Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 05:49 AM UTC

PDB ID	:	8D3C / pdb_00008d3c
EMDB ID	:	EMD-27156
Title	:	VWF tubule derived from monomeric D1-A1
Authors	:	Anderson, J.R.; Li, J.; Springer, T.A.; Brown, A.
Deposited on	:	2022-06-01
Resolution	:	3.10 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
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:

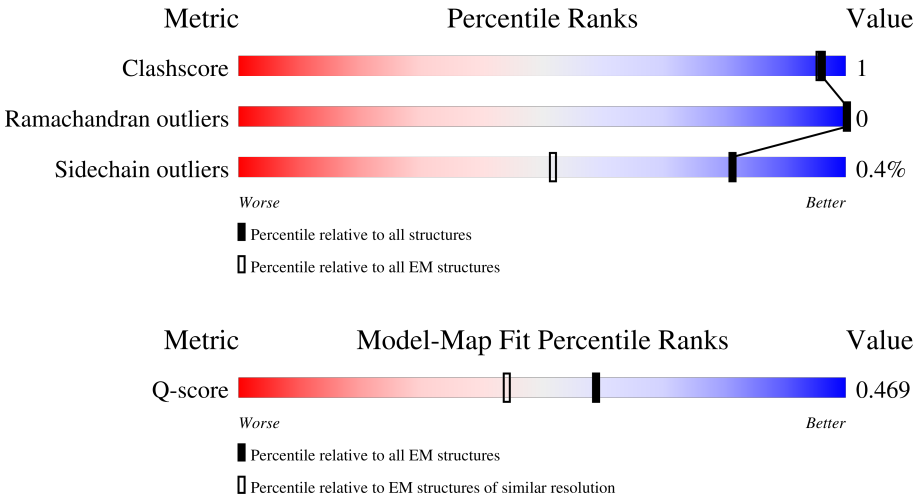
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1469	87% · 11%
1	B	1469	87% · 11%
1	C	1469	87% · 11%
1	D	1469	87% · 11%

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Mol	Chain	Length	Quality of chain
1	E	1469	87% 11%
1	F	1469	86% 11%
1	G	1469	87% 11%
1	H	1469	87% 11%
1	I	1469	87% 11%
1	J	1469	87% 11%
1	K	1469	87% 11%
1	L	1469	87% 11%
1	M	1469	87% 11%
1	N	1469	87% 11%
1	O	1469	87% 11%
1	P	1469	87% 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 162720 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 von Willebrand factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	B	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	C	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	D	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	E	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	F	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	G	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	H	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	I	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	J	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	K	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	L	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	M	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	N	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	O	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		
1	P	1305	Total	C	N	O	S	0	0
			10097	6276	1747	1942	132		

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP P04275
A	761	ALA	SER	engineered mutation	UNP P04275
A	762	SER	LYS	engineered mutation	UNP P04275
A	763	ALA	ARG	engineered mutation	UNP P04275
A	789	ALA	THR	variant	UNP P04275
A	852	ARG	GLN	variant	UNP P04275
A	1381	ALA	THR	variant	UNP P04275
A	1465	HIS	-	expression tag	UNP P04275
A	1466	HIS	-	expression tag	UNP P04275
A	1467	HIS	-	expression tag	UNP P04275
A	1468	HIS	-	expression tag	UNP P04275
A	1469	HIS	-	expression tag	UNP P04275
A	1470	HIS	-	expression tag	UNP P04275
B	?	-	ARG	deletion	UNP P04275
B	761	ALA	SER	engineered mutation	UNP P04275
B	762	SER	LYS	engineered mutation	UNP P04275
B	763	ALA	ARG	engineered mutation	UNP P04275
B	789	ALA	THR	variant	UNP P04275
B	852	ARG	GLN	variant	UNP P04275
B	1381	ALA	THR	variant	UNP P04275
B	1465	HIS	-	expression tag	UNP P04275
B	1466	HIS	-	expression tag	UNP P04275
B	1467	HIS	-	expression tag	UNP P04275
B	1468	HIS	-	expression tag	UNP P04275
B	1469	HIS	-	expression tag	UNP P04275
B	1470	HIS	-	expression tag	UNP P04275
C	?	-	ARG	deletion	UNP P04275
C	761	ALA	SER	engineered mutation	UNP P04275
C	762	SER	LYS	engineered mutation	UNP P04275
C	763	ALA	ARG	engineered mutation	UNP P04275
C	789	ALA	THR	variant	UNP P04275
C	852	ARG	GLN	variant	UNP P04275
C	1381	ALA	THR	variant	UNP P04275
C	1465	HIS	-	expression tag	UNP P04275
C	1466	HIS	-	expression tag	UNP P04275
C	1467	HIS	-	expression tag	UNP P04275
C	1468	HIS	-	expression tag	UNP P04275
C	1469	HIS	-	expression tag	UNP P04275
C	1470	HIS	-	expression tag	UNP P04275
D	?	-	ARG	deletion	UNP P04275
D	761	ALA	SER	engineered mutation	UNP P04275
D	762	SER	LYS	engineered mutation	UNP P04275
D	763	ALA	ARG	engineered mutation	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
D	789	ALA	THR	variant	UNP P04275
D	852	ARG	GLN	variant	UNP P04275
D	1381	ALA	THR	variant	UNP P04275
D	1465	HIS	-	expression tag	UNP P04275
D	1466	HIS	-	expression tag	UNP P04275
D	1467	HIS	-	expression tag	UNP P04275
D	1468	HIS	-	expression tag	UNP P04275
D	1469	HIS	-	expression tag	UNP P04275
D	1470	HIS	-	expression tag	UNP P04275
E	?	-	ARG	deletion	UNP P04275
E	761	ALA	SER	engineered mutation	UNP P04275
E	762	SER	LYS	engineered mutation	UNP P04275
E	763	ALA	ARG	engineered mutation	UNP P04275
E	789	ALA	THR	variant	UNP P04275
E	852	ARG	GLN	variant	UNP P04275
E	1381	ALA	THR	variant	UNP P04275
E	1465	HIS	-	expression tag	UNP P04275
E	1466	HIS	-	expression tag	UNP P04275
E	1467	HIS	-	expression tag	UNP P04275
E	1468	HIS	-	expression tag	UNP P04275
E	1469	HIS	-	expression tag	UNP P04275
E	1470	HIS	-	expression tag	UNP P04275
F	?	-	ARG	deletion	UNP P04275
F	761	ALA	SER	engineered mutation	UNP P04275
F	762	SER	LYS	engineered mutation	UNP P04275
F	763	ALA	ARG	engineered mutation	UNP P04275
F	789	ALA	THR	variant	UNP P04275
F	852	ARG	GLN	variant	UNP P04275
F	1381	ALA	THR	variant	UNP P04275
F	1465	HIS	-	expression tag	UNP P04275
F	1466	HIS	-	expression tag	UNP P04275
F	1467	HIS	-	expression tag	UNP P04275
F	1468	HIS	-	expression tag	UNP P04275
F	1469	HIS	-	expression tag	UNP P04275
F	1470	HIS	-	expression tag	UNP P04275
G	?	-	ARG	deletion	UNP P04275
G	761	ALA	SER	engineered mutation	UNP P04275
G	762	SER	LYS	engineered mutation	UNP P04275
G	763	ALA	ARG	engineered mutation	UNP P04275
G	789	ALA	THR	variant	UNP P04275
G	852	ARG	GLN	variant	UNP P04275
G	1381	ALA	THR	variant	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1465	HIS	-	expression tag	UNP P04275
G	1466	HIS	-	expression tag	UNP P04275
G	1467	HIS	-	expression tag	UNP P04275
G	1468	HIS	-	expression tag	UNP P04275
G	1469	HIS	-	expression tag	UNP P04275
G	1470	HIS	-	expression tag	UNP P04275
H	?	-	ARG	deletion	UNP P04275
H	761	ALA	SER	engineered mutation	UNP P04275
H	762	SER	LYS	engineered mutation	UNP P04275
H	763	ALA	ARG	engineered mutation	UNP P04275
H	789	ALA	THR	variant	UNP P04275
H	852	ARG	GLN	variant	UNP P04275
H	1381	ALA	THR	variant	UNP P04275
H	1465	HIS	-	expression tag	UNP P04275
H	1466	HIS	-	expression tag	UNP P04275
H	1467	HIS	-	expression tag	UNP P04275
H	1468	HIS	-	expression tag	UNP P04275
H	1469	HIS	-	expression tag	UNP P04275
H	1470	HIS	-	expression tag	UNP P04275
I	?	-	ARG	deletion	UNP P04275
I	761	ALA	SER	engineered mutation	UNP P04275
I	762	SER	LYS	engineered mutation	UNP P04275
I	763	ALA	ARG	engineered mutation	UNP P04275
I	789	ALA	THR	variant	UNP P04275
I	852	ARG	GLN	variant	UNP P04275
I	1381	ALA	THR	variant	UNP P04275
I	1465	HIS	-	expression tag	UNP P04275
I	1466	HIS	-	expression tag	UNP P04275
I	1467	HIS	-	expression tag	UNP P04275
I	1468	HIS	-	expression tag	UNP P04275
I	1469	HIS	-	expression tag	UNP P04275
I	1470	HIS	-	expression tag	UNP P04275
J	?	-	ARG	deletion	UNP P04275
J	761	ALA	SER	engineered mutation	UNP P04275
J	762	SER	LYS	engineered mutation	UNP P04275
J	763	ALA	ARG	engineered mutation	UNP P04275
J	789	ALA	THR	variant	UNP P04275
J	852	ARG	GLN	variant	UNP P04275
J	1381	ALA	THR	variant	UNP P04275
J	1465	HIS	-	expression tag	UNP P04275
J	1466	HIS	-	expression tag	UNP P04275
J	1467	HIS	-	expression tag	UNP P04275

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1468	HIS	-	expression tag	UNP P04275
J	1469	HIS	-	expression tag	UNP P04275
J	1470	HIS	-	expression tag	UNP P04275
K	?	-	ARG	deletion	UNP P04275
K	761	ALA	SER	engineered mutation	UNP P04275
K	762	SER	LYS	engineered mutation	UNP P04275
K	763	ALA	ARG	engineered mutation	UNP P04275
K	789	ALA	THR	variant	UNP P04275
K	852	ARG	GLN	variant	UNP P04275
K	1381	ALA	THR	variant	UNP P04275
K	1465	HIS	-	expression tag	UNP P04275
K	1466	HIS	-	expression tag	UNP P04275
K	1467	HIS	-	expression tag	UNP P04275
K	1468	HIS	-	expression tag	UNP P04275
K	1469	HIS	-	expression tag	UNP P04275
K	1470	HIS	-	expression tag	UNP P04275
L	?	-	ARG	deletion	UNP P04275
L	761	ALA	SER	engineered mutation	UNP P04275
L	762	SER	LYS	engineered mutation	UNP P04275
L	763	ALA	ARG	engineered mutation	UNP P04275
L	789	ALA	THR	variant	UNP P04275
L	852	ARG	GLN	variant	UNP P04275
L	1381	ALA	THR	variant	UNP P04275
L	1465	HIS	-	expression tag	UNP P04275
L	1466	HIS	-	expression tag	UNP P04275
L	1467	HIS	-	expression tag	UNP P04275
L	1468	HIS	-	expression tag	UNP P04275
L	1469	HIS	-	expression tag	UNP P04275
L	1470	HIS	-	expression tag	UNP P04275
M	?	-	ARG	deletion	UNP P04275
M	761	ALA	SER	engineered mutation	UNP P04275
M	762	SER	LYS	engineered mutation	UNP P04275
M	763	ALA	ARG	engineered mutation	UNP P04275
M	789	ALA	THR	variant	UNP P04275
M	852	ARG	GLN	variant	UNP P04275
M	1381	ALA	THR	variant	UNP P04275
M	1465	HIS	-	expression tag	UNP P04275
M	1466	HIS	-	expression tag	UNP P04275
M	1467	HIS	-	expression tag	UNP P04275
M	1468	HIS	-	expression tag	UNP P04275
M	1469	HIS	-	expression tag	UNP P04275
M	1470	HIS	-	expression tag	UNP P04275

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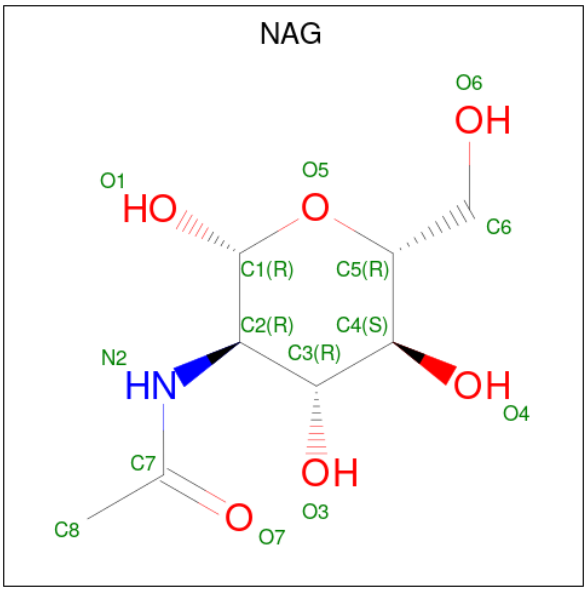
Chain	Residue	Modelled	Actual	Comment	Reference
N	?	-	ARG	deletion	UNP P04275
N	761	ALA	SER	engineered mutation	UNP P04275
N	762	SER	LYS	engineered mutation	UNP P04275
N	763	ALA	ARG	engineered mutation	UNP P04275
N	789	ALA	THR	variant	UNP P04275
N	852	ARG	GLN	variant	UNP P04275
N	1381	ALA	THR	variant	UNP P04275
N	1465	HIS	-	expression tag	UNP P04275
N	1466	HIS	-	expression tag	UNP P04275
N	1467	HIS	-	expression tag	UNP P04275
N	1468	HIS	-	expression tag	UNP P04275
N	1469	HIS	-	expression tag	UNP P04275
N	1470	HIS	-	expression tag	UNP P04275
O	?	-	ARG	deletion	UNP P04275
O	761	ALA	SER	engineered mutation	UNP P04275
O	762	SER	LYS	engineered mutation	UNP P04275
O	763	ALA	ARG	engineered mutation	UNP P04275
O	789	ALA	THR	variant	UNP P04275
O	852	ARG	GLN	variant	UNP P04275
O	1381	ALA	THR	variant	UNP P04275
O	1465	HIS	-	expression tag	UNP P04275
O	1466	HIS	-	expression tag	UNP P04275
O	1467	HIS	-	expression tag	UNP P04275
O	1468	HIS	-	expression tag	UNP P04275
O	1469	HIS	-	expression tag	UNP P04275
O	1470	HIS	-	expression tag	UNP P04275
P	?	-	ARG	deletion	UNP P04275
P	761	ALA	SER	engineered mutation	UNP P04275
P	762	SER	LYS	engineered mutation	UNP P04275
P	763	ALA	ARG	engineered mutation	UNP P04275
P	789	ALA	THR	variant	UNP P04275
P	852	ARG	GLN	variant	UNP P04275
P	1381	ALA	THR	variant	UNP P04275
P	1465	HIS	-	expression tag	UNP P04275
P	1466	HIS	-	expression tag	UNP P04275
P	1467	HIS	-	expression tag	UNP P04275
P	1468	HIS	-	expression tag	UNP P04275
P	1469	HIS	-	expression tag	UNP P04275
P	1470	HIS	-	expression tag	UNP P04275

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	AltConf
2	A	3	Total Ca 3 3	0
2	B	3	Total Ca 3 3	0
2	C	3	Total Ca 3 3	0
2	D	3	Total Ca 3 3	0
2	E	3	Total Ca 3 3	0
2	F	3	Total Ca 3 3	0
2	G	3	Total Ca 3 3	0
2	H	3	Total Ca 3 3	0
2	I	3	Total Ca 3 3	0
2	J	3	Total Ca 3 3	0
2	K	3	Total Ca 3 3	0
2	L	3	Total Ca 3 3	0
2	M	3	Total Ca 3 3	0
2	N	3	Total Ca 3 3	0
2	O	3	Total Ca 3 3	0
2	P	3	Total Ca 3 3	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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Mol	Chain	Residues	Atoms				AltConf
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	F	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	
3	G	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	H	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	I	1	Total	C	N	O	0
			14	8	1	5	
3	J	1	Total	C	N	O	0
			14	8	1	5	
3	J	1	Total	C	N	O	0
			14	8	1	5	
3	J	1	Total	C	N	O	0
			14	8	1	5	
3	J	1	Total	C	N	O	0
			14	8	1	5	
3	J	1	Total	C	N	O	0
			14	8	1	5	
3	K	1	Total	C	N	O	0
			14	8	1	5	
3	K	1	Total	C	N	O	0
			14	8	1	5	
3	K	1	Total	C	N	O	0
			14	8	1	5	
3	K	1	Total	C	N	O	0
			14	8	1	5	
3	K	1	Total	C	N	O	0
			14	8	1	5	
3	L	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
3	L	1	Total	C	N	O	0
			14	8	1	5	
3	L	1	Total	C	N	O	0
			14	8	1	5	
3	L	1	Total	C	N	O	0
			14	8	1	5	
3	L	1	Total	C	N	O	0
			14	8	1	5	
3	M	1	Total	C	N	O	0
			14	8	1	5	
3	M	1	Total	C	N	O	0
			14	8	1	5	
3	M	1	Total	C	N	O	0
			14	8	1	5	
3	M	1	Total	C	N	O	0
			14	8	1	5	
3	M	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	N	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	O	1	Total	C	N	O	0
			14	8	1	5	
3	P	1	Total	C	N	O	0
			14	8	1	5	
3	P	1	Total	C	N	O	0
			14	8	1	5	

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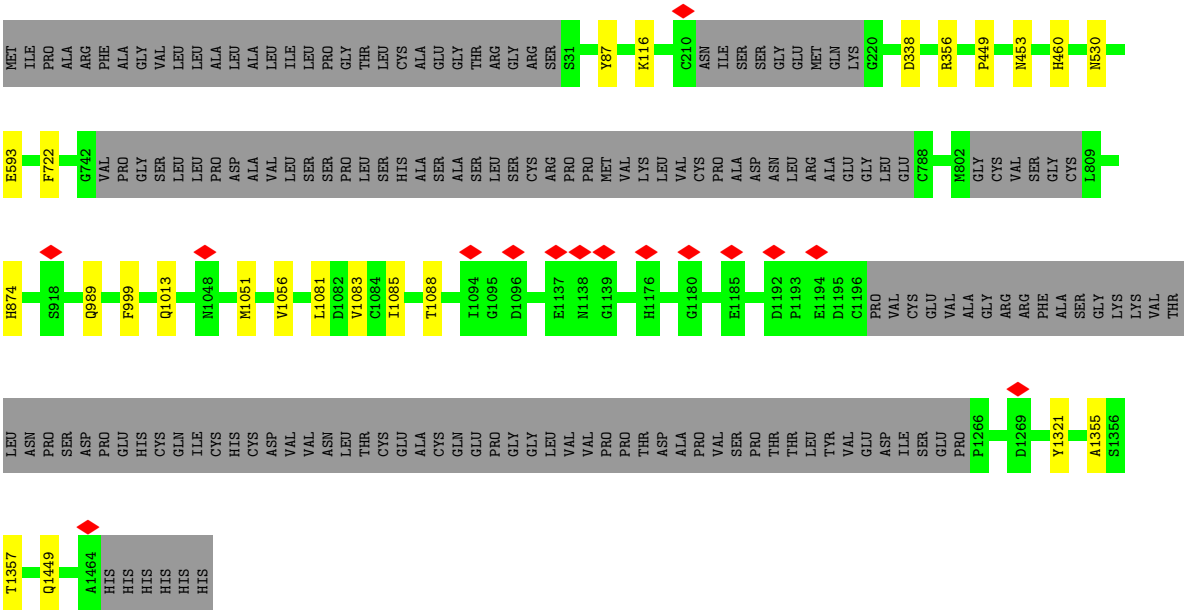
Mol	Chain	Residues	Atoms				AltConf
3	P	1	Total	C	N	O	0
			14	8	1	5	
3	P	1	Total	C	N	O	0
			14	8	1	5	
3	P	1	Total	C	N	O	0
			14	8	1	5	

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.

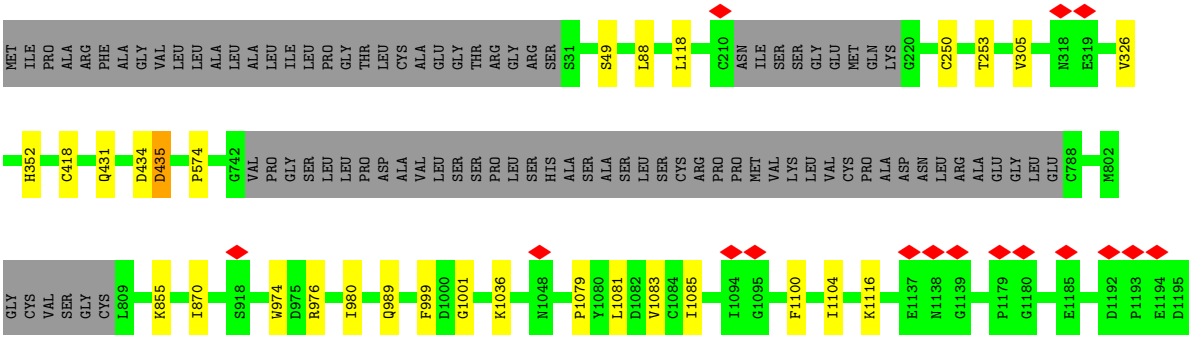
• Molecule 1: von Willebrand factor

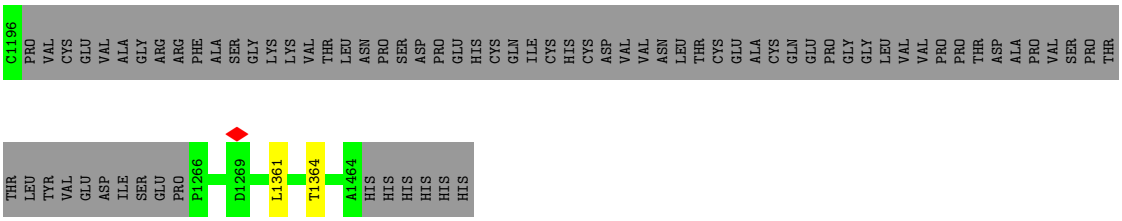
Chain A:



• Molecule 1: von Willebrand factor

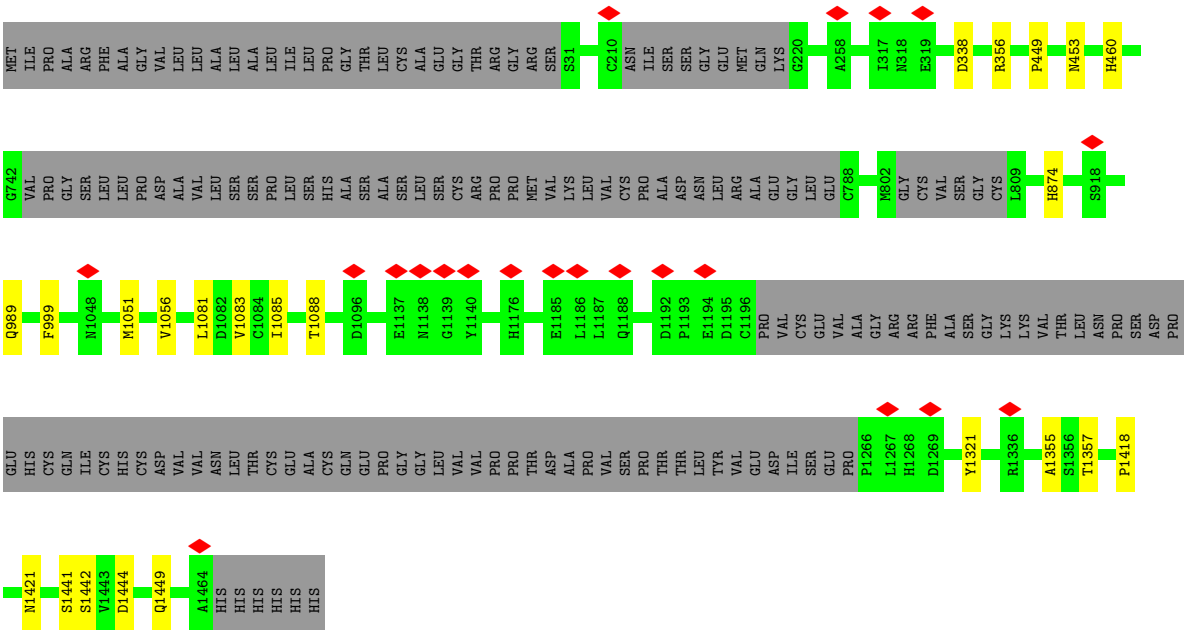
Chain B:





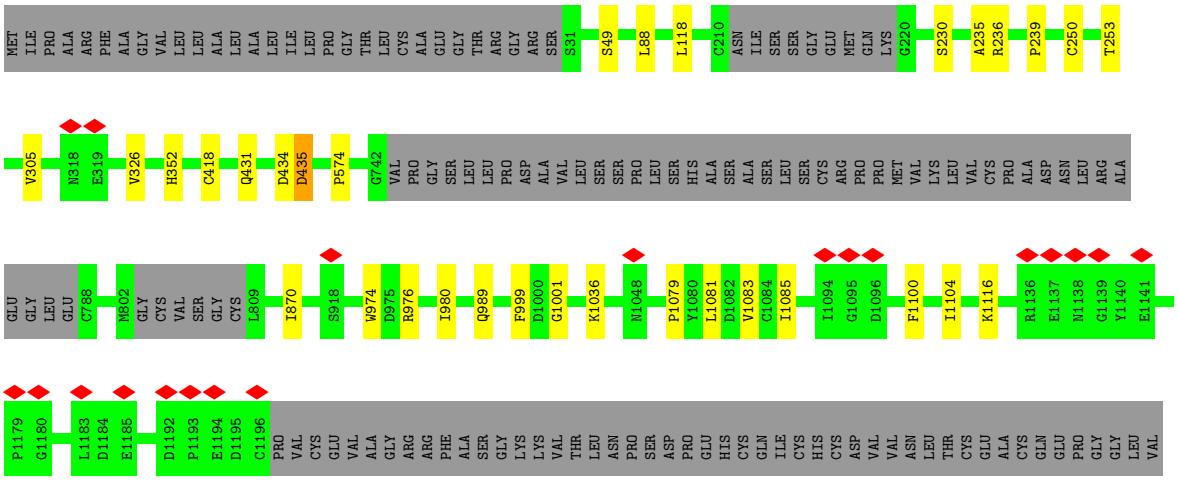
• Molecule 1: von Willebrand factor

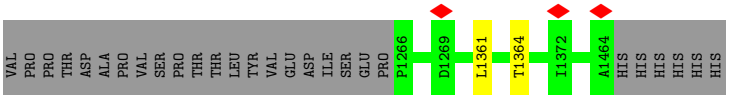
Chain C:



• Molecule 1: von Willebrand factor

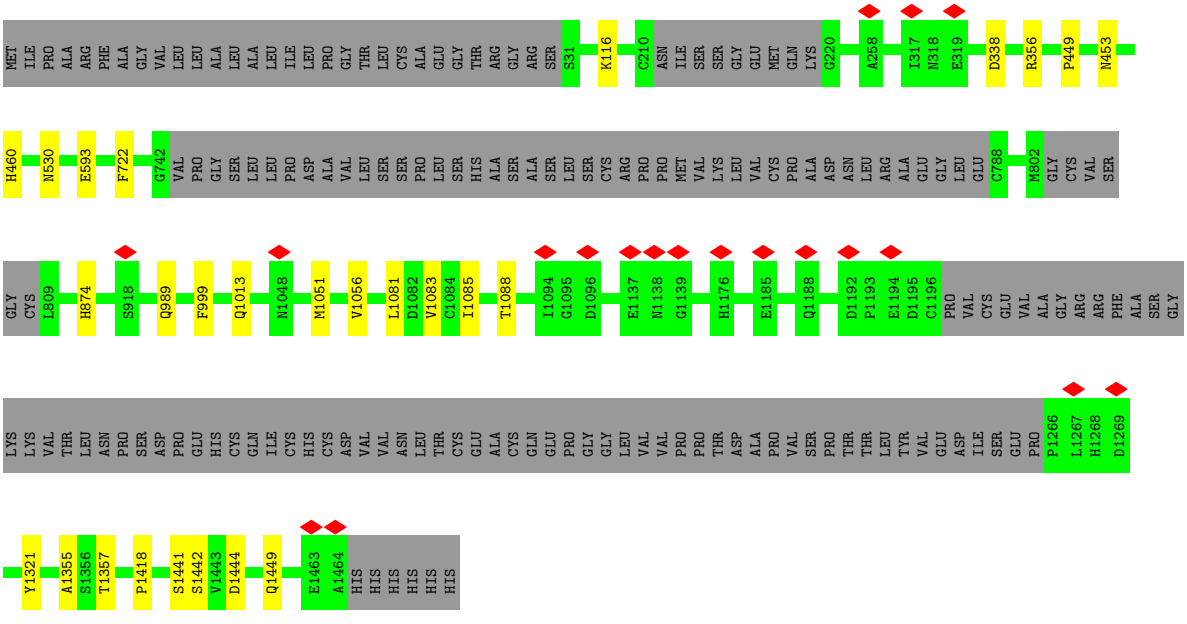
Chain D:





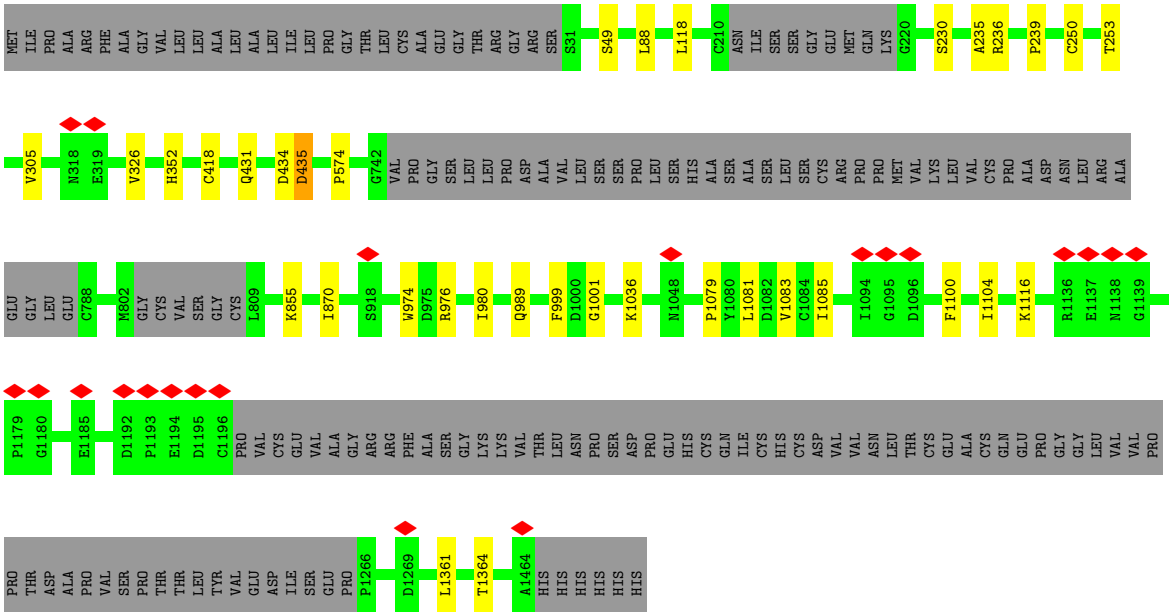
• Molecule 1: von Willebrand factor

Chain E:



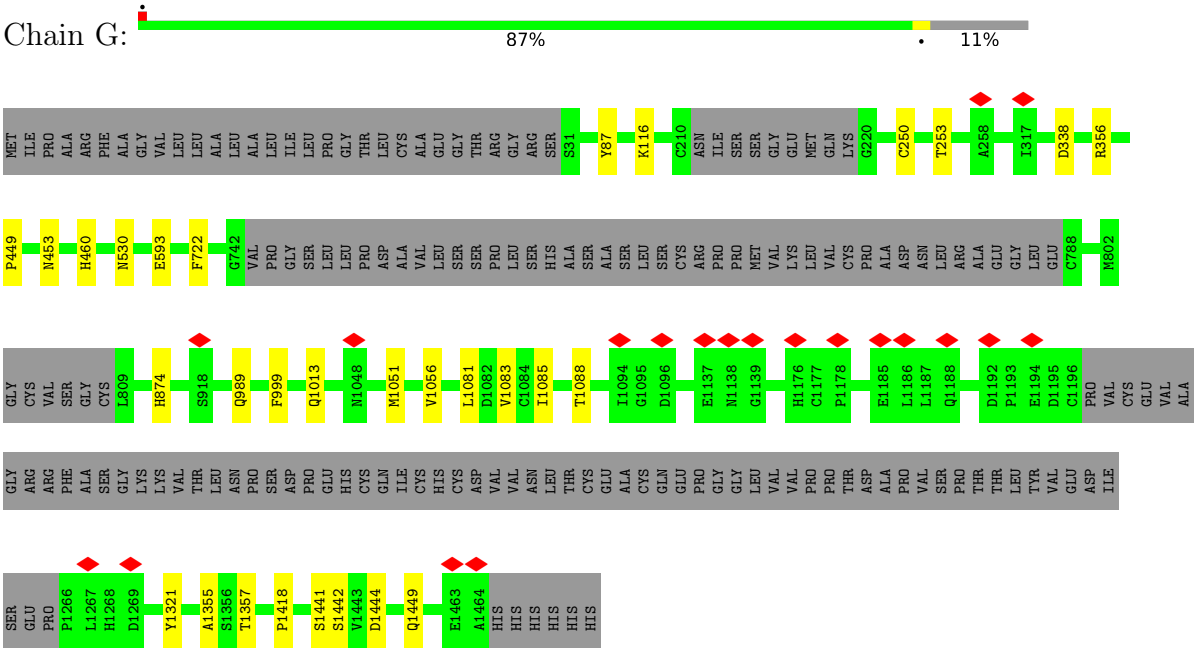
• Molecule 1: von Willebrand factor

Chain F:



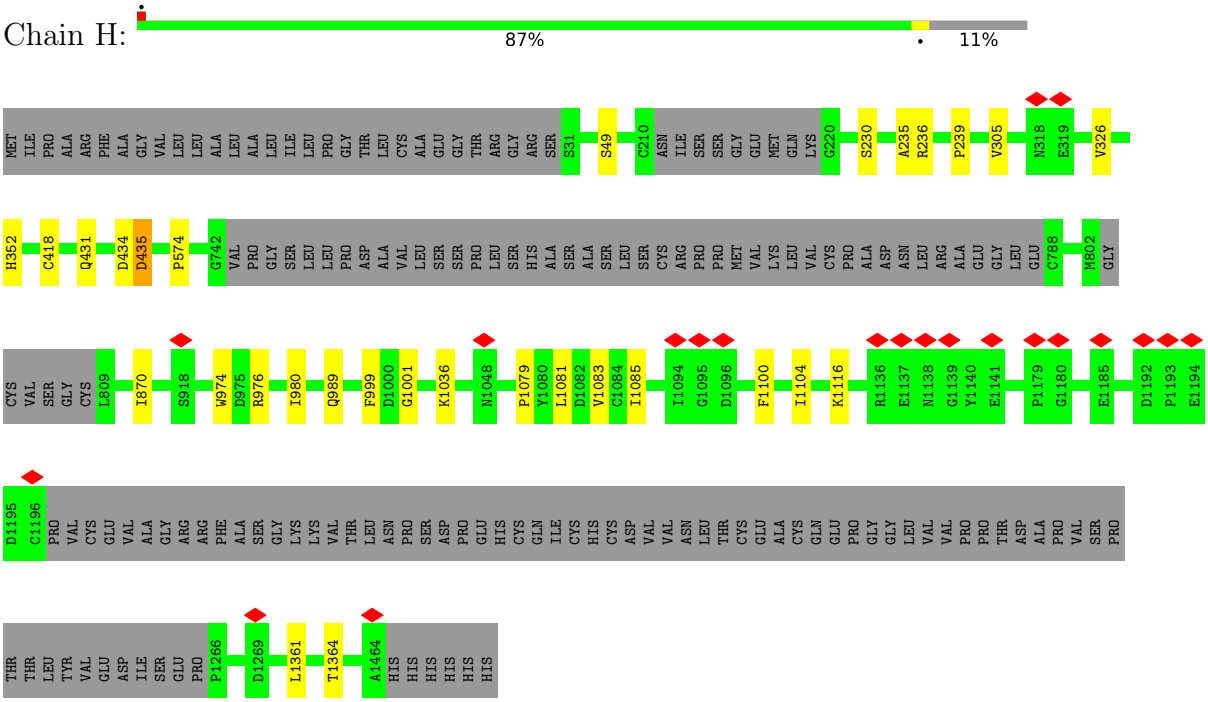
• Molecule 1: von Willebrand factor

Chain G:



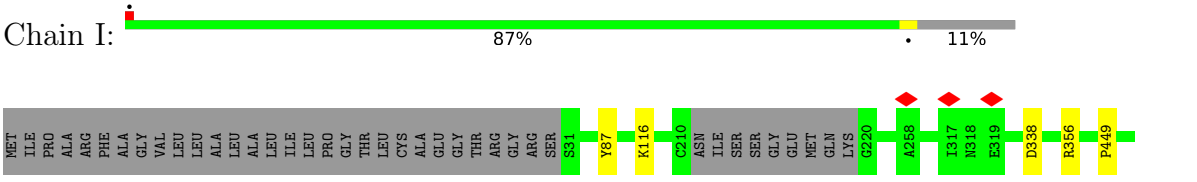
• Molecule 1: von Willebrand factor

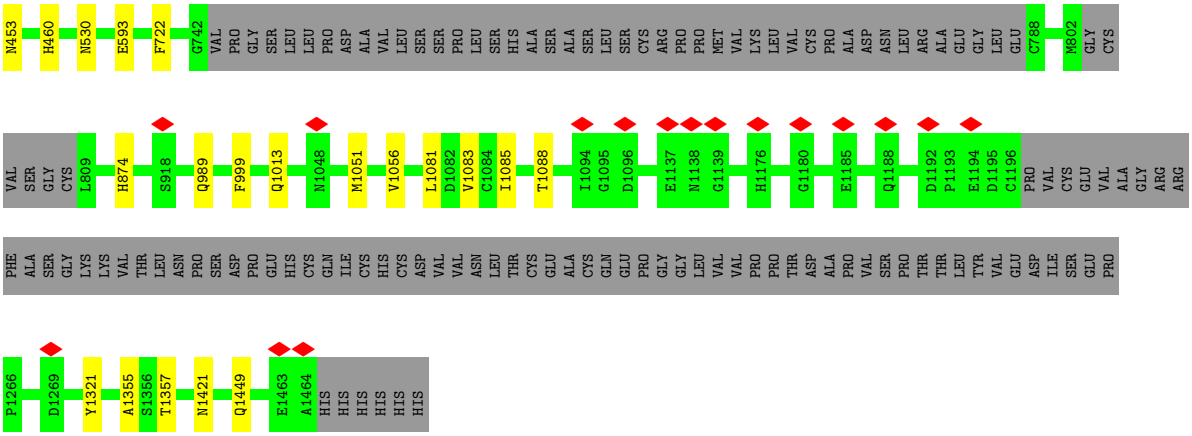
Chain H:



• Molecule 1: von Willebrand factor

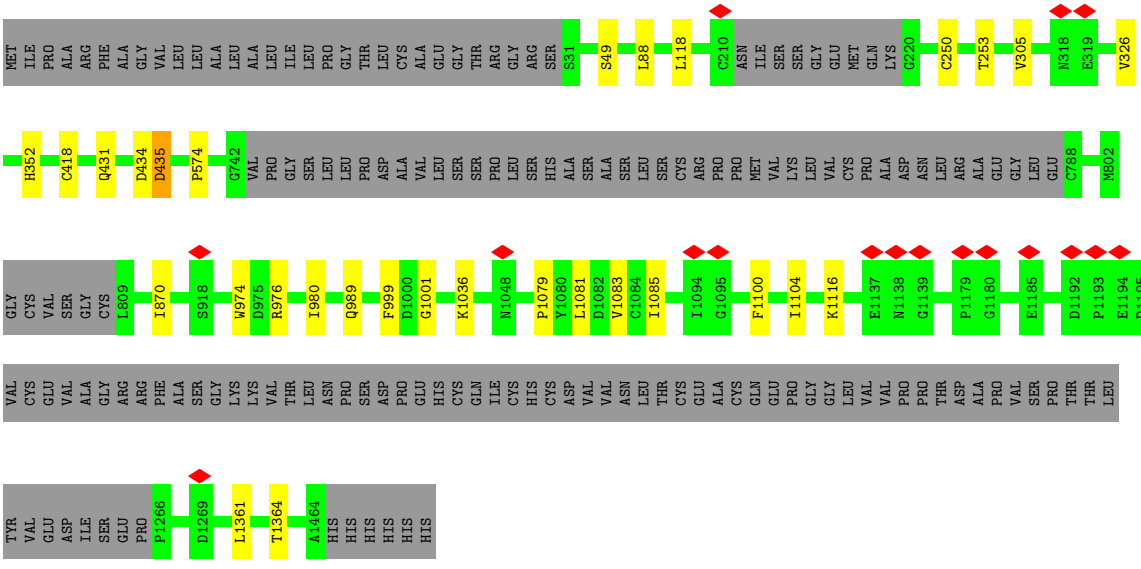
Chain I:





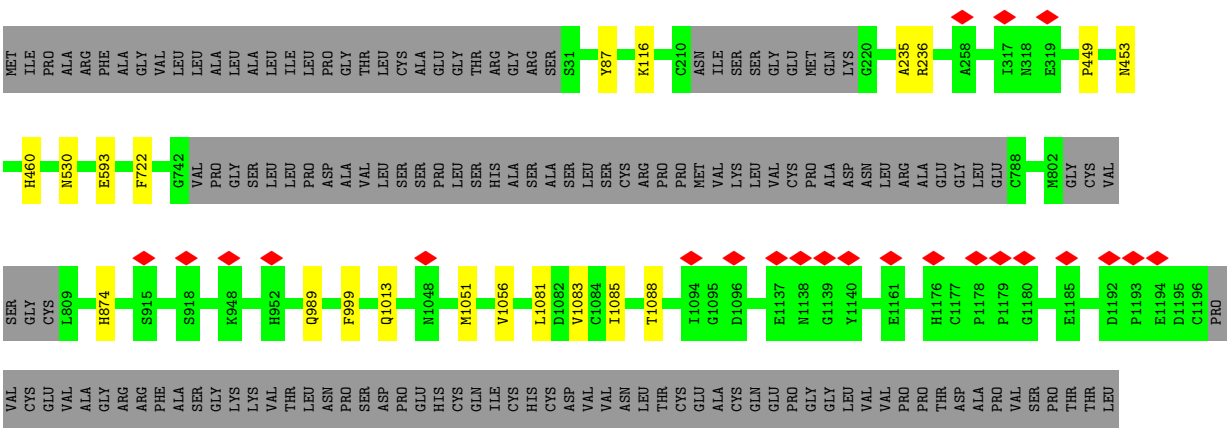
• Molecule 1: von Willebrand factor

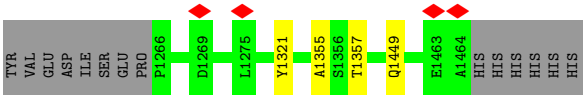
Chain J:



• Molecule 1: von Willebrand factor

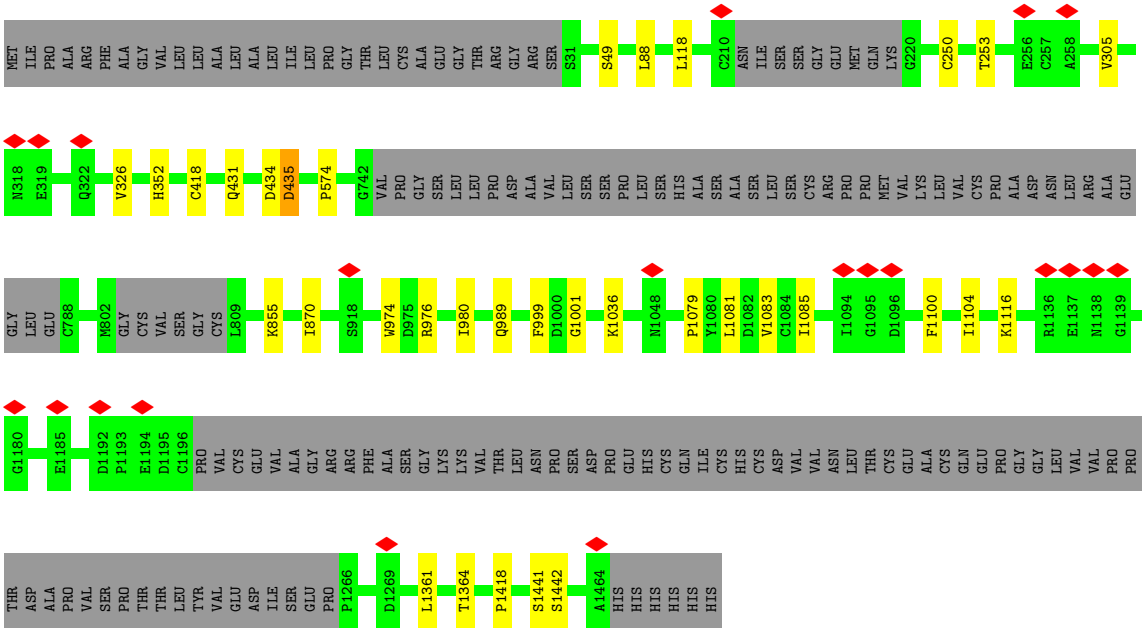
Chain K:





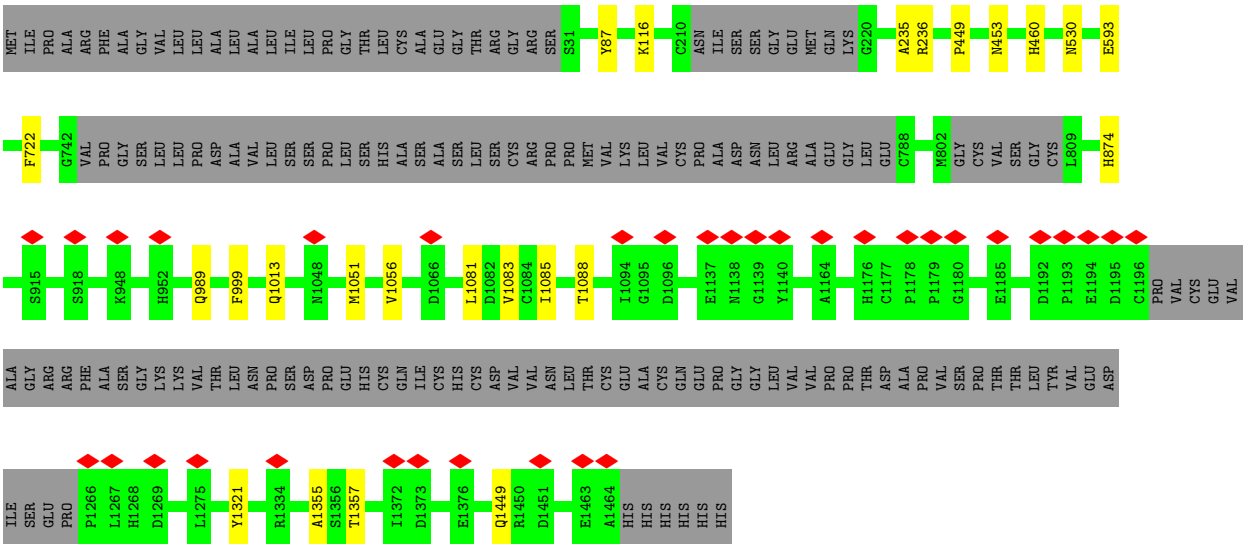
• Molecule 1: von Willebrand factor

Chain L:



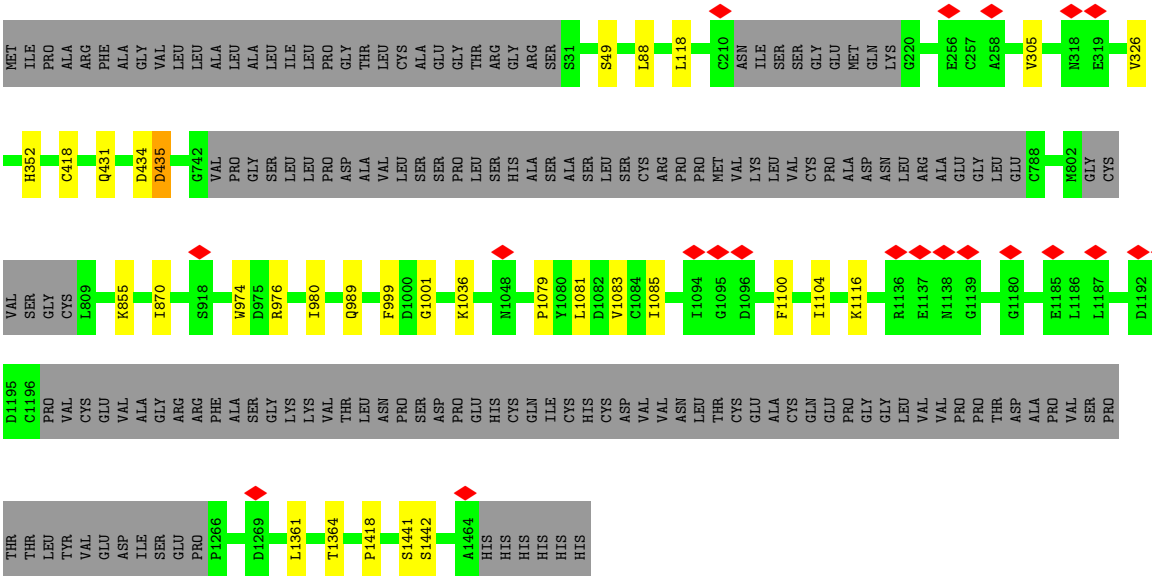
• Molecule 1: von Willebrand factor

Chain M:



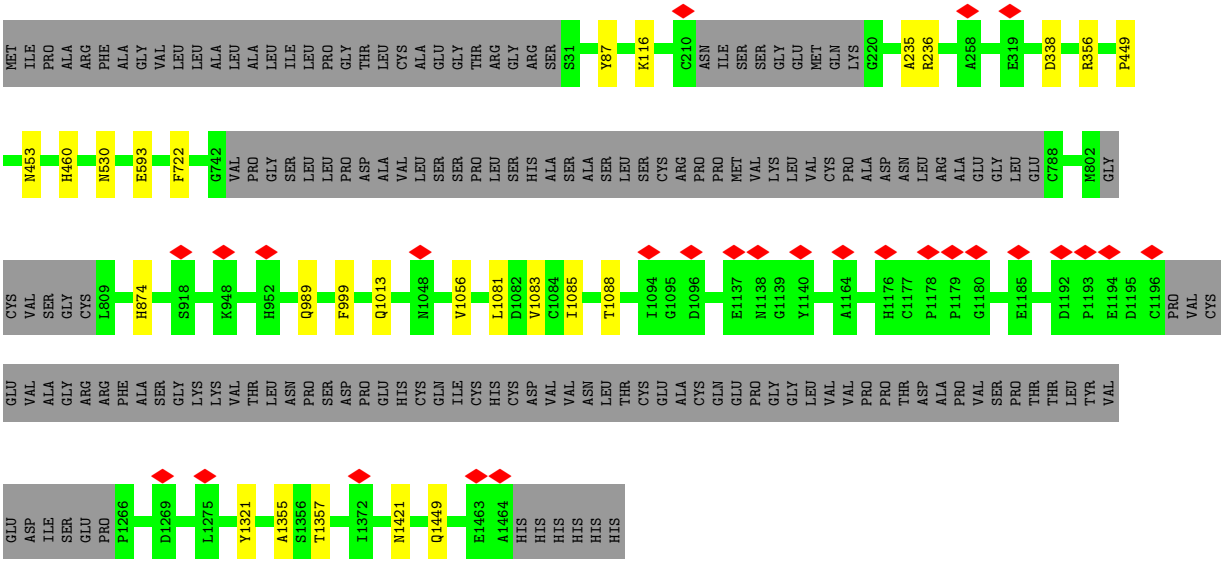
• Molecule 1: von Willebrand factor

Chain N:



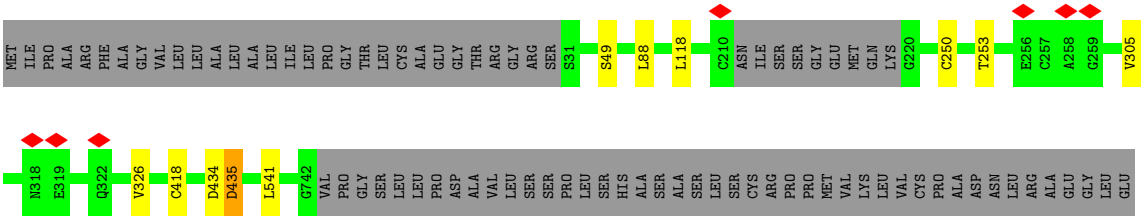
• Molecule 1: von Willebrand factor

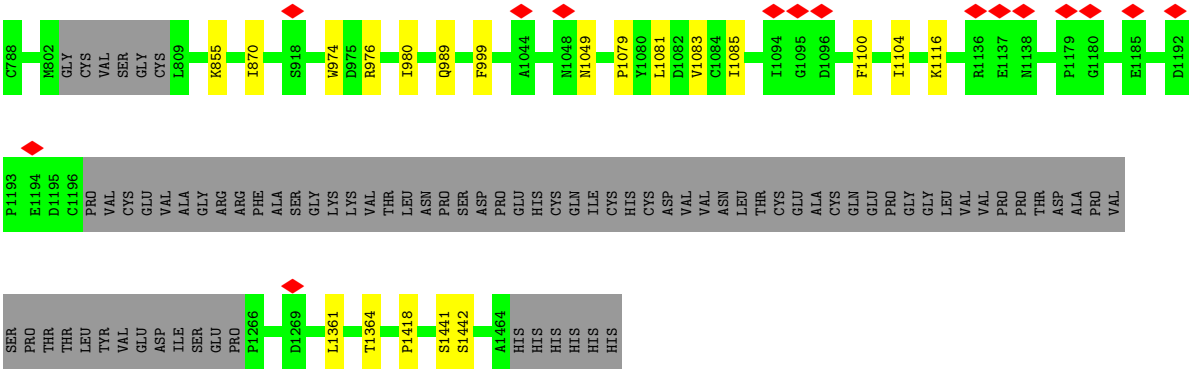
Chain O:



• Molecule 1: von Willebrand factor

Chain P:




C788 M802 GLY CYS VAL SER GLY CYS L809 K855 I870 S918 W974 D975 R976 I980 Q989 F999 A1044 N1048 N1049 P1079 Y1080 L1081 D1082 V1083 C1084 I1085 I1094 G1095 D1096 F1100 I1104 K1116 R1136 E1137 N1138 P1179 G1180 E1185 D1192

P1193 E1194 D1195 C1196 PRO VAL CYS GLU VAL ALA GLY ARG ARG PHE ALA SER GLY LYS LYS VAL THR LEU ASN PRO SER ASP PRO GLU HIS CYS GLN ILE CYS HIS CYS ASP VAL VAL ASN LEU THR CYS GLU ALA CYS GLN GLU PRO GLY GLY LEU VAL VAL PRO PRO THR ASP ALA PRO VAL

SER PRO THR THR LEU TYR VAL GLU ASP ILE SER GLU PRO P1266 D1269 L1361 T1364 P1418 S1441 S1442 A1464 HIS HIS HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=83.3°, rise=26.8 Å, axial sym=C1	Depositor
Number of segments used	373304	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	55	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	59.991	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.544	Depositor
Map value standard deviation	2.300	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.21	0/10315	0.53	0/13969
1	B	0.21	0/10315	0.54	0/13969
1	C	0.21	0/10315	0.53	0/13969
1	D	0.21	0/10315	0.54	0/13969
1	E	0.21	0/10315	0.53	0/13969
1	F	0.21	0/10315	0.54	0/13969
1	G	0.21	0/10315	0.53	0/13969
1	H	0.21	0/10315	0.54	0/13969
1	I	0.21	0/10315	0.53	0/13969
1	J	0.21	0/10315	0.54	0/13969
1	K	0.21	0/10315	0.53	0/13969
1	L	0.21	0/10315	0.54	0/13969
1	M	0.21	0/10315	0.53	0/13969
1	N	0.21	0/10315	0.54	0/13969
1	O	0.21	0/10315	0.53	0/13969
1	P	0.21	0/10315	0.54	0/13969
All	All	0.21	0/165040	0.53	0/223504

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	10097	0	9581	17	0
1	B	10097	0	9581	20	0
1	C	10097	0	9581	21	0
1	D	10097	0	9581	30	0
1	E	10097	0	9581	26	0
1	F	10097	0	9581	31	0
1	G	10097	0	9581	28	0
1	H	10097	0	9581	28	0
1	I	10097	0	9581	18	0
1	J	10097	0	9581	19	0
1	K	10097	0	9581	26	0
1	L	10097	0	9581	31	0
1	M	10097	0	9581	26	0
1	N	10097	0	9581	29	0
1	O	10097	0	9581	26	0
1	P	10097	0	9581	28	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	3	0	0	0	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	3	0	0	0	0
2	K	3	0	0	0	0
2	L	3	0	0	0	0
2	M	3	0	0	0	0
2	N	3	0	0	0	0
2	O	3	0	0	0	0
2	P	3	0	0	0	0
3	A	70	0	65	0	0
3	B	70	0	65	0	0
3	C	70	0	65	0	0
3	D	70	0	65	0	0
3	E	70	0	65	0	0
3	F	70	0	65	0	0
3	G	70	0	65	0	0
3	H	70	0	65	0	0
3	I	70	0	65	0	0
3	J	70	0	65	0	0
3	K	70	0	65	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	70	0	65	0	0
3	M	70	0	65	0	0
3	N	70	0	65	0	0
3	O	70	0	65	0	0
3	P	70	0	65	0	0
All	All	162720	0	154336	293	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 1.

All (293) 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:1441:SER:HB3	1:K:235:ALA:O	1.29	1.33
1:E:1441:SER:HB3	1:M:235:ALA:O	1.29	1.30
1:G:1441:SER:HB3	1:O:235:ALA:O	1.29	1.28
1:F:235:ALA:O	1:N:1441:SER:HB3	1.51	1.10
1:D:235:ALA:O	1:L:1441:SER:HB3	1.51	1.09
1:H:235:ALA:O	1:P:1441:SER:HB3	1.51	1.07
1:C:1418:PRO:HG3	1:K:235:ALA:HB2	1.51	0.93
1:E:1418:PRO:HG3	1:M:235:ALA:HB2	1.51	0.93
1:D:236:ARG:HG2	1:L:1442:SER:CB	2.01	0.91
1:G:1418:PRO:HG3	1:O:235:ALA:HB2	1.51	0.91
1:F:236:ARG:HG2	1:N:1442:SER:CB	2.01	0.90
1:H:236:ARG:HG2	1:P:1442:SER:CB	2.01	0.89
1:D:236:ARG:HG2	1:L:1442:SER:HB3	1.58	0.84
1:H:236:ARG:HG2	1:P:1442:SER:HB3	1.58	0.82
1:F:236:ARG:HG2	1:N:1442:SER:HB3	1.58	0.82
1:G:1442:SER:CB	1:O:236:ARG:HG2	2.10	0.82
1:E:1442:SER:CB	1:M:236:ARG:HG2	2.10	0.82
1:C:1442:SER:CB	1:K:236:ARG:HG2	2.10	0.81
1:D:235:ALA:HB2	1:L:1418:PRO:HG3	1.64	0.80
1:H:235:ALA:HB2	1:P:1418:PRO:HG3	1.64	0.80
1:F:235:ALA:HB2	1:N:1418:PRO:HG3	1.64	0.78
1:G:1418:PRO:CG	1:O:235:ALA:HB2	2.14	0.78
1:F:230:SER:O	1:N:1418:PRO:HB2	1.86	0.76
1:E:1418:PRO:CG	1:M:235:ALA:HB2	2.14	0.76
1:H:230:SER:O	1:P:1418:PRO:HB2	1.86	0.76
1:C:1418:PRO:CG	1:K:235:ALA:HB2	2.14	0.76
1:D:230:SER:O	1:L:1418:PRO:HB2	1.86	0.76
1:G:1418:PRO:HG3	1:O:235:ALA:CB	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:235:ALA:CB	1:N:1418:PRO:HG3	2.18	0.74
1:E:1418:PRO:HG3	1:M:235:ALA:CB	2.18	0.74
1:H:235:ALA:CB	1:P:1418:PRO:HG3	2.18	0.74
1:C:1418:PRO:HG3	1:K:235:ALA:CB	2.18	0.73
1:D:235:ALA:CB	1:L:1418:PRO:HG3	2.17	0.72
1:C:1442:SER:HB3	1:K:236:ARG:HG2	1.72	0.71
1:G:1442:SER:HB3	1:O:236:ARG:HG2	1.72	0.69
1:E:1442:SER:HB3	1:M:236:ARG:HG2	1.72	0.69
1:A:116:LYS:HE3	1:I:1051:MET:SD	2.35	0.67
1:K:1051:MET:SD	1:M:116:LYS:HE3	2.35	0.67
1:C:1051:MET:SD	1:E:116:LYS:HE3	2.35	0.67
1:G:1051:MET:SD	1:I:116:LYS:HE3	2.35	0.67
1:E:1051:MET:SD	1:G:116:LYS:HE3	2.35	0.67
1:M:1051:MET:SD	1:O:116:LYS:HE3	2.35	0.67
1:A:1051:MET:SD	1:K:116:LYS:HE3	2.35	0.66
1:H:230:SER:O	1:P:1418:PRO:CB	2.44	0.66
1:D:230:SER:O	1:L:1418:PRO:CB	2.44	0.66
1:F:230:SER:O	1:N:1418:PRO:CB	2.43	0.65
1:C:1418:PRO:CG	1:K:235:ALA:CB	2.76	0.63
1:E:1418:PRO:CG	1:M:235:ALA:CB	2.76	0.63
1:G:1418:PRO:CG	1:O:235:ALA:CB	2.76	0.62
1:E:1441:SER:CB	1:M:235:ALA:O	2.25	0.59
1:A:1013:GLN:HE21	1:J:352:HIS:CE1	2.22	0.57
1:D:236:ARG:CG	1:L:1442:SER:HB3	2.33	0.57
1:F:352:HIS:CE1	1:G:1013:GLN:HE21	2.22	0.57
1:H:352:HIS:CE1	1:I:1013:GLN:HE21	2.22	0.57
1:L:352:HIS:CE1	1:M:1013:GLN:HE21	2.22	0.57
1:B:352:HIS:CE1	1:K:1013:GLN:HE21	2.22	0.56
1:D:352:HIS:CE1	1:E:1013:GLN:HE21	2.22	0.56
1:F:236:ARG:CG	1:N:1442:SER:HB3	2.33	0.56
1:G:1441:SER:CB	1:O:235:ALA:O	2.25	0.56
1:N:352:HIS:CE1	1:O:1013:GLN:HE21	2.22	0.55
1:H:236:ARG:CG	1:P:1442:SER:HB3	2.33	0.55
1:H:235:ALA:CB	1:P:1418:PRO:CG	2.85	0.54
1:C:1441:SER:CB	1:K:235:ALA:O	2.25	0.54
1:D:235:ALA:CB	1:L:1418:PRO:CG	2.85	0.54
1:F:235:ALA:CB	1:N:1418:PRO:CG	2.85	0.54
1:F:235:ALA:HB2	1:N:1418:PRO:CG	2.36	0.53
1:H:235:ALA:HB2	1:P:1418:PRO:CG	2.36	0.52
1:L:1036:LYS:NZ	1:M:593:GLU:OE2	2.37	0.51
1:D:1036:LYS:NZ	1:E:593:GLU:OE2	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:1036:LYS:NZ	1:O:593:GLU:OE2	2.37	0.51
1:D:235:ALA:HB2	1:L:1418:PRO:CG	2.36	0.50
1:A:1056:VAL:HG13	1:A:1088:THR:HB	1.93	0.50
1:K:1056:VAL:HG13	1:K:1088:THR:HB	1.93	0.50
1:C:1056:VAL:HG13	1:C:1088:THR:HB	1.93	0.50
1:M:1051:MET:SD	1:O:116:LYS:CE	3.00	0.50
1:G:1051:MET:SD	1:I:116:LYS:CE	3.00	0.50
1:D:239:PRO:HD3	1:L:1441:SER:OG	2.12	0.49
1:E:1056:VAL:HG13	1:E:1088:THR:HB	1.93	0.49
1:K:1051:MET:SD	1:M:116:LYS:CE	3.00	0.49
1:O:1056:VAL:HG13	1:O:1088:THR:HB	1.93	0.49
1:E:1051:MET:SD	1:G:116:LYS:CE	3.00	0.49
1:M:1056:VAL:HG13	1:M:1088:THR:HB	1.93	0.49
1:G:1056:VAL:HG13	1:G:1088:THR:HB	1.93	0.49
1:A:116:LYS:CE	1:I:1051:MET:SD	3.00	0.49
1:H:239:PRO:HD3	1:P:1441:SER:OG	2.12	0.49
1:H:1036:LYS:NZ	1:I:593:GLU:OE2	2.37	0.48
1:I:1056:VAL:HG13	1:I:1088:THR:HB	1.93	0.48
1:K:1321:TYR:CE2	1:K:1355:ALA:HB1	2.49	0.48
1:C:1321:TYR:CE2	1:C:1355:ALA:HB1	2.49	0.48
1:A:1051:MET:SD	1:K:116:LYS:CE	3.00	0.48
1:G:1321:TYR:CE2	1:G:1355:ALA:HB1	2.49	0.48
1:P:974:TRP:CE2	1:P:976:ARG:HA	2.49	0.48
1:D:974:TRP:CE2	1:D:976:ARG:HA	2.49	0.48
1:E:1321:TYR:CE2	1:E:1355:ALA:HB1	2.49	0.48
1:A:593:GLU:OE2	1:J:1036:LYS:NZ	2.37	0.48
1:B:974:TRP:CE2	1:B:976:ARG:HA	2.49	0.48
1:F:239:PRO:HD3	1:N:1441:SER:OG	2.12	0.48
1:N:974:TRP:CE2	1:N:976:ARG:HA	2.49	0.48
1:O:1321:TYR:CE2	1:O:1355:ALA:HB1	2.49	0.48
1:J:974:TRP:CE2	1:J:976:ARG:HA	2.49	0.48
1:L:974:TRP:CE2	1:L:976:ARG:HA	2.49	0.48
1:M:1321:TYR:CE2	1:M:1355:ALA:HB1	2.49	0.48
1:P:435:ASP:OD1	1:P:435:ASP:N	2.47	0.48
1:A:1321:TYR:CE2	1:A:1355:ALA:HB1	2.49	0.47
1:H:974:TRP:CE2	1:H:976:ARG:HA	2.49	0.47
1:N:435:ASP:OD1	1:N:435:ASP:N	2.47	0.47
1:F:974:TRP:CE2	1:F:976:ARG:HA	2.49	0.47
1:I:1321:TYR:CE2	1:I:1355:ALA:HB1	2.49	0.47
1:L:435:ASP:OD1	1:L:435:ASP:N	2.47	0.47
1:C:1051:MET:SD	1:E:116:LYS:CE	3.00	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:435:ASP:OD1	1:H:435:ASP:N	2.47	0.47
1:J:435:ASP:OD1	1:J:435:ASP:N	2.47	0.47
1:B:435:ASP:OD1	1:B:435:ASP:N	2.47	0.47
1:B:1001:GLY:O	1:K:530:ASN:ND2	2.48	0.46
1:L:1001:GLY:O	1:M:530:ASN:ND2	2.48	0.46
1:A:530:ASN:ND2	1:J:1001:GLY:O	2.48	0.46
1:D:435:ASP:N	1:D:435:ASP:OD1	2.47	0.46
1:B:305:VAL:N	1:B:326:VAL:O	2.49	0.46
1:B:1079:PRO:O	1:B:1083:VAL:HG23	2.16	0.46
1:D:1001:GLY:O	1:E:530:ASN:ND2	2.48	0.46
1:D:1079:PRO:O	1:D:1083:VAL:HG23	2.16	0.46
1:H:1001:GLY:O	1:I:530:ASN:ND2	2.48	0.46
1:J:1079:PRO:O	1:J:1083:VAL:HG23	2.16	0.46
1:F:435:ASP:N	1:F:435:ASP:OD1	2.47	0.46
1:L:305:VAL:N	1:L:326:VAL:O	2.49	0.46
1:N:305:VAL:N	1:N:326:VAL:O	2.49	0.46
1:C:1442:SER:HB3	1:K:236:ARG:CG	2.45	0.46
1:D:974:TRP:CD1	1:D:980:ILE:HG12	2.51	0.46
1:B:974:TRP:CD1	1:B:980:ILE:HG12	2.51	0.46
1:D:305:VAL:N	1:D:326:VAL:O	2.49	0.46
1:G:1444:ASP:OD2	1:O:236:ARG:NE	2.35	0.46
1:H:974:TRP:CD1	1:H:980:ILE:HG12	2.51	0.46
1:P:1079:PRO:O	1:P:1083:VAL:HG23	2.16	0.46
1:F:1079:PRO:O	1:F:1083:VAL:HG23	2.16	0.46
1:H:1079:PRO:O	1:H:1083:VAL:HG23	2.16	0.46
1:N:974:TRP:CD1	1:N:980:ILE:HG12	2.51	0.46
1:J:974:TRP:CD1	1:J:980:ILE:HG12	2.51	0.46
1:N:1001:GLY:O	1:O:530:ASN:ND2	2.48	0.46
1:P:974:TRP:CD1	1:P:980:ILE:HG12	2.51	0.46
1:J:305:VAL:N	1:J:326:VAL:O	2.49	0.46
1:F:1001:GLY:O	1:G:530:ASN:ND2	2.48	0.45
1:L:1079:PRO:O	1:L:1083:VAL:HG23	2.16	0.45
1:P:305:VAL:N	1:P:326:VAL:O	2.49	0.45
1:D:1081:LEU:O	1:D:1085:ILE:HG12	2.17	0.45
1:H:305:VAL:N	1:H:326:VAL:O	2.49	0.45
1:L:974:TRP:CD1	1:L:980:ILE:HG12	2.51	0.45
1:C:1444:ASP:OD2	1:K:236:ARG:NE	2.35	0.45
1:F:974:TRP:CD1	1:F:980:ILE:HG12	2.51	0.45
1:J:1361:LEU:HA	1:J:1364:THR:HG22	1.99	0.45
1:F:305:VAL:N	1:F:326:VAL:O	2.49	0.45
1:F:1081:LEU:O	1:F:1085:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:1079:PRO:O	1:N:1083:VAL:HG23	2.16	0.45
1:N:1361:LEU:HA	1:N:1364:THR:HG22	1.99	0.45
1:H:974:TRP:CZ2	1:H:976:ARG:HA	2.52	0.45
1:J:1081:LEU:O	1:J:1085:ILE:HG12	2.17	0.45
1:P:974:TRP:CZ2	1:P:976:ARG:HA	2.52	0.45
1:P:1081:LEU:O	1:P:1085:ILE:HG12	2.17	0.45
1:B:1081:LEU:O	1:B:1085:ILE:HG12	2.17	0.45
1:K:1081:LEU:O	1:K:1085:ILE:HG12	2.17	0.45
1:H:1081:LEU:O	1:H:1085:ILE:HG12	2.17	0.44
1:A:1081:LEU:O	1:A:1085:ILE:HG12	2.17	0.44
1:C:1081:LEU:O	1:C:1085:ILE:HG12	2.17	0.44
1:G:1442:SER:HB3	1:O:236:ARG:CG	2.45	0.44
1:L:1081:LEU:O	1:L:1085:ILE:HG12	2.17	0.44
1:E:1442:SER:HB3	1:M:236:ARG:CG	2.45	0.44
1:I:1081:LEU:O	1:I:1085:ILE:HG12	2.17	0.44
1:G:1081:LEU:O	1:G:1085:ILE:HG12	2.17	0.44
1:O:1081:LEU:O	1:O:1085:ILE:HG12	2.17	0.44
1:F:1361:LEU:HA	1:F:1364:THR:HG22	1.99	0.44
1:H:1361:LEU:HA	1:H:1364:THR:HG22	1.99	0.44
1:L:974:TRP:CZ2	1:L:976:ARG:HA	2.52	0.44
1:M:1081:LEU:O	1:M:1085:ILE:HG12	2.17	0.44
1:B:1361:LEU:HA	1:B:1364:THR:HG22	1.99	0.44
1:F:974:TRP:CZ2	1:F:976:ARG:HA	2.52	0.44
1:J:974:TRP:CZ2	1:J:976:ARG:HA	2.52	0.44
1:P:1361:LEU:HA	1:P:1364:THR:HG22	1.99	0.44
1:E:1081:LEU:O	1:E:1085:ILE:HG12	2.17	0.44
1:N:1081:LEU:O	1:N:1085:ILE:HG12	2.17	0.44
1:N:974:TRP:CZ2	1:N:976:ARG:HA	2.52	0.43
1:B:974:TRP:CZ2	1:B:976:ARG:HA	2.52	0.43
1:B:1036:LYS:NZ	1:K:593:GLU:OE2	2.37	0.43
1:L:1361:LEU:HA	1:L:1364:THR:HG22	1.99	0.43
1:D:974:TRP:CZ2	1:D:976:ARG:HA	2.52	0.43
1:M:874:HIS:CG	1:M:1083:VAL:HG22	2.54	0.43
1:A:874:HIS:CG	1:A:1083:VAL:HG22	2.54	0.43
1:G:874:HIS:CG	1:G:1083:VAL:HG22	2.54	0.43
1:E:874:HIS:CG	1:E:1083:VAL:HG22	2.54	0.43
1:O:874:HIS:CG	1:O:1083:VAL:HG22	2.54	0.43
1:D:1361:LEU:HA	1:D:1364:THR:HG22	1.99	0.43
1:K:874:HIS:CG	1:K:1083:VAL:HG22	2.54	0.43
1:C:874:HIS:CG	1:C:1083:VAL:HG22	2.54	0.43
1:M:449:PRO:HA	1:M:453:ASN:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:449:PRO:HA	1:G:453:ASN:HA	2.01	0.43
1:H:1100:PHE:CE1	1:H:1104:ILE:HD11	2.54	0.42
1:E:1444:ASP:OD2	1:M:236:ARG:NE	2.35	0.42
1:E:449:PRO:HA	1:E:453:ASN:HA	2.01	0.42
1:P:1100:PHE:CE1	1:P:1104:ILE:HD11	2.54	0.42
1:K:449:PRO:HA	1:K:453:ASN:HA	2.01	0.42
1:L:1100:PHE:CE1	1:L:1104:ILE:HD11	2.54	0.42
1:N:1100:PHE:CE1	1:N:1104:ILE:HD11	2.54	0.42
1:A:87:TYR:CD2	1:H:574:PRO:HB2	2.55	0.42
1:J:1100:PHE:CE1	1:J:1104:ILE:HD11	2.54	0.42
1:L:974:TRP:CD1	1:L:980:ILE:CG1	3.03	0.42
1:A:989:GLN:HA	1:A:999:PHE:CD2	2.55	0.42
1:B:1100:PHE:CE1	1:B:1104:ILE:HD11	2.54	0.42
1:C:338:ASP:OD1	1:C:356:ARG:NH1	2.53	0.42
1:H:974:TRP:CD1	1:H:980:ILE:CG1	3.03	0.42
1:I:338:ASP:OD1	1:I:356:ARG:NH1	2.53	0.42
1:O:449:PRO:HA	1:O:453:ASN:HA	2.01	0.42
1:B:855:LYS:HB2	1:B:855:LYS:HE2	1.89	0.42
1:B:1116:LYS:HE2	1:B:1116:LYS:HA	2.01	0.42
1:F:974:TRP:CD1	1:F:980:ILE:CG1	3.03	0.42
1:F:1036:LYS:NZ	1:G:593:GLU:OE2	2.37	0.42
1:G:989:GLN:HA	1:G:999:PHE:CD2	2.55	0.42
1:I:874:HIS:CG	1:I:1083:VAL:HG22	2.54	0.42
1:N:974:TRP:CD1	1:N:980:ILE:CG1	3.03	0.42
1:D:1100:PHE:CE1	1:D:1104:ILE:HD11	2.55	0.42
1:M:989:GLN:HA	1:M:999:PHE:CD2	2.55	0.42
1:B:974:TRP:CD1	1:B:980:ILE:CG1	3.03	0.42
1:C:989:GLN:HA	1:C:999:PHE:CD2	2.55	0.42
1:E:338:ASP:OD1	1:E:356:ARG:NH1	2.53	0.42
1:I:449:PRO:HA	1:I:453:ASN:HA	2.01	0.42
1:D:1116:LYS:HE2	1:D:1116:LYS:HA	2.01	0.41
1:F:574:PRO:HB2	1:I:87:TYR:CD2	2.55	0.41
1:G:338:ASP:OD1	1:G:356:ARG:NH1	2.53	0.41
1:J:574:PRO:HB2	1:K:87:TYR:CD2	2.55	0.41
1:J:1116:LYS:HA	1:J:1116:LYS:HE2	2.01	0.41
1:L:574:PRO:HB2	1:O:87:TYR:CD2	2.55	0.41
1:O:989:GLN:HA	1:O:999:PHE:CD2	2.55	0.41
1:B:88:LEU:HD11	1:B:118:LEU:HG	2.02	0.41
1:C:449:PRO:HA	1:C:453:ASN:HA	2.01	0.41
1:D:974:TRP:CD1	1:D:980:ILE:CG1	3.03	0.41
1:F:1116:LYS:HE2	1:F:1116:LYS:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:431:GLN:O	1:O:722:PHE:HA	2.21	0.41
1:A:989:GLN:HA	1:A:999:PHE:CG	2.56	0.41
1:B:574:PRO:HB2	1:M:87:TYR:CD2	2.55	0.41
1:C:989:GLN:HA	1:C:999:PHE:CG	2.56	0.41
1:F:1100:PHE:CE1	1:F:1104:ILE:HD11	2.54	0.41
1:F:431:GLN:O	1:G:722:PHE:HA	2.21	0.41
1:O:989:GLN:HA	1:O:999:PHE:CG	2.56	0.41
1:D:574:PRO:HB2	1:G:87:TYR:CD2	2.55	0.41
1:H:1116:LYS:HA	1:H:1116:LYS:HE2	2.01	0.41
1:I:989:GLN:HA	1:I:999:PHE:CD2	2.55	0.41
1:I:989:GLN:HA	1:I:999:PHE:CG	2.56	0.41
1:I:1421:ASN:OD1	1:I:1421:ASN:N	2.53	0.41
1:J:974:TRP:CD1	1:J:980:ILE:CG1	3.03	0.41
1:O:1421:ASN:OD1	1:O:1421:ASN:N	2.53	0.41
1:P:855:LYS:HB2	1:P:855:LYS:HE2	1.89	0.41
1:P:974:TRP:CD1	1:P:980:ILE:CG1	3.03	0.41
1:B:250:CYS:HA	1:B:253:THR:HG22	2.03	0.41
1:E:989:GLN:HA	1:E:999:PHE:CG	2.56	0.41
1:F:88:LEU:HD11	1:F:118:LEU:HG	2.02	0.41
1:L:88:LEU:HD11	1:L:118:LEU:HG	2.02	0.41
1:L:1116:LYS:HE2	1:L:1116:LYS:HA	2.01	0.41
1:N:855:LYS:HB2	1:N:855:LYS:HE2	1.89	0.41
1:P:1116:LYS:HE2	1:P:1116:LYS:HA	2.01	0.41
1:A:338:ASP:OD1	1:A:356:ARG:NH1	2.53	0.41
1:C:1421:ASN:OD1	1:C:1421:ASN:N	2.53	0.41
1:D:250:CYS:HA	1:D:253:THR:HG22	2.03	0.41
1:F:989:GLN:HA	1:F:999:PHE:CD2	2.56	0.41
1:G:250:CYS:O	1:G:253:THR:OG1	2.37	0.41
1:K:989:GLN:HA	1:K:999:PHE:CD2	2.55	0.41
1:H:431:GLN:O	1:I:722:PHE:HA	2.21	0.41
1:A:449:PRO:HA	1:A:453:ASN:HA	2.01	0.41
1:B:431:GLN:O	1:K:722:PHE:HA	2.21	0.41
1:J:989:GLN:HA	1:J:999:PHE:CD2	2.56	0.41
1:E:989:GLN:HA	1:E:999:PHE:CD2	2.55	0.41
1:G:989:GLN:HA	1:G:999:PHE:CG	2.56	0.41
1:K:989:GLN:HA	1:K:999:PHE:CG	2.56	0.41
1:L:250:CYS:HA	1:L:253:THR:HG22	2.03	0.41
1:L:431:GLN:O	1:M:722:PHE:HA	2.21	0.41
1:N:989:GLN:HA	1:N:999:PHE:CD2	2.56	0.41
1:N:88:LEU:HD11	1:N:118:LEU:HG	2.02	0.40
1:A:722:PHE:HA	1:J:431:GLN:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:LEU:HD11	1:D:118:LEU:HG	2.02	0.40
1:D:989:GLN:HA	1:D:999:PHE:CD2	2.56	0.40
1:H:989:GLN:HA	1:H:999:PHE:CD2	2.56	0.40
1:J:250:CYS:HA	1:J:253:THR:HG22	2.03	0.40
1:M:989:GLN:HA	1:M:999:PHE:CG	2.56	0.40
1:N:1116:LYS:HE2	1:N:1116:LYS:HA	2.01	0.40
1:O:338:ASP:OD1	1:O:356:ARG:NH1	2.53	0.40
1:P:88:LEU:HD11	1:P:118:LEU:HG	2.02	0.40
1:D:431:GLN:O	1:E:722:PHE:HA	2.21	0.40
1:F:250:CYS:HA	1:F:253:THR:HG22	2.03	0.40
1:J:88:LEU:HD11	1:J:118:LEU:HG	2.02	0.40
1:P:541:LEU:HD23	1:P:541:LEU:HA	1.98	0.40
1:P:989:GLN:HA	1:P:999:PHE:CD2	2.56	0.40
1:B:989:GLN:HA	1:B:999:PHE:CD2	2.56	0.40
1:F:855:LYS:HE2	1:F:855:LYS:HB2	1.89	0.40
1:L:855:LYS:HE2	1:L:855:LYS:HB2	1.89	0.40
1:L:989:GLN:HA	1:L:999:PHE:CD2	2.56	0.40
1:P:250:CYS:HA	1:P:253:THR:HG22	2.03	0.40
1:P:1049:ASN:OD1	1:P:1049:ASN:N	2.54	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 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	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	B	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	C	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	D	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	E	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	G	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	H	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	I	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	J	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	K	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	L	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	M	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	N	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
1	O	1295/1469 (88%)	1240 (96%)	55 (4%)	0	100	100
1	P	1295/1469 (88%)	1248 (96%)	47 (4%)	0	100	100
All	All	20720/23504 (88%)	19904 (96%)	816 (4%)	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	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	B	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
1	C	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	D	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
1	E	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	F	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
1	G	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	H	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
1	I	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	J	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	L	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
1	M	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	N	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
1	O	1133/1270 (89%)	1130 (100%)	3 (0%)	86	87
1	P	1133/1270 (89%)	1128 (100%)	5 (0%)	84	86
All	All	18128/20320 (89%)	18064 (100%)	64 (0%)	81	86

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	460	HIS
1	A	1357	THR
1	A	1449	GLN
1	B	49	SER
1	B	418	CYS
1	B	434	ASP
1	B	435	ASP
1	B	870	ILE
1	C	460	HIS
1	C	1357	THR
1	C	1449	GLN
1	D	49	SER
1	D	418	CYS
1	D	434	ASP
1	D	435	ASP
1	D	870	ILE
1	E	460	HIS
1	E	1357	THR
1	E	1449	GLN
1	F	49	SER
1	F	418	CYS
1	F	434	ASP
1	F	435	ASP
1	F	870	ILE
1	G	460	HIS
1	G	1357	THR
1	G	1449	GLN
1	H	49	SER
1	H	418	CYS

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Mol	Chain	Res	Type
1	H	434	ASP
1	H	435	ASP
1	H	870	ILE
1	I	460	HIS
1	I	1357	THR
1	I	1449	GLN
1	J	49	SER
1	J	418	CYS
1	J	434	ASP
1	J	435	ASP
1	J	870	ILE
1	K	460	HIS
1	K	1357	THR
1	K	1449	GLN
1	L	49	SER
1	L	418	CYS
1	L	434	ASP
1	L	435	ASP
1	L	870	ILE
1	M	460	HIS
1	M	1357	THR
1	M	1449	GLN
1	N	49	SER
1	N	418	CYS
1	N	434	ASP
1	N	435	ASP
1	N	870	ILE
1	O	460	HIS
1	O	1357	THR
1	O	1449	GLN
1	P	49	SER
1	P	418	CYS
1	P	434	ASP
1	P	435	ASP
1	P	870	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (180) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	GLN
1	A	277	GLN
1	A	393	GLN

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Mol	Chain	Res	Type
1	A	401	ASN
1	A	566	HIS
1	A	725	HIS
1	A	874	HIS
1	A	916	HIS
1	A	1013	GLN
1	A	1128	GLN
1	A	1154	GLN
1	B	277	GLN
1	B	376	GLN
1	B	393	GLN
1	B	401	ASN
1	B	431	GLN
1	B	452	HIS
1	B	484	HIS
1	B	890	GLN
1	B	989	GLN
1	B	1013	GLN
1	B	1138	ASN
1	B	1268	HIS
1	C	176	GLN
1	C	277	GLN
1	C	393	GLN
1	C	401	ASN
1	C	566	HIS
1	C	725	HIS
1	C	831	HIS
1	C	874	HIS
1	C	916	HIS
1	C	1128	GLN
1	C	1154	GLN
1	D	277	GLN
1	D	376	GLN
1	D	393	GLN
1	D	431	GLN
1	D	452	HIS
1	D	484	HIS
1	D	890	GLN
1	D	989	GLN
1	D	1013	GLN
1	D	1138	ASN
1	D	1268	HIS

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Mol	Chain	Res	Type
1	E	176	GLN
1	E	277	GLN
1	E	393	GLN
1	E	401	ASN
1	E	484	HIS
1	E	566	HIS
1	E	725	HIS
1	E	874	HIS
1	E	916	HIS
1	E	1013	GLN
1	E	1128	GLN
1	E	1154	GLN
1	F	277	GLN
1	F	376	GLN
1	F	393	GLN
1	F	431	GLN
1	F	452	HIS
1	F	484	HIS
1	F	890	GLN
1	F	989	GLN
1	F	1013	GLN
1	F	1138	ASN
1	F	1268	HIS
1	G	176	GLN
1	G	277	GLN
1	G	393	GLN
1	G	401	ASN
1	G	484	HIS
1	G	566	HIS
1	G	725	HIS
1	G	874	HIS
1	G	916	HIS
1	G	1013	GLN
1	G	1128	GLN
1	G	1154	GLN
1	H	376	GLN
1	H	393	GLN
1	H	431	GLN
1	H	452	HIS
1	H	484	HIS
1	H	890	GLN
1	H	989	GLN

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Mol	Chain	Res	Type
1	H	1013	GLN
1	H	1268	HIS
1	I	176	GLN
1	I	277	GLN
1	I	393	GLN
1	I	401	ASN
1	I	566	HIS
1	I	725	HIS
1	I	737	HIS
1	I	874	HIS
1	I	916	HIS
1	I	1013	GLN
1	I	1128	GLN
1	I	1154	GLN
1	J	277	GLN
1	J	376	GLN
1	J	393	GLN
1	J	401	ASN
1	J	431	GLN
1	J	452	HIS
1	J	484	HIS
1	J	890	GLN
1	J	989	GLN
1	J	1013	GLN
1	J	1138	ASN
1	J	1268	HIS
1	K	176	GLN
1	K	277	GLN
1	K	393	GLN
1	K	401	ASN
1	K	484	HIS
1	K	566	HIS
1	K	725	HIS
1	K	874	HIS
1	K	916	HIS
1	K	1013	GLN
1	K	1128	GLN
1	K	1154	GLN
1	L	176	GLN
1	L	277	GLN
1	L	376	GLN
1	L	393	GLN

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Mol	Chain	Res	Type
1	L	431	GLN
1	L	452	HIS
1	L	484	HIS
1	L	890	GLN
1	L	989	GLN
1	L	1013	GLN
1	L	1138	ASN
1	L	1268	HIS
1	M	176	GLN
1	M	277	GLN
1	M	376	GLN
1	M	393	GLN
1	M	401	ASN
1	M	566	HIS
1	M	725	HIS
1	M	874	HIS
1	M	916	HIS
1	M	1013	GLN
1	M	1128	GLN
1	M	1154	GLN
1	N	176	GLN
1	N	376	GLN
1	N	393	GLN
1	N	431	GLN
1	N	452	HIS
1	N	484	HIS
1	N	890	GLN
1	N	989	GLN
1	N	1013	GLN
1	N	1268	HIS
1	O	176	GLN
1	O	277	GLN
1	O	393	GLN
1	O	401	ASN
1	O	566	HIS
1	O	725	HIS
1	O	737	HIS
1	O	874	HIS
1	O	916	HIS
1	O	1013	GLN
1	O	1128	GLN
1	O	1154	GLN

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Mol	Chain	Res	Type
1	P	318	ASN
1	P	393	GLN
1	P	431	GLN
1	P	452	HIS
1	P	484	HIS
1	P	831	HIS
1	P	989	GLN
1	P	1138	ASN
1	P	1268	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 128 ligands modelled in this entry, 48 are monoatomic - leaving 80 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	$\#\|Z\| > 2$
3	NAG	B	2007	1	14,14,15	0.96	2 (14%)	17,19,21	1.27	1 (5%)
3	NAG	C	2003	1	14,14,15	0.38	0	17,19,21	1.02	1 (5%)
3	NAG	M	2006	1	14,14,15	0.26	0	17,19,21	0.76	1 (5%)
3	NAG	H	2007	1	14,14,15	0.95	2 (14%)	17,19,21	1.28	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	L	2004	1	14,14,15	0.36	0	17,19,21	0.70	1 (5%)
3	NAG	G	2003	1	14,14,15	0.39	0	17,19,21	1.01	1 (5%)
3	NAG	D	2006	1	14,14,15	0.31	0	17,19,21	0.61	1 (5%)
3	NAG	O	2004	1	14,14,15	0.43	0	17,19,21	0.71	1 (5%)
3	NAG	J	2007	1	14,14,15	0.96	2 (14%)	17,19,21	1.27	1 (5%)
3	NAG	B	2004	1	14,14,15	0.37	0	17,19,21	0.70	1 (5%)
3	NAG	C	2005	1	14,14,15	0.21	0	17,19,21	0.64	1 (5%)
3	NAG	O	2003	1	14,14,15	0.38	0	17,19,21	1.02	1 (5%)
3	NAG	C	2007	1	14,14,15	0.45	0	17,19,21	0.81	1 (5%)
3	NAG	G	2007	1	14,14,15	0.45	0	17,19,21	0.80	1 (5%)
3	NAG	N	2007	1	14,14,15	0.97	2 (14%)	17,19,21	1.27	1 (5%)
3	NAG	H	2006	1	14,14,15	0.29	0	17,19,21	0.62	1 (5%)
3	NAG	K	2005	1	14,14,15	0.21	0	17,19,21	0.63	1 (5%)
3	NAG	F	2003	1	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
3	NAG	G	2006	1	14,14,15	0.27	0	17,19,21	0.76	1 (5%)
3	NAG	K	2004	1	14,14,15	0.43	0	17,19,21	0.71	1 (5%)
3	NAG	B	2003	1	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
3	NAG	K	2007	1	14,14,15	0.45	0	17,19,21	0.81	1 (5%)
3	NAG	A	2003	1	14,14,15	0.38	0	17,19,21	1.01	1 (5%)
3	NAG	P	2006	1	14,14,15	0.30	0	17,19,21	0.61	1 (5%)
3	NAG	E	2003	1	14,14,15	0.39	0	17,19,21	1.02	1 (5%)
3	NAG	K	2003	1	14,14,15	0.37	0	17,19,21	1.01	1 (5%)
3	NAG	K	2006	1	14,14,15	0.26	0	17,19,21	0.76	1 (5%)
3	NAG	O	2006	1	14,14,15	0.25	0	17,19,21	0.76	1 (5%)
3	NAG	J	2006	1	14,14,15	0.31	0	17,19,21	0.61	0
3	NAG	P	2004	1	14,14,15	0.37	0	17,19,21	0.71	1 (5%)
3	NAG	I	2003	1	14,14,15	0.38	0	17,19,21	1.02	1 (5%)
3	NAG	J	2003	1	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
3	NAG	N	2006	1	14,14,15	0.30	0	17,19,21	0.62	1 (5%)
3	NAG	M	2003	1	14,14,15	0.38	0	17,19,21	1.02	1 (5%)
3	NAG	E	2007	1	14,14,15	0.45	0	17,19,21	0.80	1 (5%)
3	NAG	A	2007	1	14,14,15	0.45	0	17,19,21	0.81	1 (5%)
3	NAG	D	2005	1	14,14,15	0.19	0	17,19,21	0.58	0
3	NAG	D	2004	1	14,14,15	0.38	0	17,19,21	0.70	1 (5%)
3	NAG	G	2005	1	14,14,15	0.22	0	17,19,21	0.64	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	F	2005	1	14,14,15	0.20	0	17,19,21	0.58	0
3	NAG	I	2004	1	14,14,15	0.43	0	17,19,21	0.70	1 (5%)
3	NAG	N	2005	1	14,14,15	0.20	0	17,19,21	0.57	0
3	NAG	F	2006	1	14,14,15	0.30	0	17,19,21	0.61	1 (5%)
3	NAG	L	2007	1	14,14,15	0.96	2 (14%)	17,19,21	1.28	1 (5%)
3	NAG	H	2004	1	14,14,15	0.36	0	17,19,21	0.70	1 (5%)
3	NAG	D	2003	1	14,14,15	0.15	0	17,19,21	0.78	1 (5%)
3	NAG	C	2006	1	14,14,15	0.27	0	17,19,21	0.76	1 (5%)
3	NAG	P	2007	1	14,14,15	0.96	2 (14%)	17,19,21	1.27	1 (5%)
3	NAG	G	2004	1	14,14,15	0.44	0	17,19,21	0.71	1 (5%)
3	NAG	C	2004	1	14,14,15	0.44	0	17,19,21	0.71	1 (5%)
3	NAG	P	2003	1	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
3	NAG	H	2005	1	14,14,15	0.20	0	17,19,21	0.58	0
3	NAG	I	2007	1	14,14,15	0.45	0	17,19,21	0.80	1 (5%)
3	NAG	O	2005	1	14,14,15	0.22	0	17,19,21	0.63	1 (5%)
3	NAG	J	2005	1	14,14,15	0.20	0	17,19,21	0.58	0
3	NAG	A	2005	1	14,14,15	0.21	0	17,19,21	0.64	1 (5%)
3	NAG	L	2006	1	14,14,15	0.31	0	17,19,21	0.61	0
3	NAG	N	2004	1	14,14,15	0.38	0	17,19,21	0.70	1 (5%)
3	NAG	M	2007	1	14,14,15	0.45	0	17,19,21	0.80	1 (5%)
3	NAG	O	2007	1	14,14,15	0.45	0	17,19,21	0.80	1 (5%)
3	NAG	B	2006	1	14,14,15	0.30	0	17,19,21	0.61	0
3	NAG	F	2004	1	14,14,15	0.38	0	17,19,21	0.70	1 (5%)
3	NAG	E	2005	1	14,14,15	0.22	0	17,19,21	0.64	1 (5%)
3	NAG	J	2004	1	14,14,15	0.37	0	17,19,21	0.71	1 (5%)
3	NAG	L	2003	1	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
3	NAG	A	2004	1	14,14,15	0.42	0	17,19,21	0.71	1 (5%)
3	NAG	L	2005	1	14,14,15	0.20	0	17,19,21	0.58	0
3	NAG	E	2004	1	14,14,15	0.41	0	17,19,21	0.71	1 (5%)
3	NAG	I	2006	1	14,14,15	0.25	0	17,19,21	0.75	1 (5%)
3	NAG	N	2003	1	14,14,15	0.15	0	17,19,21	0.78	1 (5%)
3	NAG	F	2007	1	14,14,15	0.95	2 (14%)	17,19,21	1.27	1 (5%)
3	NAG	B	2005	1	14,14,15	0.20	0	17,19,21	0.58	0
3	NAG	A	2006	1	14,14,15	0.26	0	17,19,21	0.76	1 (5%)
3	NAG	P	2005	1	14,14,15	0.20	0	17,19,21	0.58	0
3	NAG	E	2006	1	14,14,15	0.27	0	17,19,21	0.76	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	M	2004	1	14,14,15	0.43	0	17,19,21	0.70	1 (5%)
3	NAG	D	2007	1	14,14,15	0.96	2 (14%)	17,19,21	1.28	1 (5%)
3	NAG	M	2005	1	14,14,15	0.21	0	17,19,21	0.64	1 (5%)
3	NAG	H	2003	1	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
3	NAG	I	2005	1	14,14,15	0.22	0	17,19,21	0.63	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
3	NAG	B	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	C	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	M	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	H	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	L	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	G	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	D	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	O	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	J	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	B	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	C	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	O	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	C	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	G	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	N	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	H	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	K	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	F	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	G	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	K	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	B	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	K	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	A	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	P	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	E	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	K	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	K	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	O	2006	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	J	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	P	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	I	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	J	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	N	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	M	2003	1	-	0/6/23/26	0/1/1/1
3	NAG	E	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	A	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	D	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	D	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	G	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	F	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	I	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	N	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	F	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	L	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	H	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	D	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	C	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	P	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	G	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	C	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	P	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	H	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	I	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	O	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	J	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	L	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	N	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	M	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	O	2007	1	-	2/6/23/26	0/1/1/1
3	NAG	B	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	F	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	E	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	J	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	L	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	A	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	L	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	E	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	I	2006	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	N	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	F	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	B	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	P	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	E	2006	1	-	0/6/23/26	0/1/1/1
3	NAG	M	2004	1	-	0/6/23/26	0/1/1/1
3	NAG	D	2007	1	-	3/6/23/26	0/1/1/1
3	NAG	M	2005	1	-	0/6/23/26	0/1/1/1
3	NAG	H	2003	1	-	1/6/23/26	0/1/1/1
3	NAG	I	2005	1	-	0/6/23/26	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	2007	NAG	O5-C1	2.62	1.48	1.43
3	H	2007	NAG	O5-C1	2.62	1.48	1.43
3	P	2007	NAG	O5-C1	2.61	1.48	1.43
3	B	2007	NAG	O5-C1	2.61	1.48	1.43
3	D	2007	NAG	O5-C1	2.61	1.48	1.43
3	J	2007	NAG	O5-C1	2.61	1.48	1.43
3	F	2007	NAG	O5-C1	2.60	1.48	1.43
3	L	2007	NAG	O5-C1	2.60	1.48	1.43
3	N	2007	NAG	C1-C2	2.39	1.55	1.52
3	J	2007	NAG	C1-C2	2.36	1.55	1.52
3	P	2007	NAG	C1-C2	2.36	1.55	1.52
3	B	2007	NAG	C1-C2	2.33	1.55	1.52
3	D	2007	NAG	C1-C2	2.33	1.55	1.52
3	L	2007	NAG	C1-C2	2.33	1.55	1.52
3	F	2007	NAG	C1-C2	2.30	1.55	1.52
3	H	2007	NAG	C1-C2	2.28	1.55	1.52

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	2007	NAG	C1-O5-C5	5.04	118.94	112.19
3	H	2007	NAG	C1-O5-C5	5.04	118.94	112.19
3	B	2007	NAG	C1-O5-C5	5.03	118.93	112.19
3	L	2007	NAG	C1-O5-C5	5.03	118.93	112.19
3	F	2007	NAG	C1-O5-C5	5.03	118.93	112.19
3	P	2007	NAG	C1-O5-C5	5.03	118.92	112.19
3	J	2007	NAG	C1-O5-C5	5.02	118.92	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	N	2007	NAG	C1-O5-C5	5.02	118.91	112.19
3	E	2003	NAG	C1-O5-C5	3.94	117.47	112.19
3	O	2003	NAG	C1-O5-C5	3.94	117.46	112.19
3	C	2003	NAG	C1-O5-C5	3.93	117.46	112.19
3	I	2003	NAG	C1-O5-C5	3.93	117.45	112.19
3	M	2003	NAG	C1-O5-C5	3.93	117.45	112.19
3	A	2003	NAG	C1-O5-C5	3.93	117.45	112.19
3	K	2003	NAG	C1-O5-C5	3.92	117.44	112.19
3	G	2003	NAG	C1-O5-C5	3.92	117.43	112.19
3	E	2006	NAG	C1-O5-C5	2.78	115.91	112.19
3	K	2006	NAG	C1-O5-C5	2.78	115.91	112.19
3	G	2006	NAG	C1-O5-C5	2.77	115.89	112.19
3	A	2006	NAG	C1-O5-C5	2.77	115.89	112.19
3	C	2006	NAG	C1-O5-C5	2.77	115.89	112.19
3	F	2003	NAG	C1-O5-C5	2.77	115.89	112.19
3	M	2006	NAG	C1-O5-C5	2.76	115.89	112.19
3	P	2003	NAG	C1-O5-C5	2.76	115.89	112.19
3	I	2006	NAG	C1-O5-C5	2.76	115.89	112.19
3	O	2006	NAG	C1-O5-C5	2.76	115.88	112.19
3	B	2003	NAG	C1-O5-C5	2.76	115.88	112.19
3	D	2003	NAG	C1-O5-C5	2.75	115.88	112.19
3	L	2003	NAG	C1-O5-C5	2.75	115.88	112.19
3	H	2003	NAG	C1-O5-C5	2.75	115.86	112.19
3	J	2003	NAG	C1-O5-C5	2.74	115.86	112.19
3	N	2003	NAG	C1-O5-C5	2.74	115.86	112.19
3	K	2007	NAG	C1-O5-C5	2.66	115.76	112.19
3	C	2004	NAG	C1-O5-C5	2.65	115.74	112.19
3	K	2004	NAG	C1-O5-C5	2.65	115.73	112.19
3	C	2007	NAG	C1-O5-C5	2.65	115.73	112.19
3	A	2007	NAG	C1-O5-C5	2.64	115.73	112.19
3	E	2004	NAG	C1-O5-C5	2.64	115.73	112.19
3	M	2007	NAG	C1-O5-C5	2.64	115.72	112.19
3	E	2007	NAG	C1-O5-C5	2.63	115.71	112.19
3	A	2004	NAG	C1-O5-C5	2.63	115.71	112.19
3	G	2004	NAG	C1-O5-C5	2.62	115.70	112.19
3	O	2007	NAG	C1-O5-C5	2.62	115.70	112.19
3	O	2004	NAG	C1-O5-C5	2.62	115.70	112.19
3	I	2007	NAG	C1-O5-C5	2.62	115.70	112.19
3	I	2004	NAG	C1-O5-C5	2.62	115.70	112.19
3	M	2004	NAG	C1-O5-C5	2.61	115.69	112.19
3	G	2007	NAG	C1-O5-C5	2.61	115.69	112.19
3	J	2004	NAG	C1-O5-C5	2.58	115.65	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	2004	NAG	C1-O5-C5	2.57	115.63	112.19
3	D	2004	NAG	C1-O5-C5	2.57	115.63	112.19
3	F	2004	NAG	C1-O5-C5	2.56	115.62	112.19
3	L	2004	NAG	C1-O5-C5	2.56	115.62	112.19
3	B	2004	NAG	C1-O5-C5	2.56	115.62	112.19
3	H	2004	NAG	C1-O5-C5	2.55	115.60	112.19
3	N	2004	NAG	C1-O5-C5	2.55	115.60	112.19
3	M	2005	NAG	C1-O5-C5	2.23	115.17	112.19
3	E	2005	NAG	C1-O5-C5	2.22	115.16	112.19
3	C	2005	NAG	C1-O5-C5	2.22	115.16	112.19
3	G	2005	NAG	C1-O5-C5	2.21	115.15	112.19
3	A	2005	NAG	C1-O5-C5	2.21	115.14	112.19
3	K	2005	NAG	C1-O5-C5	2.20	115.13	112.19
3	I	2005	NAG	C1-O5-C5	2.19	115.12	112.19
3	O	2005	NAG	C1-O5-C5	2.19	115.12	112.19
3	H	2006	NAG	C1-O5-C5	2.02	114.89	112.19
3	F	2006	NAG	C1-O5-C5	2.01	114.88	112.19
3	D	2006	NAG	C1-O5-C5	2.01	114.88	112.19
3	P	2006	NAG	C1-O5-C5	2.00	114.87	112.19
3	N	2006	NAG	C1-O5-C5	2.00	114.87	112.19

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2007	NAG	C1-C2-N2-C7
3	B	2007	NAG	C1-C2-N2-C7
3	C	2007	NAG	C1-C2-N2-C7
3	D	2007	NAG	C1-C2-N2-C7
3	E	2007	NAG	C1-C2-N2-C7
3	F	2007	NAG	C1-C2-N2-C7
3	G	2007	NAG	C1-C2-N2-C7
3	H	2007	NAG	C1-C2-N2-C7
3	I	2007	NAG	C1-C2-N2-C7
3	J	2007	NAG	C1-C2-N2-C7
3	K	2007	NAG	C1-C2-N2-C7
3	L	2007	NAG	C1-C2-N2-C7
3	M	2007	NAG	C1-C2-N2-C7
3	N	2007	NAG	C1-C2-N2-C7
3	O	2007	NAG	C1-C2-N2-C7
3	P	2007	NAG	C1-C2-N2-C7
3	H	2003	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	A	2007	NAG	C3-C2-N2-C7
3	C	2007	NAG	C3-C2-N2-C7
3	E	2007	NAG	C3-C2-N2-C7
3	G	2007	NAG	C3-C2-N2-C7
3	I	2007	NAG	C3-C2-N2-C7
3	K	2007	NAG	C3-C2-N2-C7
3	M	2007	NAG	C3-C2-N2-C7
3	O	2007	NAG	C3-C2-N2-C7
3	D	2003	NAG	O5-C5-C6-O6
3	N	2003	NAG	O5-C5-C6-O6
3	B	2003	NAG	O5-C5-C6-O6
3	F	2003	NAG	O5-C5-C6-O6
3	J	2003	NAG	O5-C5-C6-O6
3	P	2003	NAG	O5-C5-C6-O6
3	L	2003	NAG	O5-C5-C6-O6
3	B	2007	NAG	C3-C2-N2-C7
3	D	2007	NAG	C3-C2-N2-C7
3	F	2007	NAG	C3-C2-N2-C7
3	H	2007	NAG	C3-C2-N2-C7
3	J	2007	NAG	C3-C2-N2-C7
3	L	2007	NAG	C3-C2-N2-C7
3	N	2007	NAG	C3-C2-N2-C7
3	P	2007	NAG	C3-C2-N2-C7
3	D	2007	NAG	O5-C5-C6-O6
3	J	2007	NAG	O5-C5-C6-O6
3	B	2007	NAG	O5-C5-C6-O6
3	F	2007	NAG	O5-C5-C6-O6
3	H	2007	NAG	O5-C5-C6-O6
3	N	2007	NAG	O5-C5-C6-O6
3	P	2007	NAG	O5-C5-C6-O6
3	L	2007	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

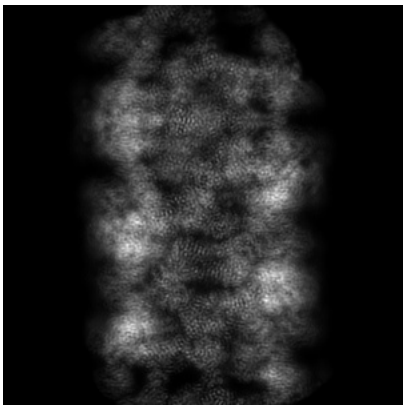
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-27156. These allow visual inspection of the internal detail of the map and identification of artifacts.

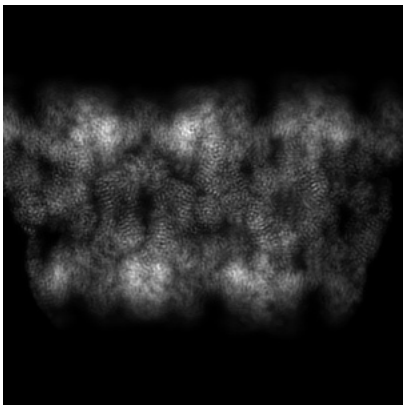
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

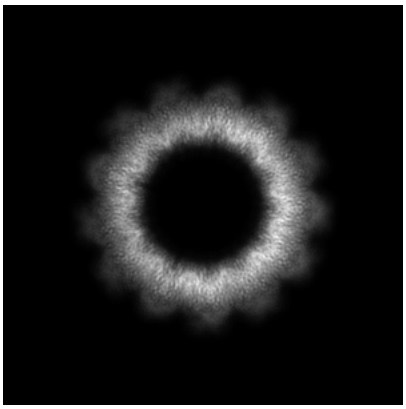
6.1.1 Primary map



X

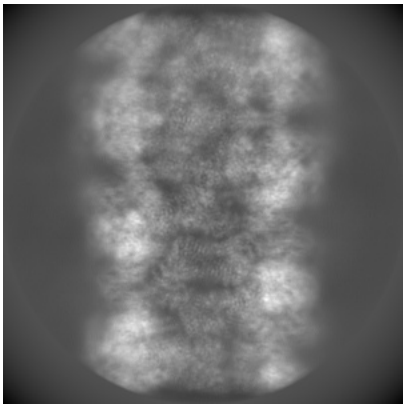


Y

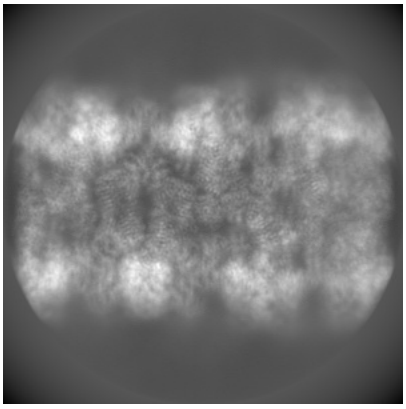


Z

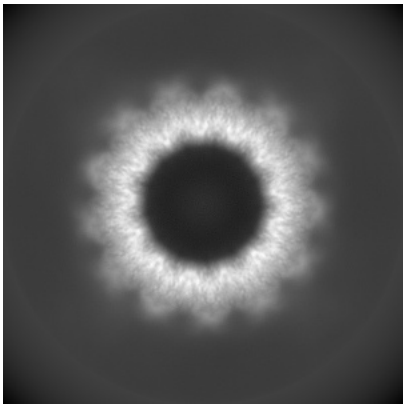
6.1.2 Raw map



X



Y

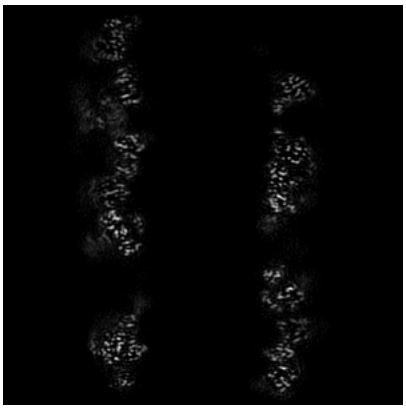


Z

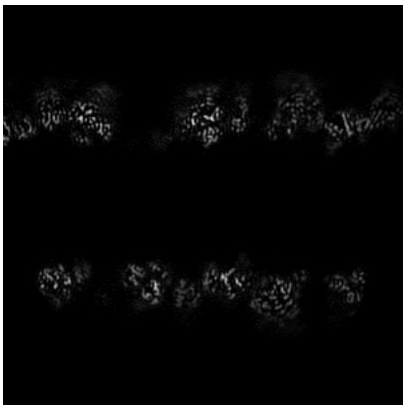
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

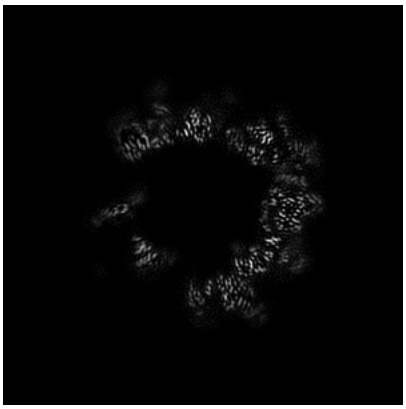
6.2.1 Primary map



X Index: 200

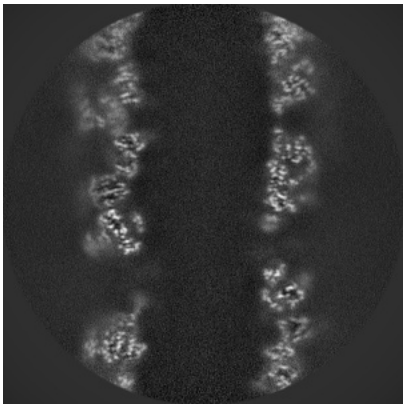


Y Index: 200



Z Index: 200

6.2.2 Raw map



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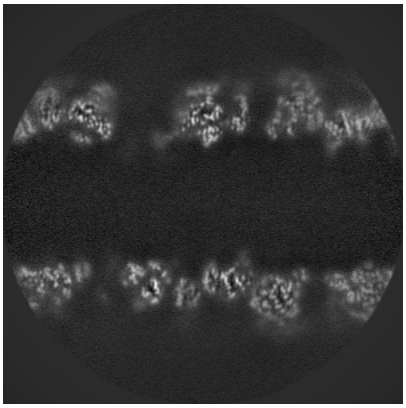
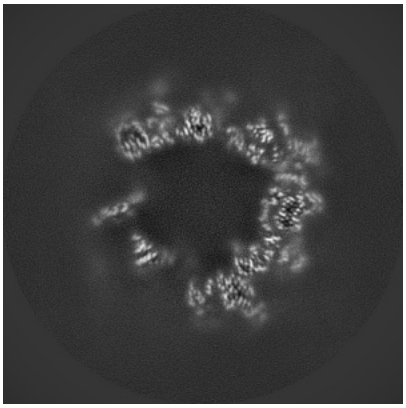


Y Index: 200

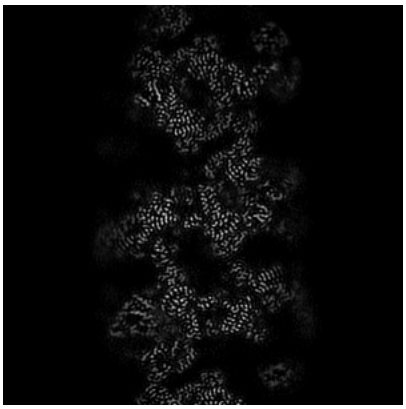


Z Index: 200

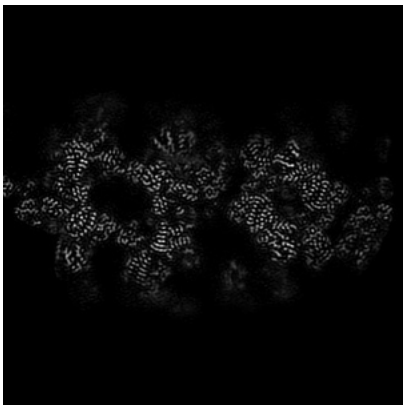
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

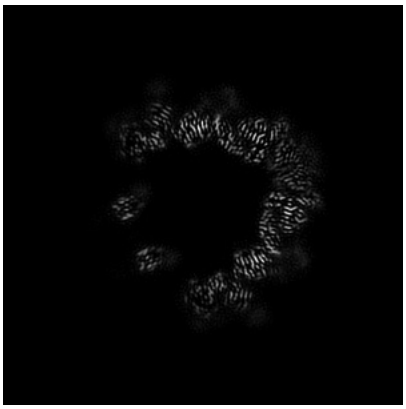
6.3.1 Primary map



X Index: 272

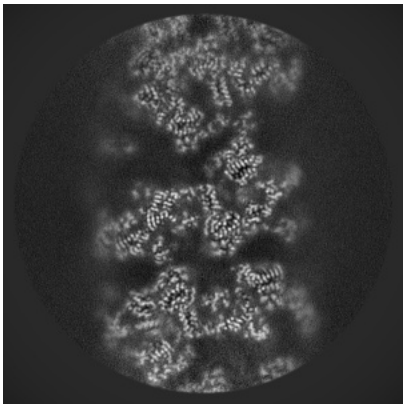


Y Index: 125

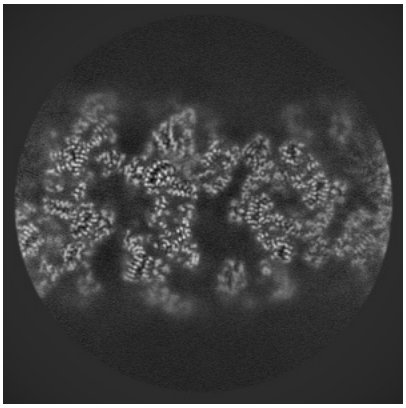


Z Index: 207

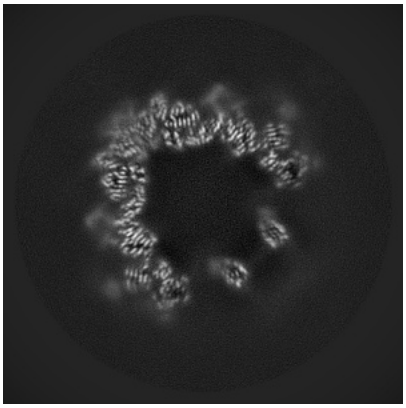
6.3.2 Raw map



X Index: 269



Y Index: 129

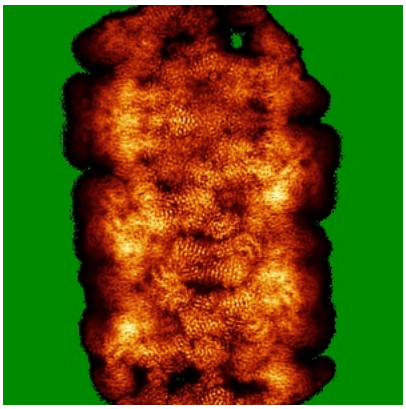


Z Index: 129

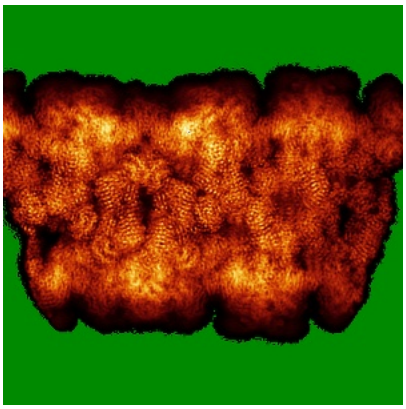
The images above show the largest variance slices of the map in three orthogonal directions.

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

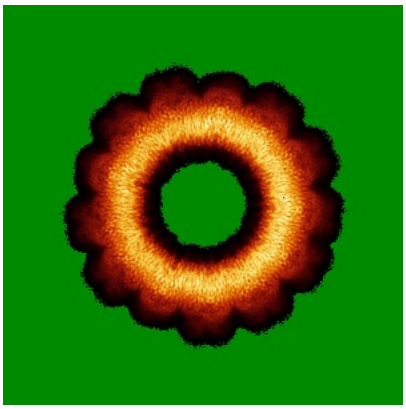
6.4.1 Primary map



X

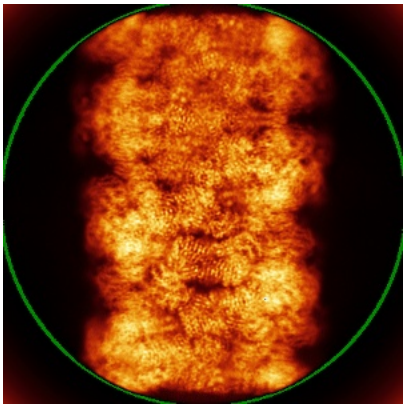


Y

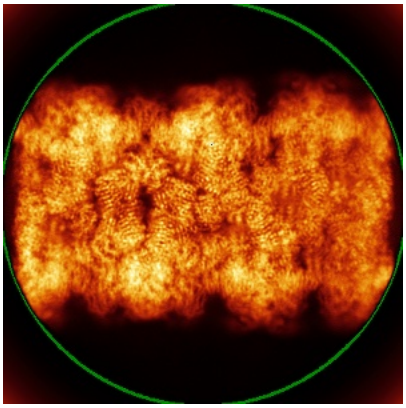


Z

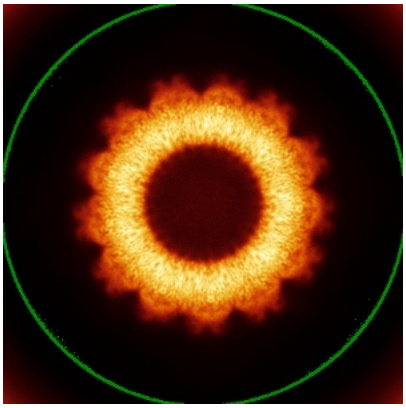
6.4.2 Raw map



X



Y

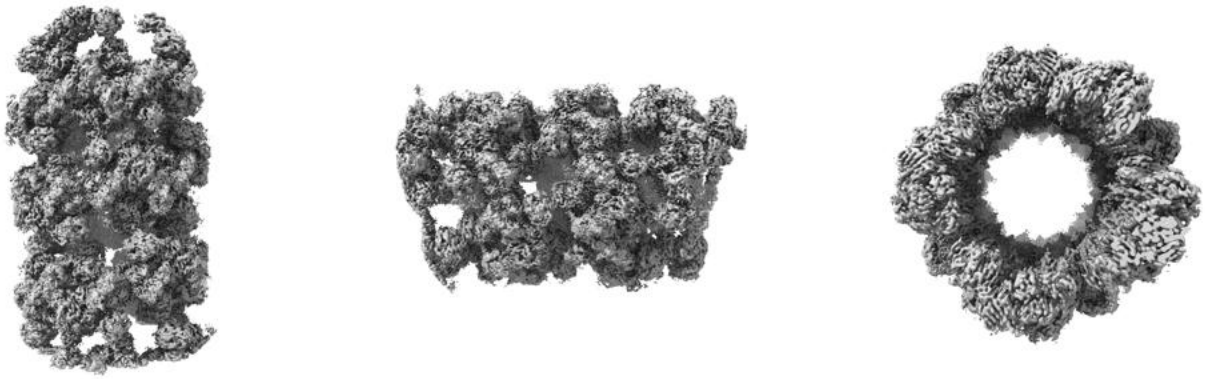


Z

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)

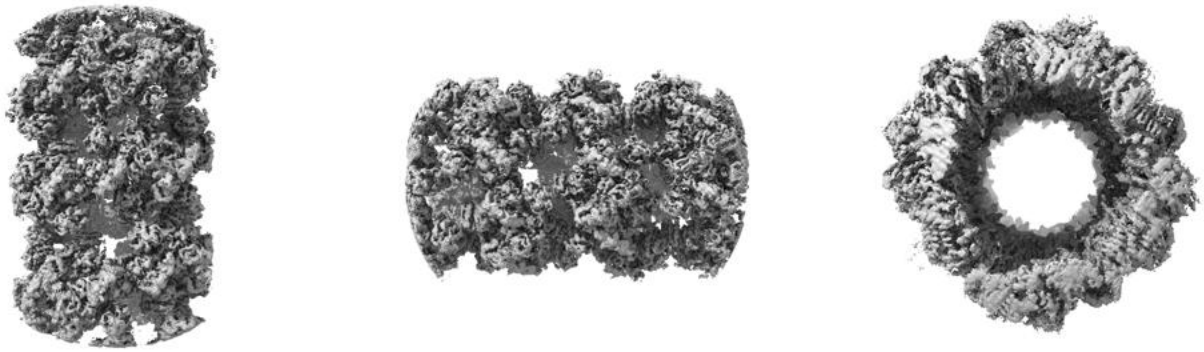
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

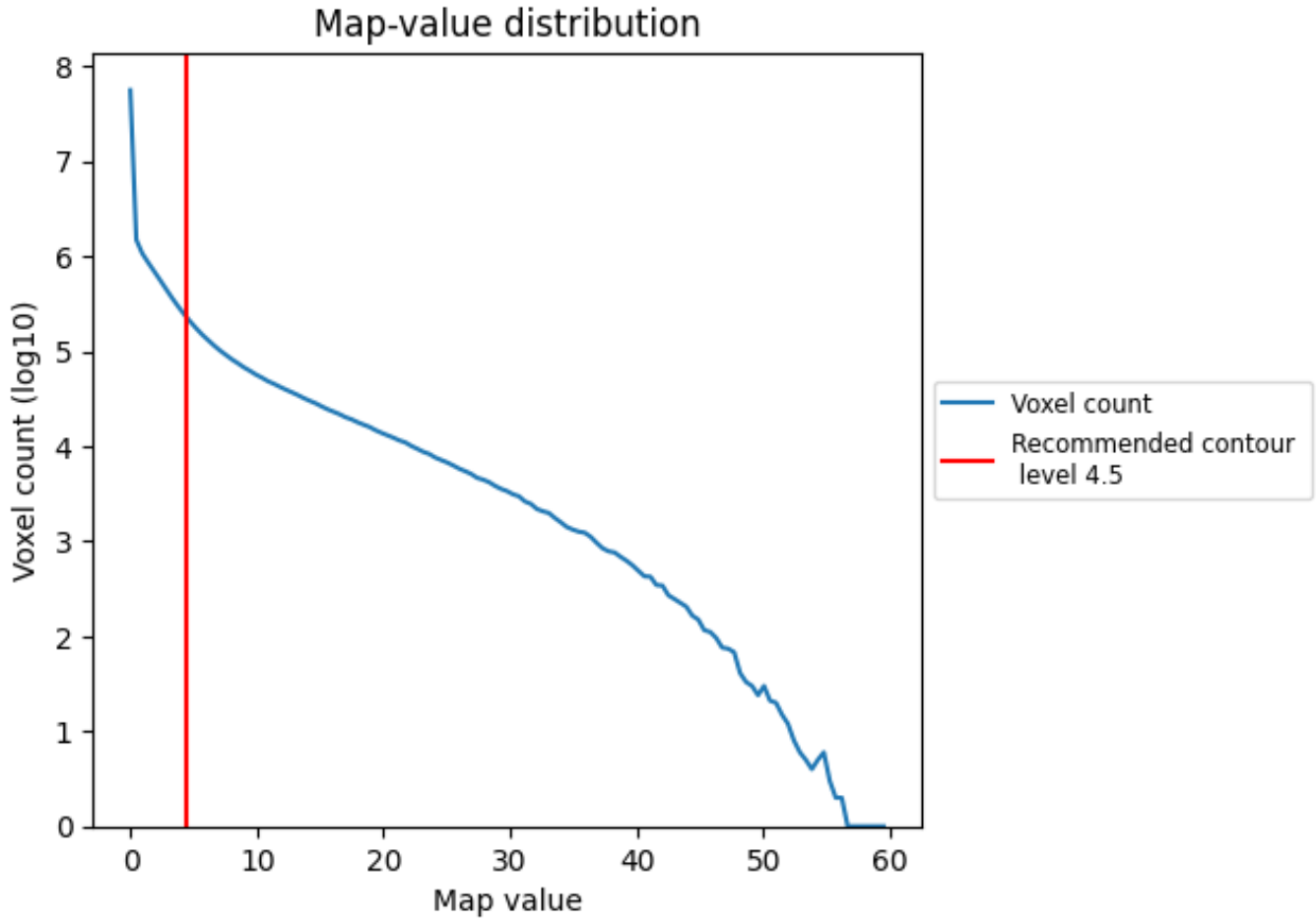
6.6 Mask visualisation (i)

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

7 Map analysis

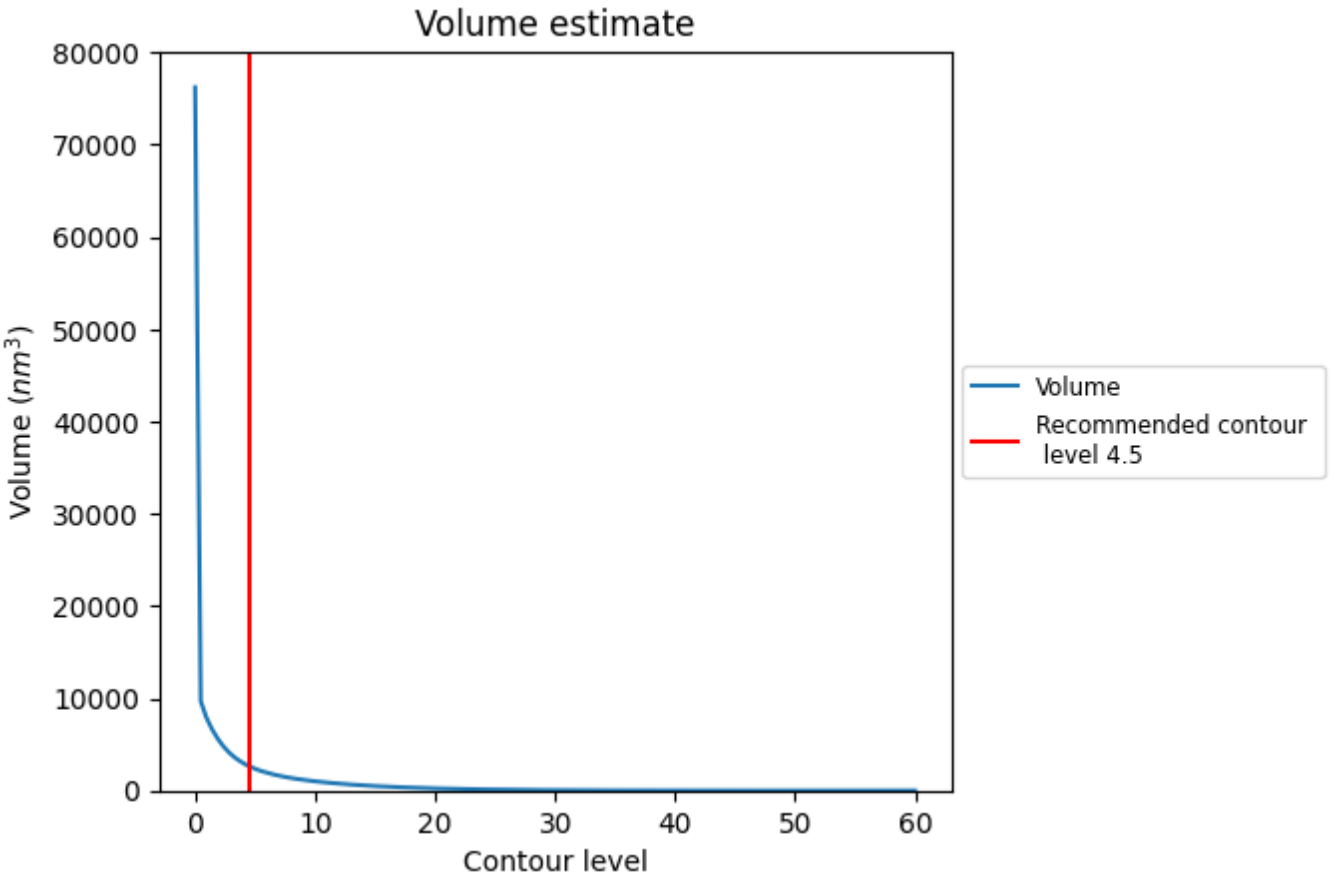
This section contains the results of statistical analysis of the map.

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.

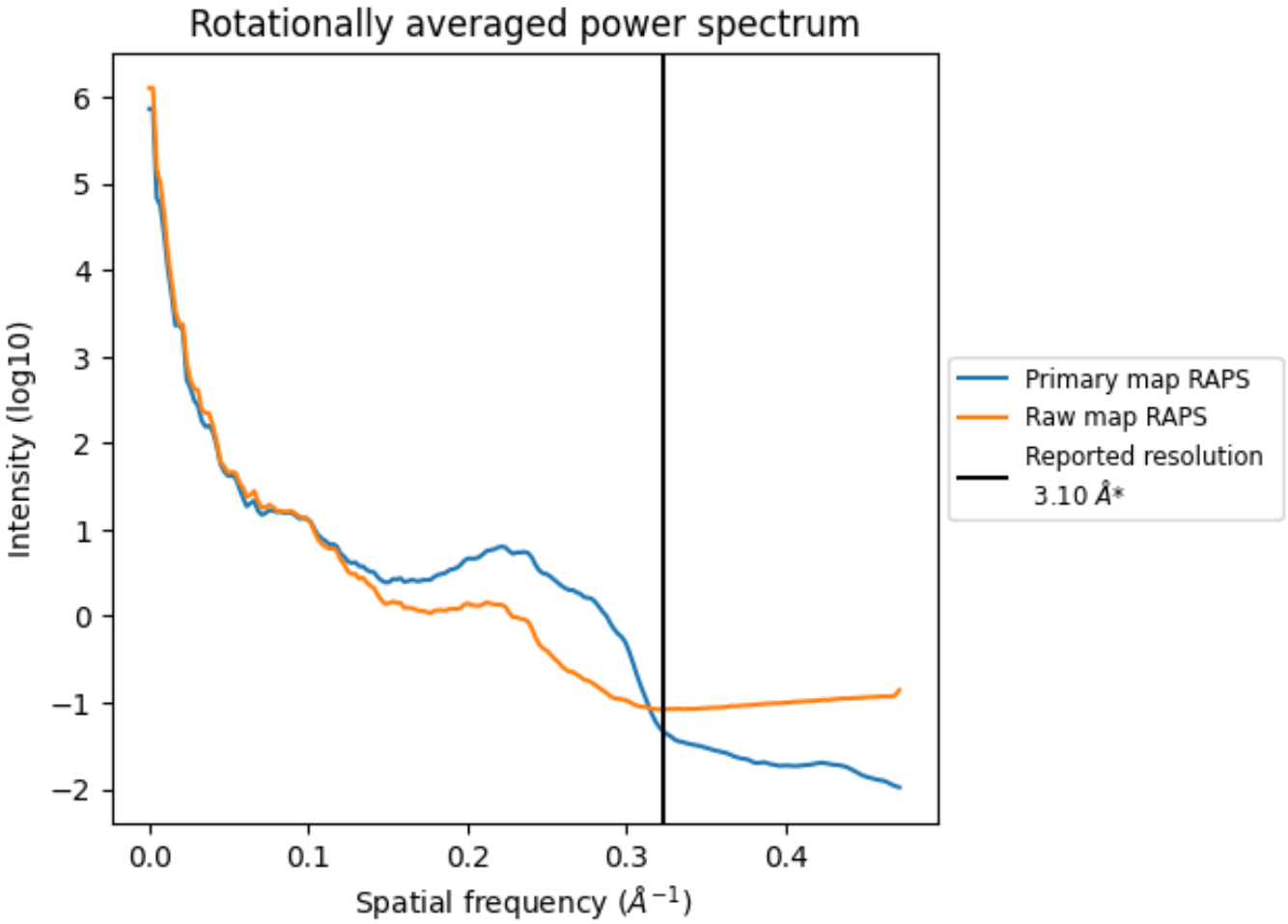
7.2 Volume estimate



The volume at the recommended contour level is 2643 nm^3; this corresponds to an approximate mass of 2388 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)

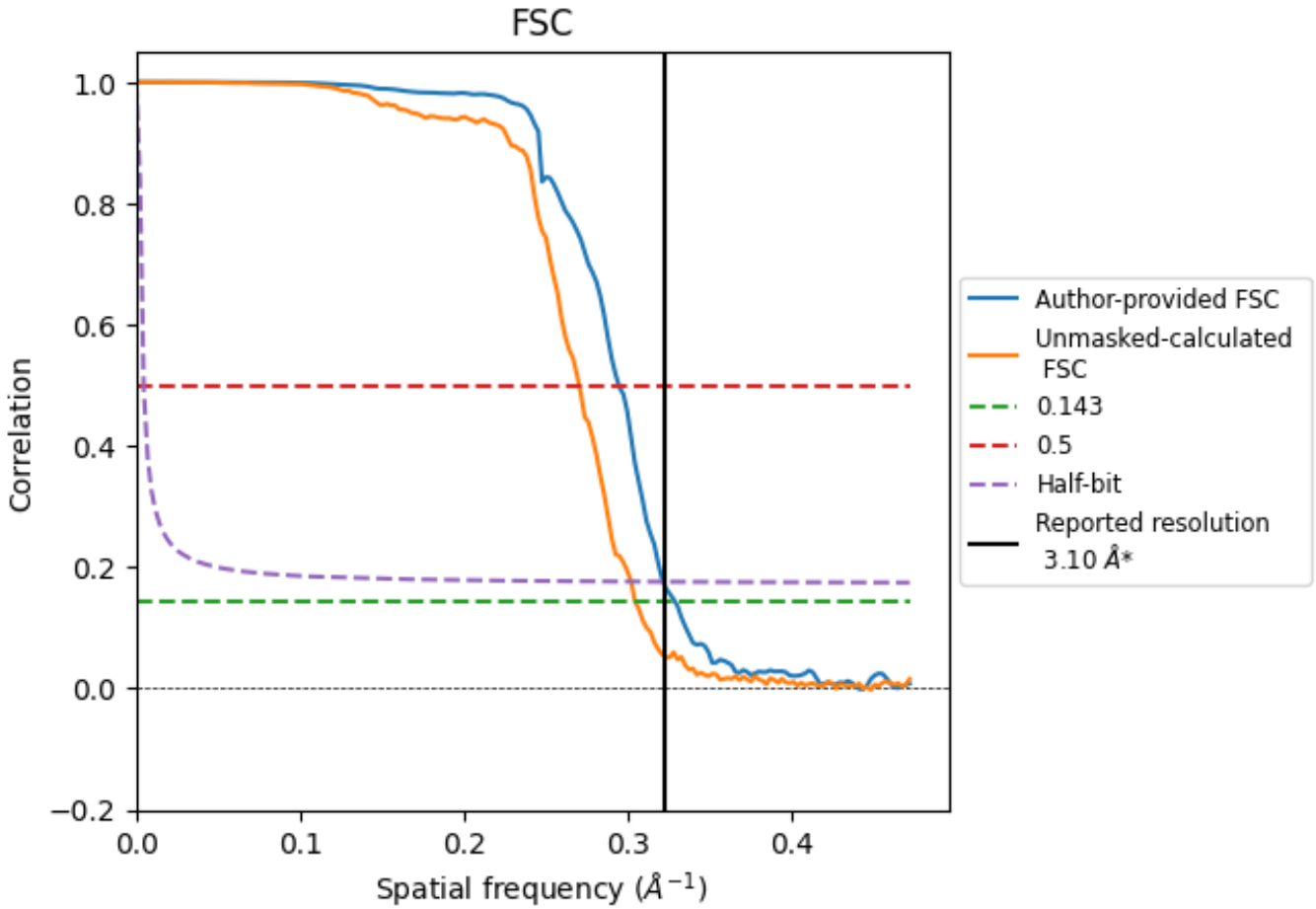


*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

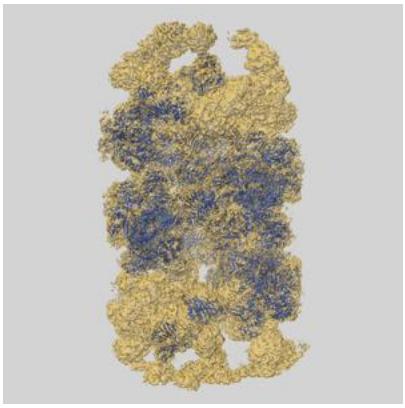
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.04	3.40	3.11
Unmasked-calculated*	3.29	3.70	3.31

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

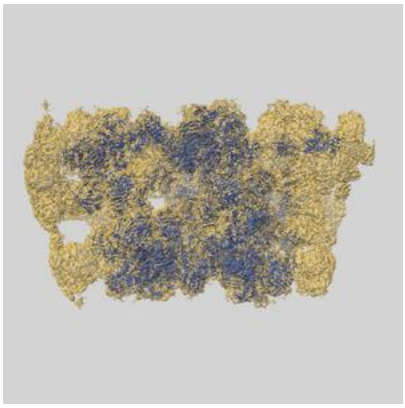
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-27156 and PDB model 8D3C. Per-residue inclusion information can be found in section 3 on page 16.

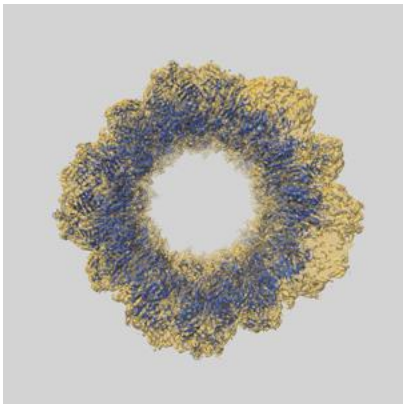
9.1 Map-model overlay



X



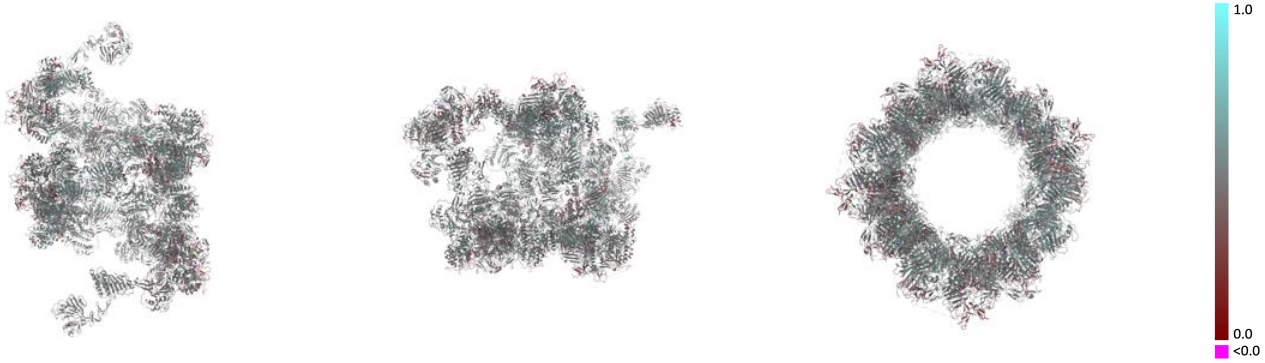
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.5 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.

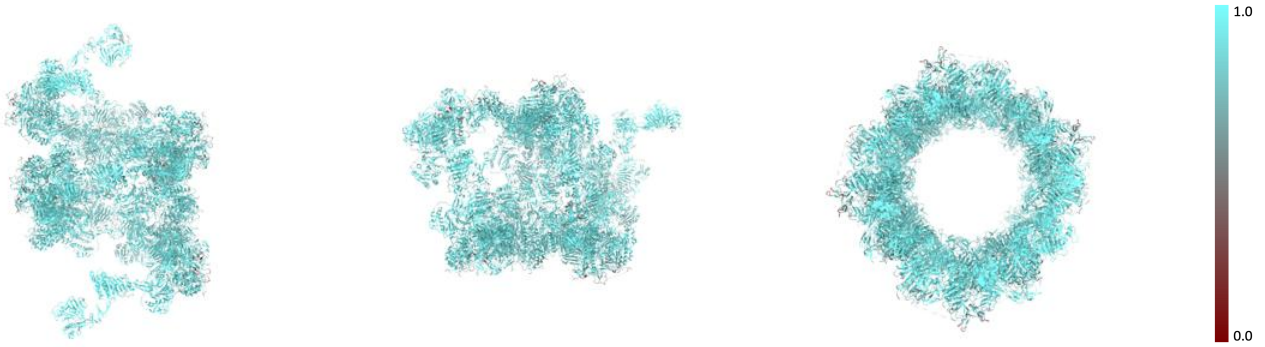
9.2 Q-score mapped to coordinate model (i)



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.

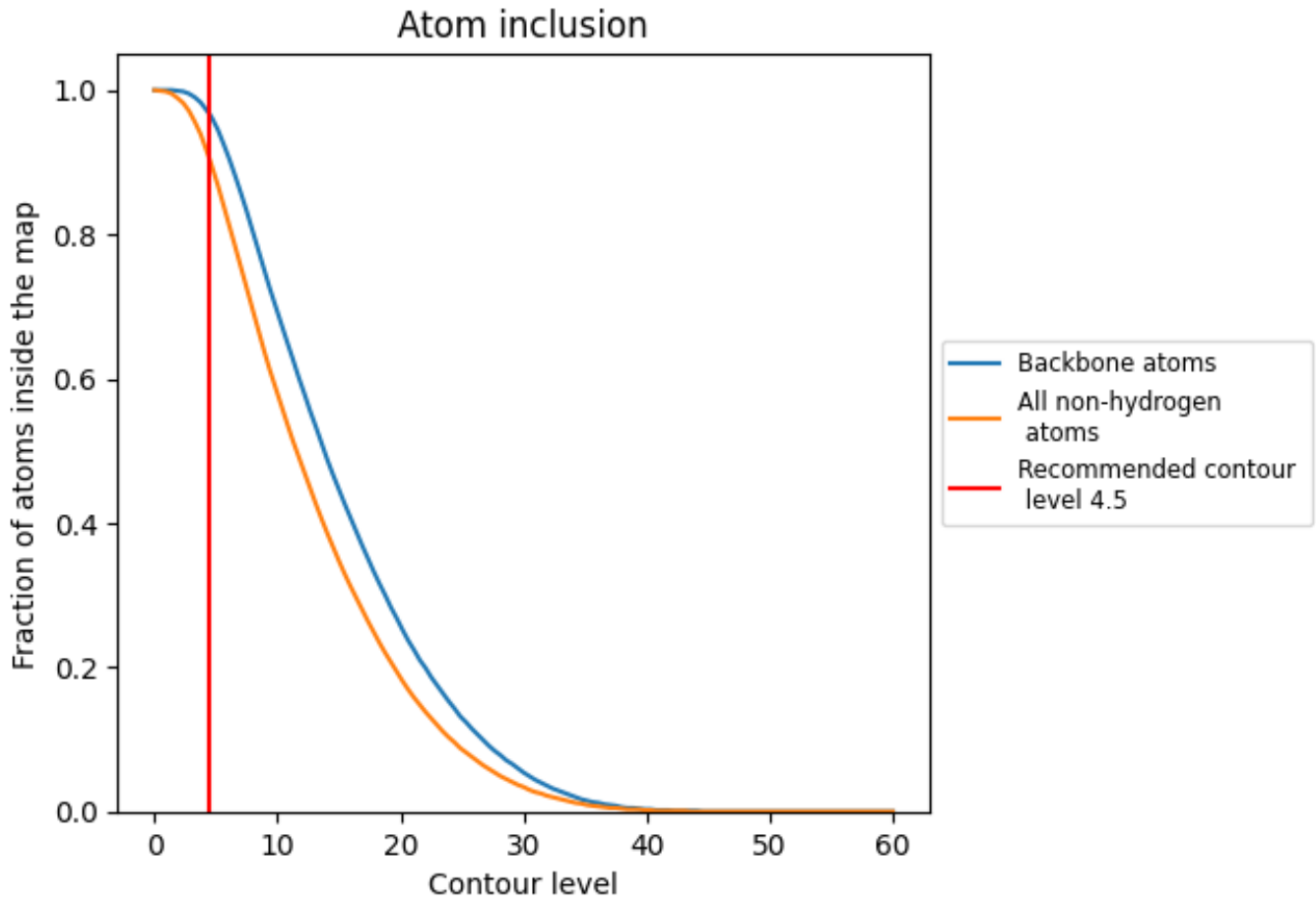
9.3 Atom inclusion mapped to coordinate model (i)



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 (4.5).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 90% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9030	0.4690
A	0.9170	0.4850
B	0.9110	0.4850
C	0.8970	0.4540
D	0.8980	0.4580
E	0.8990	0.4570
F	0.9100	0.4650
G	0.9090	0.4770
H	0.9080	0.4700
I	0.9090	0.4690
J	0.9170	0.4800
K	0.8970	0.4790
L	0.9010	0.4700
M	0.8880	0.4660
N	0.8980	0.4670
O	0.8920	0.4630
P	0.8940	0.4660