Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:46 PM GMT

PDB ID	:	4G3I
Title	:	Crystal structure of Dpo4 in complex with DNA duplex
Authors	:	Yan, Y.Y.; Gan, J.H.; Huang, Z.
Deposited on	:	2012-07-14
Resolution	:	2.50 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:

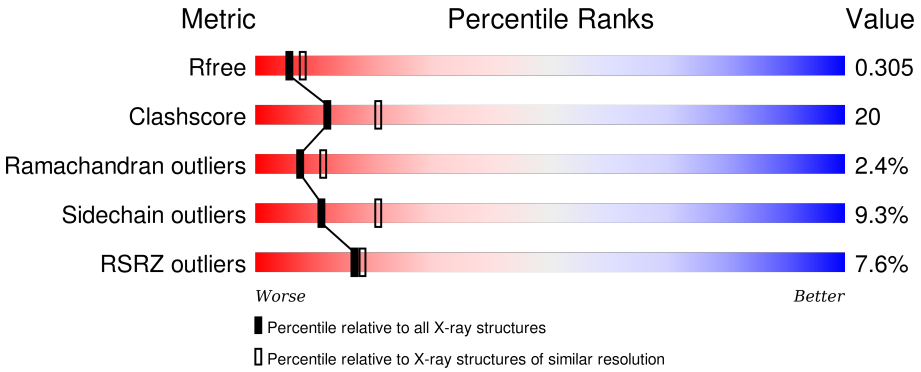
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	C	16	6% 19% 25% 19% 38%
1	E	16	6% 6% 38% 19% 38%
2	D	13	15% 8% 31% 23% 38%
2	F	13	8% 46% 15% 38%
3	A	342	9% 61% 32% 6%

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Mol	Chain	Length	Quality of chain
3	B	342	6% 64% 29% 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	CA	A	401	-	-	-	X
4	CA	B	401	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6238 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	10	Total	C	N	O	P	0	0	0
			198	96	33	60	9			
1	E	10	Total	C	N	O	P	0	0	0
			198	96	33	60	9			

- Molecule 2 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	8	Total	C	N	O	P	0	0	0
			163	78	33	45	7			
2	F	8	Total	C	N	O	P	0	0	0
			163	78	33	45	7			

- Molecule 3 is a protein called DNA polymerase IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	342	Total	C	N	O	S	0	0	0
			2750	1763	473	507	7			
3	B	341	Total	C	N	O	S	0	0	0
			2744	1760	472	505	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q97W02
B	0	SER	-	EXPRESSION TAG	UNP Q97W02

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is water.

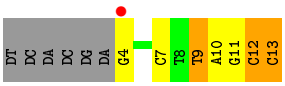
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total O 1 1	0	0
5	A	16	Total O 16 16	0	0
5	B	3	Total O 3 3	0	0

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.

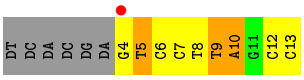
- Molecule 1: DNA

Chain C:



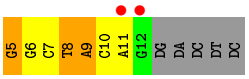
- Molecule 1: DNA

Chain E:



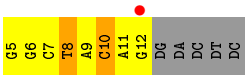
- Molecule 2: DNA

Chain D:



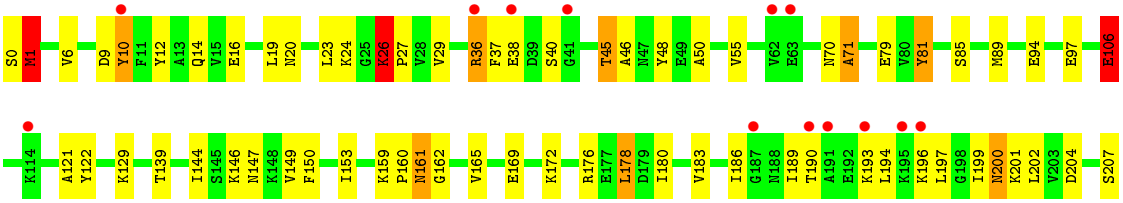
- Molecule 2: DNA

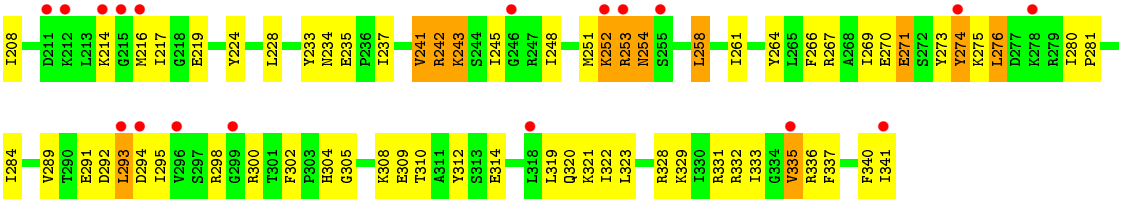
Chain F:



- Molecule 3: DNA polymerase IV

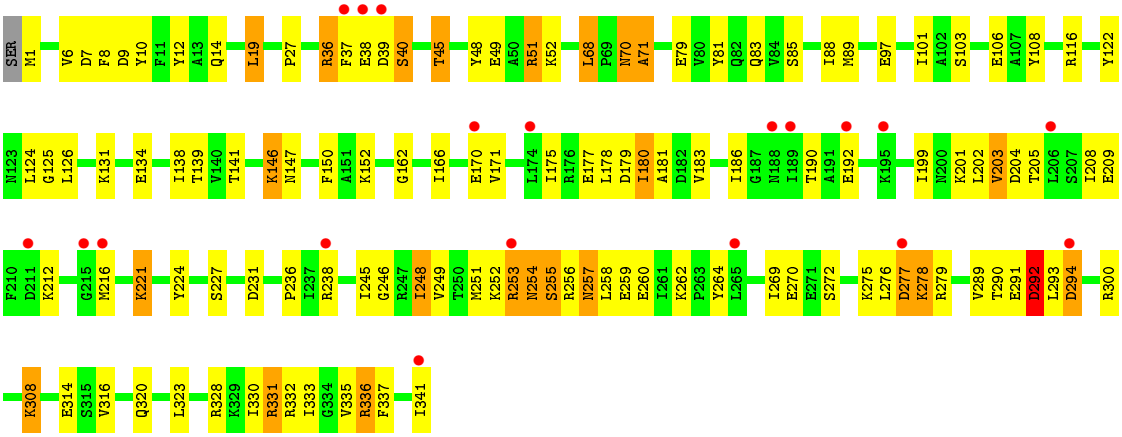
Chain A:





- Molecule 3: DNA polymerase IV

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	52.47Å 52.63Å 99.44Å 75.40° 80.35° 70.97°	Depositor
Resolution (Å)	95.81 – 2.50 28.39 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.1 (95.81-2.50) 90.7 (28.39-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	4.78 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.241 , 0.294 0.258 , 0.305	Depositor DCC
R_{free} test set	1650 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	53.7	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 42.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Outliers	0 of 32534 reflections	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	6238	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.57% 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: 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	1.38	1/220 (0.5%)	2.10	7/337 (2.1%)
1	E	1.30	0/220	2.32	16/337 (4.7%)
2	D	1.35	0/183	2.15	10/281 (3.6%)
2	F	1.32	1/183 (0.5%)	2.28	16/281 (5.7%)
3	A	0.84	2/2789 (0.1%)	0.85	1/3744 (0.0%)
3	B	0.86	0/2783	0.86	1/3736 (0.0%)
All	All	0.93	4/6378 (0.1%)	1.15	51/8716 (0.6%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	8	DT	C5-C7	5.34	1.53	1.50
3	A	106	GLU	CB-CG	5.24	1.62	1.52
3	A	79	GLU	CG-CD	5.09	1.59	1.51
1	C	11	DG	C3'-O3'	-5.01	1.37	1.44

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	12	DC	O4'-C4'-C3'	-10.35	99.79	106.00
2	D	7	DC	N3-C2-O2	-10.15	114.79	121.90
1	E	7	DC	O4'-C1'-N1	9.74	114.82	108.00
2	D	7	DC	N1-C2-O2	9.47	124.58	118.90
1	C	12	DC	N1-C2-O2	9.30	124.48	118.90
1	E	8	DT	O4'-C1'-N1	9.15	114.40	108.00
1	C	9	DT	O4'-C1'-N1	8.90	114.23	108.00
1	E	8	DT	C3'-C2'-C1'	-8.28	92.56	102.50
2	F	10	DC	C1'-O4'-C4'	-8.23	101.87	110.10
1	E	6	DC	P-O3'-C3'	8.02	129.33	119.70
1	E	6	DC	N1-C2-O2	8.00	123.70	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	4	DG	C3'-C2'-C1'	-7.98	92.92	102.50
1	E	8	DT	C1'-O4'-C4'	-7.92	102.18	110.10
2	F	6	DG	C5-C6-N1	7.79	115.40	111.50
1	E	12	DC	N3-C4-C5	7.55	124.92	121.90
1	C	13	DC	O4'-C1'-N1	-7.51	102.74	108.00
2	D	11	DA	P-O3'-C3'	7.10	128.22	119.70
2	F	6	DG	N1-C6-O6	-6.74	115.86	119.90
1	E	13	DC	O4'-C1'-C2'	6.67	111.24	105.90
1	E	6	DC	N3-C2-O2	-6.48	117.36	121.90
2	F	8	DT	N3-C4-O4	6.47	123.78	119.90
1	C	12	DC	N3-C2-O2	-6.29	117.50	121.90
1	E	5	DT	C4-C5-C7	6.25	122.75	119.00
2	F	8	DT	C5-C4-O4	-6.21	120.56	124.90
2	F	7	DC	O5'-P-OP2	-6.16	100.16	105.70
2	D	6	DG	C1'-O4'-C4'	-6.13	103.97	110.10
2	F	12	DG	C8-N9-C4	-6.06	103.98	106.40
2	D	8	DT	P-O3'-C3'	6.00	126.90	119.70
2	F	8	DT	C1'-O4'-C4'	-5.67	104.43	110.10
2	D	10	DC	P-O3'-C3'	5.67	126.50	119.70
3	B	7	ASP	CB-CG-OD1	5.63	123.37	118.30
2	F	7	DC	P-O3'-C3'	5.62	126.44	119.70
2	F	6	DG	C6-C5-N7	5.54	133.73	130.40
1	E	10	DA	N1-C6-N6	5.53	121.92	118.60
2	D	5	DG	N9-C1'-C2'	5.50	123.06	112.60
1	E	10	DA	P-O5'-C5'	-5.44	112.19	120.90
1	E	9	DT	O4'-C1'-N1	-5.42	104.20	108.00
2	D	7	DC	C2-N1-C1'	5.42	124.76	118.80
2	D	9	DA	P-O3'-C3'	5.41	126.19	119.70
2	F	10	DC	O4'-C1'-N1	5.38	111.77	108.00
1	E	10	DA	N9-C4-C5	-5.36	103.66	105.80
1	E	10	DA	C5-C6-N6	-5.32	119.45	123.70
2	F	12	DG	C5-C6-O6	-5.30	125.42	128.60
2	D	6	DG	P-O3'-C3'	5.22	125.97	119.70
2	F	5	DG	O4'-C4'-C3'	-5.22	102.41	104.50
1	C	12	DC	C2-N1-C1'	5.21	124.53	118.80
3	A	202	LEU	CA-CB-CG	5.19	127.23	115.30
2	F	7	DC	C2-N3-C4	-5.16	117.32	119.90
2	F	6	DG	C6-N1-C2	-5.12	122.03	125.10
2	F	6	DG	C1'-O4'-C4'	-5.01	105.09	110.10
1	E	5	DT	C6-C5-C7	-5.01	119.90	122.90

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	C	198	0	115	6	0
1	E	198	0	115	2	0
2	D	163	0	91	6	0
2	F	163	0	91	5	0
3	A	2750	0	2894	121	0
3	B	2744	0	2889	117	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	16	0	0	0	0
5	B	3	0	0	1	0
5	C	1	0	0	0	0
All	All	6238	0	6195	246	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 20.

All (246) 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:B:254:ASN:HB3	3:B:330:ILE:O	1.43	1.18
3:B:256:ARG:O	3:B:323:LEU:HD21	1.46	1.15
3:B:12:TYR:HB2	3:B:45:THR:HG21	1.18	1.13
3:B:116:ARG:NH1	3:B:116:ARG:HB3	1.77	0.99
3:A:294:ASP:CB	3:A:328:ARG:HH12	1.75	0.98
3:A:242:ARG:HH11	3:A:242:ARG:HG3	1.30	0.95
3:B:12:TYR:HB2	3:B:45:THR:CG2	1.98	0.91
3:B:116:ARG:HH11	3:B:116:ARG:HB3	1.36	0.91
3:A:199:ILE:HG23	3:A:204:ASP:HB2	1.55	0.89
3:A:14:GLN:NE2	3:A:139:THR:H	1.71	0.89
3:A:294:ASP:HB3	3:A:328:ARG:NH1	1.87	0.88
3:A:14:GLN:HE22	3:A:139:THR:H	0.93	0.88
3:A:149:VAL:O	3:A:153:ILE:HG13	1.74	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:254:ASN:CB	3:B:330:ILE:O	2.22	0.87
3:A:294:ASP:HB3	3:A:328:ARG:HH12	1.37	0.85
3:B:48:TYR:HA	3:B:51:ARG:HG3	1.59	0.85
3:B:248:ILE:HD11	3:B:332:ARG:HB3	1.58	0.84
3:B:12:TYR:CB	3:B:45:THR:HG21	2.06	0.84
3:B:251:MET:CE	3:B:330:ILE:HG22	2.09	0.83
3:B:38:GLU:O	3:B:39:ASP:HB2	1.79	0.83
3:A:37:PHE:CE1	3:A:40:SER:HB3	2.13	0.81
3:B:278:LYS:HA	3:B:278:LYS:HE2	1.63	0.79
3:A:0:SER:O	3:A:1:MET:HB3	1.83	0.79
3:B:166:ILE:HG23	3:B:170:GLU:HG3	1.63	0.79
3:A:14:GLN:HE22	3:A:139:THR:N	1.77	0.78
3:A:200:ASN:H	3:A:200:ASN:HD22	1.32	0.77
3:A:194:LEU:HD22	3:A:199:ILE:HD12	1.67	0.76
3:B:254:ASN:ND2	3:B:331:ARG:HD3	2.01	0.76
1:C:9:DT:H2"	1:C:10:DA:OP2	1.85	0.75
2:F:10:DC:H2'	2:F:11:DA:C8	2.22	0.74
3:B:14:GLN:NE2	3:B:139:THR:H	1.87	0.73
2:D:8:DT:O3'	3:A:242:ARG:NH1	2.21	0.72
3:A:46:ALA:HB1	3:A:50:ALA:HB3	1.70	0.72
2:D:9:DA:P	3:A:242:ARG:HH12	2.13	0.71
3:B:277:ASP:O	3:B:278:LYS:HB2	1.89	0.71
3:B:146:LYS:HD3	3:B:171:VAL:HG21	1.72	0.71
3:B:254:ASN:OD1	3:B:254:ASN:N	2.22	0.71
3:A:48:TYR:OH	3:A:159:LYS:HD3	1.91	0.71
3:A:304:HIS:HD2	3:A:305:GLY:O	1.75	0.70
3:B:254:ASN:HB3	3:B:330:ILE:C	2.13	0.69
3:A:242:ARG:NH1	3:A:242:ARG:HG3	2.04	0.69
3:B:256:ARG:O	3:B:323:LEU:CD2	2.36	0.68
2:D:8:DT:OP2	3:A:336:ARG:NH2	2.25	0.67
3:A:37:PHE:CZ	3:A:40:SER:HB3	2.30	0.66
3:B:166:ILE:HG23	3:B:170:GLU:CG	2.25	0.66
3:B:14:GLN:HE22	3:B:139:THR:H	1.41	0.65
3:A:37:PHE:CD1	3:A:40:SER:HB3	2.31	0.65
3:B:147:ASN:HD21	3:B:150:PHE:HD2	1.44	0.64
3:B:116:ARG:CB	3:B:116:ARG:NH1	2.60	0.64
3:A:271:GLU:O	3:A:274:TYR:HB3	1.98	0.64
3:B:14:GLN:HG2	3:B:138:ILE:HD13	1.80	0.63
3:B:175:ILE:HG22	3:B:203:VAL:HG23	1.80	0.63
3:B:36:ARG:NH1	3:B:331:ARG:HD2	2.13	0.63
3:A:294:ASP:HB3	3:A:328:ARG:CZ	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:8:DT:OP2	3:B:336:ARG:NH2	2.33	0.62
3:A:190:THR:HG23	3:A:217:ILE:HG21	1.80	0.62
3:A:251:MET:HG2	3:A:264:TYR:CD2	2.35	0.62
3:B:253:ARG:HG2	3:B:253:ARG:O	2.00	0.61
3:B:8:PHE:CZ	3:B:88:ILE:HG21	2.36	0.61
3:A:253:ARG:HG3	3:A:253:ARG:O	1.99	0.61
3:B:122:TYR:CE2	3:B:126:LEU:HD11	2.35	0.61
3:A:294:ASP:HB2	3:A:328:ARG:HH12	1.65	0.61
2:D:9:DA:OP1	3:A:242:ARG:NH1	2.33	0.61
3:A:6:VAL:O	3:A:106:GLU:HA	2.00	0.61
3:A:292:ASP:O	3:A:293:LEU:HB2	2.00	0.61
3:A:200:ASN:H	3:A:200:ASN:ND2	1.96	0.61
3:A:200:ASN:N	3:A:200:ASN:HD22	1.99	0.60
3:A:309:GLU:O	3:A:312:TYR:HB2	2.00	0.60
3:A:149:VAL:HG11	3:A:228:LEU:HD11	1.84	0.60
3:A:200:ASN:ND2	3:A:200:ASN:N	2.47	0.60
3:B:333:ILE:O	3:B:333:ILE:HG23	2.00	0.60
3:A:121:ALA:HB1	3:A:144:ILE:HD13	1.82	0.60
3:B:236:PRO:HG2	3:B:238:ARG:NH1	2.16	0.60
3:B:101:ILE:HD12	3:B:101:ILE:H	1.67	0.60
3:A:26:LYS:HB3	3:A:27:PRO:HD2	1.84	0.59
3:A:251:MET:HG2	3:A:264:TYR:CG	2.38	0.59
1:E:9:DT:H2"	1:E:10:DA:OP2	2.01	0.59
3:B:27:PRO:HB2	3:B:71:ALA:HB2	1.85	0.58
3:A:258:LEU:HG	3:A:323:LEU:HD22	1.86	0.58
3:B:258:LEU:HG	3:B:262:LYS:HD2	1.85	0.57
3:A:237:ILE:O	3:A:237:ILE:HG22	2.02	0.57
3:A:273:TYR:HA	3:A:276:LEU:HD12	1.85	0.57
3:A:275:LYS:O	3:A:276:LEU:C	2.43	0.57
3:B:27:PRO:HB2	3:B:71:ALA:CB	2.35	0.56
3:A:228:LEU:HD23	3:A:233:TYR:HB2	1.87	0.56
3:A:269:ILE:HG13	3:A:335:VAL:HG11	1.87	0.56
3:B:255:SER:CB	3:B:260:GLU:OE1	2.54	0.56
3:A:258:LEU:HD11	3:A:320:GLN:HG2	1.88	0.55
3:B:180:ILE:CG2	3:B:181:ALA:N	2.68	0.55
3:A:1:MET:HG2	3:A:146:LYS:O	2.07	0.55
3:B:116:ARG:CB	3:B:116:ARG:CZ	2.85	0.55
2:F:10:DC:C2'	2:F:11:DA:C8	2.89	0.55
3:A:309:GLU:N	3:A:309:GLU:OE1	2.35	0.55
3:B:36:ARG:HH12	3:B:331:ARG:NE	2.04	0.55
3:A:233:TYR:CZ	3:A:235:GLU:HB2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:294:ASP:OD2	3:A:328:ARG:NH2	2.41	0.54
3:B:289:VAL:HA	3:B:294:ASP:O	2.07	0.54
3:B:146:LYS:HE2	3:B:231:ASP:OD1	2.07	0.54
3:B:1:MET:HE3	3:B:146:LYS:O	2.08	0.54
3:A:300:ARG:HD3	3:A:314:GLU:OE1	2.08	0.54
1:C:10:DA:H3'	3:A:189:ILE:HB	1.90	0.53
3:A:9:ASP:O	3:A:10:TYR:C	2.47	0.53
3:B:36:ARG:HH12	3:B:331:ARG:HD2	1.72	0.53
3:B:180:ILE:O	3:B:183:VAL:HG23	2.09	0.53
2:D:9:DA:P	3:A:242:ARG:NH1	2.81	0.53
3:A:291:GLU:HB3	3:A:329:LYS:HB2	1.91	0.52
3:B:257:ASN:ND2	3:B:259:GLU:H	2.07	0.52
3:A:322:ILE:HG22	3:A:323:LEU:N	2.24	0.52
3:B:316:VAL:O	3:B:320:GLN:HG3	2.10	0.52
3:A:160:PRO:O	3:A:161:ASN:O	2.28	0.52
3:A:199:ILE:HD11	3:A:208:ILE:HG21	1.91	0.51
3:B:254:ASN:HD21	3:B:331:ARG:HD3	1.73	0.51
3:A:294:ASP:HB3	3:A:328:ARG:NH2	2.26	0.51
3:B:36:ARG:HH12	3:B:331:ARG:CD	2.24	0.51
3:B:146:LYS:HE2	3:B:171:VAL:HG11	1.93	0.51
3:B:246:GLY:HA3	3:B:336:ARG:NH1	2.25	0.51
3:B:9:ASP:O	3:B:10:TYR:C	2.48	0.51
3:B:186:ILE:HD12	3:B:190:THR:HG21	1.92	0.51
3:A:147:ASN:HD21	3:A:150:PHE:HD2	1.60	0.50
3:B:256:ARG:CZ	3:B:256:ARG:HB2	2.42	0.50
3:B:180:ILE:HG23	3:B:181:ALA:N	2.25	0.50
3:A:280:ILE:HB	3:A:341:ILE:HG13	1.91	0.50
3:B:278:LYS:HE2	3:B:278:LYS:CA	2.36	0.50
3:B:251:MET:HE2	3:B:330:ILE:HG22	1.89	0.50
3:A:178:LEU:O	3:A:201:LYS:HD2	2.12	0.50
3:A:310:THR:O	3:A:314:GLU:HB2	2.12	0.50
3:B:278:LYS:HA	3:B:278:LYS:CE	2.29	0.49
3:A:10:TYR:O	3:A:10:TYR:CD1	2.65	0.49
3:A:12:TYR:HB2	3:A:45:THR:CG2	2.41	0.49
2:D:5:DG:H2'	3:A:332:ARG:NH2	2.28	0.49
3:B:248:ILE:CD1	3:B:332:ARG:HE	2.25	0.49
3:A:289:VAL:HB	3:A:332:ARG:HB2	1.95	0.49
3:A:294:ASP:CB	3:A:328:ARG:NH1	2.50	0.49
3:A:200:ASN:O	3:A:201:LYS:HD3	2.13	0.49
3:B:291:GLU:C	3:B:293:LEU:H	2.16	0.49
3:B:254:ASN:CA	3:B:330:ILE:O	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:169:GLU:O	3:A:172:LYS:HB2	2.13	0.48
3:B:300:ARG:HD3	3:B:314:GLU:OE1	2.14	0.48
3:B:108:TYR:OH	3:B:152:LYS:HD2	2.14	0.48
3:A:264:TYR:HB2	3:A:333:ILE:HG21	1.96	0.48
3:B:256:ARG:HB2	3:B:256:ARG:NH1	2.28	0.48
1:C:7:DC:OP1	3:A:298:ARG:HD3	2.13	0.48
3:A:245:ILE:HG21	3:A:275:LYS:HB3	1.96	0.48
3:A:10:TYR:CE1	3:A:14:GLN:HG3	2.48	0.48
3:B:68:LEU:HD13	3:B:71:ALA:HB2	1.96	0.47
3:A:266:PHE:HA	3:A:269:ILE:HD12	1.95	0.47
3:A:190:THR:HA	3:A:193:LYS:HB2	1.96	0.47
3:B:122:TYR:CD2	3:B:126:LEU:HD11	2.49	0.47
3:B:36:ARG:HA	3:B:252:LYS:HE3	1.97	0.47
3:B:101:ILE:HD12	3:B:101:ILE:N	2.29	0.47
1:C:10:DA:H5"	3:A:189:ILE:HG21	1.96	0.47
3:A:26:LYS:CB	3:A:27:PRO:HD2	2.45	0.47
2:F:11:DA:H2'	2:F:11:DA:OP2	2.15	0.47
3:B:251:MET:HA	3:B:264:TYR:CE1	2.49	0.47
3:A:16:GLU:OE2	3:A:81:TYR:OH	2.29	0.46
3:B:289:VAL:HB	3:B:332:ARG:HB2	1.98	0.46
3:B:221:LYS:O	3:B:224:TYR:HB3	2.15	0.46
3:B:116:ARG:CZ	3:B:116:ARG:HB3	2.40	0.46
3:B:122:TYR:O	3:B:125:GLY:N	2.49	0.46
3:B:85:SER:O	3:B:89:MET:HG2	2.15	0.46
3:A:319:LEU:HD12	3:A:319:LEU:O	2.16	0.46
3:A:254:ASN:HB3	3:A:331:ARG:HA	1.98	0.46
3:B:49:GLU:HA	3:B:52:LYS:HE2	1.98	0.46
1:E:4:DG:H1'	1:E:5:DT:C2	2.51	0.45
3:A:304:HIS:CD2	3:A:304:HIS:C	2.90	0.45
3:B:209:GLU:OE1	3:B:212:LYS:HG2	2.16	0.45
3:B:289:VAL:HG13	3:B:294:ASP:O	2.17	0.45
3:A:85:SER:O	3:A:89:MET:HG2	2.17	0.45
3:B:79:GLU:HB2	5:B:501:HOH:O	2.15	0.45
3:B:1:MET:CE	3:B:146:LYS:O	2.65	0.45
3:A:172:LYS:HB3	3:A:176:ARG:HH21	1.81	0.45
3:A:252:LYS:HD2	3:A:252:LYS:HA	1.64	0.45
3:A:254:ASN:N	3:A:254:ASN:HD22	2.14	0.45
3:B:253:ARG:O	3:B:254:ASN:C	2.55	0.45
3:A:258:LEU:CD1	3:A:320:GLN:HG2	2.47	0.44
3:B:8:PHE:CZ	3:B:88:ILE:CG2	3.00	0.44
3:B:292:ASP:OD1	3:B:292:ASP:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:290:THR:HG21	3:B:328:ARG:HE	1.82	0.44
3:A:194:LEU:HA	3:A:197:LEU:HB2	2.00	0.44
3:A:10:TYR:O	3:A:10:TYR:CG	2.69	0.44
3:B:19:LEU:HA	3:B:19:LEU:HD12	1.80	0.44
3:B:178:LEU:O	3:B:201:LYS:HD3	2.18	0.44
3:A:321:LYS:HE3	3:A:321:LYS:HB2	1.64	0.44
3:B:9:ASP:HB3	3:B:10:TYR:CD2	2.53	0.44
3:B:124:LEU:HA	3:B:124:LEU:HD12	1.58	0.43
3:B:269:ILE:HG13	3:B:335:VAL:HG11	2.01	0.43
3:B:278:LYS:CE	3:B:278:LYS:CA	2.96	0.43
3:B:236:PRO:HG2	3:B:238:ARG:HH11	1.83	0.43
3:A:300:ARG:HG2	3:A:302:PHE:CE1	2.53	0.43
3:A:160:PRO:O	3:A:161:ASN:C	2.55	0.43
3:A:129:LYS:NZ	3:A:162:GLY:H	2.16	0.43
3:A:281:PRO:HA	3:A:340:PHE:HA	2.00	0.43
3:A:273:TYR:CD1	3:A:276:LEU:HD12	2.53	0.43
1:C:9:DT:C2'	1:C:10:DA:OP2	2.61	0.43
2:F:8:DT:H2"	2:F:9:DA:C8	2.54	0.43
3:B:179:ASP:O	3:B:180:ILE:C	2.57	0.43
3:A:29:VAL:HG22	3:A:55:VAL:HG11	2.00	0.43
3:A:10:TYR:CZ	3:A:14:GLN:HG3	2.54	0.42
3:A:300:ARG:NH1	3:A:314:GLU:OE1	2.48	0.42
3:A:261:ILE:HG21	3:A:319:LEU:HD21	2.01	0.42
3:A:242:ARG:NH1	3:A:242:ARG:CG	2.71	0.42
3:B:12:TYR:N	3:B:12:TYR:CD1	2.88	0.42
3:A:194:LEU:HD23	3:A:197:LEU:HD12	2.00	0.42
3:A:214:LYS:HD2	3:A:219:GLU:OE2	2.18	0.42
3:B:275:LYS:O	3:B:279:ARG:NH2	2.51	0.42
3:B:36:ARG:HB2	3:B:37:PHE:H	1.60	0.42
3:B:291:GLU:HG3	3:B:292:ASP:OD1	2.19	0.42
3:A:292:ASP:O	3:A:293:LEU:CB	2.68	0.42
3:A:241:VAL:HB	3:A:243:LYS:NZ	2.35	0.42
3:B:81:TYR:N	3:B:81:TYR:CD1	2.86	0.42
3:A:252:LYS:HE3	3:B:83:GLN:NE2	2.35	0.42
3:B:199:ILE:HG21	3:B:205:THR:HG22	2.01	0.42
3:B:272:SER:HB2	3:B:337:PHE:CE2	2.55	0.42
3:B:254:ASN:HA	3:B:330:ILE:O	2.20	0.42
3:A:294:ASP:CG	3:A:328:ARG:HH22	2.23	0.42
3:A:190:THR:HG23	3:A:217:ILE:CG2	2.49	0.42
3:A:197:LEU:HA	3:A:197:LEU:HD23	1.92	0.41
3:A:0:SER:O	3:A:1:MET:CB	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:103:SER:OG	3:B:106:GLU:HG2	2.20	0.41
3:B:270:GLU:OE1	3:B:308:LYS:NZ	2.50	0.41
3:B:70:ASN:O	3:B:70:ASN:ND2	2.53	0.41
3:B:245:ILE:CD1	3:B:279:ARG:HH21	2.34	0.41
3:A:234:ASN:CG	3:A:234:ASN:O	2.58	0.41
3:A:122:TYR:HD1	3:A:165:VAL:HG23	1.85	0.41
3:B:183:VAL:O	3:B:186:ILE:HB	2.21	0.41
3:A:81:TYR:CD1	3:A:81:TYR:N	2.85	0.41
3:A:36:ARG:HH22	3:A:254:ASN:HB3	1.86	0.41
3:B:199:ILE:HG23	3:B:204:ASP:HB2	2.03	0.41
3:A:97:GLU:CD	3:A:97:GLU:H	2.24	0.41
3:A:270:GLU:OE2	3:A:308:LYS:HD2	2.21	0.41
3:A:292:ASP:OD1	3:A:328:ARG:HD2	2.21	0.41
3:B:180:ILE:HD13	3:B:202:LEU:HA	2.02	0.41
3:B:251:MET:CE	3:B:330:ILE:CG2	2.91	0.40
3:A:292:ASP:CG	3:A:328:ARG:HH11	2.24	0.40
3:A:281:PRO:HG3	3:A:337:PHE:HB3	2.03	0.40
3:A:183:VAL:O	3:A:186:ILE:HB	2.20	0.40
3:B:293:LEU:HD23	3:B:293:LEU:HA	1.85	0.40
3:B:38:GLU:O	3:B:39:ASP:CB	2.56	0.40
3:B:141:THR:HA	3:B:162:GLY:O	2.22	0.40
3:B:36:ARG:HG3	3:B:40:SER:OG	2.20	0.40
3:B:276:LEU:O	3:B:277:ASP:C	2.60	0.40
3:B:97:GLU:CD	3:B:97:GLU:H	2.24	0.40
3:A:70:ASN:C	3:A:71:ALA:O	2.60	0.40
3:A:20:ASN:HB3	3:A:23:LEU:HG	2.04	0.40
3:B:6:VAL:O	3:B:106:GLU:HA	2.22	0.40
1:C:12:DC:H2"	1:C:13:DC:H5'	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
3	A	340/342 (99%)	302 (89%)	26 (8%)	12 (4%)	4 6
3	B	339/342 (99%)	304 (90%)	31 (9%)	4 (1%)	16 29
All	All	679/684 (99%)	606 (89%)	57 (8%)	16 (2%)	7 11

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	161	ASN
3	A	295	ILE
3	A	26	LYS
3	A	216	MET
3	B	71	ALA
3	B	277	ASP
3	A	36	ARG
3	A	1	MET
3	A	10	TYR
3	A	293	LEU
3	B	292	ASP
3	A	71	ALA
3	A	252	LYS
3	A	274	TYR
3	A	276	LEU
3	B	180	ILE

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	301/301 (100%)	275 (91%)	26 (9%)	13 24
3	B	300/301 (100%)	270 (90%)	30 (10%)	9 18
All	All	601/602 (100%)	545 (91%)	56 (9%)	11 21

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	1	MET
3	A	19	LEU
3	A	24	LYS
3	A	26	LYS
3	A	38	GLU
3	A	45	THR
3	A	81	TYR
3	A	94	GLU
3	A	106	GLU
3	A	178	LEU
3	A	180	ILE
3	A	196	LYS
3	A	200	ASN
3	A	207	SER
3	A	224	TYR
3	A	241	VAL
3	A	242	ARG
3	A	243	LYS
3	A	248	ILE
3	A	253	ARG
3	A	254	ASN
3	A	258	LEU
3	A	267	ARG
3	A	271	GLU
3	A	284	ILE
3	A	335	VAL
3	B	19	LEU
3	B	36	ARG
3	B	40	SER
3	B	45	THR
3	B	51	ARG
3	B	68	LEU
3	B	70	ASN
3	B	131	LYS
3	B	134	GLU
3	B	146	LYS
3	B	177	GLU
3	B	192	GLU
3	B	203	VAL
3	B	208	ILE
3	B	216	MET
3	B	221	LYS
3	B	227	SER

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Mol	Chain	Res	Type
3	B	248	ILE
3	B	249	VAL
3	B	253	ARG
3	B	254	ASN
3	B	255	SER
3	B	257	ASN
3	B	278	LYS
3	B	292	ASP
3	B	294	ASP
3	B	308	LYS
3	B	331	ARG
3	B	336	ARG
3	B	341	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	14	GLN
3	A	123	ASN
3	A	200	ASN
3	A	254	ASN
3	A	304	HIS
3	B	14	GLN
3	B	70	ASN
3	B	83	GLN
3	B	257	ASN
3	B	304	HIS

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

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	C	10/16 (62%)	0.61	1 (10%)	9	10	22, 46, 61, 62	0
1	E	10/16 (62%)	0.52	1 (10%)	9	10	21, 46, 61, 62	0
2	D	8/13 (61%)	0.94	2 (25%)	1	1	26, 29, 50, 51	0
2	F	8/13 (61%)	0.69	1 (12%)	5	5	25, 28, 50, 51	0
3	A	342/342 (100%)	0.67	31 (9%)	11	12	10, 30, 52, 72	1 (0%)
3	B	341/342 (99%)	0.54	19 (5%)	28	31	11, 30, 51, 62	0
All	All	719/742 (96%)	0.61	55 (7%)	17	18	10, 30, 54, 72	1 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	341	ILE	5.9
3	A	341	ILE	5.9
2	D	12	DG	4.8
3	B	188	ASN	4.8
3	A	293	LEU	4.5
3	B	216	MET	4.2
3	A	193	LYS	4.0
3	A	187	GLY	3.8
3	A	191	ALA	3.7
3	A	195	LYS	3.5
3	B	195	LYS	3.5
3	A	294	ASP	3.5
1	C	4	DG	3.3
3	A	216	MET	3.2
3	B	39	ASP	3.1
3	A	278	LYS	3.1
3	A	62	VAL	3.0
2	F	12	DG	3.0
3	A	274	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
3	B	174	LEU	2.8
3	A	63	GLU	2.8
3	B	277	ASP	2.8
3	A	335	VAL	2.7
3	A	190	THR	2.7
3	A	318	LEU	2.7
3	A	215	GLY	2.6
3	A	212	LYS	2.6
3	A	10	TYR	2.6
3	A	211	ASP	2.6
3	B	211	ASP	2.5
3	A	252	LYS	2.5
3	A	36	ARG	2.5
3	A	299	GLY	2.5
3	B	170	GLU	2.4
3	B	38	GLU	2.4
3	B	192	GLU	2.4
3	B	294	ASP	2.3
3	A	253	ARG	2.3
3	B	265	LEU	2.3
3	A	41	GLY	2.3
3	B	215	GLY	2.3
3	A	246	GLY	2.3
2	D	11	DA	2.2
3	B	37	PHE	2.2
3	A	114	LYS	2.2
3	B	189	ILE	2.2
3	A	196	LYS	2.2
3	B	238	ARG	2.2
3	B	253	ARG	2.2
1	E	4	DG	2.1
3	A	255	SER	2.1
3	B	206	LEU	2.1
3	A	214	LYS	2.1
3	A	296	VAL	2.1
3	A	38	GLU	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 carbohydrates 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. 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	CA	B	401	1/1	0.71	0.47	8.30	99,99,99,99	0
4	CA	A	401	1/1	0.87	0.40	5.69	126,126,126,126	0

6.5 Other polymers (i)

There are no such residues in this entry.