



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 02:34 PM BST

PDB ID : 1D7W
Title : CRYSTAL STRUCTURE OF HUMAN MYELOPEROXIDASE ISOFORM C
COMPLEXED WITH CYANIDE AND BROMIDE AT PH 4.0
Authors : Fiedler, T.J.; Fenna, R.E.
Deposited on : 1999-10-20
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

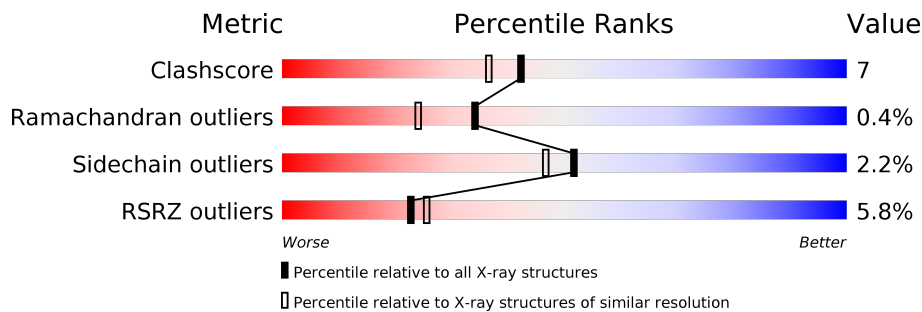
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	104	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 89%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 11%; height: 10px; background-color: yellow;"></div> </div> <p style="text-align: center;">4% 89% 11%</p>
1	B	104	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: yellow;"></div> </div> <p style="text-align: center;">4% 88% 13%</p>
2	C	466	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 83%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 15%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange;"></div> </div> <p style="text-align: center;">2% 83% 15% •</p>
2	D	466	<div style="display: flex; align-items: center;"> <div style="width: 11%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 82%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: yellow;"></div> </div> <p style="text-align: center;">11% 82% 17% •</p>
3	E	6	<div style="display: flex; align-items: center;"> <div style="width: 50%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 50%; height: 10px; background-color: yellow;"></div> </div> <p style="text-align: center;">50% 50%</p>
3	F	6	<div style="display: flex; align-items: center;"> <div style="width: 33%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 67%; height: 10px; background-color: yellow;"></div> </div> <p style="text-align: center;">33% 67%</p>

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
7	ACT	C	1606	-	-	X	-

2 Entry composition i

There are 11 unique types of molecules in this entry. The entry contains 10319 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	104	Total 838	C 529	N 148	O 156	S 5	0	0	0
1	B	104	Total 838	C 529	N 148	O 156	S 5	0	0	0

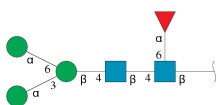
- Molecule 2 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	466	Total 3733	C 2351	N 687	O 668	S 27	0	0	0
2	D	466	Total 3733	C 2351	N 687	O 668	S 27	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	150	CSO	CYS	modified residue	UNP P05164
D	150	CSO	CYS	modified residue	UNP P05164

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[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.

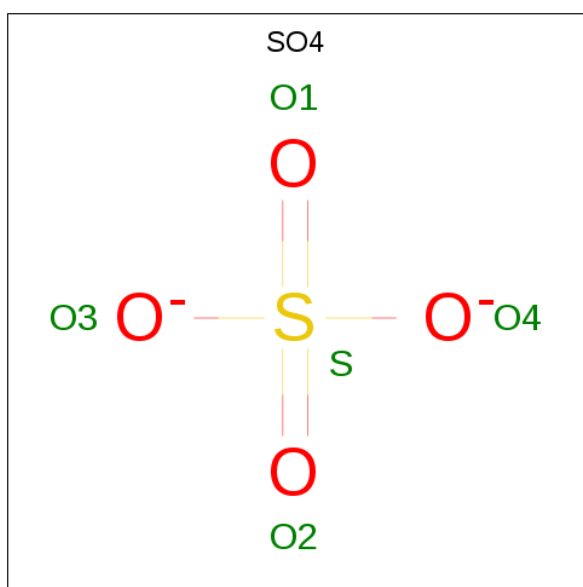


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	6	Total 71	C 40	N 2	O 29	0	0	0
3	F	6	Total 71	C 40	N 2	O 29	0	0	0

- Molecule 4 is BROMIDE ION (three-letter code: BR) (formula: Br).

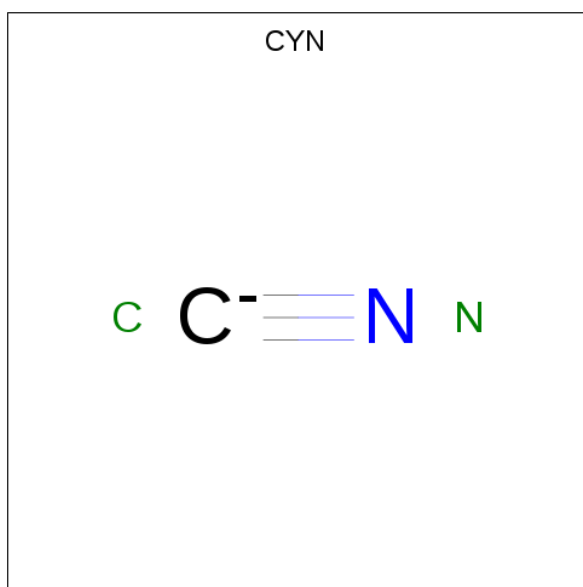
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Br 1 1	0	0
4	A	1	Total Br 1 1	0	0
4	D	3	Total Br 3 3	0	0
4	C	3	Total Br 3 3	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



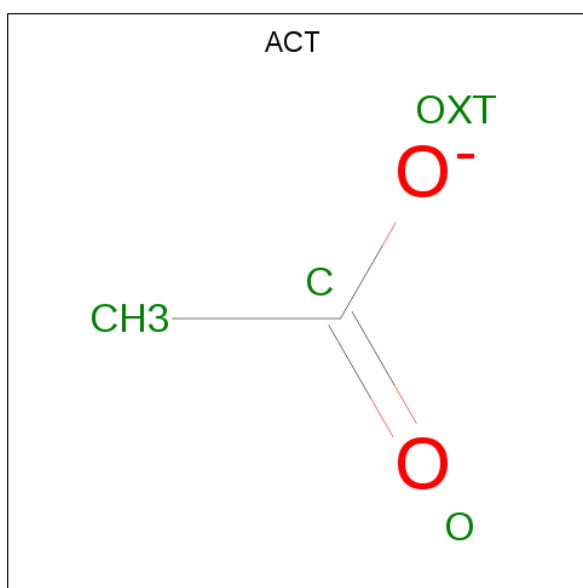
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	C	1	Total O S 5 4 1	0	0
5	C	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	D	1	Total O S 5 4 1	0	0

- Molecule 6 is CYANIDE ION (three-letter code: CYN) (formula: CN).



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

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



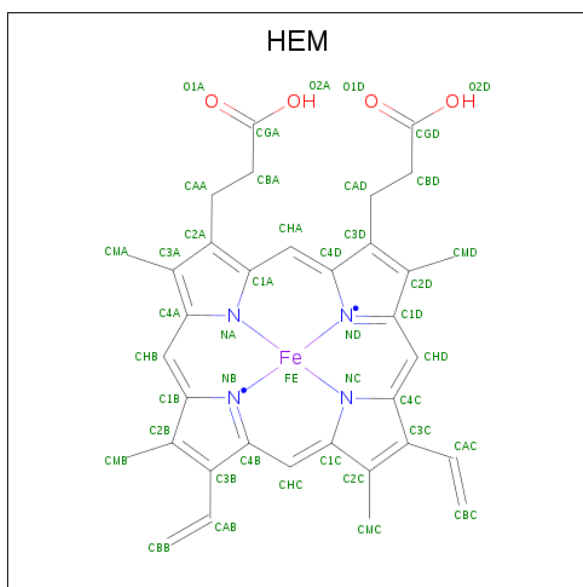
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 8 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



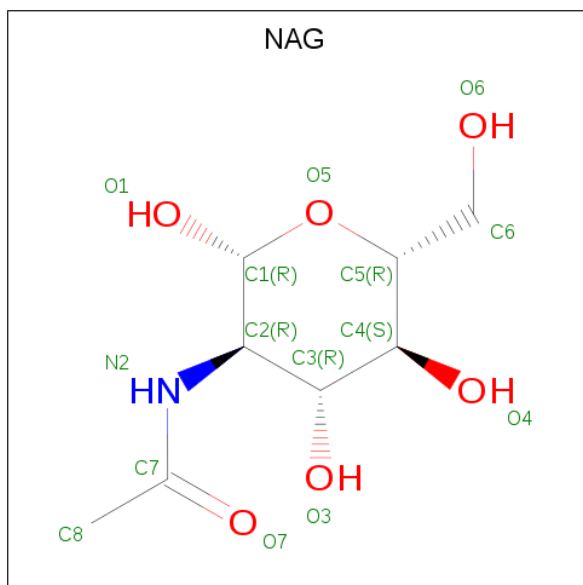
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
8	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Fe	N			O
8	B	1	43	34	1	4	4	0	0

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
9	C	1	14	8	1	5	0	0
9	C	1	14	8	1	5	0	0
9	D	1	14	8	1	5	0	0
9	D	1	14	8	1	5	0	0

- Molecule 10 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
10	D	1	1	1	0	0
10	C	1	1	1	0	0

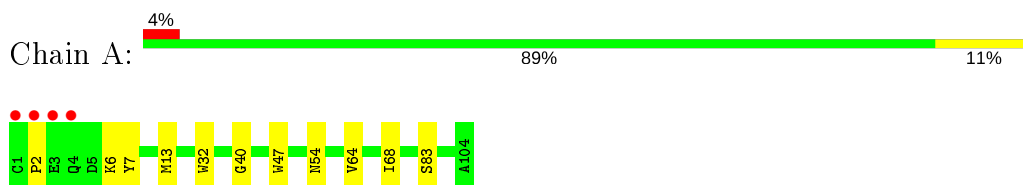
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	96	Total 96	O 96	0	0
11	C	314	Total 314	O 314	0	0
11	B	98	Total 98	O 98	0	0
11	D	298	Total 298	O 298	0	0

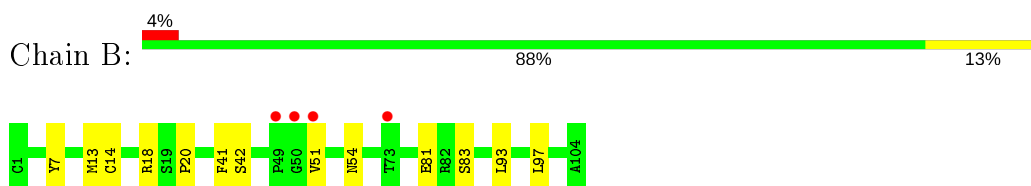
3 Residue-property plots [i](#)

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.

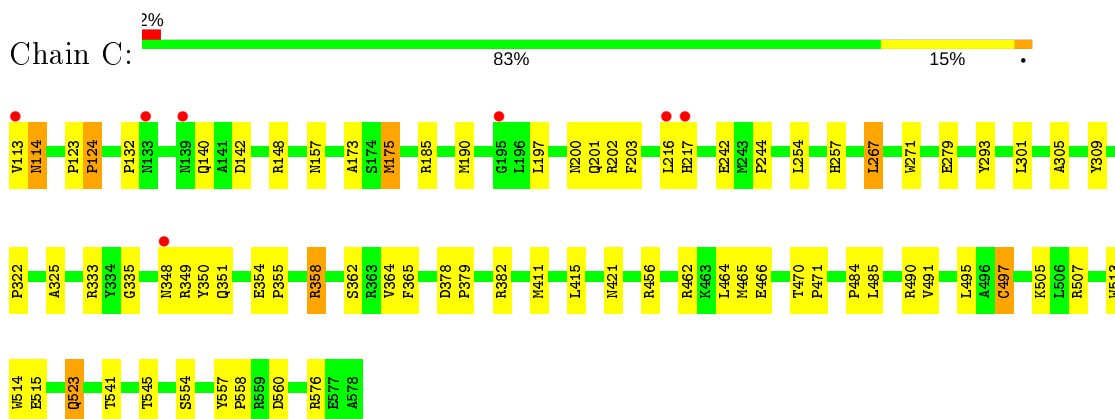
- Molecule 1: MYELOPEROXIDASE



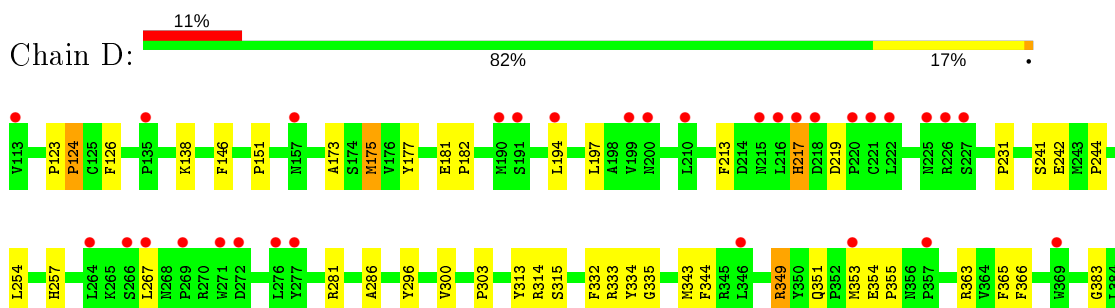
- Molecule 1: MYELOPEROXIDASE

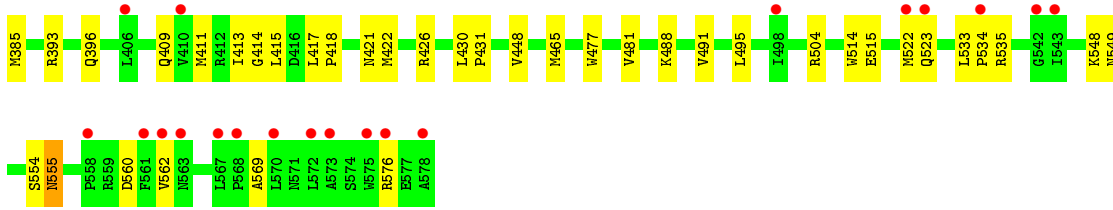


- Molecule 2: MYELOPEROXIDASE



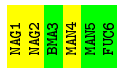
- Molecule 2: MYELOPEROXIDASE





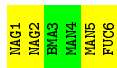
- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 50% 50%



- Molecule 3: alpha-D-mannopyranose-(1-3)-[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 F: 33% 67%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	111.34Å 63.32Å 92.26Å 90.00° 97.41° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 48.49 – 1.90	Depositor EDS
% Data completeness (in resolution range)	87.9 (30.00-1.90) 90.7 (48.49-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.00 (at 1.90Å)	Xtrriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.215 , 0.270 0.213 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	14.0	Xtrriage
Anisotropy	0.412	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10319	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CSO, BMA, NAG, SO4, CA, FUC, BR, ACT, HEM, CYN, MAN

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	0.69	0/863	0.72	0/1174
1	B	0.66	0/863	0.72	0/1174
2	C	0.67	0/3811	0.66	0/5168
2	D	0.65	0/3811	0.64	0/5168
All	All	0.66	0/9348	0.66	0/12684

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	838	0	798	10	0
1	B	838	0	798	10	0
2	C	3733	0	3725	55	0
2	D	3733	0	3725	53	0
3	E	71	0	61	0	0
3	F	71	0	61	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	3	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	10	0	0	0	0
5	D	5	0	0	1	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	4	0	3	0	0
7	B	8	0	6	0	0
7	C	20	0	15	3	0
7	D	16	0	12	2	0
8	A	43	0	30	4	0
8	B	43	0	30	3	0
9	C	28	0	26	1	0
9	D	28	0	26	0	0
10	C	1	0	0	0	0
10	D	1	0	0	0	0
11	A	96	0	0	2	0
11	B	98	0	0	5	0
11	C	314	0	0	9	0
11	D	298	0	0	9	0
All	All	10319	0	9316	129	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 7.

All (129) 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:A:6:LYS:O	11:A:726(A):HOH:O	1.75	1.02
2:D:411:MET:HE2	2:D:415:LEU:HD21	1.61	0.83
1:A:64:VAL:HG13	1:A:68:ILE:HD12	1.65	0.78
2:D:349:ARG:HG3	2:D:351:GLN:HG2	1.67	0.76
2:C:514:TRP:CE2	2:C:515:GLU:HG3	2.21	0.76
1:A:7:TYR:HE2	11:C:900(A):HOH:O	1.71	0.74
2:D:514:TRP:HB3	11:D:647(B):HOH:O	1.88	0.73
2:C:132:PRO:HG3	2:C:140:GLN:NE2	2.04	0.72
2:C:200:ASN:ND2	2:C:202:ARG:H	1.89	0.70
2:D:411:MET:CE	2:D:415:LEU:HD21	2.25	0.66
2:C:267:LEU:HD12	2:C:576:ARG:HD3	1.78	0.64
1:B:83:SER:HB3	2:D:554:SER:O	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:605:HEM:HMC2	8:A:605:HEM:HBC2	1.80	0.64
2:C:465:MET:HE1	2:C:471:PRO:HD3	1.78	0.64
2:C:200:ASN:HD22	2:C:203:PHE:H	1.43	0.63
2:C:350:TYR:CZ	2:C:382:ARG:HG2	2.34	0.62
1:A:68:ILE:HD13	2:C:464:LEU:HD23	1.83	0.61
11:D:861(B):HOH:O	3:F:1:NAG:H4	2.01	0.60
2:C:200:ASN:HD22	2:C:202:ARG:H	1.48	0.60
8:B:605:HEM:HMC2	8:B:605:HEM:HBC2	1.82	0.60
2:D:417:LEU:HB3	2:D:418:PRO:HD3	1.84	0.60
2:C:333:ARG:HH11	2:C:421:ASN:HD22	1.52	0.58
2:D:522:MET:HG3	7:D:2604:ACT:H1	1.86	0.58
2:D:241:SER:O	2:D:366:PHE:HA	2.04	0.57
2:D:514:TRP:CE2	2:D:515:GLU:HG3	2.39	0.57
2:C:200:ASN:ND2	2:C:203:PHE:H	2.02	0.57
2:D:244:PRO:HB2	2:D:343:MET:SD	2.45	0.57
1:A:47:TRP:HH2	11:C:988(A):HOH:O	1.87	0.57
1:A:7:TYR:CE2	11:C:900(A):HOH:O	2.51	0.55
2:C:358:ARG:HH11	2:C:358:ARG:HG2	1.71	0.55
2:D:333:ARG:HH11	2:D:421:ASN:ND2	2.05	0.53
2:D:242:GLU:O	2:D:365:PHE:HA	2.08	0.53
2:D:173:ALA:HA	2:D:175:MET:SD	2.48	0.53
2:C:157:ASN:HA	11:C:979(A):HOH:O	2.09	0.53
1:B:7:TYR:HE2	11:B:900(B):HOH:O	1.91	0.53
2:D:448:VAL:HB	2:D:465:MET:HG3	1.91	0.53
1:B:51:VAL:HA	11:B:935(B):HOH:O	2.08	0.52
2:C:465:MET:CE	2:C:471:PRO:HD3	2.39	0.52
2:C:333:ARG:HH11	2:C:421:ASN:ND2	2.08	0.52
2:C:456:ARG:HH21	2:C:484:PRO:HB2	1.75	0.52
2:C:148:ARG:HD3	7:C:1606:ACT:H1	1.92	0.52
2:D:123:PRO:HA	11:D:988(B):HOH:O	2.09	0.52
2:D:314:ARG:HH22	2:D:504:ARG:HH22	1.58	0.51
2:D:314:ARG:HH22	2:D:504:ARG:NH2	2.08	0.51
2:D:413:ILE:HG12	2:D:414:GLY:N	2.25	0.51
8:A:605:HEM:HBC2	8:A:605:HEM:CMC	2.40	0.51
1:B:42:SER:HB2	11:B:869(B):HOH:O	2.10	0.51
2:D:217:HIS:N	2:D:217:HIS:ND1	2.59	0.51
2:D:363:ARG:HG2	2:D:409:GLN:NE2	2.26	0.50
2:C:523:GLN:CD	2:C:523:GLN:H	2.14	0.50
2:C:411:MET:HE2	2:C:415:LEU:HD11	1.94	0.50
2:D:535:ARG:HB3	7:D:2609:ACT:O	2.11	0.50
2:D:393:ARG:HB2	2:D:396:GLN:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:197:LEU:HG	2:D:257:HIS:CD2	2.47	0.49
2:D:533:LEU:N	2:D:534:PRO:CD	2.75	0.49
2:C:462:ARG:O	2:C:466:GLU:HG2	2.12	0.49
2:D:549:ASN:ND2	11:D:829(B):HOH:O	2.46	0.48
2:C:201:GLN:NE2	9:C:1620:NAG:C7	2.77	0.47
2:D:286:ALA:HA	11:D:647(B):HOH:O	2.15	0.47
2:C:349:ARG:HG3	2:C:351:GLN:HG2	1.96	0.47
2:C:545:THR:HG21	2:C:557:TYR:HE1	1.78	0.47
2:C:485:LEU:HD13	2:C:490:ARG:HA	1.97	0.47
1:B:41:PHE:HD2	11:B:869(B):HOH:O	1.98	0.46
2:C:309:TYR:CZ	2:C:497:CYS:HA	2.50	0.46
7:C:1609:ACT:H1	11:C:874(A):HOH:O	2.16	0.46
2:C:173:ALA:HA	2:C:175:MET:SD	2.55	0.46
2:C:491:VAL:HB	2:C:495:LEU:HB2	1.97	0.46
2:D:151:PRO:HG3	11:D:871(B):HOH:O	2.15	0.46
2:D:344:PHE:O	2:D:383:GLY:HA3	2.15	0.46
2:D:569:ALA:HA	11:D:910(B):HOH:O	2.16	0.46
2:C:113:VAL:HG12	2:C:114:ASN:N	2.30	0.46
2:C:348:ASN:HA	2:C:382:ARG:NH1	2.30	0.46
2:D:296:TYR:CE2	2:D:300:VAL:HG21	2.51	0.46
8:B:605:HEM:CMC	8:B:605:HEM:HBC2	2.45	0.45
2:D:533:LEU:HB3	2:D:534:PRO:HD3	1.98	0.45
2:D:354:GLU:HB3	2:D:355:PRO:HA	1.98	0.45
2:D:181:GLU:N	2:D:182:PRO:CD	2.80	0.45
2:C:242:GLU:O	2:C:365:PHE:HA	2.17	0.45
8:B:605:HEM:CBC	2:D:335:GLY:HA3	2.47	0.45
2:D:385:MET:O	2:D:555:ASN:HA	2.17	0.45
1:B:81:GLU:HG3	5:D:2610:SO4:O4	2.16	0.45
2:C:514:TRP:HB3	11:C:647(A):HOH:O	2.16	0.44
2:C:185:ARG:HG3	2:C:190:MET:CE	2.47	0.44
2:D:213:PHE:CD2	2:D:231:PRO:HG2	2.53	0.44
2:D:477:TRP:O	2:D:481:VAL:HG22	2.18	0.44
2:D:554:SER:HB3	2:D:560:ASP:HB3	2.00	0.44
2:C:378:ASP:HB2	2:C:379:PRO:HD3	1.99	0.44
2:D:194:LEU:HD13	11:D:948(B):HOH:O	2.18	0.44
1:B:18:ARG:HB2	11:B:819(B):HOH:O	2.18	0.44
2:C:554:SER:HB3	2:C:560:ASP:HB3	2.00	0.44
2:D:313:TYR:CZ	2:D:315:SER:HA	2.53	0.44
2:C:354:GLU:HB3	2:C:355:PRO:HA	2.00	0.44
2:C:507:ARG:HG3	2:C:513:TRP:CE2	2.53	0.43
2:D:213:PHE:CG	2:D:231:PRO:HG2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:358:ARG:NH1	2:C:358:ARG:HG2	2.32	0.43
1:A:83:SER:HB3	2:C:554:SER:O	2.19	0.43
2:D:123:PRO:HA	2:D:124:PRO:HA	1.84	0.43
2:D:267:LEU:HD13	2:D:576:ARG:CZ	2.48	0.43
2:C:378:ASP:OD1	2:C:541:THR:HB	2.18	0.42
2:D:126:PHE:HB3	2:D:146:PHE:CD2	2.54	0.42
2:D:314:ARG:NH2	2:D:504:ARG:NH2	2.68	0.42
1:B:93:LEU:O	1:B:97:LEU:HG	2.19	0.42
2:D:332:PHE:C	2:D:334:TYR:H	2.23	0.42
2:D:548:LYS:HG2	2:D:562:VAL:HG13	2.00	0.42
2:C:271:TRP:CZ3	2:C:279:GLU:HG3	2.54	0.42
2:C:505:LYS:HE3	3:F:5:MAN:H61	2.02	0.42
2:C:293:TYR:CD2	2:C:513:TRP:HH2	2.38	0.42
1:A:2:PRO:HD2	11:A:791(A):HOH:O	2.20	0.41
1:B:13:MET:HG3	1:B:14:CYS:SG	2.60	0.41
8:A:605:HEM:HBB2	2:C:242:GLU:OE1	2.20	0.41
2:D:422:MET:O	2:D:426:ARG:HG3	2.19	0.41
1:A:32:TRP:CE2	2:C:325:ALA:HB2	2.55	0.41
2:C:124:PRO:HA	7:C:1606:ACT:H3	2.02	0.41
2:C:200:ASN:HD21	2:C:202:ARG:HB2	1.85	0.41
2:C:216:LEU:HD11	11:C:801(A):HOH:O	2.20	0.41
2:D:177:TYR:OH	2:D:281:ARG:HA	2.21	0.41
2:D:426:ARG:HA	11:D:727(B):HOH:O	2.20	0.41
2:C:197:LEU:HG	2:C:257:HIS:CD2	2.55	0.41
2:C:362:SER:HA	2:C:365:PHE:CE1	2.56	0.41
2:C:462:ARG:NH2	11:C:1234(A):HOH:O	2.53	0.41
2:D:491:VAL:HB	2:D:495:LEU:HB2	2.03	0.41
8:A:605:HEM:CBC	2:C:335:GLY:HA3	2.50	0.41
1:A:40:GLY:HA2	1:B:20:PRO:HD2	2.03	0.41
2:C:244:PRO:HD3	2:C:364:VAL:O	2.20	0.40
2:C:123:PRO:HA	2:C:124:PRO:HA	1.79	0.40
2:C:301:LEU:HB3	2:C:305:ALA:HB3	2.03	0.40
2:D:430:LEU:HA	2:D:431:PRO:HD3	1.98	0.40
2:C:411:MET:HE2	11:C:983(A):HOH:O	2.22	0.40
2:D:303:PRO:HD3	2:D:488:LYS:HB2	2.04	0.40

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	A	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
1	B	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
2	C	463/466 (99%)	448 (97%)	13 (3%)	2 (0%)	34	24
2	D	463/466 (99%)	448 (97%)	13 (3%)	2 (0%)	34	24
All	All	1130/1140 (99%)	1092 (97%)	34 (3%)	4 (0%)	34	24

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	114	ASN
2	C	142	ASP
2	D	555	ASN
2	D	219	ASP

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	90/90 (100%)	88 (98%)	2 (2%)	52	47
1	B	90/90 (100%)	89 (99%)	1 (1%)	73	73
2	C	410/410 (100%)	399 (97%)	11 (3%)	44	38
2	D	410/410 (100%)	402 (98%)	8 (2%)	55	51
All	All	1000/1000 (100%)	978 (98%)	22 (2%)	52	47

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	MET
1	A	54	ASN
2	C	124	PRO
2	C	175	MET
2	C	217	HIS
2	C	254	LEU
2	C	267	LEU
2	C	322	PRO
2	C	358	ARG
2	C	470	THR
2	C	497	CYS
2	C	523	GLN
2	C	558	PRO
1	B	54	ASN
2	D	124	PRO
2	D	138	LYS
2	D	175	MET
2	D	217	HIS
2	D	254	LEU
2	D	349	ARG
2	D	353	MET
2	D	523	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
2	C	133	ASN
2	C	140	GLN
2	C	200	ASN
2	C	201	GLN
2	C	348	ASN
1	B	54	ASN
2	D	204	GLN
2	D	421	ASN
2	D	549	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](#)

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
2	CSO	C	150	2	3,6,7	0.87	0	0,6,8	0.00	-
2	CSO	D	150	2	3,6,7	0.99	0	0,6,8	0.00	-

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
2	CSO	C	150	2	-	0/1/5/7	-
2	CSO	D	150	2	-	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 [i](#)

12 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$
3	NAG	E	1	3,2	14,14,15	0.76	0	17,19,21	0.94	1 (5%)
3	NAG	E	2	3	14,14,15	0.65	0	17,19,21	1.11	2 (11%)
3	BMA	E	3	3	11,11,12	0.53	0	15,15,17	0.76	0
3	MAN	E	4	3	11,11,12	0.54	0	15,15,17	0.82	1 (6%)
3	MAN	E	5	3	11,11,12	0.77	0	15,15,17	0.63	0
3	FUC	E	6	3	10,10,11	0.71	0	14,14,16	0.48	0
3	NAG	F	1	3,2	14,14,15	0.68	0	17,19,21	1.12	0
3	NAG	F	2	3	14,14,15	0.81	1 (7%)	17,19,21	0.92	1 (5%)
3	BMA	F	3	3	11,11,12	0.50	0	15,15,17	0.65	0
3	MAN	F	4	3	11,11,12	0.60	0	15,15,17	0.75	0
3	MAN	F	5	3	11,11,12	0.97	0	15,15,17	0.63	0
3	FUC	F	6	3	10,10,11	0.60	0	14,14,16	0.81	1 (7%)

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	NAG	E	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	0/2/19/22	0/1/1/1
3	FUC	E	6	3	-	-	0/1/1/1
3	NAG	F	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	0/2/19/22	0/1/1/1
3	MAN	F	5	3	-	0/2/19/22	0/1/1/1
3	FUC	F	6	3	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	NAG	C1-C2	2.02	1.55	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	2	NAG	C2-N2-C7	-2.63	119.16	122.90
3	E	2	NAG	C1-C2-N2	-2.49	106.23	110.49
3	F	2	NAG	C4-C3-C2	-2.37	107.54	111.02
3	E	4	MAN	C1-O5-C5	2.17	115.14	112.19
3	F	6	FUC	O5-C1-C2	-2.06	107.59	110.77
3	E	1	NAG	C2-N2-C7	-2.04	120.00	122.90

There are no chirality outliers.

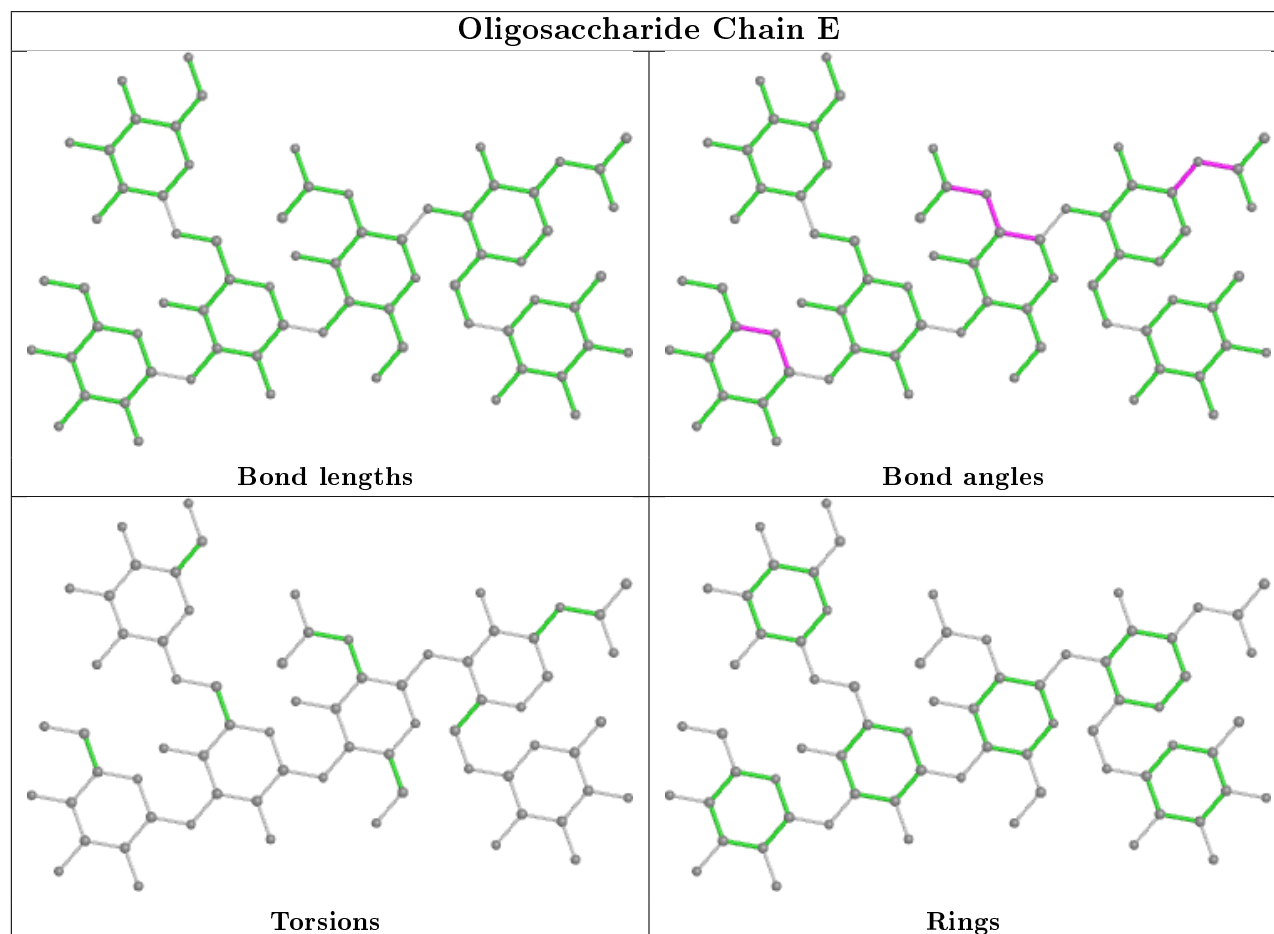
There are no torsion outliers.

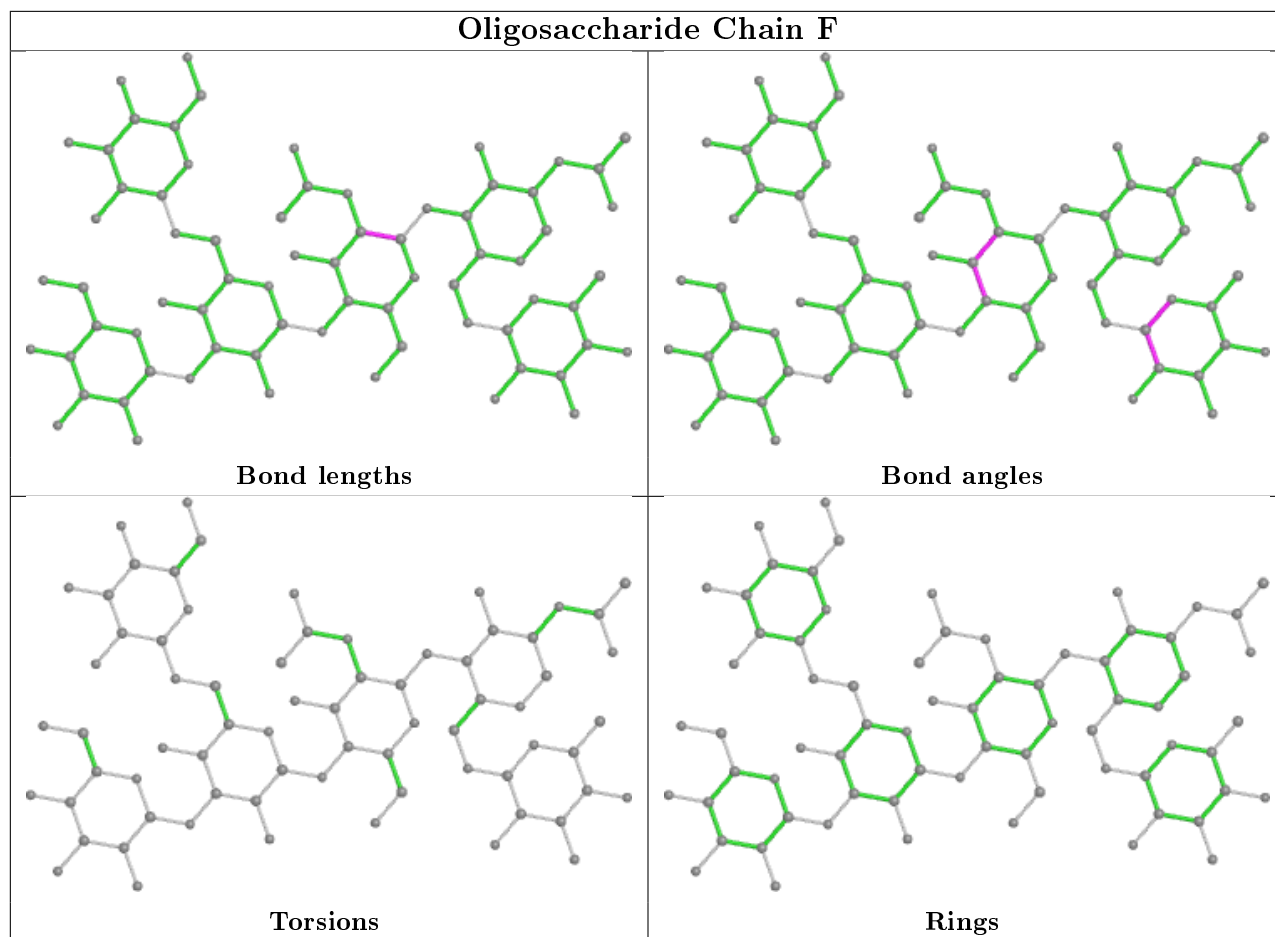
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	5	MAN	1	0
3	F	1	NAG	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 oligosaccharide.





5.6 Ligand geometry [i](#)

Of 35 ligands modelled in this entry, 10 are monoatomic - leaving 25 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$
8	HEM	B	605	1,2,6	27,50,50	1.69	6 (22%)	17,82,82	1.13	1 (5%)
9	NAG	C	1630	2	14,14,15	0.84	0	17,19,21	0.90	1 (5%)
7	ACT	B	2611	-	1,3,3	3.52	1 (100%)	0,3,3	0.00	-
7	ACT	A	2608	-	1,3,3	4.37	1 (100%)	0,3,3	0.00	-
9	NAG	D	2620	2	14,14,15	0.60	0	17,19,21	0.87	0
9	NAG	C	1620	2	14,14,15	0.44	0	17,19,21	0.96	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	A	1602	-	4,4,4	0.19	0	6,6,6	0.12	0
7	ACT	C	1609	-	1,3,3	2.10	1 (100%)	0,3,3	0.00	-
7	ACT	D	2609	-	1,3,3	2.33	1 (100%)	0,3,3	0.00	-
7	ACT	D	2607	-	1,3,3	2.70	1 (100%)	0,3,3	0.00	-
7	ACT	C	1604	-	1,3,3	2.03	1 (100%)	0,3,3	0.00	-
7	ACT	C	1606	-	1,3,3	1.16	0	0,3,3	0.00	-
7	ACT	B	1608	-	1,3,3	4.56	1 (100%)	0,3,3	0.00	-
5	SO4	D	2610	-	4,4,4	0.19	0	6,6,6	0.12	0
9	NAG	D	2630	2	14,14,15	0.68	0	17,19,21	1.05	1 (5%)
6	CYN	B	2844	8	0,1,1	0.00	-	-	-	-
8	HEM	A	605	1,2,6	27,50,50	1.62	7 (25%)	17,8,2,82	1.25	1 (5%)
7	ACT	C	1607	-	1,3,3	3.79	1 (100%)	0,3,3	0.00	-
7	ACT	D	2604	-	1,3,3	3.02	1 (100%)	0,3,3	0.00	-
7	ACT	D	2606	-	1,3,3	2.74	1 (100%)	0,3,3	0.00	-
5	SO4	C	1603	-	4,4,4	0.11	0	6,6,6	0.09	0
5	SO4	B	2602	-	4,4,4	0.27	0	6,6,6	0.06	0
6	CYN	A	1844	8	0,1,1	0.00	-	-	-	-
5	SO4	C	1610	-	4,4,4	0.20	0	6,6,6	0.15	0
7	ACT	C	1612	-	1,3,3	3.61	1 (100%)	0,3,3	0.00	-

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
8	HEM	B	605	1,2,6	-	0/6/54/54	-
9	NAG	C	1620	2	-	0/6/23/26	0/1/1/1
9	NAG	D	2630	2	-	0/6/23/26	0/1/1/1
9	NAG	C	1630	2	-	0/6/23/26	0/1/1/1
8	HEM	A	605	1,2,6	-	0/6/54/54	-
9	NAG	D	2620	2	-	2/6/23/26	0/1/1/1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1608	ACT	CH3-C	4.56	1.54	1.48
7	A	2608	ACT	CH3-C	4.37	1.54	1.48
7	C	1607	ACT	CH3-C	3.79	1.53	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	605	HEM	C3C-CAC	-3.74	1.40	1.47
8	B	605	HEM	C3B-C2B	-3.67	1.35	1.40
7	C	1612	ACT	CH3-C	3.61	1.53	1.48
7	B	2611	ACT	CH3-C	3.52	1.53	1.48
8	A	605	HEM	C3C-CAC	-3.51	1.40	1.47
8	A	605	HEM	C3B-CAB	-3.38	1.41	1.47
8	B	605	HEM	C3B-CAB	-3.13	1.41	1.47
7	D	2604	ACT	CH3-C	3.02	1.52	1.48
7	D	2606	ACT	CH3-C	2.74	1.52	1.48
7	D	2607	ACT	CH3-C	2.70	1.52	1.48
8	B	605	HEM	CBB-CAB	2.65	1.46	1.29
8	B	605	HEM	C3C-C2C	-2.64	1.36	1.40
8	A	605	HEM	CBC-CAC	2.50	1.45	1.29
8	A	605	HEM	CBB-CAB	2.50	1.45	1.29
8	B	605	HEM	CBC-CAC	2.39	1.45	1.29
7	D	2609	ACT	CH3-C	2.33	1.51	1.48
8	A	605	HEM	C3B-C2B	-2.32	1.37	1.40
8	A	605	HEM	C1B-C2B	2.17	1.47	1.42
8	A	605	HEM	C3C-C2C	-2.12	1.37	1.40
7	C	1609	ACT	CH3-C	2.10	1.51	1.48
7	C	1604	ACT	CH3-C	2.03	1.51	1.48

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	605	HEM	C3B-C4B-NB	2.52	112.47	109.21
9	D	2630	NAG	C1-C2-N2	-2.43	106.33	110.49
8	B	605	HEM	C3B-C4B-NB	2.29	112.17	109.21
9	C	1630	NAG	C1-C2-N2	-2.19	106.75	110.49
9	C	1620	NAG	C1-O5-C5	2.02	114.93	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

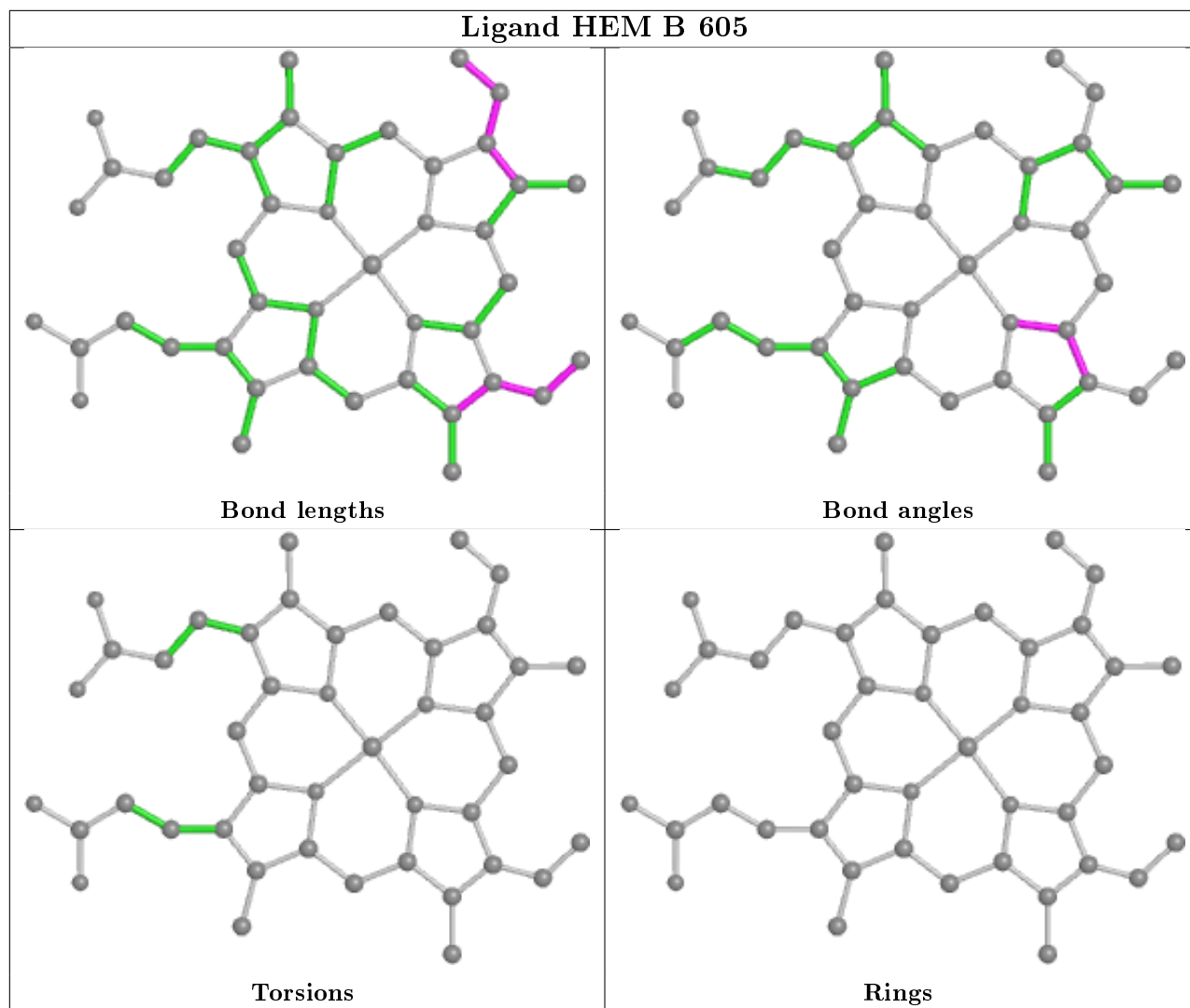
Mol	Chain	Res	Type	Atoms
9	D	2620	NAG	C4-C5-C6-O6
9	D	2620	NAG	O5-C5-C6-O6

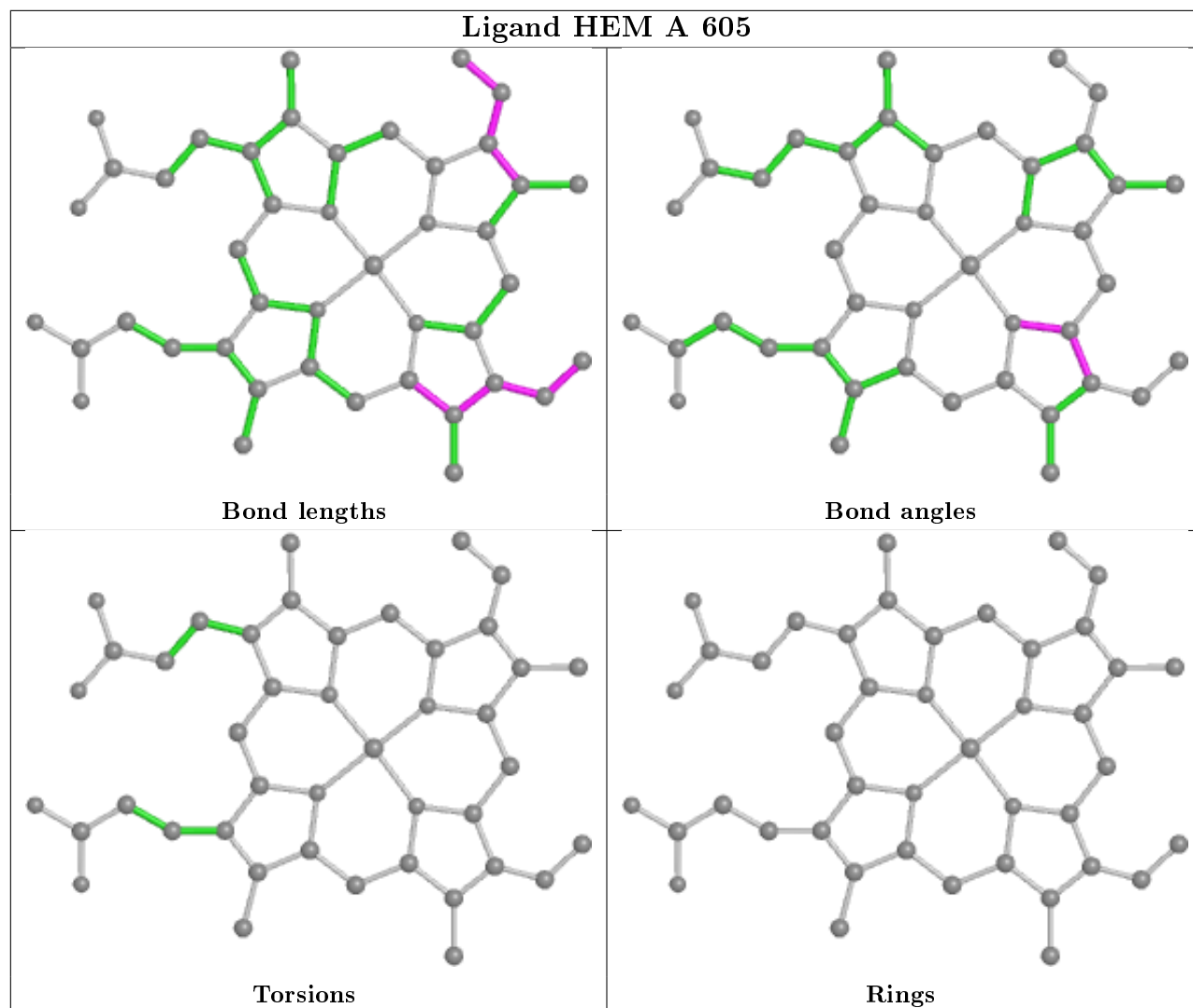
There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	605	HEM	3	0
9	C	1620	NAG	1	0
7	C	1609	ACT	1	0
7	D	2609	ACT	1	0
7	C	1606	ACT	2	0
5	D	2610	SO4	1	0
8	A	605	HEM	4	0
7	D	2604	ACT	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	A	104/104 (100%)	0.43	4 (3%) 40 43	3, 7, 24, 50	0
1	B	104/104 (100%)	0.58	4 (3%) 40 43	3, 10, 25, 29	0
2	C	465/466 (99%)	0.43	7 (1%) 73 76	2, 9, 25, 44	0
2	D	465/466 (99%)	0.78	51 (10%) 5 6	3, 14, 28, 49	0
All	All	1138/1140 (99%)	0.59	66 (5%) 23 25	2, 10, 27, 50	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	113	VAL	18.7
1	A	2	PRO	6.7
2	D	578	ALA	5.3
2	D	406	LEU	4.4
1	A	4	GLN	4.3
2	C	217	HIS	3.9
1	B	50	GLY	3.7
2	D	568	PRO	3.4
2	D	190	MET	3.4
2	C	216	LEU	3.3
2	D	225	ASN	3.3
2	C	133	ASN	3.2
2	D	269	PRO	3.2
1	A	3	GLU	3.1
2	D	567	LEU	3.0
2	D	576	ARG	3.0
2	D	575	TRP	2.9
2	D	357	PRO	2.9
2	D	522	MET	2.8
1	A	1	CYS	2.8
2	D	217	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
2	C	348	ASN	2.7
1	B	73	THR	2.7
2	D	369	TRP	2.7
2	D	135	PRO	2.7
2	D	542	GLY	2.6
2	D	113	VAL	2.6
2	D	264	LEU	2.6
2	D	498	ILE	2.5
2	D	200	ASN	2.4
2	D	523	GLN	2.4
2	D	220	PRO	2.4
2	D	272	ASP	2.4
2	C	139	ASN	2.4
2	D	271	TRP	2.4
2	D	570	LEU	2.3
2	D	561	PHE	2.3
2	D	563	ASN	2.3
2	D	543	ILE	2.3
1	B	51	VAL	2.3
2	D	210	LEU	2.3
2	D	346	LEU	2.3
2	D	157	ASN	2.3
2	D	191	SER	2.3
2	D	216	LEU	2.2
2	D	534	PRO	2.2
2	D	410	VAL	2.2
2	D	267	LEU	2.2
2	D	215	ASN	2.2
2	D	227	SER	2.1
2	D	353	MET	2.1
2	D	194	LEU	2.1
2	D	572	LEU	2.1
2	D	222	LEU	2.1
2	D	573	ALA	2.1
2	D	558	PRO	2.1
2	D	277	TYR	2.1
2	C	195	GLY	2.1
1	B	49	PRO	2.1
2	D	226	ARG	2.1
2	D	199	VAL	2.1
2	D	221	CYS	2.1
2	D	276	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	562	VAL	2.0
2	D	218	ASP	2.0
2	D	266	SER	2.0

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
2	CSO	D	150	7/8	0.92	0.13	6,7,11,13	0
2	CSO	C	150	7/8	0.94	0.10	5,6,8,11	0

6.3 Carbohydrates [i](#)

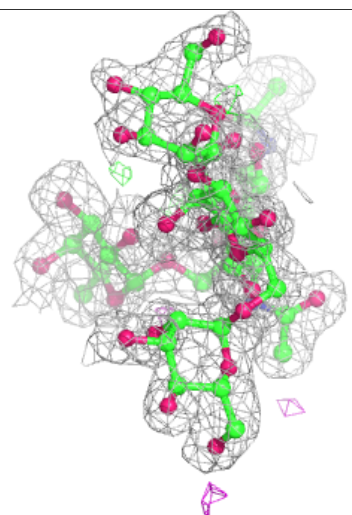
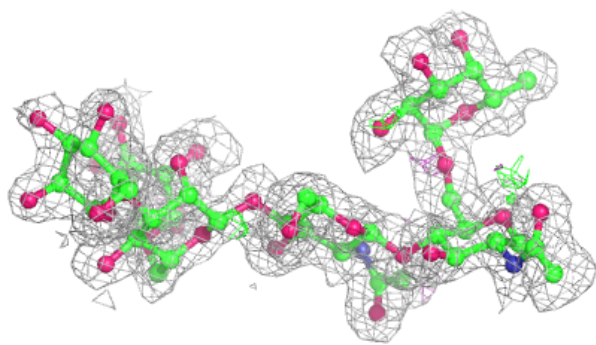
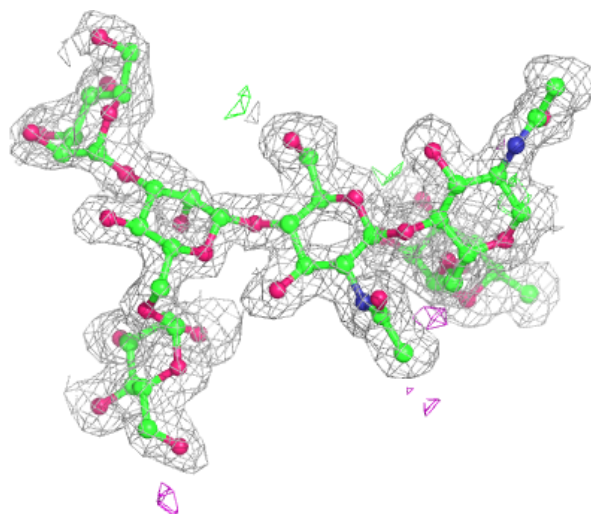
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

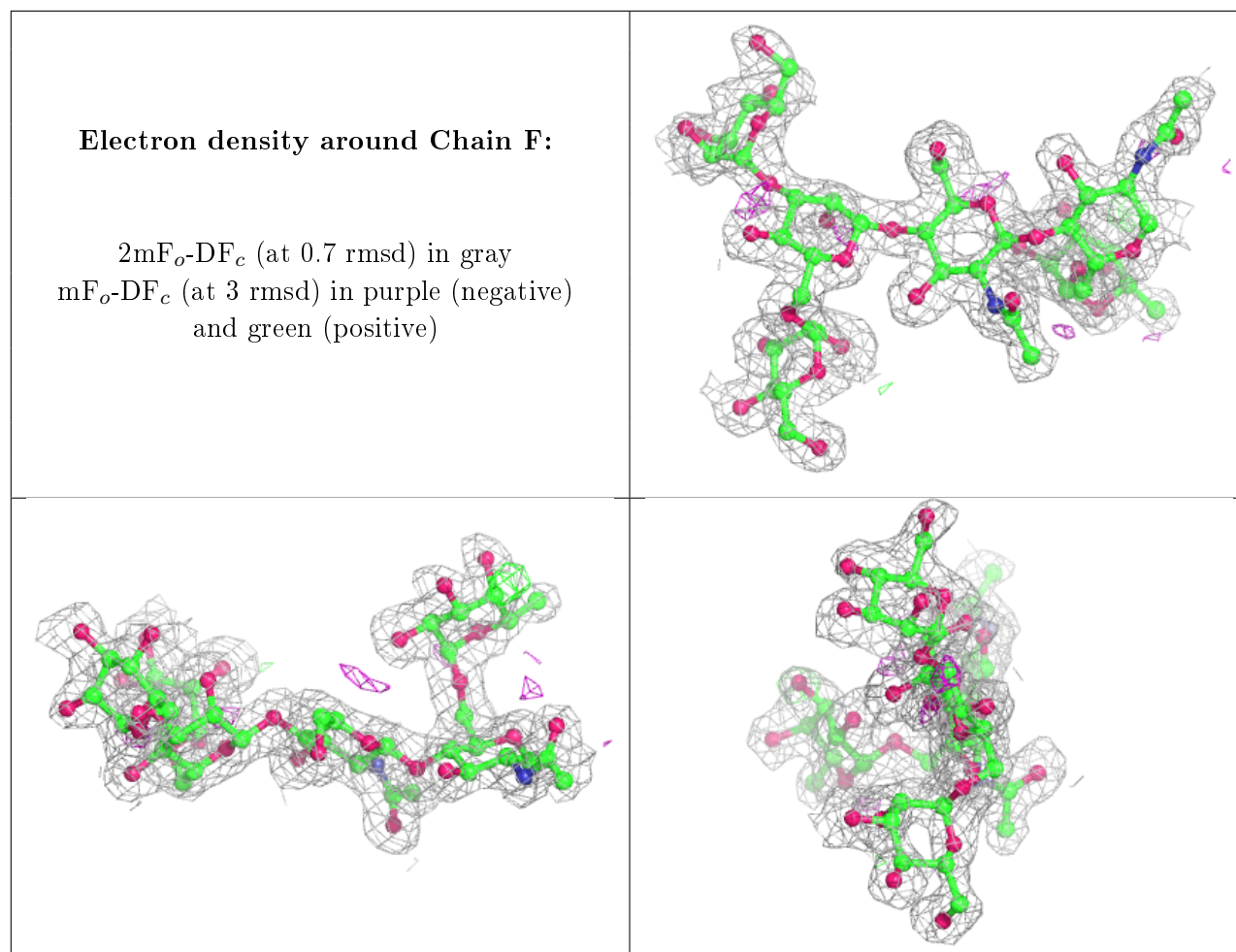
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	F	4	11/12	0.78	0.19	24,27,30,30	0
3	MAN	E	5	11/12	0.85	0.17	13,16,19,19	0
3	BMA	F	3	11/12	0.87	0.17	11,13,18,21	0
3	MAN	F	5	11/12	0.88	0.17	12,14,16,17	0
3	FUC	E	6	10/11	0.88	0.14	13,14,16,16	0
3	FUC	F	6	10/11	0.89	0.17	13,16,20,23	0
3	MAN	E	4	11/12	0.89	0.13	24,27,29,33	0
3	NAG	F	1	14/15	0.90	0.14	10,12,17,21	0
3	NAG	E	1	14/15	0.90	0.12	9,11,17,20	0
3	BMA	E	3	11/12	0.90	0.16	12,13,17,21	0
3	NAG	E	2	14/15	0.92	0.14	5,8,11,13	0
3	NAG	F	2	14/15	0.93	0.14	6,8,11,11	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.

Electron density around Chain E:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	ACT	B	1608	4/4	0.64	0.28	27,30,31,31	0
7	ACT	A	2608	4/4	0.68	0.24	24,29,30,30	0
7	ACT	C	1612	4/4	0.69	0.30	9,11,17,26	4
9	NAG	D	2630	14/15	0.75	0.21	29,32,34,36	0
7	ACT	D	2604	4/4	0.78	0.17	35,35,36,36	0
9	NAG	D	2620	14/15	0.79	0.25	17,24,31,33	0
7	ACT	D	2609	4/4	0.80	0.33	30,31,31,33	0
9	NAG	C	1630	14/15	0.81	0.14	21,25,28,30	0
7	ACT	B	2611	4/4	0.81	0.28	12,21,28,33	4
5	SO4	B	2602	5/5	0.81	0.22	22,25,25,25	5
4	BR	C	957(A)	1/1	0.81	0.14	29,29,29,29	1

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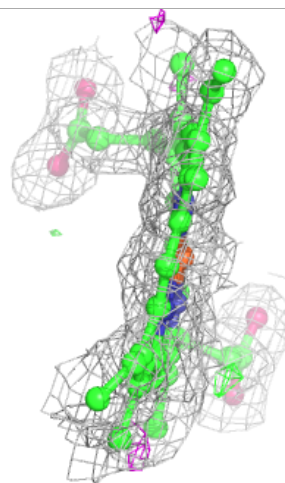
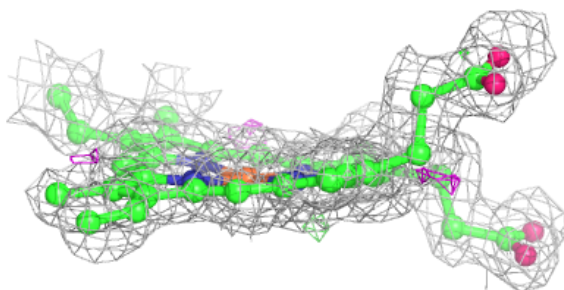
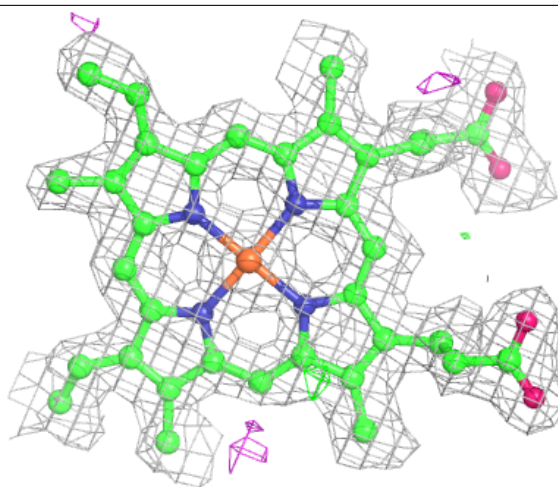
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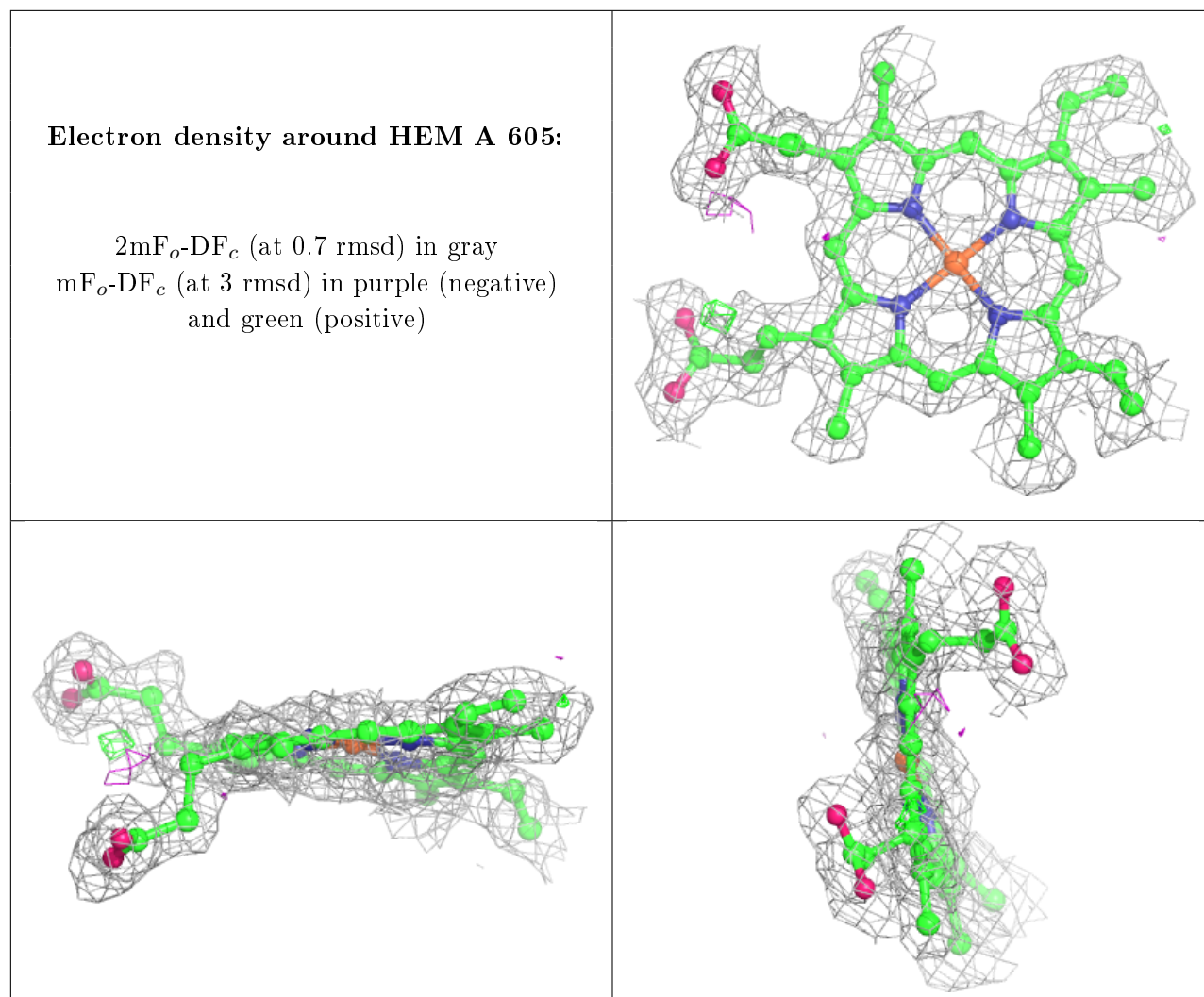
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	ACT	C	1607	4/4	0.83	0.14	22,22,23,23	0
9	NAG	C	1620	14/15	0.85	0.18	14,17,24,24	0
7	ACT	C	1609	4/4	0.88	0.19	19,21,21,26	0
7	ACT	D	2607	4/4	0.91	0.13	28,28,28,29	0
4	BR	D	957(B)	1/1	0.91	0.10	28,28,28,28	1
5	SO4	D	2610	5/5	0.91	0.25	20,20,21,22	5
7	ACT	C	1606	4/4	0.91	0.14	12,14,15,16	0
6	CYN	B	2844	2/2	0.91	0.21	18,18,18,18	0
7	ACT	C	1604	4/4	0.92	0.14	10,12,15,15	0
7	ACT	D	2606	4/4	0.93	0.11	19,21,21,22	0
5	SO4	C	1610	5/5	0.94	0.18	13,13,14,14	5
8	HEM	B	605	43/43	0.94	0.12	2,7,11,14	0
4	BR	D	889(B)	1/1	0.95	0.08	22,22,22,22	1
6	CYN	A	1844	2/2	0.95	0.15	6,6,6,6	0
8	HEM	A	605	43/43	0.96	0.12	2,5,6,10	0
5	SO4	A	1602	5/5	0.96	0.22	11,11,14,15	5
4	BR	D	758(B)	1/1	0.97	0.12	19,19,19,19	1
5	SO4	C	1603	5/5	0.97	0.11	17,18,21,23	0
4	BR	C	758(A)	1/1	0.97	0.06	22,22,22,22	1
4	BR	C	889(A)	1/1	0.99	0.09	21,21,21,21	1
4	BR	A	1601	1/1	0.99	0.10	6,6,6,6	0
10	CA	D	2600	1/1	0.99	0.13	9,9,9,9	0
10	CA	C	1600	1/1	0.99	0.08	7,7,7,7	0
4	BR	B	2601	1/1	1.00	0.12	10,10,10,10	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 B 605:

$2mF_o-DF_c$ (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.