Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 10:50 AM GMT

PDB ID	:	3N78
Title	:	SgrAI bound to Secondary Site DNA and Mg(II)
Authors	:	Horton, N.C.; Little, E.J.; Dunten, P.W.
Deposited on	:	2010-05-26
Resolution	:	2.95 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 (1)) were used in the production of this report:

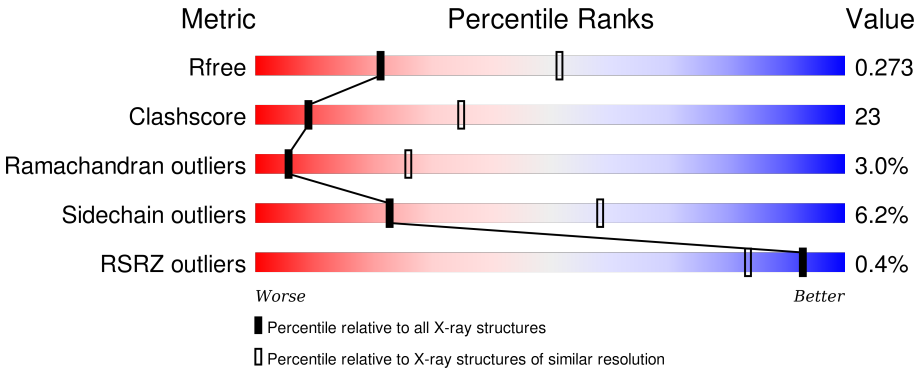
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.95 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}	91344	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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.

Mol	Chain	Length	Quality of chain
1	A	338	58% 37%
1	B	338	% 49% 43% 6%
2	C	16	75% 25%
3	D	16	6% 56% 38%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6625 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 SgraIR restriction enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2628	1667	459	493	9			
1	B	333	Total	C	N	O	S	0	0	0
			2616	1658	463	486	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	ASP	ASN	ENGINEERED MUTATION	UNP Q9F6L0
B	63	ASP	ASN	ENGINEERED MUTATION	UNP Q9F6L0

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*GP*TP*CP*CP*AP*CP*CP*GP*GP*GP*GP*GP*AP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	16	Total	C	N	O	P	0	16	0
			654	310	128	186	30			

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*GP*TP*CP*CP*CP*CP*CP*GP*GP*TP*GP*GP*AP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	16	Total	C	N	O	P	0	16	0
			646	308	118	190	30			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

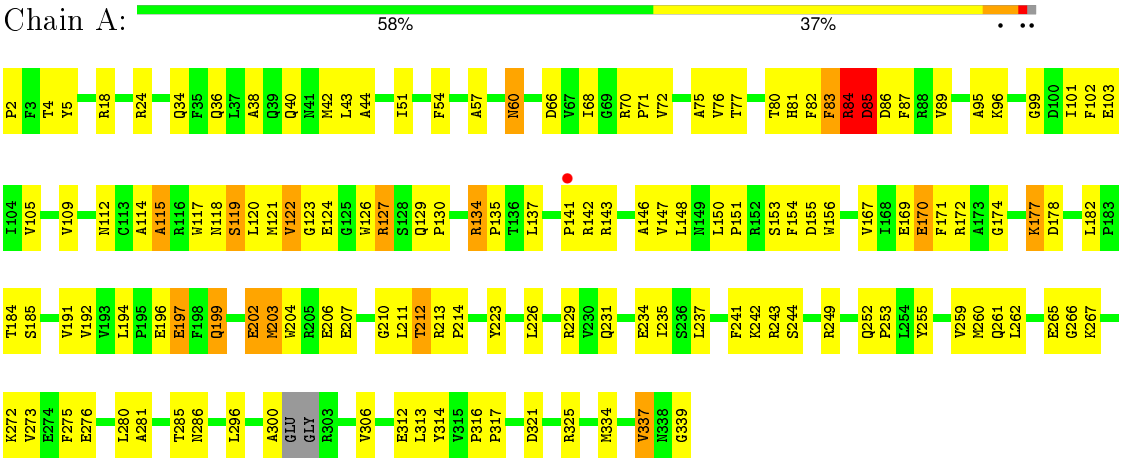
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	29	Total O 29 29	0	0
5	B	38	Total O 38 38	0	0
5	C	11	Total O 11 11	0	0
5	D	1	Total O 1 1	0	0

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.

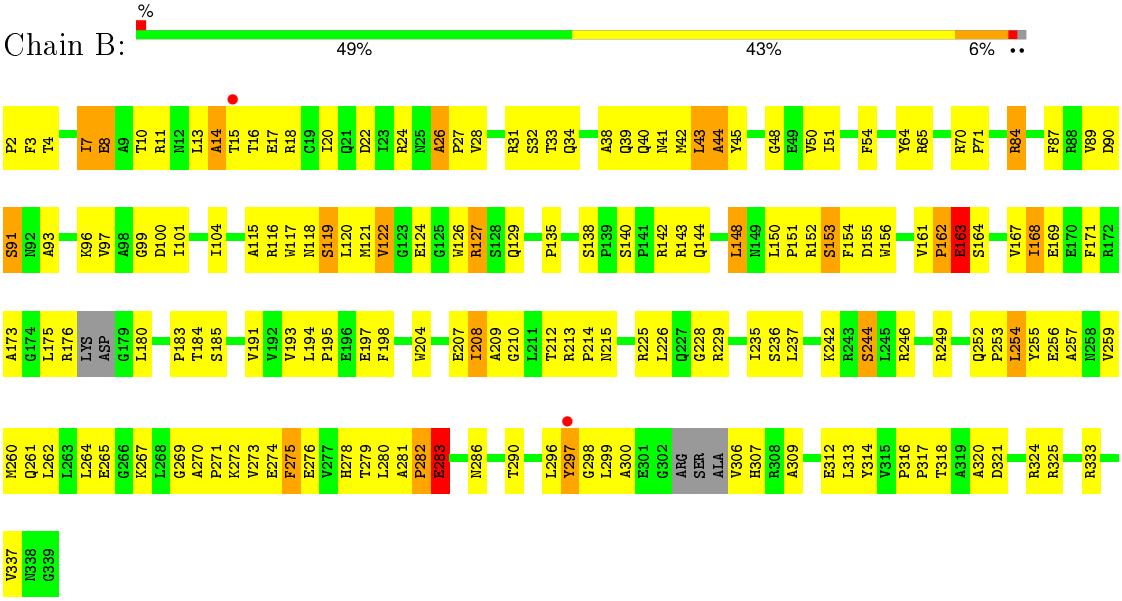
- Molecule 1: SgraIR restriction enzyme

Chain A:



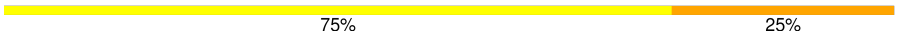
- Molecule 1: SgraIR restriction enzyme

Chain B:



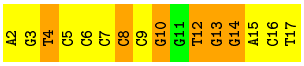
- Molecule 2: DNA (5'-D(*AP*GP*TP*CP*CP*AP*CP*CP*GP*GP*GP*GP*GP*AP*CP*T)-3')

Chain C:



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

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	108.79Å 133.00Å 64.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.35 – 2.95 84.21 – 2.95	Depositor EDS
% Data completeness (in resolution range)	97.3 (50.35-2.95) 97.3 (84.21-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	2.97 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6_289)	Depositor
R, R_{free}	0.189 , 0.281 0.179 , 0.273	Depositor DCC
R_{free} test set	959 reflections (4.84%)	DCC
Wilson B-factor (Å^2)	37.4	Xtriage
Anisotropy	0.892	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 55.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	1 of 19842 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6625	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG

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	0.85	10/2686 (0.4%)	0.68	5/3650 (0.1%)
1	B	0.82	9/2673 (0.3%)	0.69	3/3629 (0.1%)
2	C	0.80	0/734	1.64	14/1130 (1.2%)
3	D	0.90	2/722 (0.3%)	1.78	16/1110 (1.4%)
All	All	0.84	21/6815 (0.3%)	1.02	38/9519 (0.4%)

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	283	GLU	CG-CD	-17.27	1.26	1.51
1	B	283	GLU	CD-OE2	-16.84	1.07	1.25
1	A	83	PHE	CE1-CZ	-15.35	1.08	1.37
1	B	283	GLU	CD-OE1	-13.79	1.10	1.25
1	A	83	PHE	CG-CD2	-13.57	1.18	1.38
1	A	83	PHE	CE2-CZ	-13.36	1.11	1.37
1	A	83	PHE	CD1-CE1	-13.16	1.12	1.39
1	A	83	PHE	CD2-CE2	-12.99	1.13	1.39
1	A	83	PHE	CG-CD1	-10.39	1.23	1.38
1	B	282	PRO	CG-CD	-9.93	1.17	1.50
1	B	283	GLU	C-O	-9.92	1.04	1.23
1	B	283	GLU	CB-CG	-9.53	1.34	1.52
1	A	83	PHE	C-O	-8.29	1.07	1.23
1	B	282	PRO	C-O	-8.10	1.07	1.23
1	A	85	ASP	C-O	-7.24	1.09	1.23
1	B	282	PRO	CB-CG	-7.00	1.15	1.50
1	B	283	GLU	CA-C	-6.22	1.36	1.52
3	D	8[A]	DC	C3'-O3'	-5.81	1.36	1.44
3	D	8[B]	DC	C3'-O3'	-5.81	1.36	1.44
1	A	84	ARG	CZ-NH1	-5.57	1.25	1.33
1	A	83	PHE	CB-CG	-5.11	1.42	1.51

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	11[A]	DG	O4'-C1'-N9	-9.48	101.36	108.00
2	C	11[B]	DG	O4'-C1'-N9	-9.48	101.36	108.00
1	A	85	ASP	CB-CG-OD2	8.65	126.09	118.30
3	D	14[A]	DG	O4'-C1'-N9	7.90	113.53	108.00
3	D	14[B]	DG	O4'-C1'-N9	7.90	113.53	108.00
1	B	282	PRO	CA-N-CD	-7.66	100.78	111.50
3	D	12[A]	DT	O4'-C1'-N1	7.03	112.92	108.00
3	D	12[B]	DT	O4'-C1'-N1	7.03	112.92	108.00
3	D	5[A]	DC	C3'-C2'-C1'	-6.59	94.59	102.50
3	D	5[B]	DC	C3'-C2'-C1'	-6.59	94.59	102.50
2	C	5[A]	DC	N1-C2-O2	-6.56	114.96	118.90
2	C	5[B]	DC	N1-C2-O2	-6.56	114.96	118.90
2	C	4[A]	DT	N3-C4-O4	6.54	123.82	119.90
2	C	4[B]	DT	N3-C4-O4	6.54	123.82	119.90
3	D	12[A]	DT	O4'-C4'-C3'	-6.25	102.00	104.50
3	D	12[B]	DT	O4'-C4'-C3'	-6.25	102.00	104.50
1	A	84	ARG	NE-CZ-NH2	6.01	123.30	120.30
3	D	13[A]	DG	P-O3'-C3'	6.00	126.89	119.70
3	D	13[B]	DG	P-O3'-C3'	6.00	126.89	119.70
1	B	283	GLU	CA-C-N	5.89	127.98	116.20
1	A	84	ARG	N-CA-C	5.64	126.24	111.00
2	C	4[A]	DT	C5-C4-O4	-5.62	120.96	124.90
2	C	4[B]	DT	C5-C4-O4	-5.62	120.96	124.90
3	D	4[A]	DT	N3-C4-O4	5.57	123.24	119.90
3	D	4[B]	DT	N3-C4-O4	5.57	123.24	119.90
1	A	85	ASP	OD1-CG-OD2	-5.46	112.92	123.30
1	A	83	PHE	CB-CA-C	-5.36	99.69	110.40
2	C	15[A]	DA	O4'-C1'-N9	-5.34	104.26	108.00
2	C	15[B]	DA	O4'-C1'-N9	-5.34	104.26	108.00
3	D	10[A]	DG	N1-C6-O6	5.28	123.07	119.90
3	D	10[B]	DG	N1-C6-O6	5.28	123.07	119.90
3	D	13[A]	DG	OP2-P-O3'	5.07	116.35	105.20
3	D	13[B]	DG	OP2-P-O3'	5.07	116.35	105.20
2	C	2[A]	DA	N1-C6-N6	5.05	121.63	118.60
2	C	2[B]	DA	N1-C6-N6	5.05	121.63	118.60
2	C	5[A]	DC	N3-C2-O2	5.04	125.42	121.90
2	C	5[B]	DC	N3-C2-O2	5.04	125.42	121.90
1	B	282	PRO	N-CA-CB	-5.00	97.09	102.60

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	A	2628	0	2570	123	0
1	B	2616	0	2568	133	0
2	C	654	0	355	34	0
3	D	646	0	353	32	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	29	0	0	1	0
5	B	38	0	0	0	0
5	C	11	0	0	1	0
5	D	1	0	0	0	0
All	All	6625	0	5846	287	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 23.

All (287) 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:C:2[B]:DA:H2	3:D:17[B]:DT:H3	1.11	0.97
2:C:17[A]:DT:H3	3:D:2[A]:DA:H2	1.11	0.97
1:B:24:ARG:HG2	1:B:34:GLN:HE21	1.31	0.93
1:B:296:LEU:HA	1:B:299:LEU:HD12	1.52	0.91
3:D:15[A]:DA:H2"	3:D:16[A]:DC:H5"	1.56	0.87
2:C:15[B]:DA:H2"	2:C:16[B]:DC:H5"	1.56	0.87
1:A:174:GLY:O	1:A:177:LYS:HG2	1.77	0.85
1:B:246:ARG:HG2	1:B:249:ARG:HH21	1.42	0.83
1:A:148:LEU:HD21	1:A:226:LEU:HD13	1.61	0.81
1:B:168:ILE:O	1:B:168:ILE:HG22	1.81	0.80
1:A:167:VAL:O	1:A:170:GLU:HB3	1.85	0.77
1:A:262:LEU:O	1:A:266:GLY:HA3	1.85	0.75
2:C:11[B]:DG:H2"	2:C:12[B]:DG:H5"	1.67	0.75
1:B:152:ARG:O	1:B:153:SER:HB3	1.86	0.75
1:B:261:GLN:O	1:B:265:GLU:HB2	1.88	0.74
1:B:50:VAL:O	1:B:51:ILE:HD13	1.88	0.73
1:B:121:MET:HB3	1:B:140:SER:O	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ALA:HB3	1:A:207:GLU:HG2	1.72	0.70
1:B:24:ARG:HG2	1:B:34:GLN:NE2	2.06	0.70
1:B:246:ARG:HD2	3:D:7[A]:DC:H41	1.57	0.70
1:A:51:ILE:HG12	1:A:210:GLY:HA2	1.73	0.69
1:A:121:MET:CE	1:A:121:MET:HA	2.22	0.69
1:B:255:TYR:O	1:B:259:VAL:HG23	1.93	0.69
1:B:48:GLY:O	1:B:210:GLY:HA3	1.92	0.69
1:A:147:VAL:HG22	1:A:191:VAL:HG22	1.76	0.68
1:B:314:TYR:CE2	1:B:316:PRO:HG3	2.29	0.68
1:B:246:ARG:HG2	1:B:249:ARG:NH2	2.08	0.68
1:B:194:LEU:HD12	1:B:195:PRO:HD3	1.76	0.67
1:A:121:MET:HE2	1:A:121:MET:HA	1.76	0.67
1:B:26:ALA:N	1:B:27:PRO:HD3	2.08	0.66
1:B:142:ARG:O	1:B:337:VAL:HG11	1.97	0.65
1:B:185:SER:HB3	1:B:256:GLU:OE2	1.96	0.65
1:B:28:VAL:HB	1:B:31:ARG:HB2	1.78	0.65
3:D:16[A]:DC:H2'	3:D:17[A]:DT:H71	1.79	0.65
2:C:16[B]:DC:H2'	2:C:17[B]:DT:H71	1.79	0.65
1:B:148:LEU:HD11	1:B:226:LEU:HD13	1.78	0.64
2:C:2[B]:DA:H2	3:D:17[B]:DT:N3	1.90	0.64
2:C:17[A]:DT:N3	3:D:2[A]:DA:H2	1.90	0.64
1:A:244:SER:HA	1:A:281:ALA:HB3	1.80	0.64
2:C:2[B]:DA:H2"	2:C:3[B]:DG:O5'	1.98	0.63
3:D:2[A]:DA:H2"	3:D:3[A]:DG:O5'	1.98	0.63
1:B:246:ARG:HD2	3:D:7[A]:DC:N4	2.13	0.63
1:A:192:VAL:HG21	1:A:226:LEU:HD22	1.79	0.63
1:B:119:SER:HB2	1:B:127:ARG:NH2	2.14	0.62
1:A:151:PRO:HD2	1:A:154:PHE:HB2	1.81	0.62
1:A:83:PHE:O	1:A:84:ARG:HB2	1.97	0.62
1:A:96:LYS:HD3	1:A:96:LYS:C	2.19	0.62
1:A:153:SER:HB3	3:D:6[A]:DC:H5"	1.80	0.62
1:A:153:SER:HB3	2:C:6[B]:DC:H5"	1.80	0.62
1:A:72:VAL:O	1:A:76:VAL:HG23	2.00	0.62
1:B:48:GLY:C	1:B:210:GLY:HA3	2.21	0.61
1:A:314:TYR:CE1	1:A:325:ARG:HD2	2.36	0.61
1:B:151:PRO:HD2	1:B:154:PHE:HB2	1.82	0.61
1:A:171:PHE:CE1	1:A:267:LYS:HE3	2.35	0.61
1:A:252:GLN:HB3	1:A:253:PRO:HD3	1.81	0.61
1:B:120:LEU:HD22	1:B:126:TRP:CE3	2.36	0.61
1:B:2:PRO:HG2	1:B:4:THR:O	2.01	0.60
1:A:103:GLU:HG3	1:A:241:PHE:HD2	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:ILE:O	1:B:54:PHE:HB2	2.02	0.59
1:B:282:PRO:O	1:B:283:GLU:C	2.30	0.59
2:C:3[B]:DG:H2"	2:C:4[B]:DT:O5'	2.02	0.58
3:D:14[A]:DG:H2"	3:D:15[A]:DA:C8	2.39	0.58
2:C:14[B]:DG:H2"	2:C:15[B]:DA:C8	2.39	0.58
3:D:3[A]:DG:H2"	3:D:4[A]:DT:O5'	2.02	0.58
1:B:236:SER:HA	1:B:333:ARG:NH2	2.17	0.58
1:B:194:LEU:HD21	1:B:204:TRP:CD1	2.38	0.58
1:A:137:LEU:HD21	1:A:334:MET:O	2.02	0.58
1:B:312:GLU:HG2	1:B:313:LEU:N	2.18	0.58
1:B:40:GLN:OE1	1:B:213:ARG:CZ	2.51	0.58
1:A:119:SER:C	1:A:124:GLU:HB2	2.25	0.57
1:B:257:ALA:O	1:B:261:GLN:HG3	2.05	0.57
1:B:168:ILE:CG2	1:B:168:ILE:O	2.53	0.57
1:B:156:TRP:CE2	1:B:260:MET:HG2	2.40	0.57
1:A:105:VAL:O	1:A:109:VAL:HG23	2.05	0.56
3:D:15[A]:DA:C2'	3:D:16[A]:DC:H5"	2.32	0.56
2:C:15[B]:DA:C2'	2:C:16[B]:DC:H5"	2.32	0.56
1:B:2:PRO:HD2	1:B:45:TYR:CZ	2.40	0.56
1:B:84:ARG:HD3	1:B:84:ARG:C	2.25	0.56
1:A:122:VAL:CG1	1:A:123:GLY:H	2.18	0.56
1:A:334:MET:HA	1:A:337:VAL:HG21	1.88	0.56
1:B:122:VAL:CG1	1:B:124:GLU:HG3	2.35	0.56
1:A:24:ARG:HG2	1:A:34:GLN:NE2	2.21	0.56
1:B:100:ASP:O	1:B:104:ILE:HG13	2.05	0.55
1:A:81:HIS:HD2	1:A:82:PHE:CD2	2.25	0.55
1:A:242:LYS:HE3	1:A:249:ARG:O	2.06	0.55
1:A:196:GLU:O	1:A:199:GLN:HB2	2.06	0.55
1:B:265:GLU:CD	1:B:272:LYS:HA	2.26	0.55
1:A:115:ALA:CB	1:A:207:GLU:HG2	2.37	0.55
1:B:254:LEU:HD12	1:B:254:LEU:O	2.07	0.55
1:B:180:LEU:HD23	1:B:180:LEU:H	1.73	0.54
1:A:70:ARG:HB3	1:A:71:PRO:HD3	1.89	0.54
1:B:167:VAL:C	1:B:169:GLU:H	2.10	0.54
1:B:152:ARG:O	1:B:153:SER:CB	2.54	0.54
1:B:244:SER:HB2	1:B:281:ALA:HB3	1.89	0.54
1:B:96:LYS:HD3	2:C:12[B]:DG:H21	1.72	0.54
1:A:83:PHE:O	1:A:84:ARG:CB	2.53	0.54
1:B:15:THR:HA	1:B:18:ARG:HG2	1.89	0.54
1:A:212:THR:HB	1:A:214:PRO:HD2	1.90	0.54
1:B:235:ILE:O	1:B:235:ILE:HG22	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:ALA:HB3	1:B:300:ALA:CB	2.38	0.53
1:B:51:ILE:HG12	1:B:209:ALA:O	2.07	0.53
1:B:163:GLU:O	1:B:167:VAL:HG23	2.08	0.53
1:A:103:GLU:HG3	1:A:241:PHE:CD2	2.43	0.53
1:B:38:ALA:CB	1:B:41:ASN:HB2	2.38	0.53
1:A:143:ARG:NE	1:A:337:VAL:O	2.42	0.53
1:A:95:ALA:HB2	3:D:10[A]:DG:H5'	1.91	0.53
1:A:95:ALA:HB2	2:C:10[B]:DG:H5'	1.91	0.53
1:B:208:ILE:HB	1:B:215:ASN:ND2	2.24	0.52
2:C:12[B]:DG:H2'	2:C:13[B]:DG:N7	2.24	0.52
1:B:65:ARG:HG2	1:B:280:LEU:HD13	1.91	0.52
1:B:276:GLU:CD	1:B:325:ARG:HH12	2.13	0.52
1:B:122:VAL:HG12	1:B:124:GLU:HG3	1.90	0.52
2:C:10[B]:DG:O5'	2:C:10[B]:DG:H2'	2.09	0.52
3:D:10[A]:DG:O5'	3:D:10[A]:DG:H2'	2.09	0.52
1:B:38:ALA:HB1	1:B:41:ASN:HB2	1.91	0.52
1:B:143:ARG:HG2	1:B:337:VAL:HB	1.92	0.52
3:D:16[A]:DC:H2"	3:D:17[A]:DT:O5'	2.11	0.51
2:C:16[B]:DC:H2"	2:C:17[B]:DT:O5'	2.11	0.51
1:B:155:ASP:OD1	1:B:155:ASP:C	2.48	0.51
1:B:194:LEU:HD12	1:B:195:PRO:CD	2.39	0.51
1:B:171:PHE:CD1	1:B:267:LYS:HE2	2.44	0.51
1:B:118:ASN:OD1	1:B:144:GLN:HG2	2.11	0.51
1:B:286:ASN:ND2	1:B:290:THR:OG1	2.44	0.51
2:C:2[B]:DA:C2	3:D:17[B]:DT:N3	2.65	0.51
2:C:17[A]:DT:N3	3:D:2[A]:DA:C2	2.65	0.51
1:A:122:VAL:CG1	1:A:123:GLY:N	2.73	0.51
1:B:39:GLN:O	1:B:43:LEU:HG	2.11	0.51
1:B:116:ARG:HB2	1:B:207:GLU:OE2	2.12	0.50
1:A:296:LEU:HD22	1:B:262:LEU:CD1	2.41	0.50
1:B:265:GLU:OE2	1:B:272:LYS:HA	2.11	0.50
1:B:275:PHE:HD2	1:B:276:GLU:N	2.09	0.50
1:A:148:LEU:CD2	1:A:226:LEU:HD13	2.38	0.50
1:A:85:ASP:O	1:A:86:ASP:C	2.44	0.50
1:B:320:ALA:O	1:B:324:ARG:HG3	2.12	0.50
1:A:153:SER:CB	3:D:6[A]:DC:H5"	2.41	0.50
1:A:153:SER:CB	2:C:6[B]:DC:H5"	2.41	0.50
1:B:173:ALA:HA	1:B:176:ARG:NH2	2.27	0.50
1:A:5:TYR:CE2	1:A:77:THR:HG22	2.47	0.49
1:B:320:ALA:O	1:B:324:ARG:CG	2.60	0.49
1:A:57:ALA:HA	1:A:60:ASN:HD22	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:VAL:HG13	1:B:93:ALA:HB3	1.94	0.49
1:B:252:GLN:HB3	1:B:253:PRO:HD3	1.95	0.49
2:C:8[B]:DC:C2'	2:C:9[B]:DC:H5'	2.42	0.49
3:D:8[A]:DC:C2'	3:D:9[A]:DC:H5'	2.42	0.49
1:B:43:LEU:HD21	1:B:101:ILE:HG12	1.95	0.49
1:A:5:TYR:CD2	1:A:77:THR:HG21	2.47	0.49
1:A:150:LEU:HD22	1:A:154:PHE:CE2	2.48	0.48
1:B:10:THR:O	1:B:13:LEU:HB2	2.13	0.48
1:B:11:ARG:C	1:B:13:LEU:H	2.15	0.48
1:A:146:ALA:HB3	1:A:192:VAL:HG22	1.96	0.48
1:A:122:VAL:HG13	1:A:123:GLY:N	2.28	0.48
1:A:114:ALA:HA	1:A:117:TRP:HB3	1.96	0.48
2:C:2[A]:DA:O5'	2:C:2[A]:DA:C8	2.67	0.48
3:D:2[B]:DA:C8	3:D:2[B]:DA:O5'	2.67	0.48
1:A:95:ALA:HB1	3:D:9[A]:DC:O4'	2.13	0.48
1:A:95:ALA:HB1	2:C:9[B]:DC:O4'	2.13	0.48
1:A:231:GLN:HB2	1:A:234:GLU:OE1	2.14	0.48
1:A:156:TRP:CE2	1:A:260:MET:HG2	2.48	0.47
3:D:15[A]:DA:H2"	3:D:16[A]:DC:C5'	2.37	0.47
2:C:15[B]:DA:H2"	2:C:16[B]:DC:C5'	2.37	0.47
1:B:261:GLN:HE22	1:B:309:ALA:HA	1.79	0.47
1:A:147:VAL:O	1:A:147:VAL:HG12	2.13	0.47
1:B:317:PRO:HD2	1:B:321:ASP:HB3	1.96	0.47
1:B:71:PRO:HG2	1:B:101:ILE:HD13	1.96	0.47
1:A:54:PHE:CE1	1:A:112:ASN:HB3	2.50	0.47
1:A:153:SER:HB3	3:D:6[A]:DC:C4'	2.44	0.47
1:A:129:GLN:HA	1:A:130:PRO:C	2.33	0.47
1:A:153:SER:HB3	3:D:6[A]:DC:C5'	2.45	0.47
1:A:312:GLU:HG2	1:A:313:LEU:N	2.29	0.47
1:B:42:MET:CE	1:B:97:VAL:HG11	2.43	0.47
1:A:119:SER:O	1:A:120:LEU:C	2.52	0.47
1:A:262:LEU:HD23	1:A:262:LEU:C	2.36	0.47
1:B:191:VAL:HB	1:B:237:LEU:HB3	1.97	0.47
1:A:153:SER:HB3	2:C:6[B]:DC:C4'	2.44	0.47
1:B:154:PHE:CE2	1:B:156:TRP:HA	2.51	0.46
1:A:143:ARG:HE	1:A:337:VAL:HB	1.80	0.46
1:B:3:PHE:CE2	1:B:70:ARG:NH1	2.83	0.46
1:A:226:LEU:O	1:A:229:ARG:HG3	2.16	0.46
1:A:151:PRO:HG3	1:A:223:TYR:CZ	2.51	0.46
1:A:314:TYR:CD2	1:A:316:PRO:HD3	2.51	0.46
1:A:85:ASP:O	1:A:87:PHE:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:LEU:HA	1:B:150:LEU:HD23	1.71	0.46
1:B:262:LEU:O	1:B:262:LEU:HD23	2.16	0.45
1:A:203:MET:HG3	1:A:204:TRP:N	2.30	0.45
1:B:162:PRO:O	1:B:164:SER:N	2.48	0.45
1:B:15:THR:C	1:B:17:GLU:H	2.19	0.45
1:B:272:LYS:HE2	1:B:274:GLU:OE2	2.17	0.45
1:A:134:ARG:HG2	1:A:135:PRO:O	2.16	0.45
1:A:151:PRO:HD2	1:A:154:PHE:CB	2.46	0.45
1:B:297:TYR:CG	1:B:298:GLY:N	2.85	0.45
1:A:99:GLY:HA3	3:D:8[A]:DC:O3'	2.16	0.45
1:A:40:GLN:HB2	5:C:19:HOH:O	2.16	0.45
1:B:276:GLU:OE2	1:B:278:HIS:NE2	2.32	0.45
1:A:5:TYR:CE2	1:A:77:THR:CG2	3.00	0.45
1:B:244:SER:HB3	3:D:10[B]:DG:OP2	2.17	0.44
1:A:255:TYR:CE2	1:A:259:VAL:HG21	2.52	0.44
1:A:42:MET:CE	1:A:75:ALA:CB	2.96	0.44
1:B:282:PRO:O	1:B:283:GLU:O	2.34	0.44
2:C:8[A]:DC:C2'	2:C:9[A]:DC:H5'	2.47	0.44
3:D:8[B]:DC:C2'	3:D:9[B]:DC:H5'	2.47	0.44
1:B:312:GLU:CG	1:B:313:LEU:N	2.80	0.44
1:B:212:THR:O	1:B:215:ASN:N	2.51	0.44
1:A:44:ALA:HA	1:A:211:LEU:O	2.17	0.44
1:A:80:THR:O	1:A:84:ARG:N	2.41	0.44
1:A:99:GLY:HA3	2:C:8[B]:DC:O3'	2.16	0.44
1:B:99:GLY:HA3	3:D:9[B]:DC:H5'	2.00	0.44
1:A:182:LEU:HD12	1:A:182:LEU:HA	1.78	0.44
1:B:194:LEU:HD12	1:B:194:LEU:HA	1.86	0.44
1:B:193:VAL:HG12	1:B:194:LEU:O	2.17	0.44
1:B:22:ASP:OD1	1:B:24:ARG:HG3	2.17	0.44
1:B:244:SER:HB3	2:C:10[A]:DG:OP2	2.17	0.44
1:A:172:ARG:NH2	1:A:184:THR:OG1	2.50	0.44
1:A:276:GLU:CD	1:A:325:ARG:HH12	2.20	0.44
1:A:43:LEU:HD21	1:A:101:ILE:HG12	2.00	0.44
1:A:18:ARG:HG3	1:A:18:ARG:HH11	1.83	0.43
1:A:261:GLN:HG3	1:A:273:VAL:HB	2.00	0.43
1:A:285:THR:O	1:A:286:ASN:C	2.56	0.43
1:B:7:ILE:O	1:B:10:THR:N	2.51	0.43
1:A:262:LEU:O	1:A:266:GLY:CA	2.62	0.43
1:A:153:SER:HB3	2:C:6[B]:DC:H4'	1.99	0.43
1:A:153:SER:HB3	3:D:6[A]:DC:H4'	1.99	0.43
1:B:225:ARG:O	1:B:229:ARG:HD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:ASP:O	1:B:91:SER:C	2.56	0.43
1:B:33:THR:HG23	3:D:12[A]:DT:H5'	2.00	0.43
1:B:169:GLU:O	1:B:173:ALA:N	2.41	0.43
1:B:20:ILE:HG21	1:B:87:PHE:CE1	2.54	0.43
1:B:117:TRP:O	1:B:121:MET:HG2	2.19	0.43
1:A:153:SER:HB3	2:C:6[B]:DC:C5'	2.45	0.43
1:A:317:PRO:HD2	1:A:321:ASP:HB3	2.00	0.43
1:B:175:LEU:O	1:B:176:ARG:HG2	2.19	0.43
1:B:84:ARG:HD3	1:B:84:ARG:O	2.18	0.43
1:B:173:ALA:HA	1:B:176:ARG:CZ	2.49	0.43
1:A:38:ALA:O	1:A:42:MET:HG3	2.19	0.43
5:A:368:HOH:O	1:B:183:PRO:HG2	2.18	0.43
1:A:243:ARG:HG2	1:A:243:ARG:HH11	1.84	0.43
1:B:64:TYR:HB2	1:B:318:THR:HA	1.99	0.43
1:B:270:ALA:HB1	1:B:271:PRO:HD2	2.01	0.43
1:A:202:GLU:O	1:A:204:TRP:N	2.52	0.42
1:A:243:ARG:NH1	1:A:243:ARG:HG2	2.34	0.42
1:B:99:GLY:HA3	2:C:9[A]:DC:H5'	2.00	0.42
1:B:161:VAL:HA	1:B:228:GLY:O	2.19	0.42
1:B:26:ALA:N	1:B:27:PRO:CD	2.78	0.42
1:A:280:LEU:CD2	1:A:316:PRO:HG2	2.48	0.42
1:B:126:TRP:CH2	1:B:135:PRO:HD3	2.54	0.42
1:A:42:MET:HE3	1:A:75:ALA:CB	2.49	0.42
2:C:11[B]:DG:C2'	2:C:12[B]:DG:H5"	2.45	0.42
1:A:306:VAL:HG12	1:B:180:LEU:HD11	2.00	0.42
1:A:265:GLU:OE1	1:A:272:LYS:HA	2.18	0.42
2:C:7[B]:DA:H2"	2:C:8[B]:DC:OP2	2.18	0.42
1:B:13:LEU:C	1:B:14:ALA:O	2.58	0.42
1:B:14:ALA:N	1:B:17:GLU:OE1	2.51	0.42
1:B:42:MET:HE2	1:B:97:VAL:HG11	2.01	0.42
1:B:306:VAL:HG12	1:B:307:HIS:H	1.84	0.42
1:A:226:LEU:C	1:A:229:ARG:HG3	2.40	0.42
1:A:141:PRO:C	1:A:143:ARG:H	2.23	0.42
1:A:235:ILE:H	1:A:235:ILE:HG12	1.69	0.42
1:A:151:PRO:HD2	1:A:154:PHE:CG	2.55	0.42
1:A:280:LEU:HD21	1:A:316:PRO:HG2	2.00	0.42
1:B:156:TRP:CZ2	1:B:260:MET:HG2	2.55	0.42
1:B:180:LEU:HD23	1:B:180:LEU:N	2.33	0.42
1:A:70:ARG:N	1:A:71:PRO:CD	2.83	0.42
1:B:2:PRO:N	1:B:45:TYR:O	2.53	0.41
1:B:317:PRO:HD2	1:B:321:ASP:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:GLU:CG	1:A:313:LEU:N	2.83	0.41
1:A:194:LEU:HA	1:A:194:LEU:HD12	1.78	0.41
1:A:197:GLU:HG3	1:A:197:GLU:H	1.45	0.41
1:B:7:ILE:O	1:B:8:GLU:C	2.59	0.41
1:A:2:PRO:HG2	1:A:4:THR:O	2.20	0.41
1:A:36:GLN:HG2	2:C:13[A]:DG:OP2	2.20	0.41
1:A:36:GLN:HG2	3:D:13[B]:DG:OP2	2.20	0.41
1:B:242:LYS:O	1:B:279:THR:HA	2.20	0.41
1:B:208:ILE:HB	1:B:215:ASN:HD21	1.85	0.41
1:A:118:ASN:HA	1:A:121:MET:HB2	2.03	0.41
1:B:198:PHE:HD1	1:B:204:TRP:HE1	1.69	0.41
1:A:96:LYS:O	1:A:96:LYS:HD3	2.21	0.41
1:A:316:PRO:HA	1:A:317:PRO:HD3	1.82	0.41
1:A:42:MET:HE2	1:A:75:ALA:HB2	2.02	0.41
1:B:264:LEU:HD12	1:B:273:VAL:HG21	2.02	0.41
1:B:262:LEU:HD23	1:B:262:LEU:C	2.42	0.41
1:A:155:ASP:HA	1:A:185:SER:O	2.22	0.40
1:B:43:LEU:O	1:B:44:ALA:C	2.59	0.40
1:A:126:TRP:O	1:A:127:ARG:C	2.59	0.40
1:A:177:LYS:O	1:A:177:LYS:HG3	2.21	0.40
1:B:213:ARG:N	1:B:214:PRO:CD	2.84	0.40
1:A:237:LEU:HD11	1:A:276:GLU:HG2	2.03	0.40
1:A:68:ILE:HD12	1:A:102:PHE:HA	2.03	0.40
1:A:142:ARG:HD2	1:A:339:GLY:HA2	2.03	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
1	A	332/338 (98%)	279 (84%)	46 (14%)	7 (2%)	9 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	327/338 (97%)	270 (83%)	44 (14%)	13 (4%)	4 18
All	All	659/676 (98%)	549 (83%)	90 (14%)	20 (3%)	5 26

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	SER
1	B	44	ALA
1	A	203	MET
1	B	7	ILE
1	B	91	SER
1	B	168	ILE
1	A	115	ALA
1	B	8	GLU
1	B	14	ALA
1	B	43	LEU
1	B	163	GLU
1	A	60	ASN
1	A	170	GLU
1	B	153	SER
1	B	269	GLY
1	A	127	ARG
1	A	177	LYS
1	B	26	ALA
1	B	115	ALA
1	B	162	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
1	A	275/282 (98%)	259 (94%)	16 (6%)	25 62
1	B	274/282 (97%)	256 (93%)	18 (7%)	21 55
All	All	549/564 (97%)	515 (94%)	34 (6%)	23 58

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

Mol	Chain	Res	Type
1	A	66	ASP
1	A	84	ARG
1	A	85	ASP
1	A	89	VAL
1	A	122	VAL
1	A	134	ARG
1	A	169	GLU
1	A	178	ASP
1	A	197	GLU
1	A	199	GLN
1	A	202	GLU
1	A	206	GLU
1	A	212	THR
1	A	213	ARG
1	A	275	PHE
1	A	337	VAL
1	B	16	THR
1	B	32	SER
1	B	84	ARG
1	B	119	SER
1	B	122	VAL
1	B	127	ARG
1	B	129	GLN
1	B	138	SER
1	B	148	LEU
1	B	163	GLU
1	B	184	THR
1	B	197	GLU
1	B	208	ILE
1	B	244	SER
1	B	254	LEU
1	B	275	PHE
1	B	283	GLU
1	B	297	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	81	HIS
1	A	200	ASN

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Mol	Chain	Res	Type
1	B	34	GLN
1	B	92	ASN
1	B	129	GLN
1	B	224	GLN
1	B	286	ASN

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

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

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, 95^{th} 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	336/338 (99%)	-0.02	1 (0%)	94	87	9, 27, 59, 72	0
1	B	333/338 (98%)	0.05	2 (0%)	90	78	15, 31, 53, 77	0
2	C	16/16 (100%)	-0.13	0	100	100	16, 22, 44, 47	0
3	D	16/16 (100%)	-0.14	0	100	100	16, 22, 44, 47	0
All	All	701/708 (99%)	0.01	3 (0%)	93	83	9, 29, 55, 77	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	141	PRO	2.9
1	B	297	TYR	2.4
1	B	15	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
4	MG	A	340	1/1	0.96	0.10	-3.54	19,19,19,19	0
4	MG	B	1	1/1	0.97	0.11	-4.83	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.