



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 6, 2025 – 01:40 pm BST

PDB ID : 9QE3 / pdb_00009qe3
Title : Structure of native leukocyte myeloperoxidase in complex with a truncated version of the Staphylococcal Peroxidase Inhibitor SPIN and selenocyanate at pH 5.5
Authors : Leitgeb, U.; Pfanzagl, V.
Deposited on : 2025-03-07
Resolution : 2.06 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

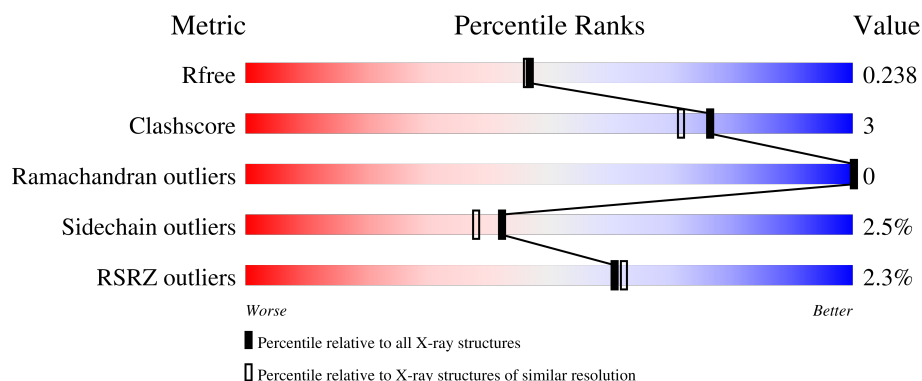
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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}	164625	3436 (2.08-2.04)
Clashscore	180529	3661 (2.08-2.04)
Ramachandran outliers	177936	3649 (2.08-2.04)
Sidechain outliers	177891	3649 (2.08-2.04)
RSRZ outliers	164620	3436 (2.08-2.04)

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	E	60	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>5%</div> </div> </div>
1	F	60	<div> <div>40%</div> <div> <div></div> <div>77%</div> <div>18%</div> <div>• •</div> </div> </div>
2	A	114	<div> <div></div> <div> <div></div> <div>82%</div> <div>10%</div> <div>8%</div> </div> </div>
2	C	114	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>13%</div> <div>• 8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	B	467	<div><div></div><div>89%</div><div>9%</div><div>.</div></div>
3	D	467	<div><div></div><div>89%</div><div>9%</div><div>..</div></div>
4	G	5	<div><div></div><div>20%</div><div>80%</div></div>
4	H	5	<div><div></div><div>40%</div><div>60%</div></div>

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 20731 atoms, of which 9899 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 Myeloperoxidase inhibitor SPIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	57	Total	C	H	N	O	0	0	0
			902	292	440	77	93			
1	F	58	Total	C	H	N	O	0	0	0
			918	298	446	80	94			

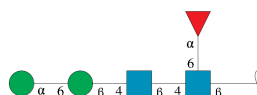
- Molecule 2 is a protein called Myeloperoxidase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	105	Total	C	H	N	O	0	0	0
			1627	532	785	149	156			
2	C	105	Total	C	H	N	O	0	0	0
			1627	532	785	149	156			

- Molecule 3 is a protein called Myeloperoxidase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	465	Total	C	H	N	O	0	0	0
			7379	2346	3654	686	666			
3	D	464	Total	C	H	N	O	0	0	0
			7369	2343	3649	685	665			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



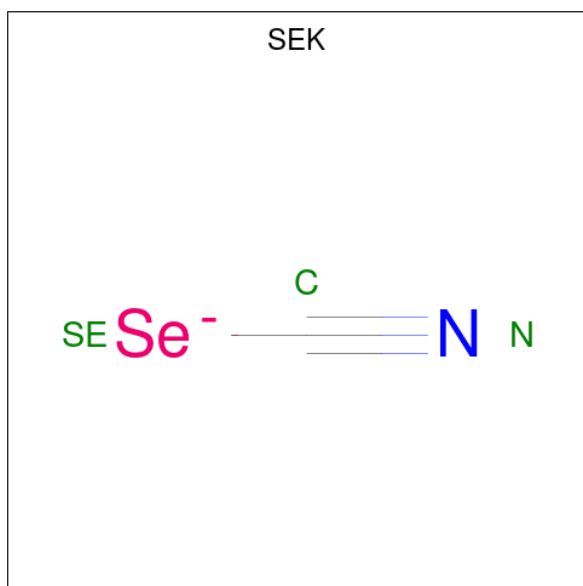
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	5	Total	C	H	N	O	0	0	0
			98	34	38	2	24			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	5	Total	C	H	N	O	0	0	0
			98	34	38	2	24			

- Molecule 5 is SELENOCYANATE ION (CCD ID: SEK) (formula: CNSe).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	Se	0	0
			3	1	1	1		
5	A	1	Total	C	N	Se	0	0
			3	1	1	1		
5	A	1	Total	C	N	Se	0	0
			3	1	1	1		
5	A	1	Total	C	N	Se	0	0
			3	1	1	1		
5	C	1	Total	C	N	Se	0	0
			3	1	1	1		
5	C	1	Total	C	N	Se	0	0
			3	1	1	1		
5	B	1	Total	C	N	Se	0	0
			3	1	1	1		
5	B	1	Total	C	N	Se	0	0
			3	1	1	1		
5	B	1	Total	C	N	Se	0	0
			3	1	1	1		
5	B	1	Total	C	N	Se	0	1
			6	2	2	2		

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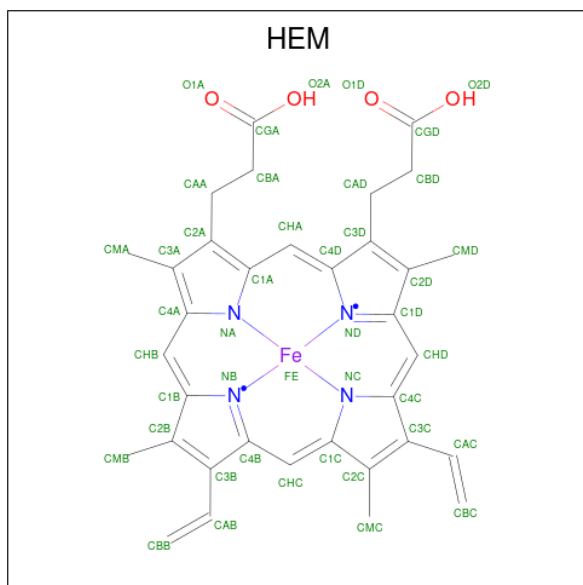
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	B	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 6	C 2	N 2	Se 2	0	1
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0
5	D	1	Total 3	C 1	N 1	Se 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	Se	0	0
			3	1	1	1		

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total 59	C 34	Fe 1	H 16	N 4	O 4	0	0
6	C	1	Total 59	C 34	Fe 1	H 16	N 4	O 4	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $\text{C}_8\text{H}_{15}\text{NO}_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	H	N	O	0	0
			22	8	8	1	5		
7	B	1	Total	C	H	N	O	0	0
			22	8	8	1	5		
7	D	1	Total	C	H	N	O	0	0
			22	8	8	1	5		
7	D	1	Total	C	H	N	O	0	0
			22	8	8	1	5		

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ca	0	0
			1	1		
8	D	1	Total	Ca	0	0
			1	1		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	E	14	Total	O	0	0
			14	14		
9	F	4	Total	O	0	0
			4	4		
9	A	56	Total	O	0	0
			56	56		

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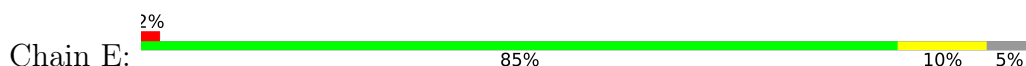
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	C	39	Total 39	O 39	0	0
9	B	174	Total 174	O 174	0	0
9	D	116	Total 116	O 116	0	0

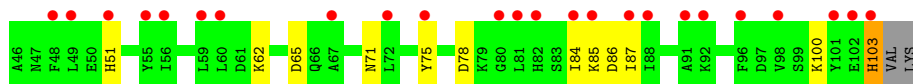
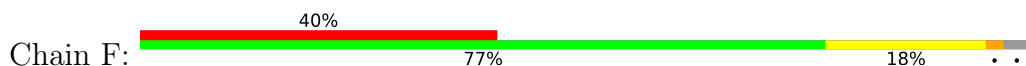
3 Residue-property plots [i](#)

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.

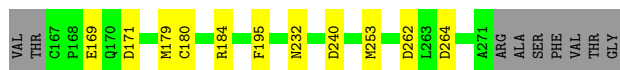
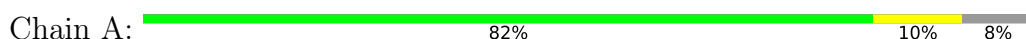
- Molecule 1: Myeloperoxidase inhibitor SPIN



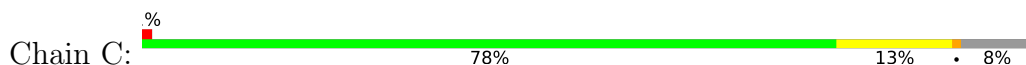
- Molecule 1: Myeloperoxidase inhibitor SPIN



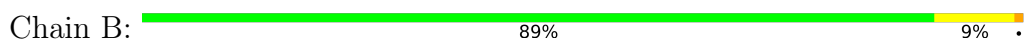
- Molecule 2: Myeloperoxidase light chain



- Molecule 2: Myeloperoxidase light chain



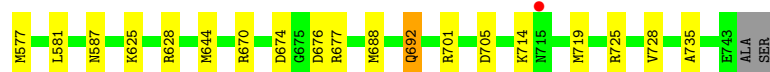
- Molecule 3: Myeloperoxidase heavy chain





- Molecule 3: Myeloperoxidase heavy chain

Chain D: 89% 9% ..



- Molecule 4: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 20% 80%



- Molecule 4: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 40% 60%



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	110.51Å 110.51Å 241.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.06 19.89 – 2.06	Depositor EDS
% Data completeness (in resolution range)	68.4 (19.89-2.06) 67.1 (19.89-2.06)	Depositor EDS
R_{merge}	0.35	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.100)	Depositor
R, R_{free}	0.179 , 0.234 0.179 , 0.238	Depositor DCC
R_{free} test set	3150 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20731	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, CA, NAG, CSO, FUC, SEK, MAN, HEM

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	E	0.65	0/469	1.31	2/629 (0.3%)
1	F	0.60	0/480	1.36	4/644 (0.6%)
2	A	0.74	0/867	1.24	5/1181 (0.4%)
2	C	0.67	0/867	1.20	4/1181 (0.3%)
3	B	0.71	0/3803	1.20	12/5158 (0.2%)
3	D	0.66	0/3798	1.19	18/5151 (0.3%)
All	All	0.68	0/10284	1.21	45/13944 (0.3%)

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
3	B	0	7
3	D	0	7
All	All	0	14

There are no bond length outliers.

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	692	GLN	N-CA-CB	9.85	124.60	110.12
3	B	506	GLN	CB-CA-C	9.58	121.88	108.76
3	D	323	ASN	CB-CA-C	-8.32	96.70	110.85
3	B	569	ARG	CD-NE-CZ	7.84	135.38	124.40
3	B	351	ARG	CB-CA-C	7.46	125.59	110.38

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	302	ARG	Sidechain
3	B	524	ARG	Sidechain
3	B	569	ARG	Sidechain
3	B	571	ARG	Sidechain
3	B	604	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	E	462	440	447	2	0
1	F	472	446	454	3	0
2	A	842	785	800	4	0
2	C	842	785	800	9	0
3	B	3725	3654	3717	29	0
3	D	3720	3649	3711	19	0
4	G	60	38	52	0	0
4	H	60	38	52	0	0
5	A	12	0	0	1	0
5	B	42	0	0	3	0
5	C	6	0	0	0	0
5	D	42	0	0	3	0
6	A	43	16	30	0	0
6	C	43	16	30	1	0
7	B	28	16	26	5	0
7	D	28	16	26	0	0
8	B	1	0	0	0	0
8	D	1	0	0	0	0
9	A	56	0	0	0	0
9	B	174	0	0	1	0
9	C	39	0	0	1	0
9	D	116	0	0	0	0
9	E	14	0	0	1	0
9	F	4	0	0	0	0
All	All	10832	9899	10145	58	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 3.

The worst 5 of 58 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)
3:B:365:VAL:H	7:B:814:NAG:H81	1.42	0.82
2:C:268:GLU:OE2	9:C:401:HOH:O	1.98	0.81
3:D:502:HIS:HD1	3:D:587:ASN:HD21	1.29	0.79
3:B:502:HIS:HD1	3:B:587:ASN:HD21	1.29	0.77
3:D:577:MET:HE1	3:D:581:LEU:HD21	1.69	0.73

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	Percentiles	
1	E	55/60 (92%)	54 (98%)	1 (2%)	0	100	100
1	F	56/60 (93%)	55 (98%)	1 (2%)	0	100	100
2	A	103/114 (90%)	101 (98%)	2 (2%)	0	100	100
2	C	103/114 (90%)	102 (99%)	1 (1%)	0	100	100
3	B	462/467 (99%)	454 (98%)	8 (2%)	0	100	100
3	D	461/467 (99%)	453 (98%)	8 (2%)	0	100	100
All	All	1240/1282 (97%)	1219 (98%)	21 (2%)	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	E	50/53 (94%)	49 (98%)	1 (2%)	50	47
1	F	51/53 (96%)	46 (90%)	5 (10%)	6	2
2	A	90/97 (93%)	88 (98%)	2 (2%)	47	43
2	C	90/97 (93%)	87 (97%)	3 (3%)	33	27
3	B	409/411 (100%)	403 (98%)	6 (2%)	60	59
3	D	409/411 (100%)	399 (98%)	10 (2%)	44	40
All	All	1099/1122 (98%)	1072 (98%)	27 (2%)	42	38

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	351	ARG
3	D	360	LEU
3	D	625	LYS
3	B	527	LEU
3	D	383	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	737	ASN
3	D	737	ASN
3	D	367	GLN
3	D	706	ASN
3	D	288	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	CSO	B	316	3	3,6,7	0.88	0	0,6,8	-	-
3	CSO	D	316	3	3,6,7	0.97	0	0,6,8	-	-

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	CSO	B	316	3	-	0/1/5/7	-
3	CSO	D	316	3	-	0/1/5/7	-

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.

5.5 Carbohydrates

10 monosaccharides 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	NAG	G	1	4,3	14,14,15	0.37	0	17,19,21	1.44	2 (11%)
4	NAG	G	2	4	14,14,15	0.33	0	17,19,21	1.00	1 (5%)
4	BMA	G	3	4	11,11,12	0.71	0	15,15,17	0.88	0
4	MAN	G	4	4	11,11,12	0.61	0	15,15,17	1.05	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FUC	G	5	4	10,10,11	0.66	0	14,14,16	1.31	3 (21%)
4	NAG	H	1	4,3	14,14,15	0.34	0	17,19,21	0.88	1 (5%)
4	NAG	H	2	4	14,14,15	0.53	0	17,19,21	1.09	2 (11%)
4	BMA	H	3	4	11,11,12	0.87	0	15,15,17	0.83	0
4	MAN	H	4	4	11,11,12	0.63	0	15,15,17	0.75	0
4	FUC	H	5	4	10,10,11	1.01	1 (10%)	14,14,16	0.78	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
4	NAG	G	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	0/1/1/1
4	FUC	G	5	4	-	-	0/1/1/1
4	NAG	H	1	4,3	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	0/2/19/22	0/1/1/1
4	MAN	H	4	4	-	0/2/19/22	0/1/1/1
4	FUC	H	5	4	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	5	FUC	C2-C3	2.86	1.56	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	1	NAG	C2-N2-C7	3.57	127.98	122.90
4	G	1	NAG	O5-C1-C2	-3.10	106.39	111.29
4	G	5	FUC	C3-C4-C5	2.63	113.87	109.77
4	G	4	MAN	C1-O5-C5	2.52	115.61	112.19
4	H	2	NAG	C2-N2-C7	2.44	126.38	122.90

There are no chirality outliers.

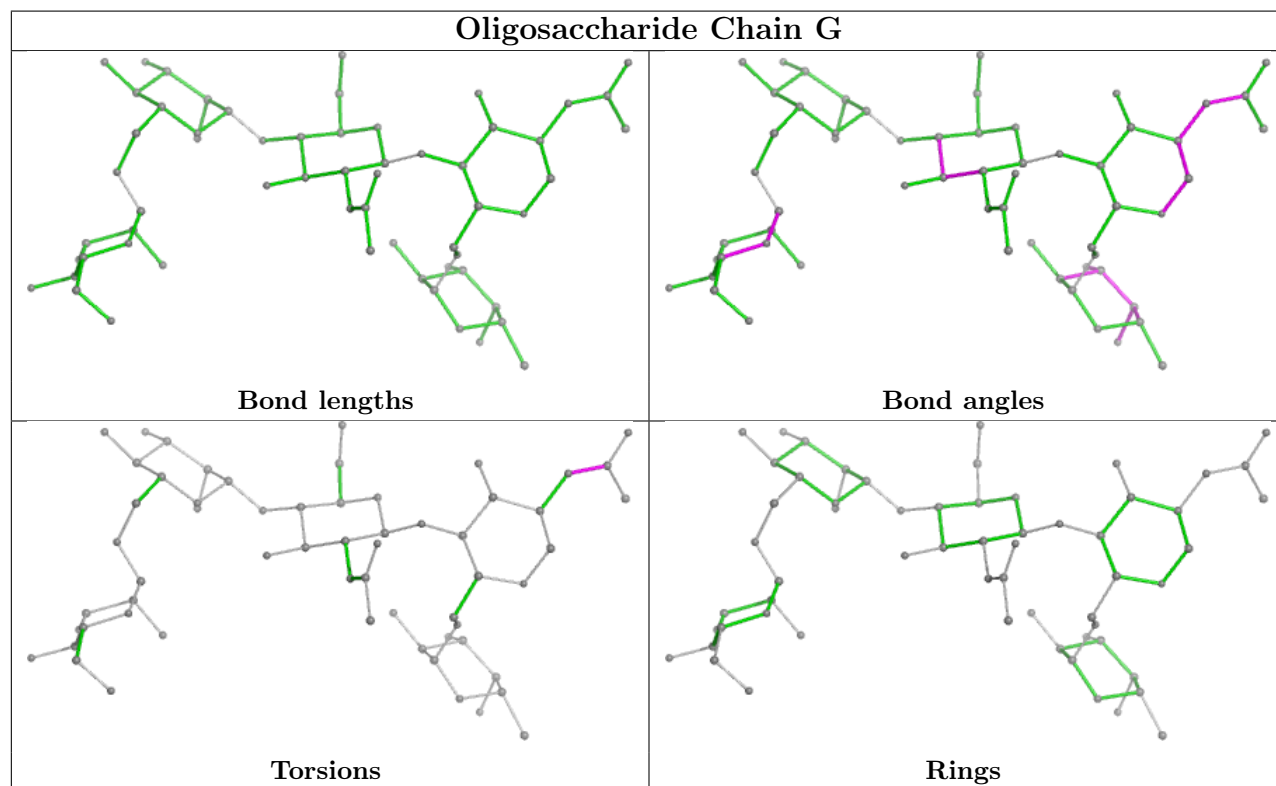
All (2) torsion outliers are listed below:

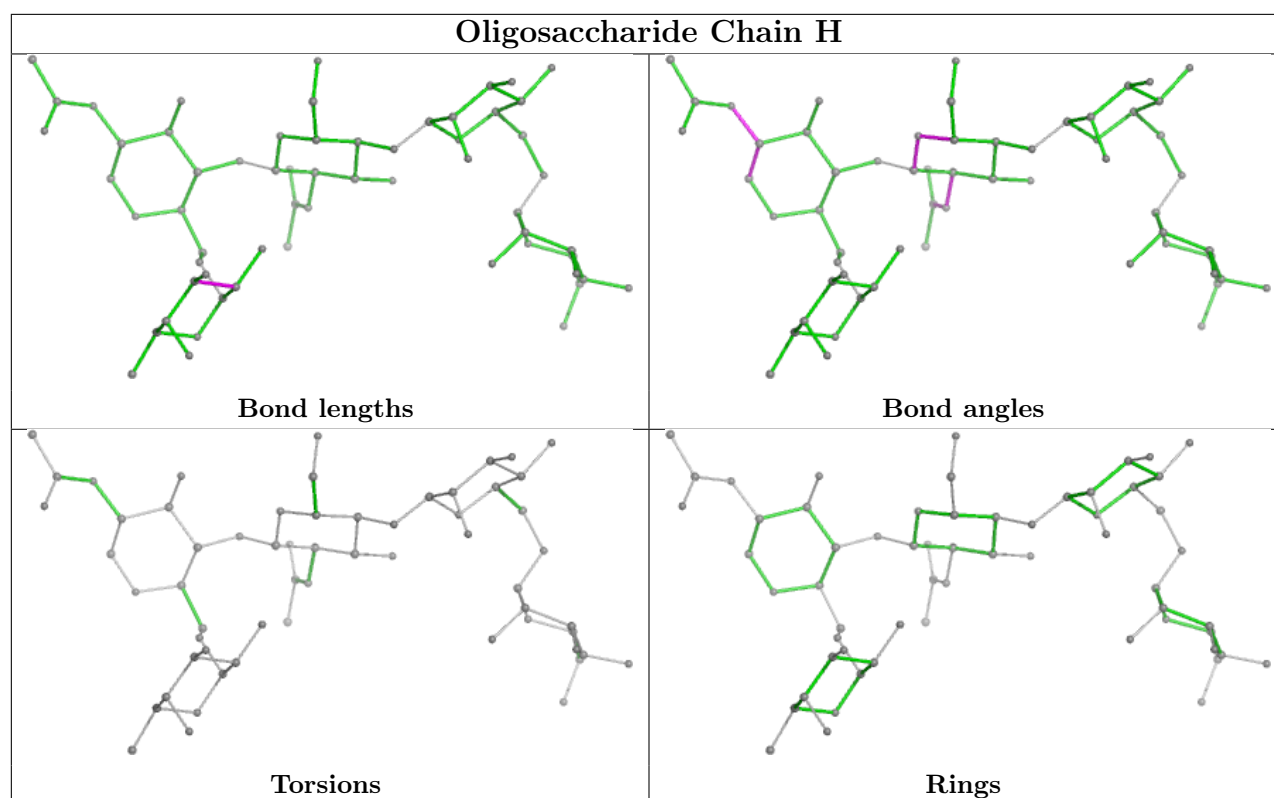
Mol	Chain	Res	Type	Atoms
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 2 are monoatomic - leaving 40 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	SEK	C	301	-	1,2,2	0.82	0	0,1,1	-	-
5	SEK	A	303	-	1,2,2	1.67	0	0,1,1	-	-
5	SEK	B	806	-	1,2,2	5.41	1 (100%)	0,1,1	-	-
5	SEK	D	804	-	1,2,2	1.14	0	0,1,1	-	-
5	SEK	D	811	-	1,2,2	0.21	0	0,1,1	-	-
6	HEM	C	302	9,3,2	41,50,50	1.55	8 (19%)	45,82,82	1.79	7 (15%)
5	SEK	D	810	-	1,2,2	1.25	0	0,1,1	-	-
5	SEK	A	301	-	1,2,2	0.56	0	0,1,1	-	-
5	SEK	A	305	-	1,2,2	0.41	0	0,1,1	-	-
5	SEK	D	806[B]	-	1,2,2	0.74	0	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SEK	B	804[A]	-	1,2,2	0.22	0	0,1,1	-	-
5	SEK	B	801	-	1,2,2	0.13	0	0,1,1	-	-
5	SEK	D	812	-	1,2,2	0.31	0	0,1,1	-	-
5	SEK	B	810	-	1,2,2	0.88	0	0,1,1	-	-
5	SEK	B	813	-	1,2,2	0.19	0	0,1,1	-	-
5	SEK	B	805	-	1,2,2	1.92	0	0,1,1	-	-
5	SEK	D	807	-	1,2,2	1.02	0	0,1,1	-	-
5	SEK	D	813	-	1,2,2	0.75	0	0,1,1	-	-
7	NAG	D	815	3	14,14,15	0.32	0	17,19,21	1.03	1 (5%)
6	HEM	A	304	9,3,2	41,50,50	1.61	8 (19%)	45,82,82	1.56	10 (22%)
5	SEK	B	803	-	1,2,2	6.09	1 (100%)	0,1,1	-	-
5	SEK	B	812	-	1,2,2	2.06	1 (100%)	0,1,1	-	-
5	SEK	B	809	-	1,2,2	0.85	0	0,1,1	-	-
5	SEK	B	807	-	1,2,2	0.50	0	0,1,1	-	-
5	SEK	B	808	-	1,2,2	0.23	0	0,1,1	-	-
7	NAG	B	815	3	14,14,15	0.47	0	17,19,21	1.66	4 (23%)
7	NAG	D	814	3	14,14,15	0.40	0	17,19,21	0.85	0
5	SEK	B	802	-	1,2,2	3.27	1 (100%)	0,1,1	-	-
5	SEK	D	801	-	1,2,2	0.29	0	0,1,1	-	-
5	SEK	D	806[A]	-	1,2,2	0.72	0	0,1,1	-	-
5	SEK	D	802	-	1,2,2	0.20	0	0,1,1	-	-
5	SEK	D	803	-	1,2,2	1.39	0	0,1,1	-	-
5	SEK	D	805	-	1,2,2	1.73	0	0,1,1	-	-
5	SEK	A	302	-	1,2,2	0.29	0	0,1,1	-	-
5	SEK	C	303	-	1,2,2	0.35	0	0,1,1	-	-
5	SEK	B	811	-	1,2,2	0.03	0	0,1,1	-	-
7	NAG	B	814	3	14,14,15	0.53	0	17,19,21	0.96	0
5	SEK	D	809	-	1,2,2	2.61	1 (100%)	0,1,1	-	-
5	SEK	D	808	-	1,2,2	0.65	0	0,1,1	-	-
5	SEK	B	804[B]	-	1,2,2	1.05	0	0,1,1	-	-

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
7	NAG	B	815	3	-	5/6/23/26	0/1/1/1
7	NAG	D	814	3	-	0/6/23/26	0/1/1/1
7	NAG	D	815	3	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEM	A	304	9,3,2	-	4/12/54/54	-
6	HEM	C	302	9,3,2	-	4/12/54/54	-
7	NAG	B	814	3	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	803	SEK	C-N	-6.09	0.97	1.15
5	B	806	SEK	C-N	-5.41	0.99	1.15
6	A	304	HEM	C4D-C3D	-4.18	1.37	1.45
6	A	304	HEM	C1D-C2D	-4.06	1.36	1.44
6	C	302	HEM	CHB-C1B	3.73	1.44	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	302	HEM	C4B-CHC-C1C	6.08	130.58	122.56
6	C	302	HEM	C4C-CHD-C1D	5.92	130.37	122.56
6	A	304	HEM	C4C-CHD-C1D	4.61	128.64	122.56
6	A	304	HEM	C4B-CHC-C1C	4.04	127.89	122.56
6	C	302	HEM	O1A-CGA-CBA	-3.61	111.47	123.08

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	815	NAG	C1-C2-N2-C7
7	B	815	NAG	C8-C7-N2-C2
7	B	815	NAG	O7-C7-N2-C2
7	D	815	NAG	C4-C5-C6-O6
7	B	814	NAG	C8-C7-N2-C2

There are no ring outliers.

9 monomers are involved in 13 short contacts:

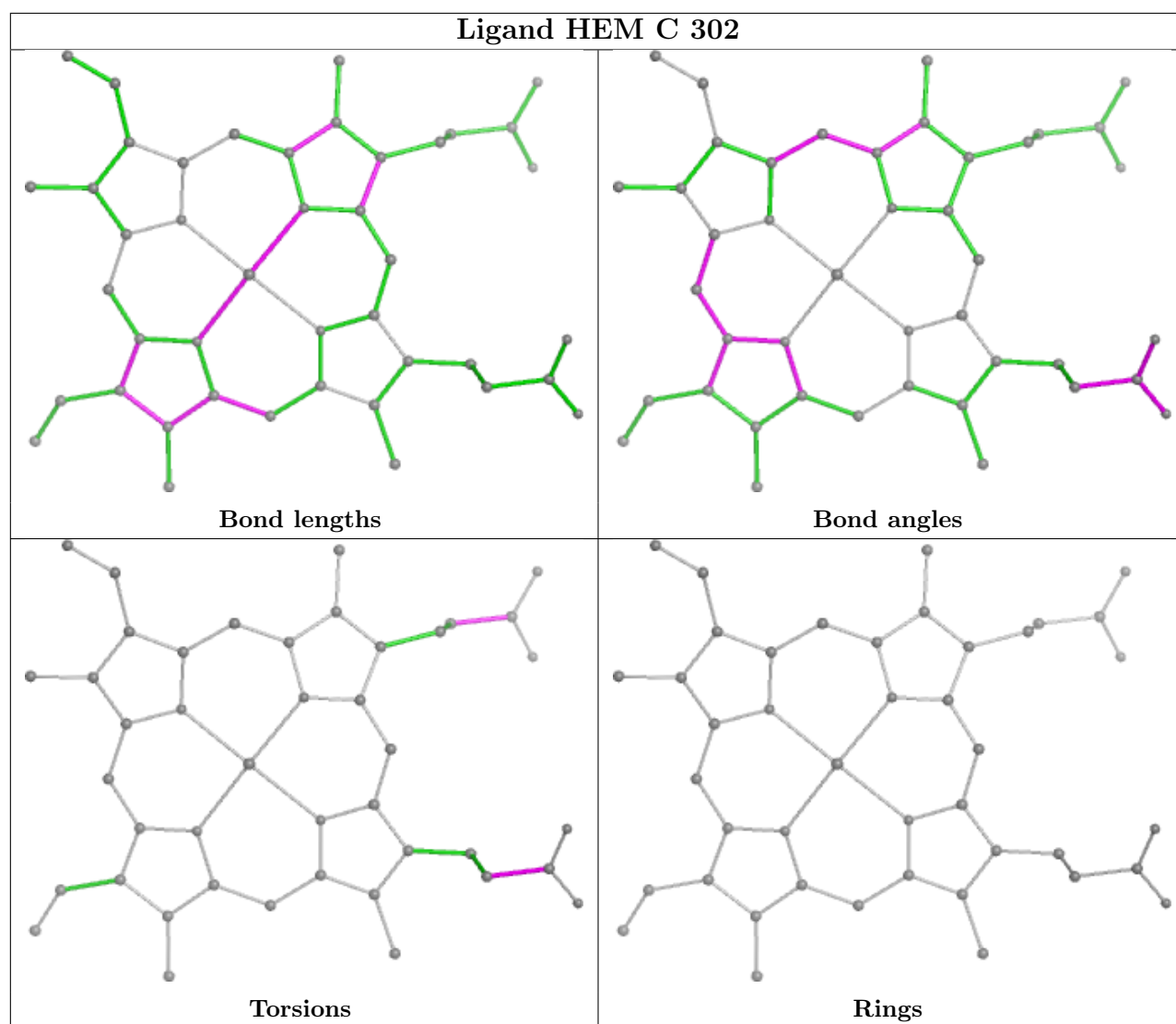
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	302	HEM	1	0
5	A	301	SEK	1	0
5	B	805	SEK	1	0
5	D	813	SEK	1	0

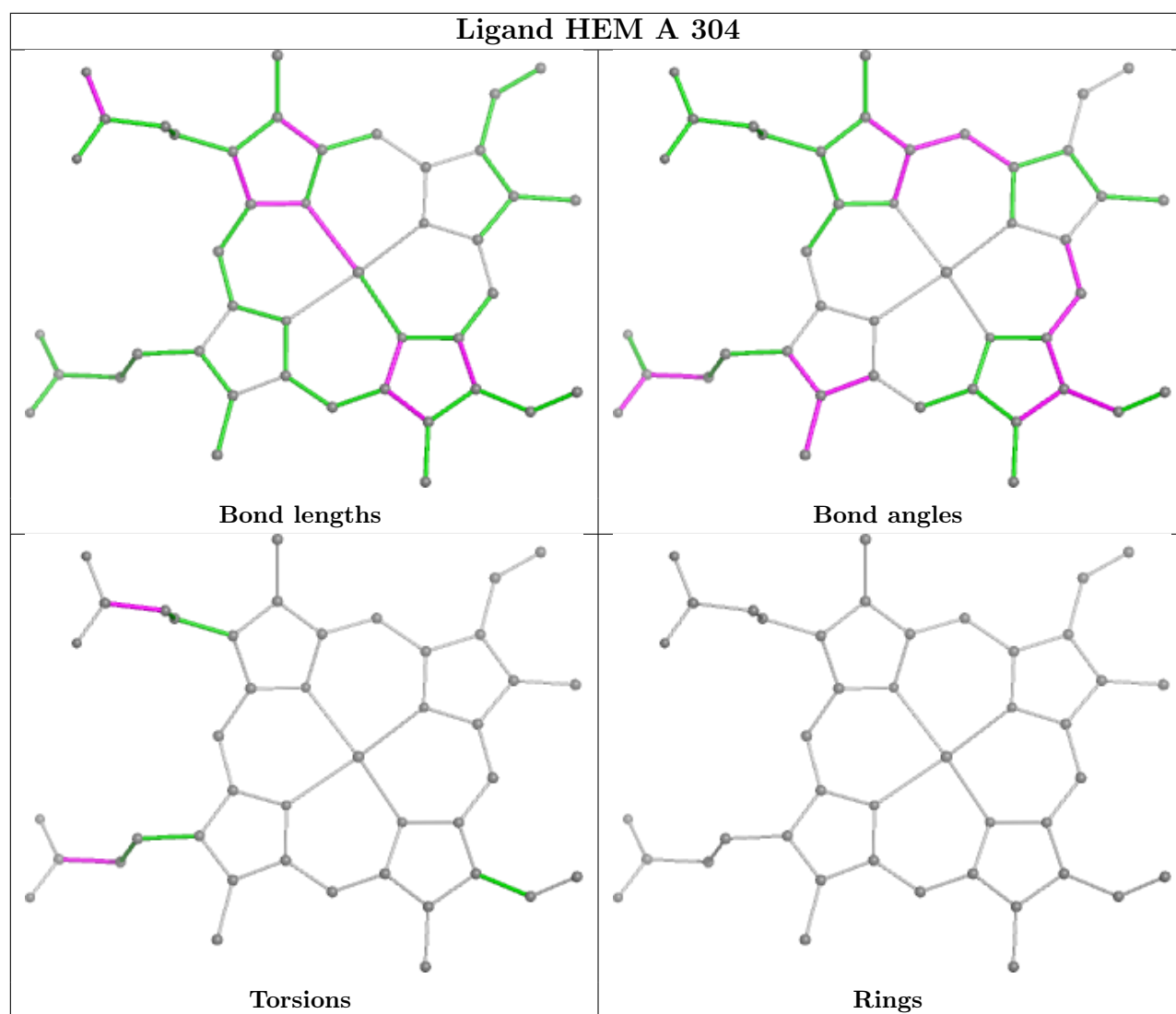
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	812	SEK	1	0
5	B	807	SEK	1	0
5	D	801	SEK	1	0
7	B	814	NAG	5	0
5	D	809	SEK	1	0

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 than 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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	E	57/60 (95%)	-0.13	1 (1%) 67 69	29, 42, 72, 105	0
1	F	58/60 (96%)	1.77	24 (41%) 1 0	83, 108, 127, 144	0
2	A	105/114 (92%)	-0.84	0 100 100	19, 26, 46, 74	0
2	C	105/114 (92%)	-0.56	1 (0%) 79 81	21, 32, 60, 84	0
3	B	464/467 (99%)	-0.76	2 (0%) 89 90	19, 28, 49, 75	0
3	D	463/467 (99%)	-0.38	1 (0%) 92 93	21, 39, 67, 88	0
All	All	1252/1282 (97%)	-0.46	29 (2%) 61 62	19, 33, 83, 144	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	96	PHE	4.6
1	F	101	TYR	3.7
1	F	56	ILE	3.3
1	F	88	ILE	3.1
1	F	103	HIS	3.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

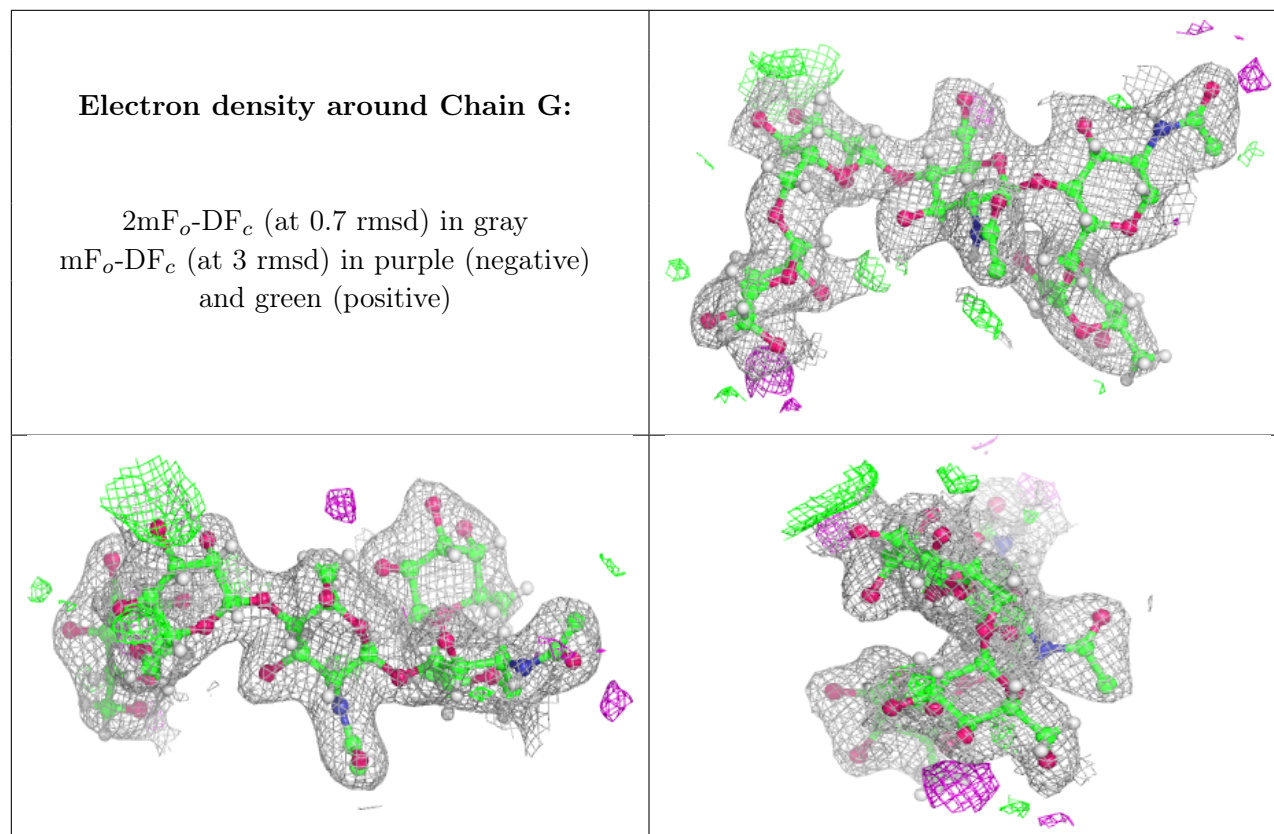
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CSO	D	316	7/8	0.93	0.06	25,27,27,30	1
3	CSO	B	316	7/8	0.97	0.05	23,24,25,25	1

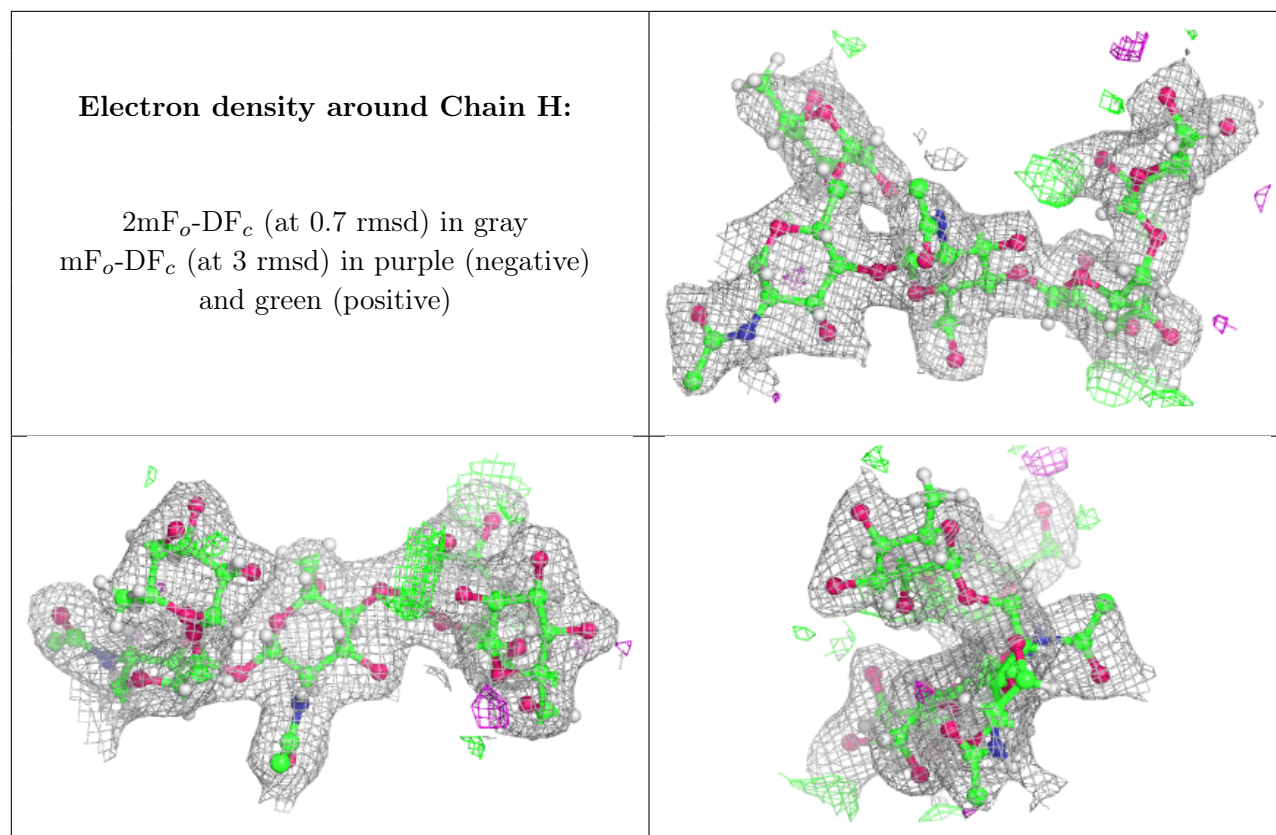
6.3 Carbohydrates [i](#)

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	NAG	G	1	14/15	0.92	0.07	24,27,30,32	0
4	BMA	G	3	11/12	0.93	0.06	31,34,37,39	0
4	FUC	G	5	10/11	0.93	0.06	33,35,37,38	0
4	NAG	G	2	14/15	0.94	0.07	24,27,30,33	0
4	MAN	H	4	11/12	0.94	0.05	27,33,37,37	0
4	FUC	H	5	10/11	0.94	0.07	34,36,39,39	0
4	MAN	G	4	11/12	0.95	0.06	32,33,35,38	0
4	BMA	H	3	11/12	0.95	0.05	29,30,32,33	0
4	NAG	H	1	14/15	0.96	0.05	27,29,31,32	0
4	NAG	H	2	14/15	0.97	0.05	22,26,30,30	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SEK	D	808	3/3	0.72	0.18	50,50,50,51	1
5	SEK	B	813	3/3	0.73	0.25	64,64,76,81	1
5	SEK	B	810	3/3	0.73	0.19	46,46,49,66	1
5	SEK	A	302	3/3	0.78	0.19	49,49,53,58	1
5	SEK	B	812	3/3	0.83	0.18	33,33,34,43	1
7	NAG	D	814	14/15	0.83	0.10	41,55,60,62	0
7	NAG	D	815	14/15	0.85	0.10	62,67,68,70	0
7	NAG	B	815	14/15	0.87	0.09	42,48,55,58	0
5	SEK	D	802	3/3	0.87	0.14	27,27,31,38	1
5	SEK	B	806	3/3	0.87	0.13	29,29,31,54	1
5	SEK	B	804[B]	3/3	0.89	0.13	28,28,34,36	3
5	SEK	B	811	3/3	0.89	0.16	30,30,37,53	1
5	SEK	B	804[A]	3/3	0.89	0.13	16,16,21,26	3
7	NAG	B	814	14/15	0.91	0.07	26,37,42,43	0

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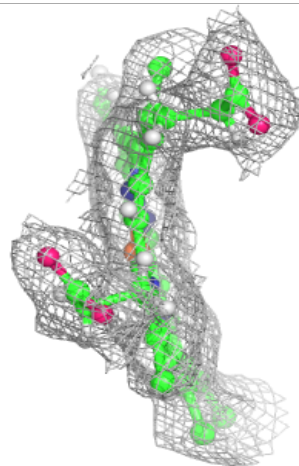
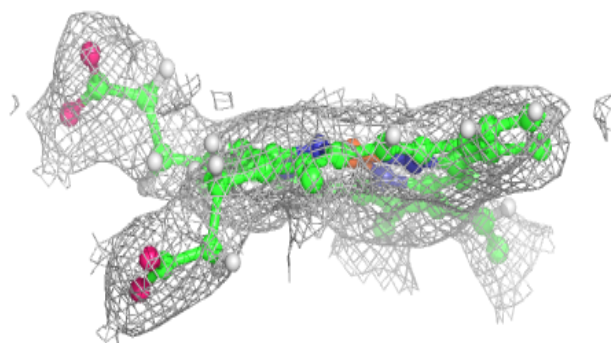
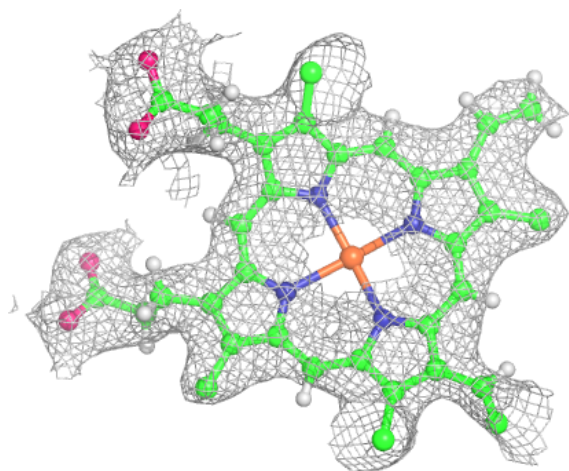
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	SEK	D	812	3/3	0.91	0.11	61,61,65,66	1
5	SEK	D	809	3/3	0.92	0.08	31,31,37,38	1
5	SEK	B	809	3/3	0.92	0.29	29,29,33,41	1
5	SEK	B	808	3/3	0.93	0.19	31,31,33,38	3
5	SEK	D	807	3/3	0.93	0.28	23,23,25,26	1
5	SEK	B	803	3/3	0.93	0.26	20,20,24,48	1
5	SEK	D	806[A]	3/3	0.95	0.12	47,47,49,51	3
5	SEK	D	806[B]	3/3	0.95	0.12	27,27,30,33	3
5	SEK	D	811	3/3	0.96	0.10	59,59,71,75	1
5	SEK	A	303	3/3	0.96	0.08	34,34,38,43	1
5	SEK	B	807	3/3	0.96	0.08	30,30,36,43	1
5	SEK	B	802	3/3	0.97	0.09	25,25,34,36	1
5	SEK	D	805	3/3	0.97	0.09	48,48,60,61	0
5	SEK	C	303	3/3	0.97	0.09	46,46,48,52	1
5	SEK	D	813	3/3	0.97	0.09	56,56,66,73	1
5	SEK	B	805	3/3	0.98	0.06	30,30,32,32	1
5	SEK	A	301	3/3	0.98	0.08	37,37,41,49	1
5	SEK	D	810	3/3	0.98	0.09	42,42,45,47	1
6	HEM	C	302	43/43	0.98	0.06	26,30,36,37	0
6	HEM	A	304	43/43	0.99	0.05	19,22,31,31	0
5	SEK	D	801	3/3	0.99	0.07	35,35,36,49	1
5	SEK	D	803	3/3	0.99	0.09	37,37,60,67	0
8	CA	B	816	1/1	0.99	0.03	23,23,23,23	0
8	CA	D	816	1/1	0.99	0.02	27,27,27,27	0
5	SEK	C	301	3/3	1.00	0.04	17,17,19,27	0
5	SEK	D	804	3/3	1.00	0.05	35,35,37,39	0
5	SEK	A	305	3/3	1.00	0.04	18,18,19,25	0
5	SEK	B	801	3/3	1.00	0.04	30,30,34,36	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.

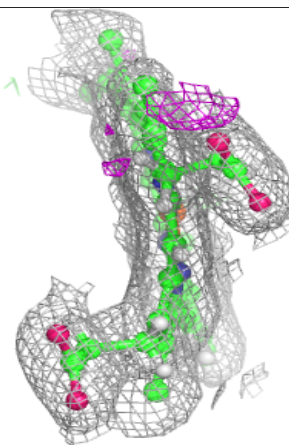
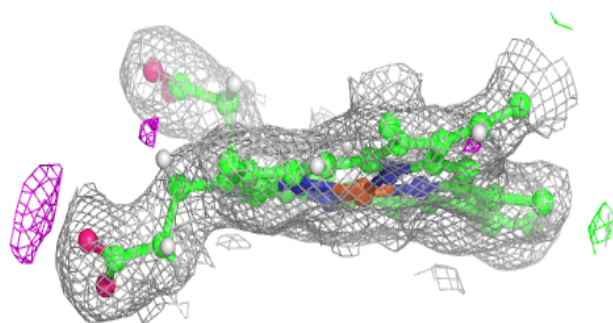
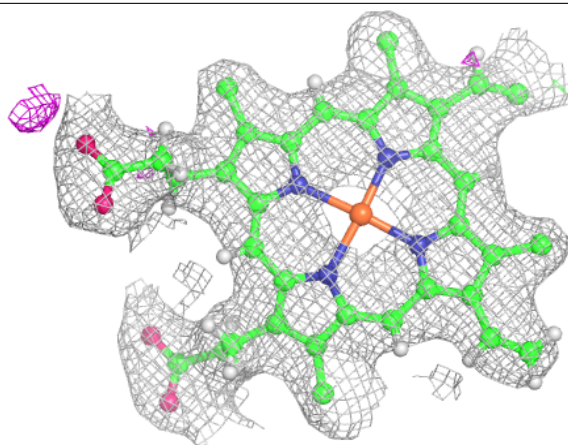
Electron density around HEM C 302:

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



Electron density around HEM A 304:

$2mF_o-DF_c$ (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.