Full wwPDB X-ray Structure Validation Report (i)

Apr 18, 2026 – 04:24 PM UTC

PDB ID	:	4EG0 / pdb_00004eg0
Title	:	Crystal Structure of D-alanine–D-alanine ligase from Burkholderia ambifaria
Authors	:	Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2012-03-30
Resolution	:	1.65 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 (1)) were used in the production of this report:

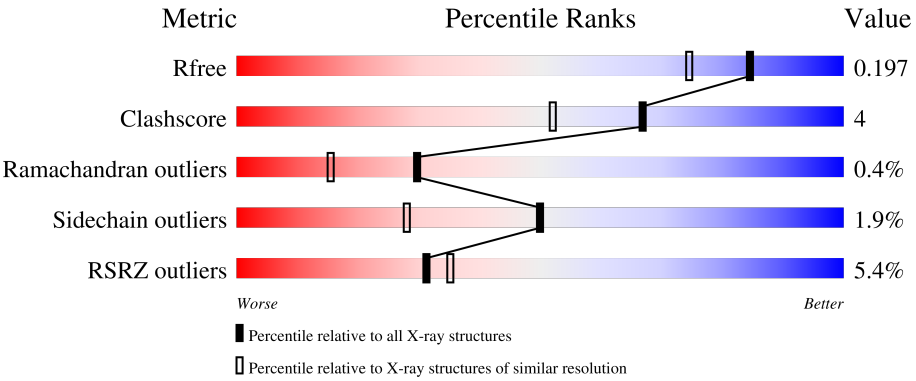
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	317	2% 84% 7% 9%
1	B	317	8% 82% 9% • 8%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4742 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.

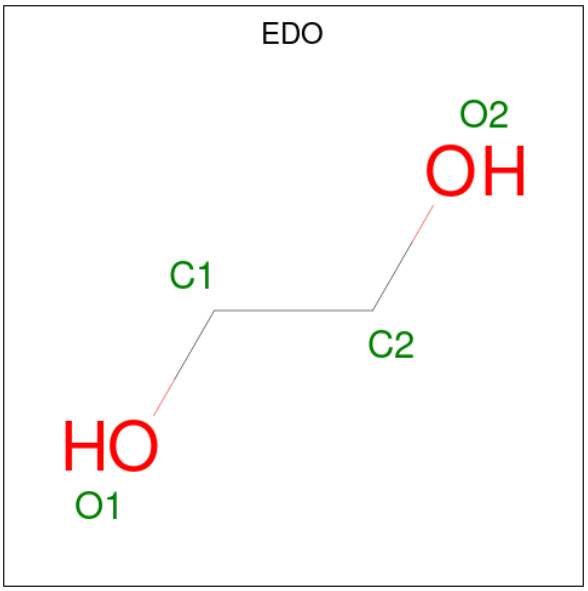
- Molecule 1 is a protein called D-alanine–D-alanine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	6	0
			2158	1381	361	410	6			
1	B	291	Total	C	N	O	S	0	5	0
			2177	1394	369	408	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP B1YSS6
A	-2	PRO	-	expression tag	UNP B1YSS6
A	-1	GLY	-	expression tag	UNP B1YSS6
A	0	SER	-	expression tag	UNP B1YSS6
B	-3	GLY	-	expression tag	UNP B1YSS6
B	-2	PRO	-	expression tag	UNP B1YSS6
B	-1	GLY	-	expression tag	UNP B1YSS6
B	0	SER	-	expression tag	UNP B1YSS6

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 3 is water.

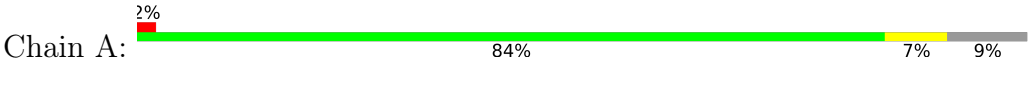
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	217	Total O 217 217	0	0
3	B	170	Total O 170 170	0	0

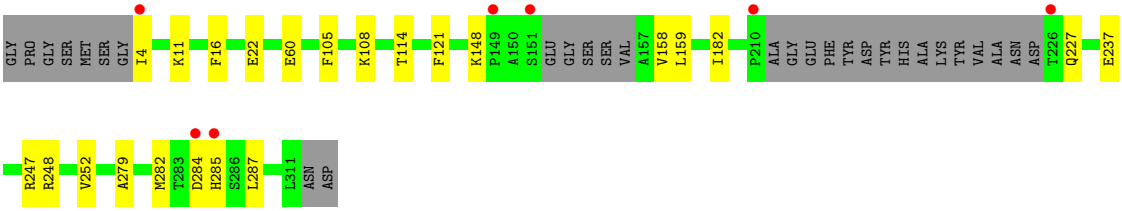
3 Residue-property plots (i)

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: D-alanine–D-alanine ligase

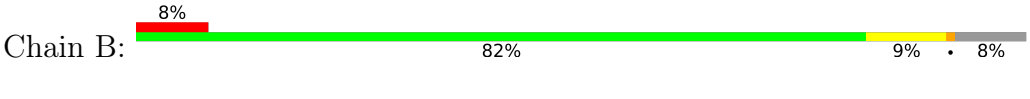
Chain A:

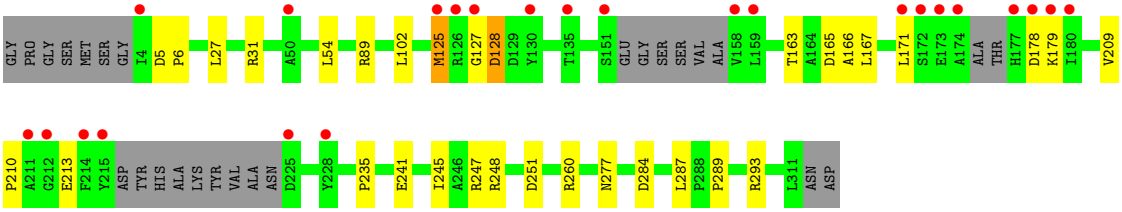




• Molecule 1: D-alanine–D-alanine ligase

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	48.38Å 118.11Å 56.93Å 90.00° 91.56° 90.00°	Depositor
Resolution (Å)	40.98 – 1.65 40.98 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.98-1.65) 95.7 (40.98-1.65)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.65 (at 1.65Å)	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
R, R_{free}	0.173 , 0.200 0.169 , 0.197	Depositor DCC
R_{free} test set	3840 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	20.5	Xtriage
Anisotropy	0.484	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	4742	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO

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	1.01	2/2218 (0.1%)	1.06	6/3018 (0.2%)
1	B	0.96	0/2235	1.05	2/3037 (0.1%)
All	All	0.99	2/4453 (0.0%)	1.06	8/6055 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	227	GLN	CG-CD	5.08	1.64	1.52
1	A	285	HIS	CA-C	5.05	1.59	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	279	ALA	CA-C-N	-7.12	112.99	120.03
1	A	279	ALA	C-N-CA	-7.12	112.99	120.03
1	A	287	LEU	CA-C-N	-6.33	113.86	120.38
1	A	287	LEU	C-N-CA	-6.33	113.86	120.38
1	B	287	LEU	CA-C-N	-5.99	114.21	120.38
1	B	287	LEU	C-N-CA	-5.99	114.21	120.38
1	A	282	MET	N-CA-C	-5.53	104.30	111.71
1	A	284	ASP	N-CA-C	-5.30	106.66	113.01

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2158	0	2147	12	0
1	B	2177	0	2142	20	1
2	A	8	0	12	0	0
2	B	12	0	18	1	0
3	A	217	0	0	2	2
3	B	170	0	0	4	1
All	All	4742	0	4319	32	2

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.

All (32) 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:A:248:ARG:NH2	3:A:582:HOH:O	2.27	0.65
1:A:237:GLU:HG2	3:A:667:HOH:O	1.99	0.63
1:A:248:ARG:HG3	1:A:248:ARG:HH11	1.64	0.61
1:A:247[A]:ARG:HH11	1:A:247[A]:ARG:HG3	1.69	0.57
1:A:105:PHE:HB2	1:A:182:ILE:HD11	1.92	0.52
1:B:248:ARG:HH11	1:B:248:ARG:HG3	1.75	0.52
1:B:27:LEU:O	1:B:31:ARG:HG3	2.09	0.52
1:A:247[A]:ARG:HG3	1:A:247[A]:ARG:NH1	2.26	0.51
1:A:114:THR:HG21	1:A:252[B]:VAL:HG21	1.91	0.51
1:A:148:LYS:HG2	1:A:158:VAL:HG13	1.93	0.51
1:A:11:LYS:NZ	1:A:60:GLU:O	2.36	0.49
1:B:251[B]:ASP:OD2	3:B:664:HOH:O	2.19	0.49
1:B:125:MET:HA	1:B:179:LYS:O	2.13	0.49
1:B:125:MET:O	1:B:128:ASP:N	2.39	0.48
1:B:284:ASP:OD1	1:B:293[A]:ARG:NH1	2.46	0.48
1:B:210:PRO:HG2	1:B:213:GLU:HB2	1.95	0.48
1:B:289:PRO:O	1:B:293[B]:ARG:HG3	2.14	0.48
1:B:289:PRO:HB2	3:B:564:HOH:O	2.13	0.47
1:B:125:MET:C	1:B:127:GLY:HA3	2.39	0.47
1:B:235:PRO:HB3	2:B:402:EDO:H22	1.98	0.46
1:B:277:ASN:ND2	3:B:654:HOH:O	2.40	0.46
1:A:248:ARG:HG3	1:A:248:ARG:NH1	2.31	0.45
1:B:165:ASP:OD1	1:B:166:ALA:N	2.51	0.44
1:B:167:LEU:O	1:B:171:LEU:HG	2.17	0.43
1:A:237:GLU:H	1:A:237:GLU:CD	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:ASP:HA	1:B:6:PRO:HD2	1.94	0.41
1:A:108:LYS:HE3	1:A:121:PHE:CD1	2.56	0.41
1:B:247[A]:ARG:NH2	3:B:644:HOH:O	2.54	0.41
1:B:260:ARG:HH11	1:B:260:ARG:HD3	1.76	0.40
1:B:102:LEU:HD23	1:B:102:LEU:HA	1.93	0.40
1:B:209:VAL:HA	1:B:210:PRO:HD2	1.83	0.40
1:B:241:GLU:OE2	1:B:245:ILE:HD11	2.20	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:508:HOH:O	3:B:599:HOH:O[2_655]	2.15	0.05
1:B:213:GLU:O	3:A:574:HOH:O[2_645]	2.15	0.05

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	288/317 (91%)	284 (99%)	4 (1%)	0	100 100
1	B	288/317 (91%)	284 (99%)	2 (1%)	2 (1%)	18 6
All	All	576/634 (91%)	568 (99%)	6 (1%)	2 (0%)	30 21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	178	ASP
1	B	128	ASP

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	221/244 (91%)	217 (98%)	4 (2%)	51 30
1	B	217/244 (89%)	213 (98%)	4 (2%)	51 30
All	All	438/488 (90%)	430 (98%)	8 (2%)	50 30

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ILE
1	A	16	PHE
1	A	22	GLU
1	A	159	LEU
1	B	54	LEU
1	B	89	ARG
1	B	125	MET
1	B	163	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	GLN
1	A	238	GLN
1	B	112	GLN
1	B	238	GLN
1	B	270	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)

5 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	EDO	A	401	-	3,3,3	0.55	0	2,2,2	0.35	0
2	EDO	B	403	-	3,3,3	0.79	0	2,2,2	0.14	0
2	EDO	B	401	-	3,3,3	0.36	0	2,2,2	0.44	0
2	EDO	B	402	-	3,3,3	0.32	0	2,2,2	0.52	0
2	EDO	A	402	-	3,3,3	0.60	0	2,2,2	0.46	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
2	EDO	A	401	-	-	1/1/1/1	-
2	EDO	B	403	-	-	1/1/1/1	-
2	EDO	B	401	-	-	0/1/1/1	-
2	EDO	B	402	-	-	1/1/1/1	-
2	EDO	A	402	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	402	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	A	401	EDO	O1-C1-C2-O2
2	B	403	EDO	O1-C1-C2-O2
2	A	402	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	402	EDO	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	288/317 (90%)	-0.07	7 (2%)	59	65	11, 26, 49, 66	6 (2%)
1	B	291/317 (91%)	0.24	24 (8%)	17	19	11, 27, 64, 80	5 (1%)
All	All	579/634 (91%)	0.09	31 (5%)	31	35	11, 27, 57, 80	11 (1%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4	ILE	6.2
1	B	177	HIS	5.4
1	B	174	ALA	4.1
1	B	172	SER	3.8
1	A	226	THR	3.6
1	B	212	GLY	3.6
1	B	126	ARG	3.6
1	A	285	HIS	3.6
1	B	215	TYR	3.5
1	A	210	PRO	3.4
1	B	178	ASP	3.4
1	B	214	PHE	3.1
1	B	173	GLU	2.9
1	B	180	ILE	2.8
1	B	4	ILE	2.8
1	B	135	THR	2.7
1	B	228	TYR	2.7
1	B	127	GLY	2.7
1	B	130	TYR	2.6
1	B	159	LEU	2.6
1	B	225	ASP	2.6
1	B	158	VAL	2.4
1	A	149	PRO	2.3
1	B	179	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	171	LEU	2.2
1	B	151	SER	2.2
1	B	125	MET	2.1
1	A	151	SER	2.1
1	B	211	ALA	2.1
1	A	284	ASP	2.1
1	B	50	ALA	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 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(Å^2)	Q<0.9
2	EDO	A	402	4/4	0.58	0.23	43,47,50,56	0
2	EDO	B	403	4/4	0.85	0.14	40,44,44,47	0
2	EDO	A	401	4/4	0.86	0.15	34,50,57,63	0
2	EDO	B	402	4/4	0.87	0.10	29,39,40,40	0
2	EDO	B	401	4/4	0.93	0.18	15,32,37,40	0

6.5 Other polymers (i)

There are no such residues in this entry.