Full wwPDB X-ray Structure Validation Report (i)

Oct 9, 2023 – 02:26 AM EDT

PDB ID	:	7JYU
Title	:	Crystal Structure of HLA-A*2402 in complex with IYFSPIRVTF, an 10-mer epitope from Influenza B virus
Authors	:	Nguyen, A.T.; Szeto, C.; Rossjohn, J.; Gras, S.
Deposited on	:	2020-09-01
Resolution	:	2.75 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 (i)) were used in the production of this report:

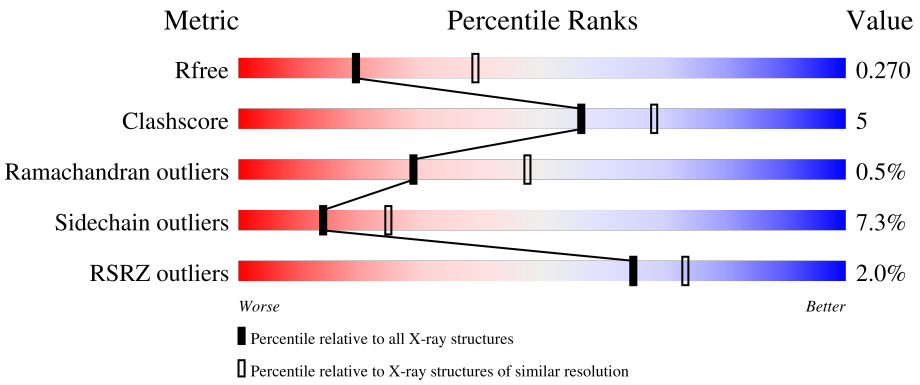
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	A	278	2%, 84%, 14%
1	D	278	3%, 81%, 16%
2	B	100	81%, 17%
2	E	100	%, 83%, 14%
3	C	10	100%

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Mol	Chain	Length	Quality of chain
3	F	10	90% 10%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6387 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 MHC class I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	275	2230	1387	404	429	10	0	0	0
1	D	274	2221	1382	403	426	10	0	0	0

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	829	528	140	158	3	0	0	0
2	E	100	837	533	141	159	4	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
E	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called NP-164-173 peptide from influenza B, IYFSPIRVTF.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	10	89	62	13	14	0	0	0
3	F	10	89	62	13	14	0	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 5 is water.

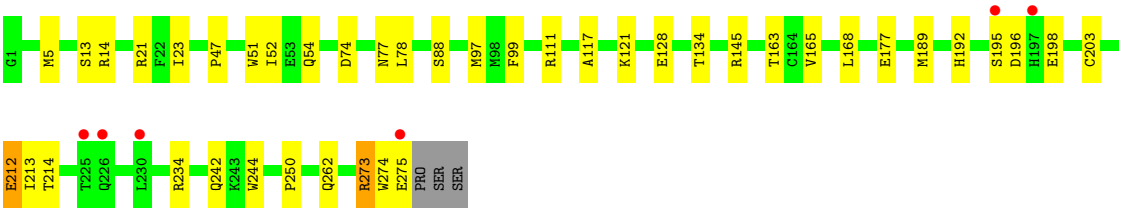
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	33	33	33	0	0
			Total	O		
5	B	19	19	19	0	0
			Total	O		
5	C	1	1	1	0	0
			Total	O		
5	D	18	18	18	0	0
			Total	O		
5	E	17	17	17	0	0
			Total	O		
5	F	3	3	3	0	0

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.

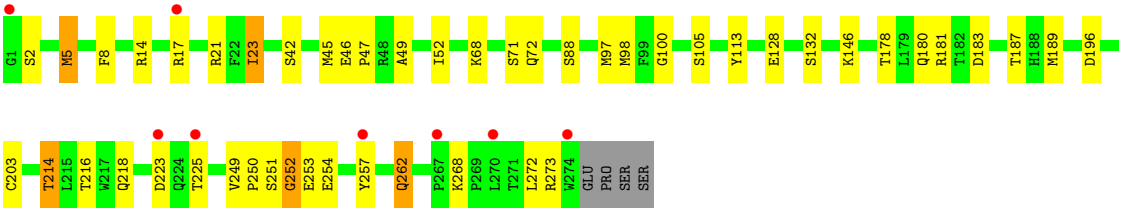
• Molecule 1: MHC class I antigen

Chain A:



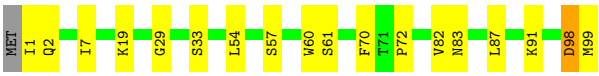
• Molecule 1: MHC class I antigen

Chain D:



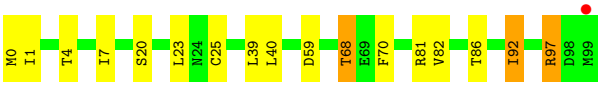
• Molecule 2: Beta-2-microglobulin

Chain B:



• Molecule 2: Beta-2-microglobulin

Chain E:



• Molecule 3: NP-164-173 peptide from influenza B, IYFSPIRVTF

Chain C:

There are no outlier residues recorded for this chain.

- Molecule 3: NP-164-173 peptide from influenza B, IYFSPIRVTF

Chain F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	79.92Å 120.25Å 187.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.95 – 2.75 46.95 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.95-2.75) 99.1 (46.95-2.75)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 2.77Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.189 , 0.259 0.201 , 0.270	Depositor DCC
R_{free} test set	1152 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	52.0	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 38.4	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	0.94	EDS
Total number of atoms	6387	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.91% 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

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	0.53	0/2290	0.72	0/3104
1	D	0.52	0/2281	0.73	0/3092
2	B	0.54	0/852	0.79	0/1152
2	E	0.58	0/860	0.77	1/1162 (0.1%)
3	C	0.53	0/92	0.77	0/123
3	F	0.61	0/92	1.03	0/123
All	All	0.54	0/6467	0.74	1/8756 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	1	ILE	N-CA-C	-6.75	92.79	111.00

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	A	2230	0	2088	22	0
1	D	2221	0	2084	25	0
2	B	829	0	794	10	0
2	E	837	0	803	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	89	0	92	0	0
3	F	89	0	92	2	0
4	A	1	0	0	0	0
5	A	33	0	0	1	0
5	B	19	0	0	0	0
5	C	1	0	0	0	0
5	D	18	0	0	0	0
5	E	17	0	0	0	0
5	F	3	0	0	0	0
All	All	6387	0	5953	61	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 5.

All (61) 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:E:4:THR:HG22	2:E:86:THR:HB	1.65	0.78
1:D:250:PRO:O	1:D:252:GLY:N	2.16	0.76
1:D:250:PRO:C	1:D:252:GLY:H	1.90	0.74
1:D:98:MET:HE1	1:D:113:TYR:CB	2.19	0.72
1:A:198:GLU:HG2	1:A:250:PRO:HA	1.71	0.71
1:A:244:TRP:NE1	2:B:99:MET:HG3	2.07	0.70
1:D:189:MET:HE3	1:D:272:LEU:HB3	1.75	0.68
2:E:25:CYS:HB2	2:E:39:LEU:HD21	1.77	0.67
1:D:250:PRO:C	1:D:252:GLY:N	2.48	0.59
1:A:23:ILE:HD12	2:B:54:LEU:HB3	1.86	0.57
1:D:98:MET:HE1	1:D:113:TYR:HB2	1.87	0.56
1:A:244:TRP:HE1	2:B:99:MET:HG3	1.69	0.56
2:B:29:GLY:HA2	2:B:61:SER:HB2	1.88	0.56
1:A:47:PRO:HB3	1:A:52:ILE:HG23	1.88	0.55
2:E:4:THR:HG22	2:E:86:THR:CB	2.34	0.55
2:E:40:LEU:HD11	2:E:81:ARG:HB2	1.90	0.53
1:D:146:LYS:NZ	3:F:9:THR:HG22	2.24	0.53
1:A:214:THR:HB	1:A:262:GLN:HB2	1.90	0.53
1:D:47:PRO:HB3	1:D:52:ILE:HG23	1.90	0.52
1:A:274:TRP:CE2	1:A:275:GLU:HG2	2.44	0.52
2:E:23:LEU:HB3	2:E:68:THR:HG22	1.92	0.52
1:D:249:VAL:HG21	1:D:254:GLU:HB3	1.91	0.52
1:D:203:CYS:SG	1:D:272:LEU:HD22	2.51	0.51
1:D:178:THR:O	1:D:181:ARG:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:PHE:CE1	1:D:98:MET:HG3	2.47	0.50
1:D:98:MET:HE1	1:D:113:TYR:HB3	1.93	0.50
2:E:92:ILE:HD12	2:E:92:ILE:H	1.75	0.50
2:B:33:SER:HB2	2:B:54:LEU:HD21	1.93	0.50
1:D:21:ARG:HD3	1:D:23:ILE:HD11	1.93	0.49
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.47	0.49
1:D:146:LYS:HZ1	3:F:9:THR:HG22	1.76	0.49
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.95	0.48
1:D:98:MET:CE	1:D:113:TYR:HB2	2.42	0.48
2:B:7:ILE:HG12	2:B:82:VAL:HG21	1.96	0.48
1:D:214:THR:HG23	1:D:262:GLN:HB2	1.96	0.47
1:D:189:MET:HE3	1:D:272:LEU:HD23	1.96	0.47
1:A:51:TRP:O	1:A:54:GLN:HG2	2.13	0.47
1:D:68:LYS:O	1:D:72:GLN:HG2	2.14	0.46
1:A:13:SER:HB3	1:A:78:LEU:HD13	1.96	0.46
1:A:273:ARG:HB2	1:A:273:ARG:HH11	1.81	0.46
1:D:5:MET:O	1:D:100:GLY:HA3	2.16	0.46
1:D:189:MET:CE	1:D:272:LEU:HD23	2.46	0.46
1:D:98:MET:CE	1:D:113:TYR:CB	2.92	0.45
1:A:274:TRP:HA	1:A:275:GLU:HA	1.74	0.45
1:A:14:ARG:HH12	1:A:21:ARG:HB2	1.82	0.44
1:A:212:GLU:HB2	5:A:423:HOH:O	2.17	0.44
1:D:49:ALA:O	1:D:52:ILE:HG22	2.17	0.44
1:A:74:ASP:HA	1:A:77:ASN:HB2	1.99	0.44
1:A:111:ARG:NH1	1:A:128:GLU:HA	2.33	0.44
2:B:1:ILE:HG23	2:B:2:GLN:H	1.83	0.43
1:D:14:ARG:HB2	1:D:17:ARG:HB3	2.00	0.43
2:B:19:LYS:O	2:B:72:PRO:HD2	2.18	0.43
1:A:192:HIS:CE1	2:B:98:ASP:HB3	2.54	0.42
2:E:97:ARG:H	2:E:97:ARG:HG3	1.44	0.42
1:A:273:ARG:HB2	1:A:273:ARG:NH1	2.35	0.42
1:A:97:MET:HE2	1:A:99:PHE:HB3	1.99	0.42
2:E:4:THR:HA	2:E:86:THR:OG1	2.20	0.42
2:E:7:ILE:HG12	2:E:82:VAL:HG21	2.02	0.41
1:D:218:GLN:O	1:D:257:TYR:HA	2.21	0.41
1:A:234:ARG:HG2	1:A:242:GLN:HB2	2.03	0.41
1:A:189:MET:HG2	1:A:274:TRP:HE3	1.86	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	273/278 (98%)	262 (96%)	11 (4%)	0	100	100
1	D	272/278 (98%)	250 (92%)	18 (7%)	4 (2%)	10	18
2	B	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
2	E	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
3	C	8/10 (80%)	7 (88%)	1 (12%)	0	100	100
3	F	8/10 (80%)	8 (100%)	0	0	100	100
All	All	756/776 (97%)	714 (94%)	38 (5%)	4 (0%)	29	47

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	251	SER
1	D	128	GLU
1	D	252	GLY
1	D	225	THR

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	231/234 (99%)	218 (94%)	13 (6%)	21	36
1	D	230/234 (98%)	208 (90%)	22 (10%)	8	14
2	B	94/95 (99%)	88 (94%)	6 (6%)	17	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	E	95/95 (100%)	88 (93%)	7 (7%)	13 24
3	C	10/10 (100%)	10 (100%)	0	100 100
3	F	10/10 (100%)	9 (90%)	1 (10%)	7 13
All	All	670/678 (99%)	621 (93%)	49 (7%)	14 25

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	SER
1	A	121	LYS
1	A	134	THR
1	A	145	ARG
1	A	163	THR
1	A	165	VAL
1	A	177	GLU
1	A	195	SER
1	A	196	ASP
1	A	203	CYS
1	A	212	GLU
1	A	213	ILE
1	A	273	ARG
2	B	57	SER
2	B	70	PHE
2	B	83	ASN
2	B	87	LEU
2	B	91	LYS
2	B	98	ASP
1	D	2	SER
1	D	5	MET
1	D	23	ILE
1	D	42	SER
1	D	45	MET
1	D	46	GLU
1	D	71	SER
1	D	88	SER
1	D	97	MET
1	D	105	SER
1	D	132	SER
1	D	180	GLN
1	D	183	ASP
1	D	187	THR

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Mol	Chain	Res	Type
1	D	196	ASP
1	D	214	THR
1	D	216	THR
1	D	223	ASP
1	D	253	GLU
1	D	262	GLN
1	D	268	LYS
1	D	273	ARG
2	E	0	MET
2	E	20	SER
2	E	59	ASP
2	E	68	THR
2	E	70	PHE
2	E	92	ILE
2	E	97	ARG
3	F	9	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 1 ligands modelled in this entry, 1 is 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	A	275/278 (98%)	-0.18	6 (2%)	62	70	24, 52, 88, 110	0
1	D	274/278 (98%)	-0.06	8 (2%)	51	61	30, 54, 100, 116	0
2	B	99/100 (99%)	-0.35	0	100	100	35, 54, 87, 93	0
2	E	100/100 (100%)	-0.35	1 (1%)	82	87	36, 53, 79, 87	0
3	C	10/10 (100%)	0.03	0	100	100	38, 42, 50, 52	0
3	F	10/10 (100%)	0.01	0	100	100	38, 44, 47, 48	0
All	All	768/776 (98%)	-0.18	15 (1%)	65	73	24, 53, 91, 116	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	GLN	4.5
1	D	225	THR	4.4
1	D	17	ARG	3.8
1	A	225	THR	2.8
1	D	1	GLY	2.8
1	D	267	PRO	2.7
1	D	257	TYR	2.7
1	A	197	HIS	2.6
1	D	274	TRP	2.5
1	A	275	GLU	2.4
1	A	230	LEU	2.3
1	A	195	SER	2.2
1	D	223	ASP	2.2
2	E	99	MET	2.0
1	D	270	LEU	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)

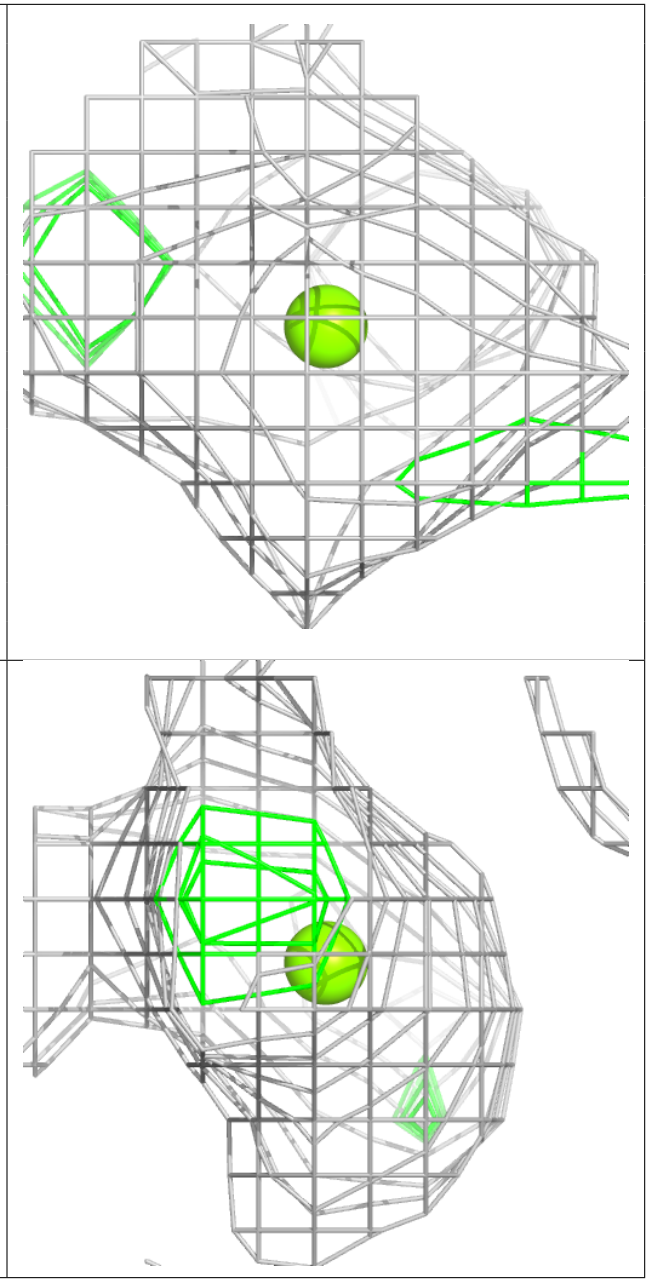
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MG	A	301	1/1	0.80	0.27	78,78,78,78	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around MG A 301:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.