



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 26, 2023 – 10:46 PM EDT

PDB ID : 3FG3
Title : Crystal structure of Delta413-417:GS I805W LOX
Authors : Neau, D.B.; Newcomer, M.E.
Deposited on : 2008-12-04
Resolution : 1.90 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

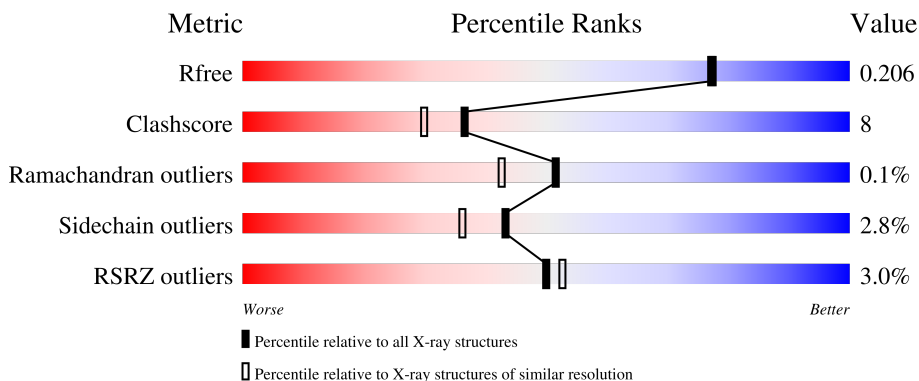
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	696	 83% 14% ..
1	B	696	 83% 14% ..
1	C	696	 84% 12% ..
1	D	696	 85% 11% ..

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
4	ACY	A	2200[B]	-	-	X	-
4	ACY	A	2201	-	-	X	-
4	ACY	A	2204	-	-	X	-
4	ACY	A	2222	-	-	X	-
4	ACY	C	2209[A]	-	-	X	-
4	ACY	C	2210	-	-	X	-
4	ACY	C	2213	-	-	X	-
4	ACY	D	2219	-	-	X	-
5	GOL	A	2303	-	-	X	-
5	GOL	A	2306	-	-	X	-
5	GOL	B	2310	-	X	X	-
5	GOL	C	2315	-	-	X	-
5	GOL	C	2321	-	-	X	-
5	GOL	C	2322	-	X	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 25025 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 Allene oxide synthase-lipoxygenase protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	687	Total 5624	C 3596	N 943	O 1071	S 14	0	25	0
1	B	682	Total 5552	C 3554	N 928	O 1056	S 14	0	23	0
1	C	686	Total 5576	C 3565	N 938	O 1060	S 13	3	21	0
1	D	681	Total 5538	C 3549	N 926	O 1049	S 14	0	22	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	368	MET	-	expression tag	UNP O16025
A	369	HIS	-	expression tag	UNP O16025
A	370	HIS	-	expression tag	UNP O16025
A	371	HIS	-	expression tag	UNP O16025
A	372	HIS	-	expression tag	UNP O16025
A	373	HIS	-	expression tag	UNP O16025
A	?	-	TRP	deletion	UNP O16025
A	?	-	PHE	deletion	UNP O16025
A	?	-	HIS	deletion	UNP O16025
A	413	GLY	ASN	engineered mutation	UNP O16025
A	414	SER	ASP	engineered mutation	UNP O16025
A	782	ILE	VAL	SEE REMARK 999	UNP O16025
A	805	TRP	ILE	engineered mutation	UNP O16025
A	963	ILE	VAL	SEE REMARK 999	UNP O16025
B	368	MET	-	expression tag	UNP O16025
B	369	HIS	-	expression tag	UNP O16025
B	370	HIS	-	expression tag	UNP O16025
B	371	HIS	-	expression tag	UNP O16025
B	372	HIS	-	expression tag	UNP O16025
B	373	HIS	-	expression tag	UNP O16025
B	?	-	TRP	deletion	UNP O16025

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PHE	deletion	UNP O16025
B	?	-	HIS	deletion	UNP O16025
B	413	GLY	ASN	engineered mutation	UNP O16025
B	414	SER	ASP	engineered mutation	UNP O16025
B	782	ILE	VAL	SEE REMARK 999	UNP O16025
B	805	TRP	ILE	engineered mutation	UNP O16025
B	963	ILE	VAL	SEE REMARK 999	UNP O16025
C	368	MET	-	expression tag	UNP O16025
C	369	HIS	-	expression tag	UNP O16025
C	370	HIS	-	expression tag	UNP O16025
C	371	HIS	-	expression tag	UNP O16025
C	372	HIS	-	expression tag	UNP O16025
C	373	HIS	-	expression tag	UNP O16025
C	?	-	TRP	deletion	UNP O16025
C	?	-	PHE	deletion	UNP O16025
C	?	-	HIS	deletion	UNP O16025
C	413	GLY	ASN	engineered mutation	UNP O16025
C	414	SER	ASP	engineered mutation	UNP O16025
C	782	ILE	VAL	SEE REMARK 999	UNP O16025
C	805	TRP	ILE	engineered mutation	UNP O16025
C	963	ILE	VAL	SEE REMARK 999	UNP O16025
D	368	MET	-	expression tag	UNP O16025
D	369	HIS	-	expression tag	UNP O16025
D	370	HIS	-	expression tag	UNP O16025
D	371	HIS	-	expression tag	UNP O16025
D	372	HIS	-	expression tag	UNP O16025
D	373	HIS	-	expression tag	UNP O16025
D	?	-	TRP	deletion	UNP O16025
D	?	-	PHE	deletion	UNP O16025
D	?	-	HIS	deletion	UNP O16025
D	413	GLY	ASN	engineered mutation	UNP O16025
D	414	SER	ASP	engineered mutation	UNP O16025
D	782	ILE	VAL	SEE REMARK 999	UNP O16025
D	805	TRP	ILE	engineered mutation	UNP O16025
D	963	ILE	VAL	SEE REMARK 999	UNP O16025

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0
2	B	1	Total Fe 1 1	0	0

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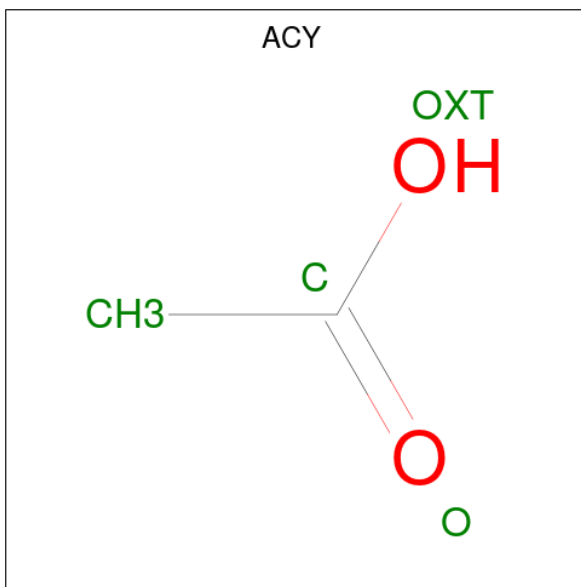
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Ca 3 3	0	0
3	B	1	Total Ca 1 1	0	0
3	C	3	Total Ca 3 3	0	0
3	D	1	Total Ca 1 1	0	0

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 8 4 4	0	1
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 8 4 4	0	1
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 12 6 6	0	1
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	D	1	Total C O 6 3 3	0	0
5	D	1	Total C O 6 3 3	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total Cl 2 2	0	0
6	B	1	Total Cl 1 1	0	0
6	C	2	Total Cl 2 2	0	0
6	D	1	Total Cl 1 1	0	0

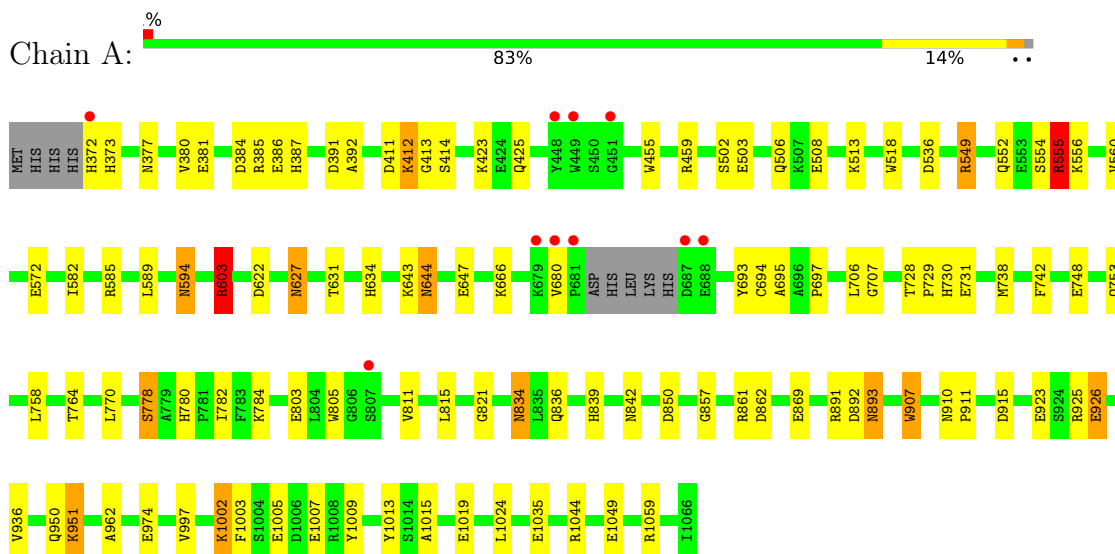
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	748	Total O 748 748	0	0
7	B	526	Total O 526 526	0	0
7	C	672	Total O 672 672	0	0
7	D	539	Total O 539 539	0	0

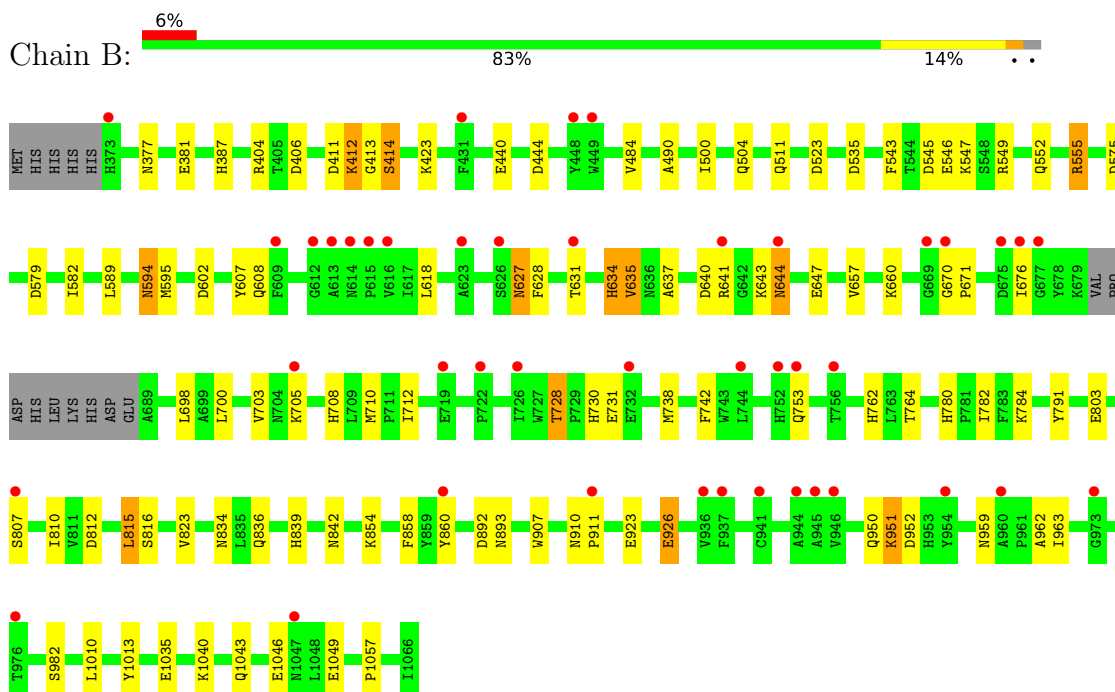
3 Residue-property plots [i](#)

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.

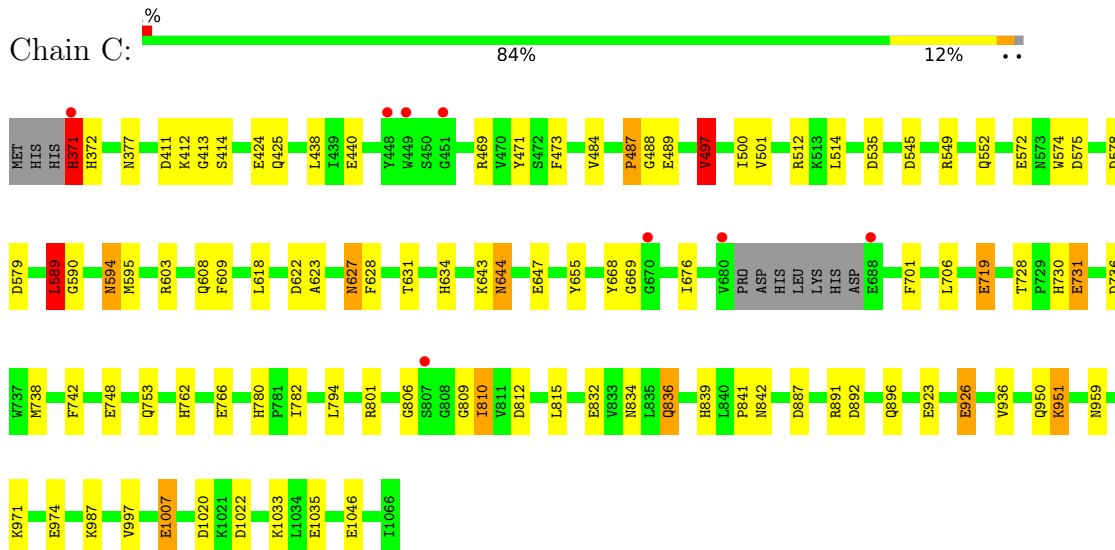
- Molecule 1: Allene oxide synthase-lipoxygenase protein



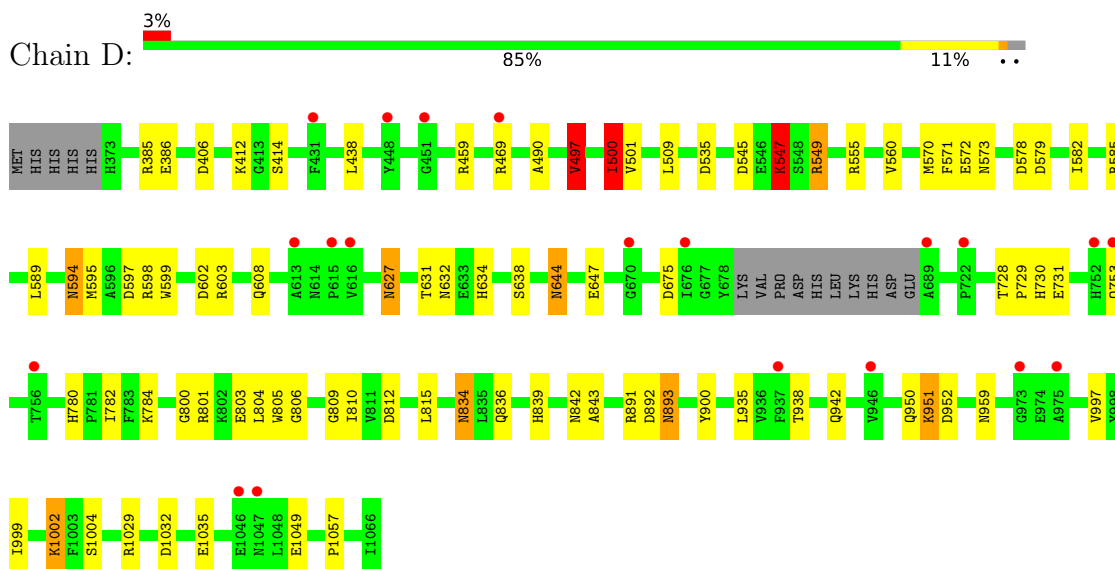
- Molecule 1: Allene oxide synthase-lipoxygenase protein



- Molecule 1: Allene oxide synthase-lipoxygenase protein



- Molecule 1: Allene oxide synthase-lipoxygenase protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.70Å 170.21Å 104.20Å 90.00° 96.13° 90.00°	Depositor
Resolution (Å)	34.54 – 1.90 34.03 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.4 (34.54-1.90) 98.4 (34.03-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 1.89Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.162 , 0.206 0.162 , 0.206	Depositor DCC
R_{free} test set	14029 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtrriage
Anisotropy	0.177	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.098 for l,-k,h	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	25025	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.88% 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: GOL, FE2, CL, CA, ACY

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	1.21	11/5851 (0.2%)	1.00	17/7955 (0.2%)
1	B	1.10	7/5773 (0.1%)	0.91	13/7856 (0.2%)
1	C	1.23	14/5791 (0.2%)	0.98	13/7878 (0.2%)
1	D	1.13	7/5754 (0.1%)	0.97	14/7827 (0.2%)
All	All	1.17	39/23169 (0.2%)	0.97	57/31516 (0.2%)

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	2
1	B	0	1
1	C	0	3
All	All	0	6

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	923[A]	GLU	CG-CD	-11.76	1.34	1.51
1	C	923[B]	GLU	CG-CD	-11.76	1.34	1.51
1	C	414	SER	C-N	7.92	1.52	1.34
1	B	414	SER	C-N	7.04	1.50	1.34
1	C	623	ALA	CA-CB	6.66	1.66	1.52

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	549	ARG	NE-CZ-NH2	-16.30	112.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	549	ARG	NE-CZ-NH1	12.25	126.42	120.30
1	B	549	ARG	NE-CZ-NH2	-11.57	114.52	120.30
1	D	585	ARG	NE-CZ-NH1	-10.28	115.16	120.30
1	A	549	ARG	NE-CZ-NH2	-8.50	116.05	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	414[A]	SER	Mainchain
1	A	680	VAL	Peptide
1	B	414	SER	Mainchain
1	C	371	HIS	Peptide
1	C	589	LEU	Peptide

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	5624	0	5393	107	0
1	B	5552	0	5281	79	0
1	C	5576	0	5311	84	1
1	D	5538	0	5281	68	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
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	C	3	0	0	0	0
3	D	1	0	0	0	0
4	A	36	0	27	11	0
4	B	16	0	12	2	0
4	C	28	0	21	9	0
4	D	20	0	15	4	0
5	A	60	0	78	17	0
5	B	24	0	32	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	36	0	48	20	0
5	D	12	0	16	3	0
6	A	2	0	0	0	0
6	B	1	0	0	0	0
6	C	2	0	0	1	0
6	D	1	0	0	0	0
7	A	748	0	0	29	0
7	B	526	0	0	16	1
7	C	672	0	0	26	0
7	D	539	0	0	9	0
All	All	25025	0	21515	349	1

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 8.

The worst 5 of 349 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:B:1035:GLU:OE2	5:B:2310:GOL:H31	1.25	1.25
1:A:459:ARG:NH2	7:A:2081:HOH:O	1.69	1.25
1:D:1002:LYS:HE2	7:D:1225:HOH:O	1.31	1.23
1:C:832:GLU:HG3	7:C:2400:HOH:O	1.40	1.21
1:C:489:GLU:CB	1:C:1020[B]:ASP:OD2	1.89	1.19

All (1) 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)
1:C:622:ASP:OD2	7:B:1106:HOH:O[1_556]	1.91	0.29

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	708/696 (102%)	684 (97%)	24 (3%)	0	100	100
1	B	700/696 (101%)	676 (97%)	22 (3%)	2 (0%)	41	31
1	C	703/696 (101%)	675 (96%)	26 (4%)	2 (0%)	41	31
1	D	699/696 (100%)	676 (97%)	23 (3%)	0	100	100
All	All	2810/2784 (101%)	2711 (96%)	95 (3%)	4 (0%)	51	42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	634	HIS
1	B	762	HIS
1	C	762	HIS
1	C	487	PRO

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	605/602 (100%)	589 (97%)	16 (3%)	46	39
1	B	590/602 (98%)	565 (96%)	25 (4%)	30	20
1	C	593/602 (98%)	578 (98%)	15 (2%)	47	41
1	D	585/602 (97%)	569 (97%)	16 (3%)	44	38
All	All	2373/2408 (98%)	2301 (97%)	72 (3%)	43	33

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	412	LYS
1	D	1057	PRO
1	D	500	ILE
1	D	644	ASN
1	B	635	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74

such sidechains are listed below:

Mol	Chain	Res	Type
1	D	594	ASN
1	D	959	ASN
1	D	627	ASN
1	D	834	ASN
1	B	627	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 65 ligands modelled in this entry, 18 are monoatomic - leaving 47 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	$\# Z > 2$
5	GOL	A	2304	-	5,5,5	0.97	0	5,5,5	1.47	2 (40%)
5	GOL	C	2321	-	5,5,5	0.90	0	5,5,5	1.36	1 (20%)
4	ACY	C	2213	-	3,3,3	0.69	0	3,3,3	1.91	1 (33%)
4	ACY	C	2209[A]	-	3,3,3	0.62	0	3,3,3	2.29	2 (66%)
5	GOL	C	2315	-	5,5,5	0.77	0	5,5,5	0.58	0
5	GOL	C	2322	-	5,5,5	0.91	0	5,5,5	3.05	2 (40%)
4	ACY	C	2210	-	3,3,3	0.91	0	3,3,3	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	A	2301	-	5,5,5	0.70	0	5,5,5	0.87	0
4	ACY	A	2201	-	3,3,3	0.72	0	3,3,3	1.24	0
4	ACY	D	2217	-	3,3,3	0.88	0	3,3,3	0.80	0
5	GOL	A	2320[A]	-	5,5,5	0.52	0	5,5,5	1.00	0
5	GOL	B	2309	-	5,5,5	0.53	0	5,5,5	0.25	0
4	ACY	A	2218	-	3,3,3	0.93	0	3,3,3	0.47	0
4	ACY	B	2208	-	3,3,3	0.86	0	3,3,3	0.46	0
4	ACY	A	2200[B]	-	3,3,3	0.92	0	3,3,3	0.97	0
4	ACY	B	2205	-	3,3,3	0.72	0	3,3,3	1.17	0
5	GOL	C	2313	-	5,5,5	0.84	0	5,5,5	1.34	1 (20%)
4	ACY	D	2216	-	3,3,3	0.83	0	3,3,3	1.01	0
4	ACY	C	2212	-	3,3,3	0.56	0	3,3,3	1.55	1 (33%)
5	GOL	B	2311	-	5,5,5	0.53	0	5,5,5	1.44	1 (20%)
4	ACY	C	2221	-	3,3,3	0.76	0	3,3,3	0.89	0
5	GOL	B	2310	-	5,5,5	0.75	0	5,5,5	2.88	2 (40%)
4	ACY	C	2211	-	3,3,3	0.65	0	3,3,3	1.49	0
4	ACY	D	2214	-	3,3,3	0.97	0	3,3,3	0.49	0
4	ACY	A	2202	-	3,3,3	1.01	0	3,3,3	2.96	2 (66%)
4	ACY	A	2204	-	3,3,3	0.60	0	3,3,3	1.64	1 (33%)
4	ACY	A	2222	-	3,3,3	0.66	0	3,3,3	1.21	0
4	ACY	B	2206	-	3,3,3	0.65	0	3,3,3	1.76	1 (33%)
4	ACY	C	2209[B]	-	3,3,3	1.12	0	3,3,3	0.53	0
5	GOL	A	2305	-	5,5,5	0.36	0	5,5,5	1.97	1 (20%)
5	GOL	A	2308	-	5,5,5	0.42	0	5,5,5	0.44	0
5	GOL	A	2307	-	5,5,5	0.86	0	5,5,5	1.23	0
5	GOL	C	2314	-	5,5,5	0.38	0	5,5,5	0.64	0
5	GOL	A	2320[B]	-	5,5,5	0.57	0	5,5,5	1.12	0
4	ACY	D	2215	-	3,3,3	0.59	0	3,3,3	2.37	1 (33%)
5	GOL	C	2317	-	5,5,5	0.42	0	5,5,5	1.16	1 (20%)
4	ACY	A	2200[A]	-	3,3,3	0.67	0	3,3,3	1.43	0
5	GOL	A	2302	-	5,5,5	0.54	0	5,5,5	0.62	0
4	ACY	A	2220	-	3,3,3	0.99	0	3,3,3	1.03	0
5	GOL	A	2306	-	5,5,5	0.34	0	5,5,5	1.90	2 (40%)
4	ACY	B	2207	-	3,3,3	0.74	0	3,3,3	1.03	0
4	ACY	A	2203	-	3,3,3	0.51	0	3,3,3	1.38	0
5	GOL	D	2318	-	5,5,5	0.44	0	5,5,5	0.53	0
5	GOL	B	2312	-	5,5,5	0.46	0	5,5,5	0.89	0
4	ACY	D	2219	-	3,3,3	0.87	0	3,3,3	0.23	0
5	GOL	D	2319	-	5,5,5	1.05	0	5,5,5	1.16	0
5	GOL	A	2303	-	5,5,5	0.77	0	5,5,5	0.82	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
5	GOL	A	2304	-	-	2/4/4/4	-
5	GOL	C	2321	-	-	2/4/4/4	-
5	GOL	C	2315	-	-	2/4/4/4	-
5	GOL	C	2322	-	-	4/4/4/4	-
5	GOL	A	2301	-	-	0/4/4/4	-
5	GOL	A	2320[A]	-	-	3/4/4/4	-
5	GOL	B	2309	-	-	0/4/4/4	-
5	GOL	C	2313	-	-	0/4/4/4	-
5	GOL	B	2311	-	-	4/4/4/4	-
5	GOL	B	2310	-	-	4/4/4/4	-
5	GOL	A	2305	-	-	3/4/4/4	-
5	GOL	A	2308	-	-	0/4/4/4	-
5	GOL	A	2307	-	-	2/4/4/4	-
5	GOL	C	2314	-	-	0/4/4/4	-
5	GOL	A	2320[B]	-	-	4/4/4/4	-
5	GOL	C	2317	-	-	2/4/4/4	-
5	GOL	A	2302	-	-	0/4/4/4	-
5	GOL	A	2306	-	-	2/4/4/4	-
5	GOL	D	2318	-	-	2/4/4/4	-
5	GOL	B	2312	-	-	4/4/4/4	-
5	GOL	D	2319	-	-	4/4/4/4	-
5	GOL	A	2303	-	-	0/4/4/4	-

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	2322	GOL	C3-C2-C1	-5.66	89.71	111.70
5	B	2310	GOL	O3-C3-C2	-4.43	88.94	110.20
5	B	2310	GOL	O2-C2-C1	3.95	126.53	109.12
4	A	2202	ACY	O-C-CH3	-3.94	106.98	122.33
5	A	2305	GOL	O1-C1-C2	-3.83	91.85	110.20

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2305	GOL	O1-C1-C2-C3
5	A	2306	GOL	O1-C1-C2-C3
5	A	2306	GOL	O2-C2-C3-O3
5	A	2307	GOL	C1-C2-C3-O3
5	A	2320[A]	GOL	O1-C1-C2-O2

There are no ring outliers.

25 monomers are involved in 74 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2304	GOL	1	0
5	C	2321	GOL	5	0
4	C	2213	ACY	2	0
4	C	2209[A]	ACY	3	0
5	C	2315	GOL	7	0
5	C	2322	GOL	8	0
4	C	2210	ACY	4	0
4	A	2201	ACY	3	0
5	A	2320[A]	GOL	2	0
4	B	2208	ACY	1	0
4	A	2200[B]	ACY	2	0
4	B	2205	ACY	1	0
5	B	2311	GOL	2	0
5	B	2310	GOL	9	0
4	D	2214	ACY	1	0
4	A	2202	ACY	1	0
4	A	2204	ACY	3	0
4	A	2222	ACY	2	0
5	A	2305	GOL	2	0
5	A	2320[B]	GOL	2	0
4	D	2215	ACY	1	0
5	A	2306	GOL	6	0
4	D	2219	ACY	2	0
5	D	2319	GOL	3	0
5	A	2303	GOL	4	0

5.7 Other polymers [i](#)

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	687/696 (98%)	-0.40	10 (1%) 73 76	14, 22, 36, 71	5 (0%)
1	B	682/696 (97%)	0.02	43 (6%) 20 22	18, 29, 52, 67	7 (1%)
1	C	686/696 (98%)	-0.39	8 (1%) 79 81	15, 23, 37, 58	13 (1%)
1	D	681/696 (97%)	-0.10	20 (2%) 51 54	17, 27, 44, 52	6 (0%)
All	All	2736/2784 (98%)	-0.22	81 (2%) 50 53	14, 25, 45, 71	31 (1%)

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	680	VAL	9.8
1	A	681	PRO	6.1
1	D	676	ILE	4.9
1	B	676	ILE	4.9
1	C	449	TRP	4.9

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(\AA^2)	Q<0.9
4	ACY	D	2219	4/4	0.79	0.18	43,44,46,48	0
4	ACY	C	2210	4/4	0.81	0.14	45,46,46,46	0
4	ACY	C	2221	4/4	0.85	0.14	41,43,44,44	0
4	ACY	A	2220	4/4	0.85	0.15	37,40,41,43	0
5	GOL	C	2321	6/6	0.85	0.14	24,40,43,50	0
4	ACY	D	2215	4/4	0.87	0.23	40,42,44,44	0
4	ACY	A	2218	4/4	0.88	0.15	40,41,41,42	0
5	GOL	A	2307	6/6	0.88	0.18	39,49,49,51	0
5	GOL	B	2310	6/6	0.88	0.21	30,38,42,44	0
4	ACY	A	2202	4/4	0.88	0.18	36,38,41,41	0
4	ACY	C	2213	4/4	0.89	0.20	39,40,42,43	0
4	ACY	A	2201	4/4	0.90	0.12	47,47,48,50	0
4	ACY	C	2212	4/4	0.90	0.13	38,39,40,40	0
5	GOL	B	2311	6/6	0.90	0.14	28,46,50,53	0
4	ACY	B	2208	4/4	0.90	0.13	53,53,54,54	0
5	GOL	C	2322	6/6	0.90	0.16	12,36,37,38	0
5	GOL	D	2319	6/6	0.90	0.13	30,38,41,41	0
6	CL	A	2402	1/1	0.90	0.08	44,44,44,44	0
4	ACY	A	2203	4/4	0.91	0.13	44,44,45,45	0
5	GOL	A	2308	6/6	0.91	0.14	47,51,52,53	0
5	GOL	A	2320[A]	6/6	0.91	0.15	15,23,27,30	6
5	GOL	A	2320[B]	6/6	0.91	0.15	25,30,31,34	6
4	ACY	A	2222	4/4	0.91	0.12	50,53,53,53	0
4	ACY	B	2207	4/4	0.92	0.12	40,43,43,43	0
5	GOL	C	2315	6/6	0.92	0.09	24,34,37,43	0
5	GOL	A	2303	6/6	0.92	0.16	28,41,41,46	0
4	ACY	D	2217	4/4	0.92	0.14	50,51,51,52	0
5	GOL	C	2313	6/6	0.93	0.10	26,30,37,39	0
5	GOL	C	2317	6/6	0.93	0.15	31,37,38,41	0
4	ACY	D	2214	4/4	0.93	0.26	34,36,37,39	0
4	ACY	A	2204	4/4	0.93	0.10	49,50,50,50	0
5	GOL	A	2305	6/6	0.93	0.12	20,36,40,41	0
5	GOL	A	2306	6/6	0.93	0.12	24,36,39,49	0
4	ACY	B	2206	4/4	0.93	0.15	45,49,49,50	0
4	ACY	C	2211	4/4	0.94	0.12	45,47,48,48	0
5	GOL	A	2304	6/6	0.94	0.14	24,33,38,43	0
5	GOL	B	2312	6/6	0.94	0.10	39,45,47,47	0
5	GOL	D	2318	6/6	0.94	0.11	29,30,31,34	0
4	ACY	D	2216	4/4	0.94	0.12	44,46,46,46	0
5	GOL	A	2301	6/6	0.94	0.08	26,34,36,39	0
4	ACY	B	2205	4/4	0.95	0.31	39,39,40,41	0
5	GOL	B	2309	6/6	0.96	0.11	29,31,35,35	0
5	GOL	C	2314	6/6	0.97	0.11	27,29,30,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ACY	C	2209[A]	4/4	0.97	0.20	16,16,16,18	4
5	GOL	A	2302	6/6	0.97	0.08	25,30,35,35	0
4	ACY	C	2209[B]	4/4	0.97	0.20	18,20,20,21	4
4	ACY	A	2200[A]	4/4	0.98	0.17	17,17,17,20	4
4	ACY	A	2200[B]	4/4	0.98	0.17	18,18,19,21	4
6	CL	C	2402	1/1	0.98	0.04	38,38,38,38	0
3	CA	C	1502	1/1	0.99	0.06	21,21,21,21	0
3	CA	D	1501	1/1	0.99	0.03	23,23,23,23	0
6	CL	B	2401	1/1	0.99	0.08	28,28,28,28	0
6	CL	C	2401	1/1	0.99	0.04	23,23,23,23	0
2	FE2	B	1500	1/1	0.99	0.07	22,22,22,22	0
2	FE2	A	1500	1/1	1.00	0.07	17,17,17,17	0
3	CA	C	1067	1/1	1.00	0.06	23,23,23,23	0
2	FE2	C	1500	1/1	1.00	0.07	18,18,18,18	0
2	FE2	D	1500	1/1	1.00	0.09	20,20,20,20	0
3	CA	A	1501	1/1	1.00	0.05	23,23,23,23	0
6	CL	A	2401	1/1	1.00	0.06	26,26,26,26	0
3	CA	A	1502	1/1	1.00	0.06	21,21,21,21	0
3	CA	A	1067	1/1	1.00	0.07	22,22,22,22	0
3	CA	B	1501	1/1	1.00	0.04	23,23,23,23	0
3	CA	C	1501	1/1	1.00	0.03	24,24,24,24	0
6	CL	D	2401	1/1	1.00	0.07	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.