



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:59 PM BST

PDB ID : 1UMT
Title : Stromelysin-1 catalytic domain with hydrophobic inhibitor bound, pH 7.0, 32°C, 20 mM CaCl₂, 15% acetonitrile; NMR average of 20 structures minimized with restraints
Authors : Van Doren, S.R.; Kurochkin, A.V.; Hu, W.; Zuiderweg, E.R.P.
Deposited on : 1995-10-31

This is a Full wwPDB NMR 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/NMRValidationReportHelp>
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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

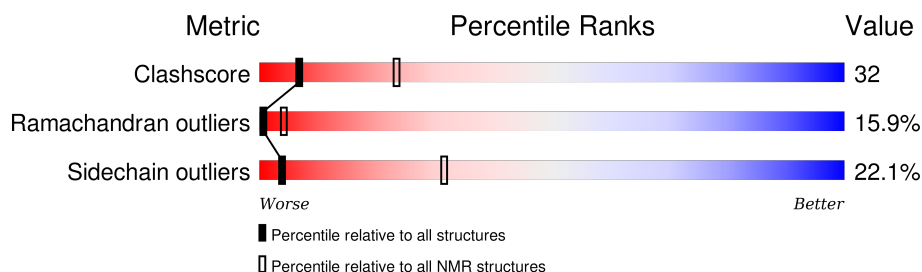
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	174	

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2643 atoms, of which 1284 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called STROMELYSIN-1.

Mol	Chain	Residues	Atoms						Trace
1	A	166	Total	C	H	N	O	S	0
			2572	851	1248	221	250	2	

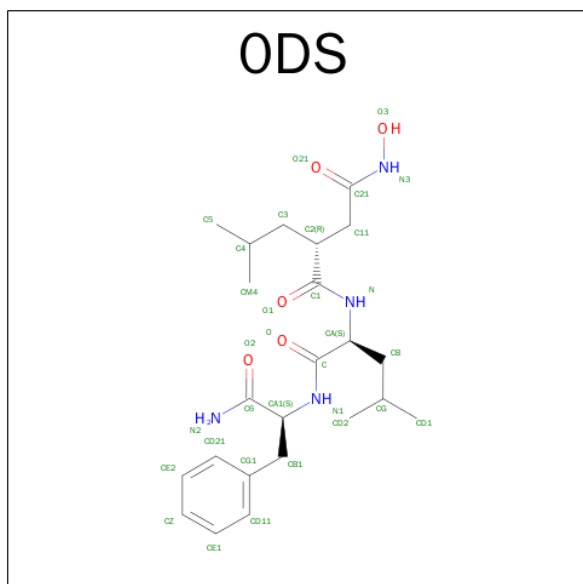
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Zn
			2	2

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
3	A	1	Total	Ca
			1	1

- Molecule 4 is N-{(2R)-2-[2-(HYDROXYAMINO)-2-OXOETHYL]-4-METHYLPENTANOYL}-L-LEUCYL-L-PHENYLALANINAMIDE (three-letter code: ODS) (formula: C₂₃H₃₆N₄O₅).

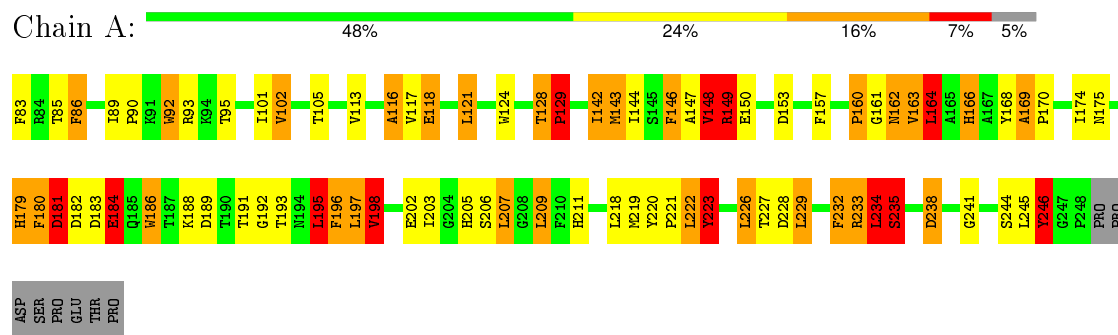


Mol	Chain	Residues	Atoms				
			Total	C	H	N	O
4	A	1	68	23	36	4	5

4 Residue-property plots [i](#)

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: STROMELYSIN-1



5 Refinement protocol and experimental data overview

The models were refined using the following method: ?.

Of the 1 calculated structures, 1 were deposited, based on the following criterion: *all calculated structures submitted*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DGII	geometry optimization	
Discover	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ODS, CA

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 (average) 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	0.76	0/1366 (0.0%)	1.74	30/1864 (1.6%)
All	All	0.76	0/1366 (0.0%)	1.74	30/1864 (1.6%)

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	Planarity
1	A	0	7
All	All	0	7

There are no bond-length outliers.

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	PRO	N-CA-CB	11.14	116.67	103.30
1	A	192	GLY	N-CA-C	-9.41	89.57	113.10
1	A	148	VAL	CG1-CB-CG2	8.72	124.86	110.90
1	A	181	ASP	CA-CB-CG	7.68	130.31	113.40
1	A	246	TYR	CB-CG-CD2	-7.25	116.65	121.00
1	A	223	TYR	CB-CG-CD1	-7.24	116.66	121.00
1	A	143	MET	CA-CB-CG	7.16	125.47	113.30
1	A	116	ALA	CB-CA-C	7.09	120.73	110.10
1	A	197	LEU	CB-CG-CD1	-7.05	99.01	111.00
1	A	166	HIS	CB-CA-C	6.86	124.12	110.40
1	A	164	LEU	CB-CG-CD2	6.77	122.51	111.00
1	A	174	ILE	N-CA-C	-6.44	93.62	111.00
1	A	203	ILE	CA-CB-CG1	6.03	122.46	111.00
1	A	246	TYR	CA-CB-CG	6.00	124.79	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	197	LEU	CB-CG-CD2	5.97	121.14	111.00
1	A	186	TRP	CB-CA-C	5.75	121.90	110.40
1	A	143	MET	CG-SD-CE	-5.65	91.15	100.20
1	A	143	MET	CB-CA-C	5.64	121.68	110.40
1	A	102	VAL	CG1-CB-CG2	-5.59	101.95	110.90
1	A	166	HIS	N-CA-C	-5.47	96.24	111.00
1	A	198	VAL	CA-CB-CG1	-5.36	102.86	110.90
1	A	163	VAL	N-CA-CB	5.29	123.13	111.50
1	A	149	ARG	C-N-CA	5.23	134.77	121.70
1	A	164	LEU	N-CA-CB	-5.18	100.04	110.40
1	A	163	VAL	CB-CA-C	5.16	121.19	111.40
1	A	195	LEU	CB-CA-C	5.11	119.92	110.20
1	A	235	SER	N-CA-CB	-5.11	102.83	110.50
1	A	148	VAL	CA-CB-CG2	-5.09	103.26	110.90
1	A	195	LEU	CB-CG-CD1	-5.08	102.37	111.00
1	A	129	PRO	CA-N-CD	-5.02	104.47	111.50

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	146	PHE	Sidechain
1	A	168	TYR	Sidechain
1	A	246	TYR	Sidechain
1	A	128	THR	Peptide
1	A	223	TYR	Sidechain
1	A	180	PHE	Sidechain
1	A	196	PHE	Sidechain

6.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1324	1248	1252	76
4	A	32	36	35	17
All	All	1359	1284	1287	84

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 32.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
4:A:261:0DS:HD1	4:A:261:0DS:CD11	1.09	0.97
4:A:261:0DS:CD21	4:A:261:0DS:HD2	1.08	0.97
4:A:261:0DS:CG1	4:A:261:0DS:CE1	0.95	2.43
4:A:261:0DS:CE2	4:A:261:0DS:CG1	0.94	2.43
4:A:261:0DS:CE2	4:A:261:0DS:HD2	0.80	2.06
4:A:261:0DS:CG1	4:A:261:0DS:HD1	0.79	2.07
4:A:261:0DS:CE1	4:A:261:0DS:HD1	0.79	2.07
1:A:116:ALA:HB1	1:A:196:PHE:N	0.79	1.93
4:A:261:0DS:CG1	4:A:261:0DS:HD2	0.78	2.07
1:A:164:LEU:HD23	1:A:198:VAL:HG21	0.70	1.63
1:A:113:VAL:HG13	1:A:195:LEU:HG	0.68	1.63
1:A:164:LEU:HD22	1:A:164:LEU:N	0.65	2.06
1:A:227:THR:HG23	1:A:232:PHE:CD1	0.65	2.26
1:A:148:VAL:CG1	1:A:181:ASP:HA	0.65	2.21
1:A:222:LEU:HD21	4:A:261:0DS:HB31	0.64	1.69
1:A:163:VAL:CG2	4:A:261:0DS:HA	0.64	2.23
1:A:163:VAL:C	1:A:164:LEU:HD13	0.63	2.13
1:A:164:LEU:HD22	1:A:198:VAL:HG11	0.62	1.70
1:A:164:LEU:CD2	1:A:198:VAL:HG21	0.62	2.23
1:A:222:LEU:HD22	1:A:223:TYR:H	0.62	1.53
1:A:163:VAL:CA	1:A:164:LEU:HD13	0.61	2.26
1:A:164:LEU:N	1:A:164:LEU:CD2	0.60	2.65
1:A:222:LEU:HD13	1:A:223:TYR:N	0.59	2.12
1:A:113:VAL:HG13	1:A:195:LEU:CG	0.59	2.28
1:A:105:THR:CG2	1:A:186:TRP:CD1	0.59	2.85
1:A:116:ALA:HB1	1:A:196:PHE:CA	0.59	2.28
1:A:169:ALA:HB1	1:A:170:PRO:CD	0.56	2.31
1:A:207:LEU:HD22	1:A:245:LEU:HD11	0.56	1.78
1:A:162:ASN:HA	4:A:261:0DS:CB1	0.55	2.32
1:A:160:PRO:HA	1:A:184:GLU:CD	0.55	2.21
1:A:162:ASN:HA	4:A:261:0DS:HB21	0.53	1.81
1:A:148:VAL:CG2	1:A:181:ASP:HA	0.52	2.34
1:A:222:LEU:CD2	1:A:223:TYR:H	0.52	2.17
1:A:164:LEU:CD2	1:A:198:VAL:HG11	0.52	2.34
1:A:142:ILE:CG2	1:A:206:SER:HB2	0.52	2.35
1:A:105:THR:HG21	1:A:186:TRP:CD1	0.51	2.40
1:A:124:TRP:CZ3	1:A:234:LEU:CD2	0.51	2.94
1:A:169:ALA:HB1	1:A:170:PRO:HD3	0.50	1.83
1:A:148:VAL:HG23	1:A:149:ARG:N	0.50	2.21

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:222:LEU:HD22	1:A:223:TYR:N	0.50	2.22
1:A:142:ILE:CG2	1:A:206:SER:CB	0.49	2.90
1:A:153:ASP:HB2	1:A:166:HIS:CE1	0.49	2.43
1:A:113:VAL:HG22	1:A:195:LEU:HG	0.48	1.85
1:A:89:ILE:CG1	1:A:245:LEU:O	0.48	2.62
1:A:163:VAL:HG22	4:A:261:ODS:H1	0.48	1.69
1:A:222:LEU:HD13	1:A:223:TYR:H	0.47	1.69
1:A:153:ASP:HB2	1:A:166:HIS:ND1	0.47	2.24
1:A:124:TRP:CZ3	1:A:234:LEU:HD23	0.46	2.45
1:A:197:LEU:CD1	1:A:223:TYR:HA	0.46	2.40
1:A:180:PHE:O	1:A:182:ASP:N	0.46	2.49
1:A:186:TRP:CE3	1:A:195:LEU:N	0.46	2.83
1:A:209:LEU:CD1	1:A:238:ASP:HB2	0.46	2.41
1:A:147:ALA:O	1:A:148:VAL:HG13	0.46	2.11
1:A:184:GLU:CG	1:A:193:THR:HG21	0.45	2.41
1:A:164:LEU:HD22	1:A:164:LEU:H	0.45	1.71
1:A:148:VAL:CG2	1:A:183:ASP:HB2	0.45	2.41
1:A:180:PHE:CD1	1:A:180:PHE:N	0.45	2.85
1:A:148:VAL:HG23	1:A:183:ASP:HB2	0.45	1.88
1:A:164:LEU:HD12	1:A:184:GLU:OE2	0.45	2.12
1:A:118:GLU:HA	1:A:121:LEU:HD23	0.44	1.88
1:A:86:PHE:CB	1:A:244:SER:CB	0.44	2.96
1:A:189:ASP:C	1:A:191:THR:H	0.44	2.16
1:A:218:LEU:HD11	1:A:232:PHE:CD2	0.43	2.48
1:A:179:HIS:N	1:A:179:HIS:CD2	0.43	2.86
1:A:163:VAL:C	1:A:164:LEU:CD1	0.43	2.85
1:A:169:ALA:CB	1:A:170:PRO:CD	0.43	2.97
1:A:148:VAL:HG21	1:A:181:ASP:OD1	0.43	2.13
1:A:162:ASN:CA	4:A:261:ODS:HB21	0.43	2.44
1:A:222:LEU:CG	1:A:223:TYR:H	0.42	2.28
1:A:220:TYR:CD1	1:A:221:PRO:HD2	0.42	2.49
1:A:163:VAL:HG22	4:A:261:ODS:N1	0.42	2.30
1:A:86:PHE:CB	1:A:244:SER:HB3	0.42	2.44
1:A:105:THR:HG21	1:A:186:TRP:NE1	0.42	2.29
1:A:144:ILE:HG23	1:A:180:PHE:CE1	0.42	2.50
1:A:113:VAL:HG13	1:A:195:LEU:CD1	0.42	2.45
1:A:222:LEU:CD2	4:A:261:ODS:HB31	0.41	2.42
1:A:153:ASP:CB	1:A:166:HIS:ND1	0.41	2.83
1:A:222:LEU:HD21	4:A:261:ODS:CB1	0.41	2.42
1:A:232:PHE:O	1:A:233:ARG:C	0.41	2.58
1:A:222:LEU:CD1	1:A:223:TYR:H	0.41	2.28
1:A:229:LEU:CD2	1:A:232:PHE:CD2	0.41	3.04

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:161:GLY:O	1:A:162:ASN:CB	0.41	2.69
1:A:235:SER:N	1:A:238:ASP:HB3	0.41	2.31
1:A:163:VAL:HG13	1:A:222:LEU:CD2	0.40	2.47

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	164/174 (94%)	88 (54%)	50 (30%)	26 (16%)	1	4
All	All	164/174 (94%)	88 (54%)	50 (30%)	26 (16%)	1	4

All 26 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	149	ARG
1	A	241	GLY
1	A	184	GLU
1	A	150	GLU
1	A	188	LYS
1	A	175	ASN
1	A	211	HIS
1	A	118	GLU
1	A	234	LEU
1	A	181	ASP
1	A	162	ASN
1	A	92	TRP
1	A	169	ALA
1	A	235	SER
1	A	246	TYR
1	A	90	PRO
1	A	226	LEU
1	A	157	PHE
1	A	102	VAL
1	A	86	PHE

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Mol	Chain	Res	Type
1	A	164	LEU
1	A	228	ASP
1	A	233	ARG
1	A	129	PRO
1	A	117	VAL
1	A	148	VAL

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	140/148 (95%)	109 (78%)	31 (22%)	4	31
All	All	140/148 (95%)	109 (78%)	31 (22%)	4	31

All 31 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	128	THR
1	A	179	HIS
1	A	101	ILE
1	A	93	ARG
1	A	184	GLU
1	A	149	ARG
1	A	83	PHE
1	A	234	LEU
1	A	85	THR
1	A	238	ASP
1	A	232	PHE
1	A	209	LEU
1	A	92	TRP
1	A	198	VAL
1	A	202	GLU
1	A	207	LEU
1	A	246	TYR
1	A	129	PRO
1	A	226	LEU

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Mol	Chain	Res	Type
1	A	219	MET
1	A	121	LEU
1	A	95	THR
1	A	205	HIS
1	A	164	LEU
1	A	146	PHE
1	A	143	MET
1	A	195	LEU
1	A	229	LEU
1	A	148	VAL
1	A	142	ILE
1	A	222	LEU

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	0DS	A	261	2	32,32,32	1.66	1 (3%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	0DS	A	261	2	40,42,42	0.98	0 (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
4	0DS	A	261	2	-	0,38,38,38	0,1,1,1

All bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	261	0DS	O3-N3	8.55	1.24	1.39

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided