	108.00
1	B	311	DT	C4-C5-C7	6.89	123.14	119.00
1	B	317	DC	P-O5'-C5'	-6.87	109.91	120.90
2	C	332	DT	C5-C4-O4	-6.67	120.23	124.90
2	C	336	DG	C4'-C3'-C2'	-6.51	97.24	103.10
2	C	338	DA	C3'-C2'-C1'	-6.31	94.92	102.50
2	C	332	DT	P-O3'-C3'	6.30	127.26	119.70
2	C	336	DG	C1'-O4'-C4'	-6.12	103.98	110.10
2	C	332	DT	N3-C4-O4	6.09	123.55	119.90
1	B	315	DT	C6-C5-C7	-6.04	119.28	122.90
2	C	338	DA	C1'-O4'-C4'	-6.00	104.10	110.10
1	B	311	DT	O4'-C1'-C2'	-5.99	101.11	105.90
1	B	320	DC	P-O5'-C5'	5.95	130.42	120.90
1	B	314	DT	C5-C4-O4	-5.75	120.88	124.90
3	A	75	ARG	NE-CZ-NH2	-5.74	117.43	120.30
2	C	338	DA	N9-C4-C5	-5.68	103.53	105.80
1	B	321	DA	C2-N3-C4	5.67	113.44	110.60
1	B	312	DA	P-O3'-C3'	5.58	126.39	119.70
2	C	336	DG	C5'-C4'-C3'	5.57	124.12	114.10
1	B	317	DC	C4'-C3'-C2'	-5.50	98.14	103.10
1	B	318	DA	C1'-O4'-C4'	-5.40	104.70	110.10
3	A	53	LEU	CA-CB-CG	5.39	127.70	115.30
1	B	316	DA	P-O3'-C3'	5.38	126.16	119.70
1	B	319	DA	P-O3'-C3'	5.32	126.08	119.70
1	B	314	DT	N3-C4-O4	5.25	123.05	119.90
1	B	318	DA	O4'-C1'-C2'	5.23	110.09	105.90
1	B	313	DG	C2-N3-C4	5.19	114.49	111.90
1	B	319	DA	O4'-C1'-C2'	5.16	110.03	105.90
1	B	313	DG	O4'-C4'-C3'	-5.12	102.45	104.50
2	C	336	DG	P-O3'-C3'	5.11	125.84	119.70
2	C	340	DC	P-O3'-C3'	-5.05	113.64	119.70
1	B	312	DA	O4'-C1'-N9	-5.04	104.47	108.00
1	B	319	DA	N1-C2-N3	-5.01	126.79	129.30
2	C	333	DG	O4'-C1'-N9	5.01	111.51	108.00

There are no chirality outliers.

There are no planarity outliers.

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	B	286	0	159	6	0
2	C	251	0	138	3	0
3	A	2495	0	2533	77	0
4	A	3	0	0	2	0
5	A	57	0	0	4	0
5	B	5	0	0	0	0
5	C	9	0	0	1	0
All	All	3106	0	2830	83	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 14.

All (83) 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)
3:A:55:ARG:HH11	3:A:55:ARG:HG2	1.13	1.13
3:A:80:GLN:HE21	3:A:80:GLN:H	0.97	0.91
3:A:110:LEU:O	3:A:114:ILE:HG12	1.79	0.81
3:A:144:HIS:HE1	3:A:150:LEU:O	1.64	0.81
1:B:323:DA:H2"	1:B:324:DC:H5'	1.65	0.79
3:A:55:ARG:HH11	3:A:55:ARG:CG	1.94	0.78
3:A:55:ARG:HD2	3:A:280:TYR:O	1.84	0.78
3:A:201:ALA:HB3	3:A:202:PRO:HD3	1.64	0.77
3:A:55:ARG:HH21	3:A:279:ASN:HD22	1.33	0.77
3:A:196:SER:HB2	3:A:197:PRO:HD3	1.67	0.77
3:A:55:ARG:HG2	3:A:55:ARG:NH1	1.93	0.76
3:A:78:PHE:H	3:A:81:GLN:HE21	1.34	0.74
3:A:232:ARG:NH1	4:A:1003:IOD:I	2.91	0.74
3:A:78:PHE:H	3:A:81:GLN:NE2	1.86	0.74
3:A:80:GLN:H	3:A:80:GLN:NE2	1.81	0.72
3:A:24:PHE:CZ	3:A:114:ILE:HD11	2.25	0.71
3:A:77:LEU:H	3:A:81:GLN:HE22	1.43	0.67
3:A:141:GLU:HB3	3:A:145:ARG:HH21	1.60	0.67
3:A:300:ILE:HD12	3:A:305:LEU:HD12	1.79	0.64
3:A:20:GLU:OE2	3:A:113:HIS:HE1	1.81	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:78:PHE:HB3	3:A:80:GLN:NE2	2.13	0.64
3:A:31:HIS:HD2	3:A:101:GLN:O	1.83	0.62
3:A:80:GLN:HE21	3:A:80:GLN:N	1.82	0.62
3:A:53:LEU:HD22	3:A:235:LYS:HE3	1.82	0.60
3:A:55:ARG:HH21	3:A:279:ASN:ND2	1.99	0.59
3:A:37:ARG:HH11	3:A:60:GLN:NE2	2.00	0.59
3:A:78:PHE:N	3:A:81:GLN:HE21	2.00	0.59
3:A:200:VAL:HG11	3:A:203:TRP:HE3	1.68	0.59
1:B:311:DT:H2"	1:B:312:DA:N7	2.18	0.59
3:A:180:ASN:ND2	3:A:229:LYS:HE2	2.18	0.57
3:A:46:LYS:O	3:A:49:GLU:HB2	2.06	0.56
3:A:102:VAL:O	3:A:265:ARG:HG3	2.06	0.55
1:B:320:DC:H5'	3:A:129:THR:HG21	1.89	0.54
3:A:204:THR:O	3:A:205:ARG:HB2	2.07	0.54
2:C:330:DT:H2"	2:C:331:DA:O4'	2.09	0.53
3:A:215:GLU:OE1	3:A:302:ARG:NH1	2.42	0.52
3:A:37:ARG:NH1	3:A:276:GLU:HB3	2.25	0.52
3:A:201:ALA:CB	3:A:202:PRO:HD3	2.38	0.51
3:A:140:PHE:O	3:A:144:HIS:HD2	1.93	0.51
1:B:311:DT:O2	3:A:288:ARG:HD2	2.11	0.51
3:A:55:ARG:CG	3:A:55:ARG:NH1	2.59	0.51
3:A:24:PHE:CZ	3:A:114:ILE:CD1	2.94	0.50
3:A:194:LEU:O	3:A:196:SER:N	2.38	0.50
3:A:9:ARG:NH2	3:A:131:GLU:OE1	2.35	0.50
3:A:145:ARG:NH1	5:A:1014:HOH:O	2.36	0.50
3:A:79:ILE:O	3:A:82:GLN:HG2	2.11	0.50
3:A:162:LEU:HD11	3:A:259:LEU:HD13	1.93	0.49
3:A:37:ARG:HH11	3:A:60:GLN:HE22	1.60	0.49
3:A:93:ARG:HG2	3:A:256:PRO:HA	1.94	0.48
3:A:228:LEU:HD23	3:A:307:VAL:HG13	1.95	0.48
3:A:83:SER:C	3:A:85:ASN:H	2.17	0.48
3:A:103:ASP:O	3:A:107:GLN:HB3	2.14	0.47
3:A:178:ILE:HA	3:A:230:ILE:O	2.14	0.47
3:A:20:GLU:OE2	3:A:113:HIS:CE1	2.65	0.47
3:A:296:LEU:HB3	3:A:306:TYR:HB3	1.96	0.47
3:A:62:LEU:O	3:A:65:ASP:HB2	2.13	0.46
3:A:74:PHE:CE1	3:A:159:LEU:CD1	2.99	0.46
1:B:311:DT:O2	3:A:288:ARG:CD	2.64	0.46
3:A:63:GLY:O	3:A:66:ALA:HB3	2.16	0.45
3:A:180:ASN:HD21	3:A:229:LYS:HE2	1.81	0.45
3:A:177:ILE:HD11	4:A:1003:IOD:I	2.87	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:204:THR:HG22	3:A:205:ARG:HG3	1.99	0.45
3:A:24:PHE:CE1	3:A:114:ILE:HD11	2.52	0.45
2:C:339:DA:H2"	2:C:340:DC:O5'	2.17	0.45
3:A:200:VAL:HG22	3:A:201:ALA:H	1.82	0.44
3:A:141:GLU:HB3	3:A:145:ARG:NH2	2.31	0.44
3:A:144:HIS:CE1	3:A:150:LEU:O	2.56	0.44
3:A:200:VAL:CG1	3:A:203:TRP:HE3	2.31	0.44
3:A:33:LEU:HD13	3:A:100:TYR:CZ	2.54	0.43
3:A:173:ALA:HB2	3:A:239:ILE:HD13	2.01	0.42
3:A:298:LEU:HD11	3:A:301:PRO:HA	2.00	0.42
3:A:195:LYS:H	3:A:195:LYS:HG3	1.64	0.42
3:A:145:ARG:NH2	5:A:1014:HOH:O	2.52	0.42
3:A:97:VAL:HG23	3:A:259:LEU:HB2	2.02	0.41
3:A:58:VAL:HG21	3:A:277:LEU:O	2.19	0.41
1:B:318:DA:O5'	1:B:318:DA:H2'	2.21	0.41
3:A:37:ARG:HD3	3:A:60:GLN:NE2	2.36	0.41
3:A:110:LEU:HD23	5:A:1010:HOH:O	2.21	0.41
3:A:15:ARG:HD3	5:A:1022:HOH:O	2.20	0.41
3:A:74:PHE:CD1	3:A:159:LEU:CD1	3.04	0.41
2:C:340:DC:H2"	2:C:341:DT:C6	2.56	0.41
3:A:121:LYS:HG2	3:A:155:ALA:O	2.21	0.41
5:C:32:HOH:O	3:A:235:LYS:HG2	2.21	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
3	A	303/309 (98%)	285 (94%)	10 (3%)	8 (3%)	5 3

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	49	GLU
3	A	194	LEU
3	A	195	LYS
3	A	196	SER
3	A	197	PRO
3	A	201	ALA
3	A	205	ARG
3	A	236	VAL

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
3	A	270/273 (99%)	236 (87%)	34 (13%)	4 3

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	6	LEU
3	A	15	ARG
3	A	19	GLN
3	A	21	LEU
3	A	53	LEU
3	A	55	ARG
3	A	65	ASP
3	A	68	SER
3	A	69	LEU
3	A	71	LEU
3	A	77	LEU
3	A	80	GLN
3	A	98	LEU
3	A	103	ASP
3	A	107	GLN
3	A	113	HIS
3	A	145	ARG
3	A	161	VAL
3	A	177	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	A	187	LEU
3	A	191	GLU
3	A	195	LYS
3	A	198	ARG
3	A	214	ARG
3	A	222	LEU
3	A	232	ARG
3	A	245	LYS
3	A	252	GLN
3	A	255	CYS
3	A	265	ARG
3	A	292	GLN
3	A	302	ARG
3	A	305	LEU
3	A	307	VAL

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

Mol	Chain	Res	Type
3	A	16	GLN
3	A	19	GLN
3	A	30	GLN
3	A	31	HIS
3	A	50	HIS
3	A	51	ASN
3	A	60	GLN
3	A	64	ASN
3	A	67	GLN
3	A	80	GLN
3	A	81	GLN
3	A	113	HIS
3	A	144	HIS
3	A	146	HIS
3	A	163	HIS
3	A	180	ASN
3	A	182	HIS
3	A	189	GLN
3	A	279	ASN
3	A	294	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 3 ligands modelled in this entry, 3 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	B	15/16 (93%)	-0.06	2 (13%)	3	3	53, 62, 83, 87	0
2	C	14/16 (87%)	0.66	3 (21%)	0	0	55, 63, 105, 112	0
3	A	305/309 (98%)	0.48	26 (8%)	10	9	48, 60, 86, 107	0
All	All	334/341 (97%)	0.47	31 (9%)	8	7	48, 60, 87, 112	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	329	DA	6.2
3	A	206	GLU	6.0
3	A	195	LYS	5.7
3	A	200	VAL	5.3
3	A	204	THR	5.1
3	A	198	ARG	5.1
3	A	194	LEU	5.0
3	A	201	ALA	4.1
3	A	309	ASP	3.8
3	A	6	LEU	3.5
3	A	292	GLN	3.4
2	C	342	DA	3.4
3	A	288	ARG	3.3
3	A	291	PRO	3.2
3	A	203	TRP	3.1
3	A	199	SER	3.0
3	A	289	TYR	2.9
3	A	205	ARG	2.9
3	A	85	ASN	2.8
2	C	341	DT	2.8
3	A	265	ARG	2.6
3	A	197	PRO	2.6
1	B	311	DT	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	325	DT	2.4
3	A	210	ARG	2.4
3	A	245	LYS	2.3
3	A	208	TRP	2.1
3	A	202	PRO	2.1
3	A	8	ASP	2.1
3	A	84	GLU	2.1
3	A	247	ASP	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
4	IOD	A	1003	1/1	0.96	0.11	88,88,88,88	1
4	IOD	A	1002	1/1	0.99	0.13	67,67,67,67	1
4	IOD	A	1001	1/1	1.00	0.14	48,48,48,48	1

6.5 Other polymers (i)

There are no such residues in this entry.