



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2016 – 08:23 AM EDT

PDB ID : 5J7T
Title : Molecular Understanding of USP7 Substrate Recognition and C-Terminal Activation
Authors : Murray, J.M.; Rouge, L.
Deposited on : 2016-04-06
Resolution : 3.20 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
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)	:	rb-20027939

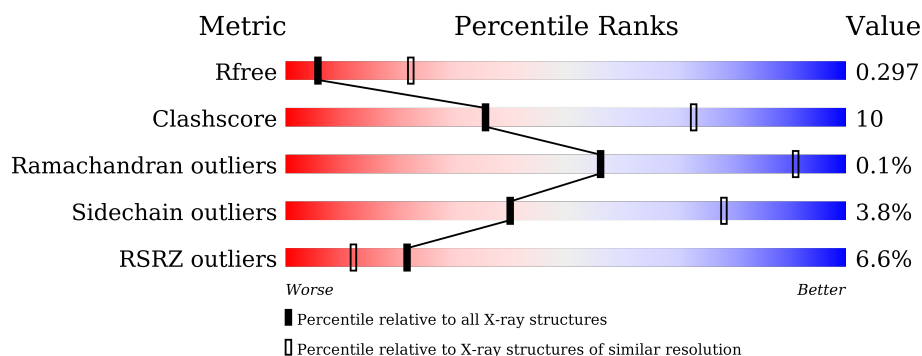
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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 $\leq 5\%$. 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	671	<div> <div>7%</div> <div>78%</div> <div>20%</div> <div>.</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5446 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.

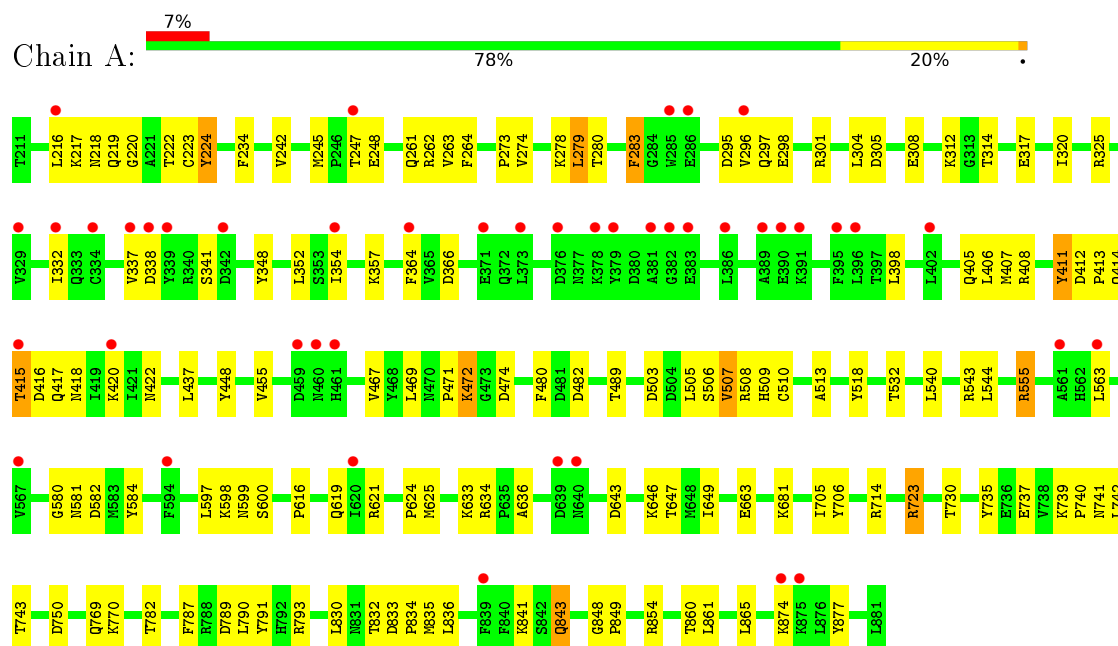
- Molecule 1 is a protein called Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	671	5446	3444	923	1046	33	0	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 ($\text{RSRZ} > 2$). 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: Ubiquitin carboxyl-terminal hydrolase 7



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	104.33Å 196.73Å 226.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.38 – 3.20 74.25 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.38-3.20) 95.4 (74.25-3.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 3.19Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.250 , 0.294 0.254 , 0.297	Depositor DCC
R_{free} test set	938 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	79.9	Xtriage
Anisotropy	0.740	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 81.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5446	wwPDB-VP
Average B, all atoms (Å ²)	127.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.26	0/5565	0.40	0/7523

There are no bond length outliers.

There are no bond angle outliers.

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	5446	0	5301	104	1
All	All	5446	0	5301	104	1

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 (104) 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:352:LEU:O	1:A:407:MET:HG2	1.40	1.16
1:A:507:VAL:HG13	1:A:508:ARG:H	1.32	0.91
1:A:219:GLN:HG3	1:A:482:ASP:OD2	1.73	0.88
1:A:352:LEU:O	1:A:407:MET:CG	2.27	0.81
1:A:220:GLY:H	1:A:222:THR:HG23	1.46	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ASN:HD22	1:A:219:GLN:N	1.81	0.77
1:A:597:LEU:HB2	1:A:600:SER:HB2	1.67	0.76
1:A:507:VAL:HG13	1:A:508:ARG:N	2.02	0.75
1:A:843:GLN:NE2	1:A:848:GLY:O	2.20	0.73
1:A:218:ASN:HD22	1:A:219:GLN:H	1.37	0.69
1:A:634:ARG:NH2	1:A:737:GLU:O	2.25	0.69
1:A:218:ASN:ND2	1:A:219:GLN:N	2.41	0.68
1:A:219:GLN:HG3	1:A:482:ASP:CG	2.15	0.66
1:A:234:PHE:CD1	1:A:471:PRO:HB3	2.32	0.65
1:A:224:TYR:HD1	1:A:224:TYR:H	1.44	0.64
1:A:414:GLN:HB3	1:A:415:THR:HB	1.79	0.63
1:A:262:ARG:NH1	1:A:278:LYS:HB3	2.13	0.63
1:A:354:ILE:HD11	1:A:406:LEU:HB3	1.80	0.63
1:A:472:LYS:NZ	1:A:472:LYS:HB3	2.14	0.62
1:A:216:LEU:HD23	1:A:274:VAL:HB	1.84	0.60
1:A:420:LYS:NZ	1:A:422:ASN:OD1	2.34	0.59
1:A:223:CYS:HB3	1:A:224:TYR:HD1	1.66	0.58
1:A:248:GLU:HA	1:A:543:ARG:HH11	1.69	0.58
1:A:599:ASN:HA	1:A:647:THR:HB	1.87	0.57
1:A:262:ARG:HH11	1:A:278:LYS:HB3	1.71	0.55
1:A:621:ARG:NH1	1:A:621:ARG:HB3	2.22	0.55
1:A:735:TYR:HB3	1:A:743:THR:HG22	1.89	0.55
1:A:467:VAL:HG13	1:A:480:PHE:HB2	1.88	0.54
1:A:741:ASN:HB2	1:A:791:TYR:CG	2.42	0.54
1:A:247:THR:O	1:A:543:ARG:NH1	2.40	0.54
1:A:865:LEU:HD13	1:A:874:LYS:HG2	1.90	0.54
1:A:663:GLU:OE1	1:A:706:TYR:OH	2.24	0.53
1:A:621:ARG:HB3	1:A:621:ARG:HH11	1.74	0.53
1:A:448:TYR:HB3	1:A:518:TYR:HB3	1.91	0.53
1:A:506:SER:O	1:A:507:VAL:HG12	2.09	0.53
1:A:304:LEU:HD22	1:A:320:ILE:HD12	1.90	0.52
1:A:625:MET:HG3	1:A:633:LYS:HG2	1.92	0.52
1:A:280:THR:HA	1:A:283:PHE:HE1	1.75	0.51
1:A:262:ARG:HG2	1:A:544:LEU:HD22	1.92	0.51
1:A:769:GLN:HE22	1:A:782:THR:HA	1.75	0.51
1:A:312:LYS:HA	1:A:317:GLU:HG3	1.92	0.51
1:A:398:LEU:HG	1:A:437:LEU:HD21	1.93	0.51
1:A:312:LYS:HD3	1:A:317:GLU:HG3	1.93	0.51
1:A:220:GLY:N	1:A:222:THR:HG23	2.23	0.50
1:A:860:THR:OG1	1:A:861:LEU:N	2.44	0.50
1:A:224:TYR:N	1:A:224:TYR:CD1	2.72	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:GLU:HG3	1:A:312:LYS:NZ	2.26	0.50
1:A:843:GLN:HE21	1:A:843:GLN:N	2.09	0.50
1:A:581:ASN:O	1:A:582:ASP:HB2	2.12	0.50
1:A:598:LYS:HE2	1:A:649:ILE:HG12	1.93	0.50
1:A:407:MET:HA	1:A:407:MET:HE3	1.94	0.49
1:A:507:VAL:CG1	1:A:508:ARG:N	2.73	0.49
1:A:705:ILE:HG23	1:A:723:ARG:HH21	1.78	0.49
1:A:332:ILE:HB	1:A:341:SER:HB3	1.94	0.49
1:A:297:GLN:HB3	1:A:405:GLN:HG2	1.95	0.48
1:A:412:ASP:N	1:A:417:GLN:O	2.27	0.48
1:A:415:THR:OG1	1:A:416:ASP:HB3	2.14	0.48
1:A:563:LEU:HA	1:A:598:LYS:HD2	1.96	0.48
1:A:263:VAL:HG21	1:A:279:LEU:HD12	1.94	0.48
1:A:219:GLN:HG3	1:A:482:ASP:OD1	2.13	0.48
1:A:740:PRO:O	1:A:741:ASN:HB3	2.14	0.48
1:A:843:GLN:H	1:A:843:GLN:HE21	1.61	0.48
1:A:411:TYR:HA	1:A:418:ASN:HA	1.95	0.46
1:A:474:ASP:N	1:A:474:ASP:OD1	2.48	0.46
1:A:405:GLN:C	1:A:406:LEU:HD23	2.37	0.45
1:A:743:THR:HG1	1:A:787:PHE:HD2	1.63	0.45
1:A:325:ARG:HB2	1:A:348:TYR:HE1	1.81	0.45
1:A:416:ASP:HB2	1:A:417:GLN:HB2	1.98	0.45
1:A:643:ASP:HB3	1:A:646:LYS:HD3	1.99	0.45
1:A:681:LYS:HE3	1:A:681:LYS:HB2	1.79	0.45
1:A:301:ARG:O	1:A:305:ASP:HB2	2.16	0.45
1:A:832:THR:OG1	1:A:833:ASP:N	2.49	0.45
1:A:833:ASP:HB3	1:A:836:LEU:HD13	1.99	0.44
1:A:469:LEU:C	1:A:471:PRO:HD3	2.38	0.44
1:A:730:THR:HG23	1:A:770:LYS:NZ	2.32	0.44
1:A:223:CYS:HB3	1:A:224:TYR:CD1	2.48	0.44
1:A:408:ARG:HD2	1:A:513:ALA:O	2.18	0.43
1:A:413:PRO:HA	1:A:414:GLN:HA	1.73	0.43
1:A:580:GLY:HA2	1:A:790:LEU:HD11	2.00	0.43
1:A:503:ASP:HB2	1:A:506:SER:HB3	2.01	0.43
1:A:242:VAL:HG21	1:A:264:PHE:HE2	1.84	0.42
1:A:295:ASP:OD1	1:A:298:GLU:HG3	2.19	0.42
1:A:508:ARG:CB	1:A:509:HIS:HD2	2.33	0.42
1:A:217:LYS:HD3	1:A:273:PRO:HB2	2.01	0.42
1:A:833:ASP:HA	1:A:834:PRO:HD2	1.93	0.42
1:A:245:MET:HB2	1:A:261:GLN:NE2	2.35	0.41
1:A:357:LYS:HZ1	1:A:366:ASP:CG	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:555:ARG:HA	1:A:555:ARG:HD2	1.64	0.41
1:A:624:PRO:O	1:A:636:ALA:N	2.43	0.41
1:A:325:ARG:HB2	1:A:348:TYR:CE1	2.56	0.41
1:A:472:LYS:HZ2	1:A:472:LYS:HB3	1.85	0.41
1:A:616:PRO:HB2	1:A:619:GLN:HG2	2.02	0.41
1:A:308:GLU:HG3	1:A:312:LYS:HZ1	1.85	0.41
1:A:507:VAL:O	1:A:510:CYS:N	2.53	0.41
1:A:337:VAL:HG12	1:A:338:ASP:H	1.86	0.41
1:A:234:PHE:CE1	1:A:471:PRO:HB3	2.56	0.41
1:A:506:SER:O	1:A:507:VAL:CG1	2.69	0.41
1:A:739:LYS:HG2	1:A:742:LEU:HD23	2.03	0.41
1:A:219:GLN:NE2	1:A:482:ASP:OD1	2.53	0.40
1:A:789:ASP:OD2	1:A:793:ARG:NH1	2.54	0.40
1:A:312:LYS:HD3	1:A:312:LYS:HA	1.92	0.40
1:A:218:ASN:C	1:A:218:ASN:ND2	2.73	0.40
1:A:308:GLU:O	1:A:312:LYS:HG2	2.21	0.40
1:A:849:PRO:HG3	1:A:877:TYR:CG	2.57	0.40

All (1) 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)
1:A:503:ASP:OD1	1:A:841:LYS:NZ[2_455]	1.93	0.27

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	669/671 (100%)	619 (92%)	49 (7%)	1 (0%)	56 91

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	507	VAL

5.3.2 Protein sidechains ⓘ

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	606/610 (99%)	583 (96%)	23 (4%)	40 78

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	TYR
1	A	279	LEU
1	A	283	PHE
1	A	296	VAL
1	A	314	THR
1	A	364	PHE
1	A	411	TYR
1	A	415	THR
1	A	455	VAL
1	A	472	LYS
1	A	489	THR
1	A	505	LEU
1	A	532	THR
1	A	540	LEU
1	A	555	ARG
1	A	584	TYR
1	A	714	ARG
1	A	723	ARG
1	A	750	ASP
1	A	830	LEU
1	A	835	MET
1	A	843	GLN
1	A	854	ARG

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	218	ASN
1	A	509	HIS
1	A	843	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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 ⓘ

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, 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	671/671 (100%)	0.61	44 (6%)	22 12	64, 120, 210, 292	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	337	VAL	7.4
1	A	332	ILE	6.1
1	A	373	LEU	5.7
1	A	461	HIS	4.9
1	A	383	GLU	4.3
1	A	334	CYS	4.2
1	A	382	GLY	3.9
1	A	459	ASP	3.6
1	A	460	ASN	3.4
1	A	395	PHE	3.4
1	A	285	TRP	3.2
1	A	561	ALA	3.2
1	A	567	VAL	3.2
1	A	376	ASP	3.1
1	A	639	ASP	3.0
1	A	396	LEU	3.0
1	A	364	PHE	2.9
1	A	379	TYR	2.8
1	A	386	LEU	2.7
1	A	874	LYS	2.7
1	A	415	THR	2.6
1	A	381	ALA	2.6
1	A	389	ALA	2.6
1	A	594	PHE	2.6
1	A	563	LEU	2.5
1	A	338	ASP	2.5
1	A	247	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	216	LEU	2.5
1	A	390	GLU	2.4
1	A	391	LYS	2.4
1	A	620	ILE	2.4
1	A	402	LEU	2.3
1	A	371	GLU	2.3
1	A	339	TYR	2.3
1	A	839	PHE	2.3
1	A	296	VAL	2.3
1	A	286	GLU	2.2
1	A	420	LYS	2.2
1	A	875	LYS	2.2
1	A	342	ASP	2.1
1	A	640	ASN	2.1
1	A	378	LYS	2.1
1	A	354	ILE	2.1
1	A	329	VAL	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 carbohydrates 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.