wwPDB X-ray Structure Validation Summary Report (i)

Mar 1, 2026 – 08:25 PM UTC

PDB ID	:	9ENI / pdb_00009eni
Title	:	L-amino acid oxidase 4 (HcLAAO4) from the fungus Hebeloma cylindrosporum in complex with L-glutamine
Authors	:	Gilzer, D.; Koopmeiners, S.; Fischer von Mollard, G.; Niemann, H.H.
Deposited on	:	2024-03-13
Resolution	:	2.10 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:

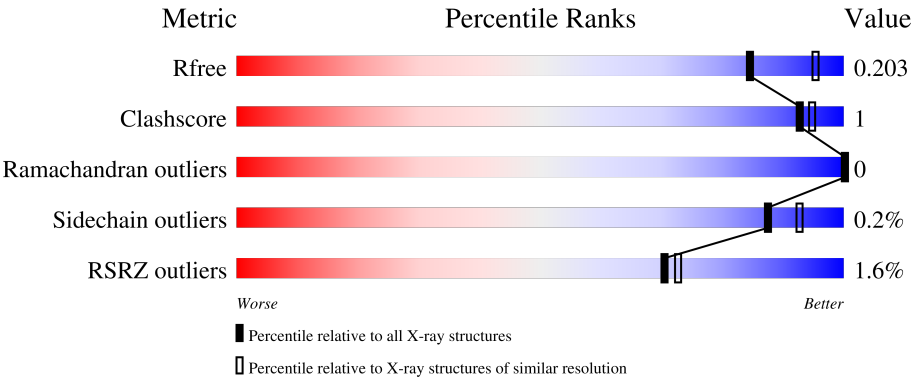
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

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

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	562	2% 91%
1	B	562	% 91% 6%
1	C	562	% 91% 5%
1	D	562	2% 92% 5%

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	SO4	B	706	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 35305 atoms, of which 16685 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.

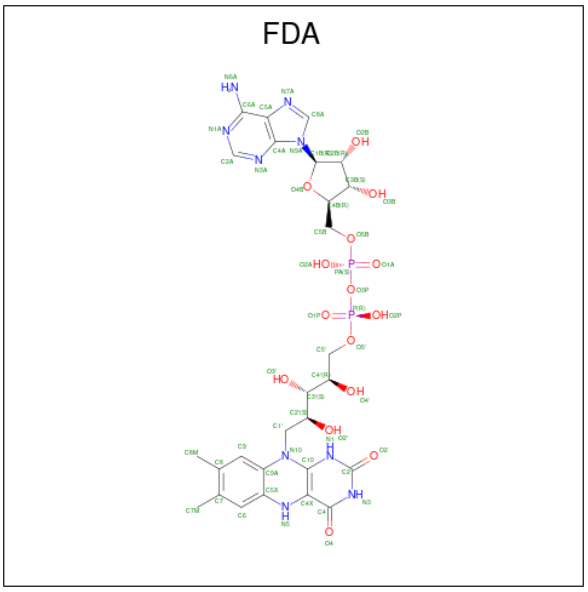
- Molecule 1 is a protein called L-amino acid oxidase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	537	Total	C	H	N	O	S	0	9	0
			8407	2746	4138	716	796	11			
1	B	531	Total	C	H	N	O	S	0	5	0
			8292	2710	4082	707	782	11			
1	C	532	Total	C	H	N	O	S	0	6	0
			8304	2713	4087	708	785	11			
1	D	535	Total	C	H	N	O	S	0	8	0
			8374	2732	4126	715	790	11			

There are 8 discrepancies between the modelled and reference sequences:

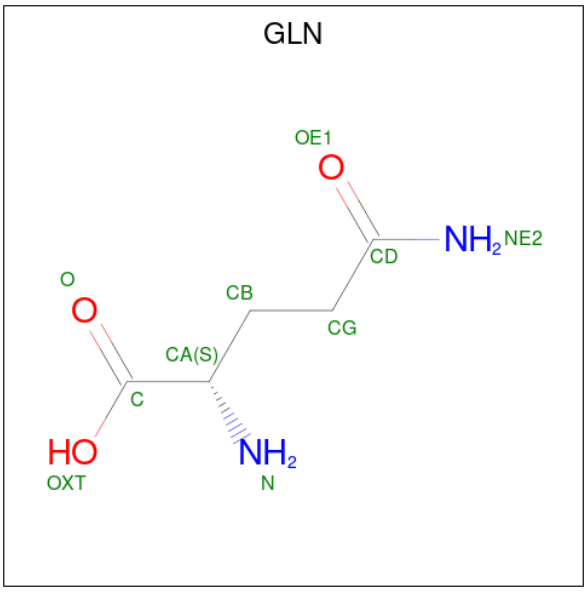
Chain	Residue	Modelled	Actual	Comment	Reference
A	474	ALA	LYS	engineered mutation	UNP S4S6Z0
A	475	ALA	LYS	engineered mutation	UNP S4S6Z0
B	474	ALA	LYS	engineered mutation	UNP S4S6Z0
B	475	ALA	LYS	engineered mutation	UNP S4S6Z0
C	474	ALA	LYS	engineered mutation	UNP S4S6Z0
C	475	ALA	LYS	engineered mutation	UNP S4S6Z0
D	474	ALA	LYS	engineered mutation	UNP S4S6Z0
D	475	ALA	LYS	engineered mutation	UNP S4S6Z0

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



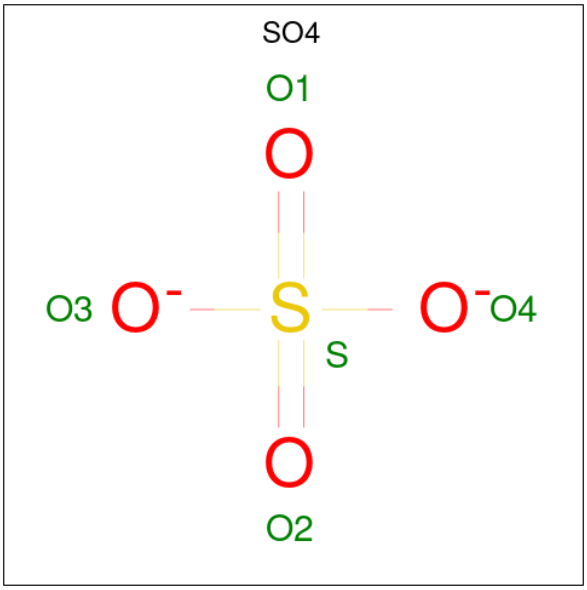
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			85	27	32	9	15	2		
2	B	1	Total	C	H	N	O	P	0	0
			85	27	32	9	15	2		
2	C	1	Total	C	H	N	O	P	0	0
			85	27	32	9	15	2		
2	D	1	Total	C	H	N	O	P	0	0
			85	27	32	9	15	2		

- Molecule 3 is GLUTAMINE (CCD ID: GLN) (formula: $C_5H_{10}N_2O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			17	5	7	2	3		
3	B	1	Total	C	H	N	O	0	0
			17	5	7	2	3		
3	C	1	Total	C	H	N	O	0	0
			17	5	7	2	3		
3	D	1	Total	C	H	N	O	0	0
			17	5	7	2	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

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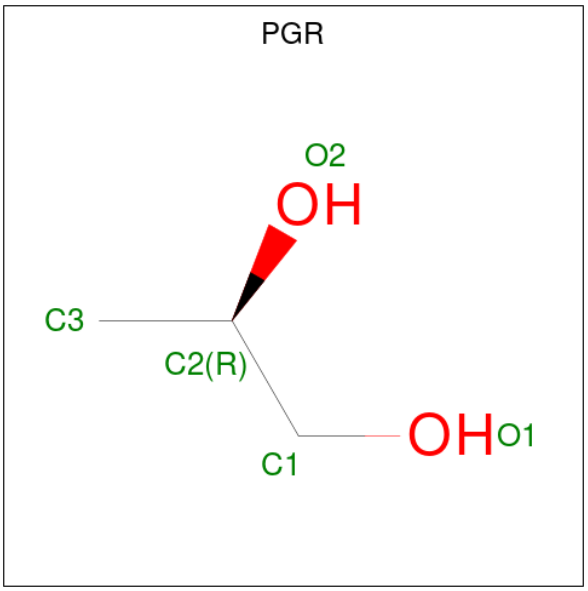
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0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

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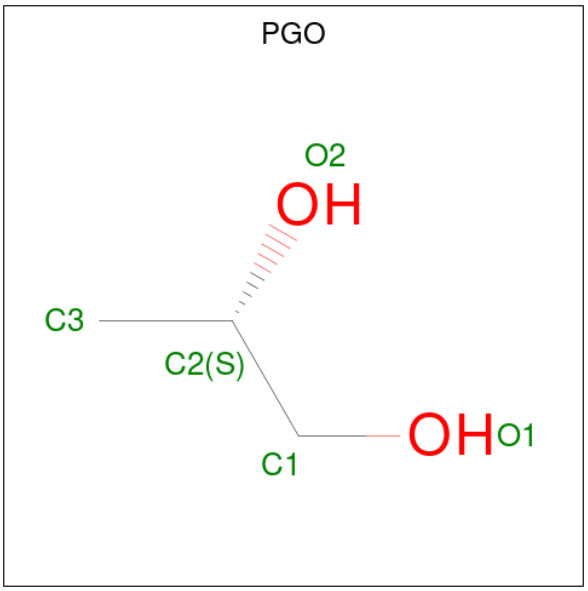
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

- Molecule 5 is R-1,2-PROPANEDIOL (CCD ID: PGR) (formula: $C_3H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H O 13 3 8 2	0	0
5	A	1	Total C H O 13 3 8 2	0	0
5	A	1	Total C H O 13 3 8 2	0	0
5	A	1	Total C H O 13 3 8 2	0	0
5	B	1	Total C H O 13 3 8 2	0	0
5	B	1	Total C H O 13 3 8 2	0	0
5	C	1	Total C H O 13 3 8 2	0	0
5	C	1	Total C H O 13 3 8 2	0	0
5	C	1	Total C H O 13 3 8 2	0	0
5	D	1	Total C H O 13 3 8 2	0	0

- Molecule 6 is S-1,2-PROPANEDIOL (CCD ID: PGO) (formula: $C_3H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C H O 13 3 8 2	0	0
6	B	1	Total C H O 13 3 8 2	0	0

- Molecule 7 is water.

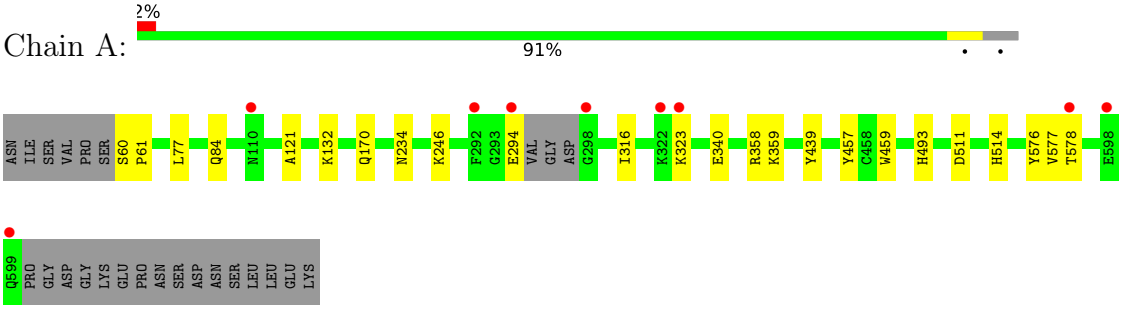
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	353	Total O 356 356	0	3
7	B	307	Total O 309 309	0	2
7	C	232	Total O 234 234	0	2
7	D	237	Total O 240 240	0	3

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.

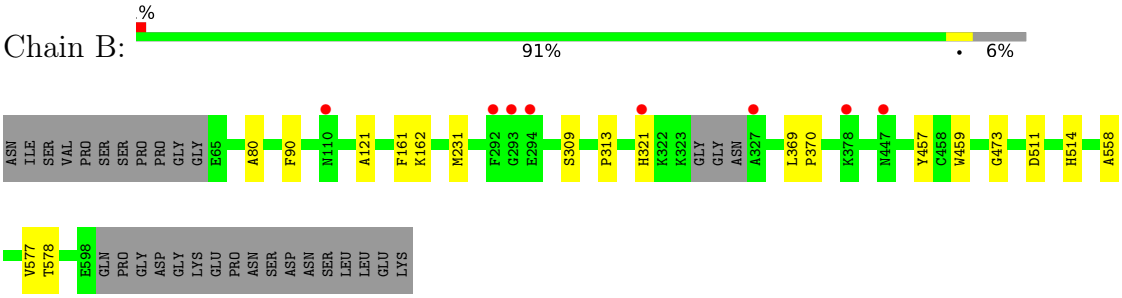
• Molecule 1: L-amino acid oxidase 4

Chain A:



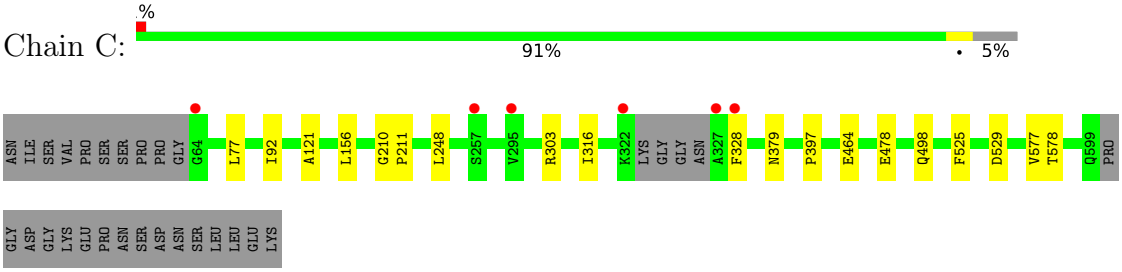
• Molecule 1: L-amino acid oxidase 4

Chain B:



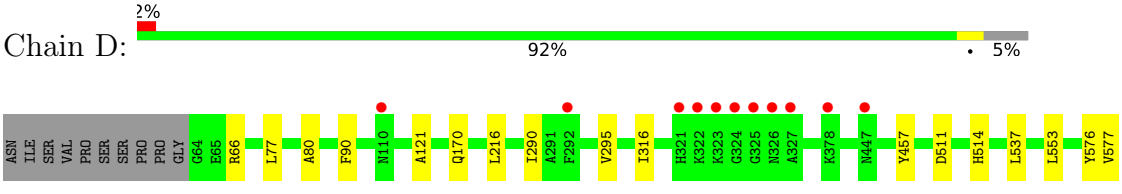
• Molecule 1: L-amino acid oxidase 4

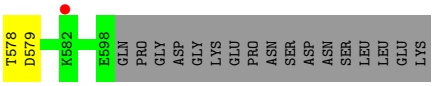
Chain C:



• Molecule 1: L-amino acid oxidase 4

Chain D:




T578
D579
K582
E598
GLN
PRO
GLY
ASP
GLY
LYS
GLU
PRO
ASN
SER
ASP
ASN
SER
LEU
LEU
GLU
LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	84.71Å 131.74Å 107.25Å 90.00° 95.95° 90.00°	Depositor
Resolution (Å)	42.13 – 2.10 42.13 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.3 (42.13-2.10) 93.3 (42.13-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.69 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.172 , 0.203 0.171 , 0.203	Depositor DCC
R_{free} test set	6356 reflections (4.23%)	wwPDB-VP
Wilson B-factor (Å^2)	40.4	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 41.9	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	0.96	EDS
Total number of atoms	35305	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: FDA, SO4, PGO, PGR

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	0.13	0/4418	0.33	0/6006
1	B	0.14	0/4347	0.32	0/5910
1	C	0.12	0/4357	0.30	0/5925
1	D	0.12	0/4393	0.30	0/5973
All	All	0.13	0/17515	0.31	0/23814

There are no bond length outliers.

There are no bond angle outliers.

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	4269	4138	4139	14	1
1	B	4210	4082	4074	14	0
1	C	4217	4087	4080	12	0
1	D	4248	4126	4124	11	2
2	A	53	32	33	1	0
2	B	53	32	33	1	0
2	C	53	32	33	1	0
2	D	53	32	33	1	0
3	A	10	7	7	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	7	7	1	0
3	C	10	7	7	0	0
3	D	10	7	7	1	0
4	A	65	0	0	2	0
4	B	55	0	0	2	0
4	C	50	0	0	2	1
4	D	55	0	0	1	0
5	A	20	32	32	2	0
5	B	10	16	16	2	0
5	C	15	24	24	0	0
5	D	5	8	8	1	0
6	A	5	8	8	0	0
6	B	5	8	8	0	0
7	A	356	0	0	2	0
7	B	309	0	0	1	0
7	C	234	0	0	1	0
7	D	240	0	0	1	0
All	All	18620	16685	16673	51	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 1.

The worst 5 of 51 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:161:PHE:N	4:B:706:SO4:O4	2.18	0.77
1:A:358:ARG:NH2	4:A:710:SO4:O1	2.22	0.72
1:D:457:TYR:O	5:D:714:PGR:H32	1.98	0.64
1:B:473:GLY:HA3	1:C:248:LEU:HD12	1.80	0.64
1:C:92:ILE:HD12	1:C:328:PHE:CE1	2.33	0.63

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)
1:D:66:ARG:NH1	4:C:705:SO4:O1[2_647]	2.07	0.13
1:A:576:TYR:O	1:D:576:TYR:OH[2_656]	2.10	0.10

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	542/562 (96%)	526 (97%)	16 (3%)	0	100	100
1	B	532/562 (95%)	517 (97%)	15 (3%)	0	100	100
1	C	534/562 (95%)	519 (97%)	15 (3%)	0	100	100
1	D	541/562 (96%)	524 (97%)	17 (3%)	0	100	100
All	All	2149/2248 (96%)	2086 (97%)	63 (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	454/467 (97%)	451 (99%)	3 (1%)	76	83
1	B	447/467 (96%)	447 (100%)	0	100	100
1	C	448/467 (96%)	448 (100%)	0	100	100
1	D	451/467 (97%)	450 (100%)	1 (0%)	87	93
All	All	1800/1868 (96%)	1796 (100%)	4 (0%)	87	93

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

Mol	Chain	Res	Type
1	A	84[A]	GLN
1	A	84[B]	GLN

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Mol	Chain	Res	Type
1	A	323	LYS
1	D	295	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	173	ASN
1	C	356	GLN
1	D	388	ASN
1	D	221	GLN
1	D	234	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

65 ligands 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	$\#\|Z\| > 2$
4	SO4	A	715	-	4,4,4	0.69	0	6,6,6	0.06	0
4	SO4	A	706	-	4,4,4	0.68	0	6,6,6	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	SO4	B	706	-	4,4,4	0.67	0	6,6,6	0.08	0
4	SO4	C	710	-	4,4,4	0.67	0	6,6,6	0.07	0
4	SO4	D	713	-	4,4,4	0.67	0	6,6,6	0.07	0
3	GLN	B	702	-	8,9,9	0.97	1 (12%)	8,11,11	0.87	0
5	PGR	D	714	-	4,4,4	0.63	0	4,4,4	0.57	0
4	SO4	A	711	-	4,4,4	0.68	0	6,6,6	0.11	0
4	SO4	B	711	-	4,4,4	0.69	0	6,6,6	0.11	0
2	FDA	C	701	-	57,58,58	0.57	0	78,89,89	0.61	0
2	FDA	D	701	-	57,58,58	0.56	0	78,89,89	0.63	0
3	GLN	D	702	-	8,9,9	0.84	1 (12%)	8,11,11	0.94	1 (12%)
4	SO4	A	709	-	4,4,4	0.69	0	6,6,6	0.07	0
4	SO4	D	705	-	4,4,4	0.69	0	6,6,6	0.07	0
4	SO4	C	706	-	4,4,4	0.69	0	6,6,6	0.08	0
4	SO4	A	703	-	4,4,4	0.67	0	6,6,6	0.10	0
5	PGR	A	716	-	4,4,4	0.61	0	4,4,4	0.56	0
4	SO4	B	713	-	4,4,4	0.70	0	6,6,6	0.08	0
4	SO4	D	709	-	4,4,4	0.67	0	6,6,6	0.11	0
4	SO4	C	712	-	4,4,4	0.69	0	6,6,6	0.08	0
5	PGR	B	715	-	4,4,4	0.64	0	4,4,4	0.59	0
4	SO4	A	712	-	4,4,4	0.67	0	6,6,6	0.09	0
4	SO4	A	704	-	4,4,4	0.65	0	6,6,6	0.16	0
4	SO4	A	707	-	4,4,4	0.67	0	6,6,6	0.09	0
5	PGR	A	717	-	4,4,4	0.66	0	4,4,4	0.53	0
4	SO4	D	711	-	4,4,4	0.67	0	6,6,6	0.06	0
5	PGR	A	719	-	4,4,4	0.64	0	4,4,4	0.43	0
4	SO4	A	714	-	4,4,4	0.68	0	6,6,6	0.08	0
4	SO4	B	708	-	4,4,4	0.68	0	6,6,6	0.07	0
5	PGR	C	715	-	4,4,4	0.62	0	4,4,4	0.48	0
4	SO4	D	710	-	4,4,4	0.69	0	6,6,6	0.10	0
4	SO4	C	708	-	4,4,4	0.68	0	6,6,6	0.08	0
4	SO4	B	705	-	4,4,4	0.67	0	6,6,6	0.06	0
4	SO4	D	703	-	4,4,4	0.67	0	6,6,6	0.10	0
4	SO4	B	707	-	4,4,4	0.68	0	6,6,6	0.09	0
4	SO4	C	705	-	4,4,4	0.66	0	6,6,6	0.10	0
4	SO4	A	710	-	4,4,4	0.68	0	6,6,6	0.09	0
4	SO4	B	710	-	4,4,4	0.68	0	6,6,6	0.09	0
2	FDA	B	701	-	57,58,58	0.54	0	78,89,89	0.62	1 (1%)
4	SO4	C	711	-	4,4,4	0.67	0	6,6,6	0.06	0
4	SO4	B	712	-	4,4,4	0.68	0	6,6,6	0.13	0
4	SO4	C	709	-	4,4,4	0.68	0	6,6,6	0.08	0
4	SO4	D	704	-	4,4,4	0.67	0	6,6,6	0.11	0
5	PGR	C	713	-	4,4,4	0.65	0	4,4,4	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	PGR	C	714	-	4,4,4	0.62	0	4,4,4	0.63	0
6	PGO	A	718	-	4,4,4	0.59	0	4,4,4	0.82	0
4	SO4	D	707	-	4,4,4	0.68	0	6,6,6	0.09	0
3	GLN	C	702	-	8,9,9	0.90	1 (12%)	8,11,11	0.99	1 (12%)
4	SO4	A	713	-	4,4,4	0.67	0	6,6,6	0.06	0
4	SO4	B	703	-	4,4,4	0.69	0	6,6,6	0.18	0
5	PGR	B	716	-	4,4,4	0.64	0	4,4,4	0.56	0
4	SO4	D	708	-	4,4,4	0.68	0	6,6,6	0.08	0
5	PGR	A	720	-	4,4,4	0.63	0	4,4,4	0.52	0
4	SO4	D	712	-	4,4,4	0.69	0	6,6,6	0.11	0
4	SO4	D	706	-	4,4,4	0.67	0	6,6,6	0.11	0
2	FDA	A	701	-	57,58,58	0.56	0	78,89,89	0.63	0
4	SO4	B	704	-	4,4,4	0.68	0	6,6,6	0.08	0
4	SO4	A	708	-	4,4,4	0.67	0	6,6,6	0.08	0
4	SO4	C	707	-	4,4,4	0.68	0	6,6,6	0.08	0
4	SO4	A	705	-	4,4,4	0.66	0	6,6,6	0.12	0
3	GLN	A	702	-	8,9,9	0.94	1 (12%)	8,11,11	1.10	1 (12%)
4	SO4	C	704	-	4,4,4	0.67	0	6,6,6	0.05	0
6	PGO	B	714	-	4,4,4	0.58	0	4,4,4	0.91	0
4	SO4	C	703	-	4,4,4	0.68	0	6,6,6	0.07	0
4	SO4	B	709	-	4,4,4	0.68	0	6,6,6	0.06	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	PGR	D	714	-	-	0/2/2/2	-
3	GLN	B	702	-	-	1/9/9/9	-
2	FDA	C	701	-	-	3/34/50/50	0/6/6/6
2	FDA	D	701	-	-	3/34/50/50	0/6/6/6
3	GLN	D	702	-	-	2/9/9/9	-
5	PGR	A	716	-	-	1/2/2/2	-
5	PGR	B	715	-	-	2/2/2/2	-
5	PGR	A	717	-	-	2/2/2/2	-
5	PGR	A	719	-	-	0/2/2/2	-
5	PGR	C	715	-	-	2/2/2/2	-
5	PGR	C	714	-	-	1/2/2/2	-
2	FDA	B	701	-	-	3/34/50/50	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PGR	C	713	-	-	2/2/2/2	-
6	PGO	A	718	-	-	0/2/2/2	-
3	GLN	C	702	-	-	2/9/9/9	-
5	PGR	B	716	-	-	2/2/2/2	-
5	PGR	A	720	-	-	2/2/2/2	-
2	FDA	A	701	-	-	3/34/50/50	0/6/6/6
3	GLN	A	702	-	-	1/9/9/9	-
6	PGO	B	714	-	-	2/2/2/2	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	GLN	OXT-C	-2.39	1.23	1.30
3	C	702	GLN	OXT-C	-2.33	1.23	1.30
3	B	702	GLN	OXT-C	-2.28	1.23	1.30
3	D	702	GLN	OXT-C	-2.23	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	702	GLN	OXT-C-O	-2.71	117.92	124.08
3	D	702	GLN	OXT-C-O	-2.59	118.20	124.08
3	C	702	GLN	OXT-C-O	-2.21	119.07	124.08
2	B	701	FDA	C4-C4X-N5	2.07	121.66	116.37

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	717	PGR	O1-C1-C2-C3
5	A	717	PGR	O1-C1-C2-O2
5	A	720	PGR	O1-C1-C2-O2
5	B	715	PGR	O1-C1-C2-O2
5	B	716	PGR	O1-C1-C2-C3

There are no ring outliers.

16 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	706	SO4	2	0

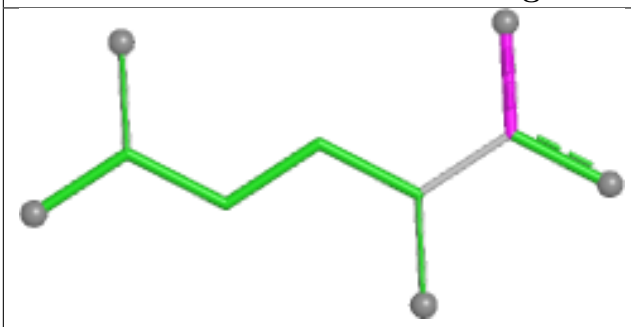
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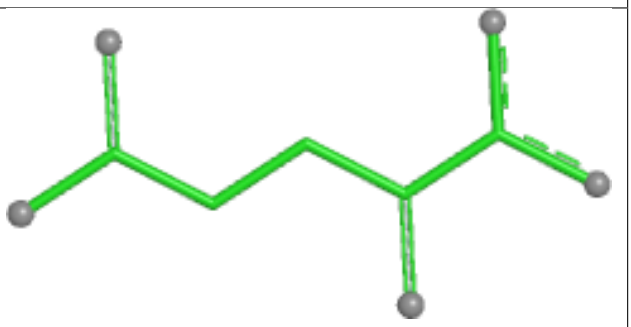
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	702	GLN	1	0
5	D	714	PGR	1	0
2	C	701	FDA	1	0
2	D	701	FDA	1	0
3	D	702	GLN	1	0
4	A	703	SO4	1	0
4	D	709	SO4	1	0
5	B	715	PGR	2	0
5	A	717	PGR	2	0
4	C	705	SO4	0	1
4	A	710	SO4	1	0
2	B	701	FDA	1	0
4	C	711	SO4	1	0
2	A	701	FDA	1	0
4	C	704	SO4	1	0

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.

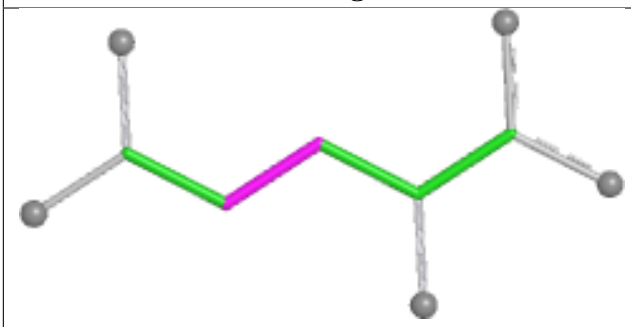
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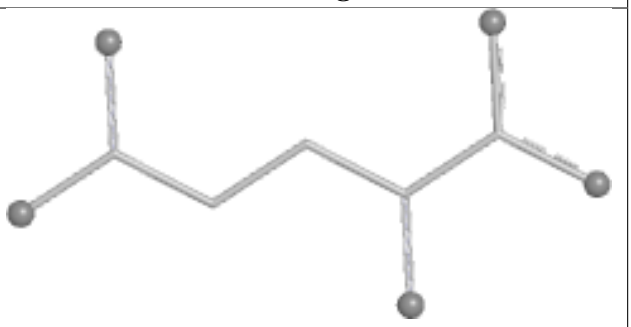
Bond lengths



Bond angles

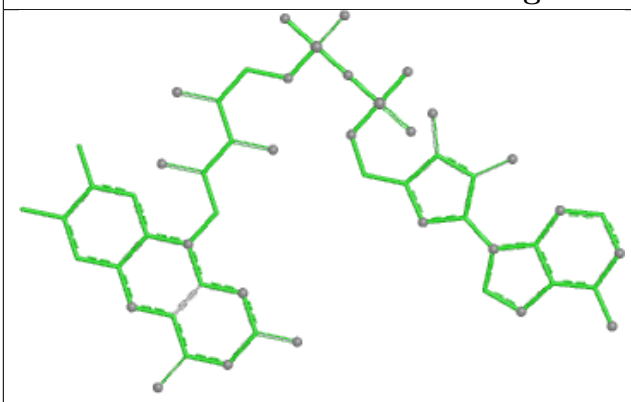


Torsions

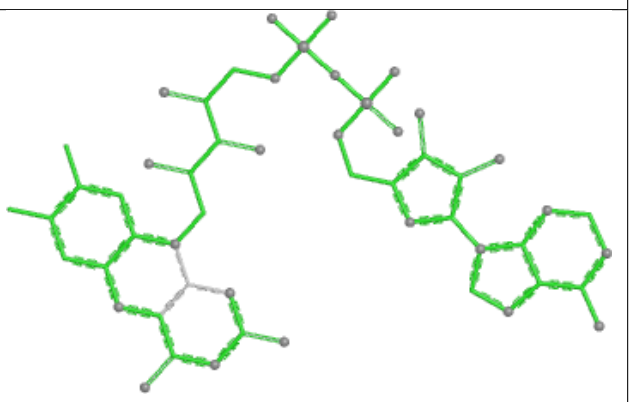


Rings

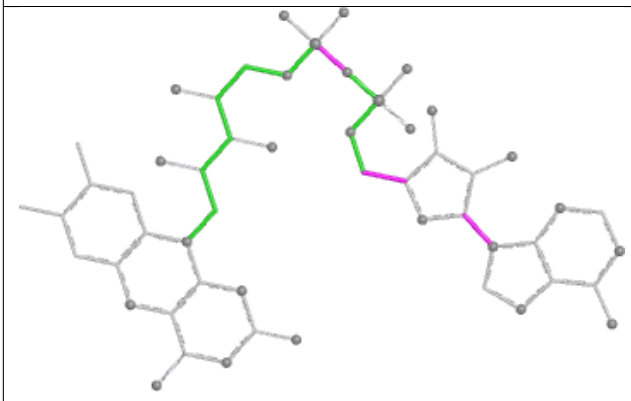
Ligand FDA C 701



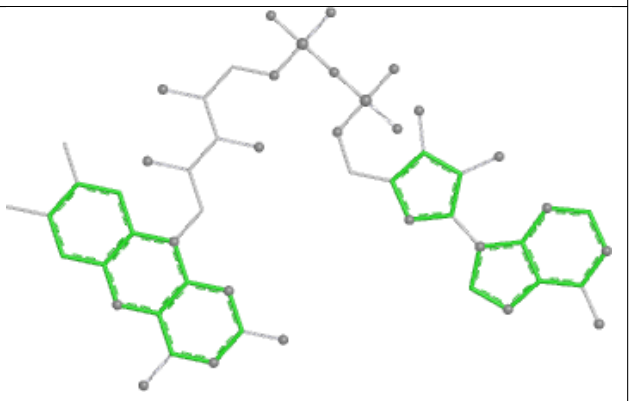
Bond lengths



Bond angles

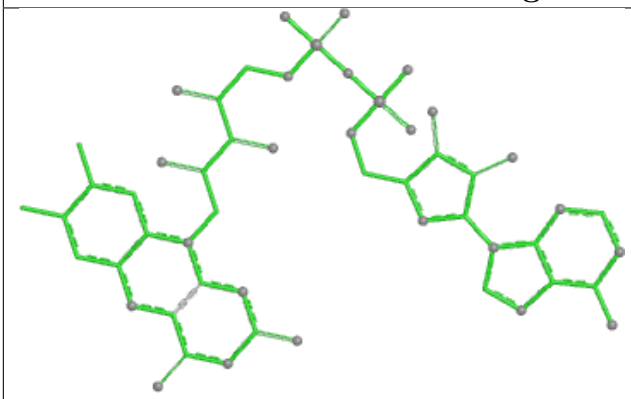


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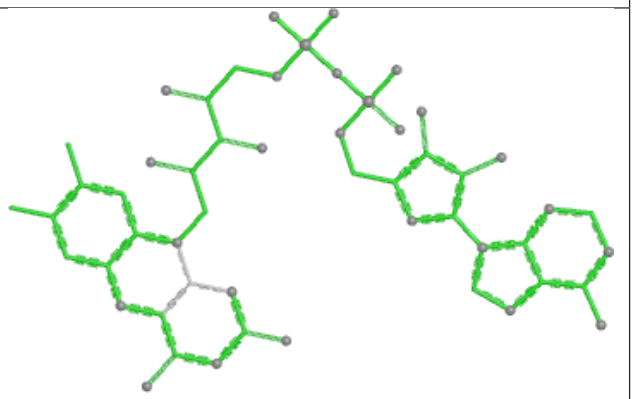


Rings

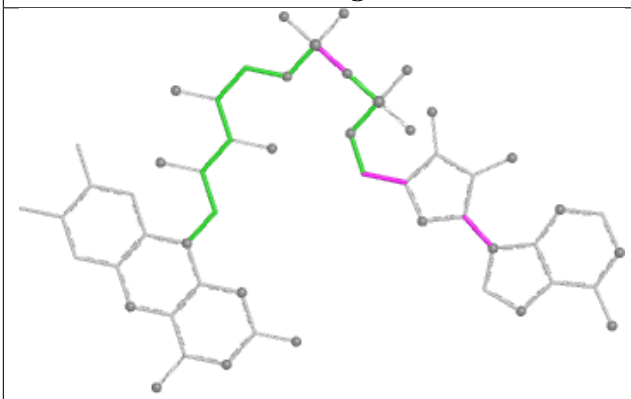
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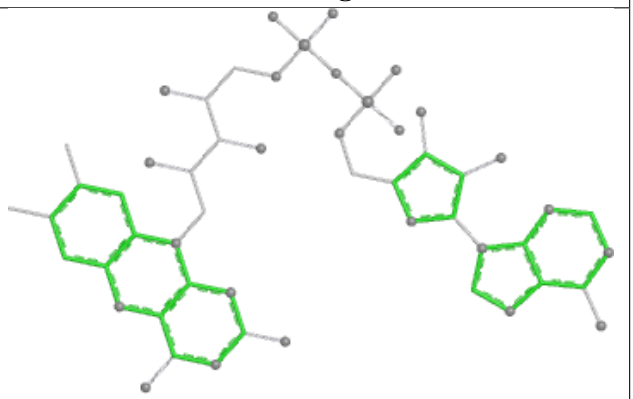
Bond lengths



Bond angles

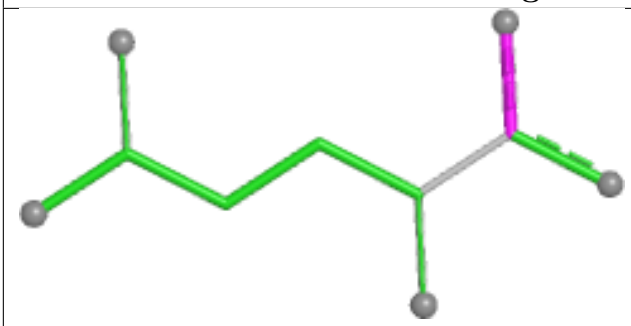


Torsions

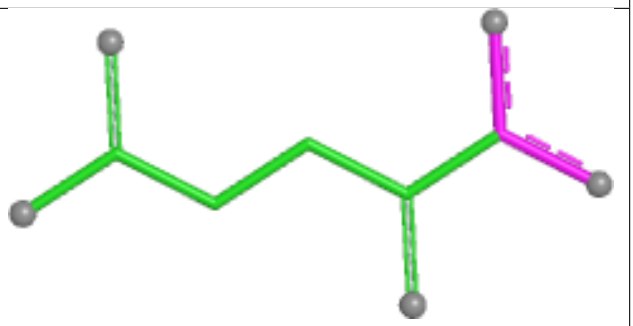


Rings

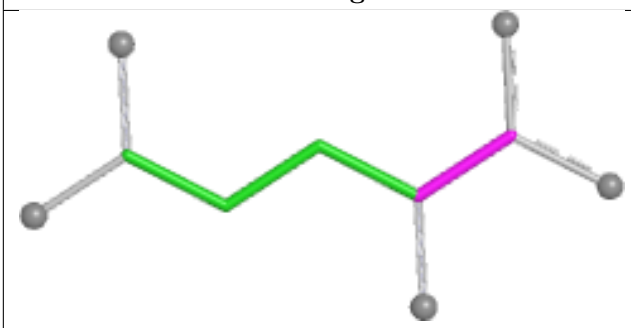
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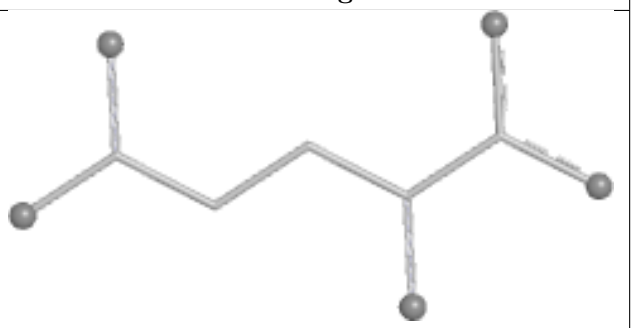
Bond lengths



Bond angles

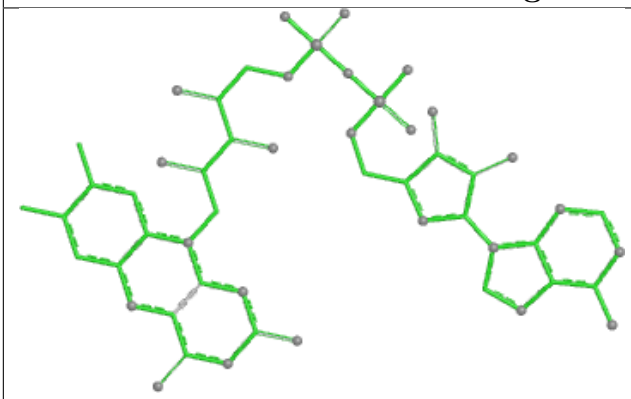


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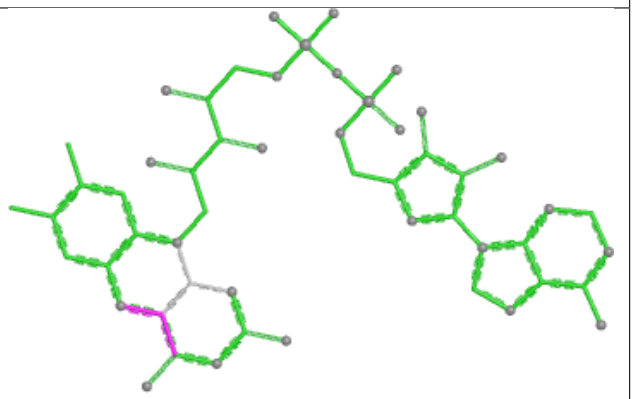


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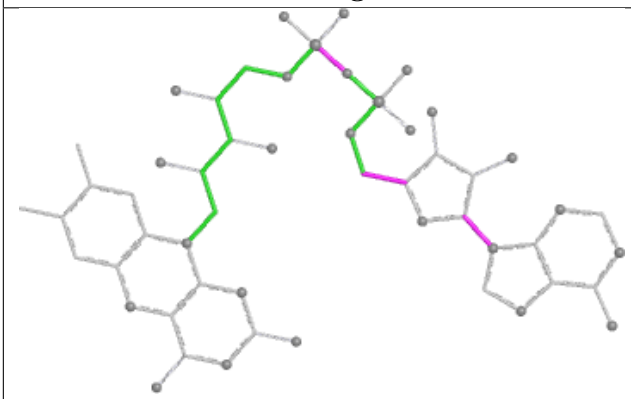
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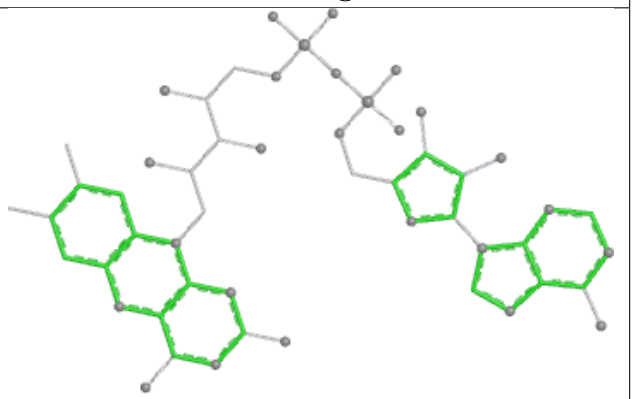
Bond lengths



Bond angles

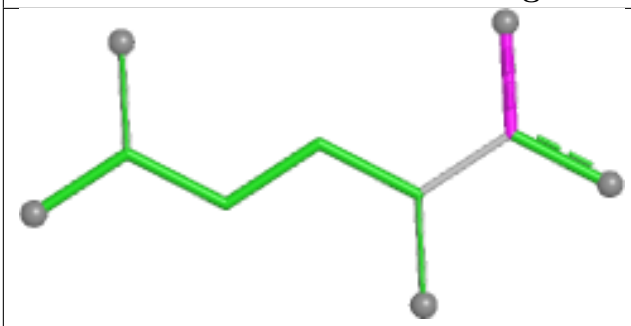


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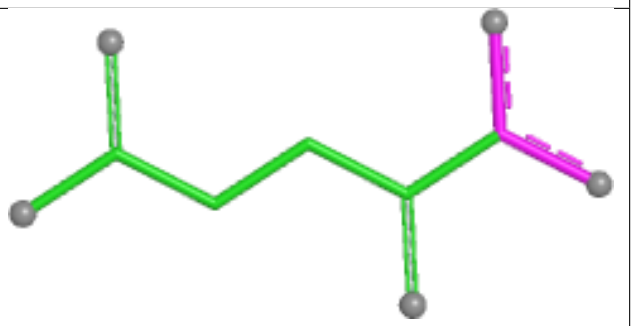


Rings

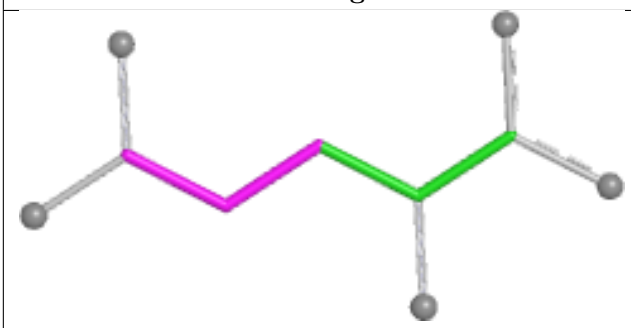
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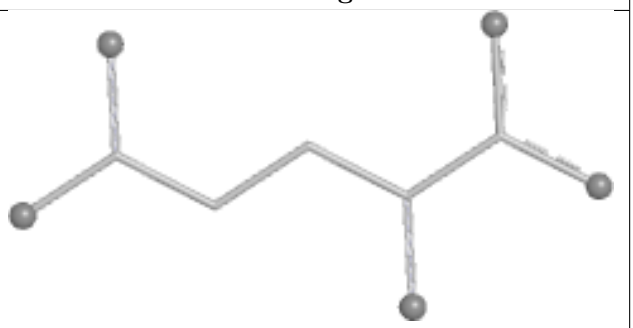
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Bond angles

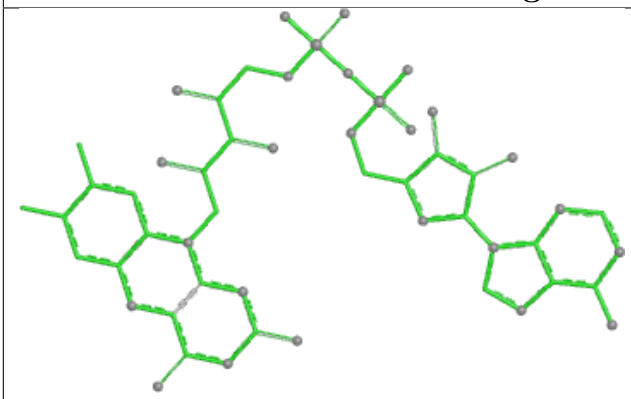


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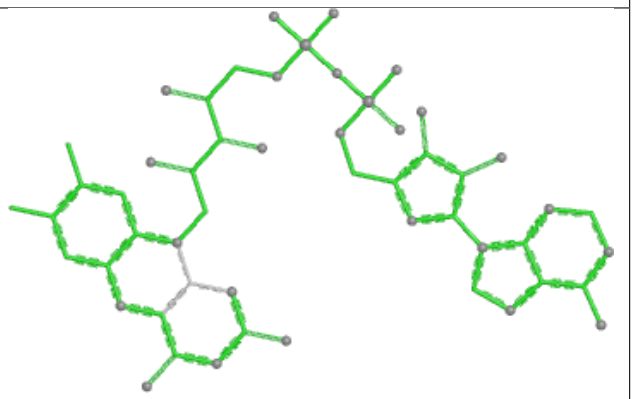


Rings

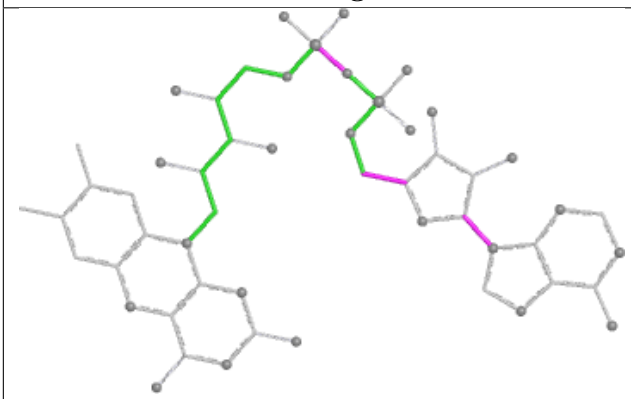
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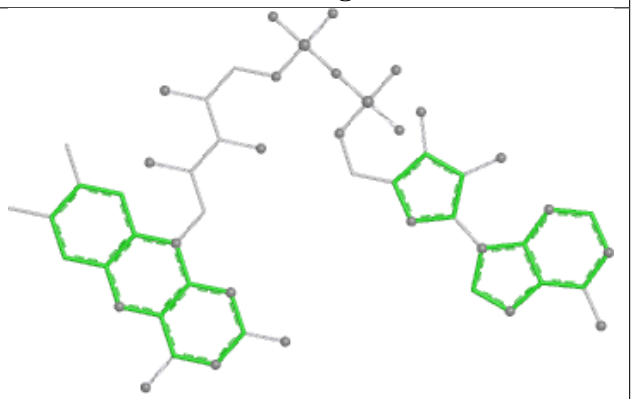
Bond lengths



Bond angles

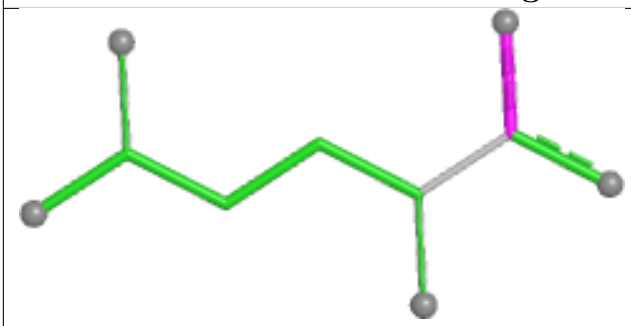


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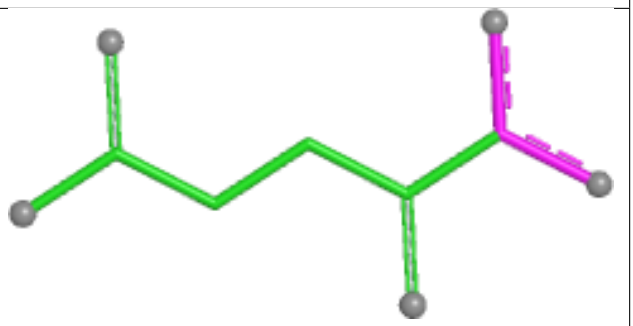


Rings

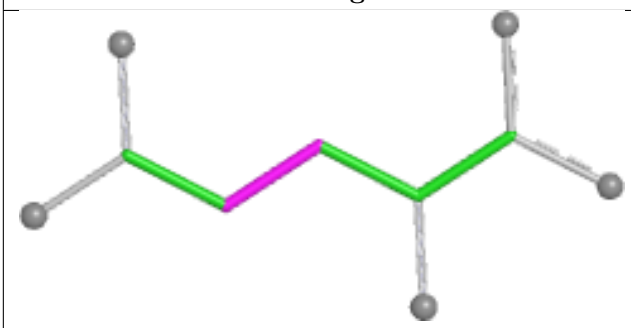
Ligand GLN A 702



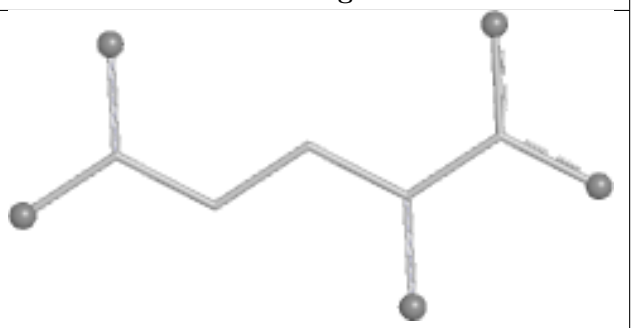
Bond lengths



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	537/562 (95%)	-0.18	9 (1%)	69	71	20, 43, 67, 140	9 (1%)
1	B	531/562 (94%)	-0.22	8 (1%)	72	74	21, 43, 66, 121	4 (0%)
1	C	532/562 (94%)	-0.01	6 (1%)	78	80	20, 50, 77, 130	5 (0%)
1	D	535/562 (95%)	0.03	12 (2%)	62	65	21, 50, 82, 149	8 (1%)
All	All	2135/2248 (94%)	-0.10	35 (1%)	70	73	20, 46, 75, 149	26 (1%)

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	327	ALA	4.6
1	A	599	GLN	3.5
1	B	321	HIS	3.2
1	A	294	GLU	3.2
1	D	327	ALA	3.1

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
4	SO4	A	710	5/5	0.64	0.14	56,57,66,71	5
4	SO4	B	711	5/5	0.69	0.20	41,47,55,58	5
4	SO4	D	709	5/5	0.71	0.21	51,55,58,58	5
4	SO4	D	713	5/5	0.71	0.13	86,86,91,103	5
4	SO4	D	710	5/5	0.72	0.13	88,95,102,120	0
4	SO4	A	708	5/5	0.72	0.11	89,96,98,105	5
4	SO4	B	713	5/5	0.73	0.17	45,52,58,63	5
4	SO4	B	707	5/5	0.74	0.14	67,68,71,83	5
4	SO4	B	709	5/5	0.75	0.10	79,81,91,97	5
4	SO4	A	713	5/5	0.75	0.11	71,76,82,84	5
4	SO4	C	710	5/5	0.76	0.11	83,85,92,95	5
4	SO4	A	714	5/5	0.77	0.12	74,76,84,89	5
5	PGR	A	717	5/5	0.78	0.21	32,38,50,50	13
5	PGR	B	715	5/5	0.78	0.21	33,40,47,47	13
5	PGR	B	716	5/5	0.78	0.16	48,57,62,65	0
4	SO4	C	707	5/5	0.80	0.11	77,82,90,96	5
4	SO4	C	708	5/5	0.81	0.10	69,72,79,87	5
4	SO4	B	708	5/5	0.81	0.11	59,59,70,73	5
4	SO4	C	712	5/5	0.81	0.17	52,52,57,60	5
4	SO4	A	711	5/5	0.82	0.12	48,53,59,62	5
4	SO4	C	703	5/5	0.82	0.11	57,60,66,66	5
4	SO4	B	710	5/5	0.82	0.13	67,68,74,83	5
4	SO4	A	715	5/5	0.82	0.18	55,56,58,62	5
5	PGR	D	714	5/5	0.82	0.21	39,47,50,50	13
4	SO4	D	708	5/5	0.83	0.11	74,82,87,96	5
4	SO4	A	703	5/5	0.83	0.17	40,46,48,50	5
4	SO4	A	712	5/5	0.83	0.13	53,55,56,58	5
4	SO4	D	711	5/5	0.83	0.14	53,56,59,62	5
4	SO4	D	712	5/5	0.83	0.19	50,52,55,58	5
5	PGR	A	720	5/5	0.84	0.13	47,57,62,62	0
4	SO4	D	704	5/5	0.84	0.14	46,50,52,53	5
4	SO4	D	707	5/5	0.84	0.10	66,69,70,75	5
5	PGR	C	715	5/5	0.84	0.13	48,57,67,67	0
4	SO4	B	703	5/5	0.84	0.16	37,45,51,53	5
4	SO4	D	705	5/5	0.85	0.10	51,54,58,61	5
4	SO4	C	711	5/5	0.85	0.13	54,58,61,63	5
4	SO4	C	705	5/5	0.86	0.12	72,75,76,77	5
4	SO4	B	706	5/5	0.86	0.15	40,43,44,45	5
4	SO4	B	712	5/5	0.86	0.12	63,66,70,77	5
4	SO4	C	709	5/5	0.87	0.09	69,75,81,91	5
4	SO4	D	703	5/5	0.88	0.11	49,51,57,58	5
3	GLN	B	702	10/10	0.88	0.12	37,44,53,53	0
3	GLN	A	702	10/10	0.88	0.13	36,46,58,58	0

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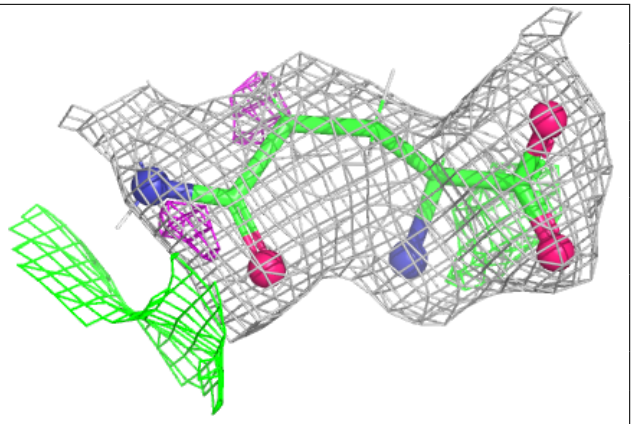
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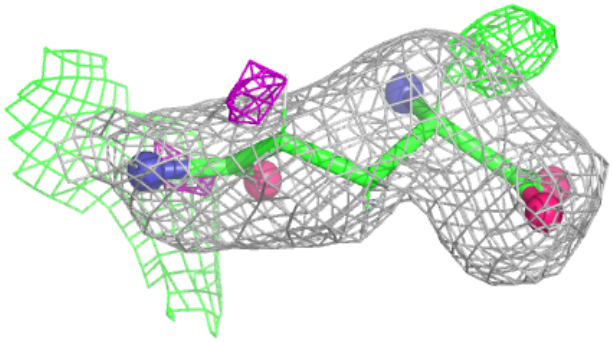
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PGR	C	713	5/5	0.88	0.17	39,47,53,53	13
4	SO4	D	706	5/5	0.88	0.14	52,55,58,62	5
5	PGR	A	719	5/5	0.88	0.12	45,54,59,65	0
6	PGO	B	714	5/5	0.88	0.10	54,65,67,75	0
4	SO4	B	705	5/5	0.89	0.10	48,48,49,51	5
4	SO4	C	706	5/5	0.89	0.12	49,52,57,59	5
4	SO4	B	704	5/5	0.89	0.10	47,47,49,55	5
4	SO4	C	704	5/5	0.89	0.10	51,53,57,63	5
5	PGR	A	716	5/5	0.90	0.11	35,44,49,56	13
3	GLN	C	702	10/10	0.90	0.12	38,47,57,57	0
5	PGR	C	714	5/5	0.90	0.12	50,63,75,75	0
4	SO4	A	709	5/5	0.90	0.14	52,53,58,59	5
4	SO4	A	705	5/5	0.90	0.13	40,44,46,48	5
4	SO4	A	706	5/5	0.90	0.09	46,47,52,53	5
6	PGO	A	718	5/5	0.92	0.11	31,43,48,51	13
4	SO4	A	704	5/5	0.92	0.12	47,51,54,58	5
3	GLN	D	702	10/10	0.94	0.09	41,45,54,54	0
4	SO4	A	707	5/5	0.95	0.09	38,41,44,45	5
2	FDA	D	701	53/53	0.96	0.07	32,38,46,47	0
2	FDA	C	701	53/53	0.96	0.07	34,38,46,47	0
2	FDA	B	701	53/53	0.97	0.06	29,34,41,43	0
2	FDA	A	701	53/53	0.97	0.06	29,34,42,43	0

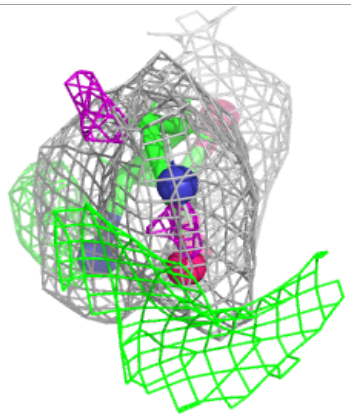
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GLN B 702:

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

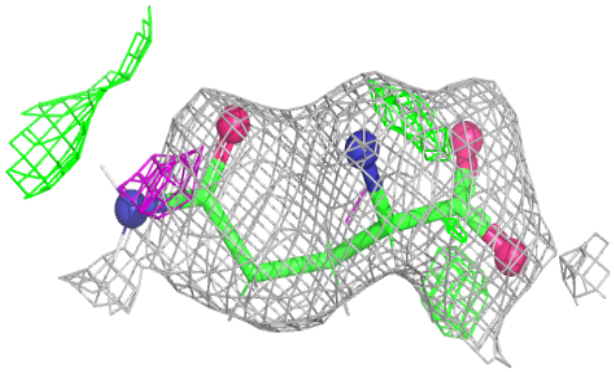


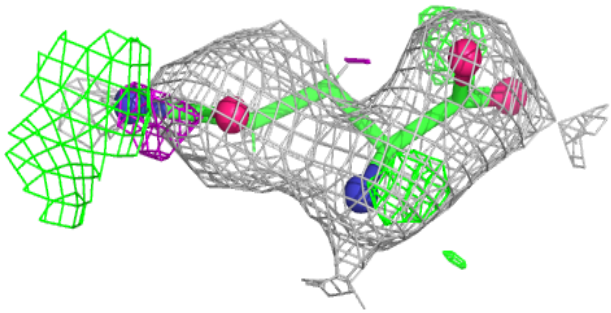


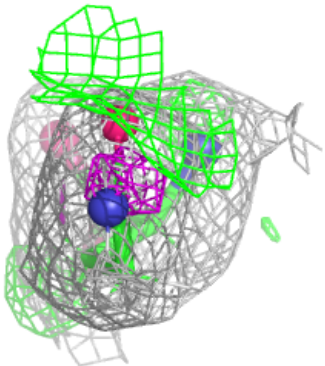


Electron density around GLN A 702:

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

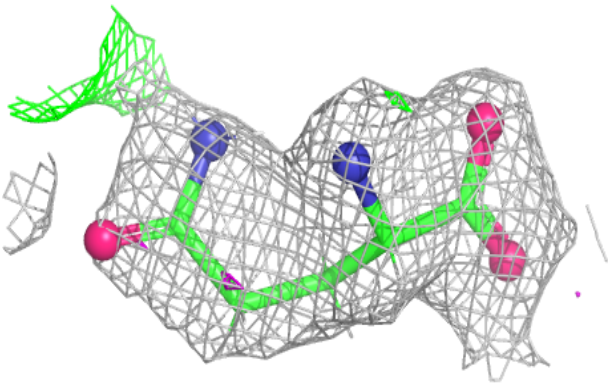


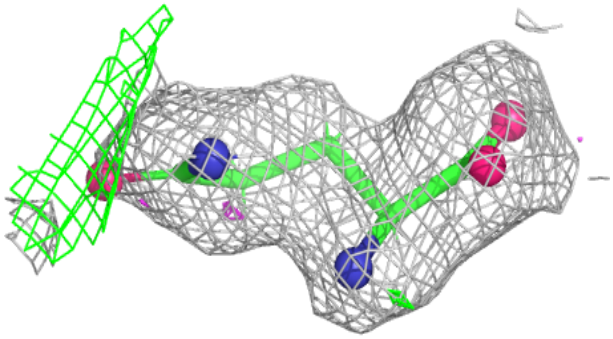


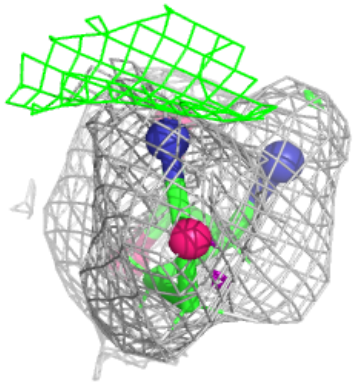


Electron density around GLN C 702:

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

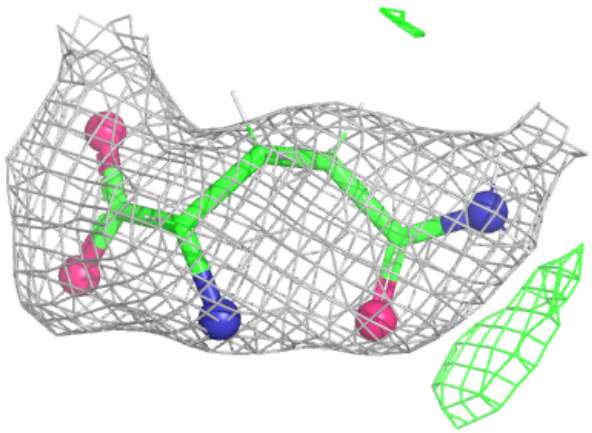


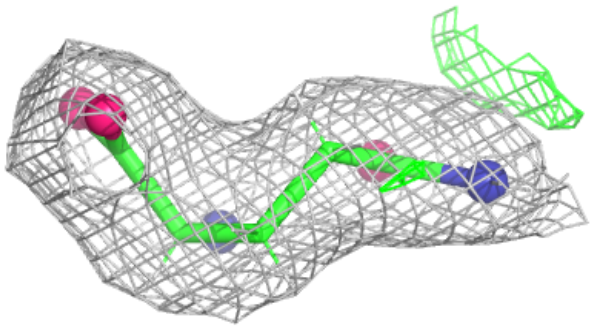


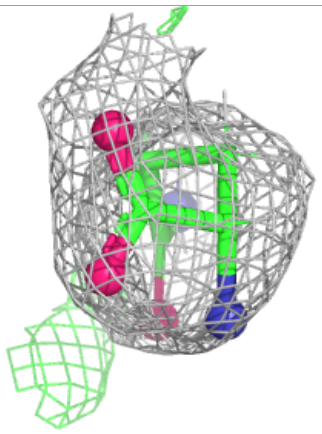


Electron density around GLN D 702:

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

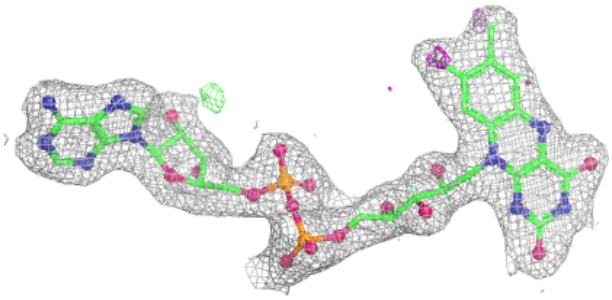


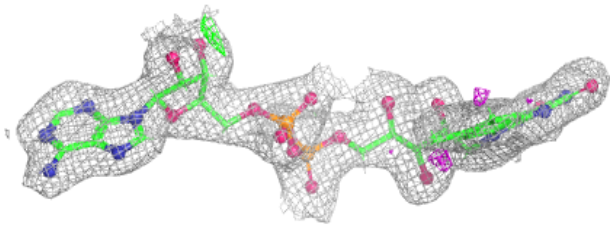


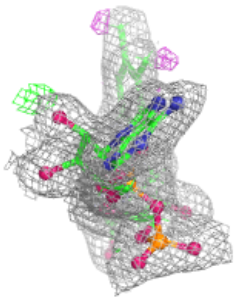


Electron density around FDA D 701:

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

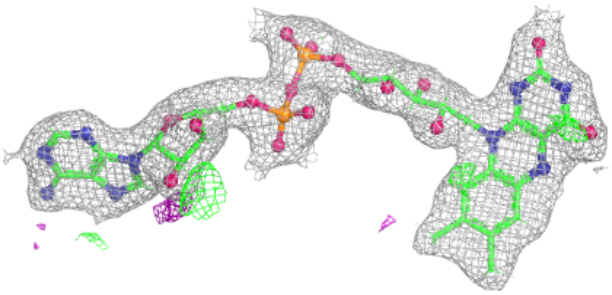


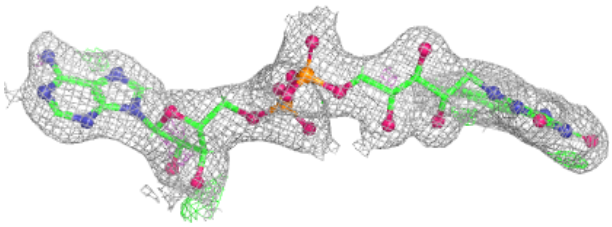


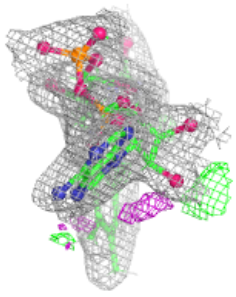


Electron density around FDA C 701:

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

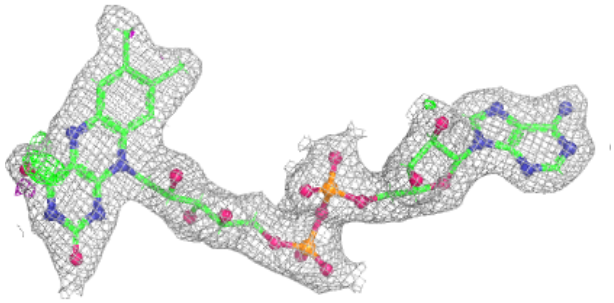


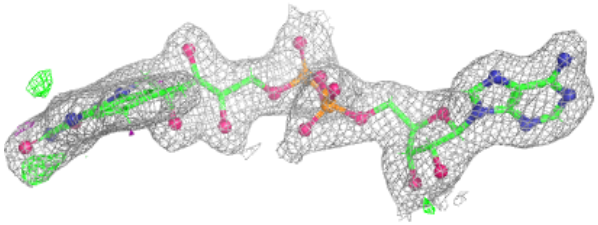


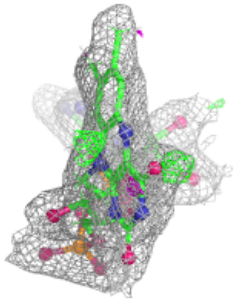


Electron density around FDA B 701:

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

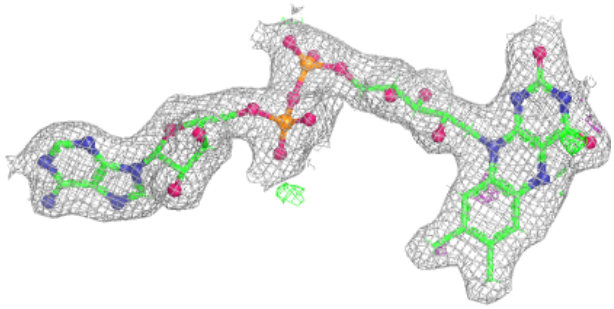


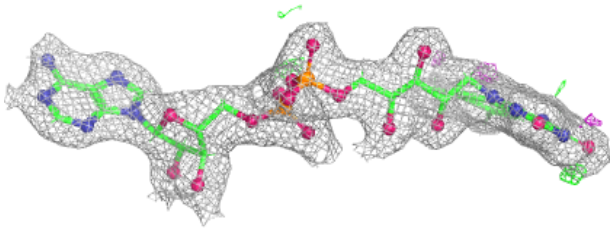


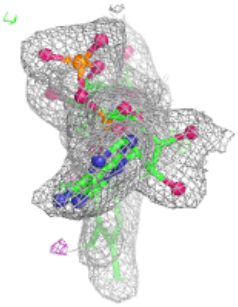


Electron density around FDA A 701:

$2mF_o$-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 (i)

There are no such residues in this entry.