Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 05:35 AM JST

PDB ID	:	7EUX
Title	:	Crystal structure of the Lon-like protease MtaLonC with D581A mutation in complex with substrate polypeptide
Authors	:	Hsieh, K.Y.; Kuo, C.I.; Su, S.C.; Huang, K.F.; Chang, C.I.
Deposited on	:	2021-05-19
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 ⓘ 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:

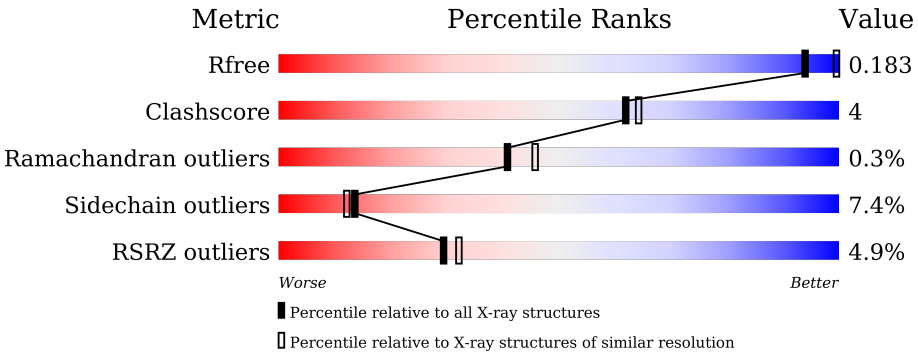
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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}	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (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% 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	732	4% 69% 10% • 20%
2	S	5	80% 20%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4804 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 Endopeptidase La.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	587	Total	C	N	O	S	0	0	0
			4508	2864	798	839	7			

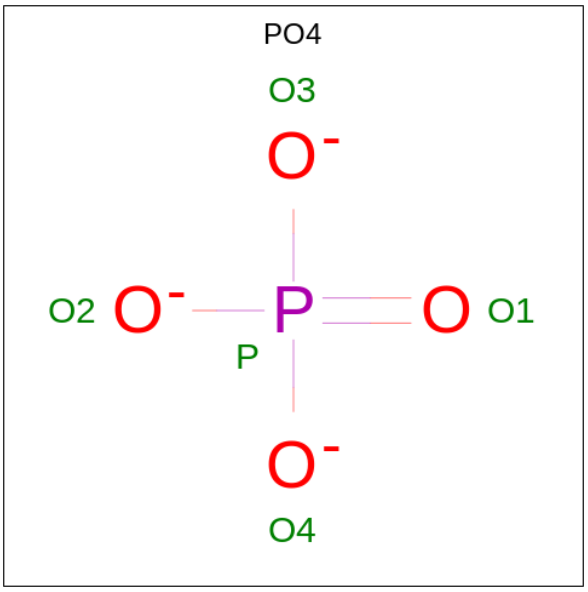
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	581	ALA	ASP	engineered mutation	UNP C9DRU9
A	720	LYS	-	expression tag	UNP C9DRU9
A	721	LEU	-	expression tag	UNP C9DRU9
A	722	ALA	-	expression tag	UNP C9DRU9
A	723	ALA	-	expression tag	UNP C9DRU9
A	724	ALA	-	expression tag	UNP C9DRU9
A	725	LEU	-	expression tag	UNP C9DRU9
A	726	GLU	-	expression tag	UNP C9DRU9
A	727	HIS	-	expression tag	UNP C9DRU9
A	728	HIS	-	expression tag	UNP C9DRU9
A	729	HIS	-	expression tag	UNP C9DRU9
A	730	HIS	-	expression tag	UNP C9DRU9
A	731	HIS	-	expression tag	UNP C9DRU9
A	732	HIS	-	expression tag	UNP C9DRU9

- Molecule 2 is a protein called ALA-PRO-GLU-ALA-VAL.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	S	5	Total	C	N	O	0	0	0
			34	21	5	8			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0

- Molecule 4 is water.

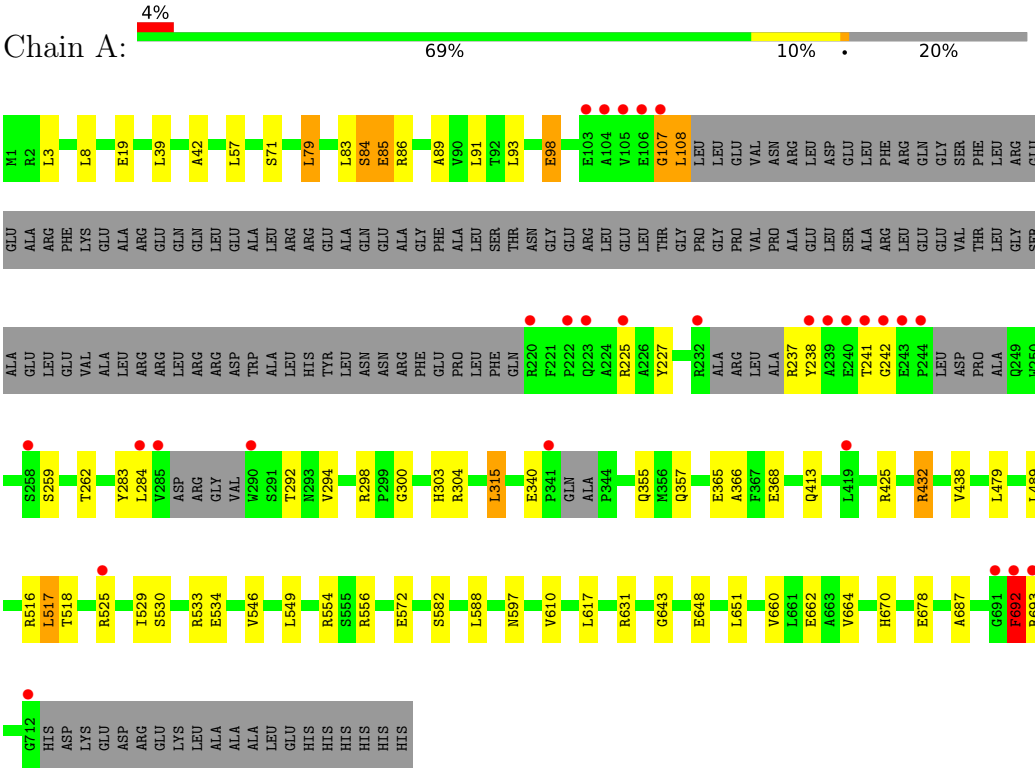
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	252	Total O 252 252	0	0
4	S	5	Total O 5 5	0	0

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.

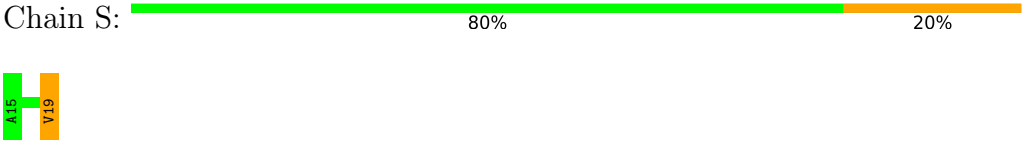
• Molecule 1: Endopeptidase La

Chain A:



• Molecule 2: ALA-PRO-GLU-ALA-VAL

Chain S:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, α, β, γ	115.74Å 115.74Å 136.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.83 – 2.25 19.83 – 2.25	Depositor EDS
% Data completeness (in resolution range)	88.5 (19.83-2.25) 89.9 (19.83-2.25)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.15 (at 2.26Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.153 , 0.193 0.153 , 0.183	Depositor DCC
R_{free} test set	2293 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å^2)	28.1	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 41.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.059 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.512 for H, K, L 0.488 for K, H, -L	Depositor
Outliers	0 of 44003 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4804	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.53	0/4598	0.75	6/6244 (0.1%)
2	S	0.72	0/34	0.84	0/45
All	All	0.54	0/4632	0.75	6/6289 (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	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	425	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	A	432	ARG	NE-CZ-NH2	-6.31	117.14	120.30
1	A	631	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	516	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	432	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	A	554	ARG	NE-CZ-NH1	5.13	122.87	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	692	PHE	Peptide

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	4508	0	4529	40	0
2	S	34	0	31	5	0
3	A	5	0	0	0	0
4	A	252	0	0	2	0
4	S	5	0	0	0	0
All	All	4804	0	4560	40	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.

All (40) 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:582:SER:OG	2:S:19:VAL:C	2.11	0.89
1:A:300:GLY:H	1:A:303:HIS:HD2	1.31	0.78
1:A:693:ARG:HA	1:A:697:GLU:OE1	1.84	0.78
1:A:98:GLU:HG2	1:A:254:LEU:HD13	1.65	0.76
1:A:83:LEU:HD11	1:A:89:ALA:HB2	1.75	0.68
1:A:107:GLY:O	1:A:108:LEU:HD12	1.95	0.65
1:A:283:TYR:HA	1:A:292:THR:HG22	1.80	0.63
1:A:582:SER:OG	2:S:19:VAL:HB	2.00	0.61
1:A:503:VAL:HG12	2:S:19:VAL:HG13	1.84	0.59
1:A:582:SER:OG	2:S:19:VAL:CA	2.50	0.58
1:A:42:ALA:O	1:A:357:GLN:NE2	2.39	0.56
1:A:648:GLU:O	1:A:651:LEU:HG	2.06	0.55
1:A:692:PHE:HA	1:A:694:GLY:H	1.71	0.55
1:A:237:ARG:N	4:A:904:HOH:O	2.40	0.53
1:A:498:GLU:HG2	1:A:518:THR:HG22	1.91	0.53
1:A:84:SER:OG	1:A:85:GLU:N	2.42	0.53
1:A:529:ILE:HG23	1:A:534:GLU:OE1	2.09	0.53
1:A:692:PHE:HA	1:A:694:GLY:N	2.25	0.52
1:A:227:TYR:OH	1:A:252:PRO:HD3	2.10	0.52
1:A:238:TYR:O	1:A:242:GLY:N	2.43	0.52
1:A:582:SER:OG	2:S:19:VAL:CB	2.59	0.51
1:A:8:LEU:HD12	1:A:664:VAL:HG11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:GLY:H	1:A:303:HIS:CD2	2.21	0.49
1:A:304:ARG:NH2	4:A:905:HOH:O	2.44	0.49
1:A:315:LEU:HD13	1:A:366:ALA:CB	2.42	0.48
1:A:549:LEU:HD22	1:A:588:LEU:HB2	1.95	0.47
1:A:315:LEU:HD13	1:A:366:ALA:HB1	1.97	0.47
1:A:283:TYR:OH	1:A:340:GLU:N	2.48	0.47
1:A:3:LEU:HD11	1:A:651:LEU:CD2	2.45	0.46
1:A:517:LEU:HD23	1:A:518:THR:N	2.30	0.46
1:A:643:GLY:HA3	1:A:670:HIS:O	2.16	0.46
1:A:19:GLU:HB3	1:A:413:GLN:HG3	1.99	0.45
1:A:660:VAL:O	1:A:664:VAL:HG23	2.17	0.44
1:A:79:LEU:HD12	1:A:91:LEU:O	2.18	0.43
1:A:549:LEU:CD2	1:A:610:VAL:HG21	2.49	0.43
1:A:79:LEU:HD12	1:A:79:LEU:N	2.33	0.42
1:A:572:GLU:OE1	1:A:572:GLU:HA	2.18	0.42
1:A:556:ARG:NH2	1:A:678:GLU:OE2	2.49	0.41
1:A:687:ALA:HB3	1:A:695:LEU:HD21	2.02	0.41
1:A:530:SER:HB2	1:A:546:VAL:HG21	2.02	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	575/732 (79%)	556 (97%)	17 (3%)	2 (0%)	41 46
2	S	3/5 (60%)	3 (100%)	0	0	100 100
All	All	578/737 (78%)	559 (97%)	17 (3%)	2 (0%)	41 46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	692	PHE
1	A	107	GLY

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	459/577 (80%)	426 (93%)	33 (7%)	14 12
2	S	3/3 (100%)	2 (67%)	1 (33%)	0 0
All	All	462/580 (80%)	428 (93%)	34 (7%)	13 12

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	57	LEU
1	A	71	SER
1	A	79	LEU
1	A	84	SER
1	A	85	GLU
1	A	86	ARG
1	A	93	LEU
1	A	98	GLU
1	A	108	LEU
1	A	225	ARG
1	A	241	THR
1	A	251	ARG
1	A	259	SER
1	A	262	THR
1	A	284	LEU
1	A	294	VAL
1	A	298	ARG
1	A	315	LEU
1	A	355	GLN
1	A	365	GLU
1	A	368	GLU

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Mol	Chain	Res	Type
1	A	432	ARG
1	A	438	VAL
1	A	479	LEU
1	A	489	LEU
1	A	517	LEU
1	A	525	ARG
1	A	533	ARG
1	A	597	ASN
1	A	617	LEU
1	A	662	GLU
1	A	692	PHE
2	S	19	VAL

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

Mol	Chain	Res	Type
1	A	303	HIS
1	A	543	HIS
1	A	597	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 monosaccharides 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	$\#\|Z\| > 2$
3	PO4	A	801	-	4,4,4	1.08	0	6,6,6	0.91	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

6.1 Protein, DNA and RNA chains

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	A	587/732 (80%)	-0.27	29 (4%) 29 32	16, 28, 80, 109	0
2	S	5/5 (100%)	-0.70	0 100 100	25, 29, 30, 31	0
All	All	592/737 (80%)	-0.27	29 (4%) 29 32	16, 28, 80, 109	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	ALA	7.9
1	A	244	PRO	6.8
1	A	285	VAL	5.2
1	A	692	PHE	4.6
1	A	241	THR	4.4
1	A	238	TYR	4.2
1	A	341	PRO	4.1
1	A	284	LEU	3.6
1	A	223	GLN	3.5
1	A	712	GLY	3.4
1	A	220	ARG	3.2
1	A	258	SER	3.1
1	A	290	TRP	3.1
1	A	225	ARG	3.0
1	A	105	VAL	3.0
1	A	240	GLU	2.9
1	A	107	GLY	2.9
1	A	243	GLU	2.8
1	A	106	GLU	2.7
1	A	222	PRO	2.7
1	A	242	GLY	2.6
1	A	691	GLY	2.5
1	A	693	ARG	2.3
1	A	251	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	232	ARG	2.1
1	A	103	GLU	2.1
1	A	525	ARG	2.1
1	A	104	ALA	2.1
1	A	419	LEU	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, 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
3	PO4	A	801	5/5	0.99	0.06	26,28,29,33	0

6.5 Other polymers (i)

There are no such residues in this entry.