



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 06:37 AM EST

PDB ID : 7KZQ
EMDB ID : EMD-23086
Title : Structure of the human Fanconi anaemia Core-ID complex
Authors : Wang, S.L.; Pavletich, N.P.
Deposited on : 2020-12-10
Resolution : 4.20 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 ⓘ 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

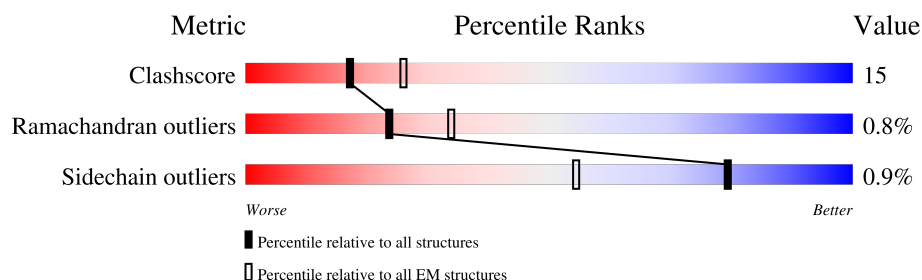
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.







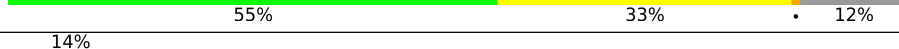
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 $\leq 5\%$. 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	1477	<div> <div>9%</div> <div>52%</div> <div>28%</div> <div>•</div> <div>20%</div> </div>
1	S	1477	<div> <div>10%</div> <div>54%</div> <div>31%</div> <div>15%</div> </div>
2	B	884	<div> <div>•</div> <div>51%</div> <div>27%</div> <div>•</div> <div>21%</div> </div>
2	O	884	<div> <div>•</div> <div>51%</div> <div>27%</div> <div>•</div> <div>21%</div> </div>
3	C	583	<div> <div>•</div> <div>68%</div> <div>25%</div> <div>•</div> <div>6%</div> </div>
4	E	555	<div> <div>•</div> <div>52%</div> <div>23%</div> <div>•</div> <div>25%</div> </div>
5	F	399	<div> <div>•</div> <div>65%</div> <div>20%</div> <div>15%</div> </div>
6	G	641	<div> <div>•</div> <div>63%</div> <div>27%</div> <div>•</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
6	H	641	
7	L	394	
7	M	394	
8	P	906	
8	Q	906	
9	W	39	
10	U	1328	
11	V	1451	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 172709 atoms, of which 87163 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 Fanconi anemia group A protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1186	Total	C	H	N	O	S	0	0
			18889	6001	9487	1650	1692	59		
1	S	1250	Total	C	H	N	O	S	0	0
			19961	6345	10028	1747	1780	61		

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1456	ALA	-	expression tag	UNP O15360
A	1457	ALA	-	expression tag	UNP O15360
A	1458	ALA	-	expression tag	UNP O15360
A	1459	LYS	-	expression tag	UNP O15360
A	1460	LEU	-	expression tag	UNP O15360
A	1461	VAL	-	expression tag	UNP O15360
A	1462	ASP	-	expression tag	UNP O15360
A	1463	GLU	-	expression tag	UNP O15360
A	1464	ASP	-	expression tag	UNP O15360
A	1465	LEU	-	expression tag	UNP O15360
A	1466	TYR	-	expression tag	UNP O15360
A	1467	PHE	-	expression tag	UNP O15360
A	1468	GLN	-	expression tag	UNP O15360
A	1469	SER	-	expression tag	UNP O15360
A	1470	ASP	-	expression tag	UNP O15360
A	1471	TYR	-	expression tag	UNP O15360
A	1472	LYS	-	expression tag	UNP O15360
A	1473	ASP	-	expression tag	UNP O15360
A	1474	ASP	-	expression tag	UNP O15360
A	1475	ASP	-	expression tag	UNP O15360
A	1476	ASP	-	expression tag	UNP O15360
A	1477	LYS	-	expression tag	UNP O15360
S	1456	ALA	-	expression tag	UNP O15360
S	1457	ALA	-	expression tag	UNP O15360
S	1458	ALA	-	expression tag	UNP O15360
S	1459	LYS	-	expression tag	UNP O15360

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Chain	Residue	Modelled	Actual	Comment	Reference
S	1460	LEU	-	expression tag	UNP O15360
S	1461	VAL	-	expression tag	UNP O15360
S	1462	ASP	-	expression tag	UNP O15360
S	1463	GLU	-	expression tag	UNP O15360
S	1464	ASP	-	expression tag	UNP O15360
S	1465	LEU	-	expression tag	UNP O15360
S	1466	TYR	-	expression tag	UNP O15360
S	1467	PHE	-	expression tag	UNP O15360
S	1468	GLN	-	expression tag	UNP O15360
S	1469	SER	-	expression tag	UNP O15360
S	1470	ASP	-	expression tag	UNP O15360
S	1471	TYR	-	expression tag	UNP O15360
S	1472	LYS	-	expression tag	UNP O15360
S	1473	ASP	-	expression tag	UNP O15360
S	1474	ASP	-	expression tag	UNP O15360
S	1475	ASP	-	expression tag	UNP O15360
S	1476	ASP	-	expression tag	UNP O15360
S	1477	LYS	-	expression tag	UNP O15360

- Molecule 2 is a protein called Fanconi anemia group B protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	701	Total	C	H	N	O	S	0	0
			11395	3619	5790	934	1013	39		
2	O	699	Total	C	H	N	O	S	0	0
			11353	3622	5759	926	1010	36		

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-24	MET	-	initiating methionine	UNP Q8NB91
B	-23	ASP	-	expression tag	UNP Q8NB91
B	-22	TYR	-	expression tag	UNP Q8NB91
B	-21	LYS	-	expression tag	UNP Q8NB91
B	-20	ASP	-	expression tag	UNP Q8NB91
B	-19	ASP	-	expression tag	UNP Q8NB91
B	-18	ASP	-	expression tag	UNP Q8NB91
B	-17	ASP	-	expression tag	UNP Q8NB91
B	-16	LYS	-	expression tag	UNP Q8NB91
B	-15	GLU	-	expression tag	UNP Q8NB91
B	-14	ASN	-	expression tag	UNP Q8NB91
B	-13	LEU	-	expression tag	UNP Q8NB91

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	TYR	-	expression tag	UNP Q8NB91
B	-11	PHE	-	expression tag	UNP Q8NB91
B	-10	GLN	-	expression tag	UNP Q8NB91
B	-9	GLY	-	expression tag	UNP Q8NB91
B	-8	GLY	-	expression tag	UNP Q8NB91
B	-7	GLY	-	expression tag	UNP Q8NB91
B	-6	ARG	-	expression tag	UNP Q8NB91
B	-5	LYS	-	expression tag	UNP Q8NB91
B	-4	LEU	-	expression tag	UNP Q8NB91
B	-3	GLY	-	expression tag	UNP Q8NB91
B	-2	THR	-	expression tag	UNP Q8NB91
B	-1	GLY	-	expression tag	UNP Q8NB91
B	0	SER	-	expression tag	UNP Q8NB91
O	-24	MET	-	initiating methionine	UNP Q8NB91
O	-23	ASP	-	expression tag	UNP Q8NB91
O	-22	TYR	-	expression tag	UNP Q8NB91
O	-21	LYS	-	expression tag	UNP Q8NB91
O	-20	ASP	-	expression tag	UNP Q8NB91
O	-19	ASP	-	expression tag	UNP Q8NB91
O	-18	ASP	-	expression tag	UNP Q8NB91
O	-17	ASP	-	expression tag	UNP Q8NB91
O	-16	LYS	-	expression tag	UNP Q8NB91
O	-15	GLU	-	expression tag	UNP Q8NB91
O	-14	ASN	-	expression tag	UNP Q8NB91
O	-13	LEU	-	expression tag	UNP Q8NB91
O	-12	TYR	-	expression tag	UNP Q8NB91
O	-11	PHE	-	expression tag	UNP Q8NB91
O	-10	GLN	-	expression tag	UNP Q8NB91
O	-9	GLY	-	expression tag	UNP Q8NB91
O	-8	GLY	-	expression tag	UNP Q8NB91
O	-7	GLY	-	expression tag	UNP Q8NB91
O	-6	ARG	-	expression tag	UNP Q8NB91
O	-5	LYS	-	expression tag	UNP Q8NB91
O	-4	LEU	-	expression tag	UNP Q8NB91
O	-3	GLY	-	expression tag	UNP Q8NB91
O	-2	THR	-	expression tag	UNP Q8NB91
O	-1	GLY	-	expression tag	UNP Q8NB91
O	0	SER	-	expression tag	UNP Q8NB91

- Molecule 3 is a protein called Fanconi anemia group C protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	550	Total	C	H	N	O	S	0	0
			8838	2826	4442	749	791	30		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-24	MET	-	initiating methionine	UNP Q00597
C	-23	ASP	-	expression tag	UNP Q00597
C	-22	TYR	-	expression tag	UNP Q00597
C	-21	LYS	-	expression tag	UNP Q00597
C	-20	ASP	-	expression tag	UNP Q00597
C	-19	ASP	-	expression tag	UNP Q00597
C	-18	ASP	-	expression tag	UNP Q00597
C	-17	ASP	-	expression tag	UNP Q00597
C	-16	LYS	-	expression tag	UNP Q00597
C	-15	GLU	-	expression tag	UNP Q00597
C	-14	ASN	-	expression tag	UNP Q00597
C	-13	LEU	-	expression tag	UNP Q00597
C	-12	TYR	-	expression tag	UNP Q00597
C	-11	PHE	-	expression tag	UNP Q00597
C	-10	GLN	-	expression tag	UNP Q00597
C	-9	GLY	-	expression tag	UNP Q00597
C	-8	GLY	-	expression tag	UNP Q00597
C	-7	GLY	-	expression tag	UNP Q00597
C	-6	ARG	-	expression tag	UNP Q00597
C	-5	LYS	-	expression tag	UNP Q00597
C	-4	LEU	-	expression tag	UNP Q00597
C	-3	GLY	-	expression tag	UNP Q00597
C	-2	THR	-	expression tag	UNP Q00597
C	-1	GLY	-	expression tag	UNP Q00597
C	0	SER	-	expression tag	UNP Q00597

- Molecule 4 is a protein called Fanconi anemia group E protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	419	Total	C	H	N	O	S	0	0
			6614	2048	3390	560	592	24		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-18	MET	-	initiating methionine	UNP Q9HB96
E	-17	ASP	-	expression tag	UNP Q9HB96

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-16	TYR	-	expression tag	UNP Q9HB96
E	-15	LYS	-	expression tag	UNP Q9HB96
E	-14	ASP	-	expression tag	UNP Q9HB96
E	-13	ASP	-	expression tag	UNP Q9HB96
E	-12	ASP	-	expression tag	UNP Q9HB96
E	-11	ASP	-	expression tag	UNP Q9HB96
E	-10	LYS	-	expression tag	UNP Q9HB96
E	-9	GLU	-	expression tag	UNP Q9HB96
E	-8	ASN	-	expression tag	UNP Q9HB96
E	-7	LEU	-	expression tag	UNP Q9HB96
E	-6	TYR	-	expression tag	UNP Q9HB96
E	-5	PHE	-	expression tag	UNP Q9HB96
E	-4	GLN	-	expression tag	UNP Q9HB96
E	-3	GLY	-	expression tag	UNP Q9HB96
E	-2	GLY	-	expression tag	UNP Q9HB96
E	-1	GLY	-	expression tag	UNP Q9HB96
E	0	ARG	-	expression tag	UNP Q9HB96

- Molecule 5 is a protein called Fanconi anemia group F protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	340	Total	C	H	N	O	S	0	0
			5466	1730	2740	506	483	7		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-24	MET	-	initiating methionine	UNP Q9NPI8
F	-23	ASP	-	expression tag	UNP Q9NPI8
F	-22	TYR	-	expression tag	UNP Q9NPI8
F	-21	LYS	-	expression tag	UNP Q9NPI8
F	-20	ASP	-	expression tag	UNP Q9NPI8
F	-19	ASP	-	expression tag	UNP Q9NPI8
F	-18	ASP	-	expression tag	UNP Q9NPI8
F	-17	ASP	-	expression tag	UNP Q9NPI8
F	-16	LYS	-	expression tag	UNP Q9NPI8
F	-15	GLU	-	expression tag	UNP Q9NPI8
F	-14	ASN	-	expression tag	UNP Q9NPI8
F	-13	LEU	-	expression tag	UNP Q9NPI8
F	-12	TYR	-	expression tag	UNP Q9NPI8
F	-11	PHE	-	expression tag	UNP Q9NPI8
F	-10	GLN	-	expression tag	UNP Q9NPI8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-9	GLY	-	expression tag	UNP Q9NPI8
F	-8	GLY	-	expression tag	UNP Q9NPI8
F	-7	GLY	-	expression tag	UNP Q9NPI8
F	-6	ARG	-	expression tag	UNP Q9NPI8
F	-5	LYS	-	expression tag	UNP Q9NPI8
F	-4	LEU	-	expression tag	UNP Q9NPI8
F	-3	GLY	-	expression tag	UNP Q9NPI8
F	-2	THR	-	expression tag	UNP Q9NPI8
F	-1	GLY	-	expression tag	UNP Q9NPI8
F	0	SER	-	expression tag	UNP Q9NPI8

- Molecule 6 is a protein called Fanconi anemia group G protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	G	577	Total	C	H	N	O	S	0	0
			9020	2843	4537	778	844	18		
6	H	544	Total	C	H	N	O	S	0	0
			8504	2676	4288	734	790	16		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-18	MET	-	initiating methionine	UNP O15287
G	-17	ASP	-	expression tag	UNP O15287
G	-16	TYR	-	expression tag	UNP O15287
G	-15	LYS	-	expression tag	UNP O15287
G	-14	ASP	-	expression tag	UNP O15287
G	-13	ASP	-	expression tag	UNP O15287
G	-12	ASP	-	expression tag	UNP O15287
G	-11	ASP	-	expression tag	UNP O15287
G	-10	LYS	-	expression tag	UNP O15287
G	-9	GLU	-	expression tag	UNP O15287
G	-8	ASN	-	expression tag	UNP O15287
G	-7	LEU	-	expression tag	UNP O15287
G	-6	TYR	-	expression tag	UNP O15287
G	-5	PHE	-	expression tag	UNP O15287
G	-4	GLN	-	expression tag	UNP O15287
G	-3	GLY	-	expression tag	UNP O15287
G	-2	GLY	-	expression tag	UNP O15287
G	-1	GLY	-	expression tag	UNP O15287
G	0	ARG	-	expression tag	UNP O15287
H	-18	MET	-	initiating methionine	UNP O15287

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-17	ASP	-	expression tag	UNP O15287
H	-16	TYR	-	expression tag	UNP O15287
H	-15	LYS	-	expression tag	UNP O15287
H	-14	ASP	-	expression tag	UNP O15287
H	-13	ASP	-	expression tag	UNP O15287
H	-12	ASP	-	expression tag	UNP O15287
H	-11	ASP	-	expression tag	UNP O15287
H	-10	LYS	-	expression tag	UNP O15287
H	-9	GLU	-	expression tag	UNP O15287
H	-8	ASN	-	expression tag	UNP O15287
H	-7	LEU	-	expression tag	UNP O15287
H	-6	TYR	-	expression tag	UNP O15287
H	-5	PHE	-	expression tag	UNP O15287
H	-4	GLN	-	expression tag	UNP O15287
H	-3	GLY	-	expression tag	UNP O15287
H	-2	GLY	-	expression tag	UNP O15287
H	-1	GLY	-	expression tag	UNP O15287
H	0	ARG	-	expression tag	UNP O15287

- Molecule 7 is a protein called E3 ubiquitin-protein ligase FANCL.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	L	370	Total	C	H	N	O	S	0	0
			5951	1914	2977	496	542	22		
7	M	370	Total	C	H	N	O	S	0	0
			5951	1914	2977	496	542	22		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-18	MET	-	initiating methionine	UNP Q9NW38
L	-17	ASP	-	expression tag	UNP Q9NW38
L	-16	TYR	-	expression tag	UNP Q9NW38
L	-15	LYS	-	expression tag	UNP Q9NW38
L	-14	ASP	-	expression tag	UNP Q9NW38
L	-13	ASP	-	expression tag	UNP Q9NW38
L	-12	ASP	-	expression tag	UNP Q9NW38
L	-11	ASP	-	expression tag	UNP Q9NW38
L	-10	LYS	-	expression tag	UNP Q9NW38
L	-9	GLU	-	expression tag	UNP Q9NW38
L	-8	ASN	-	expression tag	UNP Q9NW38
L	-7	LEU	-	expression tag	UNP Q9NW38

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-6	TYR	-	expression tag	UNP Q9NW38
L	-5	PHE	-	expression tag	UNP Q9NW38
L	-4	GLN	-	expression tag	UNP Q9NW38
L	-3	GLY	-	expression tag	UNP Q9NW38
L	-2	GLY	-	expression tag	UNP Q9NW38
L	-1	GLY	-	expression tag	UNP Q9NW38
L	0	ARG	-	expression tag	UNP Q9NW38
M	-18	MET	-	initiating methionine	UNP Q9NW38
M	-17	ASP	-	expression tag	UNP Q9NW38
M	-16	TYR	-	expression tag	UNP Q9NW38
M	-15	LYS	-	expression tag	UNP Q9NW38
M	-14	ASP	-	expression tag	UNP Q9NW38
M	-13	ASP	-	expression tag	UNP Q9NW38
M	-12	ASP	-	expression tag	UNP Q9NW38
M	-11	ASP	-	expression tag	UNP Q9NW38
M	-10	LYS	-	expression tag	UNP Q9NW38
M	-9	GLU	-	expression tag	UNP Q9NW38
M	-8	ASN	-	expression tag	UNP Q9NW38
M	-7	LEU	-	expression tag	UNP Q9NW38
M	-6	TYR	-	expression tag	UNP Q9NW38
M	-5	PHE	-	expression tag	UNP Q9NW38
M	-4	GLN	-	expression tag	UNP Q9NW38
M	-3	GLY	-	expression tag	UNP Q9NW38
M	-2	GLY	-	expression tag	UNP Q9NW38
M	-1	GLY	-	expression tag	UNP Q9NW38
M	0	ARG	-	expression tag	UNP Q9NW38

- Molecule 8 is a protein called Fanconi anemia core complex-associated protein 100.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	P	748	Total	C	H	N	O	S	0	0
			11279	3520	5681	972	1058	48		
8	Q	754	Total	C	H	N	O	S	0	0
			11355	3548	5724	978	1058	47		

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	-24	MET	-	initiating methionine	UNP Q0VG06
P	-23	ASP	-	expression tag	UNP Q0VG06
P	-22	TYR	-	expression tag	UNP Q0VG06
P	-21	LYS	-	expression tag	UNP Q0VG06

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-20	ASP	-	expression tag	UNP Q0VG06
P	-19	HIS	-	expression tag	UNP Q0VG06
P	-18	ASP	-	expression tag	UNP Q0VG06
P	-17	GLY	-	expression tag	UNP Q0VG06
P	-16	ASP	-	expression tag	UNP Q0VG06
P	-15	TYR	-	expression tag	UNP Q0VG06
P	-14	LYS	-	expression tag	UNP Q0VG06
P	-13	ASP	-	expression tag	UNP Q0VG06
P	-12	HIS	-	expression tag	UNP Q0VG06
P	-11	ASP	-	expression tag	UNP Q0VG06
P	-10	ILE	-	expression tag	UNP Q0VG06
P	-9	ASP	-	expression tag	UNP Q0VG06
P	-8	TYR	-	expression tag	UNP Q0VG06
P	-7	LYS	-	expression tag	UNP Q0VG06
P	-6	ASP	-	expression tag	UNP Q0VG06
P	-5	ASP	-	expression tag	UNP Q0VG06
P	-4	ASP	-	expression tag	UNP Q0VG06
P	-3	ASP	-	expression tag	UNP Q0VG06
P	-2	LYS	-	expression tag	UNP Q0VG06
P	-1	GLY	-	expression tag	UNP Q0VG06
P	0	SER	-	expression tag	UNP Q0VG06
Q	-24	MET	-	initiating methionine	UNP Q0VG06
Q	-23	ASP	-	expression tag	UNP Q0VG06
Q	-22	TYR	-	expression tag	UNP Q0VG06
Q	-21	LYS	-	expression tag	UNP Q0VG06
Q	-20	ASP	-	expression tag	UNP Q0VG06
Q	-19	HIS	-	expression tag	UNP Q0VG06
Q	-18	ASP	-	expression tag	UNP Q0VG06
Q	-17	GLY	-	expression tag	UNP Q0VG06
Q	-16	ASP	-	expression tag	UNP Q0VG06
Q	-15	TYR	-	expression tag	UNP Q0VG06
Q	-14	LYS	-	expression tag	UNP Q0VG06
Q	-13	ASP	-	expression tag	UNP Q0VG06
Q	-12	HIS	-	expression tag	UNP Q0VG06
Q	-11	ASP	-	expression tag	UNP Q0VG06
Q	-10	ILE	-	expression tag	UNP Q0VG06
Q	-9	ASP	-	expression tag	UNP Q0VG06
Q	-8	TYR	-	expression tag	UNP Q0VG06
Q	-7	LYS	-	expression tag	UNP Q0VG06
Q	-6	ASP	-	expression tag	UNP Q0VG06
Q	-5	ASP	-	expression tag	UNP Q0VG06
Q	-4	ASP	-	expression tag	UNP Q0VG06

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-3	ASP	-	expression tag	UNP Q0VG06
Q	-2	LYS	-	expression tag	UNP Q0VG06
Q	-1	GLY	-	expression tag	UNP Q0VG06
Q	0	SER	-	expression tag	UNP Q0VG06

- Molecule 9 is a protein called Fanconi anemia core complex-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	39	Total	C	H	N	O	0	0
			513	179	242	42	50		

- Molecule 10 is a protein called Fanconi anemia, complementation group I.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	U	1168	Total	C	H	N	O	S	0	0
			18882	5933	9626	1549	1720	54		

There are 3 discrepancies between the modelled and reference sequences:

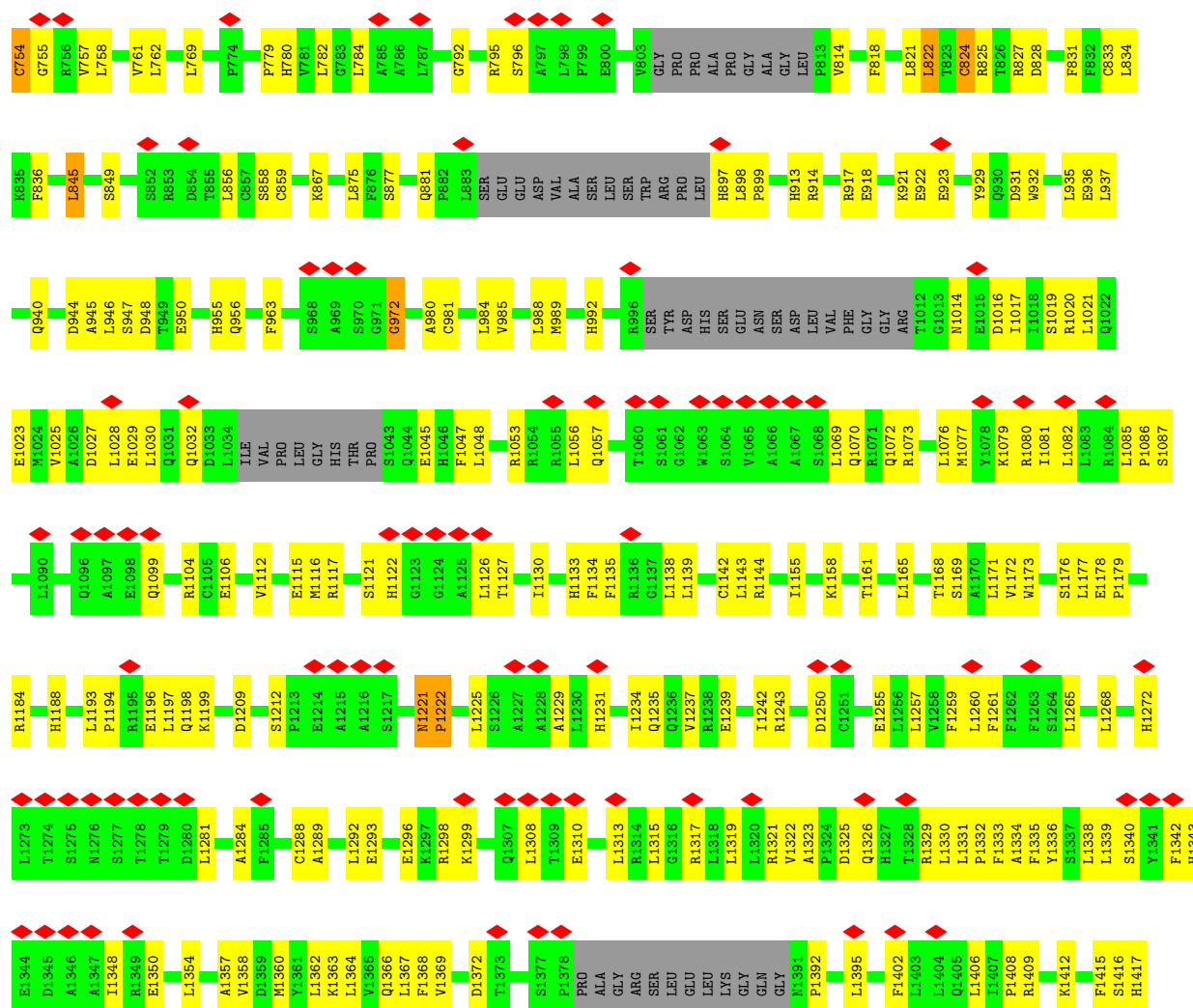
Chain	Residue	Modelled	Actual	Comment	Reference
U	877	LEU	ILE	conflict	UNP B7ZMF2
U	1235	VAL	ALA	conflict	UNP B7ZMF2
U	1274	SER	ASN	conflict	UNP B7ZMF2

- Molecule 11 is a protein called Fanconi anemia group D2 protein.

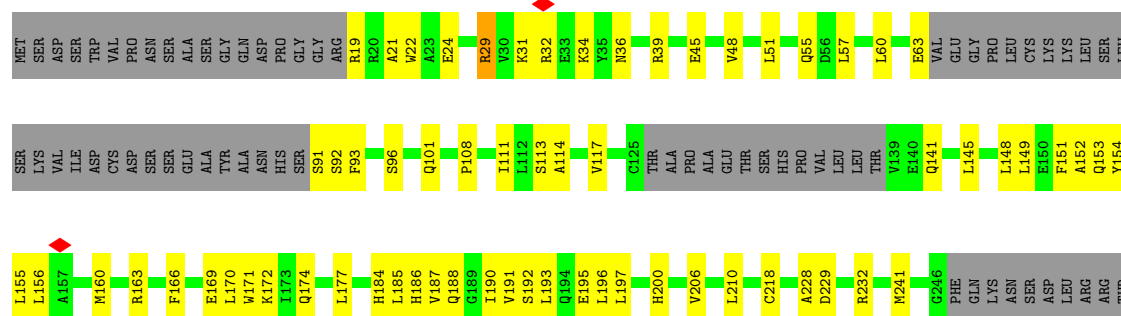
Mol	Chain	Residues	Atoms						AltConf	Trace
11	V	1153	Total	C	H	N	O	S	0	0
			18733	5970	9475	1527	1709	52		

- Molecule 12 is ZINC ION (three-letter code: ZN) (formula: Zn).

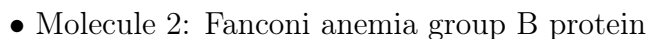
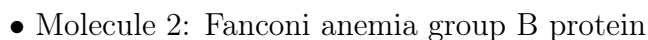
Mol	Chain	Residues	Atoms		AltConf
12	G	1	Total	Zn	0
			1	1	
12	L	2	Total	Zn	0
			2	2	
12	M	2	Total	Zn	0
			2	2	

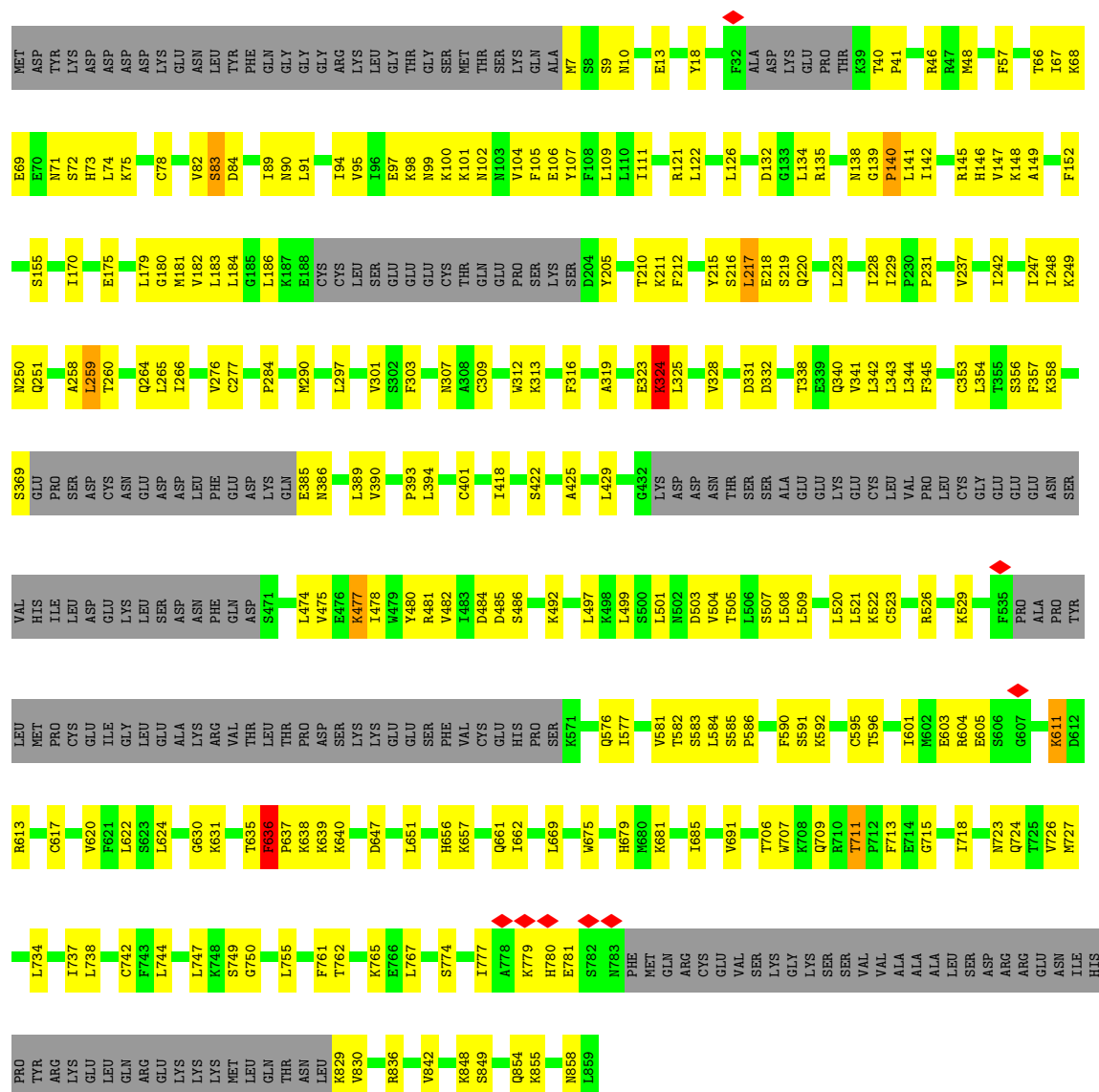


• Molecule 1: Fanconi anemia group A protein



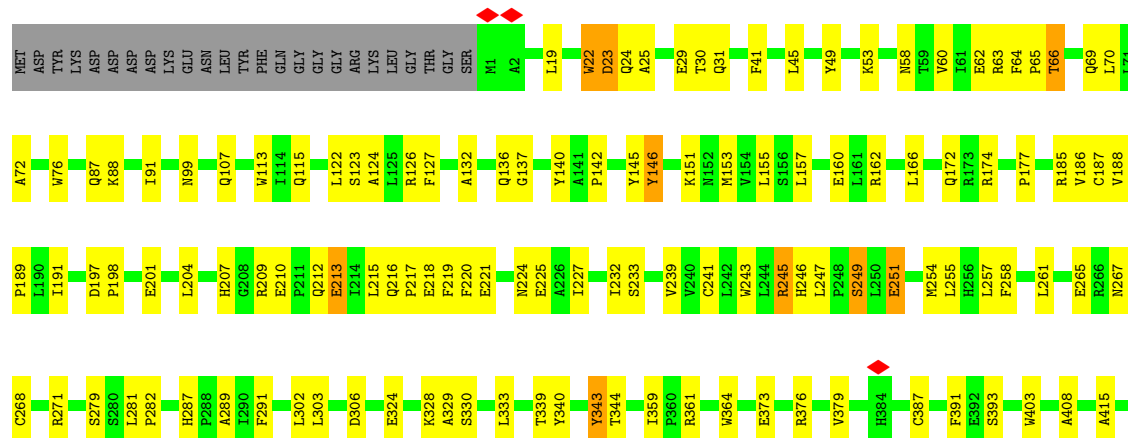
S1264	S1265	H1272	S1275	N1276	S1277	T1278	T1279	H1286	V1287	I1291	I1292	E1293	C1294	L1295	E1296	K1297	R1298	K1299	W1302	L1303	A1304	L1305	F1306	Q1307	L1308	T1309	E1310	S1311	D1312	L1313	Q1316	R1317	L1318	L1319	L1320	R1321	V1322	D1325	H1327	T1328	R1329	L1330	P1331	P1332	F1333	A1334	F1335	Y1336	S1337	L1338	L1339																																											
S1087	L1090	C1091	S1094	Q1099	P1100	I1101	T1102	A1103	M1104	E1106	Q1107	F1108	C1109	Q1110	L1111	V1112	N1113	S1114	E1115	M1116	R1117	N1118	H1122	G1123	G1124	A1125	L1126	T1127	Q1128	D1129	T1130	H1133	F1134	F1135	R1136	M1140	L1143	R1144	S1145	P1148	M1151	D1152	F1153	I1154	I1155	L1156	A1157	K1158	T1161	K1162	C1163	S1169	W1173	W1174	S1175	S1176	L1177	E1178	R1186	H1187	H1188	C1189	Q1190	S1191	P1192	L1193	P1194	R1195	E1196	L1197	L1200	F1210	E1214	A1215	A1216	S1217	P1218	A1219	N1221	P1222	A1229	L1230	E1239	I1242	R1243	E1252	R1253	E1254	E1255	L1257	L1260	F1261	F1262	F1263
S0844	L845	C846	S849	S850	Q851	S852	R853	D854	T855	S861	P862	C863	L864	R865	K866	K867	T868	R874	S877	R880	Q881	LEU	SER	GLU	GLU	ASP	VAL	ALA	ALA	SER	LEU	TRP	PRO	LEU	H897	L898	P899	S900	A901	Q904	R905	W911	T915	F916	R917	E918	Y919	L920	K921																																													
V925	T928	Y929	Q930	D931	W932	H933	H934	L935	E936	L937	E938	I939	Q940	D944	A945	L946	S947	T948	E950	Q952	H955	L964	P965	E966	S967	S968	G971	G972	C973	D974	G975	D976	L977	C981	T982	I983	L984	V985	N986	H992	S995	Y998	S1001	E1002	N1003																																																	
V1007	T1012	G1013	M1014	I1018	S1019	R1020	L1021	Q1022	E1023	M1024	D1027	L1028	E1029	L1030	Q1031	Q1032	D1033	LEU	I1034	VAL	PRO	LEU	GLY	HIS	THR	PRO	S1043	Q1044	E1045	F1052	R1053	L1056	S1061	G1062	W1063	S1064	V1065	A1066	L1069	Q1070	R1071	Q1072	E1073	L1075	L1076	R1080	T1081	L1082	L1083	R1084																																												
S0878	V679	T680	R683	L684	W685	K686	R687	P688	R674	S677	R680	Q681	LEU	SER	GLU	GLU	ASP	VAL	ALA	ALA	SER	LEU	TRP	PRO	LEU	H897	L898	P899	S900	A901	Q904	R905	W911	T915	F916	R917	E918	Y919	L920	K921																																																						
V761	L762	T763	R764	L765	C766	O767	L768	L769	L776	H780	L781	G783	L784	L787	A788	H790	L791	R795	L798	W801	L802	W803	G804	P805	PRO	PRO	GLY	ALA	GLY	P813	W814	P815	P818	D819	S820	L821	L822	T823	C824	R825	T826	S829	C833	S842	Y843																																																	
A678	V679	T680	R683	L684	W685	K686	R687	P688	R674	S677	R680	Q681	LEU	SER	GLU	GLU	ASP	VAL	ALA	ALA	SER	LEU	TRP	PRO	LEU	H897	L898	P899	S900	A901	Q904	R905	W911	T915	F916	R917	E918	Y919	L920	K921																																																						
F603	I604	E605	S606	L607	K608	R609	A610	D611	K612	I613	P614	F615	S616	L617	T620	A627	ALA	GLU	GLU	LYS	PRO	GLU	ALA	ALA	GLY	VAL	GLU	PRO	ASN	SER	ALA	E648	P649	L650	G651	Q652	L653	T654	A655	A656	L657	L660	R670	L673	S674	A675	Q676	V677																																														
S524	I525	GLU	ASN	MET	GLY	LEU	T528	A529	F452	S455	F456	R460	H463	G464	C465	F472	L473	F474	T475	F476	L477	S478	V481	E484	S485	Q490	W491	H492	T493	L494	H495	P496	P497	LEU	VAL	PRO	GLY	LYS	Y503	R504	L507	S512	L513	A514	K515	T516	R517	A430	L439	GLU	P332																																											
VAL	SER	PRO	GLU	PHE	LYS	MET	PRO	GLN	V265	T266	L270	L278	L281	G284	V285	Q286	E287	E288	S289	S290	T291	H292	K293	I294	V295	R296	F299	S303	G304	H305	I306	L307	G308	S309	V310	I311	S312	T313	D314	P315	L316	K317	F320	S321	L324	T325	Q326	I327	L328	S331																																												

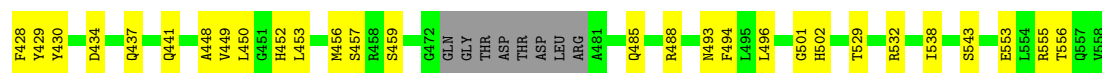




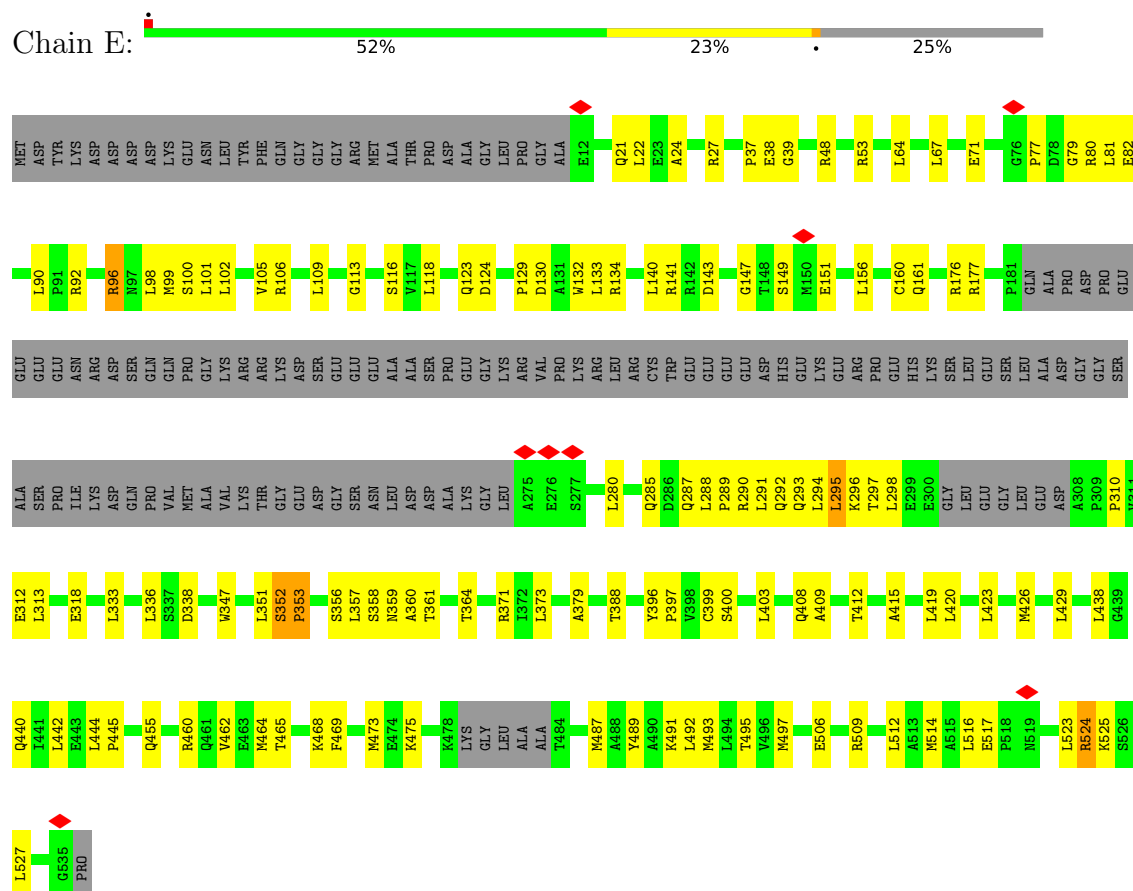
• Molecule 3: Fanconi anemia group C protein

Chain C: 68% 25% 6%

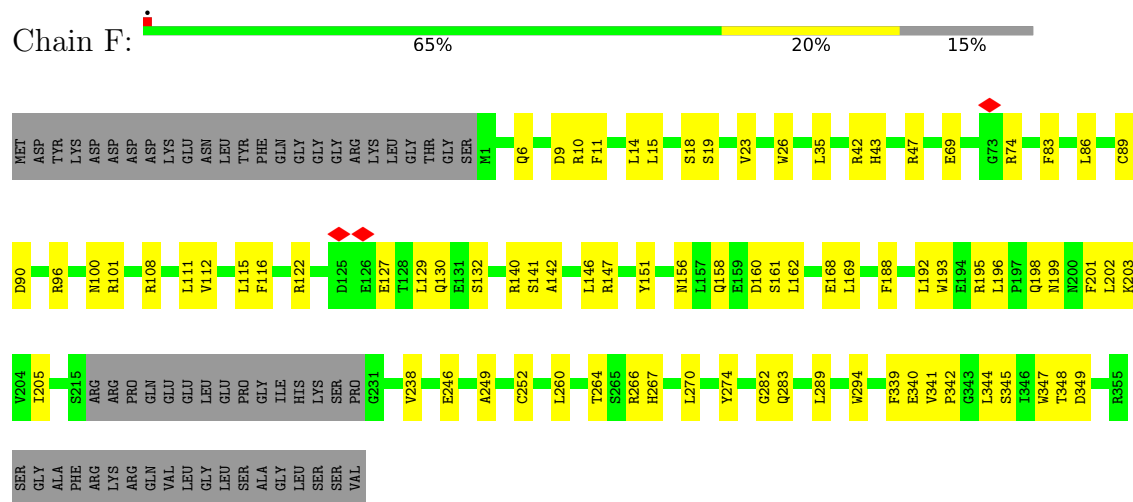




• Molecule 4: Fanconi anemia group E protein

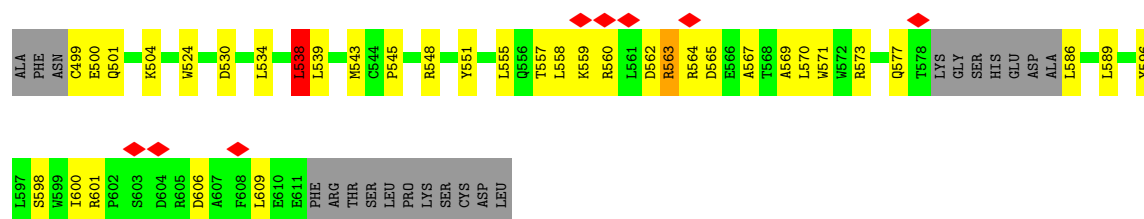


• Molecule 5: Fanconi anemia group F protein



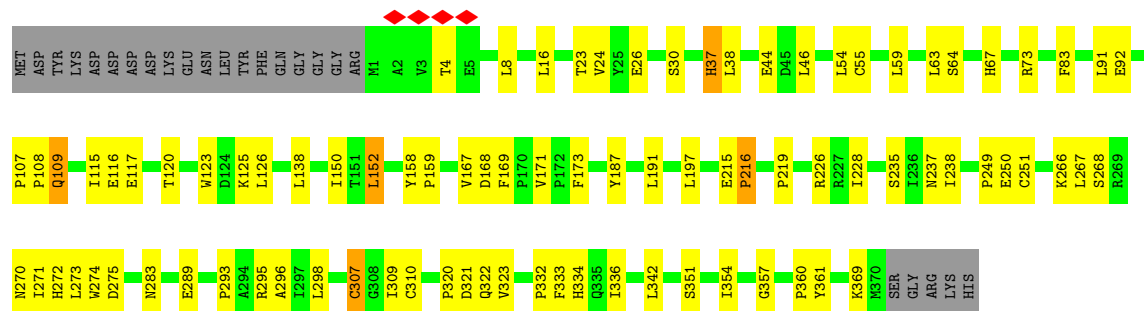
• Molecule 6: Fanconi anemia group G protein





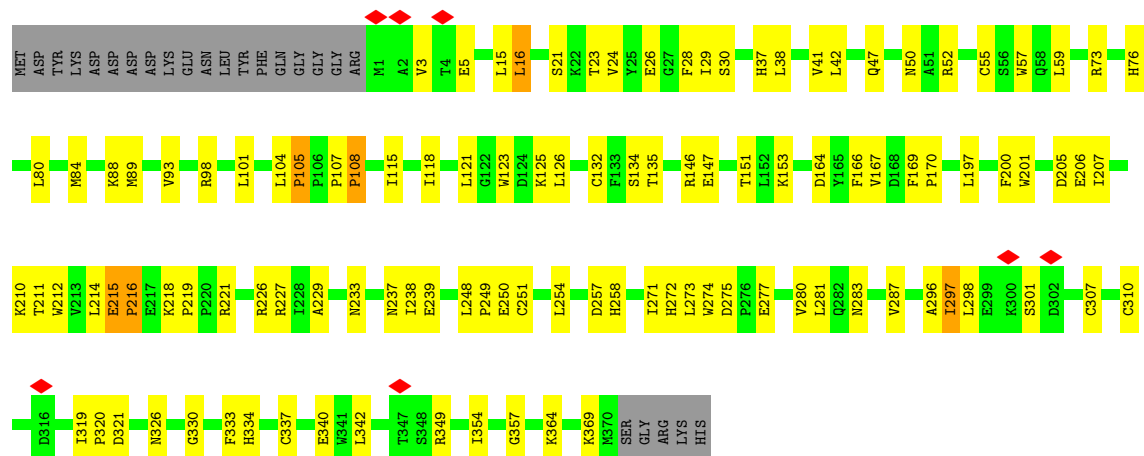
• Molecule 7: E3 ubiquitin-protein ligase FANCL

Chain L: 72% 21% 6%



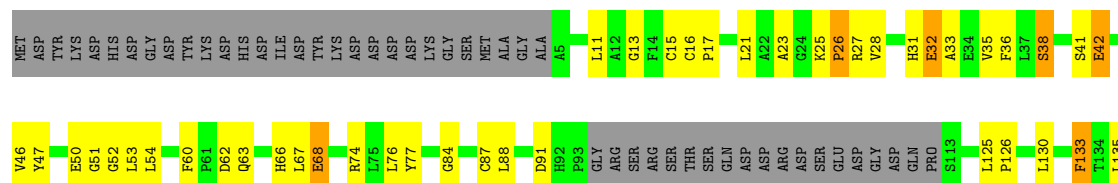
• Molecule 7: E3 ubiquitin-protein ligase FANCL

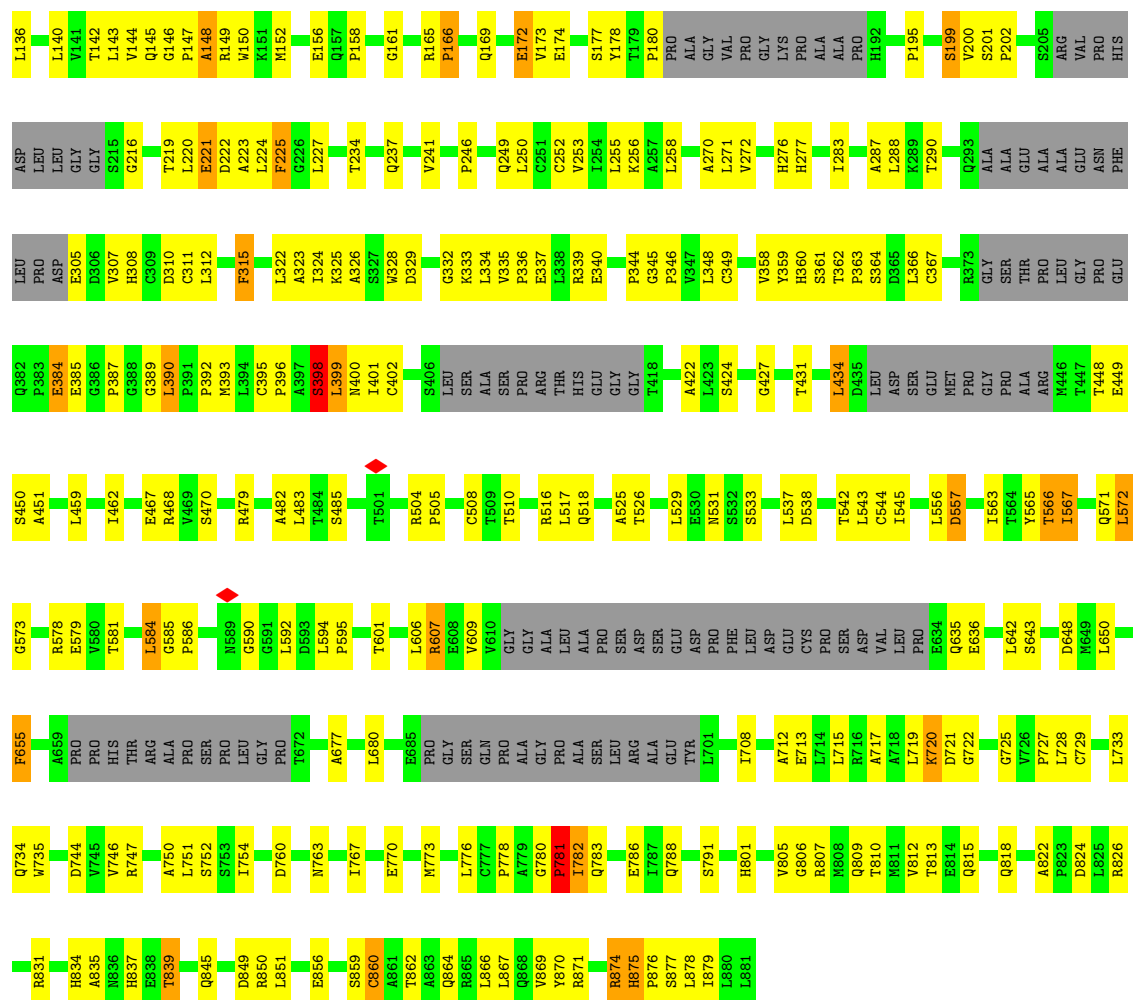
Chain M: 65% 27% 6%



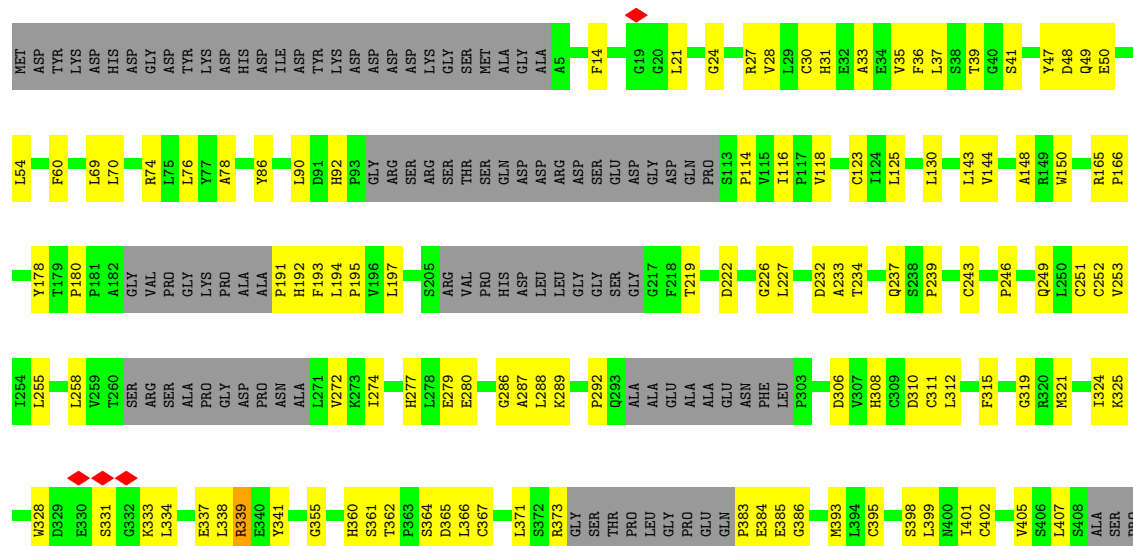
• Molecule 8: Fanconi anemia core complex-associated protein 100

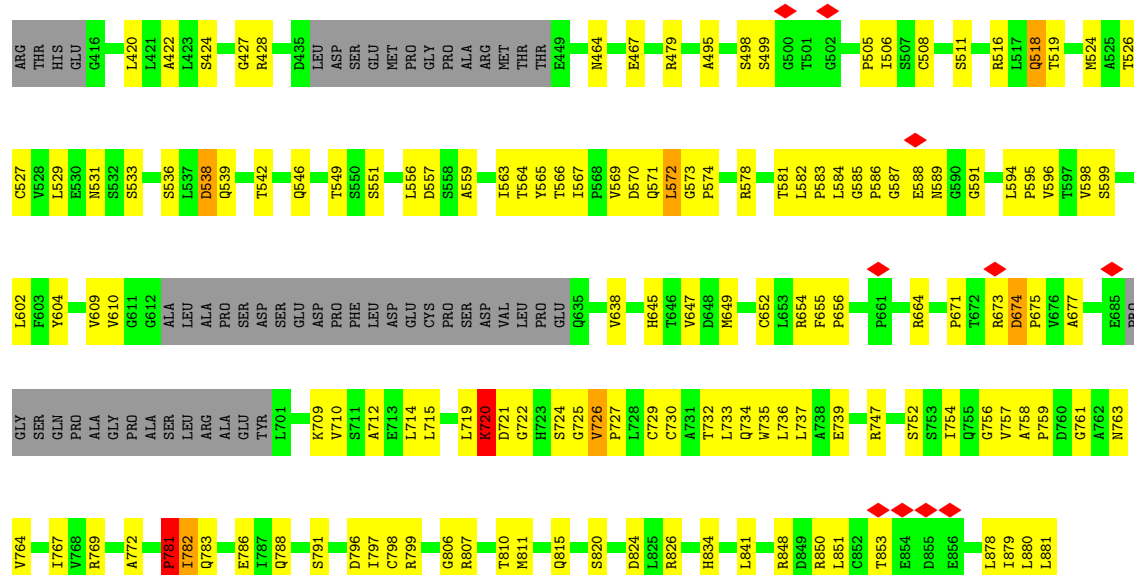
Chain P: 50% 29% 17%



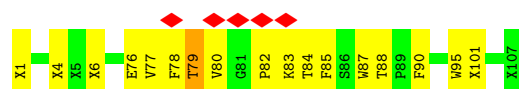


● Molecule 8: Fanconi anemia core complex-associated protein 100

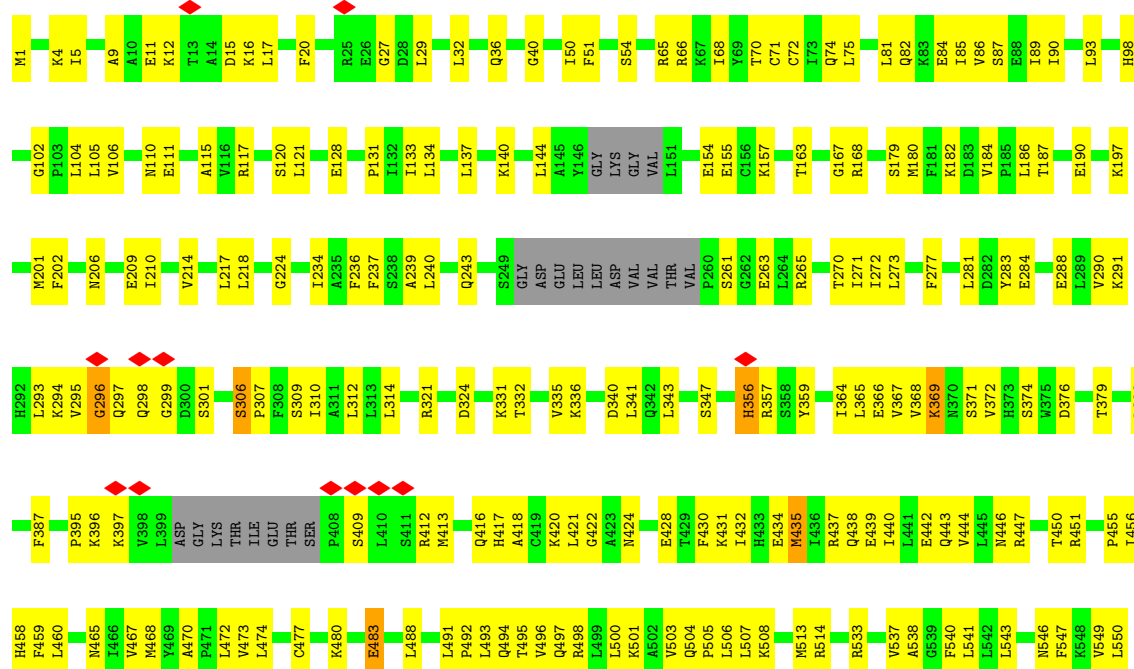


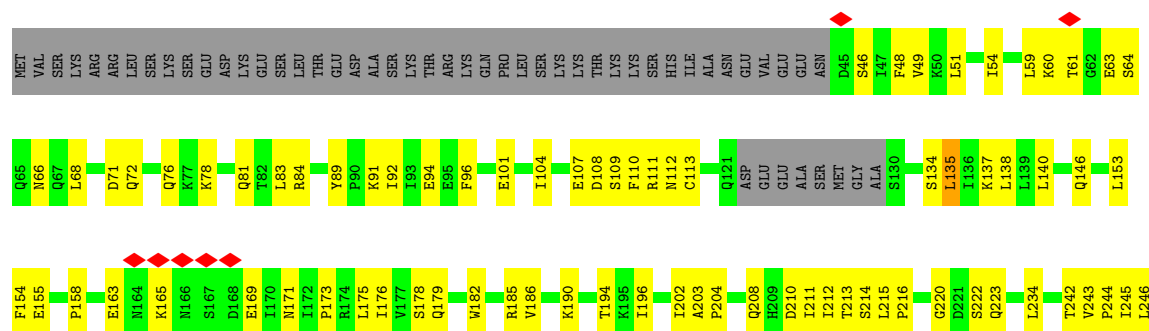
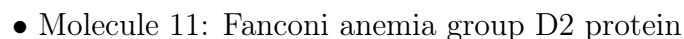


• Molecule 9: Fanconi anemia core complex-associated protein 20



• Molecule 10: Fanconi anemia, complementation group I







ALA	ASP	GLU	SER	GLU	ASP	ASP	MET	SER	SER	GLN	ALA	SER	LYS	SER	LYS	ALA	THR	GLU	GLY	GLU	GLU	ASP	GLU	VAL	SER	ALA	GLY	GLU	LYS	GLU	GLN	ASP	SER	ASP	GLU	SER	TYR	ASP	ASP	SER	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76111	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 ($e^-/\text{\AA}^2$)	65	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.071	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0055	Depositor
Map size (Å)	487.63455, 487.63455, 487.63455	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08847, 1.08847, 1.08847	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.40	0/9605	0.55	2/13008 (0.0%)
1	S	0.37	0/10153	0.43	0/13749
2	B	0.82	9/5707 (0.2%)	0.90	4/7686 (0.1%)
2	O	0.49	0/5701	0.69	1/7686 (0.0%)
3	C	0.79	12/4497 (0.3%)	0.79	2/6103 (0.0%)
4	E	0.62	4/3274 (0.1%)	0.73	1/4438 (0.0%)
5	F	0.66	3/2791 (0.1%)	0.73	0/3790
6	G	0.63	2/4568 (0.0%)	0.71	1/6215 (0.0%)
6	H	0.44	0/4293	0.60	2/5840 (0.0%)
7	L	0.73	3/3050 (0.1%)	0.80	2/4143 (0.0%)
7	M	0.48	0/3050	0.67	2/4143 (0.0%)
8	P	0.98	21/5697 (0.4%)	1.01	11/7752 (0.1%)
8	Q	0.46	0/5737	0.67	0/7810
9	W	0.34	0/202	0.44	0/281
10	U	0.42	0/9400	0.55	0/12676
11	V	0.42	0/9433	0.55	0/12760
All	All	0.57	54/87158 (0.1%)	0.67	28/118080 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9
1	S	0	4
2	B	0	8
2	O	0	4
3	C	0	2
4	E	0	1
6	G	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	H	0	3
7	L	0	2
7	M	0	2
8	P	0	12
8	Q	0	6
10	U	0	4
11	V	0	7
All	All	0	66

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	P	68	GLU	CD-OE1	9.56	1.36	1.25
8	P	68	GLU	CD-OE2	8.94	1.35	1.25
8	P	222	ASP	CG-OD1	8.80	1.45	1.25
3	C	201	GLU	CD-OE2	8.49	1.34	1.25
3	C	225	GLU	CD-OE2	8.34	1.34	1.25

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	P	359	TYR	CB-CG-CD2	-7.40	116.56	121.00
3	C	245	ARG	NE-CZ-NH2	-7.01	116.79	120.30
8	P	315	PHE	CB-CA-C	-6.79	96.82	110.40
2	B	324	LYS	CB-CG-CD	6.61	128.80	111.60
8	P	874	ARG	NE-CZ-NH1	6.46	123.53	120.30

There are no chirality outliers.

5 of 66 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	138	THR	Peptide
1	A	313	THR	Peptide
1	A	484	GLU	Peptide
1	A	824	CYS	Peptide
1	A	899	PRO	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9402	9487	9431	310	0
1	S	9933	10028	9969	345	0
2	B	5605	5790	5768	186	0
2	O	5594	5759	5740	182	0
3	C	4396	4442	4427	128	0
4	E	3224	3390	3384	107	0
5	F	2726	2740	2729	66	0
6	G	4483	4537	4523	126	0
6	H	4216	4288	4273	105	0
7	L	2974	2977	2972	60	0
7	M	2974	2977	2972	97	0
8	P	5598	5681	5652	227	0
8	Q	5631	5724	5694	191	0
9	W	271	242	195	16	0
10	U	9256	9626	9595	315	0
11	V	9258	9475	9422	329	0
12	G	1	0	0	0	0
12	L	2	0	0	0	0
12	M	2	0	0	0	0
All	All	85546	87163	86746	2627	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 15.

The worst 5 of 2627 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)
11:V:586:ALA:HB1	11:V:645:ASP:CB	1.70	1.20
11:V:586:ALA:CB	11:V:645:ASP:HB2	1.76	1.15
11:V:637:ASN:O	11:V:641:HIS:ND1	1.85	1.09
2:B:362:LEU:O	8:P:468:ARG:NH2	1.94	1.01
10:U:261:SER:O	10:U:265:ARG:HG2	1.62	0.99

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1160/1477 (78%)	1066 (92%)	86 (7%)	8 (1%)	22	62
1	S	1224/1477 (83%)	1126 (92%)	98 (8%)	0	100	100
2	B	685/884 (78%)	595 (87%)	75 (11%)	15 (2%)	6	38
2	O	685/884 (78%)	592 (86%)	84 (12%)	9 (1%)	12	48
3	C	546/583 (94%)	496 (91%)	48 (9%)	2 (0%)	34	72
4	E	411/555 (74%)	400 (97%)	9 (2%)	2 (0%)	29	68
5	F	336/399 (84%)	316 (94%)	20 (6%)	0	100	100
6	G	567/641 (88%)	514 (91%)	52 (9%)	1 (0%)	47	80
6	H	532/641 (83%)	491 (92%)	40 (8%)	1 (0%)	47	80
7	L	368/394 (93%)	334 (91%)	33 (9%)	1 (0%)	41	76
7	M	368/394 (93%)	333 (90%)	32 (9%)	3 (1%)	19	60
8	P	726/906 (80%)	626 (86%)	80 (11%)	20 (3%)	5	33
8	Q	732/906 (81%)	644 (88%)	74 (10%)	14 (2%)	8	41
9	W	21/39 (54%)	13 (62%)	8 (38%)	0	100	100
10	U	1150/1328 (87%)	1056 (92%)	88 (8%)	6 (0%)	29	68
11	V	1131/1451 (78%)	1060 (94%)	65 (6%)	6 (0%)	29	68
All	All	10642/12959 (82%)	9662 (91%)	892 (8%)	88 (1%)	24	60

5 of 88 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	754	CYS
2	B	148	LYS
2	B	324	LYS
4	E	353	PRO
2	O	147	VAL

5.3.2 Protein sidechains ⓘ

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	1034/1282 (81%)	1028 (99%)	6 (1%)	86	92
1	S	1092/1282 (85%)	1090 (100%)	2 (0%)	93	96
2	B	644/810 (80%)	640 (99%)	4 (1%)	86	92
2	O	641/810 (79%)	635 (99%)	6 (1%)	78	87
3	C	480/507 (95%)	477 (99%)	3 (1%)	86	92
4	E	358/467 (77%)	354 (99%)	4 (1%)	73	84
5	F	288/336 (86%)	287 (100%)	1 (0%)	92	95
6	G	483/538 (90%)	480 (99%)	3 (1%)	86	92
6	H	454/538 (84%)	451 (99%)	3 (1%)	84	90
7	L	334/354 (94%)	331 (99%)	3 (1%)	78	87
7	M	334/354 (94%)	333 (100%)	1 (0%)	92	95
8	P	627/749 (84%)	614 (98%)	13 (2%)	53	71
8	Q	630/749 (84%)	627 (100%)	3 (0%)	88	93
9	W	22/22 (100%)	21 (96%)	1 (4%)	27	54
10	U	1066/1204 (88%)	1052 (99%)	14 (1%)	69	82
11	V	1065/1324 (80%)	1049 (98%)	16 (2%)	65	80
All	All	9552/11326 (84%)	9469 (99%)	83 (1%)	79	87

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	U	435	MET
11	V	310	CYS
10	U	495	THR
10	U	976	ASP
11	V	436	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 163 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	1128	GLN
11	V	66	ASN
10	U	266	HIS
10	U	597	GLN
11	V	377	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	W	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	W	9:UNK	C	73:GLU	N	36.69
1	W	95:TRP	C	101:UNK	N	7.00

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23086. These allow visual inspection of the internal detail of the map and identification of artifacts.

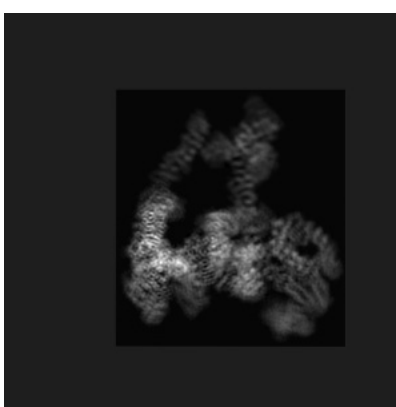
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

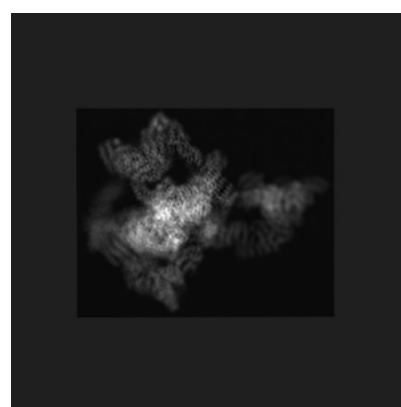
6.1.1 Primary map



X



Y



Z

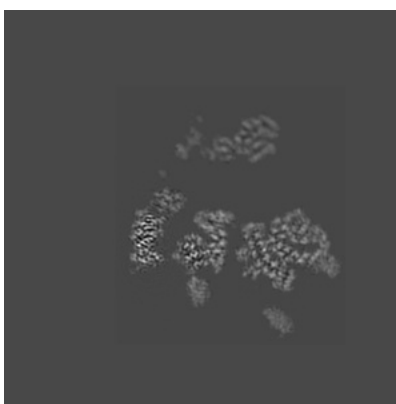
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

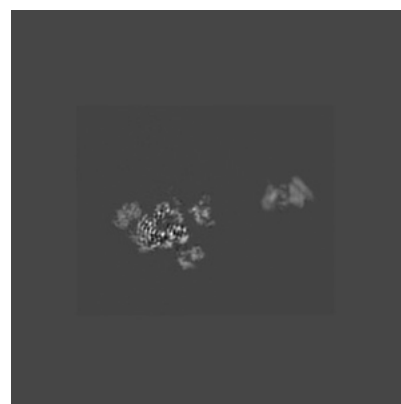
6.2.1 Primary map



X Index: 224



Y Index: 224



Z Index: 224

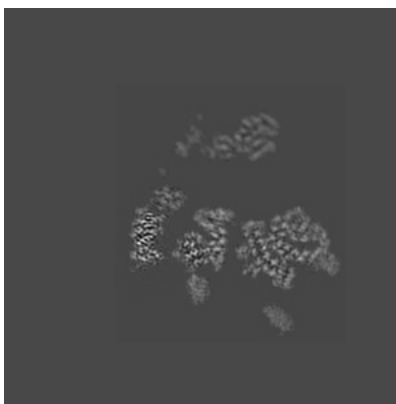
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

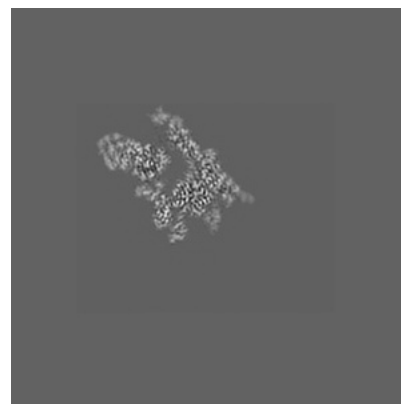
6.3.1 Primary map



X Index: 168



Y Index: 224



Z Index: 168

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

6.4 Orthogonal surface views [i](#)

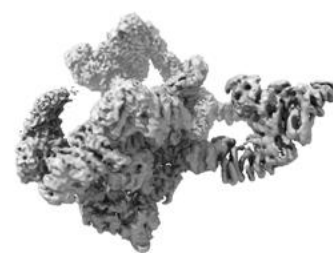
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

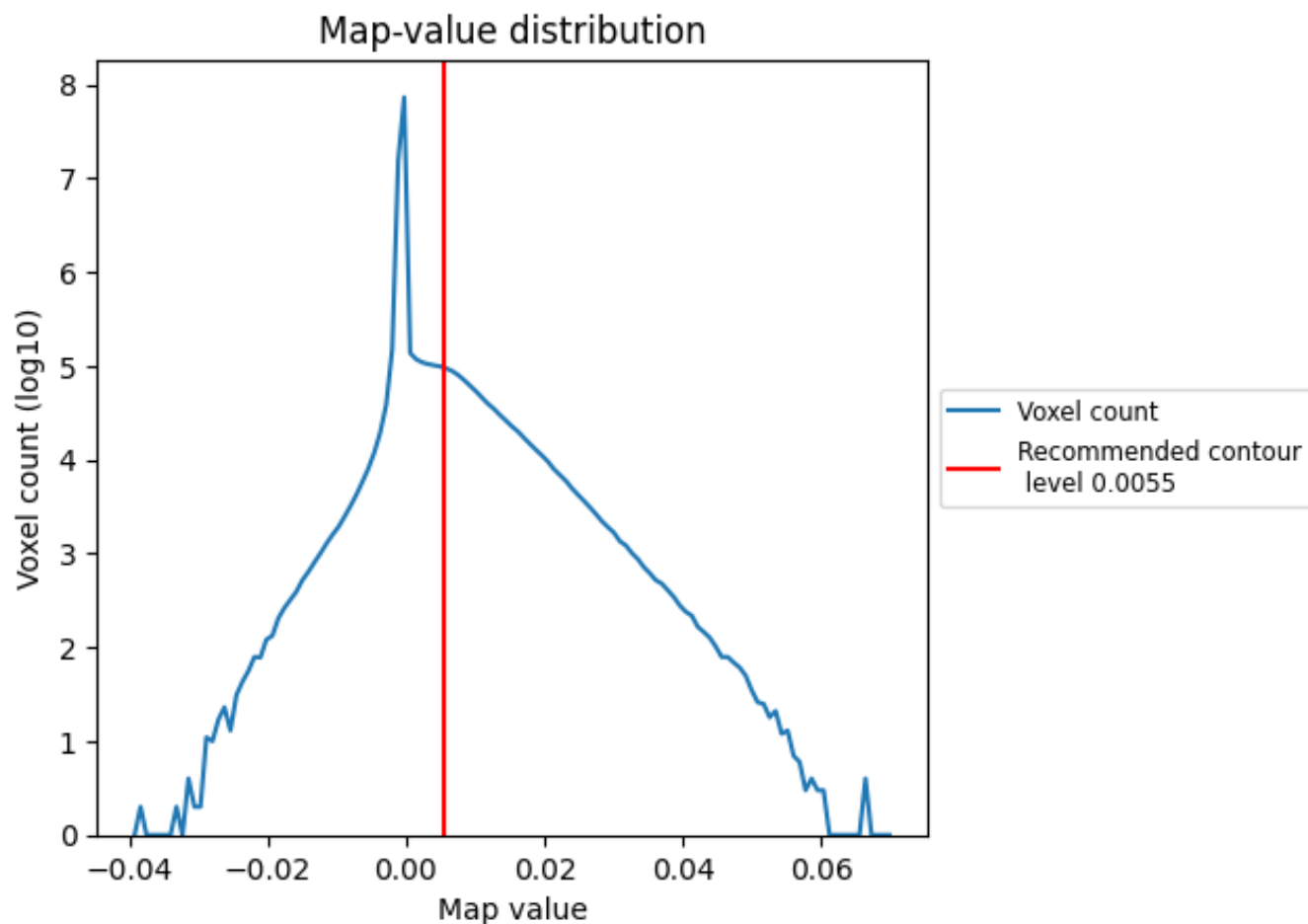
6.5 Mask visualisation

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

7 Map analysis [i](#)

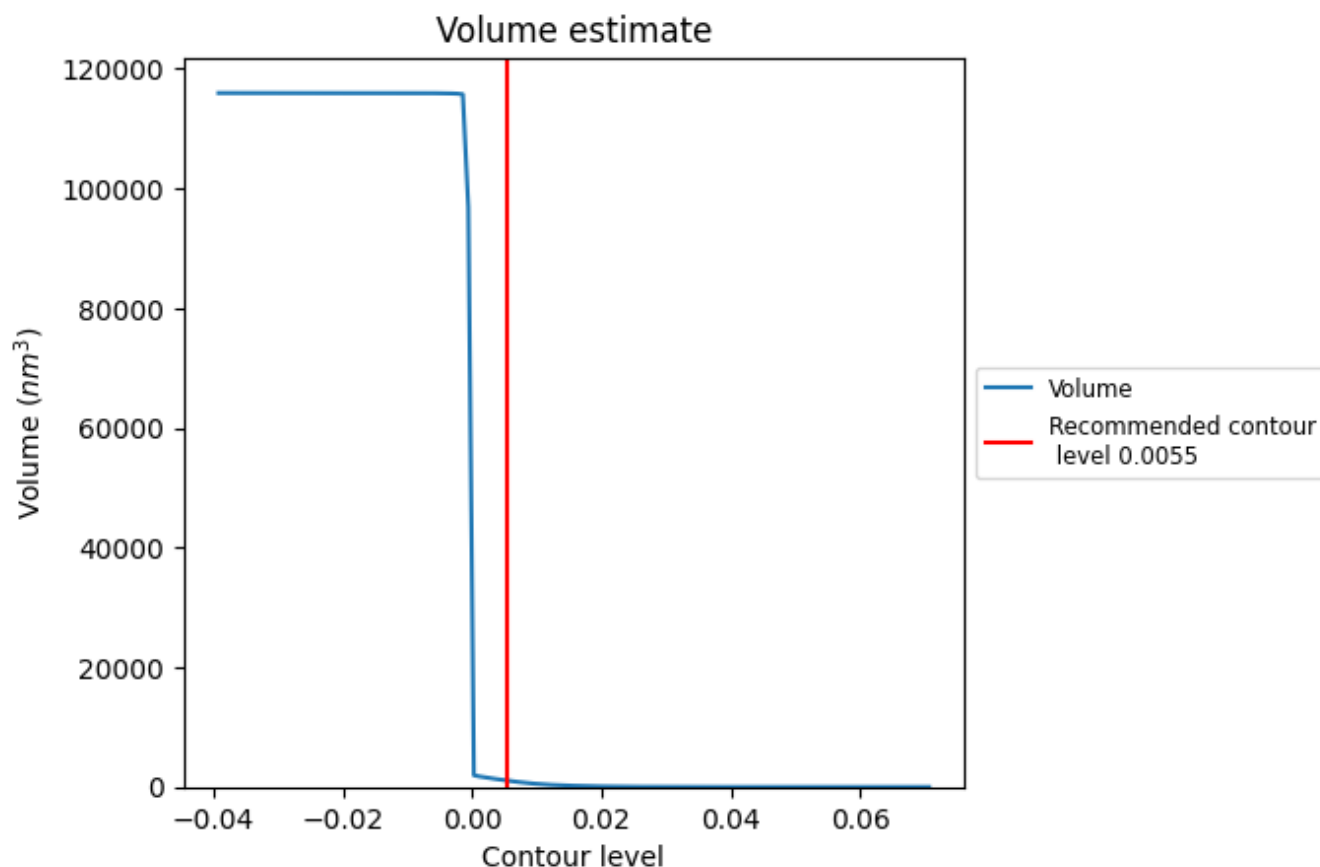
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

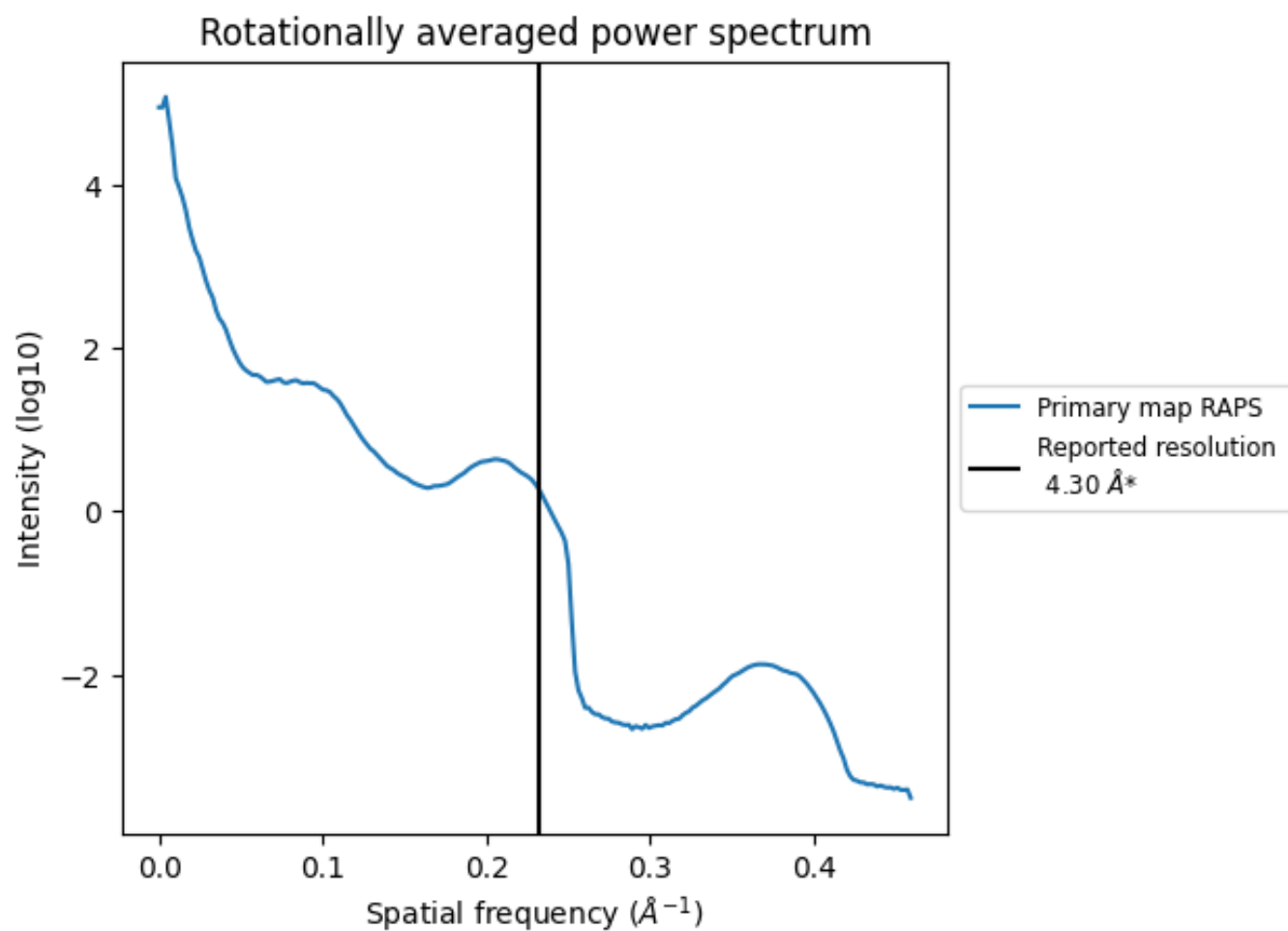
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1056 nm^3 ; this corresponds to an approximate mass of 954 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

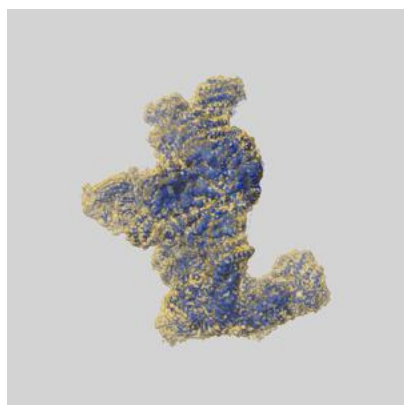
8 Fourier-Shell correlation

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

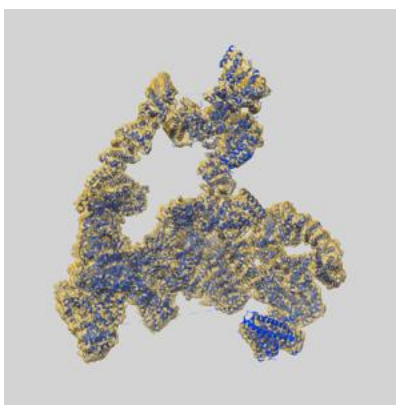
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23086 and PDB model 7KZQ. Per-residue inclusion information can be found in section 3 on page 14.

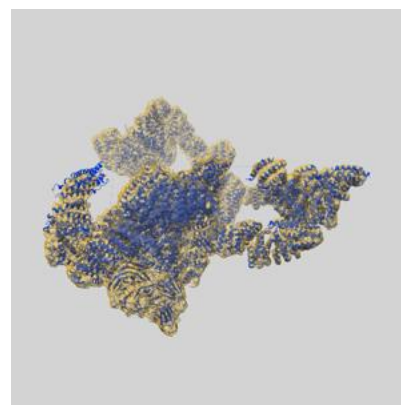
9.1 Map-model overlay [i](#)



X



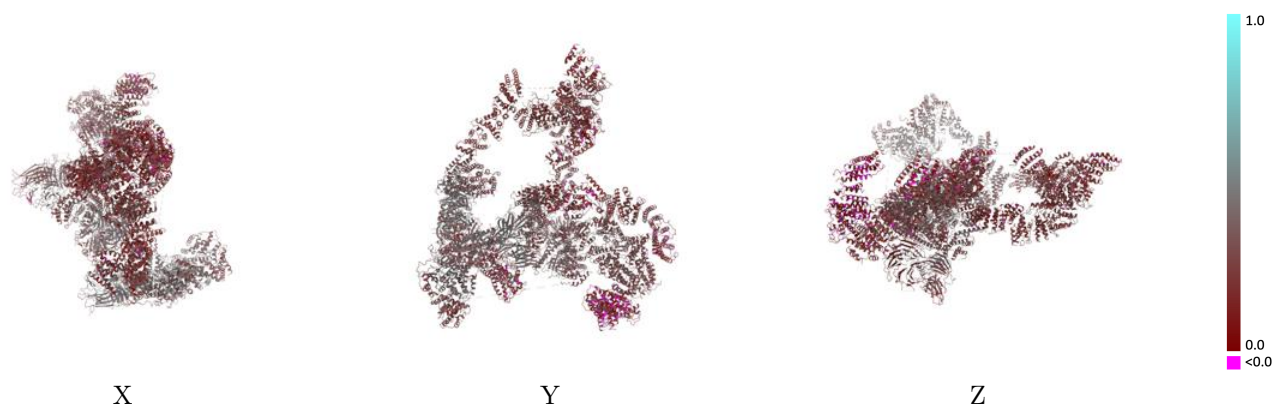
Y



Z

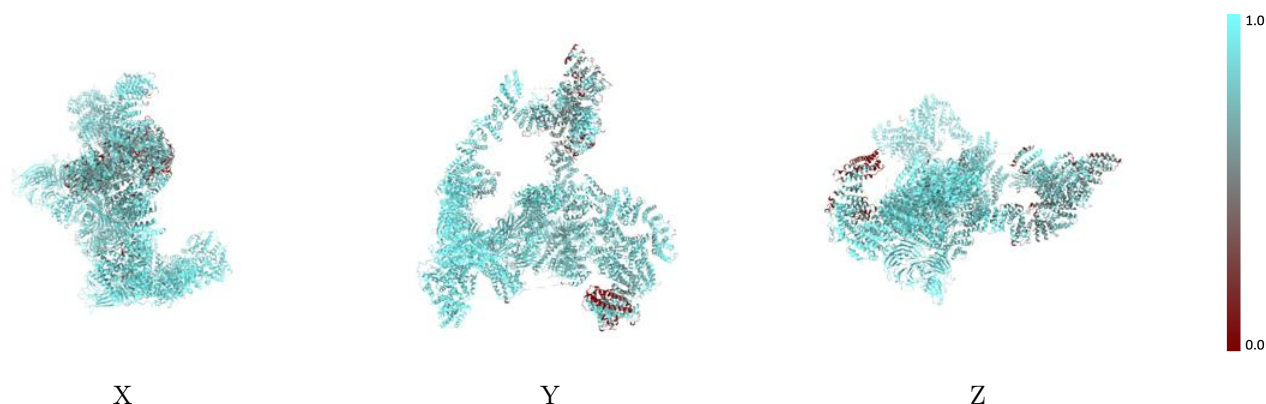
The images above show the 3D surface view of the map at the recommended contour level 0.0055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



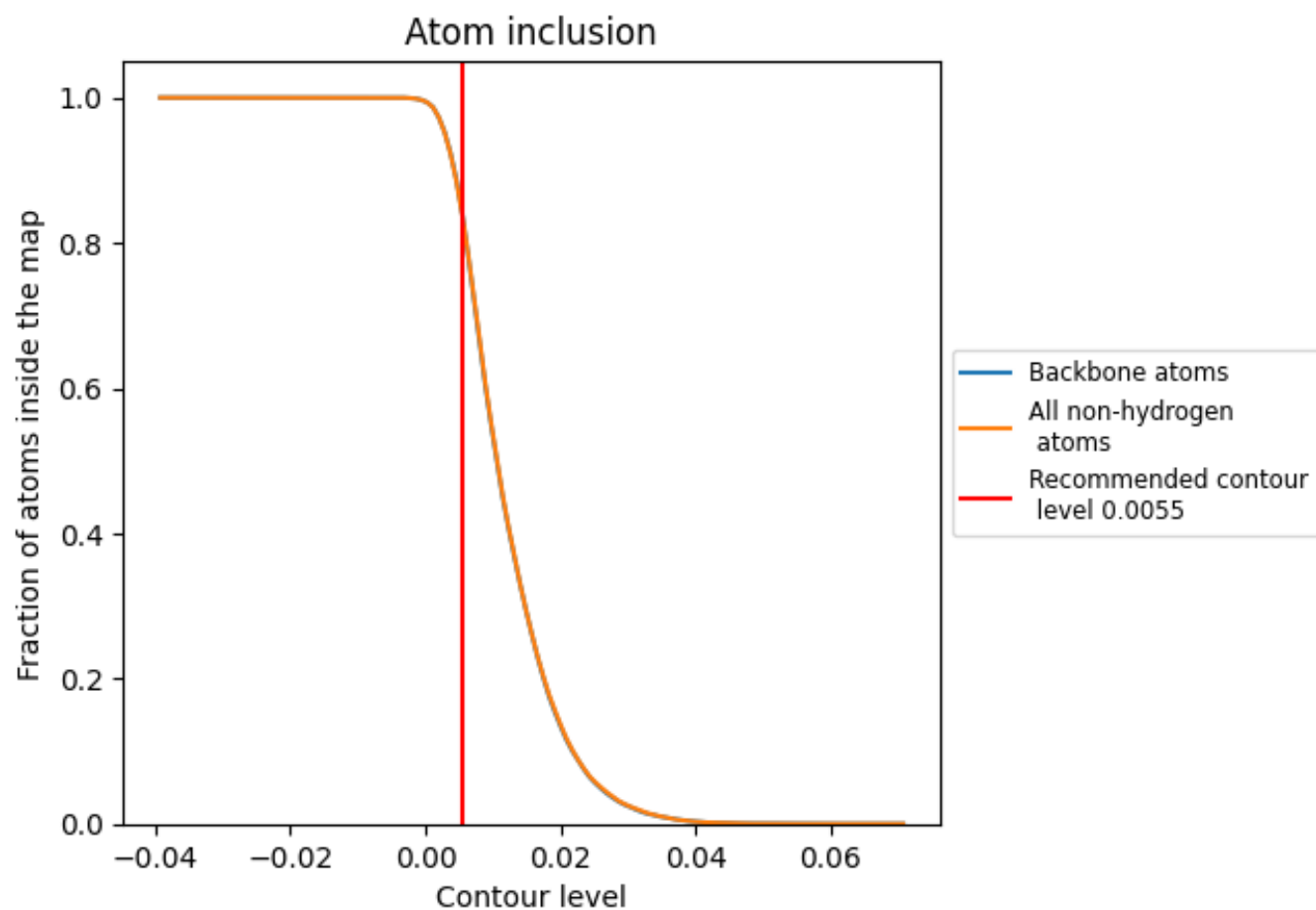
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.0055).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% 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 (0.0055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8365	<div><div></div></div> 0.2980
A	<div><div></div></div> 0.7386	<div><div></div></div> 0.2360
B	<div><div></div></div> 0.9209	<div><div></div></div> 0.3940
C	<div><div></div></div> 0.9506	<div><div></div></div> 0.3710
E	<div><div></div></div> 0.8730	<div><div></div></div> 0.3550
F	<div><div></div></div> 0.9475	<div><div></div></div> 0.3640
G	<div><div></div></div> 0.8809	<div><div></div></div> 0.3380
H	<div><div></div></div> 0.8484	<div><div></div></div> 0.2740
L	<div><div></div></div> 0.9367	<div><div></div></div> 0.3810
M	<div><div></div></div> 0.9007	<div><div></div></div> 0.3080
O	<div><div></div></div> 0.9103	<div><div></div></div> 0.3130
P	<div><div></div></div> 0.9402	<div><div></div></div> 0.4100
Q	<div><div></div></div> 0.9047	<div><div></div></div> 0.2980
S	<div><div></div></div> 0.7163	<div><div></div></div> 0.2390
U	<div><div></div></div> 0.8688	<div><div></div></div> 0.2570
V	<div><div></div></div> 0.7186	<div><div></div></div> 0.2130
W	<div><div></div></div> 0.7361	<div><div></div></div> 0.2920

