wwPDB EM Validation Summary Report (i)

Aug 26, 2026 – 05:29 pm BST

PDB ID	:	9TQD / pdb_00009tqd
EMDB ID	:	EMD-56135
Title	:	CD163 bound to haemoglobin
Authors	:	Zhou, R.X.; Higgins, M.K.
Deposited on	:	2025-12-20
Resolution	:	2.80 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp
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:

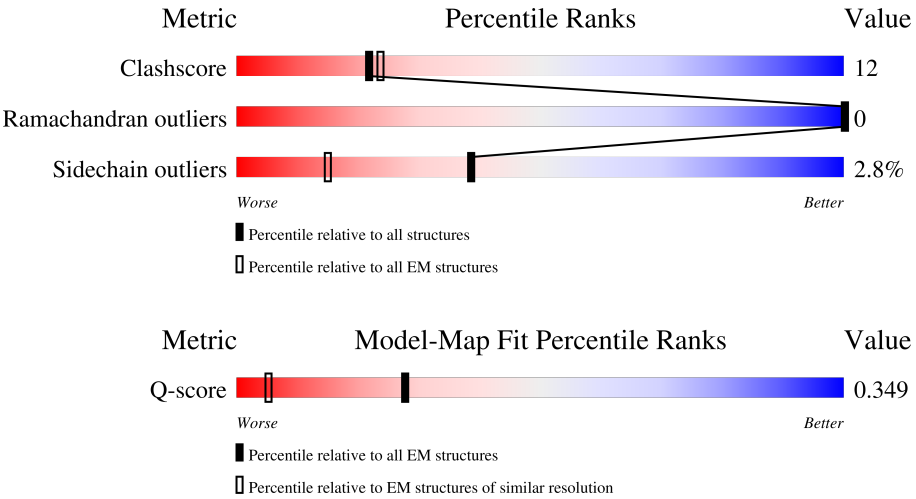
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1156	10% 55% 18% 26%
1	B	1156	13% 61% 21% 18%
1	C	1156	16% 44% 18% 36%
2	D	142	80% 18%

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Mol	Chain	Length	Quality of chain
2	F	142	11% 82% 15%
3	E	147	9% 80% 19%
3	G	147	10% 81% 18%
4	H	2	50% 50% 50%
4	I	2	50% 100%
4	J	2	50% 50%
4	K	2	100%
4	L	2	50% 50% 50%

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
8	OXY	E	202	-	-	X	-
8	OXY	G	202	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 24023 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Scavenger receptor cysteine-rich type 1 protein M130.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	851	Total	C	N	O	S	0	0
			6444	3950	1172	1251	71		
1	B	953	Total	C	N	O	S	0	0
			7214	4417	1315	1401	81		
1	C	737	Total	C	N	O	S	0	0
			5591	3435	1014	1081	61		

- Molecule 2 is a protein called Hemopressin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	140	Total	C	N	O	S	0	0
			1057	679	183	192	3		
2	F	139	Total	C	N	O	S	0	0
			1045	670	182	190	3		

- Molecule 3 is a protein called Spinorphin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	145	Total	C	N	O	S	0	0
			1112	718	192	199	3		
3	G	145	Total	C	N	O	S	0	0
			1112	718	192	199	3		

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



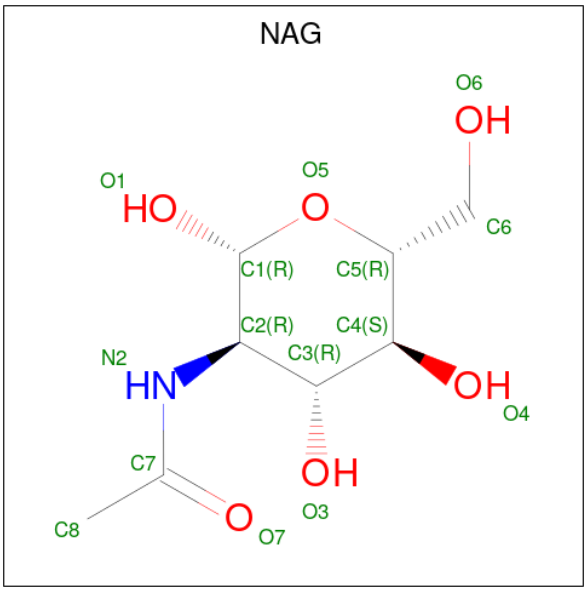
Mol	Chain	Residues	Atoms				AltConf	Trace
4	H	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms	AltConf	Trace
4	I	2	Total C N O 28 16 2 10	0	0
4	J	2	Total C N O 28 16 2 10	0	0
4	K	2	Total C N O 28 16 2 10	0	0
4	L	2	Total C N O 28 16 2 10	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	AltConf
5	A	1	Total C N O 14 8 1 5	0
5	A	1	Total C N O 14 8 1 5	0
5	A	1	Total C N O 14 8 1 5	0
5	A	1	Total C N O 14 8 1 5	0
5	B	1	Total C N O 14 8 1 5	0
5	B	1	Total C N O 14 8 1 5	0
5	B	1	Total C N O 14 8 1 5	0

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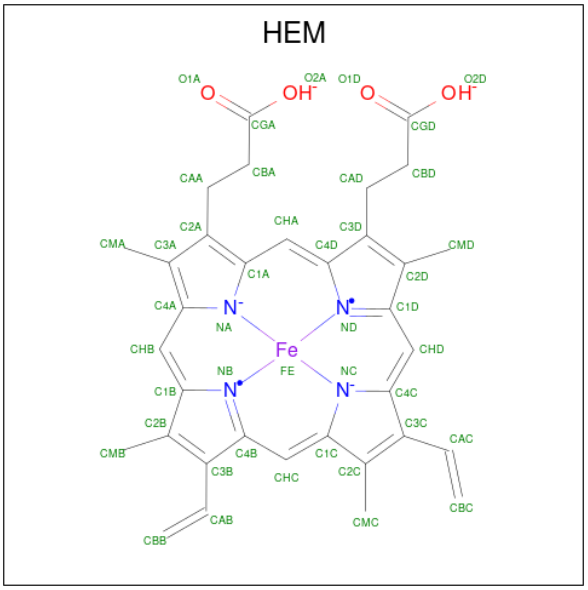
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Mol	Chain	Residues	Atoms	AltConf
5	C	1	Total C N O 14 8 1 5	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

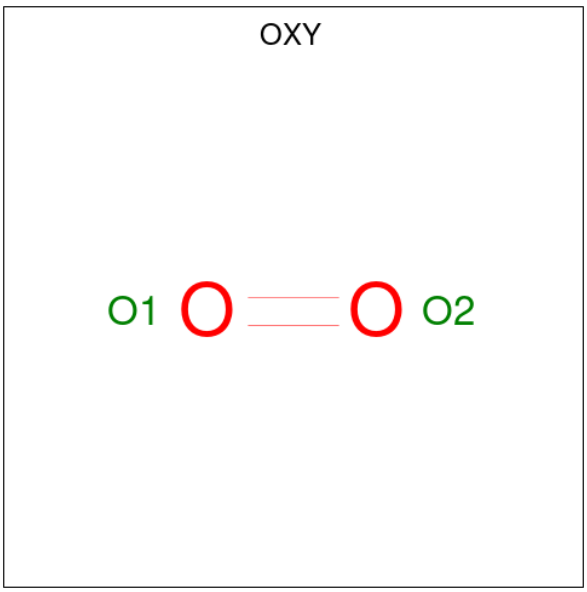
Mol	Chain	Residues	Atoms	AltConf
6	A	6	Total Ca 6 6	0
6	B	5	Total Ca 5 5	0
6	C	5	Total Ca 5 5	0

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms	AltConf
7	D	1	Total C Fe N O 43 34 1 4 4	0
7	E	1	Total C Fe N O 43 34 1 4 4	0
7	F	1	Total C Fe N O 43 34 1 4 4	0
7	G	1	Total C Fe N O 43 34 1 4 4	0

- Molecule 8 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O_2).



Mol	Chain	Residues	Atoms	AltConf
8	D	1	Total O 2 2	0
8	E	1	Total O 2 2	0
8	F	1	Total O 2 2	0
8	G	1	Total O 2 2	0

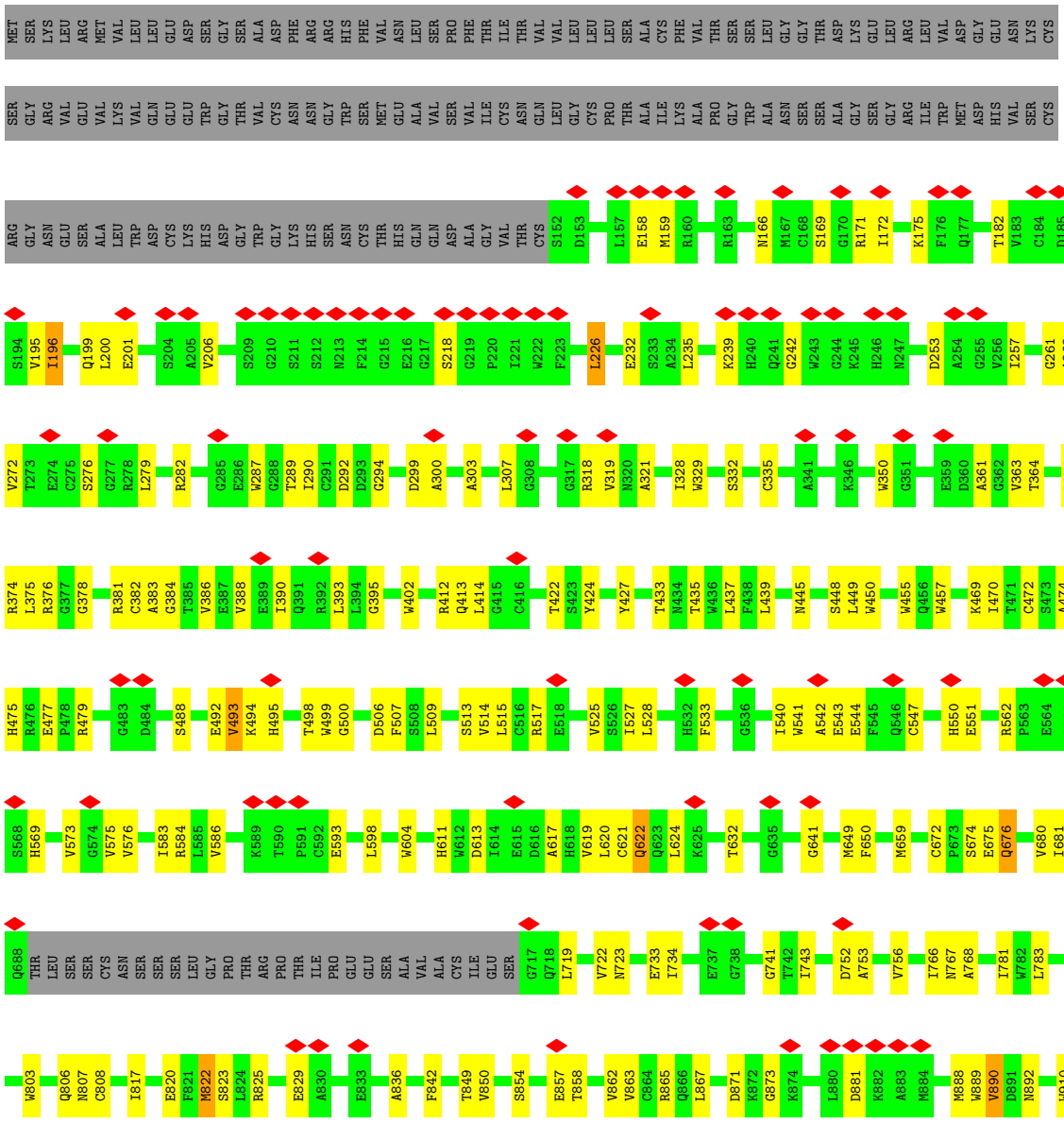
3 Residue-property plots (i)

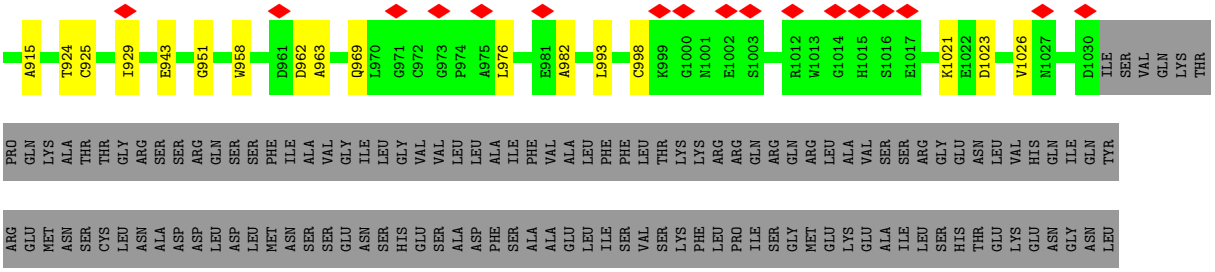
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Scavenger receptor cysteine-rich type 1 protein M130

Chain A:



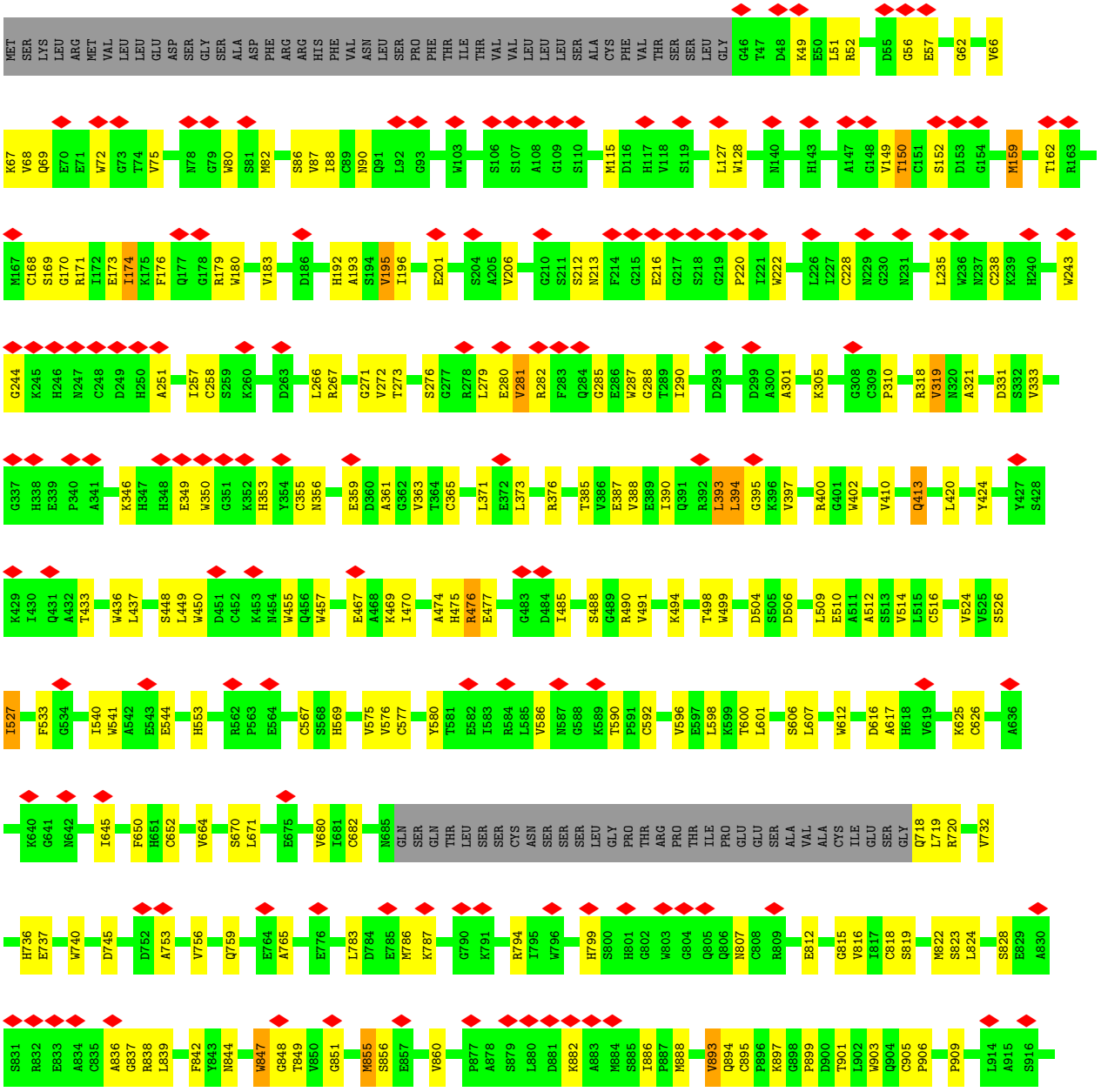


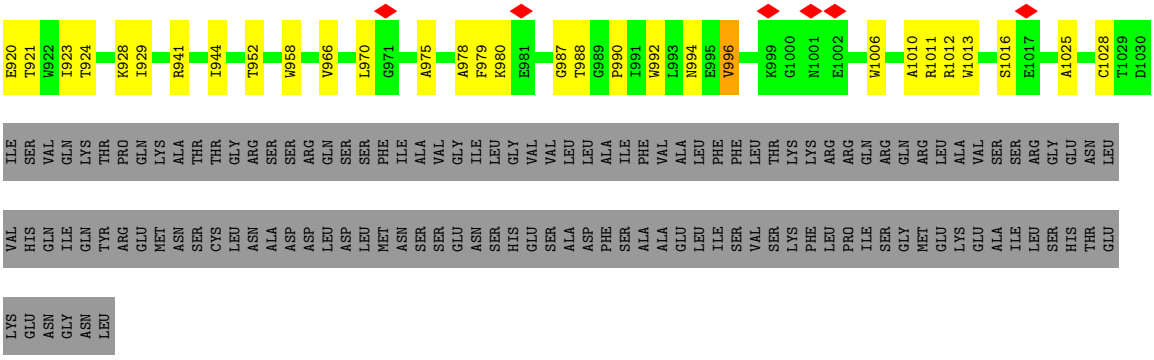


• Molecule 1: Scavenger receptor cysteine-rich type 1 protein M130

Chain B:

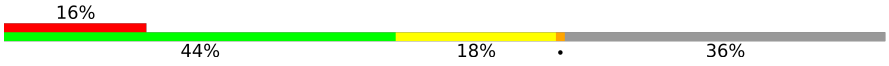


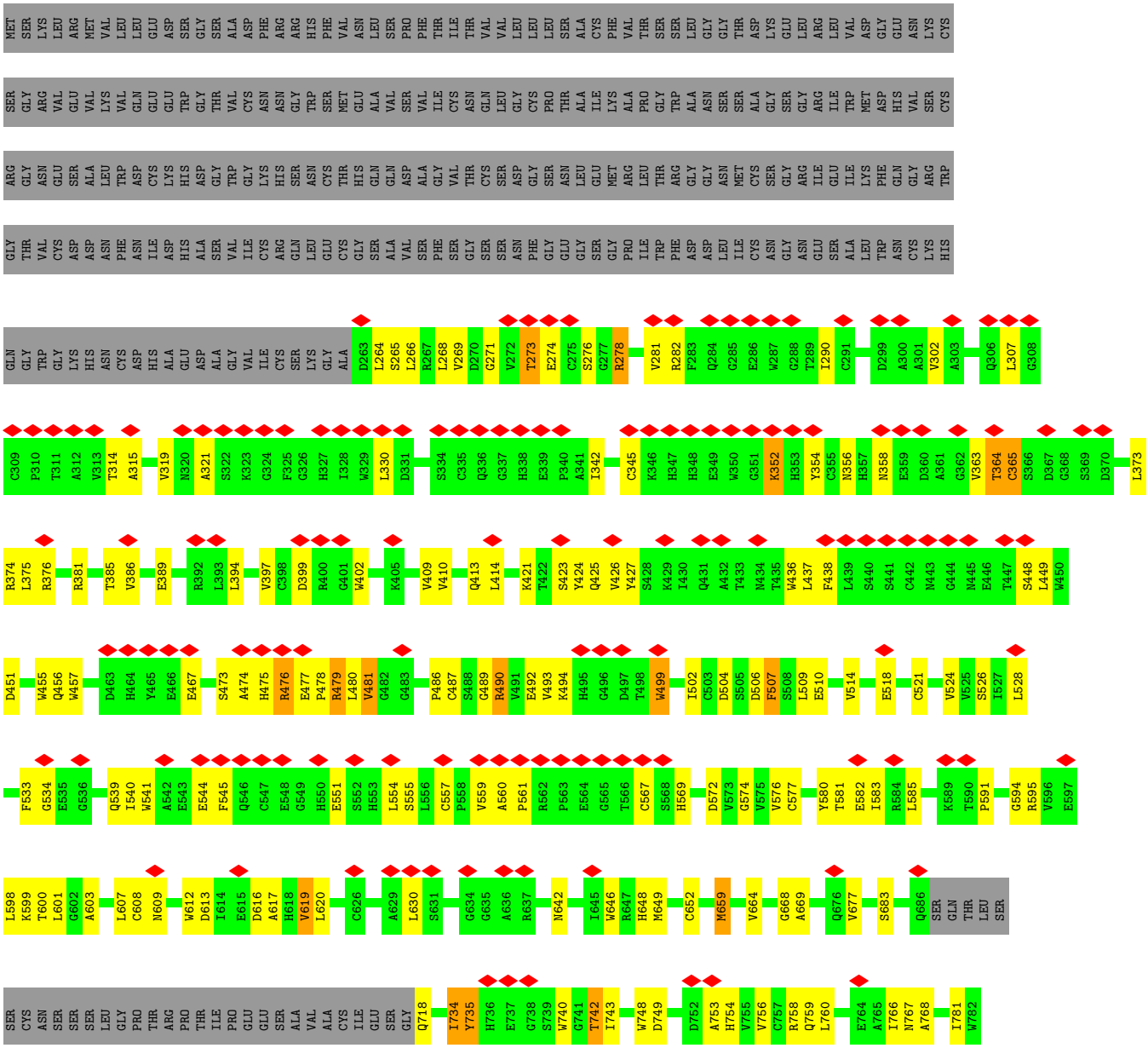


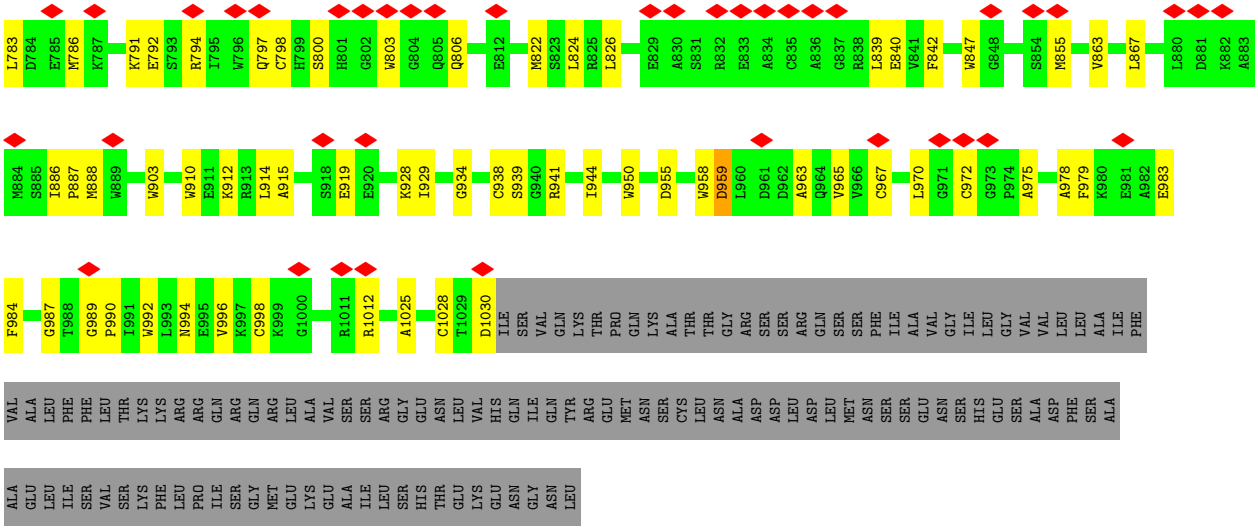


• Molecule 1: Scavenger receptor cysteine-rich type 1 protein M130

Chain C:







• Molecule 2: Hemopressin

Chain D:

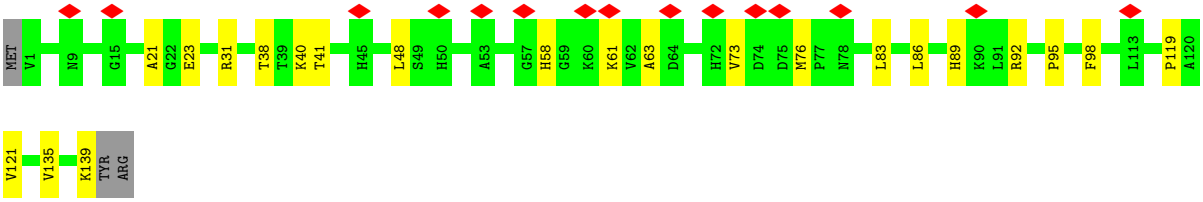




• Molecule 2: Hemopressin

Chain F:

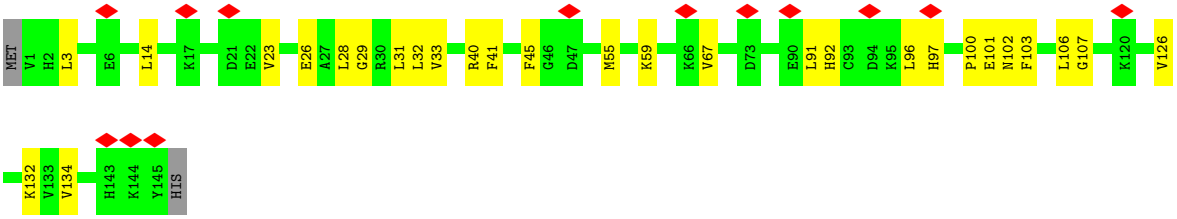




• Molecule 3: Spinorphin

Chain E:

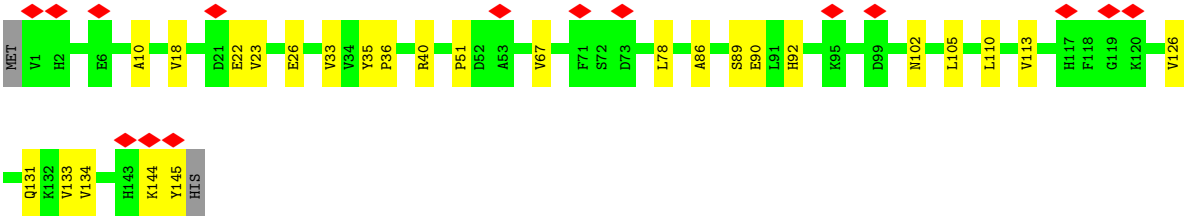




• Molecule 3: Spinorphin

Chain G:





• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

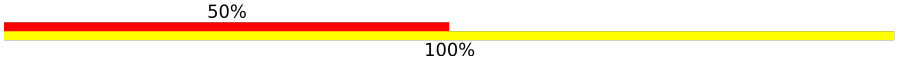
Chain H:





• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:





• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:





• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:





• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1033649	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	38.3	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.206	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	425.984, 425.984, 425.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, HEM, CA, OXY

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	0.16	0/6593	0.38	0/8926
1	B	0.14	0/7381	0.38	0/9995
1	C	0.23	0/5722	0.45	0/7754
2	D	0.14	0/1085	0.34	0/1477
2	F	0.12	0/1072	0.30	0/1459
3	E	0.14	0/1141	0.32	0/1551
3	G	0.13	0/1141	0.32	0/1551
All	All	0.17	0/24135	0.39	0/32713

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	6444	0	5980	141	0
1	B	7214	0	6688	166	0
1	C	5591	0	5210	160	0
2	D	1057	0	1060	17	0
2	F	1045	0	1051	15	0
3	E	1112	0	1111	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1112	0	1111	19	0
4	H	28	0	25	0	0
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	K	28	0	25	1	0
4	L	28	0	25	0	0
5	A	56	0	52	2	0
5	B	42	0	39	0	0
5	C	14	0	13	0	0
6	A	6	0	0	0	0
6	B	5	0	0	0	0
6	C	5	0	0	0	0
7	D	43	0	30	2	0
7	E	43	0	30	5	0
7	F	43	0	30	4	0
7	G	43	0	30	5	0
8	D	2	0	0	0	0
8	E	2	0	0	2	0
8	F	2	0	0	1	0
8	G	2	0	0	4	0
All	All	24023	0	22560	542	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 12.

The worst 5 of 542 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:C:929:ILE:HD11	1:C:970:LEU:HG	1.53	0.91
2:F:58:HIS:CE1	8:F:202:OXY:O1	2.28	0.87
1:C:475:HIS:H	1:C:555:SER:HA	1.39	0.86
1:C:490:ARG:HD2	1:C:533:PHE:HB2	1.63	0.79
1:A:822:MET:HA	1:A:842:PHE:O	1.85	0.77

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 PDB entries followed by that with respect to all EM entries.

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	847/1156 (73%)	793 (94%)	54 (6%)	0	100	100
1	B	949/1156 (82%)	884 (93%)	65 (7%)	0	100	100
1	C	733/1156 (63%)	668 (91%)	65 (9%)	0	100	100
2	D	138/142 (97%)	131 (95%)	7 (5%)	0	100	100
2	F	137/142 (96%)	133 (97%)	4 (3%)	0	100	100
3	E	143/147 (97%)	139 (97%)	4 (3%)	0	100	100
3	G	143/147 (97%)	139 (97%)	4 (3%)	0	100	100
All	All	3090/4046 (76%)	2887 (93%)	203 (7%)	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 PDB entries followed by that with respect to all EM entries.

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	691/953 (72%)	677 (98%)	14 (2%)	48	80
1	B	774/953 (81%)	751 (97%)	23 (3%)	36	72
1	C	600/953 (63%)	573 (96%)	27 (4%)	24	58
2	D	112/114 (98%)	110 (98%)	2 (2%)	51	82
2	F	111/114 (97%)	110 (99%)	1 (1%)	70	89
3	E	117/119 (98%)	114 (97%)	3 (3%)	40	75
3	G	117/119 (98%)	116 (99%)	1 (1%)	70	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2522/3325 (76%)	2451 (97%)	71 (3%)	38 73

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	822	MET
1	C	863	VAL
2	D	137	THR
1	B	394	LEU
1	B	393	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	2	HIS
3	E	97	HIS
1	B	805	GLN
1	B	946	HIS
1	C	789	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)

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	H	1	1,4	14,14,15	0.72	0	17,19,21	0.84	0
4	NAG	H	2	4	14,14,15	0.71	0	17,19,21	1.16	1 (5%)
4	NAG	I	1	1,4	14,14,15	0.75	0	17,19,21	1.37	3 (17%)
4	NAG	I	2	4	14,14,15	0.72	0	17,19,21	1.20	2 (11%)
4	NAG	J	1	4	14,14,15	0.72	0	17,19,21	0.84	0
4	NAG	J	2	4	14,14,15	0.74	0	17,19,21	2.23	2 (11%)
4	NAG	K	1	1,4	14,14,15	0.71	0	17,19,21	1.01	1 (5%)
4	NAG	K	2	4	14,14,15	0.80	0	17,19,21	1.18	1 (5%)
4	NAG	L	1	1,4	14,14,15	0.74	0	17,19,21	0.87	0
4	NAG	L	2	4	14,14,15	0.71	0	17,19,21	1.15	1 (5%)

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	H	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	NAG	I	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	1/6/23/26	0/1/1/1
4	NAG	J	1	4	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	4/6/23/26	0/1/1/1
4	NAG	K	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	K	2	4	-	1/6/23/26	0/1/1/1
4	NAG	L	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	L	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	J	2	NAG	C2-N2-C7	7.84	134.06	122.90
4	I	1	NAG	C2-N2-C7	3.17	127.42	122.90
4	I	2	NAG	C2-N2-C7	3.09	127.31	122.90
4	H	2	NAG	C2-N2-C7	3.08	127.28	122.90
4	L	2	NAG	C2-N2-C7	3.06	127.27	122.90

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	J	1	NAG	C8-C7-N2-C2
4	J	1	NAG	O7-C7-N2-C2
4	J	2	NAG	C8-C7-N2-C2
4	J	2	NAG	O7-C7-N2-C2
4	K	1	NAG	C8-C7-N2-C2

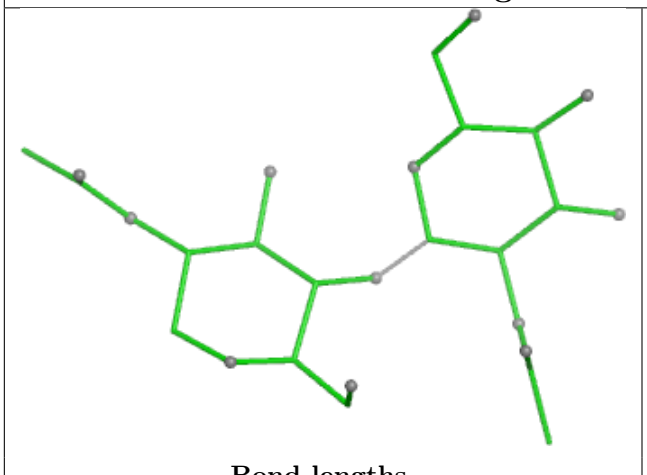
There are no ring outliers.

2 monomers are involved in 1 short contact:

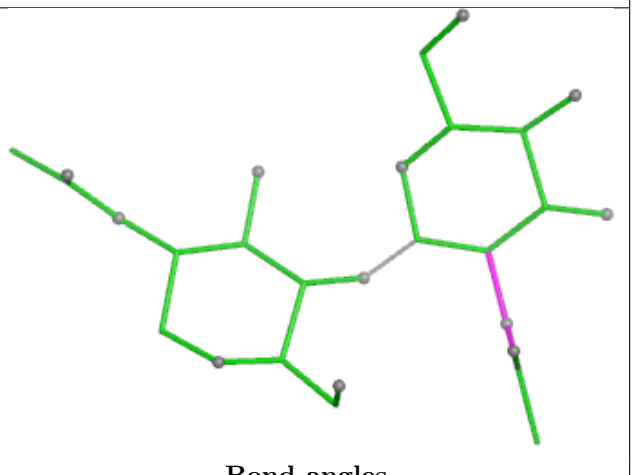
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	1	NAG	1	0
4	K	2	NAG	1	0

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

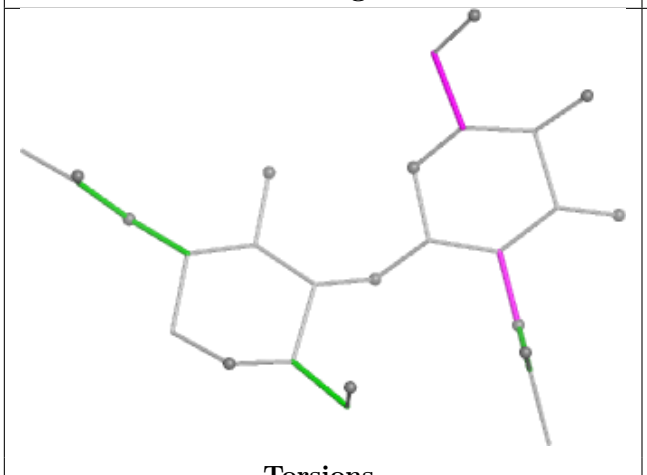
Oligosaccharide Chain H



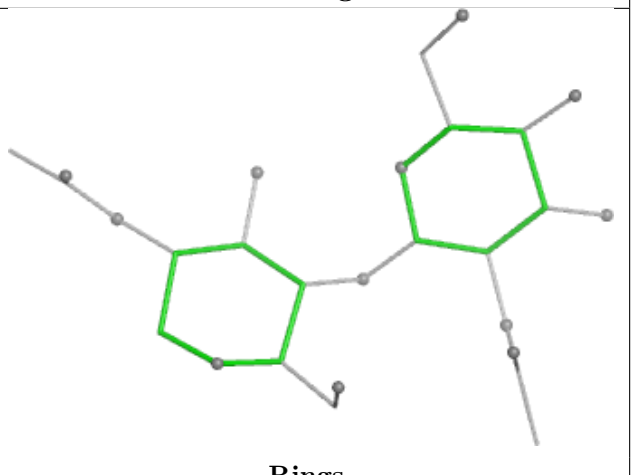
Bond lengths



Bond angles

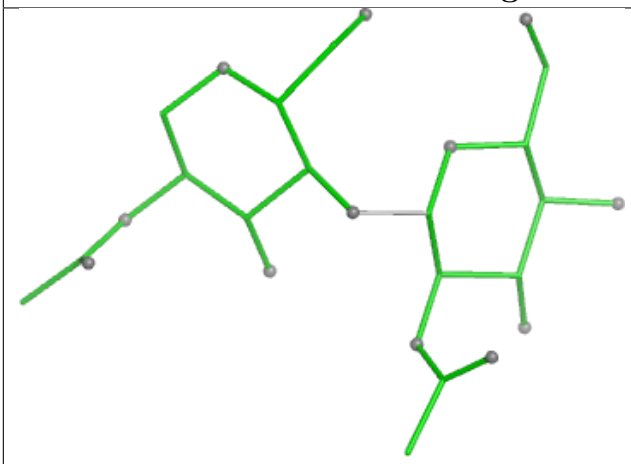


Torsions

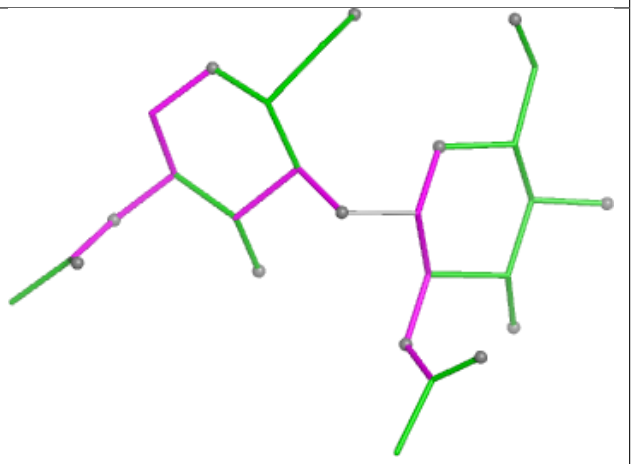


Rings

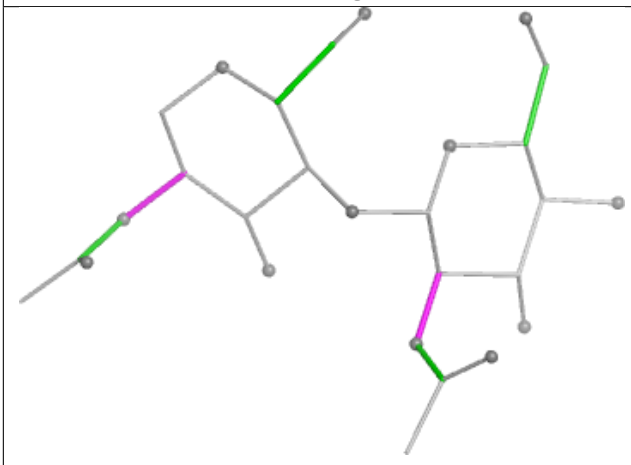
Oligosaccharide Chain I



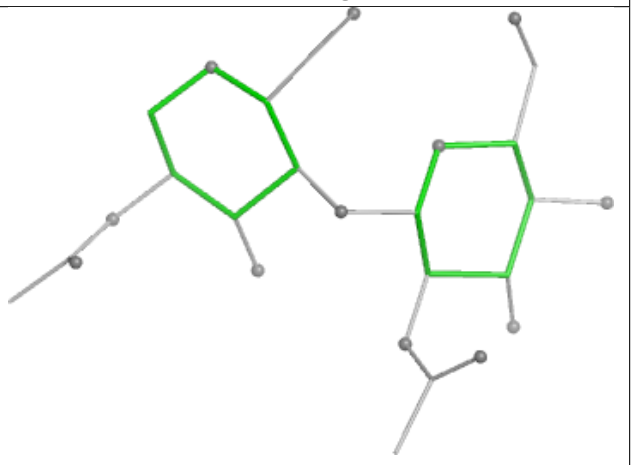
Bond lengths



Bond angles

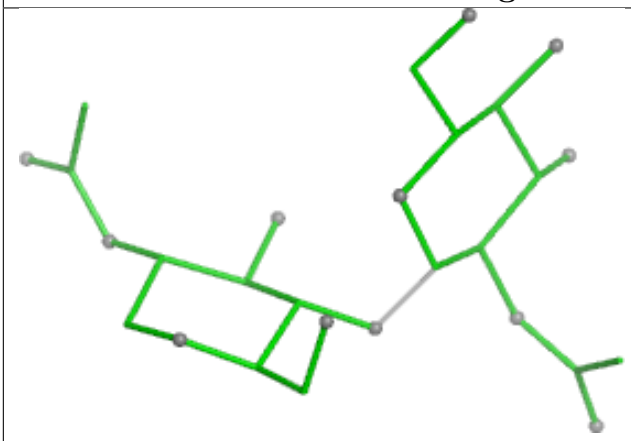


Torsions

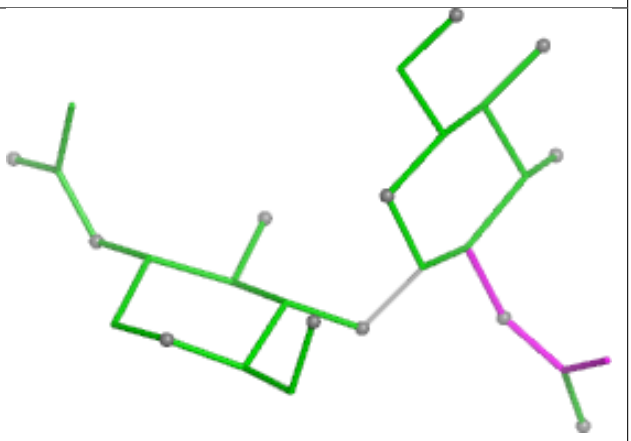


Rings

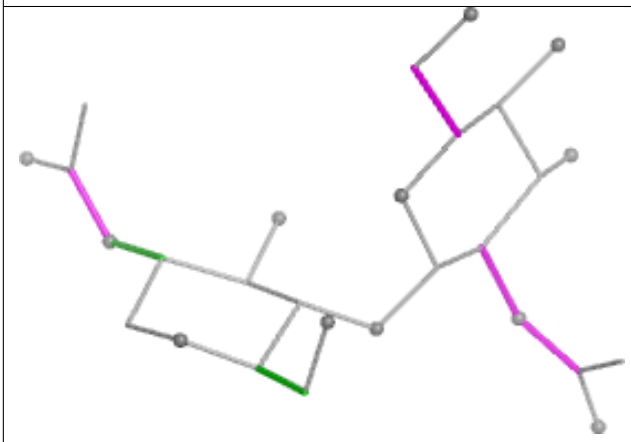
Oligosaccharide Chain J



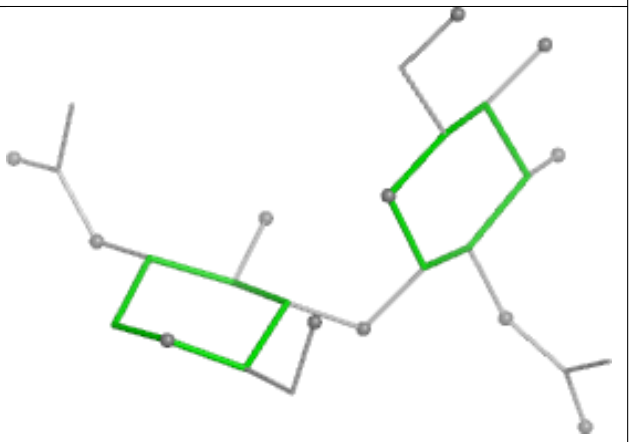
Bond lengths



Bond angles

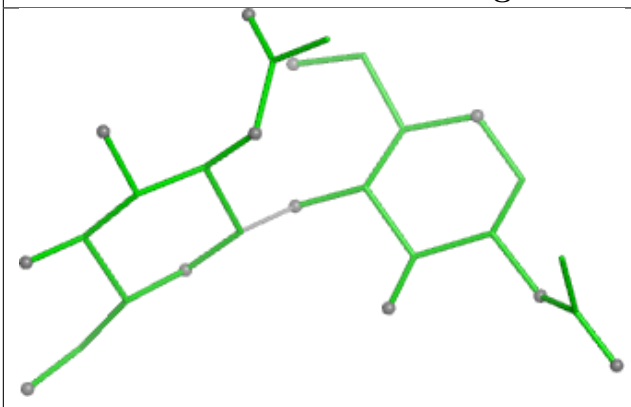


Torsions

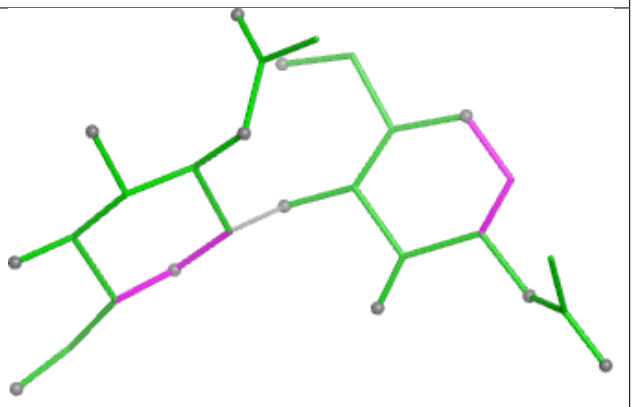


Rings

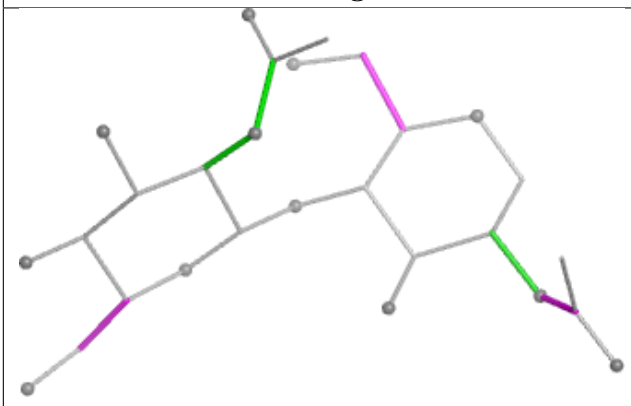
Oligosaccharide Chain K



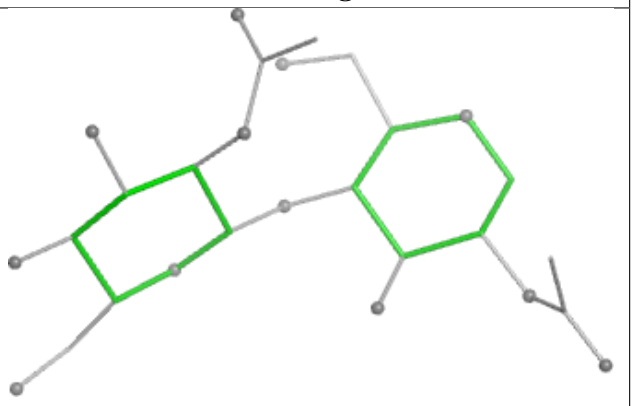
Bond lengths



Bond angles

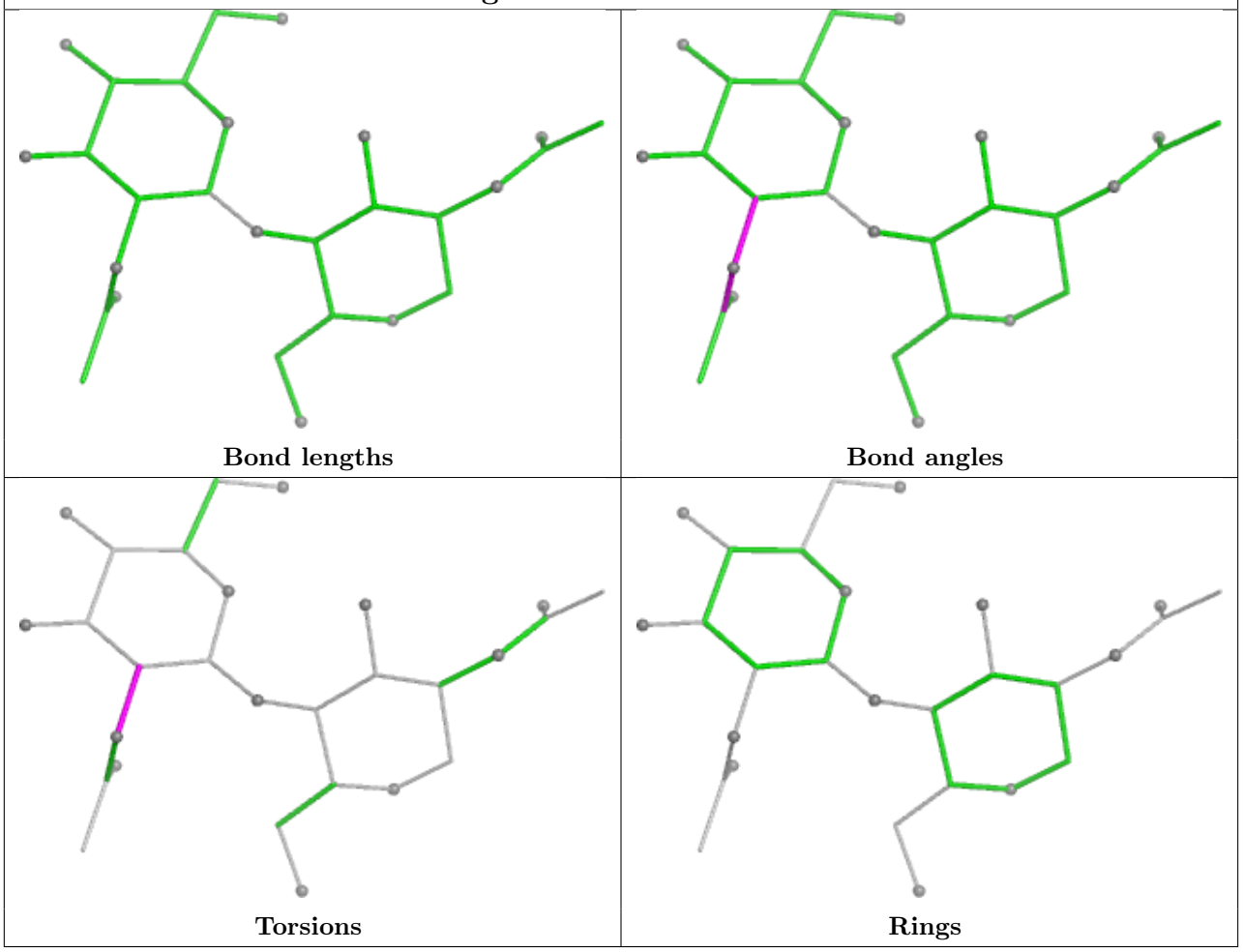


Torsions



Rings

Oligosaccharide Chain L



5.6 Ligand geometry (i)

Of 32 ligands modelled in this entry, 16 are monoatomic - leaving 16 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	OXY	G	202	7	1,1,1	0.15	0	-		
7	HEM	G	201	8,3	50,50,50	1.55	6 (12%)	66,82,82	1.24	7 (10%)
7	HEM	D	201	2,8	50,50,50	1.42	6 (12%)	66,82,82	1.27	8 (12%)
5	NAG	B	1202	-	14,14,15	0.72	0	17,19,21	0.76	0
8	OXY	D	202	7	1,1,1	0.14	0	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	NAG	B	1201	1	14,14,15	0.75	0	17,19,21	0.82	0
5	NAG	A	1201	1	14,14,15	0.72	0	17,19,21	0.80	0
5	NAG	B	1203	1	14,14,15	0.76	0	17,19,21	1.97	4 (23%)
5	NAG	A	1202	-	14,14,15	0.72	0	17,19,21	1.13	1 (5%)
7	HEM	E	201	8,3	50,50,50	1.42	6 (12%)	66,82,82	1.20	6 (9%)
5	NAG	C	1201	1	14,14,15	0.74	0	17,19,21	1.00	0
8	OXY	F	202	7	1,1,1	0.15	0	-		
5	NAG	A	1204	-	14,14,15	0.75	0	17,19,21	0.75	0
8	OXY	E	202	7	1,1,1	0.14	0	-		
5	NAG	A	1203	-	14,14,15	0.72	0	17,19,21	0.79	0
7	HEM	F	201	2,8	50,50,50	1.43	6 (12%)	66,82,82	1.35	7 (10%)

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	HEM	G	201	8,3	-	2/14/54/54	-
7	HEM	D	201	2,8	-	1/14/54/54	-
5	NAG	B	1202	-	-	0/6/23/26	0/1/1/1
5	NAG	B	1201	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1201	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1203	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1202	-	-	1/6/23/26	0/1/1/1
7	HEM	E	201	8,3	-	6/14/54/54	-
5	NAG	C	1201	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1204	-	-	0/6/23/26	0/1/1/1
5	NAG	A	1203	-	-	0/6/23/26	0/1/1/1
7	HEM	F	201	2,8	-	3/14/54/54	-

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	201	HEM	FE-ND	4.54	2.08	1.94
7	G	201	HEM	FE-NB	4.12	2.07	1.94
7	E	201	HEM	FE-NB	3.73	2.06	1.94
7	G	201	HEM	FE-NA	3.56	2.07	1.95
7	F	201	HEM	FE-NB	3.53	2.05	1.94

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	1203	NAG	C1-O5-C5	5.91	120.20	112.19
7	F	201	HEM	C3B-C2B-C1B	3.28	108.92	106.49
7	D	201	HEM	C1B-NB-C4B	3.21	108.39	105.07
5	B	1203	NAG	O5-C1-C2	3.14	116.25	111.29
7	E	201	HEM	C4D-ND-C1D	3.13	108.30	105.07

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1203	NAG	C8-C7-N2-C2
5	B	1203	NAG	O7-C7-N2-C2
5	B	1201	NAG	O5-C5-C6-O6
5	A	1201	NAG	O5-C5-C6-O6
7	F	201	HEM	C4B-C3B-CAB-CBB

There are no ring outliers.

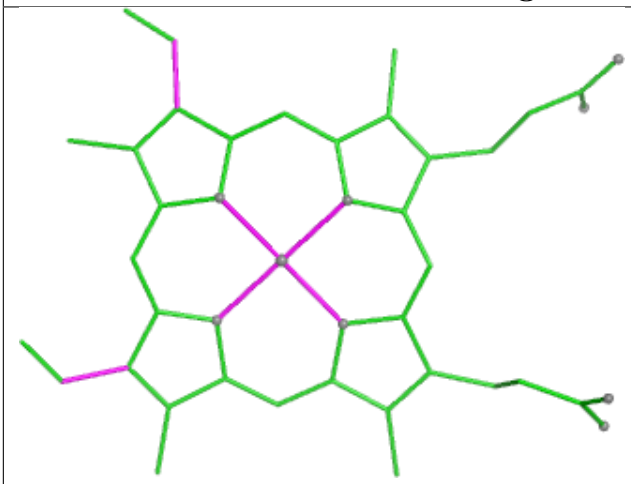
9 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	G	202	OXY	4	0
7	G	201	HEM	5	0
7	D	201	HEM	2	0
5	A	1201	NAG	1	0
7	E	201	HEM	5	0
8	F	202	OXY	1	0
8	E	202	OXY	2	0
5	A	1203	NAG	1	0
7	F	201	HEM	4	0

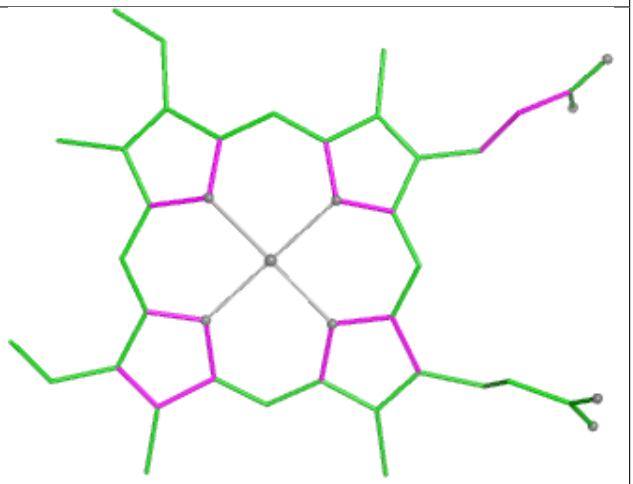
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

equivalents in the CSD to analyse the geometry.

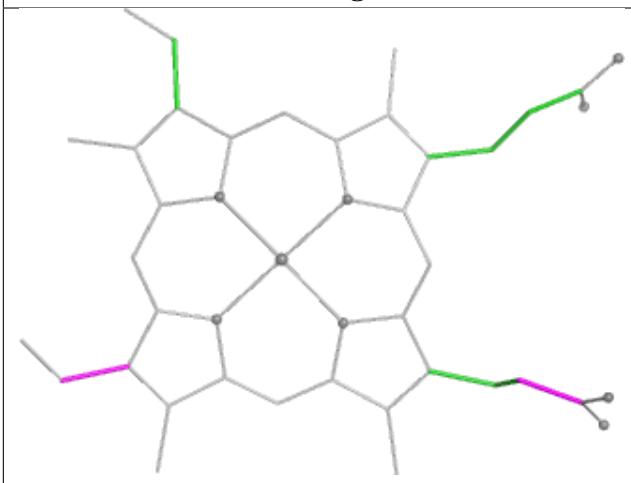
Ligand HEM G 201



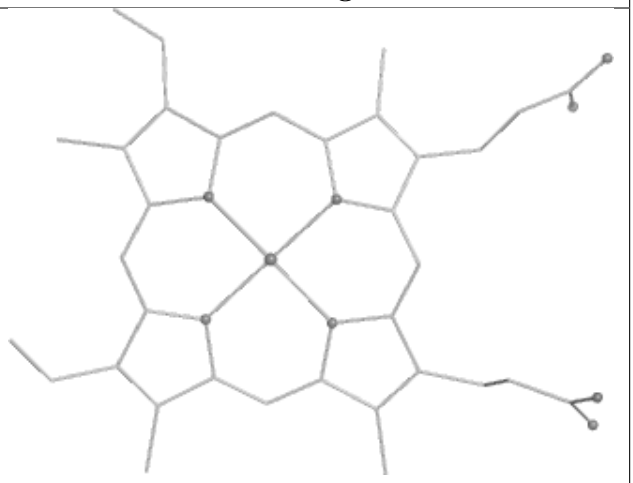
Bond lengths



Bond angles

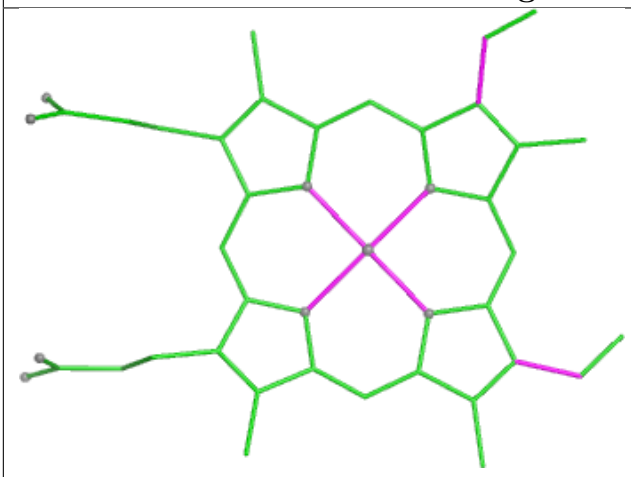


Torsions

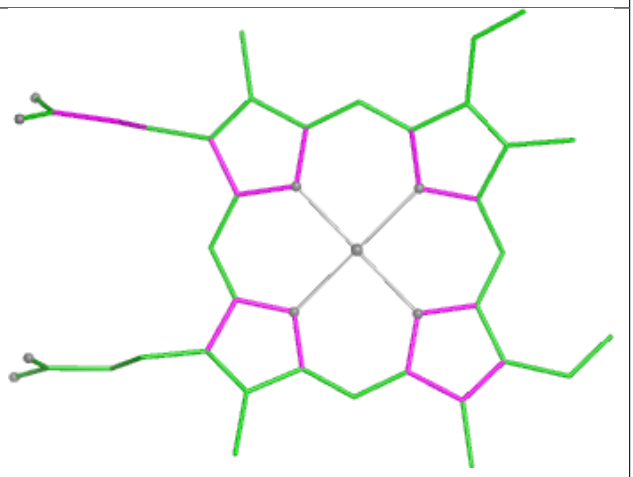


Rings

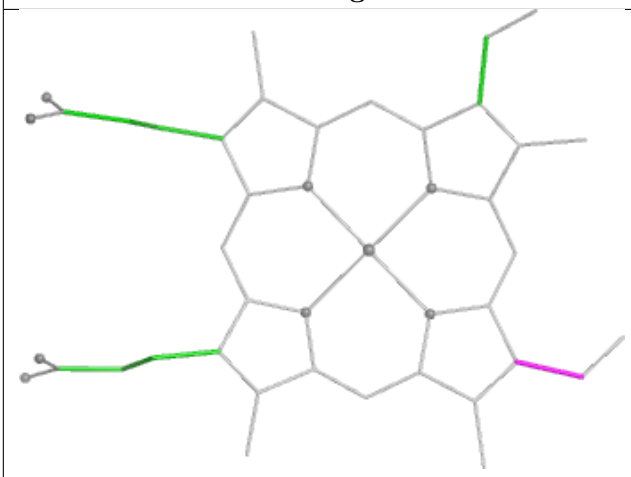
Ligand HEM D 201



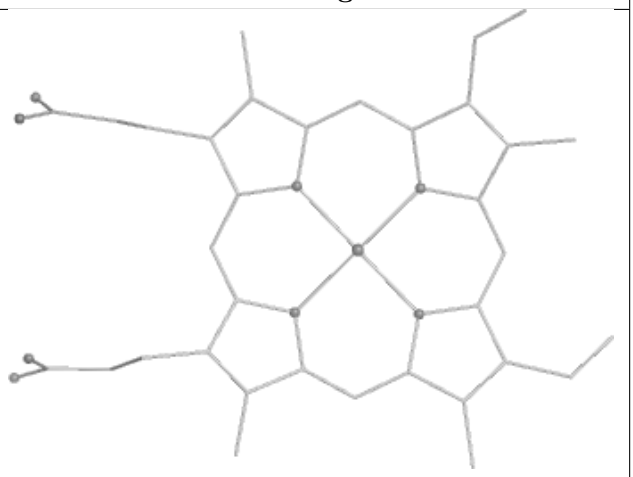
Bond lengths



Bond angles

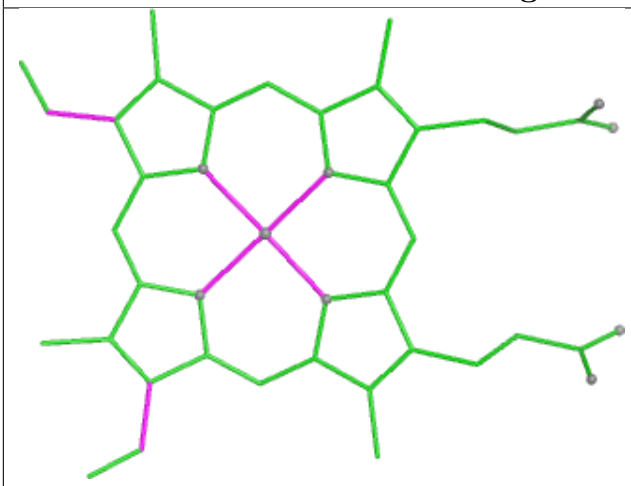


Torsions

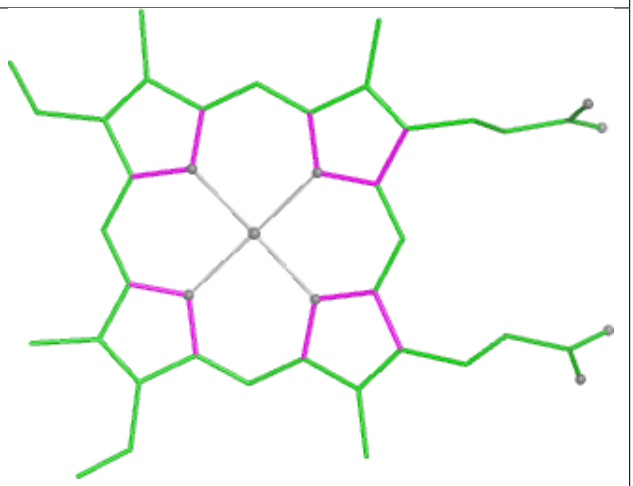


Rings

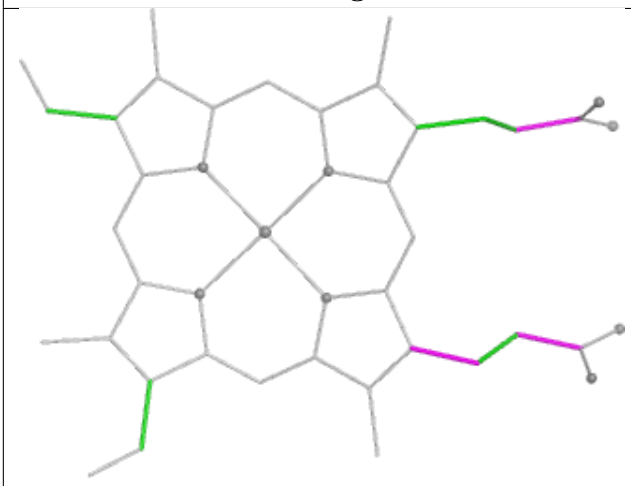
Ligand HEM E 201



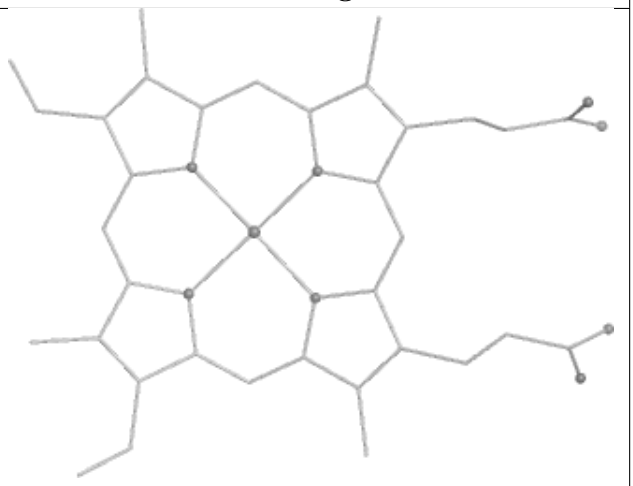
Bond lengths



Bond angles

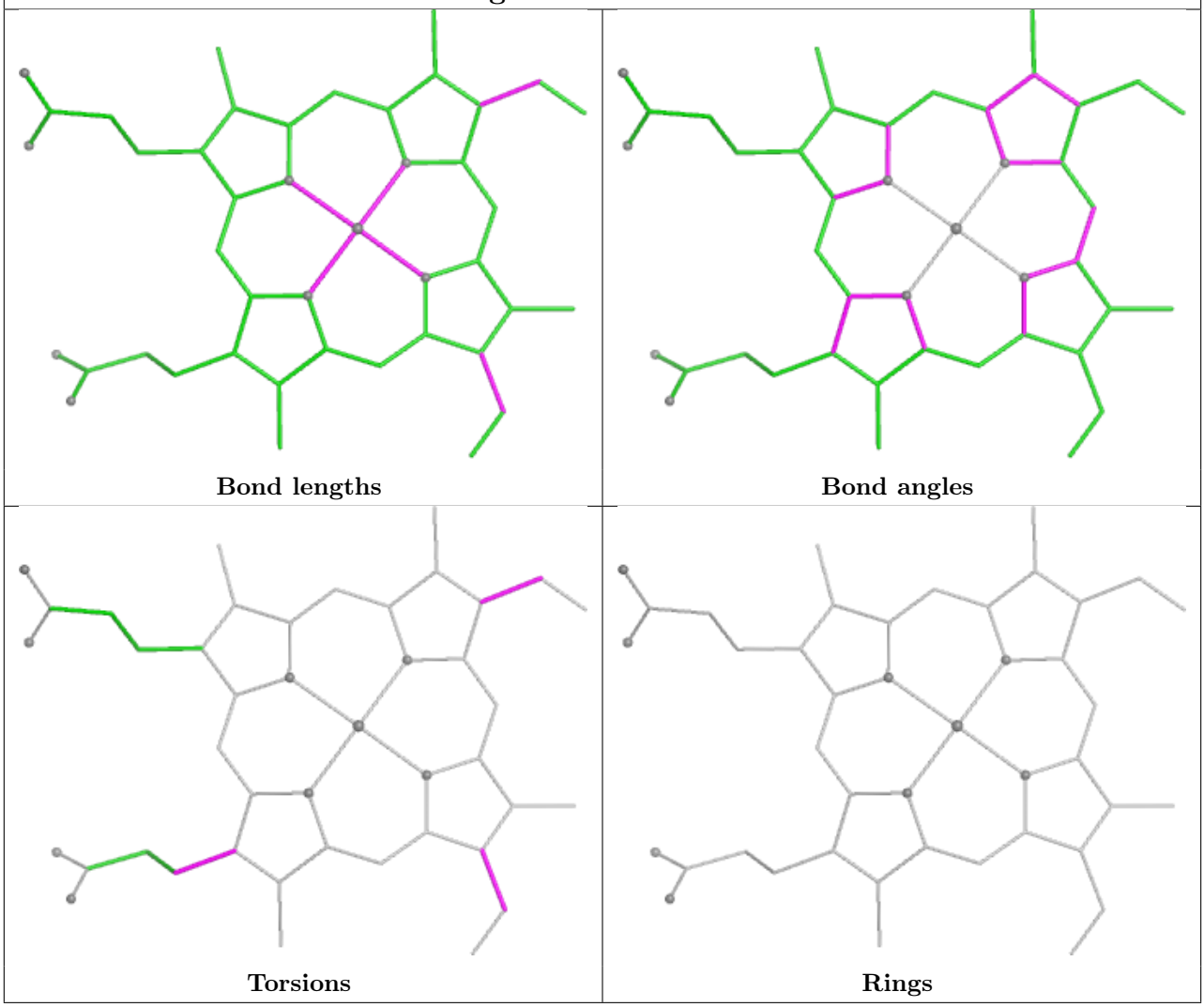


Torsions



Rings

Ligand HEM F 201



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.

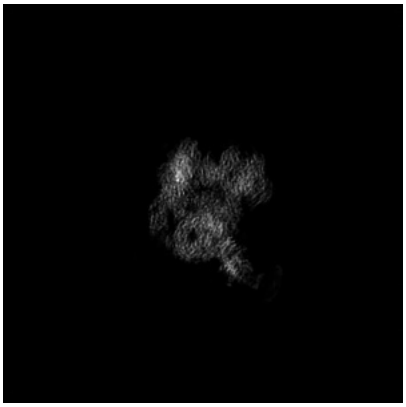
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-56135. These allow visual inspection of the internal detail of the map and identification of artifacts.

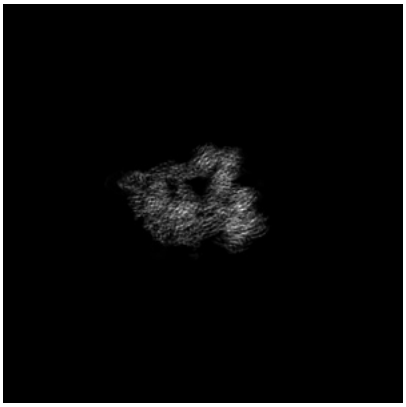
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

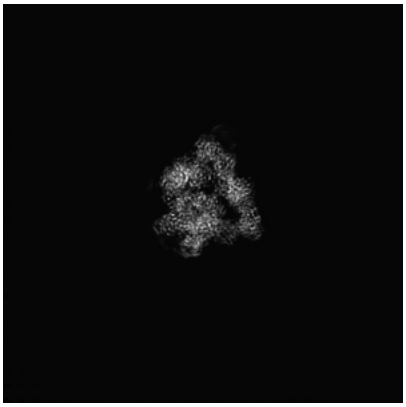
6.1.1 Primary map



X



Y



Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices

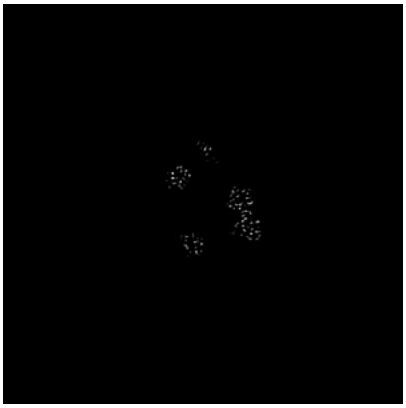
6.2.1 Primary map



X Index: 256



Y Index: 256



Z Index: 256

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

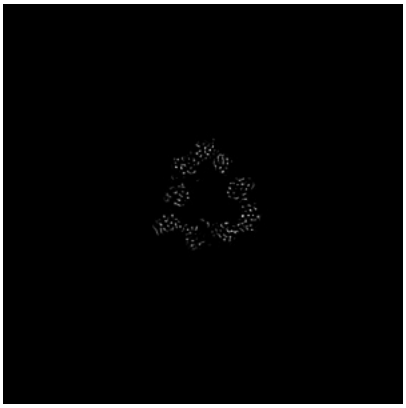
6.3.1 Primary map



X Index: 248



Y Index: 225

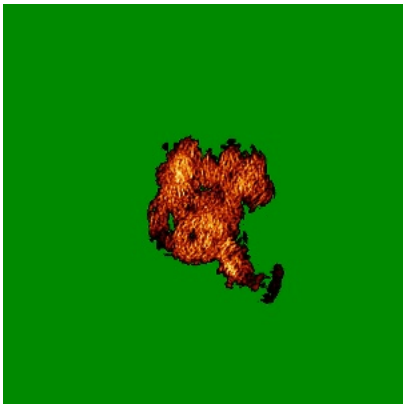


Z Index: 290

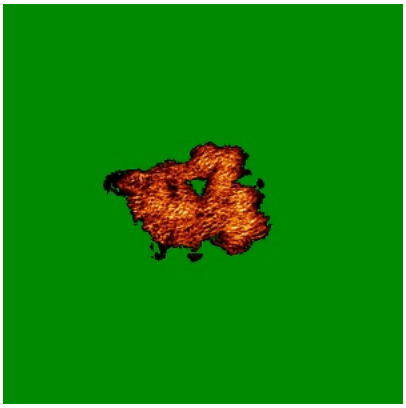
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

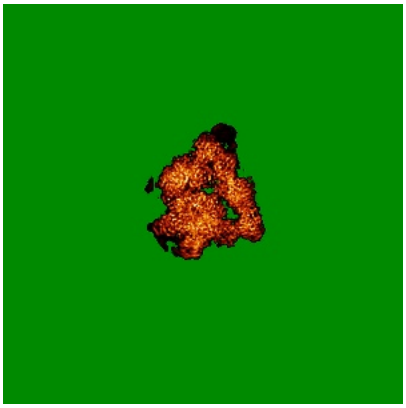
6.4.1 Primary map



X



Y

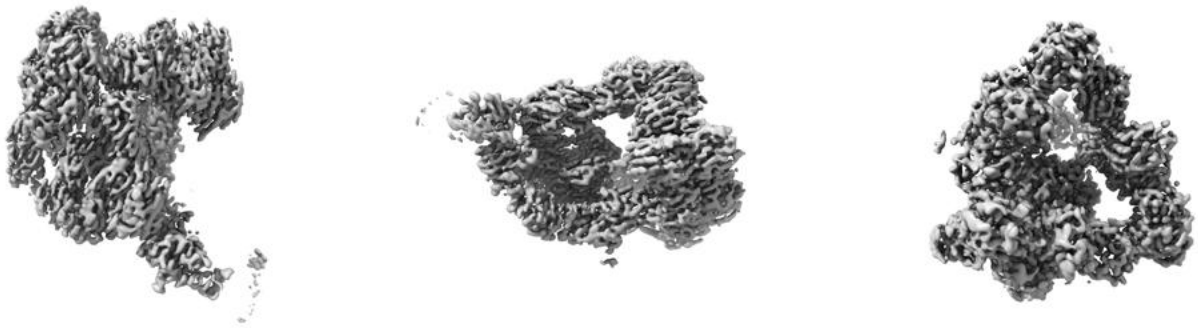


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

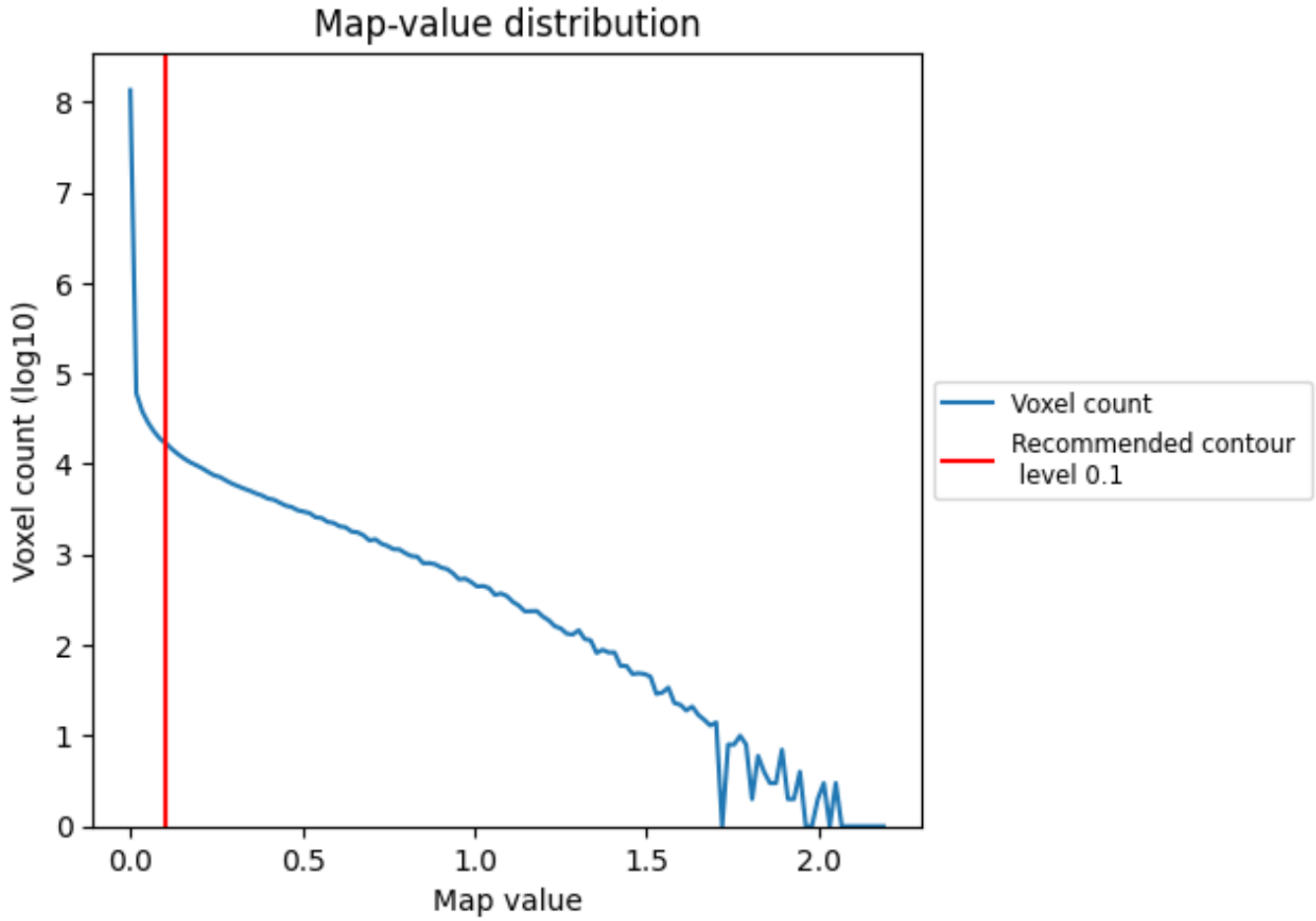
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

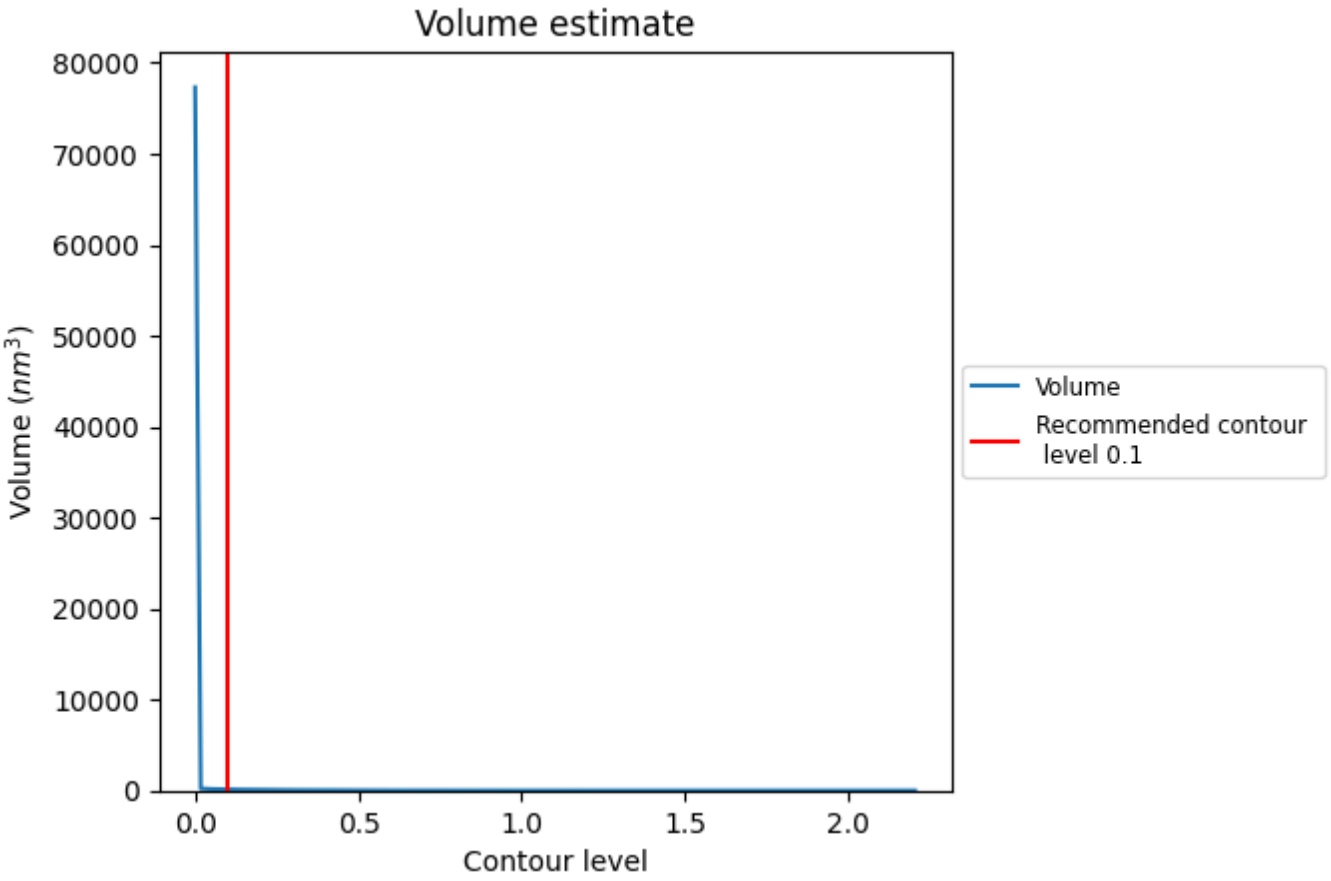
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

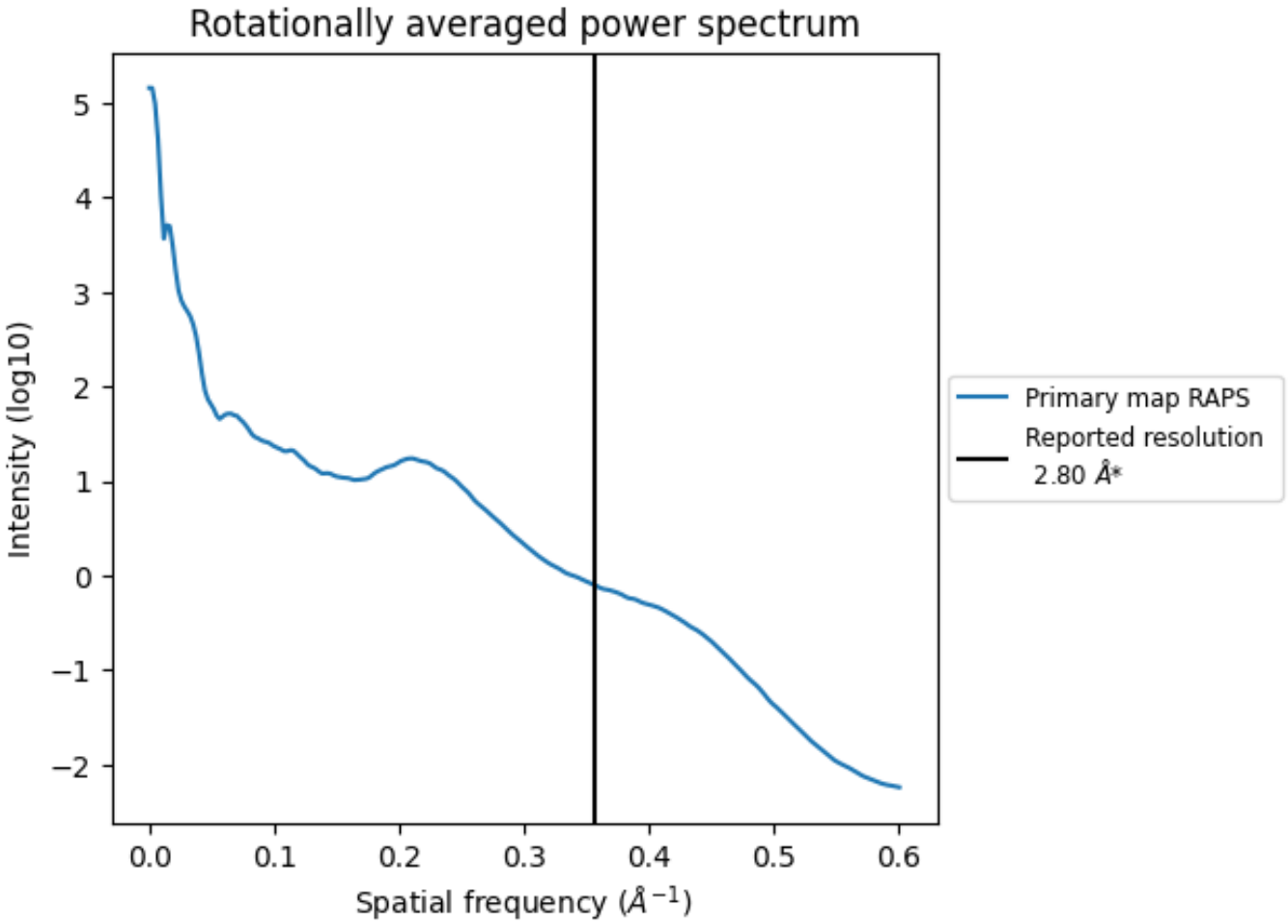
7.2 Volume estimate (i)



The volume at the recommended contour level is 125 nm^3; this corresponds to an approximate mass of 113 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

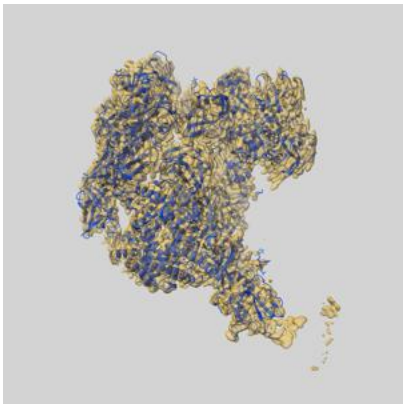
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

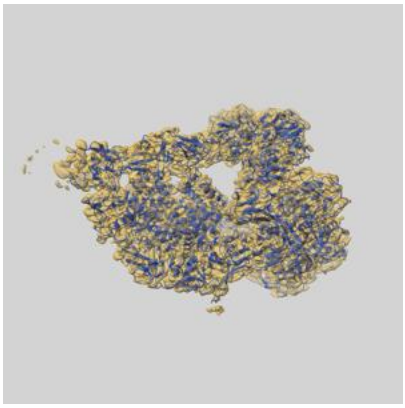
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-56135 and PDB model 9TQD. Per-residue inclusion information can be found in section 3 on page 8.

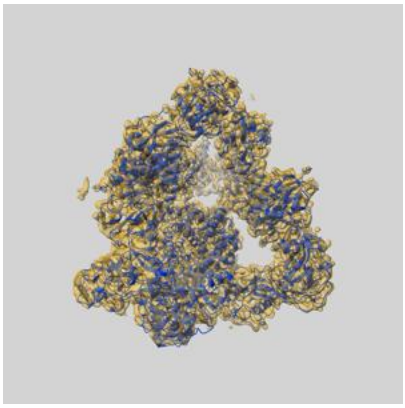
9.1 Map-model overlay



X



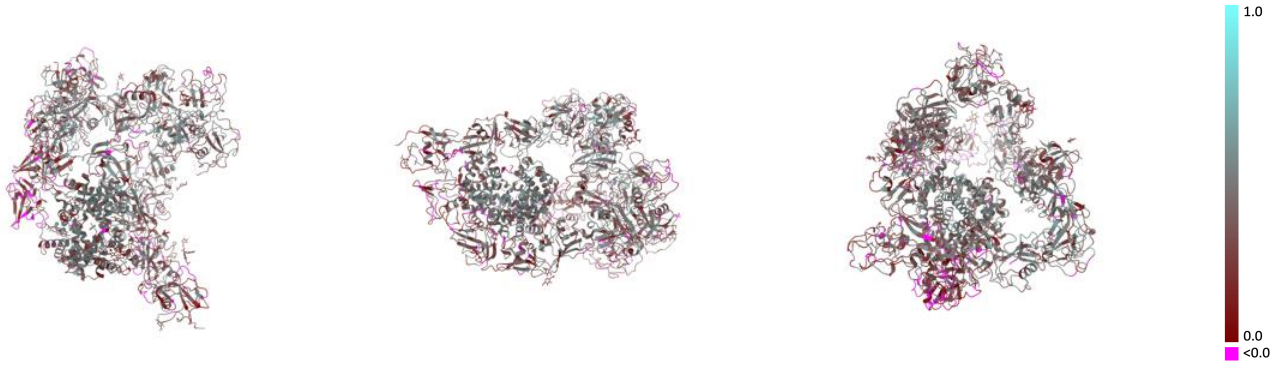
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

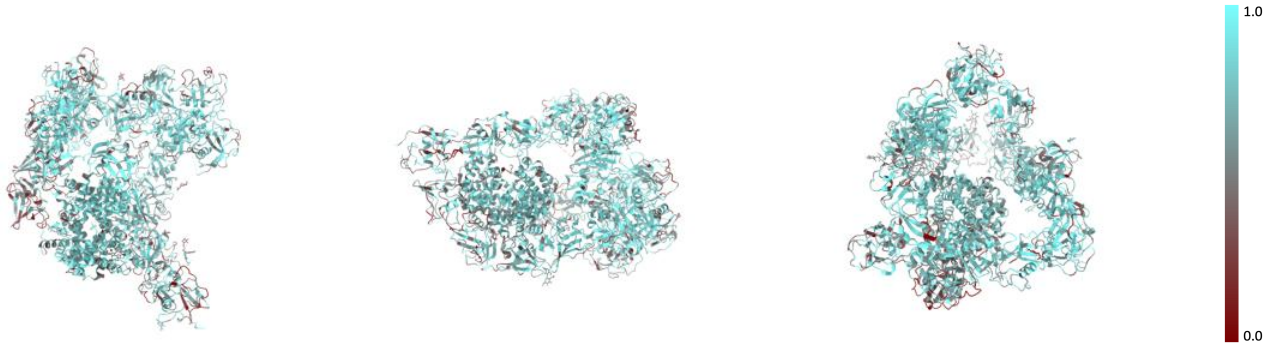
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

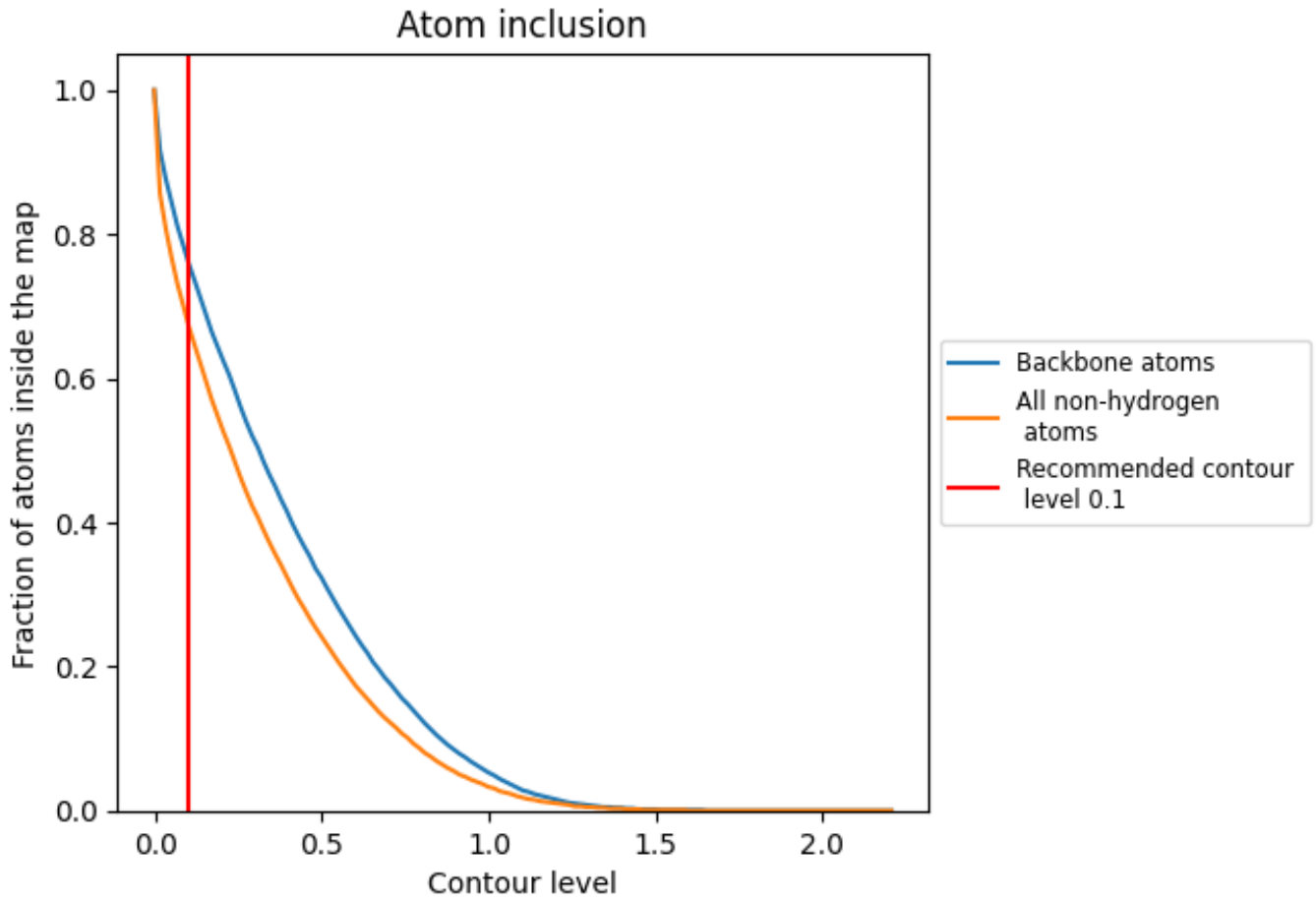
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6750	0.3490
A	0.7020	0.3830
B	0.6700	0.3460
C	0.5880	0.2550
D	0.8060	0.4660
E	0.7440	0.4200
F	0.7370	0.4020
G	0.7340	0.4090
H	0.5000	0.2870
I	0.4290	0.1170
J	0.5360	0.2510
K	0.5360	0.2200
L	0.5000	0.3190

