



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 07:52 AM UTC

PDB ID : 7CWL / pdb_00007cwl
EMDB ID : EMD-30482
Title : SARS-CoV-2 spike protein and P17 fab complex with one RBD in close state
Authors : Wang, X.; Wang, N.
Deposited on : 2020-08-29
Resolution : 3.80 Å (reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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:

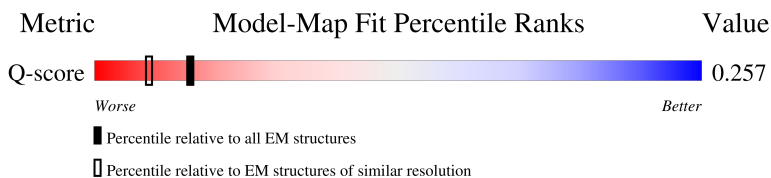
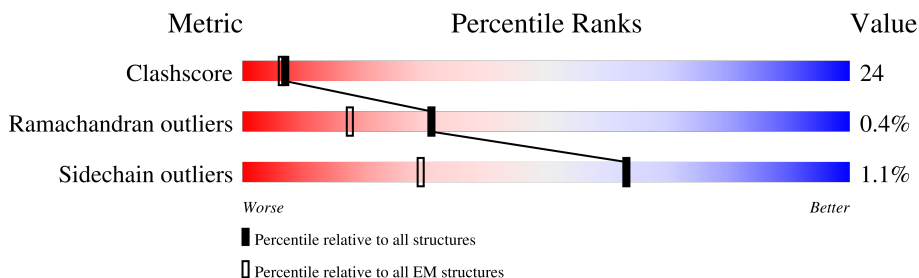
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 3.80 Å.

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



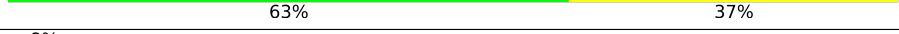

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	1273	<p>52% 32% 16%</p>
1	B	1273	<p>52% 31% 16%</p>
1	C	1273	<p>55% 29% 16%</p>
2	G	120	<p>63% 37%</p>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	120	 63% 37%
2	I	120	 52%  63% 37%
3	J	108	 8% 80% 20%
3	K	108	 63%  79% 20%
3	L	108	 81% 19%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 30638 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1073	Total 8358	C 5334	N 1396	O 1589	S 39	0	0
1	B	1070	Total 8332	C 5315	N 1393	O 1585	S 39	0	0
1	C	1074	Total 8372	C 5342	N 1399	O 1592	S 39	0	0

- Molecule 2 is a protein called Fab P17 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	120	Total 918	C 574	N 165	O 175	S 4	0	0
2	H	120	Total 918	C 574	N 165	O 175	S 4	0	0
2	I	120	Total 918	C 574	N 165	O 175	S 4	0	0

- Molecule 3 is a protein called Fab P17 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L	108	Total 814	C 510	N 137	O 165	S 2	0	0
3	J	108	Total 817	C 511	N 137	O 167	S 2	0	0
3	K	107	Total 813	C 509	N 136	O 166	S 2	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

Continued on next page...

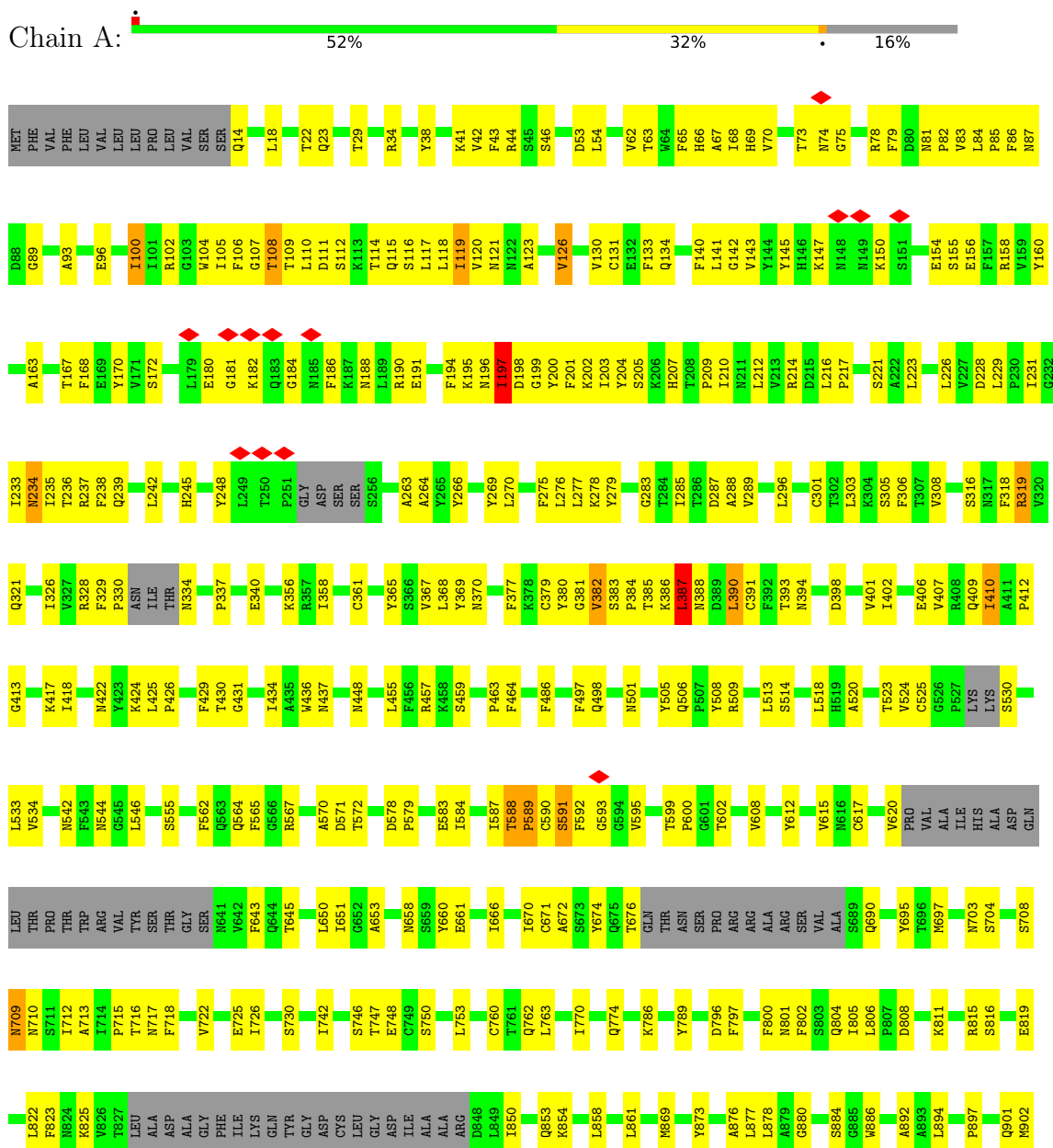
Continued from previous page...

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

3 Residue-property plots

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: Spike glycoprotein

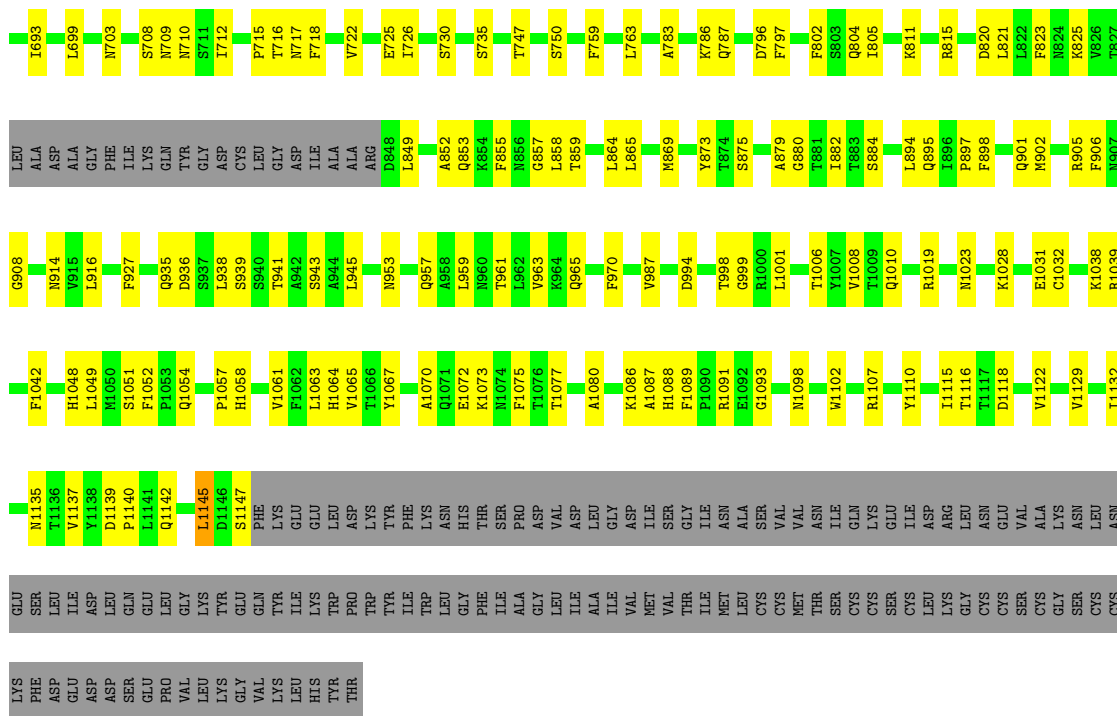


A903	R1019	I1115	ALA	CYS
Y904	R1028	I1116	LYS	GLY
R905	K1029	N1119	ASN	SER
F906	S1030	V1122	LEU	CYS
N907	E1031	S1123	ASN	LYS
G908	L1034	N1135	GLU	PHE
Q913	L1038	T1136	LEU	ASP
N914	R1039	V1137	ASP	ASP
Y915	F1042	Y1138	GLN	ASP
L916	L1049	D1139	LEU	SER
Y917	Q1054	P1140	GLU	GLU
L922	S1055	L1145	LEU	PRO
F927	A1056	D1146	GLY	VAL
N928	H1058	S1147	LYS	V16
Q935	P1057	PHE	TYR	N17
L939	H1064	LYS	GLU	L18
T941	V1065	GLU	LYS	L19
L945	H1066	TYR	TRP	T20
L959	V1067	LEU	LEU	R21
N960	V1068	LEU	LYS	T22
T961	P1069	LEU	TRP	L24
L962	A1070	LEU	PRO	T29
N963	Q1071	LEU	TRP	LYS
F970	E1072	ALA	TYR	PHE
N980	K1073	GLY	ILE	R34
F986	F1075	ASP	LEU	G35
A989	T1076	ASP	LEU	V36
E990	T1077	VAL	ALA	Y37
Y991	K1086	ILE	ILE	Y38
D994	A1087	THR	VAL	PRO
L996	H1088	ILE	ASP	ASP
L997	F1089	MET	LYS	ASP
G999	P1090	LEU	VAL	VAL
R1000	S1097	CYS	ALA	R44
T1006	N1098	CYS	SER	S45
Y1007	G1099	CYS	THR	S46
V1008	W1102	CYS	CYS	V47
T1009	Q1106	CYS	GLY	L48
Q1010	R1107	CYS	ILE	H49
Q1011	M1108	CYS	MET	S50
A1015	F1109	CYS	ALA	D63
A1016	Y1110	CYS	VAL	L64
	E1111	CYS	VAL	F65
	I1114	CYS	ASN	V62
		CYS	THR	I67
		CYS	ILE	I68
		CYS	GLN	H69
		CYS	LYS	V70
		CYS	LEU	T73
		CYS	LEU	N74
		CYS	GLY	N75
		CYS	ASN	K150
		CYS	VAL	

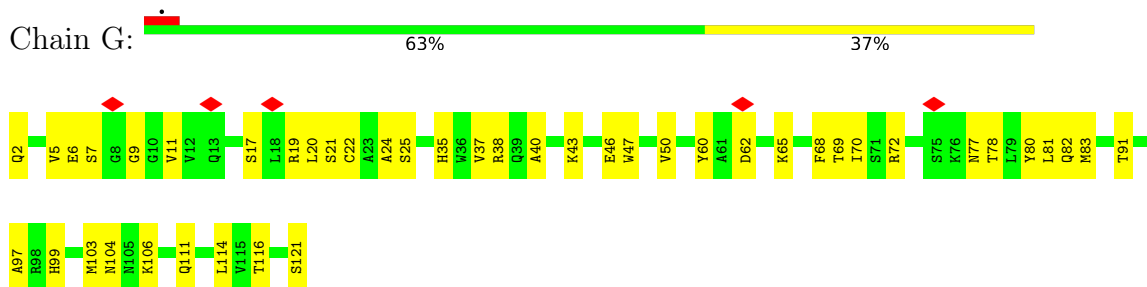
● Molecule 1: Spike glycoprotein



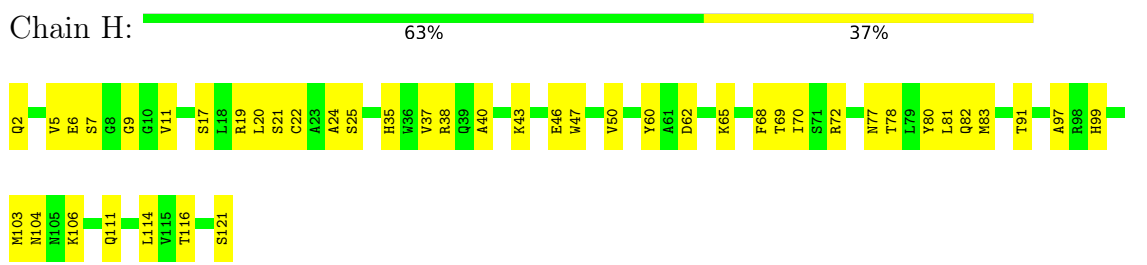
MET	N81	E154	L223	L296	M422	L552	ARG	I726
PHE	P82	E155	E224	L297	Y423	T553	VAL	S730
VAL	V83	E156	P225	S297	E554	T554	TYR	S733
PHE	L84	E157	L226	E298	K424	S555	SER	K734
LEU	P85	F158	V227	T299	G431	K558	THR	T735
VAL	F86	R159	D228	F306	M436	F559	GLY	S736
SER	N87	V159	L229	T307	M437	F562	SER	V737
LEU	D88	I160	P230	V308	M448	Q563	N641	D737
LEU	G89	S162	G232	T315	M455	Q564	N642	M740
PRO	A93	A163	I233	N317	L456	F565	T645	S746
LEU	E96	N164	H234	F318	F456	R567	G648	T747
SER	Q14	T167	I235	R319	R457	D568	C649	T748
SER	C15	F168	T236	V320	K458	L569	L650	C749
GLY	V16	E169	R237	F323	S459	D570	L653	S750
LYS	N17	G170	Q239	T323	P463	T572	A653	F759
GLU	L18	V171	L242	E324	F486	T573	V656	L763
VAL	T19	S172	L245	S325	F497	P579	N657	D775
VAL	T20	L176	H246	I326	F498	Q580	N658	D775
LYS	R21	E180	R247	V327	Q498	L584	G669	A783
TRP	Q23	G181	S247	R328	M501	T588	T676	K786
PRO	L24	K182	Y248	N331	Y505	P589	GLN	Q787
TRP	L24	L110	L249	ILE	Q506	C590	THR	A804
LYS	T29	D111	L250	THR	P507	F592	ASN	D796
TYR	T29	S112	T250	ASN	S508	G593	SER	F797
ILE	PHE	K113	G184	ASP	Y508	G594	ARG	F802
LEU	LEU	T114	N185	GLY	R509	G594	ALA	S803
GLY	LEU	Q115	F186	SER	L513	V597	ALA	Q804
LEU	LEU	S116	K187	SER	L518	T602	ARG	I805
LEU	LEU	L117	N188	SER	P521	N606	VAL	K811
LEU	LEU	L118	L189	SER	A522	Y612	ALA	R815
ALA	PRO	L119	R190	N360	V524	V615	ALA	D820
GLY	ASP	V120	E191	N365	T531	M616	ILE	L821
LEU	ASP	VAL	E191	S366	N532	C617	ASP	L822
LEU	ASP	VAL	F194	Y367	L533	C617	ASP	F823
LEU	ASP	VAL	N196	L368	N534	V620	ALA	N824
LEU	ASP	VAL	K195	T369	K535	PR0	ALA	K825
VAL	ASP	VAL	N197	N370	N536	VAL	ILE	N826
VAL	ASP	VAL	D198	N375	S375	ALA	ILE	T827
VAL	ASP	VAL	D199	C391	C538	ALA	THR	LEU
VAL	ASP	VAL	Y200	F392	V539	ILE	THR	ALA
VAL	ASP	VAL	F201	T393	N540	HIS	THR	ASP
VAL	ASP	VAL	K202	N394	F541	ALA	THR	ASP
VAL	ASP	VAL	Y204	N394	N542	ASP	THR	ASP
VAL	ASP	VAL	S205	D398	F543	GLN	THR	ASP
VAL	ASP	VAL	P209	V401	L546	LEU	THR	ASP
VAL	ASP	VAL	I210	K417	G550	THR	THR	ASP
VAL	ASP	VAL	R211	I418	V551	TRP	TRP	ASP
VAL	ASP	VAL	L212					
VAL	ASP	VAL	V213					
VAL	ASP	VAL	R214					
VAL	ASP	VAL	D215					
VAL	ASP	VAL	L216					
VAL	ASP	VAL	P217					
VAL	ASP	VAL	S221					
VAL	ASP	VAL	A222					



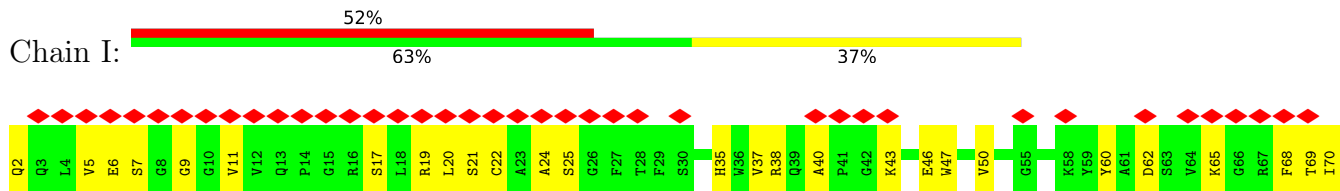
• Molecule 2: Fab P17 heavy chain

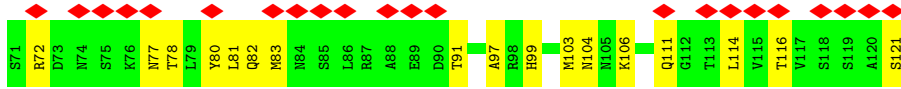


• Molecule 2: Fab P17 heavy chain

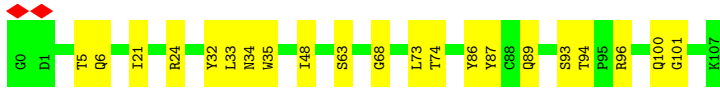
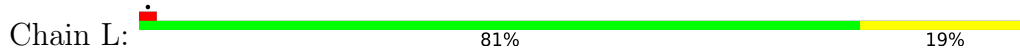


• Molecule 2: Fab P17 heavy chain

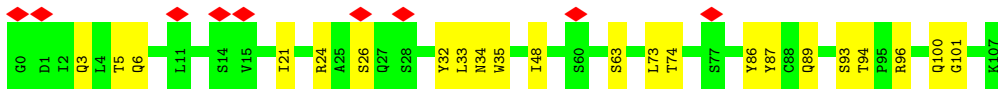
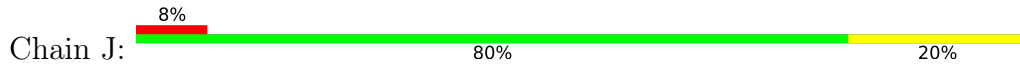




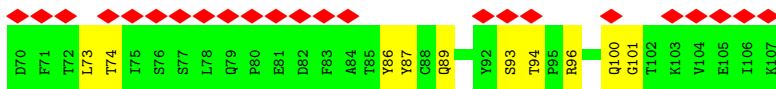
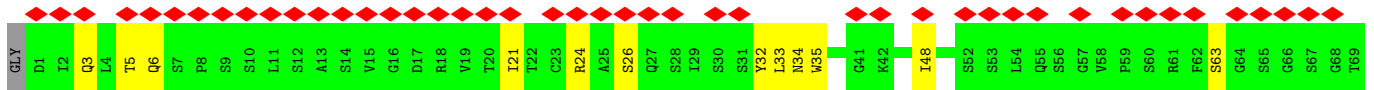
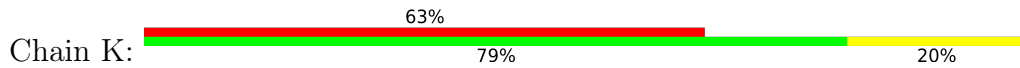
• Molecule 3: Fab P17 light chain



• Molecule 3: Fab P17 light chain



• Molecule 3: Fab P17 light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98932	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00502	Depositor
Map size (\AA)	416.0, 416.0, 416.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	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: 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	0.59	2/8549 (0.0%)	0.80	6/11634 (0.1%)
1	B	0.53	0/8521	0.76	8/11596 (0.1%)
1	C	0.47	0/8563	0.69	5/11653 (0.0%)
2	G	0.32	0/937	0.64	0/1269
2	H	0.32	0/937	0.64	0/1269
2	I	0.32	0/937	0.64	0/1269
3	J	0.33	0/834	0.63	0/1131
3	K	0.33	0/830	0.63	0/1126
3	L	0.33	0/831	0.63	0/1127
All	All	0.51	2/30939 (0.0%)	0.73	19/42074 (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	2
1	B	0	5
1	C	0	4
2	G	0	1
2	H	0	1
2	I	0	1
All	All	0	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	589	PRO	N-CA	21.25	1.70	1.47
1	A	588	THR	C-N	9.98	1.45	1.33

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	588	THR	CA-C-N	19.20	139.52	120.52
1	A	588	THR	C-N-CA	19.20	139.52	120.52
1	A	100	ILE	N-CA-C	-10.80	102.83	113.20
1	B	100	ILE	N-CA-C	-10.78	102.85	113.20
1	C	301	CYS	N-CA-C	-8.72	102.42	113.23

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1145	LEU	Peptide
1	A	248	TYR	Peptide
1	B	248	TYR	Peptide
1	B	278	LYS	Mainchain
1	B	391	CYS	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	8358	0	8130	514	0
1	B	8332	0	8105	489	0
1	C	8372	0	8149	470	0
2	G	918	0	885	27	0
2	H	918	0	885	26	0
2	I	918	0	885	27	0
3	J	817	0	800	16	0
3	K	813	0	797	16	0
3	L	814	0	798	16	0
4	A	126	0	117	7	0
4	B	126	0	117	1	0
4	C	126	0	117	4	0
All	All	30638	0	29785	1450	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 24.

The worst 5 of 1450 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:276:LEU:HD11	1:C:306:PHE:CE1	1.32	1.61
1:A:63:THR:HG21	1:A:65:PHE:CZ	1.36	1.60
1:A:22:THR:CG2	1:A:78:ARG:HD2	1.28	1.54
1:A:63:THR:CG2	1:A:65:PHE:CZ	1.85	1.54
1:C:296:LEU:HD12	1:C:608:VAL:CG1	1.40	1.52

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	1059/1273 (83%)	971 (92%)	79 (8%)	9 (1%)	16	48
1	B	1056/1273 (83%)	977 (92%)	76 (7%)	3 (0%)	36	67
1	C	1060/1273 (83%)	984 (93%)	72 (7%)	4 (0%)	30	62
2	G	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
2	H	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
2	I	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
3	J	106/108 (98%)	97 (92%)	9 (8%)	0	100	100
3	K	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
3	L	106/108 (98%)	97 (92%)	9 (8%)	0	100	100
All	All	3846/4503 (85%)	3538 (92%)	292 (8%)	16 (0%)	31	62

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	LEU
1	A	197	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	198	ASP
1	B	197	ILE
1	B	198	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	929/1112 (84%)	916 (99%)	13 (1%)	59	70
1	B	926/1112 (83%)	910 (98%)	16 (2%)	53	67
1	C	932/1112 (84%)	925 (99%)	7 (1%)	73	76
2	G	96/98 (98%)	96 (100%)	0	100	100
2	H	96/98 (98%)	96 (100%)	0	100	100
2	I	96/98 (98%)	96 (100%)	0	100	100
3	J	93/93 (100%)	93 (100%)	0	100	100
3	K	93/93 (100%)	93 (100%)	0	100	100
3	L	92/93 (99%)	92 (100%)	0	100	100
All	All	3353/3909 (86%)	3317 (99%)	36 (1%)	63	73

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	984	LEU
1	C	708	SER
1	C	68	ILE
1	C	524	VAL
1	A	709	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	784	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	K	90	GLN
1	C	148	ASN
3	K	79	GLN
3	L	38	GLN

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](#)

27 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	B	1303	1	14,14,15	0.27	0	17,19,21	0.63	0
4	NAG	A	1303	1	14,14,15	0.28	0	17,19,21	0.60	0
4	NAG	B	1304	1	14,14,15	0.27	0	17,19,21	0.63	0
4	NAG	C	1309	1	14,14,15	0.26	0	17,19,21	0.54	0
4	NAG	B	1306	1	14,14,15	0.27	0	17,19,21	0.62	0
4	NAG	A	1307	1	14,14,15	0.28	0	17,19,21	0.63	0
4	NAG	A	1306	1	14,14,15	0.26	0	17,19,21	0.65	0
4	NAG	B	1307	1	14,14,15	0.27	0	17,19,21	0.65	0
4	NAG	B	1309	1	14,14,15	0.28	0	17,19,21	0.66	0
4	NAG	C	1301	1	14,14,15	0.28	0	17,19,21	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1301	1	14,14,15	0.27	0	17,19,21	0.61	0
4	NAG	C	1302	1	14,14,15	0.27	0	17,19,21	0.64	0
4	NAG	B	1308	1	14,14,15	0.30	0	17,19,21	0.67	0
4	NAG	B	1305	1	14,14,15	0.27	0	17,19,21	0.54	0
4	NAG	A	1302	1	14,14,15	0.30	0	17,19,21	0.68	0
4	NAG	B	1302	1	14,14,15	0.28	0	17,19,21	0.57	0
4	NAG	C	1308	1	14,14,15	0.26	0	17,19,21	0.66	0
4	NAG	A	1305	1	14,14,15	0.27	0	17,19,21	0.70	0
4	NAG	C	1303	1	14,14,15	0.29	0	17,19,21	0.64	0
4	NAG	C	1305	1	14,14,15	0.26	0	17,19,21	0.68	0
4	NAG	B	1301	1	14,14,15	0.35	0	17,19,21	0.75	0
4	NAG	C	1306	1	14,14,15	0.28	0	17,19,21	0.62	0
4	NAG	C	1307	1	14,14,15	0.27	0	17,19,21	0.66	0
4	NAG	A	1309	1	14,14,15	0.27	0	17,19,21	0.61	0
4	NAG	A	1308	1	14,14,15	0.30	0	17,19,21	0.70	0
4	NAG	C	1304	1	14,14,15	0.28	0	17,19,21	0.66	0
4	NAG	A	1304	1	14,14,15	0.27	0	17,19,21	0.61	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1303	1	-	4/6/23/26	0/1/1/1
4	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1309	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1307	1	-	3/6/23/26	0/1/1/1
4	NAG	A	1306	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1307	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1309	1	-	3/6/23/26	0/1/1/1
4	NAG	C	1301	1	-	3/6/23/26	0/1/1/1
4	NAG	A	1301	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1302	1	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1303	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1306	1	-	1/6/23/26	0/1/1/1
4	NAG	C	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1309	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1304	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1301	NAG	C3-C2-N2-C7
4	A	1301	NAG	C8-C7-N2-C2
4	A	1301	NAG	O7-C7-N2-C2
4	A	1303	NAG	C1-C2-N2-C7
4	A	1303	NAG	C8-C7-N2-C2

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1307	NAG	1	0
4	A	1306	NAG	4	0
4	C	1301	NAG	1	0
4	A	1301	NAG	1	0
4	C	1308	NAG	2	0
4	A	1305	NAG	1	0
4	C	1303	NAG	1	0
4	B	1301	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

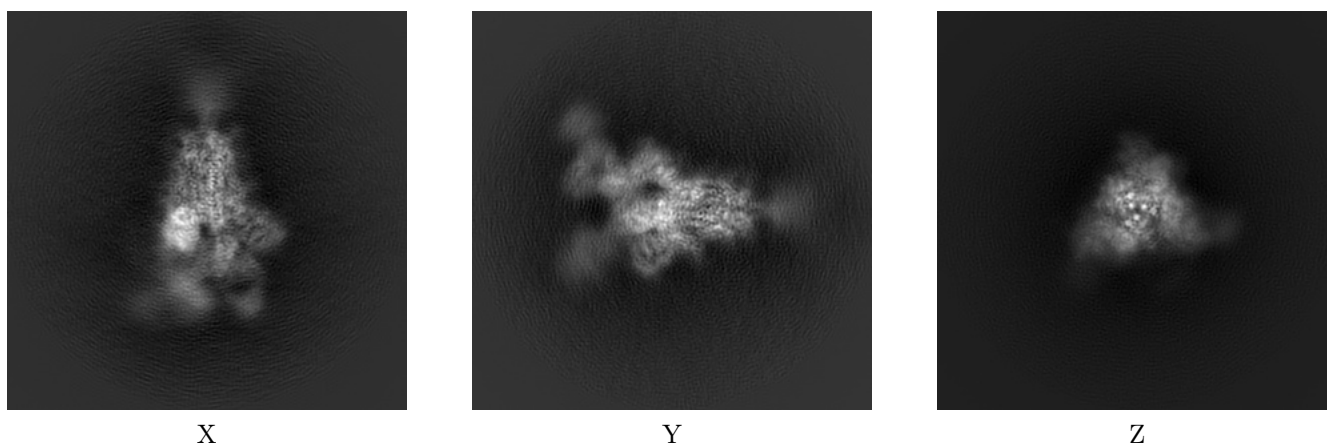
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30482. 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](#)

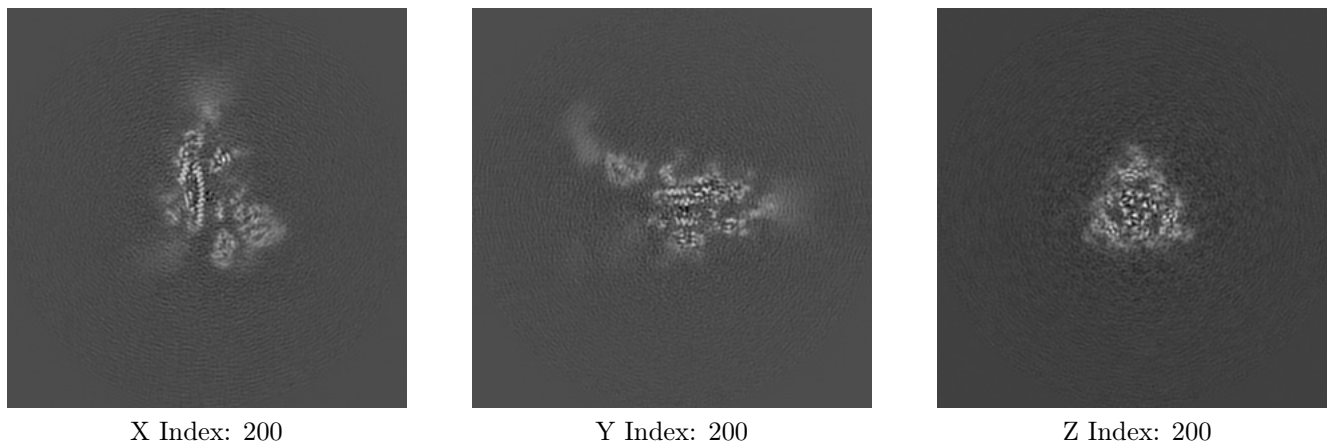
6.1.1 Primary map



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

6.2 Central slices [i](#)

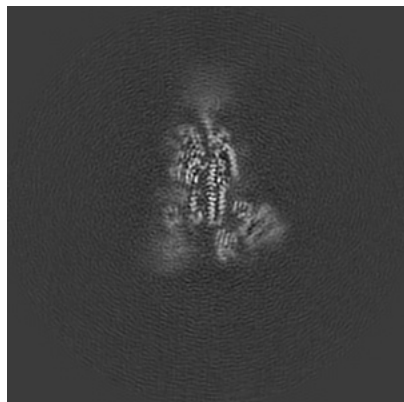
6.2.1 Primary map



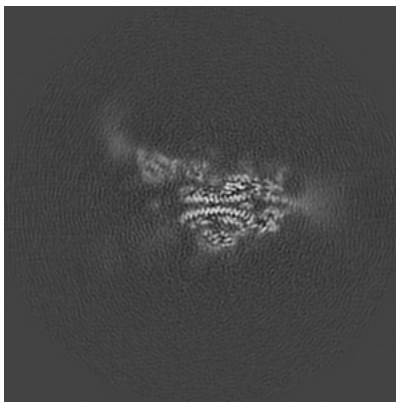
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

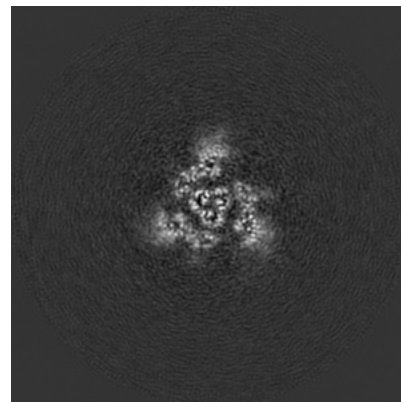
6.3.1 Primary map



X Index: 193



Y Index: 204

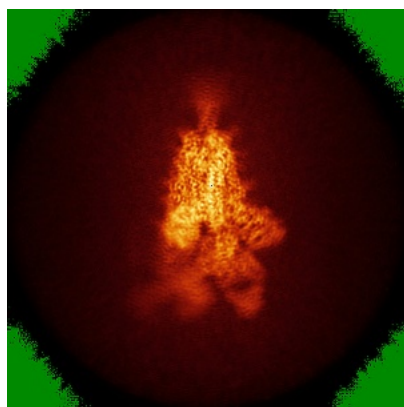


Z Index: 189

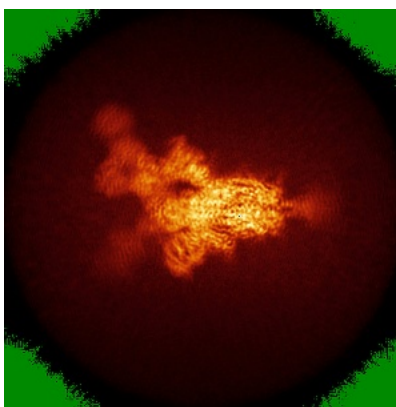
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [\(i\)](#)

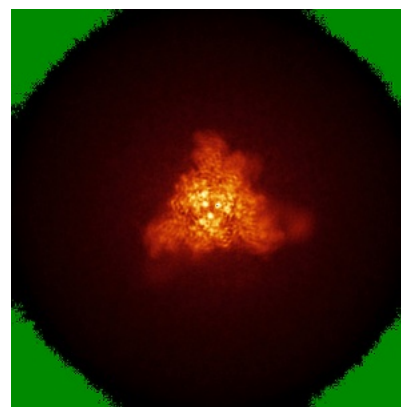
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00502. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

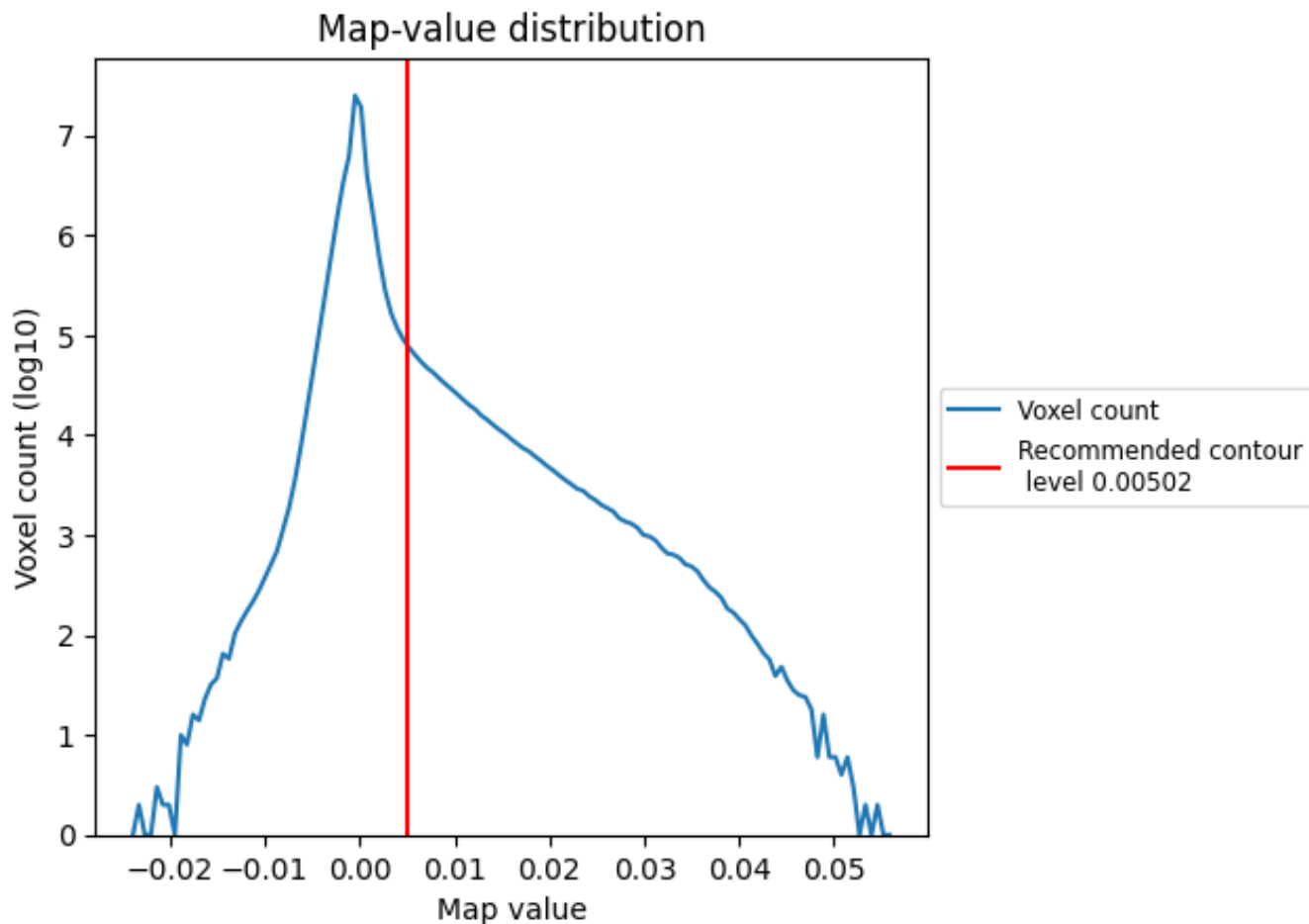
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

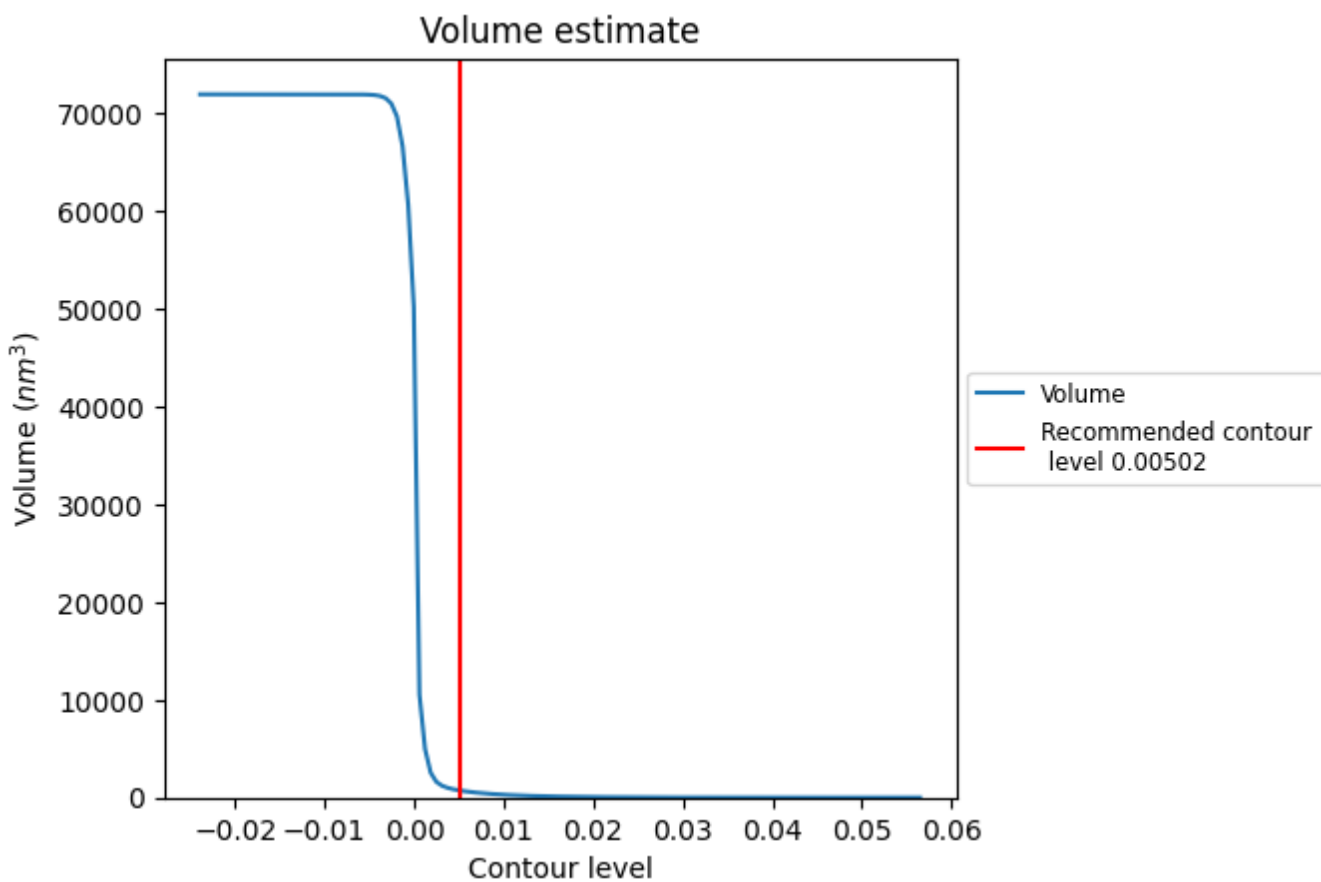
This section contains the results of statistical analysis of the map.

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.

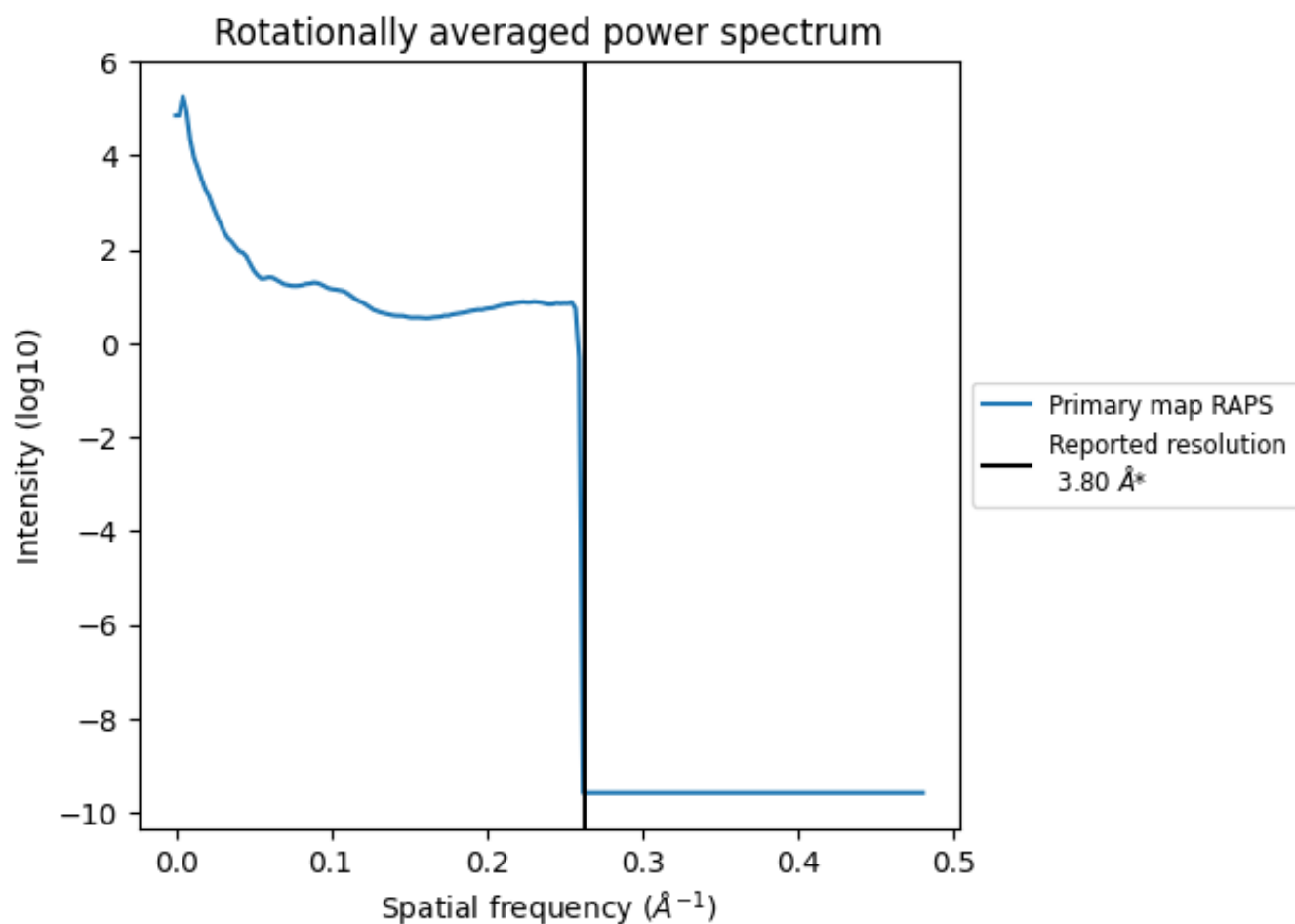
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 737 nm³; this corresponds to an approximate mass of 666 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 0.263 Å⁻¹

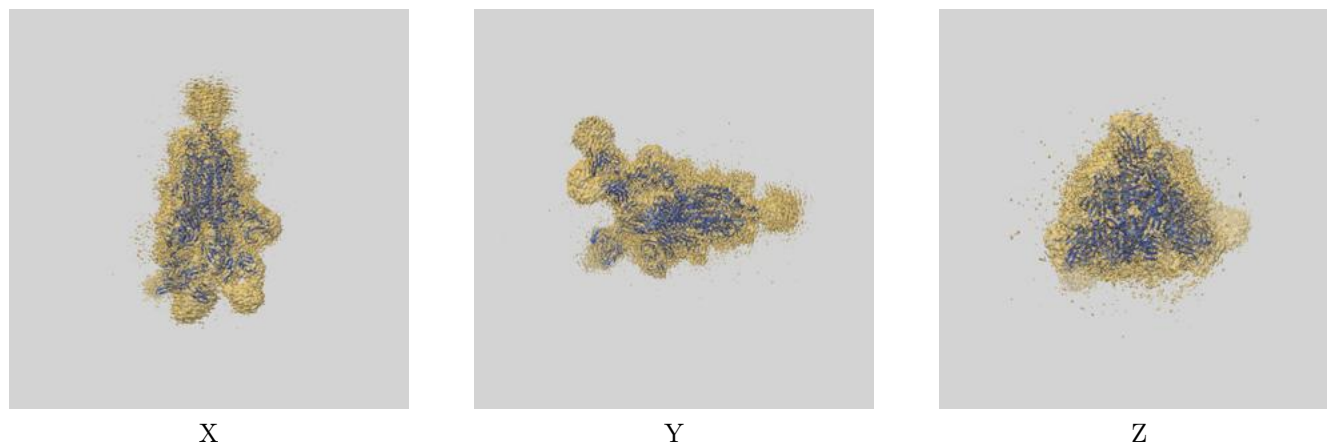
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

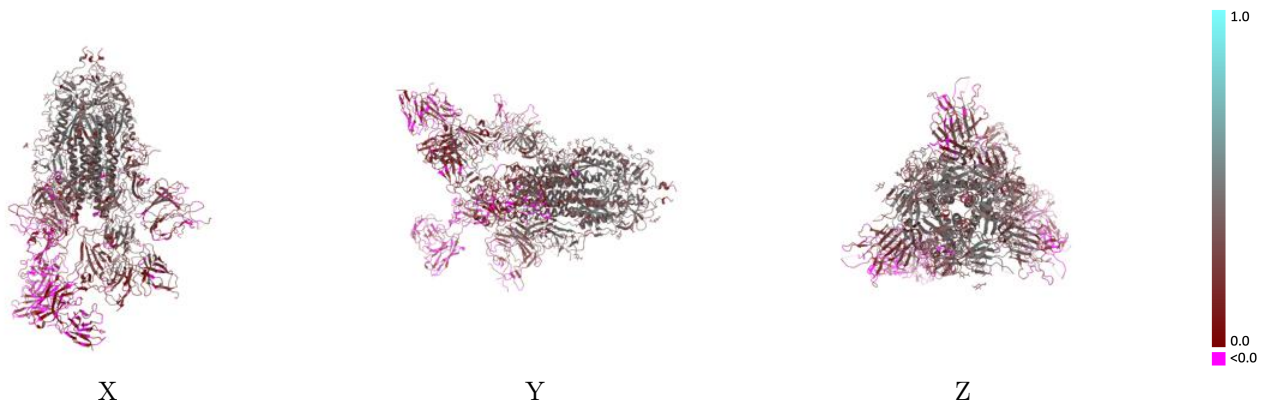
This section contains information regarding the fit between EMDB map EMD-30482 and PDB model 7CWL. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



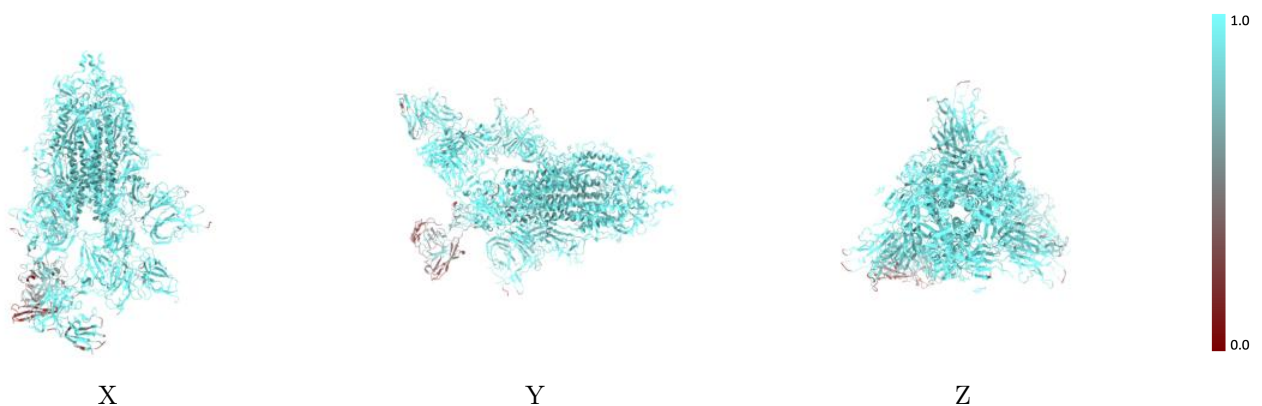
The images above show the 3D surface view of the map at the recommended contour level 0.00502 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



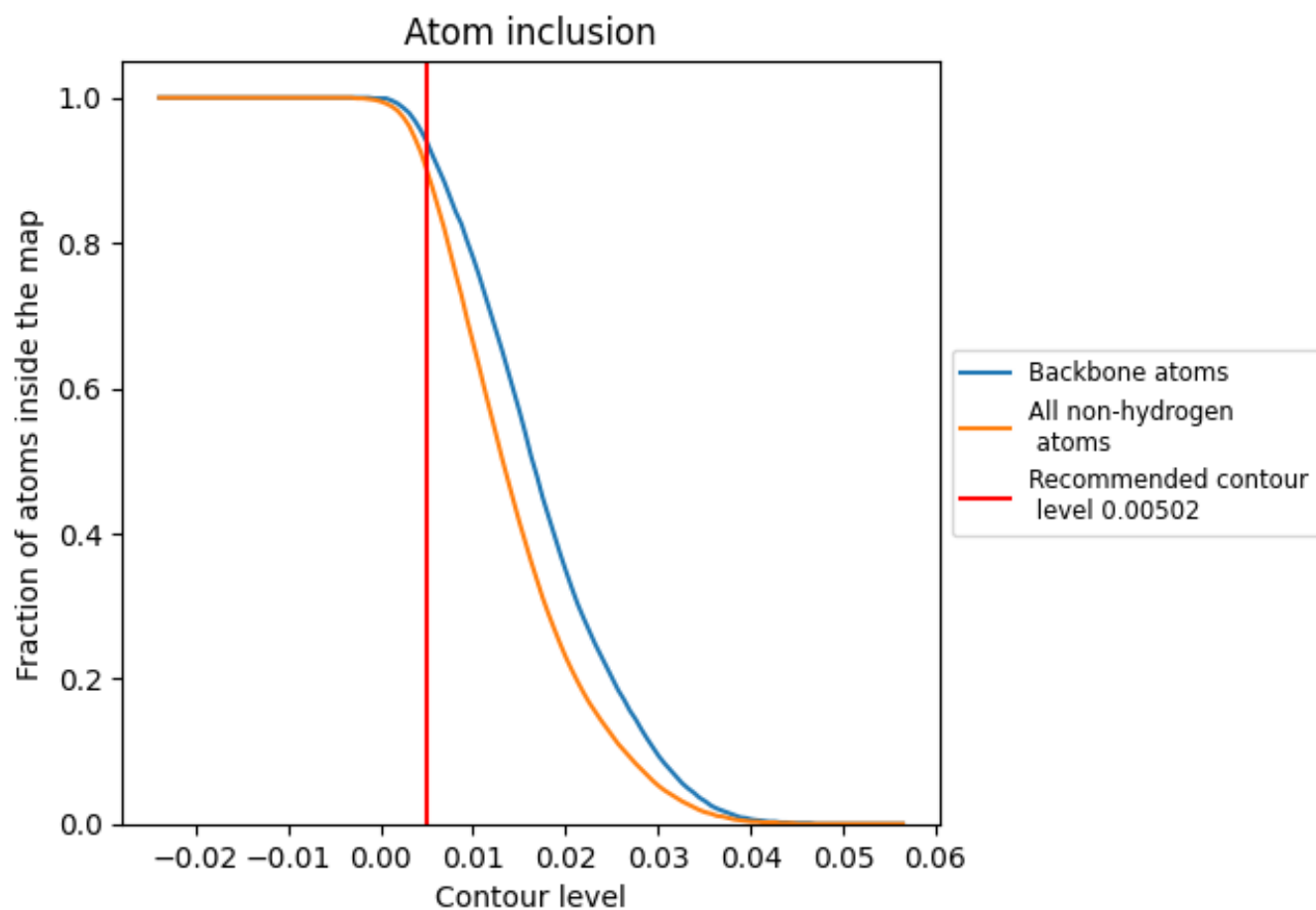
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00502).





















9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.00502) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.2570
A	 0.9450	 0.3080
B	 0.9380	 0.2800
C	 0.9190	 0.2780
G	 0.8810	 0.0550
H	 0.9680	 0.2230
I	 0.4410	 0.0100
J	 0.8240	 0.0490
K	 0.3450	 0.0600
L	 0.9360	 0.2280

