



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 05:12 PM UTC

PDB ID : 4LGT / pdb_00004lgt
Title : Crystal structure of the catalytic domain of RluB in complex with a 21-nucleotide RNA substrate
Authors : Czudnochowski, N.; Finer-Moore, J.S.; Stroud, R.M.
Deposited on : 2013-06-28
Resolution : 1.30 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

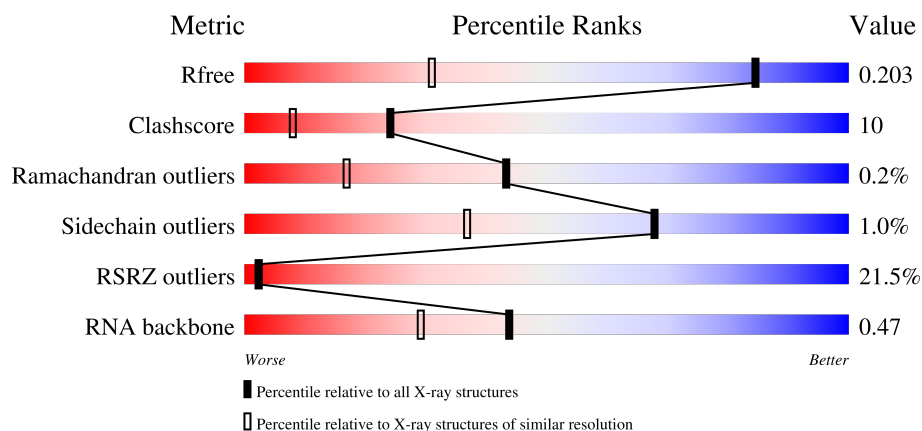
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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	1553 (1.30-1.30)
Clashscore	190562	1595 (1.30-1.30)
Ramachandran outliers	187476	1551 (1.30-1.30)
Sidechain outliers	187428	1551 (1.30-1.30)
RSRZ outliers	180081	1549 (1.30-1.30)
RNA backbone	3983	1020 (2.10-0.62)

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	255	5% 87% 11% ••
1	D	255	37% 80% 16% ••
2	E	21	5% 76% 19% 5%
2	F	21	29% 52% 33% 10% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9941 atoms, of which 4452 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 Ribosomal large subunit pseudouridine synthase B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	251	Total	C	H	N	O	S	0	6	0
			4048	1254	2036	376	376	6			
1	D	247	Total	C	H	N	O	S	0	5	0
			3930	1225	1970	364	365	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P37765
A	-2	PRO	-	expression tag	UNP P37765
A	-1	GLY	-	expression tag	UNP P37765
A	0	SER	-	expression tag	UNP P37765
D	-3	GLY	-	expression tag	UNP P37765
D	-2	PRO	-	expression tag	UNP P37765
D	-1	GLY	-	expression tag	UNP P37765
D	0	SER	-	expression tag	UNP P37765

- Molecule 2 is a RNA chain called stem-loop of 23S rRNA.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
2	E	21	Total	C	F	H	N	O	P	0	0	0
			682	202	1	228	85	145	21			
2	F	20	Total	C	F	H	N	O	P	0	0	0
			651	192	1	218	80	140	20			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	347	Total	O	0	0
			347	347		
3	E	134	Total	O	0	0
			134	134		

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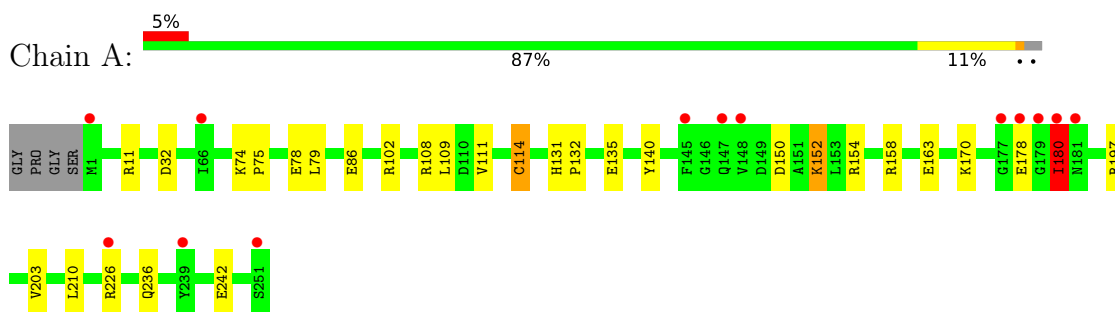
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	109	Total	O	0	0
			109	109		
3	F	40	Total	O	0	0
			40	40		

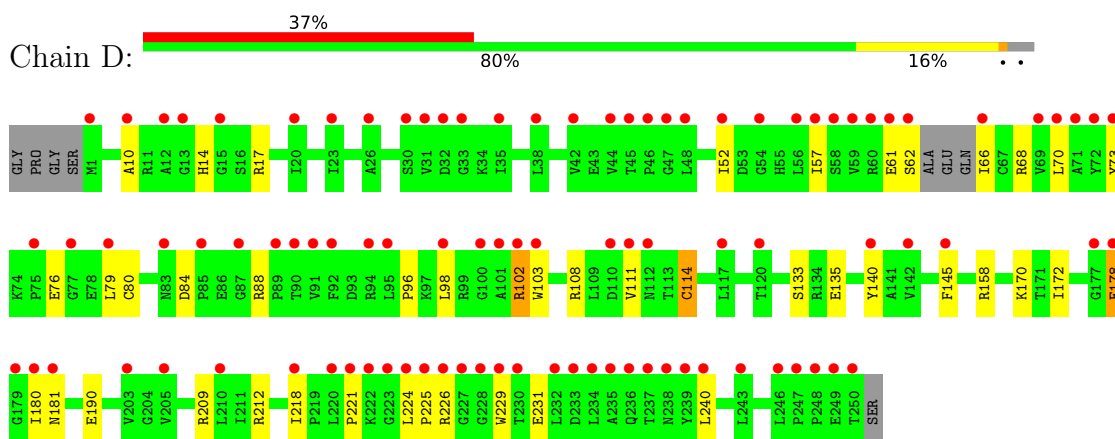
3 Residue-property plots [i](#)

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.

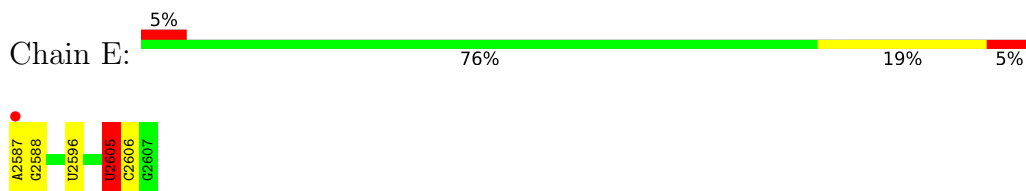
- Molecule 1: Ribosomal large subunit pseudouridine synthase B



- Molecule 1: Ribosomal large subunit pseudouridine synthase B

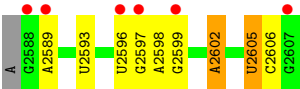


- Molecule 2: stem-loop of 23S rRNA



- Molecule 2: stem-loop of 23S rRNA





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	80.94Å 42.20Å 169.43Å 90.00° 102.61° 90.00°	Depositor
Resolution (Å)	40.46 – 1.30 40.46 – 1.30	Depositor EDS
% Data completeness (in resolution range)	92.0 (40.46-1.30) 92.0 (40.46-1.30)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.30Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069), ELVES	Depositor
R, R_{free}	0.173 , 0.203 0.174 , 0.203	Depositor DCC
R_{free} test set	1991 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	10.2	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9941	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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 38.31 % 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 3.7598e-04. 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: OCS, FHU

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	0.63	0/2041	0.80	0/2757
1	D	0.46	0/1986	0.77	2/2686 (0.1%)
2	E	0.59	0/485	0.78	0/755
2	F	0.37	0/460	0.62	0/716
All	All	0.54	0/4972	0.77	2/6914 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	178	GLU	N-CA-C	-6.82	100.65	108.49
1	D	172	ILE	CB-CA-C	-5.12	102.90	111.29

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	2012	2036	2036	41	0
1	D	1960	1970	1965	63	0
2	E	454	228	227	3	2
2	F	433	218	218	9	0
3	A	347	0	0	7	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	109	0	0	5	0
3	E	134	0	0	2	0
3	F	40	0	0	2	0
All	All	5489	4452	4446	93	2

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.

The worst 5 of 93 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:170:LYS:HG3	1:D:170:LYS:HG3	1.51	0.92
1:D:158[B]:ARG:NH2	3:D:327:HOH:O	2.04	0.88
1:A:170:LYS:CE	1:D:170:LYS:HE2	2.08	0.83
1:A:170:LYS:HE2	1:D:170:LYS:CE	2.13	0.78
1:A:158[A]:ARG:NH2	3:A:447:HOH:O	2.17	0.78

All (2) 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)
2:E:2587:A:OP1	3:A:439:HOH:O[4_556]	2.09	0.11
2:E:2587:A:H61	3:A:515:HOH:O[1_565]	1.56	0.04

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	253/255 (99%)	251 (99%)	1 (0%)	1 (0%)	30 9
1	D	246/255 (96%)	241 (98%)	5 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	499/510 (98%)	492 (99%)	6 (1%)	1 (0%)	43 17

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	ILE

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	212/212 (100%)	209 (99%)	3 (1%)	59 24
1	D	204/212 (96%)	203 (100%)	1 (0%)	81 60
All	All	416/424 (98%)	412 (99%)	4 (1%)	68 37

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	LYS
1	A	180	ILE
1	A	226	ARG
1	D	102	ARG

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	193	ASN
1	D	14	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	20/21 (95%)	4 (20%)	0
2	F	19/21 (90%)	6 (31%)	0
All	All	39/42 (92%)	10 (25%)	0

5 of 10 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	2588	G
2	E	2596	U
2	E	2605	FHU
2	E	2606	C
2	F	2589	A

There are no RNA pucker outliers to report.

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

6 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	OCS	D	114[B]	1	6,8,9	0.83	0	7,11,13	1.32	0
2	FHU	F	2605	2	16,23,24	1.27	2 (12%)	18,35,38	1.81	6 (33%)
1	OCS	A	114[B]	1	6,8,9	1.48	1 (16%)	7,11,13	2.58	2 (28%)
2	FHU	E	2605	1,2	17,22,24	1.54	2 (11%)	18,33,38	1.24	3 (16%)
1	OCS	D	114[A]	1	6,8,9	0.87	0	7,11,13	1.61	1 (14%)
1	OCS	A	114[A]	1	6,8,9	1.24	0	7,11,13	1.60	1 (14%)

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
1	OCS	D	114[B]	1	-	0/4/7/9	-
2	FHU	F	2605	2	-	0/3/47/48	0/2/2/2
1	OCS	A	114[B]	1	-	0/4/7/9	-
2	FHU	E	2605	1,2	-	0/5/43/48	0/2/2/2
1	OCS	D	114[A]	1	-	4/4/7/9	-
1	OCS	A	114[A]	1	-	0/4/7/9	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2605	FHU	F5-C5	-4.88	1.33	1.40
2	F	2605	FHU	F5-C5	-3.62	1.33	1.39
1	A	114[B]	OCS	CB-CA	3.05	1.55	1.53
2	E	2605	FHU	C4-N3	-2.52	1.33	1.37
2	F	2605	FHU	O4'-C1'	-2.16	1.41	1.44

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114[B]	OCS	CA-CB-SG	5.18	121.31	113.61
2	F	2605	FHU	N3-C2-N1	3.75	119.82	116.06
1	A	114[B]	OCS	OD1-SG-CB	3.58	112.09	106.76
2	F	2605	FHU	C5-C6-N1	-3.21	107.24	111.64
1	A	114[A]	OCS	OD2-SG-CB	2.99	111.74	105.97

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	114[A]	OCS	N-CA-CB-SG
1	D	114[A]	OCS	CA-CB-SG-OD1
1	D	114[A]	OCS	CA-CB-SG-OD2
1	D	114[A]	OCS	CA-CB-SG-OD3

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	114[B]	OCS	2	0
2	F	2605	FHU	3	0
1	A	114[B]	OCS	1	0
2	E	2605	FHU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 [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	250/255 (98%)	-0.06	13 (5%) 33 37	7, 17, 41, 65	5 (2%)
1	D	246/255 (96%)	1.75	95 (38%) 1 0	12, 43, 72, 79	4 (1%)
2	E	20/21 (95%)	-0.56	1 (5%) 34 39	7, 12, 22, 55	0
2	F	19/21 (90%)	1.64	6 (31%) 1 1	23, 36, 59, 67	0
All	All	535/552 (96%)	0.82	115 (21%) 2 2	7, 27, 65, 79	9 (1%)

The worst 5 of 115 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	229[A]	TRP	6.4
1	D	66	ILE	6.0
1	A	145	PHE	5.9
1	D	228	GLY	5.9
1	D	79	LEU	5.7

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	OCS	D	114[A]	9/10	0.86	0.14	35,43,52,52	14
1	OCS	D	114[B]	9/10	0.86	0.14	34,43,51,54	14
2	FHU	F	2605	22/23	0.94	0.10	24,31,43,47	0
1	OCS	A	114[B]	9/10	0.95	0.08	12,17,20,21	14
1	OCS	A	114[A]	9/10	0.95	0.08	14,19,23,23	14
2	FHU	E	2605	21/23	0.98	0.05	11,15,18,20	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.