



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 09:49 AM EDT

PDB ID : 5MZZ
Title : Crystal structure of the decarboxylase AibA/AibB in complex with 3-methylglutaconate
Authors : Bock, T.; Luxenburger, E.; Hoffmann, J.; Schuetza, V.; Feiler, C.; Mueller, R.; Blankenfeldt, W.
Deposited on : 2017-02-02
Resolution : 2.30 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 ⓘ 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

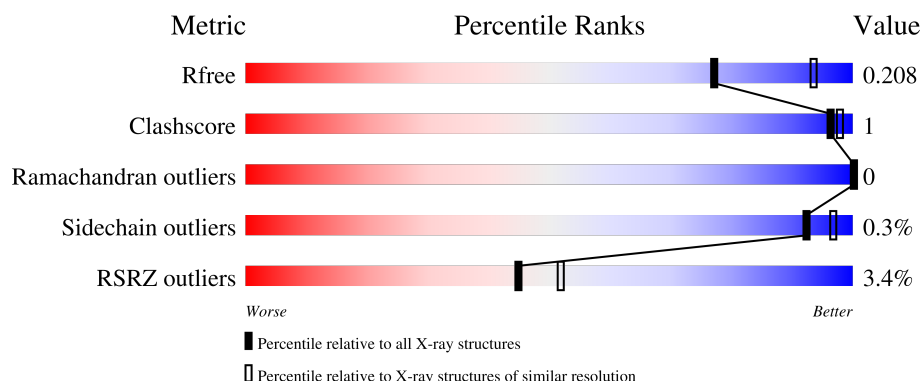
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	265	<div> <div>4%</div> <div>98%</div> <div>..</div> </div>
1	C	265	<div> <div>%</div> <div>97%</div> <div>..</div> </div>
2	B	248	<div> <div>6%</div> <div>93%</div> <div>..</div> </div>
2	D	248	<div> <div>2%</div> <div>95%</div> <div>..</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15409 atoms, of which 7481 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 Glutaconate CoA-transferase family, subunit A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	261	Total	C	H	N	O	S	0	6	0
			3923	1251	1953	337	368	14			
1	C	263	Total	C	H	N	O	S	0	7	0
			3966	1258	1988	339	367	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	ALA	LYS	engineered mutation	UNP Q1D4I4
C	191	ALA	LYS	engineered mutation	UNP Q1D4I4

- Molecule 2 is a protein called Glutaconate CoA-transferase family, subunit B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	D	241	Total	C	H	N	O	S	0	2	0
			3565	1121	1781	329	332	2			
2	B	241	Total	C	H	N	O	S	0	3	0
			3537	1122	1756	327	330	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	PRO	-	expression tag	UNP Q1D4I3
D	0	HIS	-	expression tag	UNP Q1D4I3
D	200	ALA	GLU	engineered mutation	UNP Q1D4I3
D	201	ALA	GLU	engineered mutation	UNP Q1D4I3
B	-1	PRO	-	expression tag	UNP Q1D4I3
B	0	HIS	-	expression tag	UNP Q1D4I3
B	200	ALA	GLU	engineered mutation	UNP Q1D4I3
B	201	ALA	GLU	engineered mutation	UNP Q1D4I3

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



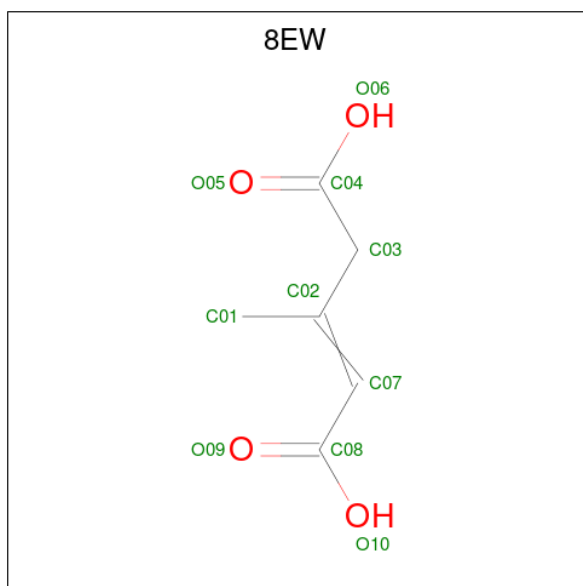
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 5 is 3-methylpent-2-enedioic acid (three-letter code: 8EW) (formula: $C_6H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		

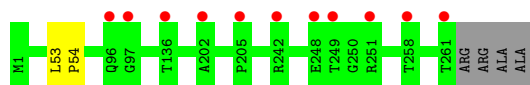
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	80	Total	O	0	1
			81	81		
6	C	116	Total	O	0	0
			116	116		
6	D	100	Total	O	0	0
			100	100		
6	B	72	Total	O	0	0
			72	72		

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: Glutaconate CoA-transferase family, subunit A



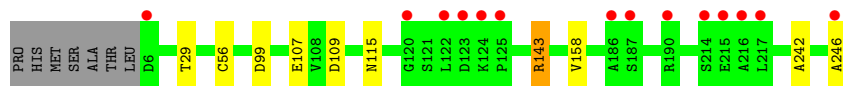
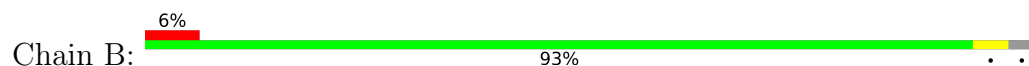
- Molecule 1: Glutaconate CoA-transferase family, subunit A



- Molecule 2: Glutaconate CoA-transferase family, subunit B



- Molecule 2: Glutaconate CoA-transferase family, subunit B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.96Å 93.13Å 90.80Å 90.00° 104.36° 90.00°	Depositor
Resolution (Å)	26.82 – 2.30 26.83 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (26.82-2.30) 99.1 (26.83-2.30)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.179 , 0.207 0.180 , 0.208	Depositor DCC
R_{free} test set	2401 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	16.6	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15409	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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: GOL, ACT, 8EW

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	0.28	0/2026	0.45	0/2761
1	C	0.30	1/2040 (0.0%)	0.45	0/2779
2	B	0.24	0/1825	0.45	0/2499
2	D	0.24	0/1825	0.46	0/2496
All	All	0.27	1/7716 (0.0%)	0.45	0/10535

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	179	ASP	C-N	6.48	1.46	1.34

There are no bond angle outliers.

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	1970	1953	1987	1	0
1	C	1978	1988	2007	3	0
2	B	1781	1756	1801	8	0
2	D	1784	1781	1801	3	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	6	0	8	0	0
4	C	4	0	3	0	0
4	D	4	3	3	0	0
5	B	10	0	0	1	0
5	D	10	0	0	0	0
6	A	81	0	0	0	0
6	B	72	0	0	0	0
6	C	116	0	0	0	0
6	D	100	0	0	2	0
All	All	7928	7481	7626	15	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 1.

All (15) 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:D:72:GLU:OE2	6:D:401:HOH:O	2.12	0.67
1:C:47:ASP:O	1:C:70[A]:ARG:NH2	2.29	0.65
2:D:245:GLY:O	2:D:246:ALA:HB3	2.12	0.49
2:B:143:ARG:HH21	2:B:143:ARG:HG2	1.78	0.49
2:B:29:THR:O	2:B:56:CYS:HB3	2.13	0.48
2:D:205:GLU:OE2	6:D:402:HOH:O	2.20	0.47
2:B:56:CYS:HB2	5:B:301:8EW:C01	2.45	0.47
1:C:53:LEU:HB3	1:C:54:PRO:HD2	1.98	0.45
1:A:53:LEU:HB3	1:A:54:PRO:CD	2.50	0.42
2:B:143:ARG:HG2	2:B:143:ARG:NH2	2.34	0.42
2:B:242:ALA:O	2:B:246:ALA:HB2	2.20	0.41
2:B:99:ASP:HA	2:B:143:ARG:HB2	2.02	0.41
2:B:109:ASP:HA	2:B:158:VAL:O	2.20	0.41
2:B:107:GLU:HB2	2:B:115:ASN:HB3	2.02	0.41
1:C:170:ASP:HA	1:C:201:VAL:O	2.20	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	265/265 (100%)	259 (98%)	6 (2%)	0	100	100
1	C	267/265 (101%)	261 (98%)	6 (2%)	0	100	100
2	B	242/248 (98%)	235 (97%)	7 (3%)	0	100	100
2	D	241/248 (97%)	234 (97%)	7 (3%)	0	100	100
All	All	1015/1026 (99%)	989 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	202/201 (100%)	202 (100%)	0	100	100
1	C	203/201 (101%)	203 (100%)	0	100	100
2	B	183/193 (95%)	182 (100%)	1 (0%)	88	95
2	D	183/193 (95%)	182 (100%)	1 (0%)	88	95
All	All	771/788 (98%)	769 (100%)	2 (0%)	92	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	139	ARG
2	B	143	ARG

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

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

7 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	$\# Z > 2$
5	8EW	B	301	-	9,9,9	4.08	2 (22%)	10,11,11	2.85	2 (20%)
4	ACT	D	303	-	3,3,3	0.79	0	3,3,3	1.28	0
3	GOL	B	302	-	5,5,5	0.35	0	5,5,5	0.27	0
5	8EW	D	301	-	9,9,9	4.10	2 (22%)	10,11,11	2.63	2 (20%)
4	ACT	C	301	-	3,3,3	0.75	0	3,3,3	1.34	0
3	GOL	D	302	-	5,5,5	0.35	0	5,5,5	0.28	0
3	GOL	A	301	-	5,5,5	0.37	0	5,5,5	0.35	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	8EW	B	301	-	-	4/8/8/8	-
3	GOL	B	302	-	-	2/4/4/4	-
5	8EW	D	301	-	-	6/8/8/8	-
3	GOL	D	302	-	-	0/4/4/4	-
3	GOL	A	301	-	-	4/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	301	8EW	C07-C02	9.78	1.52	1.33
5	B	301	8EW	C07-C02	9.67	1.52	1.33
5	B	301	8EW	C03-C02	-6.80	1.35	1.51
5	D	301	8EW	C03-C02	-6.68	1.35	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	301	8EW	C02-C07-C08	-7.80	112.44	127.11
5	D	301	8EW	C02-C07-C08	-7.09	113.77	127.11
5	B	301	8EW	O10-C08-C07	2.13	120.12	113.50
5	D	301	8EW	O10-C08-C07	2.09	119.99	113.50

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	GOL	O1-C1-C2-C3
3	B	302	GOL	C1-C2-C3-O3
3	B	302	GOL	O2-C2-C3-O3
5	D	301	8EW	C01-C02-C03-C04
5	D	301	8EW	C01-C02-C07-C08
5	D	301	8EW	C03-C02-C07-C08
5	B	301	8EW	C01-C02-C07-C08
5	B	301	8EW	C03-C02-C07-C08
3	A	301	GOL	O1-C1-C2-O2
5	B	301	8EW	C02-C07-C08-O10
3	A	301	GOL	O2-C2-C3-O3
5	B	301	8EW	C02-C07-C08-O09
5	D	301	8EW	C02-C03-C04-O06
3	A	301	GOL	C1-C2-C3-O3
5	D	301	8EW	C02-C03-C04-O05

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Mol	Chain	Res	Type	Atoms
5	D	301	8EW	C07-C02-C03-C04

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	301	8EW	1	0

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(Å ²)	Q<0.9
1	A	261/265 (98%)	0.10	11 (4%) 36 43	12, 18, 34, 48	0
1	C	263/265 (99%)	-0.11	3 (1%) 80 85	12, 15, 23, 35	0
2	B	241/248 (97%)	0.13	14 (5%) 23 29	14, 19, 32, 53	0
2	D	241/248 (97%)	0.01	6 (2%) 57 64	13, 17, 26, 35	0
All	All	1006/1026 (98%)	0.03	34 (3%) 45 52	12, 17, 29, 53	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	246	ALA	7.1
1	A	249	THR	4.5
2	B	214	SER	4.2
2	B	120	GLY	4.0
2	B	216	ALA	3.5
2	B	215	GLU	3.5
2	D	216	ALA	3.2
2	D	246	ALA	3.2
2	B	217	LEU	3.1
1	A	261	THR	3.0
1	A	248	GLU	2.9
2	B	6	ASP	2.9
2	B	122	LEU	2.9
2	B	186	ALA	2.8
1	A	205	PRO	2.8
1	A	96	GLN	2.7
1	C	261	THR	2.5
2	B	123	ASP	2.5
1	A	97	GLY	2.5
2	B	187	SER	2.5
1	A	251	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	258	THR	2.3
1	C	1[A]	MET	2.3
2	B	190	ARG	2.3
2	D	6	ASP	2.3
2	B	124	LYS	2.3
2	D	123	ASP	2.2
2	D	190	ARG	2.1
1	A	242	ARG	2.1
2	D	126	ARG	2.1
2	B	125	PRO	2.1
1	A	136	THR	2.1
1	A	202	ALA	2.1
1	C	262	ARG	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(\AA^2)	Q<0.9
3	GOL	B	302	6/6	0.75	0.24	20,22,25,26	0
5	8EW	D	301	10/10	0.85	0.25	21,23,25,26	0
5	8EW	B	301	10/10	0.87	0.21	20,22,25,26	0
4	ACT	D	303	4/4	0.88	0.15	18,20,24,24	0
3	GOL	D	302	6/6	0.91	0.18	23,25,26,27	0
3	GOL	A	301	6/6	0.92	0.29	21,23,25,25	0
4	ACT	C	301	4/4	0.95	0.12	16,18,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.