



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:35 AM UTC

PDB ID : 7EV4 / pdb\_00007ev4  
Title : Crystal structure of the Lon-like protease MtaLonC with S582A mutation in complex with F-b20-Q  
Authors : Hsieh, K.Y.; Kuo, C.I.; Su, S.C.; Huang, K.F.; Chang, C.I.  
Deposited on : 2021-05-20  
Resolution : 2.12 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](mailto: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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

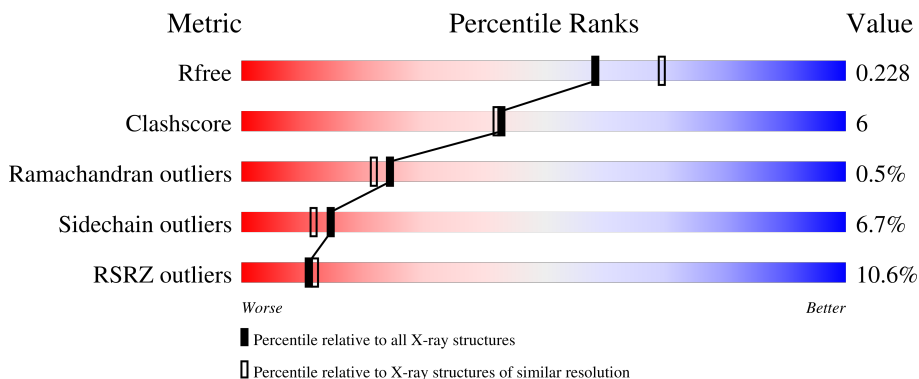
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.12 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))
$R_{free}$	180053	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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  $\geq 3$ , 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	732	 9% 67% 12% 19%
2	S	4	 100%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4963 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
			Total	C	N	O	S			
1	A	592	4553	2894	805	846	8	0	1	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	582	ALA	SER	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 F-b20-Q peptide {ortho-aminobenzoic acid (Abz)- QLRSLNG EWRFAWFPAPEAV[Tyr(3-NO<sub>2</sub>)]A}.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	S	4	33	20	5	8	0	0	0

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	370	Total	O	0	0
			370	370		
4	S	2	Total	O	0	0
			2	2		



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.60Å 115.60Å 135.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.93 – 2.12 29.93 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.93-2.12) 99.7 (29.93-2.12)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.55 (at 2.12Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.180 , 0.220 (Not available) , 0.228	Depositor DCC
$R_{free}$ test set	2934 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.0	Xtrriage
Anisotropy	0.068	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 41.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.052 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4963	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NIY, 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	1.15	7/4648 (0.2%)	1.37	9/6314 (0.1%)
2	S	0.99	0/16	1.28	0/18
All	All	1.15	7/4664 (0.2%)	1.37	9/6332 (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	4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	573	GLN	N-CA	7.01	1.55	1.46
1	A	579	GLU	CD-OE1	-6.61	1.12	1.25
1	A	585	LEU	C-O	6.27	1.31	1.24
1	A	399	ALA	C-O	5.85	1.30	1.24
1	A	657	ARG	C-O	5.32	1.30	1.23
1	A	500	ASN	C-O	5.30	1.30	1.24
1	A	543	HIS	C-O	5.26	1.30	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	572	GLU	CA-C-N	-14.47	93.90	121.54
1	A	572	GLU	C-N-CA	-14.47	93.90	121.54
1	A	572	GLU	O-C-N	-11.19	109.39	122.15
1	A	579	GLU	CB-CG-CD	6.25	123.23	112.60

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	THR	CB-CA-C	5.73	117.74	110.98
1	A	665	ARG	CG-CD-NE	-5.11	100.75	112.00
1	A	576	VAL	N-CA-CB	-5.07	102.98	112.36
1	A	438	VAL	CA-C-O	-5.04	115.51	120.85
1	A	432	ARG	NE-CZ-NH2	-5.04	114.67	119.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	106	GLU	Peptide
1	A	290	TRP	Peptide
1	A	691	GLY	Peptide
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	4553	0	4572	57	0
2	S	33	0	26	3	0
3	A	5	0	0	0	0
4	A	370	0	0	3	2
4	S	2	0	0	0	0
All	All	4963	0	4598	57	2

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 (57) 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:549:LEU:CD2	1:A:610:VAL:HG21	2.06	0.85
1:A:300:GLY:H	1:A:303:HIS:HD2	1.31	0.79
1:A:692:PHE:HA	1:A:694:GLY:H	1.52	0.73

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:LEU:HD21	1:A:610:VAL:HG21	1.72	0.70
1:A:582:ALA:HB3	2:S:20:ALA:C	2.19	0.67
1:A:48:HIS:HD2	1:A:358:VAL:H	1.42	0.66
1:A:692:PHE:HA	1:A:694:GLY:N	2.14	0.63
1:A:549:LEU:CD2	1:A:610:VAL:CG2	2.78	0.60
1:A:576:VAL:HG13	2:S:17:ALA:HA	1.84	0.60
1:A:48:HIS:CD2	1:A:358:VAL:H	2.19	0.59
1:A:693:ARG:HA	1:A:697:GLU:OE1	2.03	0.59
1:A:549:LEU:HD22	1:A:588:LEU:HB2	1.84	0.58
1:A:249:GLN:HA	1:A:293:ASN:HB2	1.84	0.58
1:A:549:LEU:HD23	1:A:610:VAL:HG21	1.82	0.58
1:A:300:GLY:H	1:A:303:HIS:CD2	2.17	0.57
1:A:549:LEU:HD21	1:A:610:VAL:CG2	2.34	0.57
1:A:88:VAL:HG12	1:A:294:VAL:HG13	1.87	0.56
1:A:106:GLU:HA	1:A:106:GLU:OE1	2.05	0.56
1:A:94:PRO:HD3	1:A:223:GLN:HE22	1.71	0.55
1:A:237:ARG:HA	1:A:240:GLU:HB3	1.89	0.55
1:A:98:GLU:HG2	1:A:254:LEU:HD12	1.90	0.53
1:A:426[B]:MET:HE2	1:A:426[B]:MET:HA	1.91	0.53
1:A:228:LEU:O	1:A:231:LEU:HB3	2.08	0.53
1:A:632:VAL:HG23	4:A:1079:HOH:O	2.09	0.52
1:A:240:GLU:O	1:A:240:GLU:HG3	2.10	0.52
1:A:389:THR:OG1	1:A:432:ARG:HD3	2.10	0.51
1:A:274:ALA:HB3	1:A:275:PRO:HD3	1.92	0.51
1:A:549:LEU:HD23	1:A:610:VAL:CG2	2.41	0.51
1:A:304:ARG:NH2	4:A:912:HOH:O	2.44	0.50
1:A:418:ARG:NE	1:A:461:GLU:OE2	2.42	0.49
1:A:578:ILE:HG23	2:S:18:VAL:HG23	1.93	0.49
1:A:554:ARG:HG2	4:A:1075:HOH:O	2.11	0.48
1:A:105:VAL:HG21	1:A:252:PRO:HD3	1.96	0.48
1:A:98:GLU:CG	1:A:254:LEU:HD12	2.45	0.47
1:A:692:PHE:CD2	1:A:692:PHE:O	2.68	0.46
1:A:517:LEU:HD11	1:A:587:GLU:HG3	1.98	0.46
1:A:94:PRO:CD	1:A:223:GLN:HE22	2.30	0.45
1:A:238:TYR:CD2	1:A:238:TYR:C	2.95	0.44
1:A:648:GLU:HG3	1:A:651:LEU:HD11	1.99	0.44
1:A:498:GLU:HG2	1:A:518:THR:HG22	2.00	0.43
1:A:692:PHE:O	1:A:692:PHE:CG	2.70	0.43
1:A:72:VAL:O	1:A:261:GLY:HA3	2.19	0.42
1:A:82:PRO:HD3	1:A:294:VAL:HG11	1.99	0.42
1:A:688:ARG:HA	1:A:688:ARG:HD2	1.88	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:VAL:CG1	1:A:294:VAL:HG13	2.49	0.42
1:A:537:LEU:O	1:A:577:SER:HA	2.19	0.42
1:A:530:SER:HB2	1:A:546:VAL:HG21	2.02	0.42
1:A:403:TRP:O	1:A:407:GLN:HG2	2.20	0.42
1:A:597:ASN:HD22	1:A:597:ASN:HA	1.71	0.41
1:A:710:GLU:HA	1:A:710:GLU:OE1	2.22	0.40
1:A:12:THR:HB	1:A:417:THR:CG2	2.52	0.40
1:A:79:LEU:HD21	1:A:93:LEU:HD22	2.02	0.40
1:A:57:LEU:HD12	1:A:57:LEU:HA	1.99	0.40
1:A:283:TYR:CD1	1:A:292:THR:CG2	3.04	0.40
1:A:711:GLU:O	1:A:711:GLU:CG	2.70	0.40
1:A:283:TYR:HA	1:A:292:THR:HG22	2.03	0.40
1:A:283:TYR:CE1	1:A:343:ALA:CB	3.05	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1111:HOH:O	4:A:1233:HOH:O[4_565]	1.97	0.23
4:A:1092:HOH:O	4:A:1196:HOH:O[6_555]	2.15	0.05

## 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	583/732 (80%)	559 (96%)	21 (4%)	3 (0%)	24	22
2	S	1/4 (25%)	1 (100%)	0	0	100	100
All	All	584/736 (79%)	560 (96%)	21 (4%)	3 (0%)	24	22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	692	PHE
1	A	107	GLY
1	A	294	VAL

### 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	463/577 (80%)	432 (93%)	31 (7%)	15	12
2	S	1/1 (100%)	1 (100%)	0	100	100
All	All	464/578 (80%)	433 (93%)	31 (7%)	15	12

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	52	VAL
1	A	57	LEU
1	A	73	GLU
1	A	79	LEU
1	A	85	GLU
1	A	86	ARG
1	A	93	LEU
1	A	98	GLU
1	A	220	ARG
1	A	240	GLU
1	A	251	ARG
1	A	259	SER
1	A	262	THR
1	A	294	VAL
1	A	296	LEU
1	A	315	LEU
1	A	355	GLN
1	A	365	GLU
1	A	368	GLU
1	A	377	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	432	ARG
1	A	494	ARG
1	A	505	VAL
1	A	525	ARG
1	A	576	VAL
1	A	578	ILE
1	A	579	GLU
1	A	617	LEU
1	A	662	GLU
1	A	692	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	HIS
1	A	70	GLN
1	A	223	GLN
1	A	249	GLN
1	A	303	HIS
1	A	429	GLN
1	A	462	GLN
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](#)

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
2	NIY	S	19	2	14,15,16	1.83	4 (28%)	11,20,22	1.15	1 (9%)

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	NIY	S	19	2	-	0/7/10/12	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	19	NIY	CE1-NN	-3.91	1.38	1.45
2	S	19	NIY	CE2-CD2	3.40	1.44	1.38
2	S	19	NIY	CB-CG	-2.84	1.44	1.51
2	S	19	NIY	O-C	2.53	1.29	1.20

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	19	NIY	CD2-CE2-CZ	-2.63	117.87	120.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	0.92	0	6,6,6	0.92	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	592/732 (80%)	0.38	63 (10%) 11 12	17, 33, 93, 135	1 (0%)
2	S	3/4 (75%)	1.10	0 100 100	30, 30, 33, 41	0
All	All	595/736 (80%)	0.39	63 (10%) 11 12	17, 33, 93, 135	1 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	284	LEU	7.7
1	A	285	VAL	7.2
1	A	712	GLY	6.8
1	A	108	LEU	6.7
1	A	692	PHE	6.6
1	A	105	VAL	6.5
1	A	244	PRO	5.3
1	A	228	LEU	5.3
1	A	218	PHE	5.1
1	A	290	TRP	4.7
1	A	236	ALA	4.6
1	A	250	TRP	4.4
1	A	342	GLN	4.2
1	A	99	ILE	4.2
1	A	294	VAL	4.1
1	A	283	TYR	4.1
1	A	341	PRO	4.1
1	A	249	GLN	3.9
1	A	344	PRO	3.9
1	A	101	LEU	3.9
1	A	104	ALA	3.8
1	A	369	GLY	3.8
1	A	231	LEU	3.8
1	A	232	ARG	3.7

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	230	ALA	3.7
1	A	221	PHE	3.6
1	A	254	LEU	3.5
1	A	224	ALA	3.4
1	A	343	ALA	3.4
1	A	80	TYR	3.2
1	A	98	GLU	3.1
1	A	222	PRO	3.0
1	A	226	ALA	3.0
1	A	239	ALA	2.9
1	A	281	LEU	2.9
1	A	96	GLY	2.9
1	A	227	TYR	2.9
1	A	93	LEU	2.9
1	A	81	VAL	2.9
1	A	258	SER	2.9
1	A	102	ALA	2.8
1	A	576	VAL	2.8
1	A	79	LEU	2.6
1	A	291	SER	2.6
1	A	292	THR	2.6
1	A	219	GLN	2.6
1	A	298	ARG	2.6
1	A	560	HIS	2.5
1	A	106	GLU	2.5
1	A	90	VAL	2.4
1	A	525	ARG	2.3
1	A	100	HIS	2.3
1	A	82	PRO	2.3
1	A	426[A]	MET	2.2
1	A	262	THR	2.2
1	A	340	GLU	2.2
1	A	256	THR	2.1
1	A	237	ARG	2.1
1	A	83	LEU	2.1
1	A	259	SER	2.1
1	A	97	GLN	2.1
1	A	84	SER	2.0
1	A	107	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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NIY	S	19	15/16	0.94	0.09	24,29,49,53	0

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	PO4	A	801	5/5	0.98	0.05	28,30,35,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.