wwPDB X-ray Structure Validation Summary Report (i)

Aug 25, 2026 – 08:54 am BST

PDB ID	:	8A1H / pdb_00008a1h
Title	:	Bacterial 6-4 photolyase from Vibrio cholerase
Authors	:	Essen, L.-O.; Emmerich, H.J.
Deposited on	:	2022-06-01
Resolution	:	1.65 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

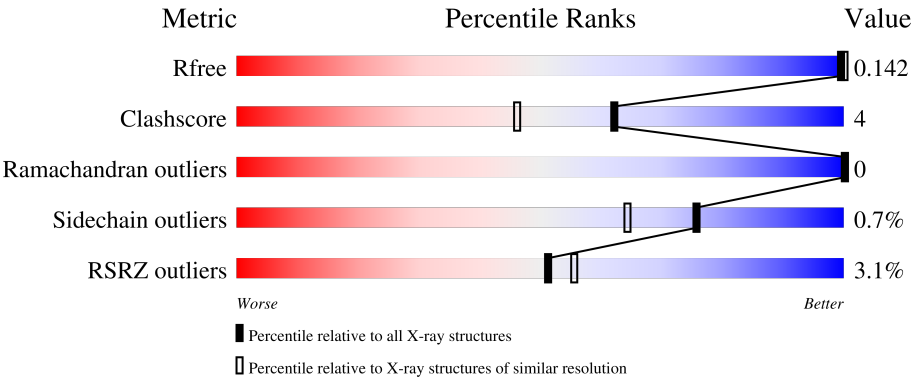
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	536	3% 90% 6% ·

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
6	GOL	A	612	-	X	-	-

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 9432 atoms, of which 4302 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.

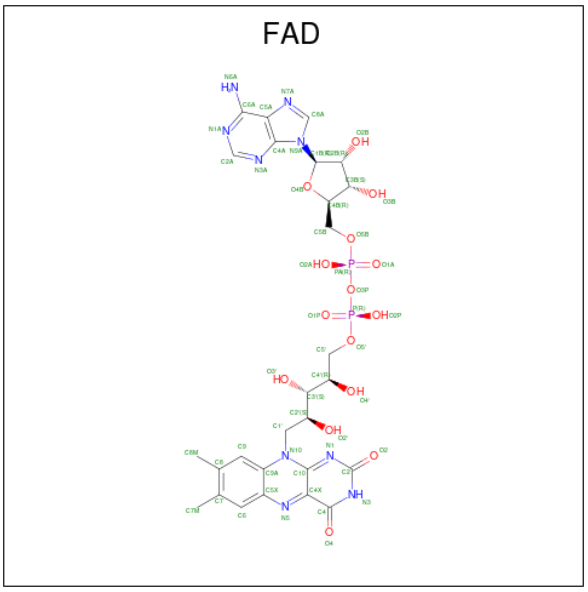
- Molecule 1 is a protein called 6-4 photolyase (FeS-BCP, CryPro).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	516	8468	2744	4173	757	766	28	0	22	0

There are 20 discrepancies between the modelled and reference sequences:

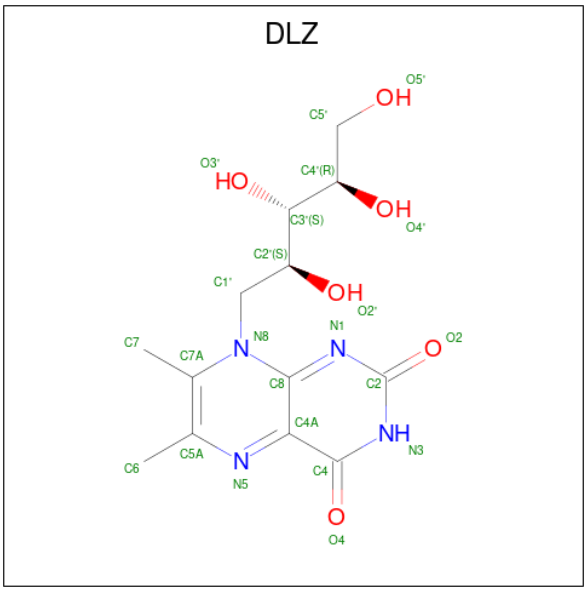
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q9KLD7
A	2	GLY	-	expression tag	UNP Q9KLD7
A	3	SER	-	expression tag	UNP Q9KLD7
A	4	SER	-	expression tag	UNP Q9KLD7
A	5	HIS	-	expression tag	UNP Q9KLD7
A	6	HIS	-	expression tag	UNP Q9KLD7
A	7	HIS	-	expression tag	UNP Q9KLD7
A	8	HIS	-	expression tag	UNP Q9KLD7
A	9	HIS	-	expression tag	UNP Q9KLD7
A	10	HIS	-	expression tag	UNP Q9KLD7
A	11	SER	-	expression tag	UNP Q9KLD7
A	12	SER	-	expression tag	UNP Q9KLD7
A	13	GLY	-	expression tag	UNP Q9KLD7
A	14	LEU	-	expression tag	UNP Q9KLD7
A	15	VAL	-	expression tag	UNP Q9KLD7
A	16	PRO	-	expression tag	UNP Q9KLD7
A	17	ARG	-	expression tag	UNP Q9KLD7
A	18	GLY	-	expression tag	UNP Q9KLD7
A	19	SER	-	expression tag	UNP Q9KLD7
A	20	HIS	-	expression tag	UNP Q9KLD7

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



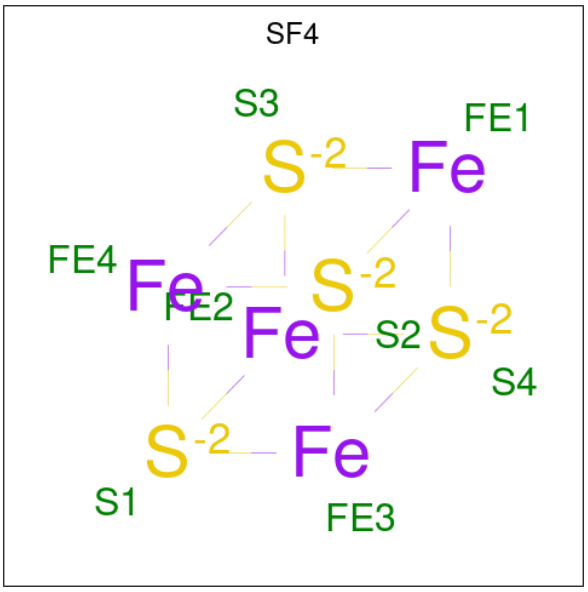
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		

- Molecule 3 is 1-deoxy-1-(6,7-dimethyl-2,4-dioxo-3,4-dihydropteridin-8(2H)-yl)-D-ribitol (CCD ID: DLZ) (formula: $C_{13}H_{18}N_4O_6$).



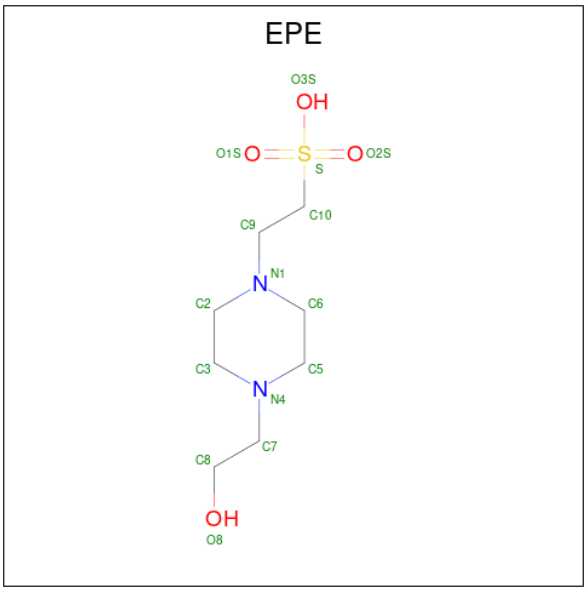
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			23	13	4	6		

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



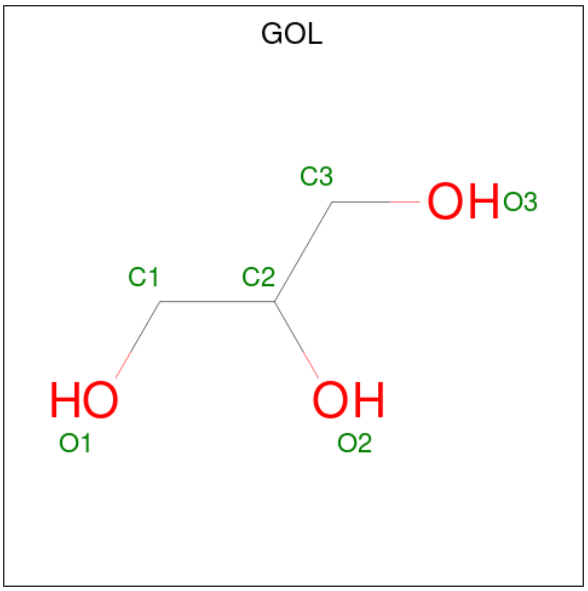
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe S 8 4 4	0	0

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



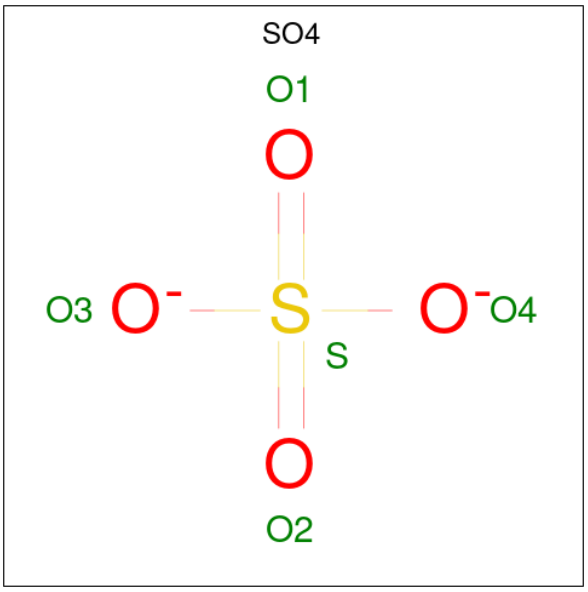
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H N O S 32 8 17 2 4 1	0	0

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C H O 9 3 3 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 13 3 7 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O S 5 4 1	0	0
7	A	1	Total O S 5 4 1	0	0
7	A	1	Total O S 5 4 1	0	0
7	A	1	Total O S 5 4 1	0	0
7	A	1	Total O S 5 4 1	0	0
7	A	1	Total O S 5 4 1	0	0
7	A	1	Total O S 5 4 1	0	0

- Molecule 8 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	6	Total Na 6 6	0	0

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total Cl 1 1	0	0

- Molecule 10 is water.

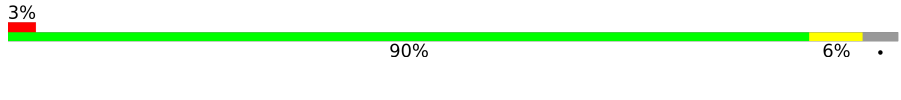
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	622	Total	O	0	6
			628	628		

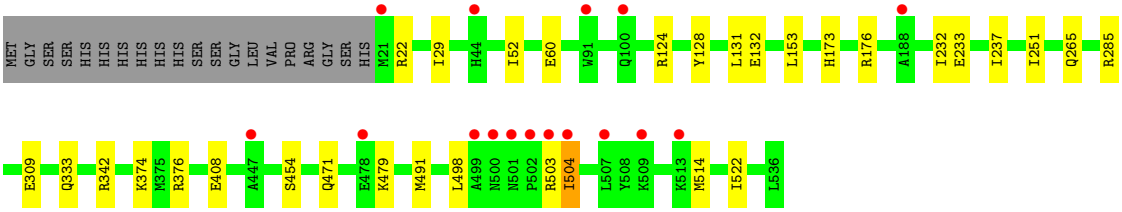
3 Residue-property plots (i)

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: 6-4 photolyase (FeS-BCP, CryPro)

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α, β, γ	199.69Å 199.69Å 77.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.59 – 1.65 34.59 – 1.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.59-1.65) 100.0 (34.59-1.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.32 (at 1.65Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.119 , 0.136 0.125 , 0.142	Depositor DCC
R_{free} test set	2158 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	19.9	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 61.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	9432	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, FAD, DLZ, GOL, SO4, CL, SF4, EPE

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	0.82	1/4481 (0.0%)	0.77	0/6076

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	309	GLU	CD-OE2	5.79	1.36	1.25

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	ARG	Sidechain
1	A	342	ARG	Sidechain

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	4295	4173	4198	29	0
2	A	53	30	31	1	0
3	A	23	0	18	0	0
4	A	8	0	0	0	0
5	A	15	17	17	4	0
6	A	66	82	84	9	1
7	A	35	0	0	1	0
8	A	6	0	0	0	0
9	A	1	0	0	1	0
10	A	628	0	0	17	5
All	All	5130	4302	4348	36	5

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 36 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)
6:A:611:GOL:O3	10:A:701:HOH:O	1.74	1.04
1:A:514:MET:HE1	1:A:522:ILE:CD1	2.04	0.87
1:A:514:MET:HE1	1:A:522:ILE:HD12	1.56	0.85
1:A:479:LYS:NZ	10:A:707:HOH:O	2.13	0.79
5:A:604:EPE:O2S	10:A:702:HOH:O	2.01	0.77

All (5) 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)
10:A:1142:HOH:O	10:A:1215:HOH:O[8_555]	1.84	0.36
10:A:717:HOH:O	10:A:1045:HOH:O[10_555]	1.99	0.21
10:A:1045:HOH:O	10:A:1265:HOH:O[10_555]	1.99	0.21
10:A:1117:HOH:O	10:A:1320:HOH:O[10_555]	2.05	0.15
6:A:611:GOL:O1	10:A:705:HOH:O[10_555]	2.17	0.03

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	536/536 (100%)	521 (97%)	15 (3%)	0	100 100

There are no Ramachandran outliers to report.

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	461/458 (101%)	458 (99%)	3 (1%)	76 64

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ARG
1	A	503	ARG
1	A	504	ILE

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

Mol	Chain	Res	Type
1	A	116	GLN
1	A	281	GLN
1	A	333	GLN
1	A	520	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 29 ligands modelled in this entry, 7 are monoatomic - leaving 22 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	GOL	A	613	-	5,5,5	2.44	3 (60%)	5,5,5	0.62	0
7	SO4	A	616	-	4,4,4	0.43	0	6,6,6	0.26	0
7	SO4	A	618	-	4,4,4	0.18	0	6,6,6	0.42	0
6	GOL	A	605	-	5,5,5	0.82	0	5,5,5	1.11	1 (20%)
6	GOL	A	608	-	5,5,5	1.75	2 (40%)	5,5,5	0.67	0
6	GOL	A	610	-	5,5,5	0.77	0	5,5,5	1.04	0
2	FAD	A	601	-	56,58,58	0.72	1 (1%)	81,89,89	0.68	0
3	DLZ	A	602	-	23,24,24	2.01	9 (39%)	29,35,35	2.06	11 (37%)
6	GOL	A	614	-	5,5,5	0.41	0	5,5,5	1.22	1 (20%)
6	GOL	A	607	-	5,5,5	1.29	1 (20%)	5,5,5	0.82	0
7	SO4	A	622	-	4,4,4	0.21	0	6,6,6	0.25	0
5	EPE	A	604	-	15,15,15	0.84	0	18,20,20	1.57	3 (16%)
7	SO4	A	619	-	4,4,4	0.30	0	6,6,6	0.49	0
4	SF4	A	603	1	0,12,12	-	-	-		
7	SO4	A	620	-	4,4,4	0.47	0	6,6,6	0.49	0
7	SO4	A	617	-	4,4,4	0.38	0	6,6,6	0.69	0
7	SO4	A	621	-	4,4,4	0.17	0	6,6,6	0.21	0
6	GOL	A	612	-	5,5,5	1.58	1 (20%)	5,5,5	1.12	1 (20%)
6	GOL	A	606	-	5,5,5	1.85	2 (40%)	5,5,5	0.95	0
6	GOL	A	615	-	5,5,5	0.97	0	5,5,5	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	GOL	A	611	-	5,5,5	1.17	1 (20%)	5,5,5	0.86	0
6	GOL	A	609	8	5,5,5	1.89	1 (20%)	5,5,5	0.68	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
3	DLZ	A	602	-	-	1/14/14/14	0/2/2/2
6	GOL	A	614	-	-	0/4/4/4	-
6	GOL	A	607	-	-	0/4/4/4	-
6	GOL	A	611	-	-	4/4/4/4	-
5	EPE	A	604	-	-	2/9/19/19	0/1/1/1
6	GOL	A	613	-	-	0/4/4/4	-
6	GOL	A	612	-	-	4/4/4/4	-
6	GOL	A	606	-	-	3/4/4/4	-
6	GOL	A	609	8	-	2/4/4/4	-
6	GOL	A	615	-	-	3/4/4/4	-
4	SF4	A	603	1	-	-	0/6/5/5
6	GOL	A	605	-	-	0/4/4/4	-
6	GOL	A	608	-	-	0/4/4/4	-
6	GOL	A	610	-	-	0/4/4/4	-
2	FAD	A	601	-	-	2/34/50/50	0/6/6/6

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	DLZ	C1'-C2'	4.42	1.58	1.52
3	A	602	DLZ	C7-C7A	4.03	1.55	1.49
6	A	613	GOL	O2-C2	-4.01	1.31	1.43
6	A	609	GOL	O2-C2	-3.70	1.32	1.43
6	A	608	GOL	C1-C2	3.28	1.65	1.51

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	604	EPE	C5-N4-C3	4.15	118.16	108.83
3	A	602	DLZ	O4-C4-N3	3.94	127.68	120.12
3	A	602	DLZ	C4A-C8-N8	-3.82	110.99	116.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	602	DLZ	C6-C5A-N5	3.60	118.20	112.53
3	A	602	DLZ	C1'-N8-C7A	3.04	126.64	121.74

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	606	GOL	O1-C1-C2-C3
6	A	611	GOL	O1-C1-C2-C3
6	A	611	GOL	C1-C2-C3-O3
6	A	612	GOL	O1-C1-C2-C3
6	A	609	GOL	O1-C1-C2-O2

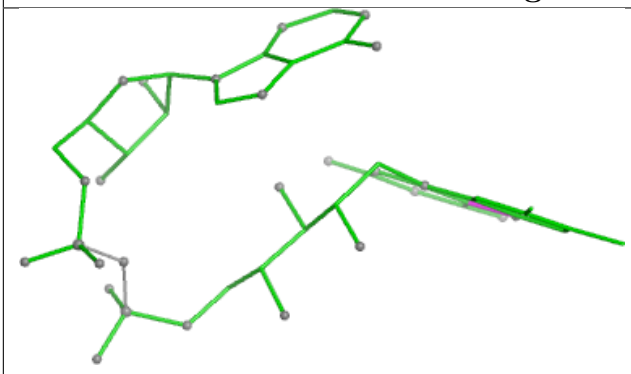
There are no ring outliers.

8 monomers are involved in 16 short contacts:

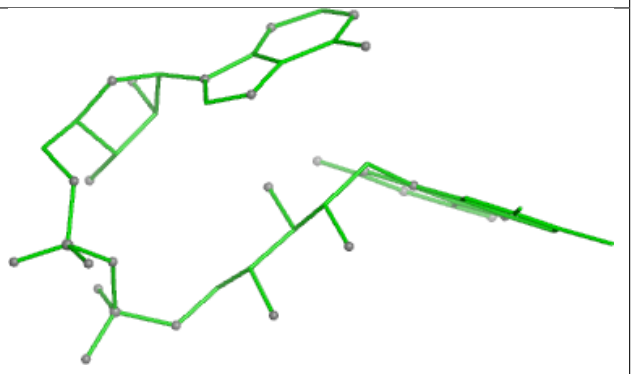
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	608	GOL	2	0
6	A	610	GOL	1	0
2	A	601	FAD	1	0
5	A	604	EPE	4	0
7	A	619	SO4	1	0
6	A	615	GOL	3	0
6	A	611	GOL	2	1
6	A	609	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

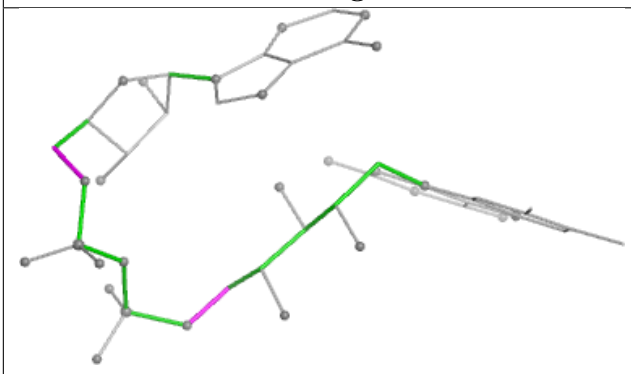
Ligand FAD A 601



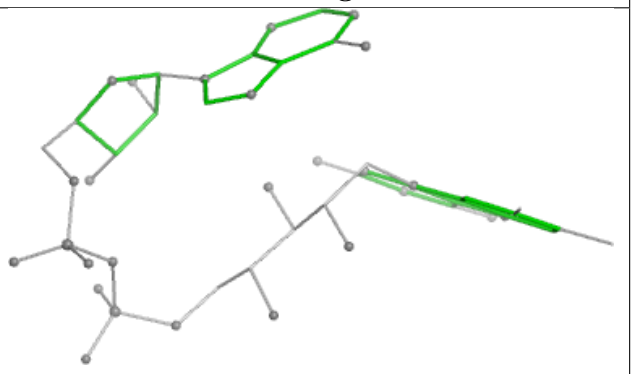
Bond lengths



Bond angles

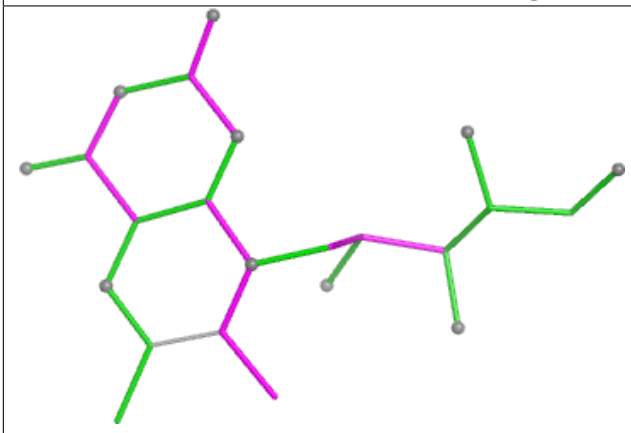


Torsions

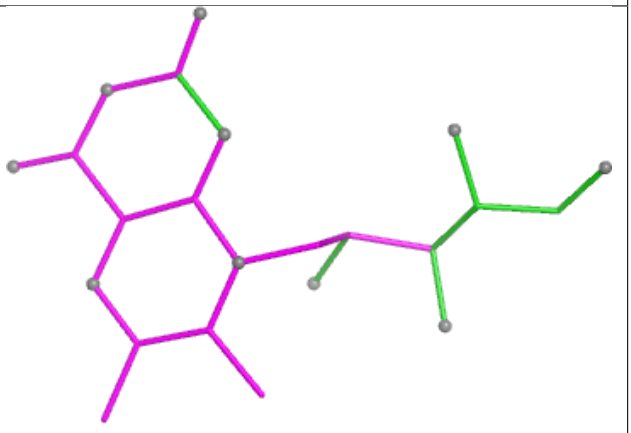


Rings

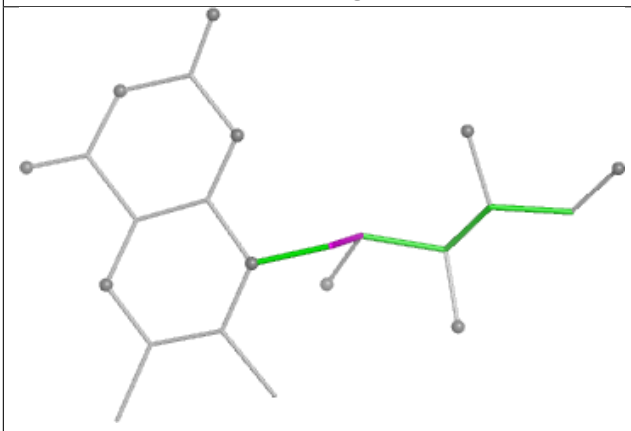
Ligand DLZ A 602



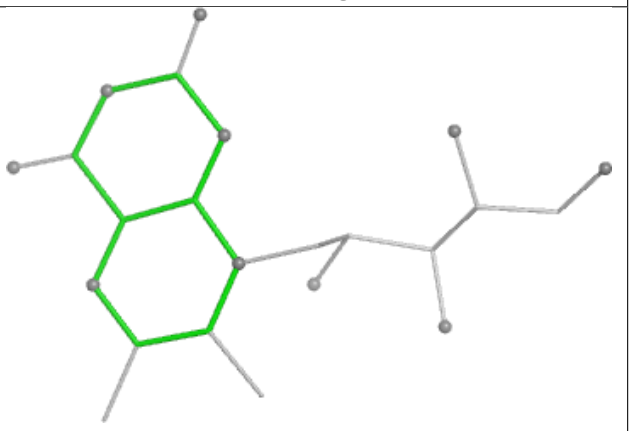
Bond lengths



Bond angles



Torsions



Rings

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, 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>2	OWAB(Å^2)	Q<0.9
1	A	516/536 (96%)	-0.66	16 (3%) 51 55	11, 24, 62, 138	21 (4%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	MET	6.1
1	A	504	ILE	5.0
1	A	502	PRO	4.2
1	A	507	LEU	4.1
1	A	44[A]	HIS	3.3

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, 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	B-factors(Å^2)	Q<0.9
5	EPE	A	604	15/15	0.77	0.29	24,73,95,103	32
6	GOL	A	610	6/6	0.80	0.26	41,55,59,67	14

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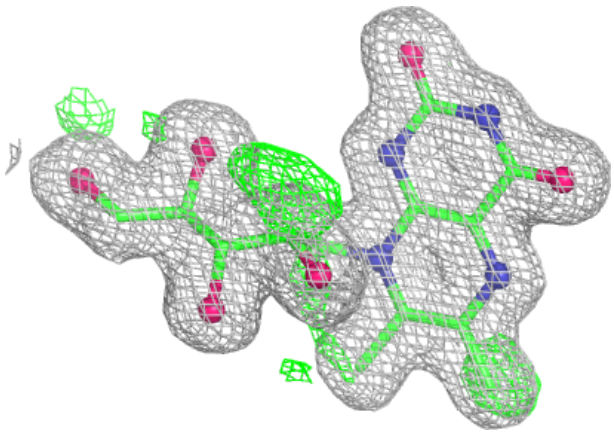
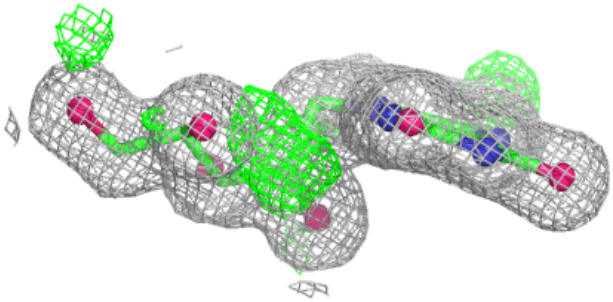
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	NA	A	627	1/1	0.80	0.21	66,66,66,66	1
7	SO4	A	617	5/5	0.81	0.23	32,48,75,102	5
6	GOL	A	614	6/6	0.81	0.24	36,60,69,76	14
6	GOL	A	612	6/6	0.83	0.21	25,36,76,91	14
8	NA	A	625	1/1	0.84	0.26	56,56,56,56	1
6	GOL	A	611	6/6	0.84	0.16	21,36,46,55	14
8	NA	A	626	1/1	0.85	0.19	64,64,64,64	1
7	SO4	A	618	5/5	0.85	0.16	33,38,59,80	5
6	GOL	A	609	6/6	0.87	0.20	22,49,59,69	13
6	GOL	A	607	6/6	0.87	0.21	51,73,83,92	0
6	GOL	A	605	6/6	0.88	0.16	30,41,48,56	9
8	NA	A	624	1/1	0.89	0.13	65,65,65,65	0
7	SO4	A	620	5/5	0.89	0.16	37,42,60,76	5
7	SO4	A	621	5/5	0.90	0.14	50,58,60,75	5
6	GOL	A	606	6/6	0.91	0.13	24,31,41,49	14
7	SO4	A	619	5/5	0.92	0.12	28,46,54,75	5
6	GOL	A	615	6/6	0.92	0.13	32,56,76,91	0
7	SO4	A	616	5/5	0.92	0.17	22,34,42,47	5
7	SO4	A	622	5/5	0.92	0.13	36,46,57,76	5
6	GOL	A	608	6/6	0.93	0.15	28,42,59,64	14
8	NA	A	623	1/1	0.94	0.16	27,27,27,27	1
6	GOL	A	613	6/6	0.95	0.11	23,36,54,54	14
9	CL	A	629	1/1	0.96	0.09	60,60,60,60	0
8	NA	A	628	1/1	0.97	0.09	67,67,67,67	1
3	DLZ	A	602	23/23	0.98	0.05	15,17,19,19	0
2	FAD	A	601	53/53	0.99	0.03	13,15,21,22	0
4	SF4	A	603	8/8	1.00	0.01	18,19,20,21	0

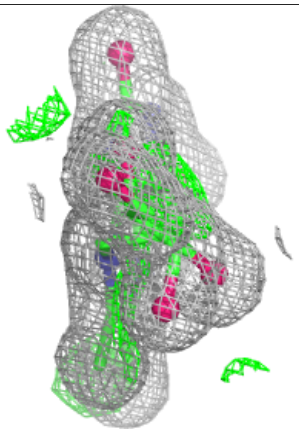
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DLZ A 602:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

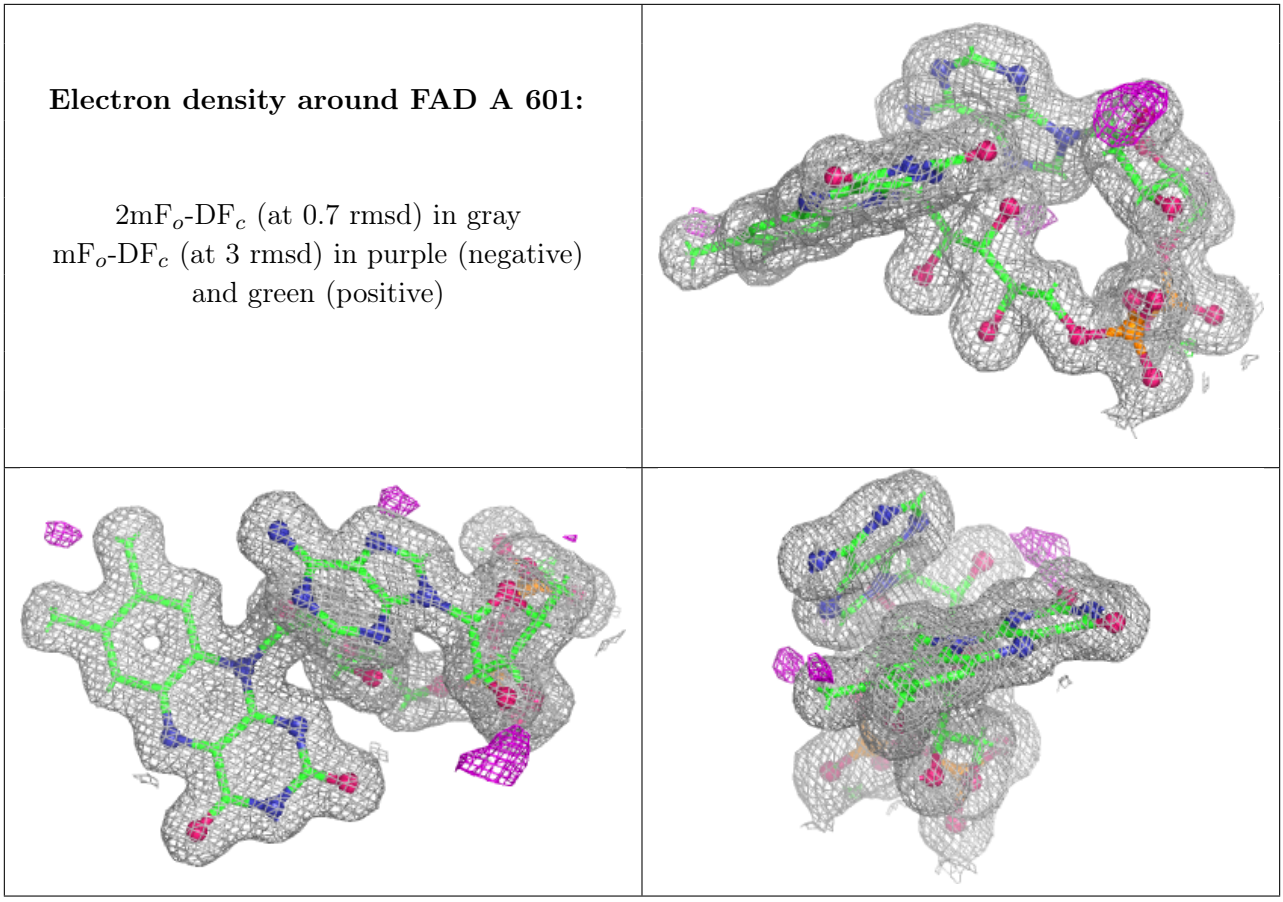






Electron density around FAD A 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.