



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 04:52 PM GMT

PDB ID : 1O4Z
Title : THE THREE-DIMENSIONAL STRUCTURE OF BETA-AGARASE B
FROM ZOBELLIA GALACTANIVORANS
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Deposited on : 2003-07-29
Resolution : 2.30 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

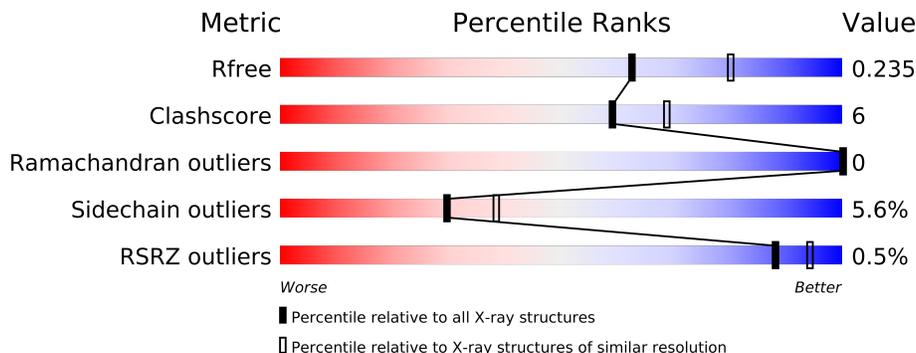
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	346	
1	B	346	
1	C	346	
1	D	346	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	MG	C	1002	-	X
3	NA	A	1007	-	X
4	EPE	A	2002	-	X
4	EPE	B	2004	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	EPE	C	2001	-	X
4	EPE	D	2003	-	X

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 10647 atoms, of which 0 are hydrogen and 0 are deuterium.

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 beta-agarase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	295	Total 2413	C 1532	N 402	O 473	S 6	0	0	0
1	B	297	Total 2428	C 1543	N 404	O 475	S 6	0	0	0
1	C	296	Total 2421	C 1537	N 403	O 475	S 6	0	1	0
1	D	297	Total 2428	C 1543	N 404	O 475	S 6	0	0	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MET	-	CLONING ARTIFACT	UNP Q9RGX8
A	17	ASP	-	CLONING ARTIFACT	UNP Q9RGX8
A	18	ILE	-	CLONING ARTIFACT	UNP Q9RGX8
A	354	LEU	-	CLONING ARTIFACT	UNP Q9RGX8
A	355	GLU	-	CLONING ARTIFACT	UNP Q9RGX8
A	356	HIS	-	EXPRESSION TAG	UNP Q9RGX8
A	357	HIS	-	EXPRESSION TAG	UNP Q9RGX8
A	358	HIS	-	EXPRESSION TAG	UNP Q9RGX8
A	359	HIS	-	EXPRESSION TAG	UNP Q9RGX8
A	360	HIS	-	EXPRESSION TAG	UNP Q9RGX8
A	361	HIS	-	EXPRESSION TAG	UNP Q9RGX8
B	16	MET	-	CLONING ARTIFACT	UNP Q9RGX8
B	17	ASP	-	CLONING ARTIFACT	UNP Q9RGX8
B	18	ILE	-	CLONING ARTIFACT	UNP Q9RGX8
B	354	LEU	-	CLONING ARTIFACT	UNP Q9RGX8
B	355	GLU	-	CLONING ARTIFACT	UNP Q9RGX8
B	356	HIS	-	EXPRESSION TAG	UNP Q9RGX8
B	357	HIS	-	EXPRESSION TAG	UNP Q9RGX8
B	358	HIS	-	EXPRESSION TAG	UNP Q9RGX8
B	359	HIS	-	EXPRESSION TAG	UNP Q9RGX8
B	360	HIS	-	EXPRESSION TAG	UNP Q9RGX8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	361	HIS	-	EXPRESSION TAG	UNP Q9RGX8
C	16	MET	-	CLONING ARTIFACT	UNP Q9RGX8
C	17	ASP	-	CLONING ARTIFACT	UNP Q9RGX8
C	18	ILE	-	CLONING ARTIFACT	UNP Q9RGX8
C	354	LEU	-	CLONING ARTIFACT	UNP Q9RGX8
C	355	GLU	-	CLONING ARTIFACT	UNP Q9RGX8
C	356	HIS	-	EXPRESSION TAG	UNP Q9RGX8
C	357	HIS	-	EXPRESSION TAG	UNP Q9RGX8
C	358	HIS	-	EXPRESSION TAG	UNP Q9RGX8
C	359	HIS	-	EXPRESSION TAG	UNP Q9RGX8
C	360	HIS	-	EXPRESSION TAG	UNP Q9RGX8
C	361	HIS	-	EXPRESSION TAG	UNP Q9RGX8
D	16	MET	-	CLONING ARTIFACT	UNP Q9RGX8
D	17	ASP	-	CLONING ARTIFACT	UNP Q9RGX8
D	18	ILE	-	CLONING ARTIFACT	UNP Q9RGX8
D	354	LEU	-	CLONING ARTIFACT	UNP Q9RGX8
D	355	GLU	-	CLONING ARTIFACT	UNP Q9RGX8
D	356	HIS	-	EXPRESSION TAG	UNP Q9RGX8
D	357	HIS	-	EXPRESSION TAG	UNP Q9RGX8
D	358	HIS	-	EXPRESSION TAG	UNP Q9RGX8
D	359	HIS	-	EXPRESSION TAG	UNP Q9RGX8
D	360	HIS	-	EXPRESSION TAG	UNP Q9RGX8
D	361	HIS	-	EXPRESSION TAG	UNP Q9RGX8

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

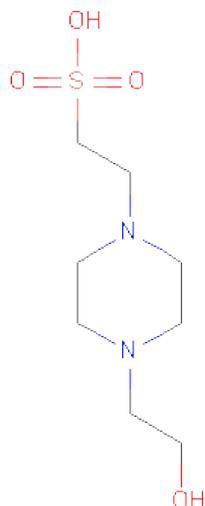
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Na 2 2	0	0
3	A	2	Total Na 2 2	0	0
3	D	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	2	Total	Na	0	0
			2	2		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINEETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is water.

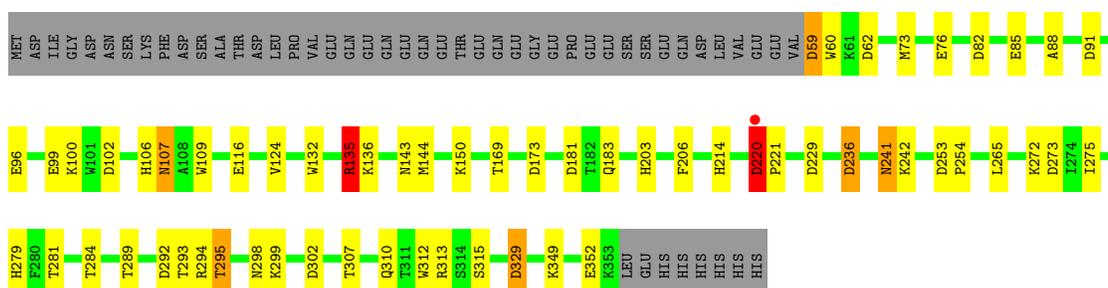
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	226	Total	O	0	0
			226	226		
5	B	230	Total	O	0	0
			230	230		
5	C	213	Total	O	0	0
			213	213		
5	D	219	Total	O	0	0
			219	219		

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 errors 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.

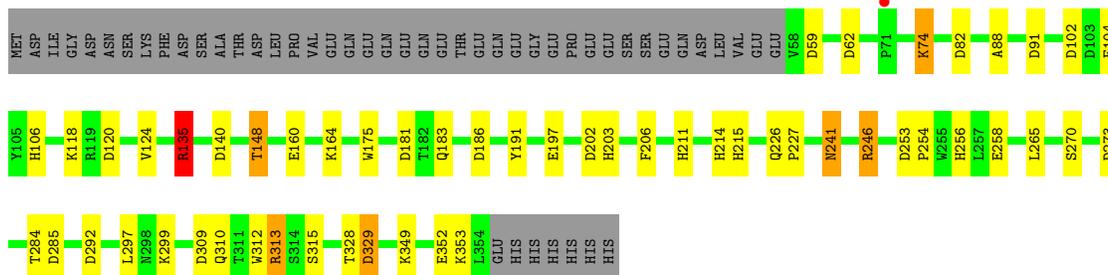
- Molecule 1: beta-agarase B

Chain A:



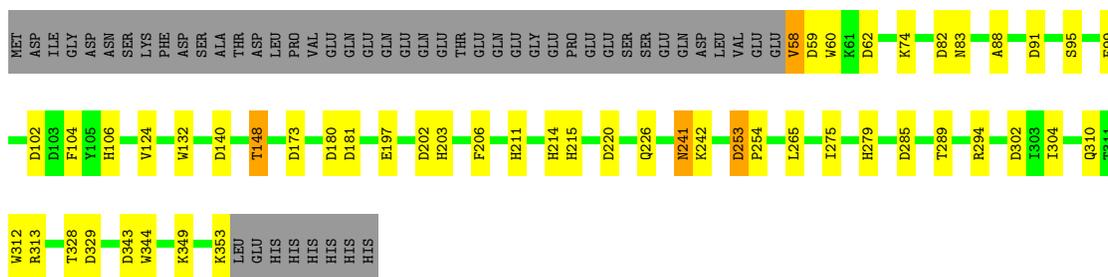
- Molecule 1: beta-agarase B

Chain B:



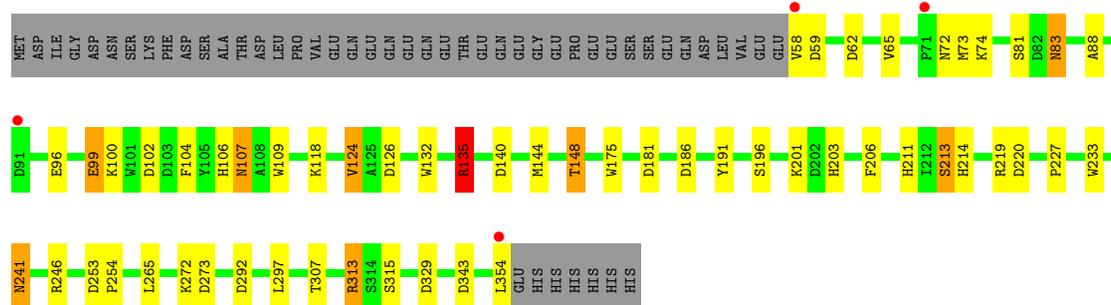
- Molecule 1: beta-agarase B

Chain C:



- Molecule 1: beta-agarase B

Chain D: 



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.45Å 105.35Å 97.37Å 90.00° 94.13° 90.00°	Depositor
Resolution (Å)	25.00 – 2.30 24.75 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.00-2.30) 99.9 (24.75-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 2.31Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.166 , 0.224 0.179 , 0.235	Depositor DCC
R_{free} test set	3282 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	17.0	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 26.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 125926 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10647	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.19 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.3258e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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: NA, MG, EPE

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	0.52	0/2487	0.87	14/3386 (0.4%)
1	B	0.50	0/2502	0.89	18/3407 (0.5%)
1	C	0.51	0/2500	0.87	18/3404 (0.5%)
1	D	0.51	0/2502	0.86	15/3407 (0.4%)
All	All	0.51	0/9991	0.87	65/13604 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	313	ARG	NE-CZ-NH2	-7.84	116.38	120.30
1	B	292	ASP	CB-CG-OD2	7.70	125.23	118.30
1	B	246	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	A	91	ASP	CB-CG-OD1	7.08	124.67	118.30
1	A	236	ASP	CB-CG-OD2	6.94	124.55	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	220	ASP	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2413	0	2244	32	0
1	B	2428	0	2264	29	0
1	C	2421	0	2254	25	0
1	D	2428	0	2264	28	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	15	0	17	0	0
4	B	15	0	17	1	0
4	C	15	0	17	0	0
4	D	15	0	17	1	0
5	A	226	0	0	3	1
5	B	230	0	0	4	0
5	C	213	0	0	3	0
5	D	219	0	0	2	1
All	All	10647	0	9094	114	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

The worst 5 of 114 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:211:HIS:HD2	1:D:233:TRP:CZ2	1.90	0.90
1:B:197:GLU:OE2	5:B:2157:HOH:O	1.95	0.85
1:D:211:HIS:HD2	1:D:233:TRP:CE2	2.00	0.80
1:A:295:THR:HG23	1:A:298:ASN:OD1	1.84	0.78
1:D:273:ASP:OD1	5:D:2206:HOH:O	2.01	0.78

All (1) 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	Distance(Å)	Clash(Å)
5:A:2219:HOH:O	5:D:2198:HOH:O[2_546]	2.14	0.06

5.3 Torsion angles

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	293/346 (85%)	287 (98%)	6 (2%)	0	100	100
1	B	295/346 (85%)	289 (98%)	6 (2%)	0	100	100
1	C	295/346 (85%)	289 (98%)	6 (2%)	0	100	100
1	D	295/346 (85%)	290 (98%)	5 (2%)	0	100	100
All	All	1178/1384 (85%)	1155 (98%)	23 (2%)	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	260/308 (84%)	245 (94%)	15 (6%)	28	36
1	B	262/308 (85%)	252 (96%)	10 (4%)	44	59
1	C	262/308 (85%)	249 (95%)	13 (5%)	34	45
1	D	262/308 (85%)	241 (92%)	21 (8%)	17	20
All	All	1046/1232 (85%)	987 (94%)	59 (6%)	30	38

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	60	TRP
1	C	148	THR

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Mol	Chain	Res	Type
1	D	241	ASN
1	C	74	LYS
1	C	95[B]	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	323	ASN
1	C	215	HIS
1	D	226	GLN
1	C	92	ASN
1	A	310	GLN

5.3.3 RNA [i](#)

There are no RNA chains 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 13 ligands modelled in this entry, 9 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
4	EPE	A	2002	-	15,15,15	0.81	1 (6%)	20,20,20	1.60	5 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EPE	B	2004	-	15,15,15	0.79	1 (6%)	20,20,20	1.43	3 (15%)
4	EPE	C	2001	-	15,15,15	0.57	0	20,20,20	1.45	3 (15%)
4	EPE	D	2003	-	15,15,15	0.72	1 (6%)	20,20,20	1.42	2 (10%)

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
4	EPE	A	2002	-	-	0/9/19/19	0/1/1/1
4	EPE	B	2004	-	-	0/9/19/19	0/1/1/1
4	EPE	C	2001	-	-	0/9/19/19	0/1/1/1
4	EPE	D	2003	-	-	0/9/19/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2004	EPE	C10-S	2.77	1.81	1.77
4	A	2002	EPE	C10-S	2.69	1.81	1.77
4	D	2003	EPE	C10-S	2.23	1.80	1.77

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	2003	EPE	O2S-S-C10	4.33	110.52	106.81
4	B	2004	EPE	O2S-S-C10	4.24	110.44	106.81
4	A	2002	EPE	O2S-S-C10	3.51	109.82	106.81
4	C	2001	EPE	C6-C5-N4	3.37	117.25	110.61
4	A	2002	EPE	O3S-S-C10	3.02	109.75	105.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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	295/346 (85%)	-0.32	1 (0%) 91 96	14, 20, 29, 38	16 (5%)
1	B	297/346 (85%)	-0.36	1 (0%) 91 96	15, 21, 32, 36	21 (7%)
1	C	296/346 (85%)	-0.30	0 100 100	15, 21, 32, 38	15 (5%)
1	D	297/346 (85%)	-0.31	4 (1%) 74 82	15, 21, 33, 40	20 (6%)
All	All	1185/1384 (85%)	-0.32	6 (0%) 88 94	14, 21, 32, 40	72 (6%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	71	PRO	3.3
1	A	220	ASP	2.7
1	D	354	LEU	2.4
1	B	71	PRO	2.2
1	D	58	VAL	2.2

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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	EPE	B	2004	15/15	0.26	11.78	40,45,48,48	6
4	EPE	D	2003	15/15	0.24	8.52	37,39,45,46	6
3	NA	A	1007	1/1	0.17	8.24	38,38,38,38	0
2	MG	C	1002	1/1	0.25	5.30	40,40,40,40	0
4	EPE	C	2001	15/15	0.17	2.95	28,35,37,37	6
4	EPE	A	2002	15/15	0.17	2.93	36,37,38,39	6
2	MG	B	1001	1/1	0.13	1.53	33,33,33,33	0
3	NA	B	1008	1/1	0.10	-0.76	45,45,45,45	0
3	NA	D	1003	1/1	0.07	-1.33	21,21,21,21	0
3	NA	C	1006	1/1	0.05	-1.92	21,21,21,21	0
3	NA	B	1005	1/1	0.06	-2.25	25,25,25,25	0
3	NA	A	1004	1/1	0.05	-2.30	23,23,23,23	0
3	NA	C	1009	1/1	0.05	-6.32	18,18,18,18	0

6.5 Other polymers i

There are no such residues in this entry.