



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7WG4
Title : DVAA-KlAtel
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Deposited on : 2021-12-28
Resolution : 1.51 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
Xtriage (Phenix) : 1.13
EDS : 2.30
buster-report : 1.1.7 (2018)
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) : 2.30

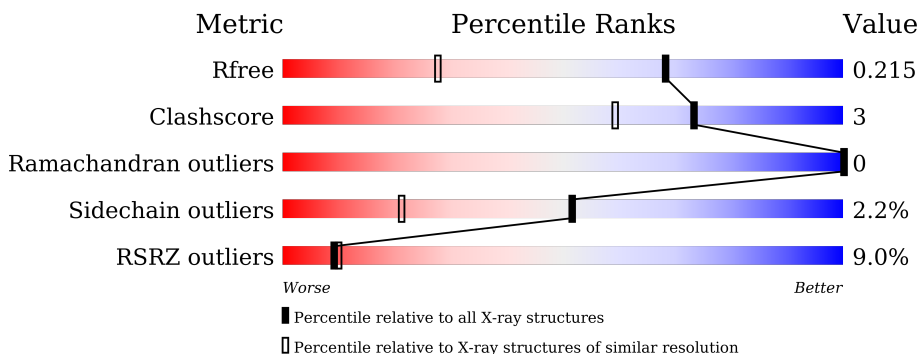
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.51 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	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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 $\leq 5\%$. 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	507	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8183 atoms, of which 3907 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 Arginyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	491	7878	2547	3907	647	760	17	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	ASP	-	expression tag	UNP Q6CXX6
A	-2	VAL	-	expression tag	UNP Q6CXX6
A	-1	ALA	-	expression tag	UNP Q6CXX6
A	0	ALA	-	expression tag	UNP Q6CXX6

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

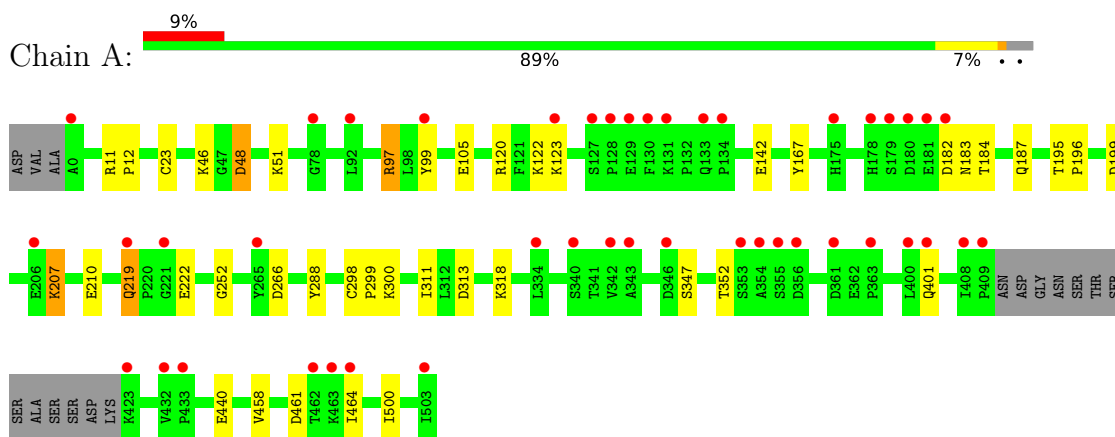
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	304	Total	O	0	0
			304	304		

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: Arginyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	86.46Å 86.46Å 160.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.57 – 1.51 28.57 – 1.51	Depositor EDS
% Data completeness (in resolution range)	97.6 (28.57-1.51) 97.6 (28.57-1.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 1.51Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.185 , 0.216 0.185 , 0.215	Depositor DCC
R_{free} test set	4682 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtrriage
Anisotropy	0.124	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8183	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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](#)

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

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	0.84	1/4068 (0.0%)	0.84	1/5510 (0.0%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	23	CYS	CB-SG	-5.73	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	313	ASP	CB-CG-OD1	7.44	124.99	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	97	ARG	Sidechain

5.2 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 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	3971	3907	3905	26	0
2	A	1	0	0	0	0
3	A	304	0	0	2	0
All	All	4276	3907	3905	26	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 3.

All (26) 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:167:TYR:OH	1:A:183:ASN:O	2.06	0.73
1:A:461:ASP:CG	1:A:464:ILE:HD12	2.17	0.65
1:A:347:SER:N	3:A:702:HOH:O	2.31	0.63
1:A:99:TYR:HB3	1:A:311:ILE:HG23	1.82	0.61
1:A:300:LYS:H	1:A:300:LYS:HE2	1.64	0.61
1:A:299:PRO:HD2	1:A:300:LYS:NZ	2.16	0.60
1:A:299:PRO:HD2	1:A:300:LYS:HZ1	1.67	0.57
1:A:352:THR:N	1:A:440:GLU:OE2	2.34	0.56
1:A:252:GLY:HA3	1:A:288:TYR:O	2.08	0.54
1:A:352:THR:HG22	3:A:900:HOH:O	2.08	0.53
1:A:122:LYS:NZ	1:A:142:GLU:OE2	2.44	0.51
1:A:219:GLN:O	1:A:222:GLU:HG3	2.10	0.50
1:A:352:THR:OG1	1:A:440:GLU:OE2	2.18	0.50
1:A:300:LYS:H	1:A:300:LYS:CE	2.25	0.50
1:A:207:LYS:C	1:A:207:LYS:HD2	2.33	0.49
1:A:184:THR:OG1	1:A:187:GLN:HG3	2.13	0.49
1:A:120:ARG:NH2	1:A:266:ASP:OD2	2.48	0.47
1:A:401:GLN:OE1	1:A:401:GLN:N	2.28	0.45
1:A:298:CYS:SG	1:A:300:LYS:HE2	2.59	0.43
1:A:195:THR:HB	1:A:196:PRO:HD2	2.00	0.42
1:A:207:LYS:HD2	1:A:207:LYS:O	2.20	0.41
1:A:458:VAL:HB	1:A:500:ILE:HG12	2.02	0.41
1:A:48:ASP:HB3	1:A:51:LYS:HE3	2.01	0.41
1:A:300:LYS:H	1:A:300:LYS:CD	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ARG:HA	1:A:12:PRO:HD3	1.89	0.40
1:A:182:ASP:C	1:A:187:GLN:OE1	2.59	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	487/507 (96%)	479 (98%)	8 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	448/461 (97%)	438 (98%)	10 (2%)	52 21

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LYS
1	A	48	ASP
1	A	97	ARG
1	A	105	GLU

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Mol	Chain	Res	Type
1	A	123	LYS
1	A	199	ASP
1	A	207	LYS
1	A	210	GLU
1	A	219	GLN
1	A	318	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	HIS
1	A	214	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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, 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	491/507 (96%)	0.35	44 (8%) 9 10	17, 28, 69, 112	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	464	ILE	7.4
1	A	182	ASP	6.9
1	A	354	ALA	6.8
1	A	409	PRO	6.7
1	A	355	SER	6.6
1	A	178	HIS	6.3
1	A	463	LYS	6.1
1	A	408	ILE	6.0
1	A	356	ASP	5.8
1	A	0	ALA	5.8
1	A	180	ASP	5.8
1	A	130	PHE	5.2
1	A	181	GLU	5.1
1	A	346	ASP	4.8
1	A	353	SER	4.6
1	A	128	PRO	4.3
1	A	343	ALA	4.1
1	A	131	LYS	4.1
1	A	129	GLU	3.9
1	A	342	VAL	3.6
1	A	134	PRO	3.4
1	A	400	LEU	3.3
1	A	503	ILE	3.3
1	A	361	ASP	3.1
1	A	340	SER	3.1
1	A	179	SER	3.0
1	A	363	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	433	PRO	2.9
1	A	462	THR	2.8
1	A	423	LYS	2.7
1	A	432	VAL	2.7
1	A	99	TYR	2.5
1	A	92	LEU	2.4
1	A	334	LEU	2.4
1	A	265	TYR	2.4
1	A	219	GLN	2.3
1	A	127	SER	2.3
1	A	133	GLN	2.2
1	A	206	GLU	2.1
1	A	221	GLY	2.1
1	A	123	LYS	2.1
1	A	78	GLY	2.0
1	A	401	GLN	2.0
1	A	175	HIS	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](#)

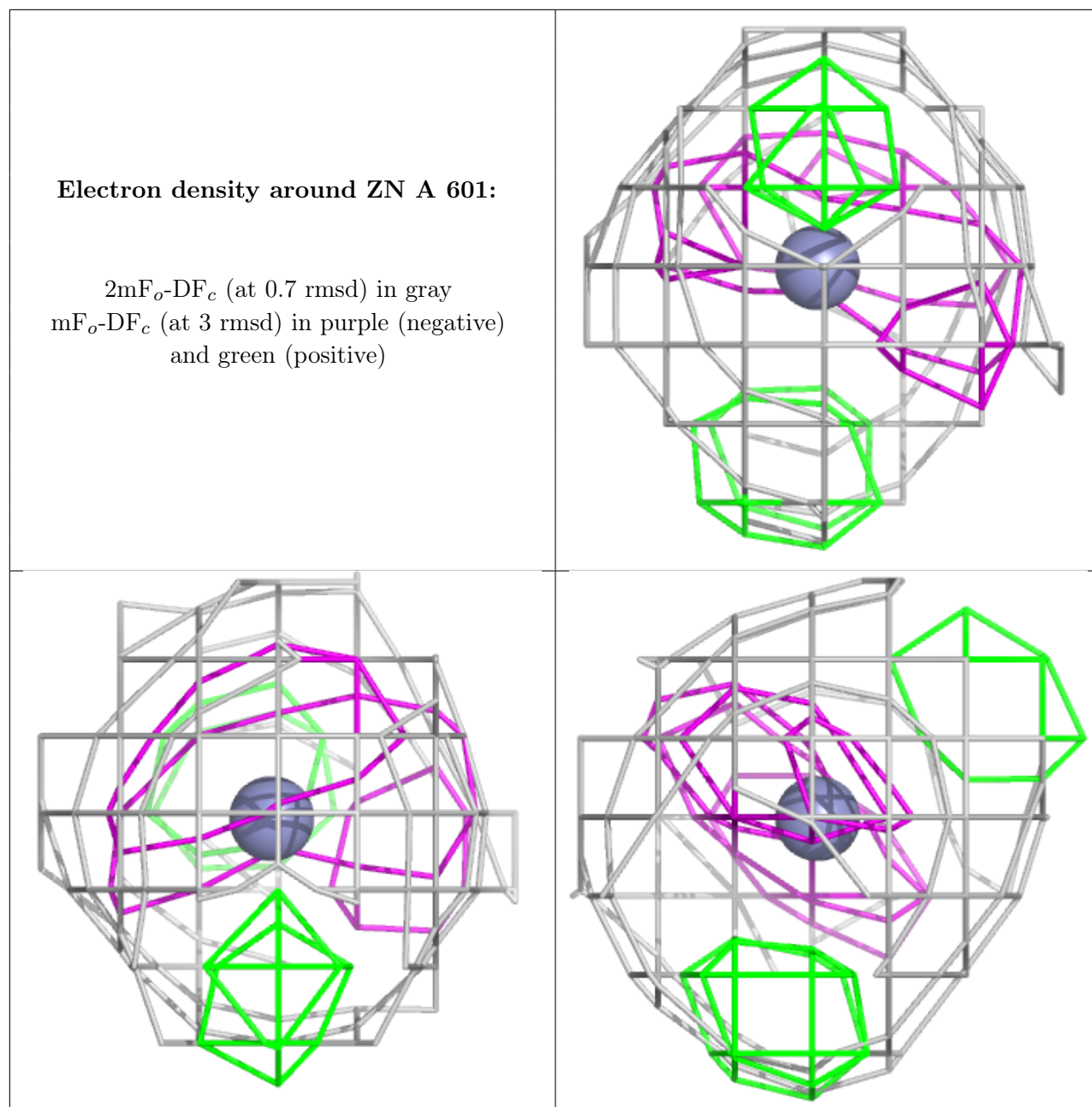
There are no monosaccharides in this entry.

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	ZN	A	601	1/1	0.99	0.04	22,22,22,22	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.