W O R L D W I D E

wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

May 29, 2020 – 05:59 am BST

PDB ID	:	4QKO
Title	:	The Crystal Structure of the Pyocin S2 Nuclease Domain, Immunity Protein Complex at 1.8 Angstroms
Authors	:	Grinter, R.; Josts, I.; Roszak, A.W.; Cogdell, C.J.; Walker, D.
Deposited on	:	2014-06-07
Resolution	:	1.80 Å(reported)

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	:	2.11
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)	:	2.11

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 1.80 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.
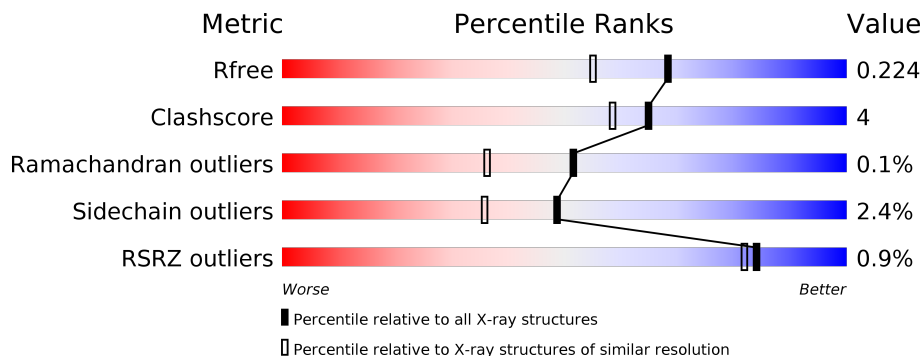
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 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	A	95	% 83% 8% 8%
1	C	95	2% 86% · · 8%
1	E	95	2% 85% 5% · 8%
1	G	95	83% 7% 9%
2	B	134	% 92% · · ·
2	D	134	87% 13% ·

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	134	88% 10%
2	H	134	90% 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
3	BR	D	704	-	-	X	-
3	BR	D	705	-	-	X	-
3	BR	D	708	-	-	X	-
3	BR	F	705	-	-	X	-
3	BR	F	708	-	-	X	-
3	BR	H	704	-	-	X	-
3	BR	H	705	-	-	X	-

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 7820 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 Pyocin-S2 immunity protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	87	Total	C	N	O	S	0	2	0
			724	465	118	140	1			
1	C	87	Total	C	N	O	S	0	0	0
			709	455	116	137	1			
1	E	87	Total	C	N	O	S	0	1	0
			715	459	117	138	1			
1	G	86	Total	C	N	O		0	1	0
			706	452	115	139				

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	LEU	-	EXPRESSION TAG	UNP Q06579
A	89	GLU	-	EXPRESSION TAG	UNP Q06579
A	90	HIS	-	EXPRESSION TAG	UNP Q06579
A	91	HIS	-	EXPRESSION TAG	UNP Q06579
A	92	HIS	-	EXPRESSION TAG	UNP Q06579
A	93	HIS	-	EXPRESSION TAG	UNP Q06579
A	94	HIS	-	EXPRESSION TAG	UNP Q06579
A	95	HIS	-	EXPRESSION TAG	UNP Q06579
C	88	LEU	-	EXPRESSION TAG	UNP Q06579
C	89	GLU	-	EXPRESSION TAG	UNP Q06579
C	90	HIS	-	EXPRESSION TAG	UNP Q06579
C	91	HIS	-	EXPRESSION TAG	UNP Q06579
C	92	HIS	-	EXPRESSION TAG	UNP Q06579
C	93	HIS	-	EXPRESSION TAG	UNP Q06579
C	94	HIS	-	EXPRESSION TAG	UNP Q06579
C	95	HIS	-	EXPRESSION TAG	UNP Q06579
E	88	LEU	-	EXPRESSION TAG	UNP Q06579
E	89	GLU	-	EXPRESSION TAG	UNP Q06579
E	90	HIS	-	EXPRESSION TAG	UNP Q06579
E	91	HIS	-	EXPRESSION TAG	UNP Q06579
E	92	HIS	-	EXPRESSION TAG	UNP Q06579

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	93	HIS	-	EXPRESSION TAG	UNP Q06579
E	94	HIS	-	EXPRESSION TAG	UNP Q06579
E	95	HIS	-	EXPRESSION TAG	UNP Q06579
G	88	LEU	-	EXPRESSION TAG	UNP Q06579
G	89	GLU	-	EXPRESSION TAG	UNP Q06579
G	90	HIS	-	EXPRESSION TAG	UNP Q06579
G	91	HIS	-	EXPRESSION TAG	UNP Q06579
G	92	HIS	-	EXPRESSION TAG	UNP Q06579
G	93	HIS	-	EXPRESSION TAG	UNP Q06579
G	94	HIS	-	EXPRESSION TAG	UNP Q06579
G	95	HIS	-	EXPRESSION TAG	UNP Q06579

- Molecule 2 is a protein called Pyocin-S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	131	Total 1023	C 638	N 198	O 185	S 2	0	2	0
2	D	133	Total 1042	C 650	N 200	O 190	S 2	0	4	0
2	F	131	Total 1041	C 651	N 203	O 185	S 2	0	4	0
2	H	131	Total 1006	C 629	N 193	O 182	S 2	0	0	0

- Molecule 3 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	3	Total 3	Br 3	0	0
3	D	7	Total 7	Br 7	0	0
3	E	3	Total 3	Br 3	0	0
3	H	6	Total 6	Br 6	0	0
3	B	3	Total 3	Br 3	0	0
3	C	3	Total 3	Br 3	0	0
3	A	3	Total 3	Br 3	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	7	Total 7	Br 7	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total 1	Mg 1	0	0
4	B	1	Total 1	Mg 1	0	0
4	D	1	Total 1	Mg 1	0	0
4	F	1	Total 1	Mg 1	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	82	Total 82	O 82	0	0
5	B	123	Total 123	O 123	0	0
5	C	82	Total 82	O 82	0	0
5	D	139	Total 139	O 139	0	0
5	E	96	Total 96	O 96	0	0
5	F	124	Total 124	O 124	0	0
5	G	73	Total 73	O 73	0	0
5	H	96	Total 96	O 96	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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.
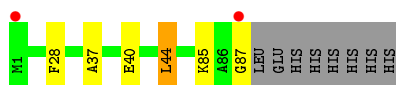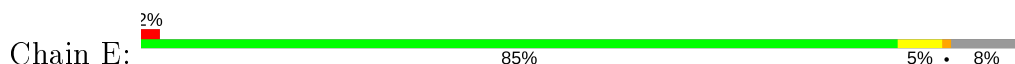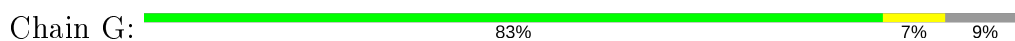
- Molecule 1: Pyocin-S2 immunity protein
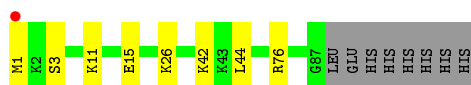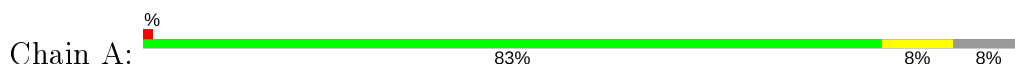
- Molecule 1: Pyocin-S2 immunity protein
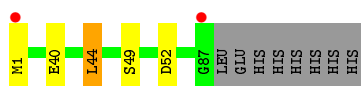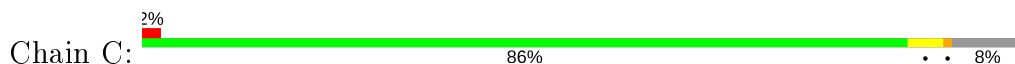
- Molecule 1: Pyocin-S2 immunity protein

- Molecule 1: Pyocin-S2 immunity protein

- Molecule 2: Pyocin-S2
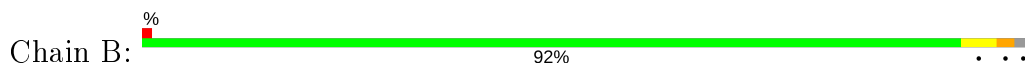
- Molecule 2: Pyocin-S2

Chain D:

87%   13%

R556 D557 P558 R559 D560 G583 E584 K602 N603 D606 K623 R642 E645 R650 I655 H656 H657 R660 G666 G688 LYS

● Molecule 2: Pyocin-S2

Chain F:

%

88%   10%

R556 D557 P558 W576 Q582 G583 E584 R597 R605 Q624 R634 R642 H656 V674 E683 K686 GLY GLY LYS

● Molecule 2: Pyocin-S2

Chain H:

90%   7%

R556 D557 P558 Q582 K595 L596 R597 D635 R642 R660 H685 K686 GLY GLY LYS
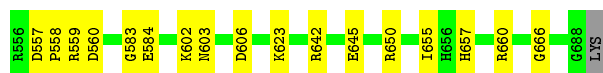
4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	65.39Å 114.42Å 120.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	82.88 – 1.80 43.06 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (82.88-1.80) 98.8 (43.06-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.00 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.172 , 0.215 0.182 , 0.224	Depositor DCC
R_{free} test set	4150 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	22.8	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.4	EDS
L-test for twinning[2]	$<|L|> = 0.46, <L^2> = 0.29$	Xtriage
Estimated twinning fraction	0.024 for -h,l,k	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7820	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.00% 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: MG, BR

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	0.92	0/744	0.90	1/997 (0.1%)
1	C	0.98	0/726	0.89	0/974
1	E	0.86	0/735	0.85	0/986
1	G	0.87	0/723	0.82	0/972
2	B	0.93	0/1047	1.00	4/1412 (0.3%)
2	D	1.02	2/1073 (0.2%)	0.95	3/1447 (0.2%)
2	F	0.96	0/1070	0.91	3/1444 (0.2%)
2	H	0.82	0/1030	0.86	2/1390 (0.1%)
All	All	0.93	2/7148 (0.0%)	0.91	13/9622 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	645	GLU	CD-OE1	5.40	1.31	1.25
2	D	645	GLU	CD-OE2	5.35	1.31	1.25

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	642	ARG	NE-CZ-NH2	-6.96	116.82	120.30
2	B	591	GLN	CB-CA-C	-6.77	96.86	110.40
2	F	642	ARG	NE-CZ-NH2	-6.63	116.99	120.30
2	F	597	ARG	NE-CZ-NH1	6.09	123.35	120.30
2	B	634	ARG	NE-CZ-NH2	-5.98	117.31	120.30

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	724	0	722	8	0
1	C	709	0	704	2	0
1	E	715	0	712	4	0
1	G	706	0	686	5	0
2	B	1023	0	1011	6	0
2	D	1042	0	1025	13	0
2	F	1041	0	1028	7	0
2	H	1006	0	995	8	0
3	A	3	0	0	0	0
3	B	3	0	0	1	0
3	C	3	0	0	1	0
3	D	7	0	0	10	0
3	E	3	0	0	0	0
3	F	7	0	0	5	0
3	G	3	0	0	1	0
3	H	6	0	0	5	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
5	A	82	0	0	4	0
5	B	123	0	0	1	0
5	C	82	0	0	1	0
5	D	139	0	0	3	0
5	E	96	0	0	2	0
5	F	124	0	0	3	0
5	G	73	0	0	2	0
5	H	96	0	0	3	0
All	All	7820	0	6883	57	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 4.

The worst 5 of 57 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:B:605[A]:ARG:HG2	2:B:605[A]:ARG:HH11	0.94	1.10
2:B:605[A]:ARG:HG2	2:B:605[A]:ARG:NH1	1.57	1.05
2:B:605[A]:ARG:HH11	2:B:605[A]:ARG:CG	1.72	1.01
3:F:705:BR:BR	5:F:874:HOH:O	2.47	0.85
3:H:705:BR:BR	5:H:886:HOH:O	2.52	0.81

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	87/95 (92%)	86 (99%)	1 (1%)	0	100	100
1	C	85/95 (90%)	85 (100%)	0	0	100	100
1	E	86/95 (90%)	85 (99%)	1 (1%)	0	100	100
1	G	85/95 (90%)	85 (100%)	0	0	100	100
2	B	131/134 (98%)	128 (98%)	3 (2%)	0	100	100
2	D	135/134 (101%)	131 (97%)	3 (2%)	1 (1%)	22	10
2	F	133/134 (99%)	130 (98%)	3 (2%)	0	100	100
2	H	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
All	All	871/916 (95%)	857 (98%)	13 (2%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	583	GLY

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	80/86 (93%)	77 (96%)	3 (4%)	33	18
1	C	78/86 (91%)	76 (97%)	2 (3%)	46	32
1	E	79/86 (92%)	77 (98%)	2 (2%)	47	34
1	G	77/86 (90%)	76 (99%)	1 (1%)	69	62
2	B	103/102 (101%)	98 (95%)	5 (5%)	25	11
2	D	105/102 (103%)	105 (100%)	0	100	100
2	F	105/102 (103%)	103 (98%)	2 (2%)	57	46
2	H	101/102 (99%)	98 (97%)	3 (3%)	41	27
All	All	728/752 (97%)	710 (98%)	18 (2%)	49	34

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1	MET
1	C	44	LEU
1	G	59	GLU
2	B	605[A]	ARG
2	B	605[B]	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
2	F	685	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 (i)

Of 39 ligands modelled in this entry, 39 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 ⓘ

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, 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(Å²)	Q<0.9
1	A	87/95 (91%)	-0.46	1 (1%)	80	78	16, 26, 45, 57	0
1	C	87/95 (91%)	-0.56	2 (2%)	60	56	14, 24, 44, 70	0
1	E	87/95 (91%)	-0.37	2 (2%)	60	56	16, 29, 51, 89	0
1	G	86/95 (90%)	-0.39	0	100	100	18, 31, 49, 57	0
2	B	131/134 (97%)	-0.32	2 (1%)	73	70	16, 25, 48, 90	0
2	D	133/134 (99%)	-0.54	0	100	100	14, 20, 36, 59	0
2	F	131/134 (97%)	-0.40	1 (0%)	86	84	14, 22, 41, 82	0
2	H	131/134 (97%)	-0.45	0	100	100	18, 29, 46, 68	0
All	All	873/916 (95%)	-0.44	8 (0%)	84	82	14, 26, 48, 90	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	MET	6.9
1	C	1	MET	3.1
2	B	556	ARG	2.9
2	F	556	ARG	2.5
1	E	87	GLY	2.3

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 (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	MG	B	704	1/1	0.91	0.07	38,38,38,38	0
3	BR	D	705	1/1	0.94	0.10	40,40,40,40	1
3	BR	E	103	1/1	0.94	0.19	48,48,48,48	1
3	BR	E	102	1/1	0.94	0.17	56,56,56,56	1
4	MG	D	707	1/1	0.96	0.06	34,34,34,34	0
3	BR	G	101	1/1	0.96	0.06	42,42,42,42	1
3	BR	C	103	1/1	0.96	0.22	50,50,50,50	1
3	BR	C	102	1/1	0.96	0.16	49,49,49,49	1
3	BR	F	706	1/1	0.97	0.08	34,34,34,34	1
3	BR	G	103	1/1	0.97	0.05	37,37,37,37	1
3	BR	E	101	1/1	0.97	0.14	39,39,39,39	1
3	BR	H	702	1/1	0.97	0.05	35,35,35,35	0
3	BR	G	102	1/1	0.97	0.15	59,59,59,59	1
3	BR	F	703	1/1	0.98	0.06	33,33,33,33	1
3	BR	A	101	1/1	0.98	0.09	37,37,37,37	1
3	BR	H	705	1/1	0.98	0.09	44,44,44,44	1
3	BR	F	705	1/1	0.98	0.11	35,35,35,35	1
4	MG	F	707	1/1	0.98	0.05	33,33,33,33	0
3	BR	D	708	1/1	0.98	0.18	40,40,40,40	1
3	BR	A	102	1/1	0.98	0.14	46,46,46,46	1
3	BR	H	704	1/1	0.98	0.04	45,45,45,45	1
3	BR	F	704	1/1	0.98	0.05	36,36,36,36	1
3	BR	H	706	1/1	0.98	0.04	33,33,33,33	1
3	BR	C	101	1/1	0.99	0.10	33,33,33,33	1
4	MG	H	707	1/1	0.99	0.04	28,28,28,28	0
3	BR	F	702	1/1	0.99	0.03	28,28,28,28	0
3	BR	A	103	1/1	0.99	0.17	44,44,44,44	1
3	BR	D	702	1/1	0.99	0.03	28,28,28,28	1
3	BR	F	701	1/1	0.99	0.02	24,24,24,24	0
3	BR	D	703	1/1	0.99	0.03	29,29,29,29	1
3	BR	H	703	1/1	0.99	0.03	26,26,26,26	1
3	BR	D	704	1/1	0.99	0.05	39,39,39,39	1
3	BR	F	708	1/1	0.99	0.06	33,33,33,33	1
3	BR	B	701	1/1	0.99	0.02	27,27,27,27	0
3	BR	H	701	1/1	0.99	0.03	24,24,24,24	0
3	BR	B	703	1/1	0.99	0.10	36,36,36,36	1
3	BR	D	706	1/1	1.00	0.04	34,34,34,34	1

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
3	BR	D	701	1/1	1.00	0.02	20,20,20,20	0
3	BR	B	702	1/1	1.00	0.04	30,30,30,30	0

6.5 Other polymers (i)

There are no such residues in this entry.