



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:17 PM UTC

PDB ID : 4H2H / pdb_00004h2h
Title : Crystal structure of an enolase (mandalate racemase subgroup, target EFI-502101) from *Pelagibaca bermudensis* htcc2601, with bound mg and l-4-hydroxyproline betaine (betonicine)
Authors : Vetting, M.W.; Morisco, L.L.; Wasserman, S.R.; Sojitra, S.; Imker, H.J.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)
Deposited on : 2012-09-12
Resolution : 1.70 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

<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)
Xtriage (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

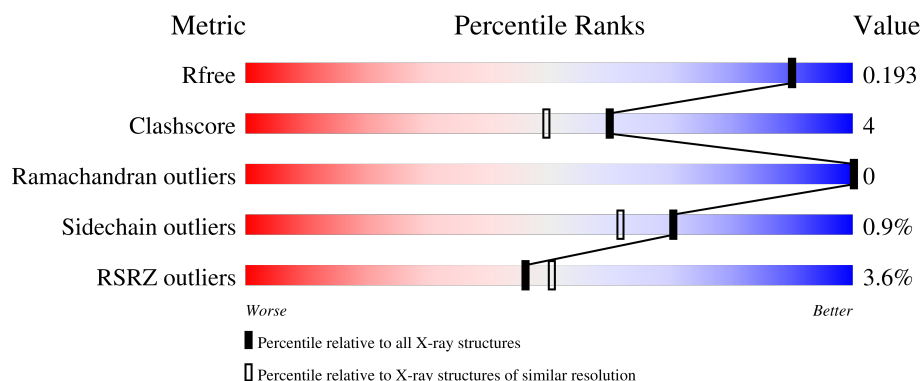
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	376	5% 88% 9% ..
1	B	376	5% 89% 9% .
1	C	376	4% 93% 5% .
1	D	376	5% 90% 7% ..

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Mol	Chain	Length	Quality of chain
1	E	376	
1	F	376	
1	G	376	
1	H	376	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	IOD	A	404	-	-	X	-
5	IOD	A	405	-	-	X	-
5	IOD	D	409	-	-	X	-
5	IOD	D	411	-	-	X	-
5	IOD	E	409	-	-	X	-
5	IOD	G	409	-	-	X	-
5	IOD	G	410	-	-	X	-
5	IOD	H	406	-	-	X	-
5	IOD	H	408	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 24627 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 Mandelate racemase/muconate lactonizing enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	5	0
			2829	1785	498	530	16			
1	B	367	Total	C	N	O	S	0	5	0
			2828	1783	500	530	15			
1	C	367	Total	C	N	O	S	0	2	0
			2800	1766	494	525	15			
1	D	367	Total	C	N	O	S	0	4	0
			2809	1771	494	529	15			
1	E	355	Total	C	N	O	S	0	4	0
			2713	1707	478	512	16			
1	F	367	Total	C	N	O	S	0	1	0
			2792	1762	492	523	15			
1	G	367	Total	C	N	O	S	0	2	0
			2800	1768	493	524	15			
1	H	367	Total	C	N	O	S	0	2	0
			2803	1768	496	524	15			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP Q0FPQ4
A	-7	ALA	-	expression tag	UNP Q0FPQ4
A	-6	HIS	-	expression tag	UNP Q0FPQ4
A	-5	HIS	-	expression tag	UNP Q0FPQ4
A	-4	HIS	-	expression tag	UNP Q0FPQ4
A	-3	HIS	-	expression tag	UNP Q0FPQ4
A	-2	HIS	-	expression tag	UNP Q0FPQ4
A	-1	HIS	-	expression tag	UNP Q0FPQ4
A	0	SER	-	expression tag	UNP Q0FPQ4
A	1	LEU	-	expression tag	UNP Q0FPQ4
B	-8	MET	-	expression tag	UNP Q0FPQ4
B	-7	ALA	-	expression tag	UNP Q0FPQ4
B	-6	HIS	-	expression tag	UNP Q0FPQ4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	expression tag	UNP Q0FPQ4
B	-4	HIS	-	expression tag	UNP Q0FPQ4
B	-3	HIS	-	expression tag	UNP Q0FPQ4
B	-2	HIS	-	expression tag	UNP Q0FPQ4
B	-1	HIS	-	expression tag	UNP Q0FPQ4
B	0	SER	-	expression tag	UNP Q0FPQ4
B	1	LEU	-	expression tag	UNP Q0FPQ4
C	-8	MET	-	expression tag	UNP Q0FPQ4
C	-7	ALA	-	expression tag	UNP Q0FPQ4
C	-6	HIS	-	expression tag	UNP Q0FPQ4
C	-5	HIS	-	expression tag	UNP Q0FPQ4
C	-4	HIS	-	expression tag	UNP Q0FPQ4
C	-3	HIS	-	expression tag	UNP Q0FPQ4
C	-2	HIS	-	expression tag	UNP Q0FPQ4
C	-1	HIS	-	expression tag	UNP Q0FPQ4
C	0	SER	-	expression tag	UNP Q0FPQ4
C	1	LEU	-	expression tag	UNP Q0FPQ4
D	-8	MET	-	expression tag	UNP Q0FPQ4
D	-7	ALA	-	expression tag	UNP Q0FPQ4
D	-6	HIS	-	expression tag	UNP Q0FPQ4
D	-5	HIS	-	expression tag	UNP Q0FPQ4
D	-4	HIS	-	expression tag	UNP Q0FPQ4
D	-3	HIS	-	expression tag	UNP Q0FPQ4
D	-2	HIS	-	expression tag	UNP Q0FPQ4
D	-1	HIS	-	expression tag	UNP Q0FPQ4
D	0	SER	-	expression tag	UNP Q0FPQ4
D	1	LEU	-	expression tag	UNP Q0FPQ4
E	-8	MET	-	expression tag	UNP Q0FPQ4
E	-7	ALA	-	expression tag	UNP Q0FPQ4
E	-6	HIS	-	expression tag	UNP Q0FPQ4
E	-5	HIS	-	expression tag	UNP Q0FPQ4
E	-4	HIS	-	expression tag	UNP Q0FPQ4
E	-3	HIS	-	expression tag	UNP Q0FPQ4
E	-2	HIS	-	expression tag	UNP Q0FPQ4
E	-1	HIS	-	expression tag	UNP Q0FPQ4
E	0	SER	-	expression tag	UNP Q0FPQ4
E	1	LEU	-	expression tag	UNP Q0FPQ4
F	-8	MET	-	expression tag	UNP Q0FPQ4
F	-7	ALA	-	expression tag	UNP Q0FPQ4
F	-6	HIS	-	expression tag	UNP Q0FPQ4
F	-5	HIS	-	expression tag	UNP Q0FPQ4
F	-4	HIS	-	expression tag	UNP Q0FPQ4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	HIS	-	expression tag	UNP Q0FPQ4
F	-2	HIS	-	expression tag	UNP Q0FPQ4
F	-1	HIS	-	expression tag	UNP Q0FPQ4
F	0	SER	-	expression tag	UNP Q0FPQ4
F	1	LEU	-	expression tag	UNP Q0FPQ4
G	-8	MET	-	expression tag	UNP Q0FPQ4
G	-7	ALA	-	expression tag	UNP Q0FPQ4
G	-6	HIS	-	expression tag	UNP Q0FPQ4
G	-5	HIS	-	expression tag	UNP Q0FPQ4
G	-4	HIS	-	expression tag	UNP Q0FPQ4
G	-3	HIS	-	expression tag	UNP Q0FPQ4
G	-2	HIS	-	expression tag	UNP Q0FPQ4
G	-1	HIS	-	expression tag	UNP Q0FPQ4
G	0	SER	-	expression tag	UNP Q0FPQ4
G	1	LEU	-	expression tag	UNP Q0FPQ4
H	-8	MET	-	expression tag	UNP Q0FPQ4
H	-7	ALA	-	expression tag	UNP Q0FPQ4
H	-6	HIS	-	expression tag	UNP Q0FPQ4
H	-5	HIS	-	expression tag	UNP Q0FPQ4
H	-4	HIS	-	expression tag	UNP Q0FPQ4
H	-3	HIS	-	expression tag	UNP Q0FPQ4
H	-2	HIS	-	expression tag	UNP Q0FPQ4
H	-1	HIS	-	expression tag	UNP Q0FPQ4
H	0	SER	-	expression tag	UNP Q0FPQ4
H	1	LEU	-	expression tag	UNP Q0FPQ4

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	F	1	Total Mg 1 1	0	0
2	G	1	Total Mg 1 1	0	0

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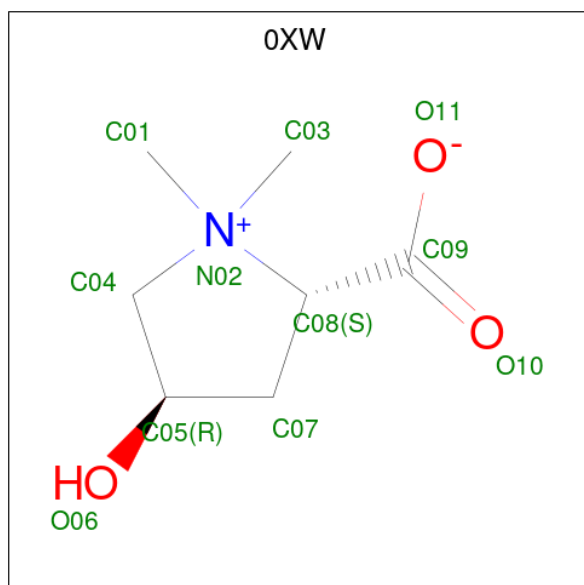
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total	Mg	0	0
			1	1		

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ni	0	0
			1	1		
3	B	1	Total	Ni	0	0
			1	1		

- Molecule 4 is (2S,4R)-4-hydroxy-1,1-dimethylpyrrolidinium-2-carboxylate (CCD ID: 0XW) (formula: C₇H₁₃NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	7	1	3		
4	B	1	Total	C	N	O	0	0
			11	7	1	3		
4	C	1	Total	C	N	O	0	0
			11	7	1	3		
4	D	1	Total	C	N	O	0	0
			11	7	1	3		
4	E	1	Total	C	N	O	0	0
			11	7	1	3		
4	F	1	Total	C	N	O	0	0
			11	7	1	3		

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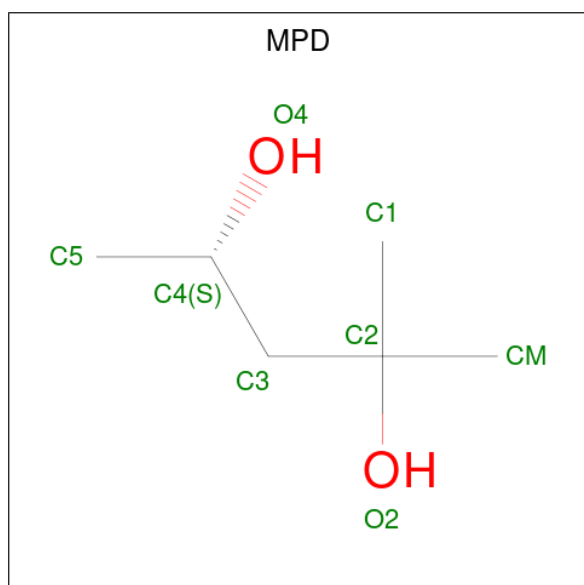
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	G	1	Total	C	N	O	0	0
			11	7	1	3		
4	H	1	Total	C	N	O	0	0
			11	7	1	3		

- Molecule 5 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	8	Total	I	0	0
			8	8		
5	B	6	Total	I	0	0
			6	6		
5	C	10	Total	I	0	0
			10	10		
5	D	8	Total	I	0	0
			8	8		
5	E	7	Total	I	0	0
			7	7		
5	F	8	Total	I	0	0
			8	8		
5	G	8	Total	I	0	0
			8	8		
5	H	6	Total	I	0	0
			6	6		

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			8	6	2		
6	D	1	Total	C	O	0	0
			8	6	2		
6	E	1	Total	C	O	0	0
			8	6	2		

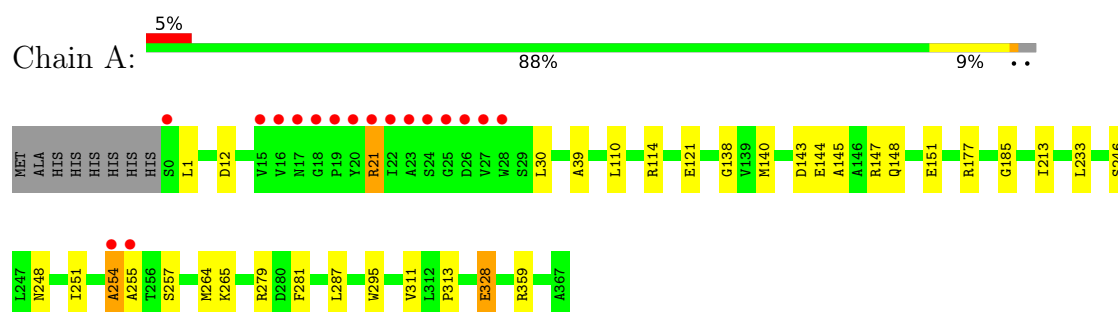
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	275	Total	O	0	0
			275	275		
7	B	293	Total	O	0	1
			294	294		
7	C	272	Total	O	0	1
			273	273		
7	D	251	Total	O	0	0
			251	251		
7	E	250	Total	O	0	1
			251	251		
7	F	266	Total	O	0	0
			266	266		
7	G	227	Total	O	0	1
			228	228		
7	H	232	Total	O	0	0
			232	232		

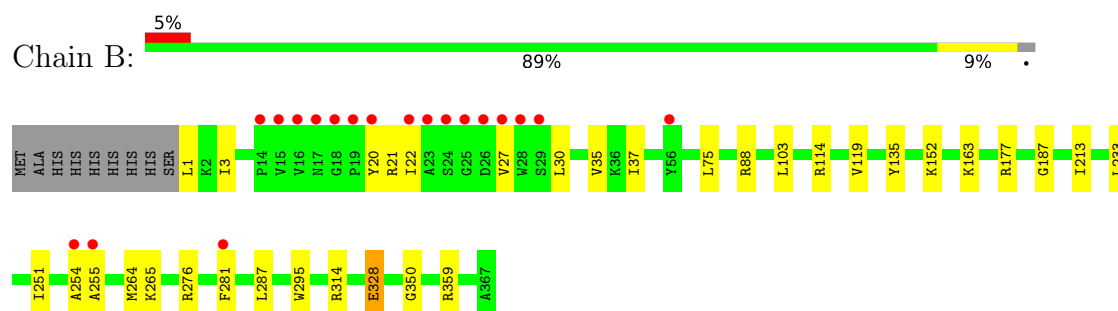
3 Residue-property plots [i](#)

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.

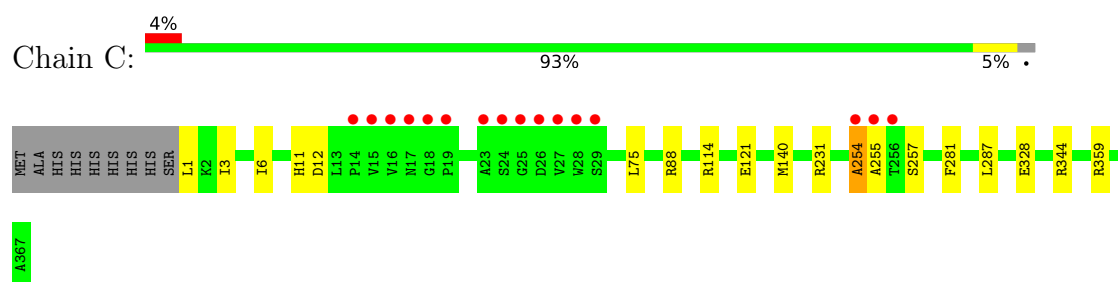
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



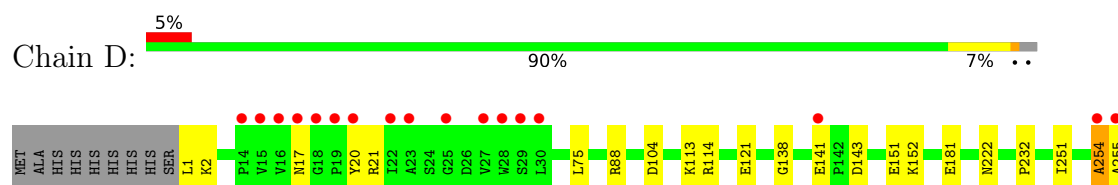
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme

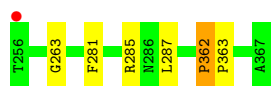


- Molecule 1: Mandelate racemase/muconate lactonizing enzyme

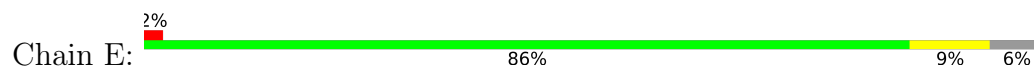


- Molecule 1: Mandelate racemase/muconate lactonizing enzyme

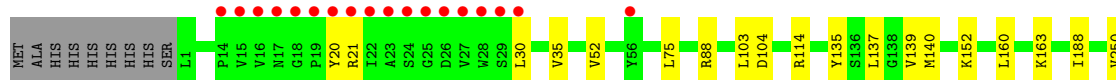
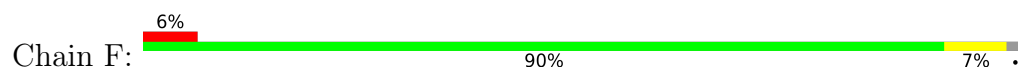




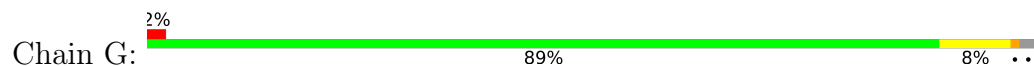
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



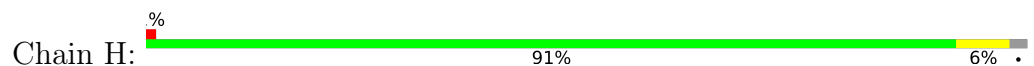
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.03Å 152.82Å 113.03Å 90.00° 105.20° 90.00°	Depositor
Resolution (Å)	25.68 – 1.70 25.68 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.68-1.70) 99.9 (25.68-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.159 , 0.192 0.159 , 0.193	Depositor DCC
R_{free} test set	16437 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	18.0	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	24627	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.87 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.0650e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MPD, NI, MG, IOD, 0XW

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	0.46	1/2894 (0.0%)	0.77	0/3936
1	B	0.44	0/2893	0.77	0/3936
1	C	0.43	1/2865 (0.0%)	0.76	2/3899 (0.1%)
1	D	0.43	1/2879 (0.0%)	0.76	2/3918 (0.1%)
1	E	0.42	0/2772	0.76	0/3770
1	F	0.43	0/2857	0.73	0/3888
1	G	0.42	1/2865 (0.0%)	0.77	0/3899
1	H	0.41	0/2868	0.75	1/3902 (0.0%)
All	All	0.43	4/22893 (0.0%)	0.76	5/31148 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	254	ALA	CA-CB	-5.32	1.45	1.53
1	A	254	ALA	CA-CB	-5.20	1.45	1.53
1	C	254	ALA	CA-CB	-5.06	1.45	1.53
1	G	254	ALA	CA-CB	-5.02	1.45	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	362	PRO	O-C-N	5.61	123.79	121.15
1	C	231	ARG	CA-C-N	-5.52	114.33	120.45
1	C	231	ARG	C-N-CA	-5.52	114.33	120.45
1	H	330	TYR	N-CA-C	-5.49	106.08	112.89
1	D	263	GLY	N-CA-C	-5.12	101.06	113.18

There are no chirality outliers.

There are no planarity outliers.

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	2829	0	2785	32	0
1	B	2828	0	2782	29	0
1	C	2800	0	2751	18	0
1	D	2809	0	2758	26	0
1	E	2713	0	2672	29	0
1	F	2792	0	2746	20	0
1	G	2800	0	2756	29	0
1	H	2803	0	2758	20	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	11	0	13	1	0
4	B	11	0	13	0	0
4	C	11	0	13	0	0
4	D	11	0	13	0	0
4	E	11	0	13	1	0
4	F	11	0	13	0	0
4	G	11	0	13	1	0
4	H	11	0	13	2	0
5	A	8	0	0	5	0
5	B	6	0	0	1	0
5	C	10	0	0	1	0
5	D	8	0	0	8	0
5	E	7	0	0	6	0
5	F	8	0	0	2	0
5	G	8	0	0	6	0
5	H	6	0	0	7	0
6	C	8	0	14	0	0
6	D	8	0	14	0	0
6	E	8	0	14	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	275	0	0	5	0
7	B	294	0	0	4	0
7	C	273	0	0	6	0
7	D	251	0	0	5	0
7	E	251	0	0	7	0
7	F	266	0	0	2	0
7	G	228	0	0	7	0
7	H	232	0	0	3	0
All	All	24627	0	22154	192	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 192 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)
5:E:406:IOD:I	7:E:693:HOH:O	2.33	1.16
5:A:407:IOD:I	7:A:663:HOH:O	2.39	1.08
5:D:406:IOD:I	7:D:638:HOH:O	2.44	1.06
5:G:404:IOD:I	7:G:614:HOH:O	2.49	1.00
5:F:403:IOD:I	7:F:667:HOH:O	2.59	0.91

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	371/376 (99%)	367 (99%)	4 (1%)	0	100	100
1	B	370/376 (98%)	365 (99%)	5 (1%)	0	100	100
1	C	367/376 (98%)	362 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	369/376 (98%)	364 (99%)	5 (1%)	0	100	100
1	E	355/376 (94%)	351 (99%)	4 (1%)	0	100	100
1	F	366/376 (97%)	360 (98%)	6 (2%)	0	100	100
1	G	367/376 (98%)	362 (99%)	5 (1%)	0	100	100
1	H	367/376 (98%)	363 (99%)	4 (1%)	0	100	100
All	All	2932/3008 (98%)	2894 (99%)	38 (1%)	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	292/294 (99%)	288 (99%)	4 (1%)	59	46
1	B	291/294 (99%)	289 (99%)	2 (1%)	76	69
1	C	288/294 (98%)	286 (99%)	2 (1%)	76	69
1	D	290/294 (99%)	288 (99%)	2 (1%)	76	69
1	E	281/294 (96%)	278 (99%)	3 (1%)	65	54
1	F	287/294 (98%)	284 (99%)	3 (1%)	68	58
1	G	288/294 (98%)	284 (99%)	4 (1%)	59	46
1	H	288/294 (98%)	287 (100%)	1 (0%)	86	83
All	All	2305/2352 (98%)	2284 (99%)	21 (1%)	70	62

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	250	VAL
1	G	160	LEU
1	H	141	GLU
1	G	186	THR
1	G	104	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	273	GLN
1	H	11	HIS
1	H	273	GLN
1	H	153	GLN
1	E	273	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 82 ligands modelled in this entry, 71 are monoatomic - leaving 11 for Mogul analysis.

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	$\# Z > 2$
6	MPD	E	403	-	7,7,7	0.33	0	9,10,10	0.58	0
4	0XW	C	402	2	9,11,11	2.17	3 (33%)	8,17,17	2.92	3 (37%)
4	0XW	H	402	2	9,11,11	2.15	2 (22%)	8,17,17	2.92	3 (37%)
4	0XW	B	403	2	9,11,11	2.15	2 (22%)	8,17,17	2.83	3 (37%)
4	0XW	D	402	2	9,11,11	2.14	2 (22%)	8,17,17	2.79	3 (37%)
4	0XW	G	402	2	9,11,11	2.21	2 (22%)	8,17,17	2.53	3 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	0XW	F	402	2	9,11,11	2.23	3 (33%)	8,17,17	2.55	3 (37%)
6	MPD	D	403	-	7,7,7	0.29	0	9,10,10	0.60	0
4	0XW	A	403	2	9,11,11	2.29	2 (22%)	8,17,17	2.41	3 (37%)
6	MPD	C	403	-	7,7,7	0.26	0	9,10,10	0.74	0
4	0XW	E	402	2	9,11,11	2.11	2 (22%)	8,17,17	2.68	3 (37%)

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
6	MPD	E	403	-	-	5/5/5/5	-
4	0XW	C	402	2	-	3/4/19/19	0/1/1/1
4	0XW	H	402	2	-	3/4/19/19	0/1/1/1
4	0XW	B	403	2	-	3/4/19/19	0/1/1/1
4	0XW	D	402	2	-	3/4/19/19	0/1/1/1
4	0XW	G	402	2	-	3/4/19/19	0/1/1/1
4	0XW	F	402	2	-	4/4/19/19	0/1/1/1
6	MPD	D	403	-	-	3/5/5/5	-
4	0XW	A	403	2	-	3/4/19/19	0/1/1/1
6	MPD	C	403	-	-	3/5/5/5	-
4	0XW	E	402	2	-	2/4/19/19	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	403	0XW	C07-C08	3.94	1.61	1.53
4	F	402	0XW	C07-C08	3.89	1.61	1.53
4	H	402	0XW	C07-C08	3.89	1.61	1.53
4	C	402	0XW	C07-C08	3.89	1.61	1.53
4	A	403	0XW	C07-C05	-3.86	1.45	1.52

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	402	0XW	O06-C05-C07	6.38	125.60	110.10
4	C	402	0XW	O06-C05-C07	6.25	125.28	110.10
4	G	402	0XW	O06-C05-C07	6.23	125.24	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	402	0XW	O06-C05-C07	6.16	125.07	110.10
4	D	402	0XW	O06-C05-C07	6.14	125.02	110.10

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	0XW	C07-C08-C09-O10
4	A	403	0XW	C07-C08-C09-O11
4	C	402	0XW	N02-C08-C09-O11
4	F	402	0XW	C07-C08-C09-O10
4	F	402	0XW	C07-C08-C09-O11

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	403	MPD	2	0
4	H	402	0XW	2	0
4	G	402	0XW	1	0
4	A	403	0XW	1	0
4	E	402	0XW	1	0

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	368/376 (97%)	-0.30	17 (4%)	37	41	5, 17, 39, 78	5 (1%)
1	B	367/376 (97%)	-0.28	19 (5%)	33	36	6, 17, 42, 73	5 (1%)
1	C	367/376 (97%)	-0.31	16 (4%)	39	42	7, 19, 39, 74	2 (0%)
1	D	367/376 (97%)	-0.20	18 (4%)	35	38	6, 19, 41, 68	4 (1%)
1	E	355/376 (94%)	-0.27	6 (1%)	69	73	7, 20, 39, 47	4 (1%)
1	F	367/376 (97%)	-0.24	21 (5%)	29	32	7, 19, 44, 86	1 (0%)
1	G	367/376 (97%)	-0.11	6 (1%)	70	75	7, 25, 46, 72	2 (0%)
1	H	367/376 (97%)	-0.20	3 (0%)	82	85	7, 23, 43, 73	2 (0%)
All	All	2925/3008 (97%)	-0.24	106 (3%)	46	50	5, 20, 42, 86	25 (0%)

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	254	ALA	6.1
1	H	254	ALA	6.0
1	F	29	SER	6.0
1	E	254	ALA	5.9
1	B	23	ALA	5.6

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
6	MPD	D	403	8/8	0.69	0.20	43,48,49,50	0
6	MPD	E	403	8/8	0.71	0.19	32,45,48,50	0
5	IOD	D	410	1/1	0.72	0.14	91,91,91,91	1
5	IOD	D	409	1/1	0.79	0.21	77,77,77,77	1
5	IOD	C	413	1/1	0.81	0.16	79,79,79,79	1
4	0XW	E	402	11/11	0.82	0.14	39,40,45,49	0
5	IOD	H	406	1/1	0.82	0.15	64,64,64,64	1
6	MPD	C	403	8/8	0.85	0.12	32,35,39,40	0
5	IOD	G	408	1/1	0.85	0.13	76,76,76,76	1
4	0XW	F	402	11/11	0.85	0.11	29,35,40,40	0
5	IOD	C	411	1/1	0.86	0.12	62,62,62,62	1
5	IOD	B	409	1/1	0.87	0.10	83,83,83,83	1
5	IOD	H	407	1/1	0.88	0.11	73,73,73,73	1
4	0XW	C	402	11/11	0.88	0.12	23,38,45,47	0
5	IOD	G	410	1/1	0.88	0.12	66,66,66,66	1
4	0XW	B	403	11/11	0.88	0.10	24,28,31,32	0
5	IOD	E	407	1/1	0.89	0.11	50,50,50,50	1
4	0XW	G	402	11/11	0.89	0.12	23,36,41,42	0
4	0XW	H	402	11/11	0.89	0.13	27,39,45,48	0
5	IOD	C	412	1/1	0.89	0.14	65,65,65,65	1
5	IOD	A	408	1/1	0.90	0.10	52,52,52,52	1
4	0XW	D	402	11/11	0.91	0.10	24,38,43,45	0
5	IOD	E	408	1/1	0.91	0.15	65,65,65,65	1
5	IOD	A	410	1/1	0.91	0.11	69,69,69,69	1
5	IOD	F	410	1/1	0.92	0.10	49,49,49,49	1
5	IOD	G	407	1/1	0.92	0.09	47,47,47,47	1
4	0XW	A	403	11/11	0.92	0.08	25,29,31,32	0
5	IOD	G	409	1/1	0.92	0.08	52,52,52,52	1
5	IOD	B	407	1/1	0.92	0.09	53,53,53,53	1
5	IOD	G	406	1/1	0.93	0.09	64,64,64,64	1
5	IOD	B	404	1/1	0.93	0.08	46,46,46,46	1
5	IOD	A	409	1/1	0.93	0.08	57,57,57,57	1
5	IOD	E	410	1/1	0.93	0.09	47,47,47,47	1
5	IOD	E	404	1/1	0.93	0.08	45,45,45,45	1
5	IOD	H	405	1/1	0.94	0.07	35,35,35,35	1
5	IOD	D	408	1/1	0.94	0.09	49,49,49,49	1
5	IOD	D	405	1/1	0.95	0.07	41,41,41,41	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	IOD	H	408	1/1	0.95	0.07	45,45,45,45	1
5	IOD	E	409	1/1	0.95	0.07	40,40,40,40	1
5	IOD	D	404	1/1	0.95	0.07	46,46,46,46	1
5	IOD	F	405	1/1	0.95	0.07	41,41,41,41	1
5	IOD	C	408	1/1	0.96	0.06	40,40,40,40	1
2	MG	E	401	1/1	0.96	0.06	18,18,18,18	0
5	IOD	F	404	1/1	0.96	0.05	35,35,35,35	1
5	IOD	C	404	1/1	0.96	0.06	34,34,34,34	1
5	IOD	C	406	1/1	0.96	0.05	29,29,29,29	1
5	IOD	G	405	1/1	0.96	0.06	34,34,34,34	1
5	IOD	A	404	1/1	0.97	0.06	44,44,44,44	1
5	IOD	G	403	1/1	0.97	0.04	30,30,30,30	1
5	IOD	A	411	1/1	0.97	0.05	31,31,31,31	1
5	IOD	C	410	1/1	0.97	0.05	34,34,34,34	1
5	IOD	F	406	1/1	0.97	0.05	31,31,31,31	1
5	IOD	A	406	1/1	0.98	0.03	23,23,23,23	1
5	IOD	A	407	1/1	0.98	0.03	20,20,20,20	1
5	IOD	B	408	1/1	0.98	0.04	22,22,22,22	1
5	IOD	D	411	1/1	0.98	0.05	39,39,39,39	1
5	IOD	H	403	1/1	0.98	0.04	27,27,27,27	1
5	IOD	C	409	1/1	0.98	0.03	23,23,23,23	1
5	IOD	F	407	1/1	0.98	0.04	27,27,27,27	1
5	IOD	F	409	1/1	0.98	0.03	24,24,24,24	1
5	IOD	E	405	1/1	0.98	0.04	29,29,29,29	1
5	IOD	E	406	1/1	0.98	0.04	29,29,29,29	1
2	MG	H	401	1/1	0.98	0.05	16,16,16,16	0
5	IOD	D	407	1/1	0.98	0.04	28,28,28,28	1
2	MG	F	401	1/1	0.99	0.05	15,15,15,15	0
5	IOD	C	407	1/1	0.99	0.03	23,23,23,23	1
5	IOD	G	404	1/1	0.99	0.03	23,23,23,23	1
2	MG	G	401	1/1	0.99	0.07	17,17,17,17	0
2	MG	B	401	1/1	0.99	0.02	15,15,15,15	0
3	NI	A	402	1/1	0.99	0.04	12,12,12,12	1
3	NI	B	402	1/1	0.99	0.02	12,12,12,12	1
5	IOD	B	405	1/1	0.99	0.03	23,23,23,23	1
5	IOD	B	406	1/1	0.99	0.03	25,25,25,25	1
2	MG	C	401	1/1	0.99	0.03	14,14,14,14	0
5	IOD	H	404	1/1	0.99	0.03	22,22,22,22	1
5	IOD	F	403	1/1	0.99	0.03	27,27,27,27	1
5	IOD	A	405	1/1	0.99	0.03	30,30,30,30	1
5	IOD	D	406	1/1	0.99	0.03	18,18,18,18	1
2	MG	D	401	1/1	0.99	0.04	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	401	1/1	0.99	0.03	14,14,14,14	0
5	IOD	F	408	1/1	0.99	0.04	19,19,19,19	1
5	IOD	C	405	1/1	0.99	0.03	23,23,23,23	1

6.5 Other polymers [i](#)

There are no such residues in this entry.