Full wwPDB X-ray Structure Validation Report (i)

Sep 29, 2024 – 06:28 PM EDT

PDB ID	:	3FRL
Title	:	The 2.25 A crystal structure of LipL32, the major surface antigen of Leptospira interrogans serovar Copenhageni
Authors	:	Farah, C.S.; Guzzo, C.R.; Hauk, P.; Ho, P.L.
Deposited on	:	2009-01-08
Resolution	:	2.25 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 (i)) were used in the production of this report:

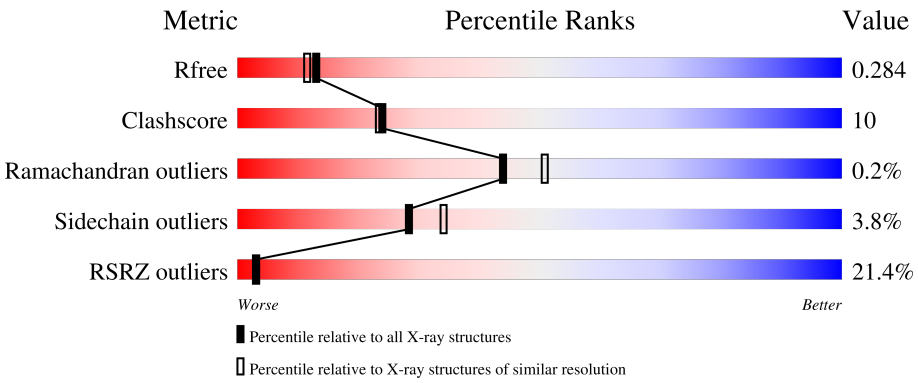
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.25 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}	164625	1763 (2.26-2.26)
Clashscore	180529	1919 (2.26-2.26)
Ramachandran outliers	177936	1884 (2.26-2.26)
Sidechain outliers	177891	1885 (2.26-2.26)
RSRZ outliers	164620	1763 (2.26-2.26)

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%

Mol	Chain	Length	Quality of chain
1	A	252	12% 78% 13% 8%
1	B	252	27% 73% 19% 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	211	A	1	-	-	X	-
3	OXL	A	273	-	X	-	-
3	OXL	B	2	-	X	-	-

2 Entry composition (i)

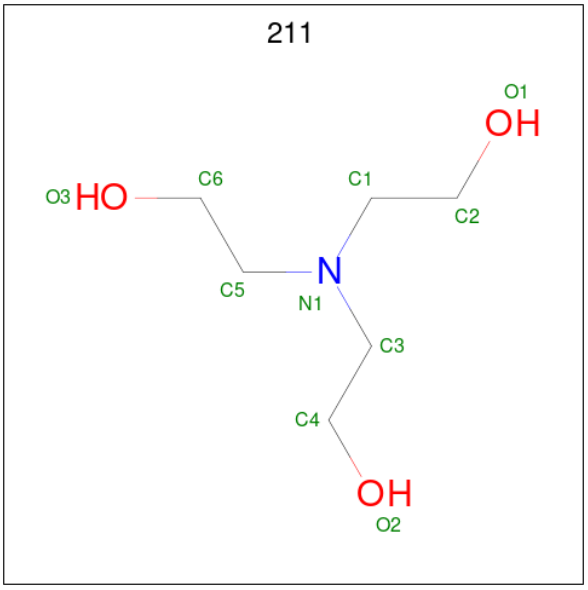
There are 5 unique types of molecules in this entry. The entry contains 3919 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 LipL32.

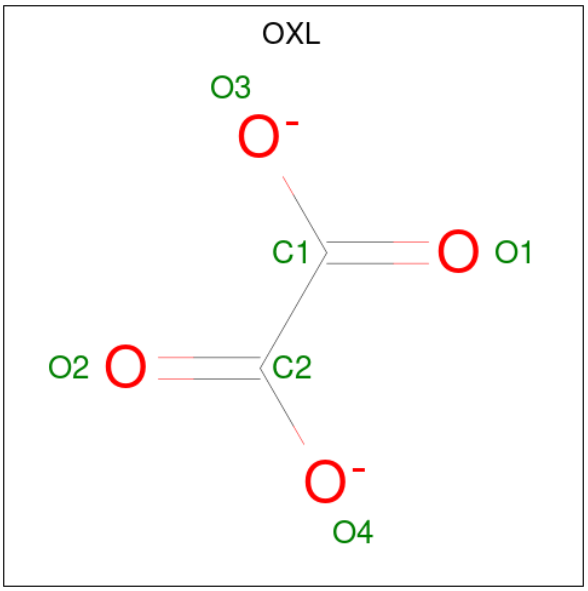
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	231	1817	1169	299	343	6	0	3	0
1	B	232	1807	1160	296	346	5	0	1	0

- Molecule 2 is 2,2',2''-NITRILOTRIETHANOL (three-letter code: 211) (formula: $C_6H_{15}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	10	6	1	3	0	0

- Molecule 3 is OXALATE ION (three-letter code: OXL) (formula: C_2O_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 2 4	0	0
3	B	1	Total C O 6 2 4	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0

- Molecule 5 is water.

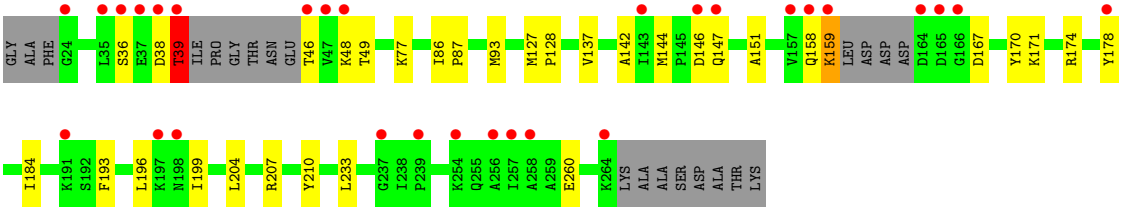
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	191	Total O 191 191	0	0
5	B	81	Total O 81 81	0	0

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. 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. 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.

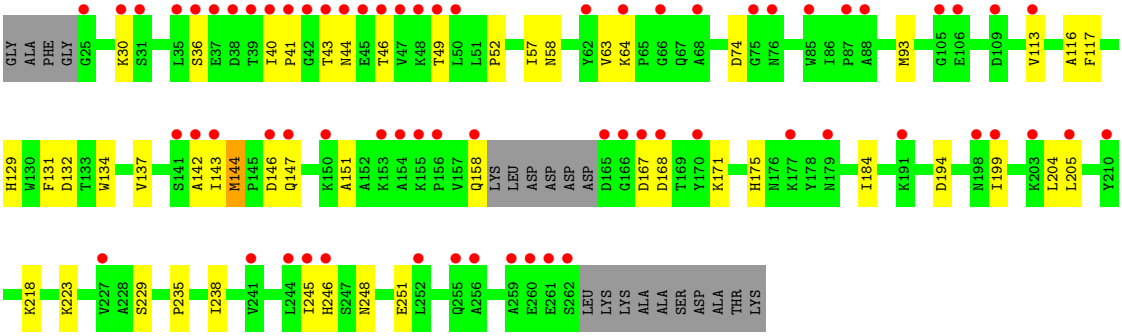
- Molecule 1: LipL32

Chain A:



- Molecule 1: LipL32

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	126.72Å 126.72Å 96.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 2.25 35.00 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.4 (35.00-2.25) 99.3 (35.00-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.02 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.181 , 0.227 0.246 , 0.284	Depositor DCC
R_{free} test set	2129 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	44.9	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 59.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3919	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, OXL, 211

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	0.82	0/1859	0.77	1/2510 (0.0%)
1	B	0.70	0/1848	0.71	0/2502
All	All	0.77	0/3707	0.74	1/5012 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	39	THR	CA-C-O	5.14	130.90	120.10

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	1817	0	1832	35	0
1	B	1807	0	1804	38	0
2	A	10	0	15	8	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
4	A	1	0	0	0	0
5	A	191	0	0	8	0
5	B	81	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3919	0	3651	72	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 10.

All (72) 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:207:ARG:HD3	5:A:437:HOH:O	1.49	1.11
1:A:49:THR:OG1	1:B:49:THR:HG21	1.71	0.89
1:A:38:ASP:HB2	1:A:39:THR:HG22	1.58	0.83
1:B:113:VAL:HG13	1:B:117:PHE:CD2	2.13	0.83
1:A:77:LYS:HZ1	2:A:1:211:H22	1.48	0.79
1:A:87:PRO:HD3	5:A:383:HOH:O	1.85	0.77
2:A:1:211:H41	5:A:421:HOH:O	1.84	0.77
1:A:49:THR:OG1	1:B:49:THR:CG2	2.33	0.76
1:B:168:ASP:HB3	1:B:205:LEU:HD22	1.71	0.73
1:B:113:VAL:CG1	1:B:117:PHE:HD2	2.04	0.69
1:B:113:VAL:CG1	1:B:117:PHE:CD2	2.76	0.68
1:A:77:LYS:HE3	2:A:1:211:H21	1.77	0.67
1:B:93:MSE:HE1	1:B:137:VAL:HG11	1.77	0.66
1:A:87:PRO:O	1:A:207:ARG:CD	2.44	0.66
1:A:87:PRO:HD2	5:A:438:HOH:O	1.95	0.66
1:A:93:MSE:CE	1:A:137:VAL:HG11	2.27	0.65
1:B:248:ASN:ND2	1:B:251:GLU:H	1.95	0.64
1:B:64:LYS:HE2	1:B:116:ALA:HB1	1.81	0.63
1:A:87:PRO:O	1:A:207:ARG:NE	2.33	0.62
1:B:143:ILE:HD11	1:B:144:MSE:HE2	1.83	0.59
1:A:77:LYS:HZ1	2:A:1:211:C2	2.14	0.58
1:A:193:PHE:CD1	1:A:196:LEU:HD12	2.39	0.58
1:B:184:ILE:HG22	1:B:205:LEU:HD13	1.87	0.56
1:B:129:HIS:CE1	1:B:223:LYS:HE3	2.41	0.56
1:A:144[B]:MSE:CG	1:A:147:GLN:HG3	2.36	0.56
1:A:144[B]:MSE:HG3	1:A:147:GLN:HG3	1.90	0.54
1:B:63:VAL:HB	1:B:223:LYS:HA	1.90	0.54
1:A:77:LYS:NZ	2:A:1:211:H31	2.24	0.53
1:B:132:ASP:OD2	1:B:175:HIS:HD2	1.92	0.53
1:A:158[B]:GLN:NE2	1:A:158[B]:GLN:HA	2.25	0.52
1:B:248:ASN:HD22	1:B:251:GLU:H	1.55	0.52
1:A:87:PRO:CD	5:A:383:HOH:O	2.51	0.52
1:B:58:ASN:ND2	1:B:229:SER:OG	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:MSE:HE1	1:A:137:VAL:HG11	1.90	0.51
1:A:38:ASP:HB2	1:A:39:THR:CG2	2.37	0.51
1:B:93:MSE:CE	1:B:137:VAL:HG11	2.40	0.51
1:B:184:ILE:HG22	1:B:205:LEU:CD1	2.41	0.50
1:B:167:ASP:HB3	1:B:184:ILE:HG23	1.94	0.50
1:B:142:ALA:HB2	1:B:151:ALA:HB2	1.94	0.50
1:A:77:LYS:HZ1	2:A:1:211:H31	1.75	0.49
1:B:144:MSE:HE3	1:B:147:GLN:NE2	2.27	0.49
1:A:199:ILE:HG21	1:A:204:LEU:HD21	1.94	0.49
1:A:167:ASP:O	1:A:184:ILE:HD12	2.12	0.48
1:A:171:LYS:HB3	1:A:184:ILE:HD11	1.96	0.48
1:A:77:LYS:HZ1	2:A:1:211:C3	2.28	0.46
1:A:142:ALA:HB2	1:A:151:ALA:CB	2.45	0.46
1:A:86:ILE:HD12	1:A:210:TYR:CD2	2.50	0.46
1:B:142:ALA:HB2	1:B:151:ALA:CB	2.46	0.46
1:A:159:LYS:HD3	1:A:170:TYR:CG	2.50	0.46
5:A:284:HOH:O	1:B:40:ILE:HD12	2.15	0.45
1:A:167:ASP:HB3	1:A:184:ILE:HG23	1.98	0.45
1:A:87:PRO:O	1:A:207:ARG:CG	2.65	0.45
1:B:40:ILE:N	5:B:342:HOH:O	2.49	0.45
1:A:77:LYS:NZ	2:A:1:211:H22	2.25	0.44
1:B:171:LYS:HG2	1:B:184:ILE:HD13	1.99	0.44
5:A:284:HOH:O	1:B:43:THR:HB	2.17	0.44
1:B:171:LYS:HB3	1:B:184:ILE:CD1	2.48	0.44
1:A:127:MSE:HE3	1:A:128:PRO:O	2.17	0.44
1:B:235:PRO:HD2	1:B:238:ILE:HD12	2.00	0.44
1:B:246:HIS:CE1	1:B:251:GLU:HG2	2.53	0.43
1:B:74:ASP:HB2	1:B:134:TRP:CH2	2.54	0.43
1:A:193:PHE:HD1	1:A:196:LEU:HD12	1.83	0.43
1:B:30:LYS:HA	1:B:52:PRO:HA	2.00	0.43
1:B:57:ILE:CG2	1:B:245:ILE:HD12	2.49	0.43
1:B:168:ASP:CB	1:B:205:LEU:HD22	2.46	0.42
1:A:174:ARG:NH2	5:A:379:HOH:O	2.51	0.42
1:B:248:ASN:HD22	1:B:251:GLU:CB	2.32	0.42
1:B:44:ASN:O	1:B:46:THR:HG23	2.19	0.42
1:B:199:ILE:HG21	1:B:204:LEU:HD21	2.02	0.42
1:B:248:ASN:HD22	1:B:251:GLU:HB3	1.85	0.41
1:A:144[B]:MSE:HE2	1:A:146:ASP:OD2	2.21	0.41
1:B:113:VAL:HG11	1:B:117:PHE:HD2	1.84	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	Percentiles	
1	A	228/252 (90%)	225 (99%)	3 (1%)	0	100	100
1	B	229/252 (91%)	217 (95%)	11 (5%)	1 (0%)	30	32
All	All	457/504 (91%)	442 (97%)	14 (3%)	1 (0%)	44	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	41	PRO

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	199/206 (97%)	191 (96%)	8 (4%)	27	32
1	B	198/206 (96%)	190 (96%)	8 (4%)	27	32
All	All	397/412 (96%)	381 (96%)	16 (4%)	28	32

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	SER
1	A	39	THR
1	A	46	THR
1	A	48	LYS
1	A	159	LYS

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Mol	Chain	Res	Type
1	A	178	TYR
1	A	233	LEU
1	A	260	GLU
1	B	36	SER
1	B	131	PHE
1	B	144	MSE
1	B	146[A]	ASP
1	B	146[B]	ASP
1	B	158	GLN
1	B	194	ASP
1	B	218	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	ASN
1	B	58	ASN
1	B	175	HIS
1	B	248	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)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\#\|Z\| > 2$
2	211	A	1	-	9,9,9	0.49	0	9,9,9	1.02	0
3	OXL	A	273	-	5,5,5	1.91	2 (40%)	6,6,6	3.73	5 (83%)
3	OXL	B	2	-	5,5,5	2.04	2 (40%)	6,6,6	2.47	4 (66%)

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	211	A	1	-	-	4/9/9/9	-
3	OXL	A	273	-	-	4/4/4/4	-
3	OXL	B	2	-	-	4/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2	OXL	C2-C1	-3.05	1.49	1.54
3	A	273	OXL	O2-C2	2.91	1.29	1.22
3	A	273	OXL	O1-C1	2.41	1.28	1.22
3	B	2	OXL	O2-C2	2.03	1.27	1.22

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	273	OXL	O3-C1-O1	-4.76	112.56	123.90
3	A	273	OXL	O2-C2-C1	4.60	130.22	120.63
3	B	2	OXL	O3-C1-C2	4.40	121.37	112.83
3	A	273	OXL	O4-C2-O2	-3.79	114.87	123.90
3	A	273	OXL	O1-C1-C2	3.72	128.38	120.63
3	A	273	OXL	O3-C1-C2	3.19	119.03	112.83
3	B	2	OXL	O4-C2-C1	2.54	117.75	112.83
3	B	2	OXL	O3-C1-O1	-2.23	118.60	123.90
3	B	2	OXL	O4-C2-O2	-2.05	119.02	123.90

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	211	N1-C5-C6-O3
3	A	273	OXL	O1-C1-C2-O2
3	A	273	OXL	O1-C1-C2-O4
3	A	273	OXL	O3-C1-C2-O2
3	A	273	OXL	O3-C1-C2-O4
2	A	1	211	N1-C3-C4-O2
2	A	1	211	N1-C1-C2-O1
3	B	2	OXL	O1-C1-C2-O2
3	B	2	OXL	O3-C1-C2-O4
2	A	1	211	C2-C1-N1-C3
3	B	2	OXL	O3-C1-C2-O2
3	B	2	OXL	O1-C1-C2-O4

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	211	8	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)

Warning: The R factor obtained from EDS is 0.2517,which does not match the depositor's R factor of 0.18134. Please interpret the results in this section carefully.

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	226/252 (89%)	0.68	29 (12%)	9	8	22, 39, 58, 63	23 (10%)
1	B	227/252 (90%)	1.64	68 (29%)	1	1	25, 53, 64, 71	26 (11%)
All	All	453/504 (89%)	1.16	97 (21%)	3	3	22, 49, 63, 71	49 (10%)

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	48	LYS	6.1
1	B	41	PRO	6.0
1	A	46	THR	5.9
1	A	164	ASP	5.9
1	B	153	LYS	5.1
1	B	155	LYS	4.9
1	A	165	ASP	4.8
1	B	44	ASN	4.8
1	A	24	GLY	4.7
1	B	42	GLY	4.5
1	A	37	GLU	4.4
1	B	150	LYS	4.4
1	B	47	VAL	4.4
1	B	37	GLU	4.4
1	A	47	VAL	4.3
1	B	191	LYS	4.2
1	B	35	LEU	3.9
1	B	40	ILE	3.8
1	B	75	GLY	3.7
1	A	39	THR	3.6
1	B	38	ASP	3.6
1	A	38	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	191	LYS	3.5
1	B	39	THR	3.5
1	B	45	GLU	3.4
1	B	165	ASP	3.4
1	B	260	GLU	3.4
1	A	146	ASP	3.3
1	B	241	VAL	3.2
1	B	141	SER	3.2
1	B	256	ALA	3.0
1	A	258	ALA	3.0
1	B	252	LEU	2.9
1	B	203	LYS	2.9
1	B	46	THR	2.9
1	B	25	GLY	2.9
1	B	154	ALA	2.9
1	B	177	LYS	2.8
1	B	245	ILE	2.8
1	A	257	ILE	2.8
1	B	64	LYS	2.8
1	A	48	LYS	2.8
1	B	49	THR	2.8
1	B	36	SER	2.7
1	A	264	LYS	2.7
1	A	35	LEU	2.6
1	B	76	ASN	2.6
1	B	262	SER	2.6
1	B	43	THR	2.6
1	B	113	VAL	2.6
1	B	166	GLY	2.6
1	B	168	ASP	2.6
1	B	143	ILE	2.5
1	B	85	TRP	2.5
1	B	146[A]	ASP	2.5
1	B	244	LEU	2.5
1	B	106	GLU	2.5
1	A	147	GLN	2.5
1	B	62	TYR	2.4
1	B	109	ASP	2.4
1	A	166	GLY	2.4
1	B	105	GLY	2.4
1	A	36	SER	2.4
1	B	261	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	158	GLN	2.4
1	A	198	ASN	2.4
1	B	30	LYS	2.4
1	B	66	GLY	2.4
1	A	159	LYS	2.4
1	B	167	ASP	2.4
1	B	205	LEU	2.3
1	A	197	LYS	2.3
1	B	50	LEU	2.3
1	B	88	ALA	2.3
1	A	143	ILE	2.3
1	A	158[A]	GLN	2.3
1	B	259	ALA	2.2
1	A	239	PRO	2.2
1	B	227	VAL	2.2
1	B	87	PRO	2.2
1	B	31	SER	2.2
1	B	199	ILE	2.2
1	A	178	TYR	2.2
1	B	179	ASN	2.1
1	B	156	PRO	2.1
1	B	142	ALA	2.1
1	A	157	VAL	2.1
1	B	246	HIS	2.1
1	B	198	ASN	2.1
1	A	256	ALA	2.1
1	B	147	GLN	2.1
1	B	170	TYR	2.1
1	B	255	GLN	2.1
1	A	254	LYS	2.0
1	B	68	ALA	2.0
1	B	210	TYR	2.0
1	A	237	GLY	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 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(Å^2)	Q<0.9
2	211	A	1	10/10	0.83	0.26	77,86,87,87	2
3	OXL	B	2	6/6	0.89	0.25	82,86,88,89	0
3	OXL	A	273	6/6	0.92	0.16	51,63,67,68	0
4	CL	A	274	1/1	0.99	0.17	52,52,52,52	0

6.5 Other polymers (i)

There are no such residues in this entry.