



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 5, 2017 – 12:22 PM EDT

PDB ID : 5WX3
Title : Alkyldiketide-CoA synthase from Evodia rutaecarpa
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Deposited on : 2017-01-06
Resolution : 1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029077
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029077

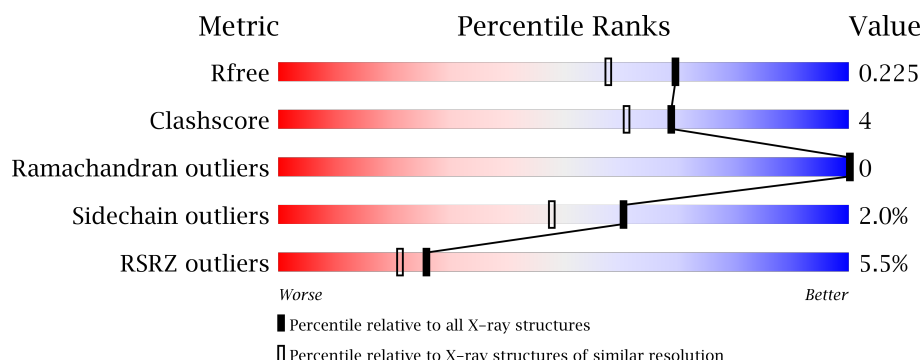
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	100719	4827 (1.80-1.80)
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)
RSRZ outliers	101464	4906 (1.80-1.80)

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	396	<div> <div>4%</div> <div>88%</div> <div>7%</div> <div>5%</div> </div>
1	B	396	<div> <div>4%</div> <div>82%</div> <div>9%</div> <div>8%</div> </div>
1	C	396	<div> <div>6%</div> <div>76%</div> <div>13%</div> <div>11%</div> </div>
1	D	396	<div> <div>7%</div> <div>81%</div> <div>12%</div> <div>7%</div> </div>

2 Entry composition [i](#)

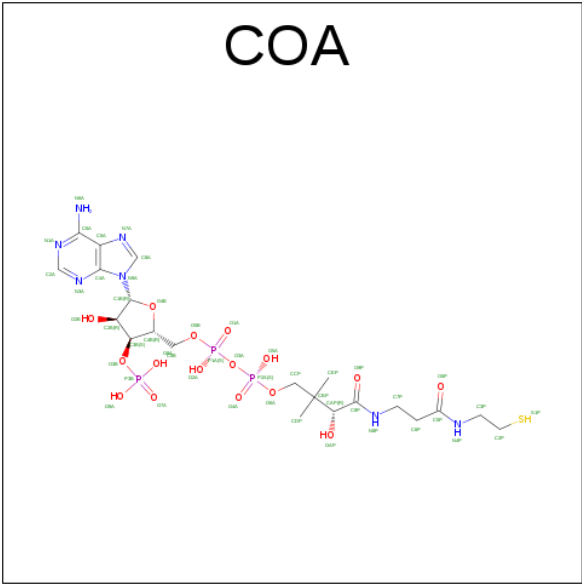
There are 4 unique types of molecules in this entry. The entry contains 12075 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alkyldiketide-CoA synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total	C	N	O	S	0	0	0
			2920	1859	496	539	26			
1	B	363	Total	C	N	O	S	0	1	0
			2845	1815	484	520	26			
1	C	353	Total	C	N	O	S	0	1	0
			2761	1764	466	507	24			
1	D	370	Total	C	N	O	S	0	0	0
			2883	1837	491	529	26			

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



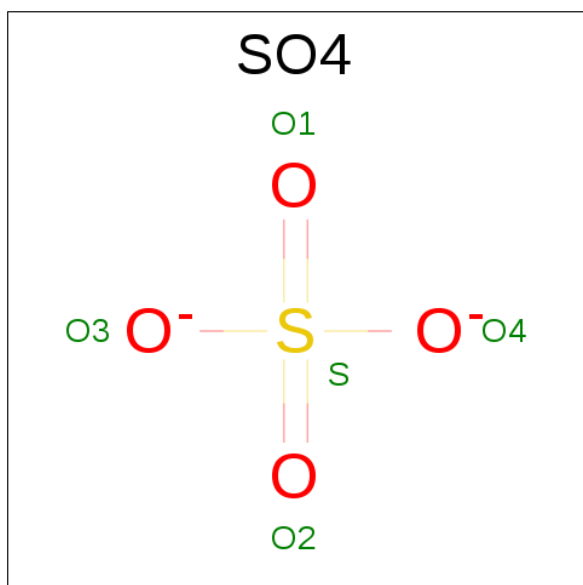
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P S	0	0
			48	21	7	16	3 1		
2	B	1	Total	C	N	O	P S	0	0
			48	21	7	16	3 1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	140	Total	O	0	0
			140	140		
4	B	122	Total	O	0	0
			122	122		
4	C	130	Total	O	0	0
			130	130		

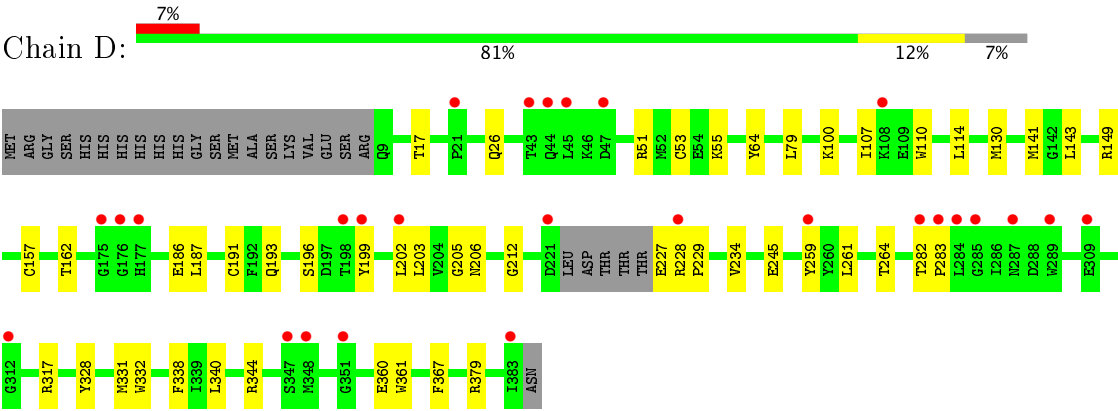
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	62	Total	O	0	0
			62	62		

- Molecule 1: Alkyldiketide-CoA synthase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	164.59 Å 84.12 Å 138.67 Å 90.00° 124.74° 90.00°	Depositor
Resolution (Å)	39.74 – 1.80 39.74 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.74-1.80) 99.5 (39.74-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.81 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.192 , 0.226 0.188 , 0.225	Depositor DCC
R_{free} test set	7145 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
Reported twinning fraction	0.040 for h,-k,-h-l	Depositor
Outliers	1 of 142922 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12075	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: COA, SO4

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	0.41	0/2983	0.57	1/4040 (0.0%)
1	B	0.40	0/2906	0.56	1/3929 (0.0%)
1	C	0.42	1/2820 (0.0%)	0.55	0/3815
1	D	0.37	0/2945	0.50	0/3985
All	All	0.40	1/11654 (0.0%)	0.54	2/15769 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	297	HIS	C-N	5.23	1.44	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	LEU	CA-CB-CG	5.13	127.09	115.30
1	B	340	LEU	CA-CB-CG	5.09	127.00	115.30

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	2920	0	2923	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2845	0	2844	24	0
1	C	2761	0	2774	32	0
1	D	2883	0	2886	31	0
2	A	48	0	32	2	0
2	B	48	0	32	2	0
2	C	48	0	32	2	0
2	D	48	0	32	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	140	0	0	1	0
4	B	122	0	0	0	0
4	C	130	0	0	0	0
4	D	62	0	0	0	0
All	All	12075	0	11555	100	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.

The worst 5 of 100 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)
2:A:401:COA:O4B	2:A:401:COA:C1B	1.67	1.28
2:B:401:COA:C1B	2:B:401:COA:O4B	1.67	1.27
2:D:401:COA:O4B	2:D:401:COA:C1B	1.66	1.14
2:C:401:COA:O4B	2:C:401:COA:C1B	1.66	1.13
1:D:360:GLU:OE2	1:D:379:ARG:NH1	2.21	0.73

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	373/396 (94%)	363 (97%)	10 (3%)	0	100	100
1	B	358/396 (90%)	351 (98%)	7 (2%)	0	100	100
1	C	350/396 (88%)	341 (97%)	9 (3%)	0	100	100
1	D	366/396 (92%)	357 (98%)	9 (2%)	0	100	100
All	All	1447/1584 (91%)	1412 (98%)	35 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	317/335 (95%)	310 (98%)	7 (2%)	57	44
1	B	307/335 (92%)	299 (97%)	8 (3%)	51	36
1	C	298/335 (89%)	292 (98%)	6 (2%)	60	48
1	D	312/335 (93%)	307 (98%)	5 (2%)	68	58
All	All	1234/1340 (92%)	1208 (98%)	26 (2%)	60	46

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	277	CYS
1	B	344	ARG
1	D	340	LEU
1	B	315	LYS
1	B	340	LEU

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

Mol	Chain	Res	Type
1	A	275	GLN
1	D	19	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 ligands are 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	COA	A	401	-	43,50,50	4.17	14 (32%)	48,75,75	2.21	10 (20%)
3	SO4	A	402	-	4,4,4	0.22	0	6,6,6	0.11	0
2	COA	B	401	-	43,50,50	4.23	15 (34%)	48,75,75	2.09	7 (14%)
3	SO4	B	402	-	4,4,4	0.21	0	6,6,6	0.17	0
2	COA	C	401	-	43,50,50	4.15	15 (34%)	48,75,75	2.24	5 (10%)
3	SO4	C	402	-	4,4,4	0.22	0	6,6,6	0.15	0
2	COA	D	401	-	43,50,50	4.15	15 (34%)	48,75,75	2.28	8 (16%)
3	SO4	D	402	-	4,4,4	0.16	0	6,6,6	0.20	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
2	COA	A	401	-	-	0/44/64/64	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	402	-	-	0/0/0/0	0/0/0/0
2	COA	B	401	-	-	0/44/64/64	0/3/3/3
3	SO4	B	402	-	-	0/0/0/0	0/0/0/0
2	COA	C	401	-	-	0/44/64/64	0/3/3/3
3	SO4	C	402	-	-	0/0/0/0	0/0/0/0
2	COA	D	401	-	-	0/44/64/64	0/3/3/3
3	SO4	D	402	-	-	0/0/0/0	0/0/0/0

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	COA	C2B-C1B	-13.05	1.32	1.53
2	B	401	COA	C2B-C1B	-12.82	1.33	1.53
2	A	401	COA	C2B-C1B	-12.44	1.33	1.53
2	C	401	COA	C2B-C1B	-12.34	1.34	1.53
2	C	401	COA	O4B-C4B	-6.21	1.31	1.45

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	COA	N3A-C2A-N1A	-10.15	120.02	128.86
2	C	401	COA	N3A-C2A-N1A	-9.83	120.30	128.86
2	A	401	COA	N3A-C2A-N1A	-9.80	120.33	128.86
2	B	401	COA	N3A-C2A-N1A	-8.96	121.05	128.86
2	C	401	COA	N6A-C6A-N1A	-6.24	106.39	118.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	COA	2	0
2	B	401	COA	2	0
2	C	401	COA	2	0
2	D	401	COA	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	375/396 (94%)	-0.00	15 (4%) 39 33	14, 22, 40, 68	0
1	B	363/396 (91%)	0.02	15 (4%) 38 32	15, 24, 50, 70	0
1	C	353/396 (89%)	0.16	23 (6%) 20 16	13, 23, 52, 82	0
1	D	370/396 (93%)	0.34	27 (7%) 16 13	17, 37, 60, 80	0
All	All	1461/1584 (92%)	0.13	80 (5%) 26 21	13, 25, 52, 82	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	199	TYR	6.5
1	B	259[A]	TYR	6.2
1	C	223	ASP	5.6
1	D	176	GLY	5.4
1	C	224	THR	5.4

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	COA	D	401	48/48	0.81	0.20	1.80	59,73,75,76	0
2	COA	B	401	48/48	0.78	0.19	1.73	46,64,76,79	0
2	COA	A	401	48/48	0.85	0.16	1.48	21,43,56,61	0
2	COA	C	401	48/48	0.86	0.19	1.31	37,50,57,72	0
3	SO4	D	402	5/5	0.94	0.14	-0.21	50,57,59,61	0
3	SO4	A	402	5/5	0.96	0.10	-0.30	40,48,50,52	0
3	SO4	B	402	5/5	0.95	0.13	-	56,58,62,64	0
3	SO4	C	402	5/5	0.92	0.13	-	51,55,57,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.