

wwPDB X-ray Structure Validation Summary Report (i)

Oct 12, 2021 – 10:04 am BST

PDB ID : 7AJ0

Title : Crystal structure of PsFucS1 sulfatase from Pseudoalteromonas sp.

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Deposited on : 2020-09-28

Resolution : 2.50 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467 Xtriage (Phenix): 1.13

EDS : 2.23.2 buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0267

 $\begin{array}{cccc} & CCP4 & : & 7.1.010 \; (Gargrove) \\ Ideal \; geometry \; (proteins) & : & Engh \; \& \; Huber \; (2001) \end{array}$

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

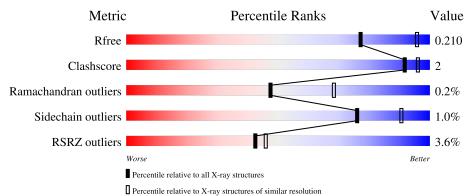
 $\begin{tabular}{lll} Validation Pipeline (wwPDB-VP) & : & 2.23.2 \end{tabular}$

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ range(\AA)}) \end{array}$
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	515	93%		_
			3%		_
1	В	515	93%	•	•
1	С	515	93%	٠	•
1	D	515	91%	6%	-
1	Е	515	94%		-

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Mol	Chain	Length	Quality of chain			
1	F	515	93%	•	-	-



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 48247 atoms, of which 23325 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 Arylsulfatase.

Mol	Chain	Residues			Atom	ıs			ZeroOcc	AltConf	Trace
1	A	501	Total	С	Н	N	О	S	0	0	0
1	Λ	301	7824	2505	3893	669	738	19	0	0	0
1	В	501	Total	С	Н	N	О	S	0	0	0
1	Ъ	301	7794	2499	3871	667	738	19	0	U	0
1	С	501	Total	С	Н	N	О	S	0	0	0
1		301	7824	2505	3893	669	738	19	U	U	U
1	D	501	Total	С	Η	N	О	S	0	0	0
1	D	501	7824	2505	3893	669	738	19	0	U	U
1	Е	501	Total	С	Η	N	Ο	S	0	0	0
1	ш	501	7824	2505	3893	669	738	19	U	U	U
1	F	501	Total	С	Н	N	О	S	0	0	0
1	I.	501	7809	2502	3882	668	738	19	0	U	U

• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	В	1	Total Ca 1 1	0	0
2	С	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0
2	F	1	Total Ca 1 1	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Cl 2 2	0	0
3	В	2	Total Cl 2 2	0	0
3	С	2	Total Cl 2 2	0	0
3	D	2	Total Cl 2 2	0	0
3	Е	2	Total Cl 2 2	0	0
3	F	2	Total Cl 2 2	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	240	Total O 240 240	0	0
4	В	220	Total O 220 220	0	0
4	С	212	Total O 212 212	0	0
4	D	246	Total O 246 246	0	0
4	E	187	Total O 187 187	0	0
4	F	225	Total O 225 225	0	0



3 Residue-property plots (i)

• Molecule 1: Arylsulfatase

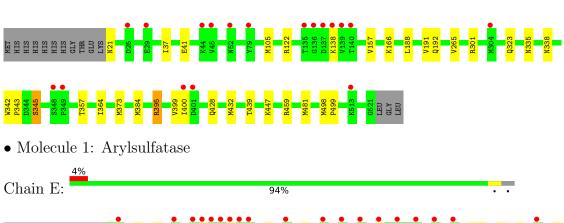
Chain D:

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: Arylsulfatase Chain A: • Molecule 1: Arylsulfatase Chain B: 93% • Molecule 1: Arylsulfatase Chain C:

91%

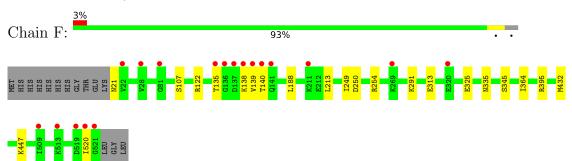








• Molecule 1: Arylsulfatase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	86.20Å 182.34Å 209.85Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.66 - 2.50	Depositor
Resolution (A)	46.66 - 2.50	EDS
% Data completeness	99.9 (46.66-2.50)	Depositor
(in resolution range)	99.9 (46.66-2.50)	EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.29 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
D D.	0.172 , 0.210	Depositor
R, R_{free}	0.172 , 0.210	DCC
R_{free} test set	5742 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	48247	wwPDB-VP
Average B, all atoms $(Å^2)$	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 15.00% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: CA, CL

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.26	0/4027	0.45	0/5460	
1	В	0.27	0/4019	0.47	$2/5452 \ (0.0\%)$	
1	С	0.27	0/4027	0.45	0/5460	
1	D	0.27	0/4027	0.46	0/5460	
1	Е	0.26	0/4027	0.44	0/5460	
1	F	0.26	0/4023	0.45	0/5456	
All	All	0.27	0/24150	0.45	$2/32748 \ (0.0\%)$	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	В	188	LEU	CB-CG-CD2	7.67	124.03	111.00
1	В	188	LEU	CA-CB-CG	5.55	128.07	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	3931	3893	3892	15	0
1	В	3923	3871	3870	12	0
1	С	3931	3893	3892	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3931	3893	3892	22	0
1	Ε	3931	3893	3892	9	0
1	F	3927	3882	3881	10	0
2	A	1	0	0	0	0
2	В	1	0	0	0	0
2	С	1	0	0	0	0
2	D	1	0	0	0	0
2	Е	1	0	0	0	0
2	F	1	0	0	0	0
3	A	2	0	0	0	0
3	В	2	0	0	0	0
3	С	2	0	0	0	0
3	D	2	0	0	0	0
3	Ε	2	0	0	0	0
3	F	2	0	0	0	0
4	A	240	0	0	1	0
4	В	220	0	0	2	0
4	С	212	0	0	1	0
4	D	246	0	0	4	0
4	Ε	187	0	0	2	0
4	F	225	0	0	3	0
All	All	24922	23325	23319	74	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 2.

The worst 5 of 74 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:D:21:ASN:N	4:D:701:HOH:O	2.07	0.87
1:D:373:MET:SD	4:D:936:HOH:O	2.32	0.86
1:A:94:LYS:NZ	1:A:98:GLU:OE2	2.15	0.78
1:B:454:ASN:OD1	4:B:701:HOH:O	2.11	0.68
1:A:421:ASP:O	4:A:701:HOH:O	2.12	0.66

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	Perce	ntiles
1	A	499/515~(97%)	483 (97%)	16 (3%)	0	100	100
1	В	499/515 (97%)	481 (96%)	15 (3%)	3 (1%)	25	43
1	С	499/515 (97%)	485 (97%)	14 (3%)	0	100	100
1	D	499/515 (97%)	475 (95%)	24 (5%)	0	100	100
1	E	499/515 (97%)	479 (96%)	19 (4%)	1 (0%)	47	68
1	F	499/515 (97%)	478 (96%)	20 (4%)	1 (0%)	47	68
All	All	2994/3090 (97%)	2881 (96%)	108 (4%)	5 (0%)	47	68

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	135	THR
1	В	138	LYS
1	F	138	LYS
1	В	136	GLY
1	Е	136	GLY

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	Perce	ntiles
1	A	421/433~(97%)	419 (100%)	2 (0%)	88	96
1	В	419/433~(97%)	415 (99%)	4 (1%)	76	90
1	С	421/433~(97%)	418 (99%)	3 (1%)	84	94

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	D	421/433 (97%)	416 (99%)	5 (1%)	71	88
1	E	421/433 (97%)	415 (99%)	6 (1%)	67	86
1	F	420/433 (97%)	414 (99%)	6 (1%)	67	86
All	All	2523/2598 (97%)	2497 (99%)	26 (1%)	76	90

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

Mol	Chain	Res	Type
1	Е	156	LYS
1	Е	325	GLU
1	F	345	SER
1	Е	282	ASN
1	Е	335	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	454	ASN
1	С	263	GLN
1	С	378	GLN
1	F	491	HIS

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 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (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, 95^{th} 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>	# RSRZ > 2	$OWAB(Å^2)$	Q < 0.9
1	A	501/515~(97%)	0.14	14 (2%) 53 56	21, 27, 38, 51	0
1	В	501/515~(97%)	0.18	18 (3%) 42 46	23, 29, 40, 52	0
1	С	501/515 (97%)	0.17	18 (3%) 42 46	22, 29, 41, 55	0
1	D	501/515~(97%)	0.16	18 (3%) 42 46	21, 27, 39, 48	0
1	Е	501/515 (97%)	0.15	22 (4%) 34 37	23, 29, 41, 50	0
1	F	501/515~(97%)	0.18	18 (3%) 42 46	23, 28, 39, 50	0
All	All	3006/3090 (97%)	0.16	108 (3%) 42 46	21, 28, 40, 55	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	LYS	5.2
1	В	140	THR	4.9
1	D	137	ASP	4.3
1	В	139	VAL	4.3
1	Ε	135	THR	4.2

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.



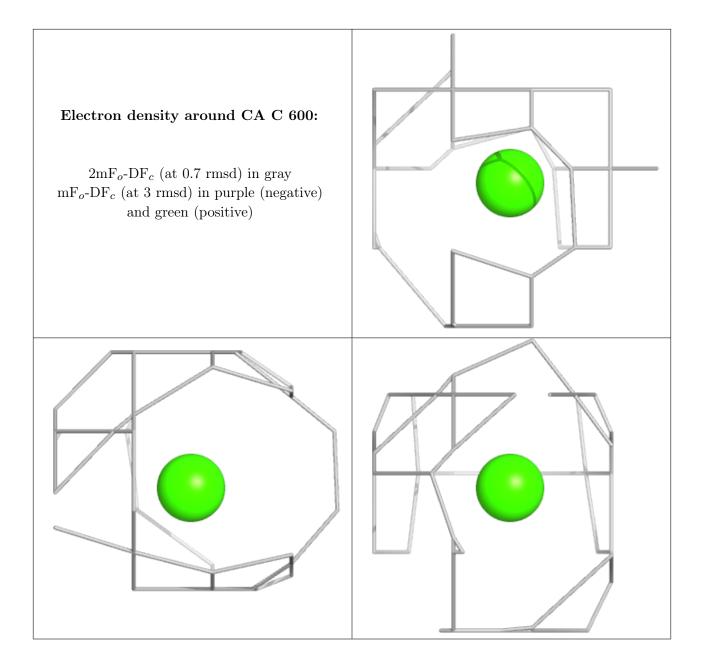
6.4 Ligands (i)

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, 95^{th} 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.

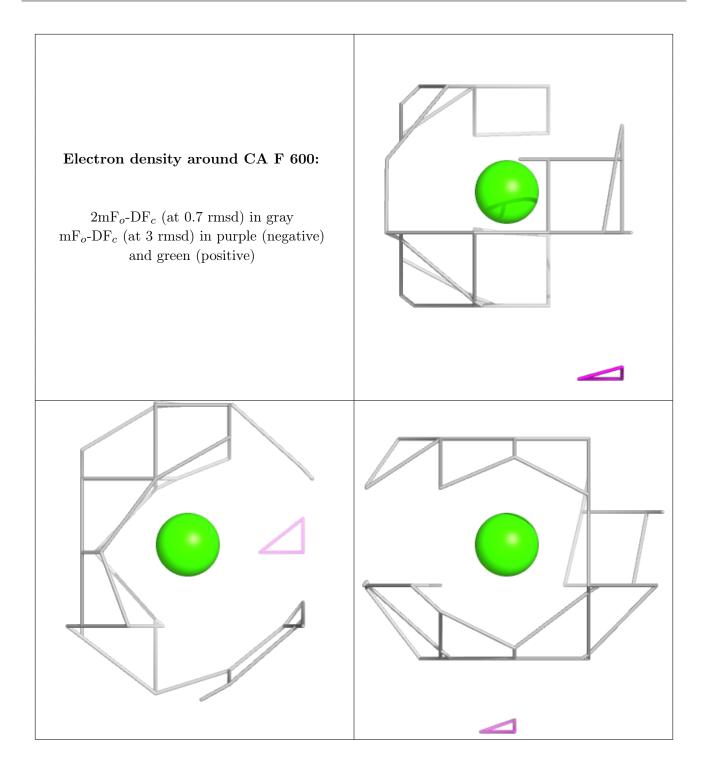
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathrm{\AA}^2)$	Q<0.9
3	CL	С	602	1/1	0.92	0.15	53,53,53,53	0
3	CL	A	602	1/1	0.93	0.09	35,35,35,35	0
3	CL	Е	602	1/1	0.94	0.10	43,43,43,43	0
3	CL	В	602	1/1	0.95	0.07	44,44,44	0
3	CL	С	601	1/1	0.96	0.07	26,26,26,26	0
3	CL	D	602	1/1	0.97	0.09	42,42,42,42	0
3	CL	F	602	1/1	0.97	0.10	44,44,44	0
3	CL	D	603	1/1	0.98	0.24	24,24,24,24	0
2	CA	С	600	1/1	0.98	0.06	31,31,31,31	0
3	CL	F	601	1/1	0.98	0.15	24,24,24,24	0
3	CL	В	601	1/1	0.98	0.11	25,25,25,25	0
2	CA	F	600	1/1	0.99	0.04	22,22,22,22	0
3	CL	A	601	1/1	0.99	0.13	26,26,26,26	0
2	CA	В	600	1/1	0.99	0.06	22,22,22,22	0
3	CL	Ε	601	1/1	0.99	0.15	28,28,28,28	0
2	CA	A	600	1/1	0.99	0.09	22,22,22,22	0
2	CA	D	601	1/1	0.99	0.08	22,22,22,22	0
2	CA	Ε	600	1/1	0.99	0.04	22,22,22,22	0

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

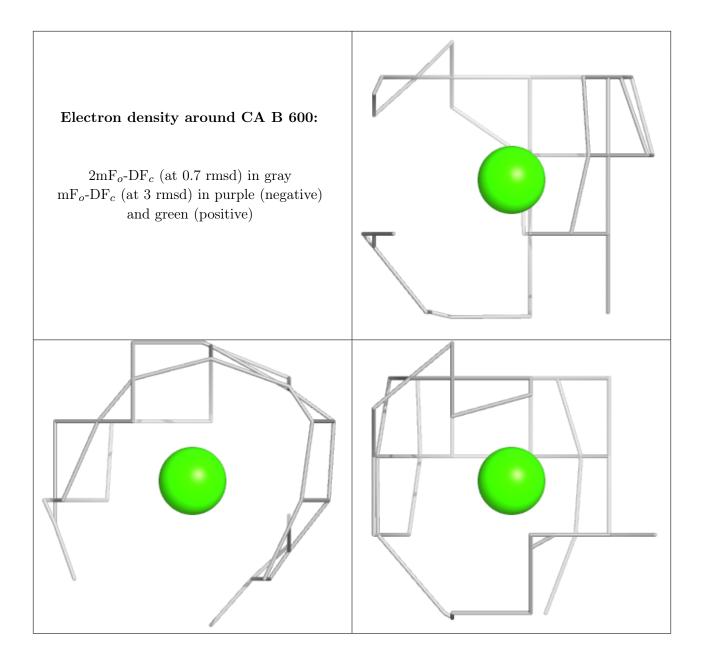




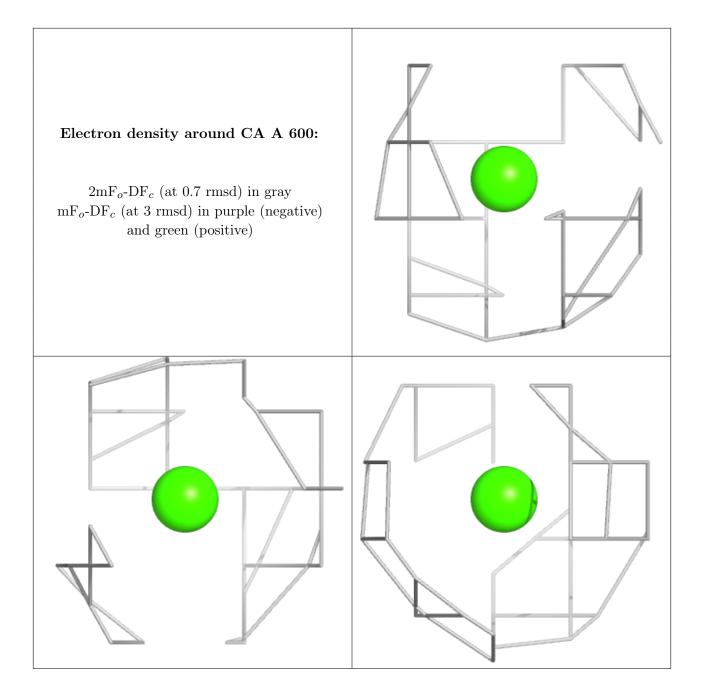




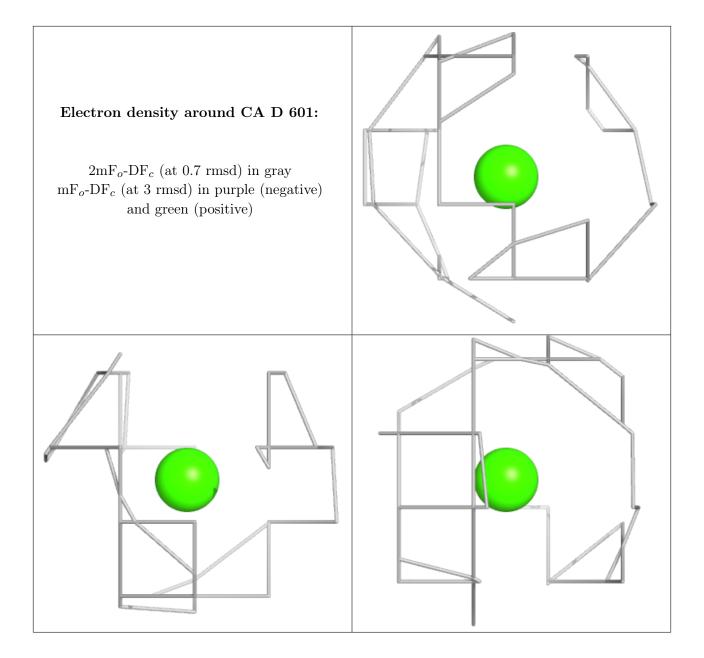




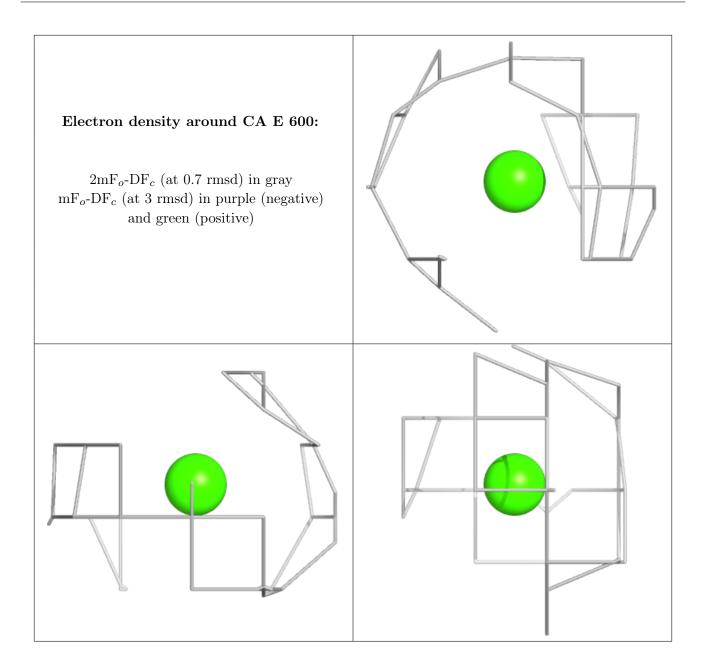












6.5 Other polymers (i)

There are no such residues in this entry.

