



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 10:55 AM UTC

PDB ID : 1S8A / pdb_00001s8a
Title : H98Q Mutant of Methylglyoxal Synthase from E. coli complexed with Phosphoglycolic Acid
Authors : Harrison, D.H.; Marks, G.T.; Susler, M.
Deposited on : 2004-01-31
Resolution : 2.20 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

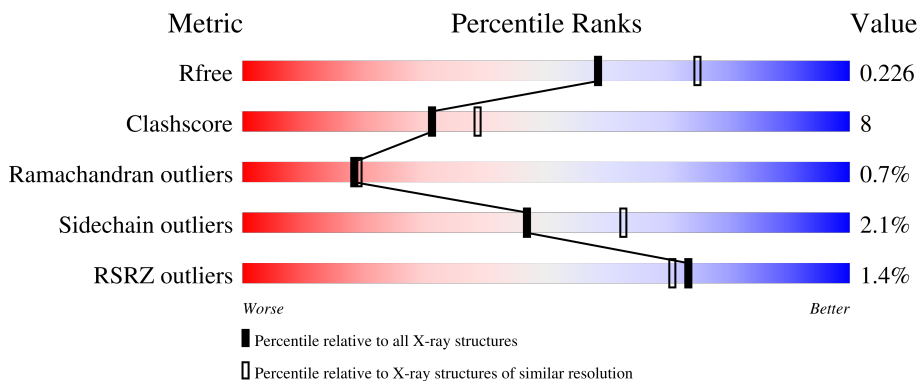
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	152	 2% 79% 18%
1	B	152	 0% 80% 18%
1	C	152	 3% 85% 15%
1	D	152	 0% 80% 19%
1	E	152	 0% 72% 27%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	152	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into two segments: a green segment on the left representing 78% and a yellow segment on the right representing 21%. A small red square is at the beginning of the bar, and a small black dot is at the end. A '%' symbol is positioned above the start of the bar.</p>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7159 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.

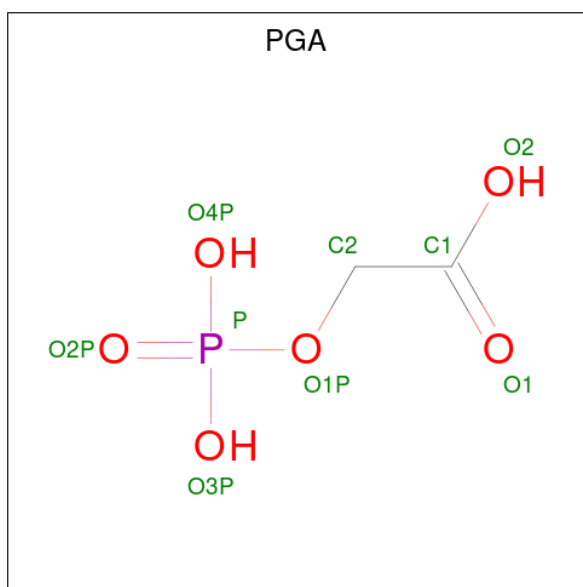
- Molecule 1 is a protein called Methylglyoxal synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	152	1166	747	200	213	6	0	0	0
1	B	152	1168	748	200	213	7	0	0	0
1	C	152	1162	744	200	211	7	0	0	0
1	D	151	1163	744	199	213	7	0	0	0
1	E	151	1173	749	203	214	7	0	0	0
1	F	152	1177	753	206	211	7	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	98	GLN	HIS	engineered mutation	UNP P0A731
B	98	GLN	HIS	engineered mutation	UNP P0A731
C	98	GLN	HIS	engineered mutation	UNP P0A731
D	98	GLN	HIS	engineered mutation	UNP P0A731
E	98	GLN	HIS	engineered mutation	UNP P0A731
F	98	GLN	HIS	engineered mutation	UNP P0A731

- Molecule 2 is 2-PHOSPHOGLYCOLIC ACID (CCD ID: PGA) (formula: C₂H₅O₆P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
2	A	1	9	2	6	1	0	0
2	B	1	9	2	6	1	0	0
2	C	1	9	2	6	1	0	0
2	D	1	9	2	6	1	0	0
2	E	1	9	2	6	1	0	0
2	F	1	9	2	6	1	0	0

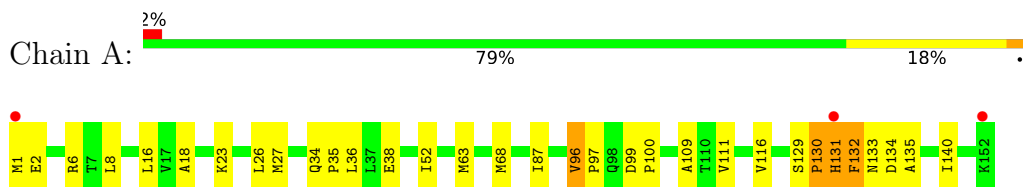
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	16	16	16	0	0
3	B	18	18	18	0	0
3	C	17	17	17	0	0
3	D	13	13	13	0	0
3	E	16	16	16	0	0
3	F	16	16	16	0	0

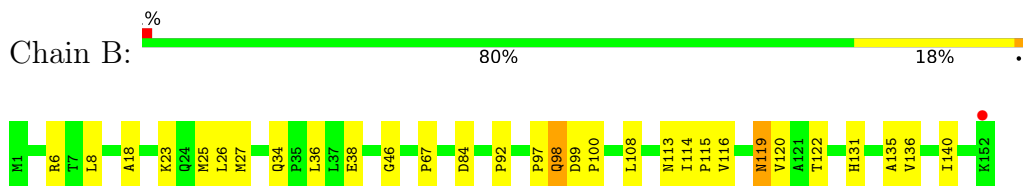
3 Residue-property plots [i](#)

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.

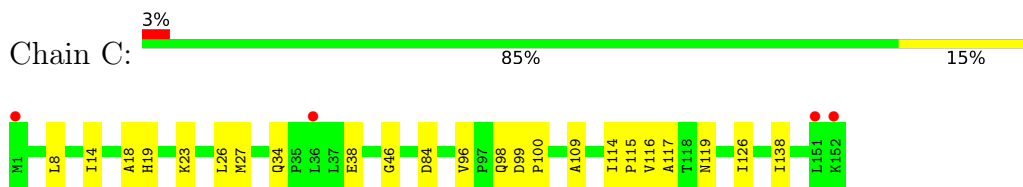
- Molecule 1: Methylglyoxal synthase



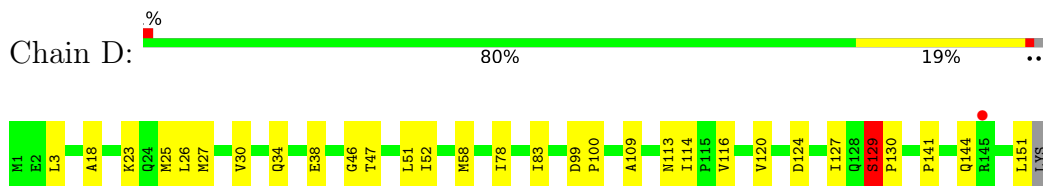
- Molecule 1: Methylglyoxal synthase



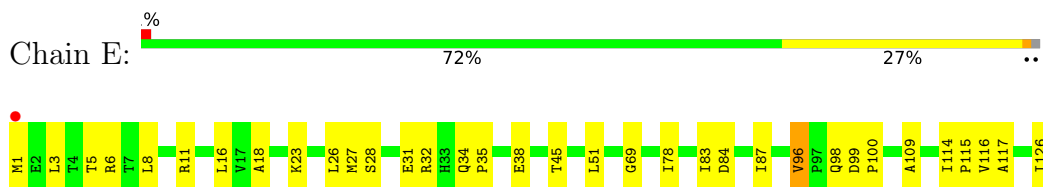
- Molecule 1: Methylglyoxal synthase

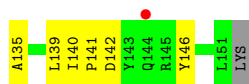


- Molecule 1: Methylglyoxal synthase

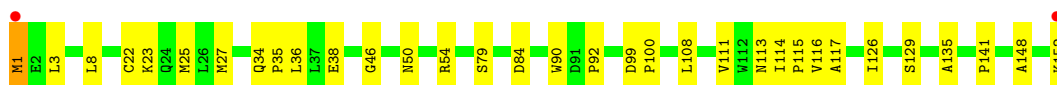
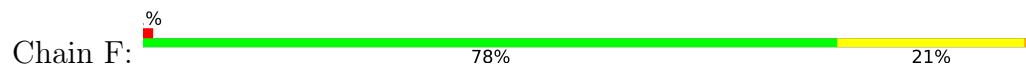


- Molecule 1: Methylglyoxal synthase





- Molecule 1: Methylglyoxal synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	53.08Å 129.96Å 178.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.65 – 2.20 29.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.9 (29.65-2.20) 89.8 (29.65-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.10 (at 2.20Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.192 , 0.227 0.192 , 0.226	Depositor DCC
R_{free} test set	4305 reflections (7.51%)	wwPDB-VP
Wilson B-factor (Å ²)	26.5	Xtrriage
Anisotropy	0.055	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 31.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7159	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: PGA

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	0.45	0/1193	0.88	1/1632 (0.1%)
1	B	0.46	0/1195	0.91	1/1634 (0.1%)
1	C	0.43	0/1188	0.87	1/1625 (0.1%)
1	D	0.43	0/1190	0.87	3/1628 (0.2%)
1	E	0.47	0/1200	0.89	0/1640
1	F	0.42	0/1204	0.87	0/1644
All	All	0.45	0/7170	0.88	6/9803 (0.1%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	132	PHE	N-CA-C	-6.84	104.40	112.89
1	D	129	SER	CA-C-N	5.71	125.18	119.24
1	D	129	SER	C-N-CA	5.71	125.18	119.24
1	C	14	ILE	N-CA-C	5.38	115.70	108.17
1	B	113	ASN	N-CA-C	5.21	118.59	111.39

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	1166	0	1160	21	0
1	B	1168	0	1165	25	0
1	C	1162	0	1158	12	0
1	D	1163	0	1158	16	0
1	E	1173	0	1175	24	0
1	F	1177	0	1185	22	0
2	A	9	0	2	0	0
2	B	9	0	2	0	0
2	C	9	0	2	0	0
2	D	9	0	2	0	0
2	E	9	0	2	0	0
2	F	9	0	2	0	0
3	A	16	0	0	1	0
3	B	18	0	0	3	0
3	C	17	0	0	0	0
3	D	13	0	0	0	0
3	E	16	0	0	0	0
3	F	16	0	0	3	0
All	All	7159	0	7013	115	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 8.

The worst 5 of 115 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)
1:F:79:SER:HB3	3:F:212:HOH:O	1.68	0.93
1:A:131:HIS:N	3:A:213:HOH:O	2.06	0.88
1:B:34:GLN:O	1:B:38:GLU:HG3	1.86	0.76
1:C:23:LYS:O	1:C:27:MET:HG2	1.89	0.73
1:A:131:HIS:HB3	1:A:134:ASP:HB2	1.70	0.72

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	150/152 (99%)	143 (95%)	5 (3%)	2 (1%)	9	8
1	B	150/152 (99%)	147 (98%)	2 (1%)	1 (1%)	18	19
1	C	150/152 (99%)	147 (98%)	2 (1%)	1 (1%)	18	19
1	D	149/152 (98%)	146 (98%)	2 (1%)	1 (1%)	18	19
1	E	149/152 (98%)	146 (98%)	3 (2%)	0	100	100
1	F	150/152 (99%)	147 (98%)	2 (1%)	1 (1%)	18	19
All	All	898/912 (98%)	876 (98%)	16 (2%)	6 (1%)	18	19

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	F	46	GLY
1	A	130	PRO
1	C	46	GLY
1	B	46	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	124/129 (96%)	120 (97%)	4 (3%)	34	47
1	B	125/129 (97%)	123 (98%)	2 (2%)	55	71
1	C	123/129 (95%)	123 (100%)	0	100	100
1	D	125/129 (97%)	121 (97%)	4 (3%)	34	47
1	E	127/129 (98%)	124 (98%)	3 (2%)	43	58
1	F	126/129 (98%)	123 (98%)	3 (2%)	43	58
All	All	750/774 (97%)	734 (98%)	16 (2%)	47	63

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	36	LEU
1	F	1	MET
1	D	144	GLN
1	E	96	VAL
1	D	129	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	33	HIS
1	F	59	ASN
1	B	98	GLN
1	B	119	ASN
1	C	94	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PGA	F	206	-	8,8,8	1.15	0	10,11,11	1.10	0
2	PGA	B	202	-	8,8,8	1.18	0	10,11,11	1.12	0
2	PGA	E	205	-	8,8,8	1.31	0	10,11,11	1.10	0
2	PGA	A	201	-	8,8,8	1.12	0	10,11,11	1.10	0
2	PGA	D	204	-	8,8,8	1.22	0	10,11,11	1.12	0
2	PGA	C	203	-	8,8,8	1.15	0	10,11,11	1.13	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PGA	F	206	-	-	3/6/6/6	-
2	PGA	B	202	-	-	2/6/6/6	-
2	PGA	E	205	-	-	2/6/6/6	-
2	PGA	A	201	-	-	2/6/6/6	-
2	PGA	D	204	-	-	2/6/6/6	-
2	PGA	C	203	-	-	2/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	204	PGA	O1-C1-C2-O1P
2	E	205	PGA	O2-C1-C2-O1P
2	F	206	PGA	O1-C1-C2-O1P
2	D	204	PGA	O2-C1-C2-O1P
2	F	206	PGA	O2-C1-C2-O1P

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

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	152/152 (100%)	-0.03	3 (1%) 65 62	15, 29, 44, 63	0
1	B	152/152 (100%)	-0.21	1 (0%) 84 82	15, 26, 42, 51	0
1	C	152/152 (100%)	-0.12	4 (2%) 57 54	16, 28, 44, 53	0
1	D	151/152 (99%)	-0.08	1 (0%) 84 82	16, 30, 42, 58	0
1	E	151/152 (99%)	-0.16	2 (1%) 75 73	15, 26, 42, 57	0
1	F	152/152 (100%)	-0.12	2 (1%) 75 73	17, 29, 43, 51	0
All	All	910/912 (99%)	-0.12	13 (1%) 73 71	15, 28, 43, 63	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	4.5
1	A	131	HIS	3.9
1	A	152	LYS	3.3
1	E	144	GLN	2.6
1	E	1	MET	2.4

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 oligosaccharides 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(\AA^2)	Q<0.9
2	PGA	A	201	9/9	0.97	0.09	23,26,34,36	0
2	PGA	C	203	9/9	0.97	0.08	21,25,29,32	0
2	PGA	B	202	9/9	0.98	0.09	28,30,34,36	0
2	PGA	D	204	9/9	0.98	0.06	25,29,30,33	0
2	PGA	E	205	9/9	0.98	0.07	24,26,27,31	0
2	PGA	F	206	9/9	0.98	0.06	25,27,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.