Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 11:38 PM GMT

PDB ID	:	1Y4I
Title	:	Crystal structure of Citrobacter Freundii L-methionine-lyase
Authors	:	Revtovich, S.V.; Mamaeva, D.V.; Morozova, E.A.; Nikulin, A.D.; Nikonov, S.V.; Garber, M.B.; Demidkina, T.V.
Deposited on	:	2004-12-01
Resolution	:	1.90 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
http://wwpdb.org/validation/2016/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:

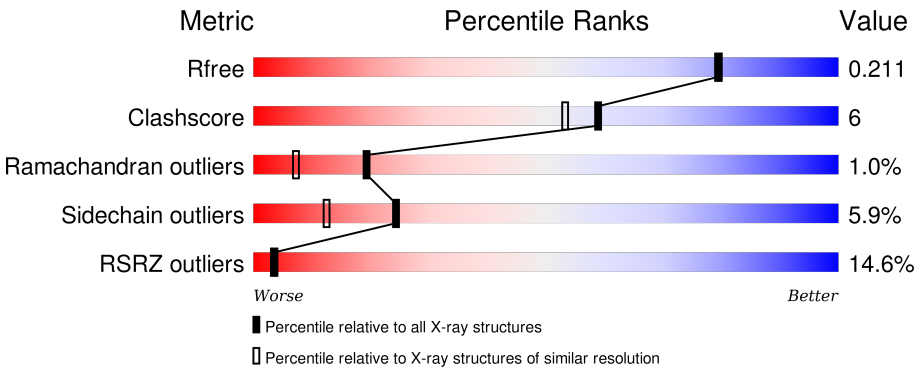
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

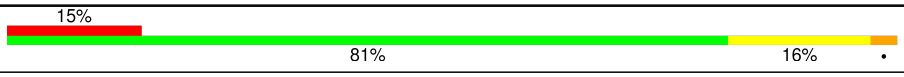
The reported resolution of this entry is 1.90 Å.

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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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. 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	398	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3133 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.

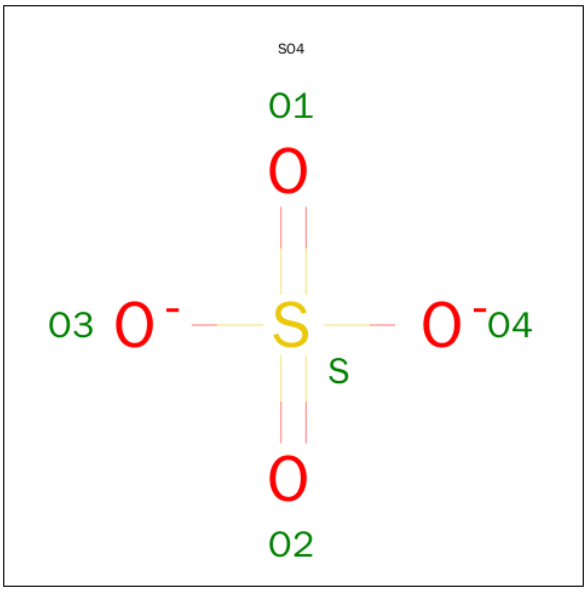
- Molecule 1 is a protein called methionine gamma-lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	397	3024	1905	522	581	1	15	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	133	PHE	LEU	SEE REMARK 999	UNP Q84AR1
A	210	LLP	LYS	MODIFIED RESIDUE	UNP Q84AR1

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is water.

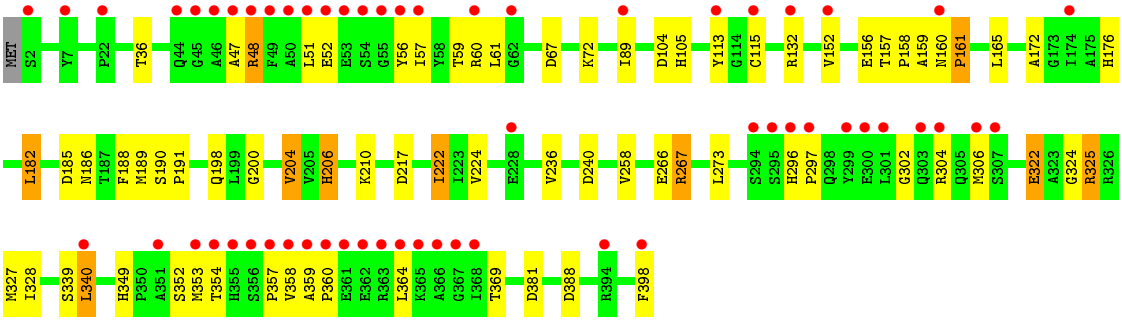
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	104	104	104	0	0

3 Residue-property plots (i)

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: methionine gamma-lyase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	56.35Å 121.83Å 127.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.66 – 1.90 18.66 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.9 (18.66-1.90) 98.7 (18.66-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.41 (at 1.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.206 , 0.209 0.208 , 0.211	Depositor DCC
R_{free} test set	1722 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	23.3	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 63.4	EDS
Estimated twinning fraction	0.018 for -h,-l,-k	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 34432 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3133	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: LLP, 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	0.99	2/3058 (0.1%)	0.79	6/4150 (0.1%)

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	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	266	GLU	C-N	8.51	1.53	1.34
1	A	267	ARG	C-N	-6.22	1.19	1.34

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	357	PRO	CA-N-CD	-7.04	101.64	111.50
1	A	104	ASP	CB-CG-OD2	6.33	124.00	118.30
1	A	217	ASP	CB-CG-OD2	6.33	123.99	118.30
1	A	388	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	67	ASP	CB-CG-OD2	5.58	123.32	118.30
1	A	381	ASP	CB-CG-OD2	5.15	122.94	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	ALA	Peptide
1	A	206	HIS	Peptide
1	A	267	ARG	Mainchain

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	3024	0	3006	35	0
2	A	5	0	0	0	0
3	A	104	0	0	0	0
All	All	3133	0	3006	35	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 6.

All (35) 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:364:LEU:HD23	1:A:369:THR:HA	1.60	0.82
1:A:48:ARG:HD2	1:A:57:ILE:HB	1.71	0.72
1:A:302:GLY:HA2	1:A:306:MET:HE2	1.75	0.69
1:A:59:THR:HG23	1:A:61:LEU:H	1.57	0.67
1:A:191:PRO:HD3	1:A:206:HIS:CE1	2.28	0.67
1:A:339:SER:O	1:A:340:LEU:HD13	1.94	0.67
1:A:322:GLU:OE2	1:A:325:ARG:HD3	1.94	0.67
1:A:105:HIS:NE2	1:A:132:ARG:HG3	2.10	0.67
1:A:302:GLY:HA2	1:A:306:MET:CE	2.25	0.67
1:A:324:GLY:HA3	1:A:349:HIS:CE1	2.35	0.61
1:A:113:TYR:CE2	1:A:115:CYS:HB2	2.35	0.61
1:A:160:ASN:HB3	1:A:161:PRO:HD3	1.82	0.61
1:A:206:HIS:HB2	1:A:222:ILE:HG22	1.84	0.58
1:A:360:PRO:O	1:A:364:LEU:HD12	2.03	0.58
1:A:157:THR:HA	1:A:158:PRO:C	2.24	0.57
1:A:204:VAL:HG13	1:A:224:VAL:HB	1.87	0.57
1:A:186:ASN:HB3	1:A:206:HIS:CE1	2.41	0.55
1:A:302:GLY:O	1:A:306:MET:HG2	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:VAL:O	1:A:240:ASP:HB2	2.07	0.53
1:A:172:ALA:HB2	1:A:182:LEU:HD12	1.92	0.52
1:A:48:ARG:HB3	1:A:57:ILE:HG21	1.93	0.51
1:A:72:LYS:HD2	1:A:258:VAL:HG11	1.93	0.50
1:A:156:GLU:HG2	1:A:185:ASP:HB3	1.95	0.49
1:A:176:HIS:HE1	1:A:200:GLY:O	1.95	0.49
1:A:364:LEU:CD2	1:A:369:THR:HA	2.38	0.48
1:A:188:PHE:CE2	1:A:210:LLP:H2'1	2.50	0.47
1:A:165:LEU:HD13	1:A:306:MET:HE3	1.97	0.47
1:A:51:LEU:O	1:A:52:GLU:HB2	2.16	0.45
1:A:158:PRO:HD2	1:A:189:MET:HG2	2.00	0.43
1:A:59:THR:HG23	1:A:61:LEU:N	2.31	0.43
1:A:89:ILE:HD11	1:A:115:CYS:CB	2.49	0.42
1:A:328:ILE:HG13	1:A:349:HIS:HB2	2.02	0.41
1:A:349:HIS:ND1	1:A:352:SER:HB2	2.35	0.41
1:A:349:HIS:CG	1:A:352:SER:HB2	2.56	0.41
1:A:296:HIS:HA	1:A:297:PRO:HD3	1.90	0.41

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	394/398 (99%)	372 (94%)	18 (5%)	4 (1%)	19 7

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	VAL
1	A	161	PRO
1	A	47	ALA
1	A	359	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	A	323/324 (100%)	304 (94%)	19 (6%)	24 12

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	THR
1	A	48	ARG
1	A	56	TYR
1	A	60	ARG
1	A	152	VAL
1	A	182	LEU
1	A	190	SER
1	A	198	GLN
1	A	204	VAL
1	A	222	ILE
1	A	273	LEU
1	A	304	ARG
1	A	322	GLU
1	A	325	ARG
1	A	327	MET
1	A	340	LEU
1	A	353	MET
1	A	354	THR
1	A	398	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	101	GLN
1	A	227	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	LLP	A	210	1	23,24,25	2.30	8 (34%)	28,32,34	1.54	6 (21%)

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	A	210	1	-	0/15/17/19	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210	LLP	O3-C3	-4.87	1.25	1.37
1	A	210	LLP	P-OP2	-2.93	1.44	1.54
1	A	210	LLP	CG-CB	2.21	1.62	1.52
1	A	210	LLP	CB-CA	2.32	1.56	1.53
1	A	210	LLP	C3-C2	2.46	1.42	1.40
1	A	210	LLP	CD-CE	3.79	1.63	1.51
1	A	210	LLP	C4'-NZ	3.89	1.39	1.27
1	A	210	LLP	C4-C4'	5.43	1.56	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	210	LLP	OP4-P-OP1	-2.92	99.72	107.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	210	LLP	C4-C4'-NZ	-2.57	110.75	125.06
1	A	210	LLP	O-C-CA	-2.56	118.81	125.49
1	A	210	LLP	CE-NZ-C4'	-2.34	112.20	118.97
1	A	210	LLP	OP2-P-OP1	2.07	117.25	110.58
1	A	210	LLP	OP4-C5'-C5	4.46	116.37	108.99

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
1	A	210	LLP	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	A	399	-	4,4,4	0.22	0	6,6,6	0.32	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	SO4	A	399	-	-	0/0/0/0	0/0/0/0

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.

No monomer is involved in short contacts.

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	396/398 (99%)	0.85	58 (14%) 3 3	13, 27, 76, 98	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	358	VAL	15.4
1	A	359	ALA	13.1
1	A	357	PRO	13.0
1	A	56	TYR	11.5
1	A	55	GLY	11.3
1	A	364	LEU	11.3
1	A	398	PHE	9.1
1	A	54	SER	8.7
1	A	360	PRO	7.4
1	A	299	TYR	7.1
1	A	363	ARG	6.6
1	A	355	HIS	6.6
1	A	361	GLU	6.6
1	A	356	SER	6.1
1	A	50	ALA	5.4
1	A	295	SER	5.2
1	A	2	SER	5.0
1	A	51	LEU	4.6
1	A	354	THR	4.5
1	A	365	LYS	4.4
1	A	53	GLU	4.3
1	A	48	ARG	4.2
1	A	160	ASN	4.2
1	A	362	GLU	4.1
1	A	367	GLY	4.0
1	A	294	SER	4.0
1	A	297	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	46	ALA	3.6
1	A	353	MET	3.4
1	A	57	ILE	3.3
1	A	368	ILE	3.3
1	A	307	SER	3.3
1	A	366	ALA	3.2
1	A	47	ALA	3.1
1	A	113	TYR	3.1
1	A	300	GLU	3.0
1	A	132	ARG	3.0
1	A	228	GLU	3.0
1	A	304	ARG	2.7
1	A	22	PRO	2.7
1	A	49	PHE	2.6
1	A	44	GLN	2.6
1	A	394	ARG	2.6
1	A	351	ALA	2.5
1	A	340	LEU	2.5
1	A	60	ARG	2.5
1	A	7	TYR	2.4
1	A	296	HIS	2.4
1	A	89	ILE	2.3
1	A	152	VAL	2.3
1	A	303	GLN	2.3
1	A	115	CYS	2.2
1	A	174	ILE	2.1
1	A	52	GLU	2.1
1	A	306	MET	2.1
1	A	301	LEU	2.0
1	A	45	GLY	2.0
1	A	62	GLY	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. 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	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	LLP	A	210	24/25	0.93	0.15	-	23,34,38,41	0

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	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	SO4	A	399	5/5	0.95	0.18	-	49,49,50,51	0

6.5 Other polymers (i)

There are no such residues in this entry.