

Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	7CIF
Title	:	Crystal structure of L-methionine decarboxylase from Streptomyces sp.590 (in-
		ternal aldimine form).
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Deposited on	:	2020-07-07
Resolution	:	1.80 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 following versions of software and data (see references (1)) 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	:	2.16
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)	:	2.16

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$		
R_{free}	130704	5950(1.80-1.80)		
Clashscore	141614	6793 (1.80-1.80)		
Ramachandran outliers	138981	6697 (1.80-1.80)		
Sidechain outliers	138945	6696 (1.80-1.80)		
RSRZ outliers	127900	5850 (1.80-1.80)		

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	А	557	9%	8% • 6%
1	В	557	83%	10% • 7%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8502 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 L-methionine decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	Λ	526	Total	С	Ν	Ο	Р	\mathbf{S}	0	2	0
	520	4139	2632	722	769	1	15	0	2	0	
1	В	510	Total	С	Ν	Ο	Р	S	0	0	0
I D	519	4082	2598	710	758	1	15	0	U	0	

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	132	Total O 132 132	0	0
2	В	149	Total O 149 149	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: L-methionine decarboxylase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	124.63Å 147.50Å 53.90Å	Depositor
a, b, c, α , β , γ	90.00° 99.87° 90.00°	Depositor
Bosolution (Å)	19.89 - 1.80	Depositor
	19.89 - 1.80	EDS
% Data completeness	98.1 (19.89-1.80)	Depositor
(in resolution range)	98.1 (19.89-1.80)	EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.95 (at 1.80 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R R.	0.190 , 0.231	Depositor
II, II, <i>free</i>	0.199 , 0.237	DCC
R_{free} test set	4308 reflections $(4.97%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	28.7	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 43.6	EDS
L-test for $twinning^2$	$ < L >=0.51, < L^2>=0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8502	wwPDB-VP
Average B, all atoms $(Å^2)$	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 9.54% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: LLP

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).

Mal	Chain	Bond	lengths	Bond angles		
1VIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.61	0/4234	0.78	4/5773~(0.1%)	
1	В	0.64	0/4176	0.78	1/5691~(0.0%)	
All	All	0.63	0/8410	0.78	5/11464~(0.0%)	

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	470	ARG	NE-CZ-NH1	5.19	122.90	120.30
1	А	537	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	А	425	PRO	N-CA-C	5.13	125.44	112.10
1	А	470	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	А	150	ARG	NE-CZ-NH1	-5.04	117.78	120.30

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	А	4139	0	3981	24	0
1	В	4082	0	3930	28	0
2	А	132	0	0	0	0
2	В	149	0	0	2	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8502	0	7911	51	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 3.

All (51) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:516:VAL:HG22	1:B:522:THR:HG21	1.56	0.88
1:A:516:VAL:HG22	1:A:522:THR:HG21	1.69	0.72
1:B:482:LEU:HD11	1:B:553:ILE:HG23	1.74	0.68
1:A:284:PHE:O	1:A:528:HIS:HD2	1.82	0.63
1:B:354:PRO:HB2	1:B:360:THR:HG22	1.81	0.63
1:A:537:ARG:NH1	1:A:541:ASP:OD2	2.32	0.62
1:B:284:PHE:O	1:B:528:HIS:HD2	1.83	0.61
1:B:424:ALA:HB1	1:B:425:PRO:CD	2.33	0.59
1:B:354:PRO:CB	1:B:360:THR:HG22	2.34	0.57
1:B:116:HIS:HD2	1:B:369:ASP:OD2	1.87	0.56
1:A:182:ASN:HD21	1:A:217:LYS:NZ	2.04	0.55
1:B:69:MET:HB2	1:B:72:THR:HG23	1.88	0.55
1:B:69:MET:HB2	1:B:72:THR:CG2	2.37	0.54
1:A:516:VAL:HG23	1:A:519:ASP:HB3	1.90	0.53
1:A:313:VAL:HG12	1:A:325:VAL:HG22	1.89	0.53
1:B:208:GLU:HG3	2:B:627:HOH:O	2.10	0.52
1:A:102:VAL:HG22	1:A:105:ARG:NH2	2.27	0.49
1:A:537:ARG:HG2	1:A:537:ARG:HH11	1.78	0.48
1:B:218:TYR:OH	1:B:272:HIS:HE1	1.97	0.48
1:A:265:GLU:OE1	1:A:304:ARG:NH1	2.47	0.48
1:A:178:ARG:HD3	1:A:179:ARG:HA	1.96	0.48
1:B:424:ALA:HB1	1:B:425:PRO:HD2	1.97	0.47
1:B:509:SER:HB3	1:B:528:HIS:CE1	2.50	0.47
1:A:185:HIS:O	1:A:272:HIS:HD2	1.98	0.47
1:B:202:VAL:HG13	1:B:207:VAL:O	2.14	0.47
1:B:62:GLY:HA3	1:B:508:LEU:HA	1.96	0.47
1:B:146:LEU:HG	1:B:207:VAL:HG21	1.96	0.46
1:B:480:VAL:HG23	1:B:482:LEU:HD13	1.97	0.46
1:A:423:GLY:C	1:A:425:PRO:HD2	2.36	0.46
1:B:75:ASP:OD2	1:B:447:ARG:NH2	2.49	0.46
1:B:461:GLN:HE22	1:B:489:GLY:HA2	1.80	0.45
1:A:54:THR:O	1:A:58:LYS:HE3	2.15	0.45
1:A:218:TYR:OH	1:A:272:HIS:HE1	2.00	0.45



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:509:SER:HB3	1:A:528:HIS:CE1	2.52	0.45
1:B:444:HIS:HE1	2:B:716:HOH:O	2.01	0.44
1:A:393:HIS:CD2	1:A:393:HIS:H	2.34	0.44
1:A:310[A]:ARG:O	1:A:310[A]:ARG:HG3	2.16	0.44
1:B:110:TYR:CE1	1:B:445:LEU:HD22	2.53	0.44
1:A:190:TYR:HB3	1:A:277:ASN:HB3	2.01	0.43
1:B:337:GLY:O	1:B:338:ALA:C	2.57	0.42
1:B:159:ILE:HG22	1:B:160:GLN:HG2	2.01	0.42
1:B:393:HIS:H	1:B:393:HIS:CD2	2.37	0.42
1:A:344:ALA:N	1:A:345:PRO:CD	2.81	0.42
1:B:185:HIS:O	1:B:272:HIS:HD2	2.03	0.42
1:B:182:ASN:OD1	1:B:217:LYS:NZ	2.53	0.41
1:A:393:HIS:CD2	1:A:401:PRO:HA	2.55	0.41
1:A:258[B]:ASP:OD1	1:A:297:ARG:NH2	2.53	0.41
1:B:146:LEU:HD23	1:B:205:LEU:HD12	2.02	0.41
1:A:89:ASP:HB2	1:A:425:PRO:HA	2.03	0.41
1:A:393:HIS:HE1	1:B:432:SER:OG	2.04	0.40
1:A:516:VAL:O	1:A:516:VAL:HG23	2.21	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	Perce	ntiles
1	А	523/557~(94%)	497~(95%)	20~(4%)	6 (1%)	14	4
1	В	514/557~(92%)	496 (96%)	17 (3%)	1 (0%)	47	33
All	All	1037/1114~(93%)	993~(96%)	37~(4%)	7 (1%)	22	10

All (7) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	А	425	PRO
1	В	424	ALA
1	А	319	GLN
1	А	323	PRO
1	А	423	GLY
1	А	180	ASN
1	А	424	ALA

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	А	426/449~(95%)	412 (97%)	14 (3%)	38 23	3	
1	В	421/449 (94%)	406 (96%)	15 (4%)	35 20)	
All	All	847/898~(94%)	818~(97%)	29~(3%)	38 22	2	

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	41	ARG
1	А	224	LEU
1	А	292	ARG
1	А	309	GLN
1	А	310[A]	ARG
1	А	310[B]	ARG
1	А	322	ARG
1	А	418	GLN
1	А	420	ASP
1	А	421	TYR
1	А	425	PRO
1	А	436	PHE
1	А	494	ARG
1	А	528	HIS
1	В	25	LEU
1	В	57	ARG
1	В	72	THR



Mol	Chain	\mathbf{Res}	Type
1	В	92	GLN
1	В	178	ARG
1	В	179	ARG
1	В	197	SER
1	В	198	PHE
1	В	292	ARG
1	В	319	GLN
1	В	320	THR
1	В	427	THR
1	В	436	PHE
1	В	494	ARG
1	В	528	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	92	GLN
1	А	180	ASN
1	А	182	ASN
1	А	184	HIS
1	А	272	HIS
1	А	279	ASN
1	А	393	HIS
1	А	528	HIS
1	В	116	HIS
1	В	272	HIS
1	В	279	ASN
1	В	309	GLN
1	В	319	GLN
1	В	393	HIS
1	В	444	HIS
1	В	461	GLN
1	В	528	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)

2 non-standard protein/DNA/RNA residues 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	Trune	Chain	Dec	Tinle	Bond lengths			Bond angles		
INIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
1	LLP	В	394	1	23,24,25	2.69	4 (17%)	$25,\!32,\!34$	1.50	6 (24%)
1	LLP	А	394	1	23,24,25	2.59	4 (17%)	25,32,34	1.90	7 (28%)

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
1	LLP	В	394	1	-	4/16/17/19	0/1/1/1
1	LLP	А	394	1	-	4/16/17/19	0/1/1/1

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	В	394	LLP	C3-C2	7.95	1.48	1.40
1	А	394	LLP	C3-C2	6.73	1.47	1.40
1	А	394	LLP	C4-C5	6.71	1.50	1.42
1	А	394	LLP	C4'-NZ	5.42	1.45	1.27
1	В	394	LLP	C4-C5	5.39	1.48	1.42
1	В	394	LLP	C4-C3	5.35	1.48	1.40
1	В	394	LLP	C4'-NZ	5.25	1.44	1.27
1	А	394	LLP	C4-C3	4.43	1.47	1.40

All (8) bond length outliers are listed below:

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	394	LLP	C4-C3-C2	-4.15	117.62	120.19
1	А	394	LLP	C6-N1-C2	3.88	126.36	119.17
1	А	394	LLP	C4-C4'-NZ	-3.34	108.96	124.31



Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	Ideal(°)
1	В	394	LLP	C4-C4'-NZ	-3.01	110.48	124.31
1	А	394	LLP	OP3-P-OP1	2.82	121.71	110.68
1	В	394	LLP	C6-N1-C2	2.69	124.16	119.17
1	В	394	LLP	C4-C3-C2	-2.51	118.63	120.19
1	В	394	LLP	OP3-P-OP4	-2.23	100.80	106.73
1	В	394	LLP	OP2-P-OP1	2.22	119.36	110.68
1	В	394	LLP	OP3-P-OP1	2.08	118.82	110.68
1	А	394	LLP	OP4-C5'-C5	-2.03	105.47	109.35
1	А	394	LLP	O3-C3-C2	2.02	121.89	117.49
1	А	394	LLP	OP3-P-OP4	-2.02	101.37	106.73

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	В	394	LLP	C4-C4'-NZ-CE
1	А	394	LLP	C4-C4'-NZ-CE
1	В	394	LLP	CG-CD-CE-NZ
1	А	394	LLP	CG-CD-CE-NZ
1	А	394	LLP	C3-C4-C4'-NZ
1	В	394	LLP	CD-CE-NZ-C4'
1	А	394	LLP	CD-CE-NZ-C4'
1	В	394	LLP	C3-C4-C4'-NZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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, 95^{th} 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	А	525/557~(94%)	0.54	52 (9%) 7	5	20, 31, 69, 146	0
1	В	518/557~(92%)	0.35	37 (7%) 16	12	18, 30, 67, 122	0
All	All	1043/1114~(93%)	0.45	89 (8%) 10	8	18, 30, 69, 146	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	163	THR	14.0
1	А	422	ILE	12.4
1	А	162	PRO	12.2
1	А	161	PRO	12.1
1	В	423	GLY	11.4
1	А	317	CYS	11.2
1	В	421	TYR	11.2
1	А	164	ALA	10.6
1	А	320	THR	10.3
1	А	421	TYR	9.9
1	В	417	SER	9.8
1	В	422	ILE	9.7
1	А	322	ARG	9.5
1	В	424	ALA	8.8
1	А	417	SER	8.3
1	А	556	ALA	8.2
1	В	318	PRO	6.9
1	В	161	PRO	6.8
1	В	419	PRO	6.6
1	А	424	ALA	6.6
1	В	162	PRO	6.6
1	А	419	PRO	6.5
1	В	420	ASP	6.2
1	А	319	GLN	6.1



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Mol	Chain	Res	Type	RSRZ			
1	В	418	GLN	6.0			
1	А	178	ARG	5.9			
1	В	325	VAL	5.9			
1	А	423	GLY	5.9			
1	А	430	ALA	5.8			
1	В	179	ARG	5.8			
1	А	416	PRO	5.6			
1	В	322	ARG	5.3			
1	В	319	GLN	5.0			
1	А	418	GLN	4.9			
1	А	321	GLY	4.9			
1	В	557	PRO	4.8			
1	А	420	ASP	4.8			
1	А	179	ARG	4.7			
1	А	315	GLY	4.7			
1	В	324	LEU	4.5			
1	В	416	PRO	4.2			
1	В	317	CYS	4.2			
1	В	25	LEU	4.2			
1	А	518	GLY	4.2			
1	А	324	LEU	4.2			
1	А	323	PRO	4.1			
1	В	320	THR	4.0			
1	А	318	PRO	4.0			
1	В	26	ASP	4.0			
1	А	22	GLY	3.9			
1	А	316	SER	3.8			
1	А	425	PRO	3.8			
1	В	24	GLU	3.7			
1	В	379	HIS	3.7			
1	В	316	SER	3.6			
1	В	323	PRO	3.5			
1	А	379	HIS	3.5			
1	В	518	GLY	3.4			
1	А	520	GLU	3.4			
1	В	315	GLY	3.2			
1	А	429	PHE	3.2			
1	В	425	PRO	3.2			
1	В	415	PRO	3.1			
1	А	93	SER	3.0			
1	В	160	GLN	3.0			
1	А	314	TYR	3.0			
			-				



\mathbf{Mol}	Chain	\mathbf{Res}	Type	RSRZ
1	А	355	GLU	3.0
1	А	18	ALA	2.9
1	А	555	GLY	2.8
1	А	377	ALA	2.8
1	В	216	GLU	2.8
1	А	160	GLN	2.7
1	В	312	VAL	2.6
1	В	313	VAL	2.5
1	А	414	SER	2.5
1	А	68	ASP	2.5
1	А	380	GLY	2.4
1	А	313	VAL	2.3
1	А	232	ARG	2.3
1	А	519	ASP	2.3
1	В	93	SER	2.2
1	А	352	GLU	2.2
1	В	355	GLU	2.1
1	А	378	GLY	2.1
1	А	376	THR	2.1
1	В	426	ASP	2.1
1	А	215	LEU	2.1
1	А	21	PRO	2.0
1	А	24	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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
1	LLP	А	394	24/25	0.96	0.09	21,24,28,28	0
1	LLP	В	394	24/25	0.97	0.08	21,24,26,28	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

