



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 07:08 AM EDT

PDB ID : 6NST
Title : Crystal structure of branched chain amino acid aminotransferase from *Pseudomonas aeruginosa*
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Deposited on : 2019-01-25
Resolution : 2.14 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
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)	:	2.36.2

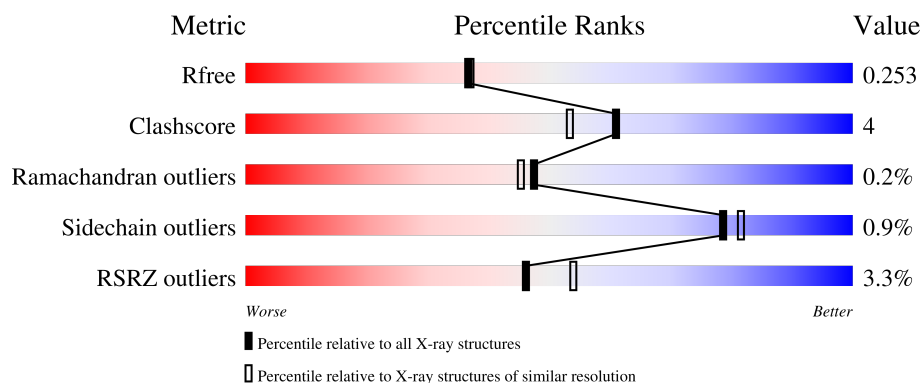
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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	307	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div>..</div> </div> </div>
1	B	307	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>.</div> </div> </div>
1	C	307	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>14%</div> <div>.</div> </div> </div>
1	D	307	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>15%</div> <div>.</div> </div> </div>
1	E	307	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	307	<div><div></div><div>2%</div><div>91%</div><div>7%</div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14476 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 Branched-chain-amino-acid aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	0	0
			2349	1475	416	446	12			
1	B	301	Total	C	N	O	S	0	1	0
			2341	1470	414	446	11			
1	C	295	Total	C	N	O	S	0	1	0
			2295	1441	408	434	12			
1	D	299	Total	C	N	O	S	0	1	0
			2314	1451	412	440	11			
1	E	300	Total	C	N	O	S	0	1	0
			2326	1458	413	443	12			
1	F	300	Total	C	N	O	S	0	1	0
			2334	1464	415	443	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	HIS	LEU	engineered mutation	UNP O86428
B	31	HIS	LEU	engineered mutation	UNP O86428
C	31	HIS	LEU	engineered mutation	UNP O86428
D	31	HIS	LEU	engineered mutation	UNP O86428
E	31	HIS	LEU	engineered mutation	UNP O86428
F	31	HIS	LEU	engineered mutation	UNP O86428

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

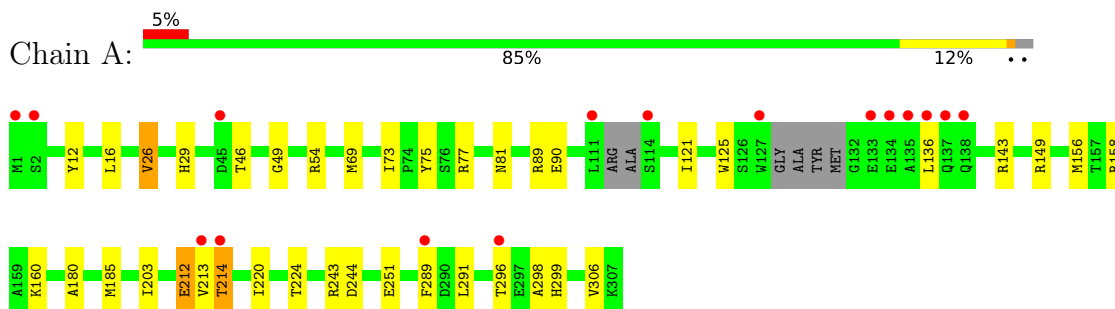
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	84	Total	O	0	0
			84	84		
3	B	68	Total	O	0	0
			68	68		
3	C	82	Total	O	0	0
			82	82		
3	D	85	Total	O	0	0
			85	85		
3	E	73	Total	O	0	0
			73	73		
3	F	95	Total	O	0	0
			95	95		

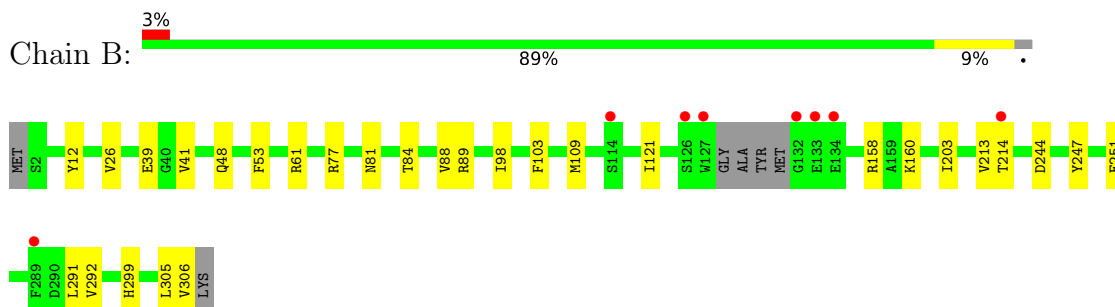
3 Residue-property plots

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.

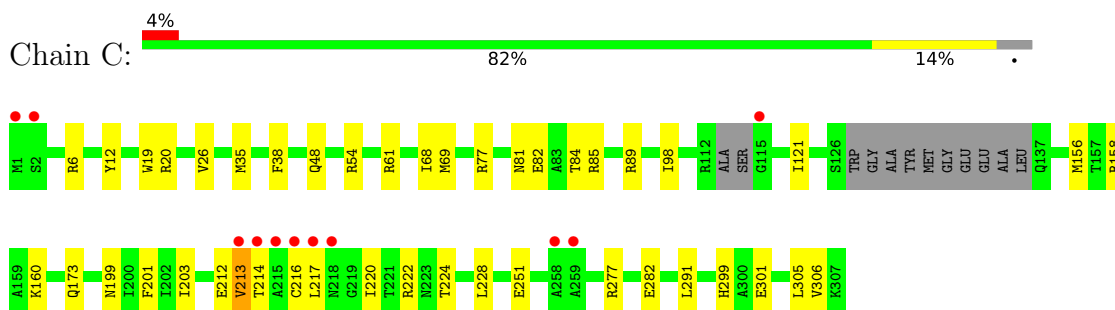
- Molecule 1: Branched-chain-amino-acid aminotransferase



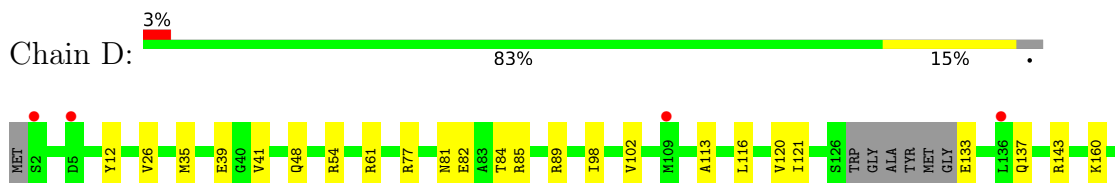
- Molecule 1: Branched-chain-amino-acid aminotransferase



- Molecule 1: Branched-chain-amino-acid aminotransferase

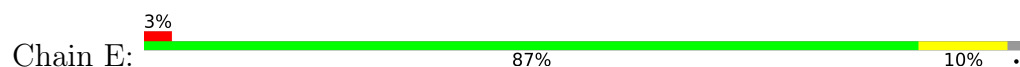


- Molecule 1: Branched-chain-amino-acid aminotransferase

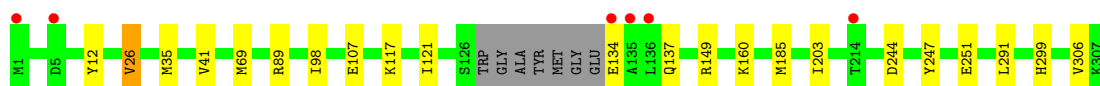




- Molecule 1: Branched-chain-amino-acid aminotransferase



- Molecule 1: Branched-chain-amino-acid aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.84Å 129.64Å 85.79Å 90.00° 114.25° 90.00°	Depositor
Resolution (Å)	49.92 – 2.14 49.92 – 2.14	Depositor EDS
% Data completeness (in resolution range)	83.4 (49.92-2.14) 83.5 (49.92-2.14)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.195 , 0.253 0.195 , 0.253	Depositor DCC
R_{free} test set	3816 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14476	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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: SO4

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	0.24	0/2395	0.43	0/3239
1	B	0.24	0/2388	0.43	0/3235
1	C	0.25	0/2339	0.43	0/3164
1	D	0.24	0/2358	0.43	0/3193
1	E	0.24	0/2371	0.43	0/3211
1	F	0.25	0/2379	0.44	0/3219
All	All	0.25	0/14230	0.43	0/19261

There are no bond length outliers.

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	2349	0	2290	23	0
1	B	2341	0	2261	19	0
1	C	2295	0	2227	31	0
1	D	2314	0	2234	29	0
1	E	2326	0	2257	20	0
1	F	2334	0	2279	14	0
2	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	1	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	84	0	0	2	0
3	B	68	0	0	1	0
3	C	82	0	0	5	0
3	D	85	0	0	2	0
3	E	73	0	0	0	0
3	F	95	0	0	1	0
All	All	14476	0	13548	124	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 4.

The worst 5 of 124 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:121:ILE:HG21	1:B:26:VAL:HG21	1.70	0.73
1:C:26:VAL:HG21	1:D:121:ILE:HG21	1.70	0.72
1:C:173[B]:GLN:NE2	3:C:502:HOH:O	2.25	0.69
1:C:277:ARG:NH2	3:C:503:HOH:O	2.28	0.66
1:B:203:ILE:HB	1:B:251:GLU:HB2	1.78	0.66

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	295/307 (96%)	287 (97%)	7 (2%)	1 (0%)	41 36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	298/307 (97%)	290 (97%)	8 (3%)	0	100	100
1	C	290/307 (94%)	285 (98%)	4 (1%)	1 (0%)	41	36
1	D	294/307 (96%)	287 (98%)	7 (2%)	0	100	100
1	E	297/307 (97%)	285 (96%)	11 (4%)	1 (0%)	41	36
1	F	297/307 (97%)	285 (96%)	12 (4%)	0	100	100
All	All	1771/1842 (96%)	1719 (97%)	49 (3%)	3 (0%)	47	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	VAL
1	C	213	VAL
1	E	213	VAL

5.3.2 Protein sidechains ⓘ

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	242/246 (98%)	238 (98%)	4 (2%)	60	63
1	B	238/246 (97%)	237 (100%)	1 (0%)	91	93
1	C	234/246 (95%)	233 (100%)	1 (0%)	91	93
1	D	235/246 (96%)	233 (99%)	2 (1%)	78	81
1	E	238/246 (97%)	235 (99%)	3 (1%)	69	73
1	F	240/246 (98%)	238 (99%)	2 (1%)	81	85
All	All	1427/1476 (97%)	1414 (99%)	13 (1%)	78	81

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	35	MET
1	E	12	TYR
1	F	26	VAL

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Mol	Chain	Res	Type
1	E	136	LEU
1	F	12	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	137	GLN
1	E	29	HIS

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](#)

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	SO4	D	401	-	4,4,4	0.15	0	6,6,6	0.06	0
2	SO4	E	401	-	4,4,4	0.15	0	6,6,6	0.05	0
2	SO4	F	401	-	4,4,4	0.14	0	6,6,6	0.06	0
2	SO4	B	401	-	4,4,4	0.13	0	6,6,6	0.06	0
2	SO4	C	401	-	4,4,4	0.14	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	401	-	4,4,4	0.12	0	6,6,6	0.05	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	SO4	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 [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	301/307 (98%)	0.02	16 (5%) 26 33	12, 27, 59, 116	0
1	B	301/307 (98%)	0.09	8 (2%) 54 61	11, 32, 60, 116	0
1	C	295/307 (96%)	-0.01	11 (3%) 41 49	14, 28, 54, 104	0
1	D	299/307 (97%)	-0.07	8 (2%) 54 61	8, 26, 56, 87	0
1	E	300/307 (97%)	0.14	10 (3%) 46 54	11, 29, 61, 118	0
1	F	300/307 (97%)	-0.06	6 (2%) 65 71	11, 23, 55, 125	0
All	All	1796/1842 (97%)	0.02	59 (3%) 46 54	8, 28, 59, 125	0

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	MET	13.3
1	A	1	MET	12.1
1	F	1	MET	10.4
1	F	135	ALA	6.9
1	D	217	LEU	6.8

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
2	SO4	D	401	5/5	0.95	0.17	46,48,60,64	0
2	SO4	C	401	5/5	0.96	0.11	36,46,54,59	0
2	SO4	A	401	5/5	0.96	0.10	28,28,38,40	0
2	SO4	B	401	5/5	0.98	0.10	24,27,36,42	0
2	SO4	E	401	5/5	0.98	0.09	22,28,32,43	0
2	SO4	F	401	5/5	0.99	0.07	18,21,27,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.