



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 10:43 AM UTC

PDB ID : 6PSU / pdb_00006psu
EMDB ID : EMD-20464
Title : Escherichia coli RNA polymerase promoter unwinding intermediate (TRPi2)
with TraR and rpsT P2 promoter
Authors : Chen, J.; Chiu, C.E.; Campbell, E.A.; Darst, S.A.
Deposited on : 2019-07-13
Resolution : 3.90 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:

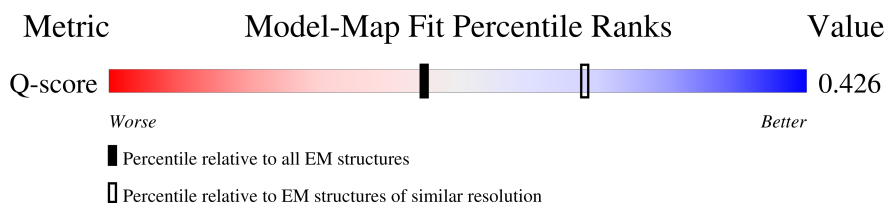
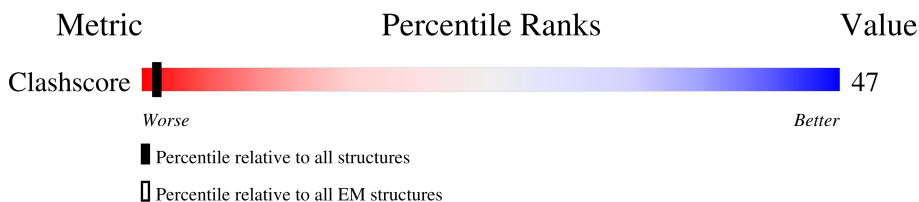
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

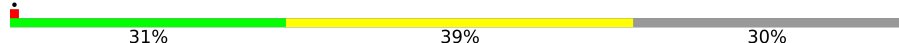



The reported resolution of this entry is 3.90 Å.

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



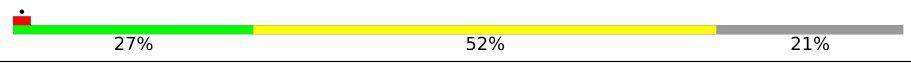



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	N	72	 43% 57%
2	G	329	 31% 39% 30%
2	H	329	 23% 43% 34%
2	M	329	 9% 13% 22% 78%
3	I	1342	 35% 64%
4	J	1430	 6% 34% 60% 6%

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Mol	Chain	Length	Quality of chain
5	K	91	
6	L	616	
7	O	85	
8	P	85	

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 32323 atoms, of which 156 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 Protein TraR.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	N	72	571	353	105	108	5	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	230	1775	1108	314	347	6	0	0
2	H	217	1668	1043	293	326	6	0	0
2	M	73	572	362	100	108	2	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	I	1340	10567	6631	1841	2052	43	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	1344	10433	6556	1856	1971	50	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	VAL	-	expression tag	UNP P0A8T7
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	LEU	-	expression tag	UNP P0A8T7
J	1411	GLU	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1412	VAL	-	expression tag	UNP P0A8T7
J	1413	LEU	-	expression tag	UNP P0A8T7
J	1414	PHE	-	expression tag	UNP P0A8T7
J	1415	GLN	-	expression tag	UNP P0A8T7
J	1416	GLY	-	expression tag	UNP P0A8T7
J	1417	PRO	-	expression tag	UNP P0A8T7
J	1418	SER	-	expression tag	UNP P0A8T7
J	1419	SER	-	expression tag	UNP P0A8T7
J	1420	GLY	-	expression tag	UNP P0A8T7
J	1421	HIS	-	expression tag	UNP P0A8T7
J	1422	HIS	-	expression tag	UNP P0A8T7
J	1423	HIS	-	expression tag	UNP P0A8T7
J	1424	HIS	-	expression tag	UNP P0A8T7
J	1425	HIS	-	expression tag	UNP P0A8T7
J	1426	HIS	-	expression tag	UNP P0A8T7
J	1427	HIS	-	expression tag	UNP P0A8T7
J	1428	HIS	-	expression tag	UNP P0A8T7
J	1429	HIS	-	expression tag	UNP P0A8T7
J	1430	HIS	-	expression tag	UNP P0A8T7

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	72	577	352	110	114	1	0	0

- Molecule 6 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L	529	4277	2677	753	821	26	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-2	SER	-	expression tag	UNP Q0P6L9
L	-1	GLU	-	expression tag	UNP Q0P6L9
L	0	PHE	-	expression tag	UNP Q0P6L9

- Molecule 7 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	O	42	863	411	168	242	42	0	0

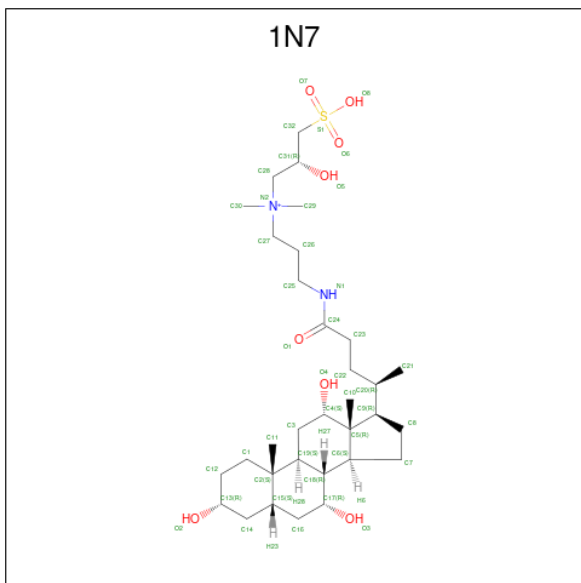
- Molecule 8 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	P	37	752	363	117	235	37	0	0

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
9	N	1	1	1	0
9	J	2	2	2	0

- Molecule 10 is CHAPSO (CCD ID: 1N7) (formula: C₃₂H₅₉N₂O₈S).

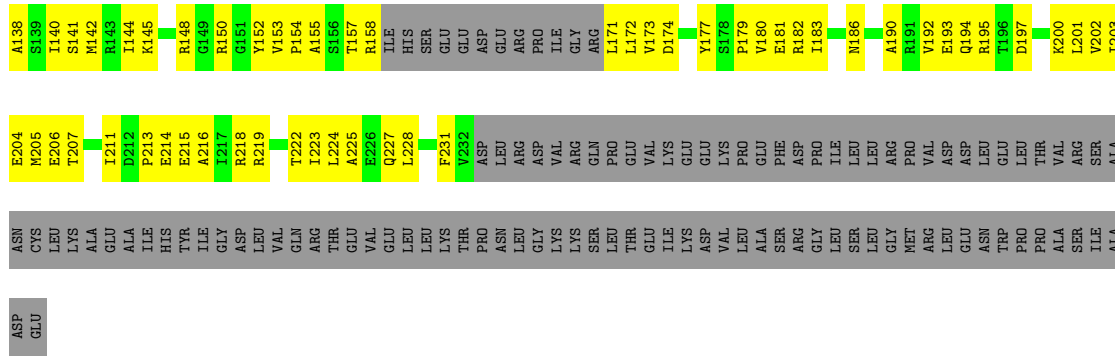


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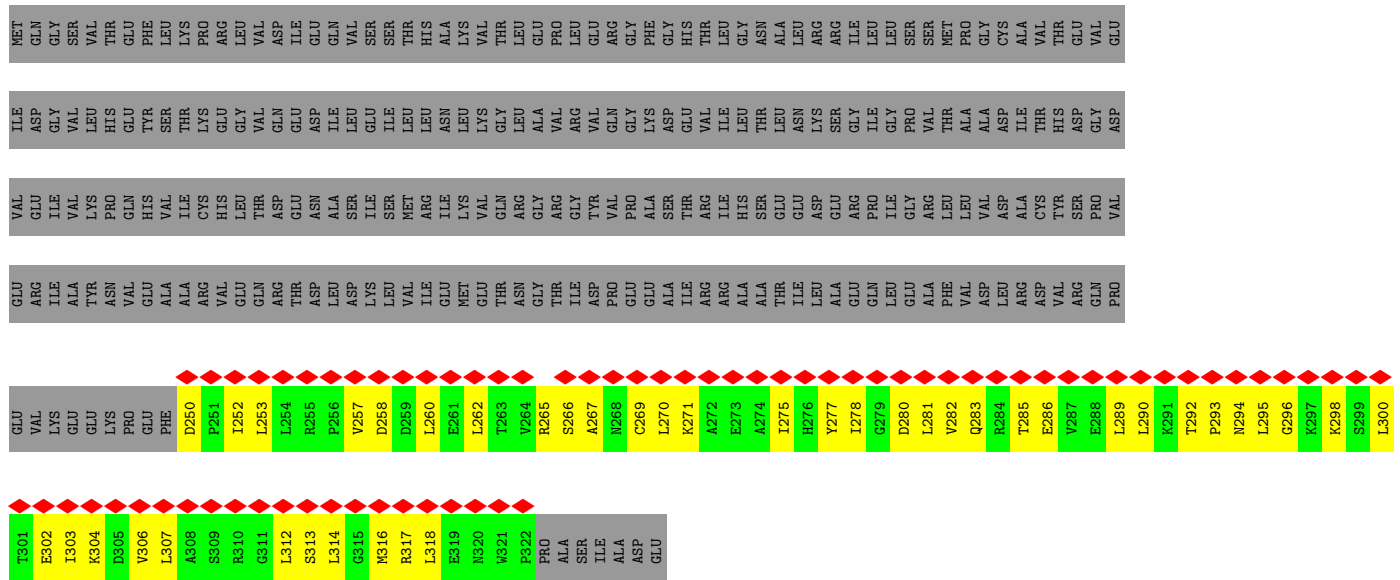
Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	O	
10	L	1	66	24	39	3	0

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

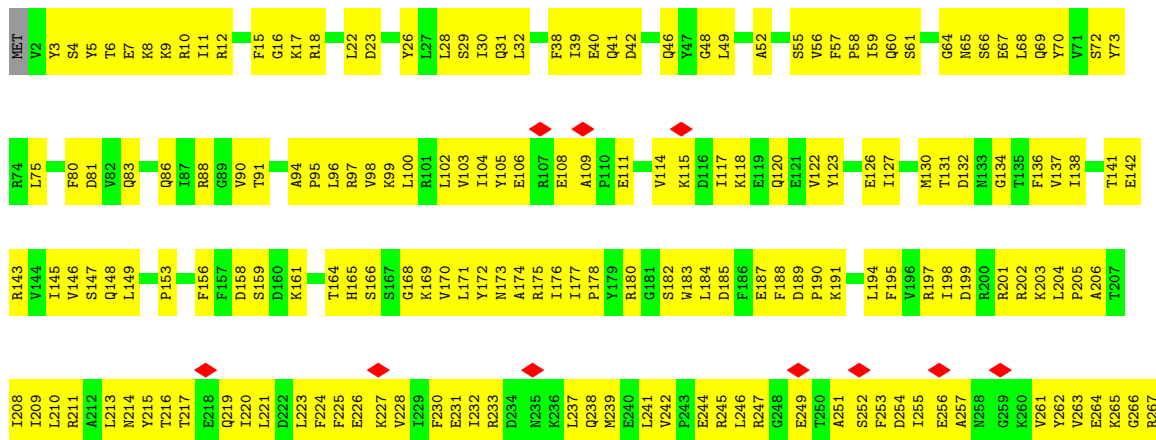
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
11	J	1	1	1	0



● Molecule 2: DNA-directed RNA polymerase subunit alpha



● Molecule 3: DNA-directed RNA polymerase subunit beta



Q1288	Q1300	Q1303	Q1304	Q1306	Q1307	Q1308	Q1309	Q1312	Q1319	Q1320	Q1321	Q1322	Q1323	Q1324	Q1325	Q1326	Q1327	Q1328	Q1329	Q1330	Q1331	Q1332	Q1333	Q1334	Q1335	Q1339	Q1340	Q1341	GLU
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• Molecule 4: DNA-directed RNA polymerase subunit beta'



VAL	LYS	ASP	LEU	LEU	LEU	PHE	LEU	LEU	ALA	GLN	THR	LYS	THR	GLU	E16	F17	E25	A19	I20	S26	M29	I30	W33	S34	F35	G36	E37	V38	K39	K40	P41	E42	T43	I44	M45	Y46	T48	P51	E52	R53	D54	G55	F57	C58	A59	R60	I61	L126	L127	I61	L128	L129	M130	P131	L132	E69
C70	L71	C72	G73	K74	W75	L78	K79	H80	V83	I84	C85	E86	K87	C88	G89	V90	E91	I92	T93	Q94	T95	R98	R99	E100	S101	M102	G103	L104	H105	E106	P107	P110	T111	A112	H113	I114	W115	F116	L117	K118	S119	S122	R123	I124	G125	L126	L127	I61	L128	L129	M130	P131	L132	E69		
D134	I135	R136	R137	V138	L139	Y140	F141	E142	S143	Y144	V145	V146	I147	E148	M151	C152	M153	L154	E155	Q158	I159	T160	T161	E162	Q164	Y165	L166	D167	E170	E171	F172	G173	D174	E175	F176	D177	A178	K179	M180	G181	A182	I185	L188	L189	D193	L194	E195	Q196	E197	C198	E199	Q200				
L201	R202	E203	E204	E211	K216	L217	T218	K219	R220	R221	K222	L223	L224	E225	A226	F227	V228	Q229	K233	P234	E235	W236	M237	V241	L242	P243	V244	L245	P246	L249	R250	P251	L252	V253	P254	R259	F260	A261	T262	L265	D267	L268	Y269	R270	R271	R275	N276	L279	K280							
R281	L282	D283	D284	L285	A286	A287	P288	D289	L290	L291	V292	R293	M294	E295	K296	R297	M298	L299	Q300	D304	A305	L306	L307	D308	R311	T317	G318	R322	K325	S326	L327	A328	D329	K330	L331	K332	G333	K334	Q335	M400	G336	R337	F338	R339	Q340	R341	V408	L342	L343	G344	K345	R346	V347	Y349	S350	
G351	R352	S353	V354	L355	T356	V357	G358	P359	L360	L361	R362	L363	H364	R365	C366	G367	L368	P369	K370	K371	K372	L374	E375	L376	F377	K378	P379	Y382	G383	K384	L385	E386	L387	R388	G389	L390	T393	L394	K398	K399	M400	G401	E405	A406	V407	V408	A409	D410	G344	K345	R346	V347	Y349	S350		
E418	H419	P420	V421	L422	L423	M424	R425	A426	P427	T428	L429	H430	R431	L432	F437	E438	P439	V440	L441	I442	E443	G444	K445	Q448	L449	H450	P451	L452	V453	C454	M458	A459	D460	F461	D462	G463	D464	Q465	M466	V468	H469	P471	L472	T473	L474	E475	A476	Q477	L478	E479	E482	L483	M484			
M485	S486	D487	M488	M489	L490	L491	S492	M495	G496	L499	M500	V501	P502	S503	V506	V507	L508	G509	L510	V511	M512	N513	T514	R515	P516	K517	G518	L519	M520	V521	L522	P523	K531	E532	A533	L536	V537	R538	S539	G540	L541	A542	R545	A546	R547	V548	K549	V550	R551	L552	T553	E554	V555			
E556	K557	D558	A559	E562	L563	V564	A565	L566	T567	S568	L569	M644	V645	P647	G653	E658	V661	I662	L664	Q667	V673	R678	M680	G681	V682	I683	D684	I685	W686	A687	A688	L605	R606	T607	C608	L609	M604	L606	R607	V693	S694	M697	M700	L701	K615	P616	K619	F620	M708	R709	D710	G623	L624			
M625	V626	T627	A632	A633	R634	V639	G640	I641	D642	D643	M644	V645	P647	L653	E658	V661	I662	L664	Q667	V673	R678	M680	G681	V682	I683	D684	I685	W686	A687	A688	L605	R606	T607	C608	L609	M604	L606	R607	V693	S694	M697	M700	L701	K615	P616	K619	F620	M708	R709	D710	G623	L624				
G712	E713	E714	V717	S718	F719	M720	S721	I722	Y723	M724	M725	S728	R731	G732	S733	A734	I735	Q736	R738	Q739	L740	A741	G742	G745	L746	M747	A748	K749	P750	D751	G752	S753	I754	I755	E756	I757	P758	I759	M762	F763	R764	G765	G766	M768	Q771	L774	S775	I776	A779							
R780	K781	G782	L783	T786	A787	L788	M792	I795	Y796	L797	I799	R799	L800	M802	M803	A804	R805	V808	M809	T810	E811	D812	D813	M821	M822	V825	R826	D830	K832	L835	R836	R838	V839	H842	V843	T844	A845	E846	D847	V848	L849	K850	P851	D855	G824	E825	R856	P926								
V858	P859	R860	N861	L863	L864	H865	E866	Q867	W868	C869	D870	L871	E872	R873	S876	V877	D878	A879	V882	R883	S884	V885	V886	D889	T890	D891	V894	C895	C898	Y899	R901	K832	L835	R836	R838	V839	H842	V843	T844	A845	E846	D847	V848	L849	K850	P851	D855	G824	E825	R856	P926					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46553	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 ($e^-/\text{\AA}^2$)	80	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	0.150	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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: MG, 1N7, 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	N	0.30	0/581	0.53	0/785
2	G	0.36	0/1797	0.54	0/2437
2	H	0.33	0/1687	0.62	1/2287 (0.0%)
2	M	0.19	0/579	0.52	0/784
3	I	0.39	0/10736	0.59	5/14487 (0.0%)
4	J	0.37	0/10592	0.57	0/14308
5	K	0.28	0/579	0.51	0/779
6	L	0.23	0/4329	0.51	1/5820 (0.0%)
7	O	0.25	0/971	0.43	0/1495
8	P	0.25	0/837	0.47	0/1290
All	All	0.35	0/32688	0.56	7/44472 (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
3	I	0	4
4	J	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1167	GLU	N-CA-C	7.51	126.79	110.80
2	H	14	VAL	N-CA-C	-5.84	107.60	113.20
3	I	1166	ASP	CA-C-N	5.74	132.50	121.54
3	I	1166	ASP	C-N-CA	5.74	132.50	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	516	ASP	N-CA-C	-5.38	99.75	108.41

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	I	1165	SER	Peptide
3	I	1166	ASP	Peptide
3	I	1240	ASP	Peptide
3	I	247	ARG	Peptide
4	J	47	ARG	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	N	571	0	556	52	0
2	G	1775	0	1803	133	0
2	H	1668	0	1702	185	0
2	M	572	0	602	61	0
3	I	10567	0	10585	1051	0
4	J	10433	0	10625	1045	0
5	K	577	0	588	54	0
6	L	4277	0	4325	546	0
7	O	863	0	471	74	0
8	P	752	0	426	74	0
9	J	2	0	0	0	0
9	N	1	0	0	0	0
10	I	27	39	39	7	0
10	J	27	39	38	4	0
10	L	27	39	37	3	0
10	N	27	39	38	4	0
11	J	1	0	0	0	0
All	All	32167	156	31835	3030	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 47.

The worst 5 of 3030 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)
10:L:701:1N7:C19	10:L:701:1N7:C3	1.83	1.57
10:N:102:1N7:C19	10:N:102:1N7:C3	1.83	1.51
10:I:1401:1N7:C3	10:I:1401:1N7:C19	1.82	1.51
10:J:1504:1N7:C19	10:J:1504:1N7:C3	1.83	1.50
6:L:284:GLU:HA	6:L:287:ILE:HB	1.36	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
10	1N7	I	1401	-	30,30,46	4.97	15 (50%)	47,48,72	2.27	15 (31%)
10	1N7	L	701	-	30,30,46	5.18	16 (53%)	47,48,72	2.17	14 (29%)
10	1N7	N	102	-	30,30,46	5.11	15 (50%)	47,48,72	2.28	16 (34%)
10	1N7	J	1504	-	30,30,46	5.11	15 (50%)	47,48,72	2.12	14 (29%)

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
10	1N7	I	1401	-	-	0/7/72/92	0/4/4/4
10	1N7	L	701	-	-	5/7/72/92	0/4/4/4
10	1N7	N	102	-	-	7/7/72/92	0/4/4/4
10	1N7	J	1504	-	-	1/7/72/92	0/4/4/4

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	L	701	1N7	C3-C19	18.52	1.83	1.53
10	J	1504	1N7	C3-C19	18.23	1.83	1.53
10	N	102	1N7	C3-C19	18.12	1.83	1.53
10	I	1401	1N7	C3-C19	17.68	1.82	1.53
10	N	102	1N7	C3-C4	12.34	1.73	1.53

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	N	102	1N7	C7-C6-C18	-7.38	108.23	118.36
10	I	1401	1N7	C7-C6-C18	-6.22	109.83	118.36
10	J	1504	1N7	C7-C6-C18	-5.97	110.17	118.36
10	L	701	1N7	C9-C5-C4	-5.58	112.65	117.67
10	L	701	1N7	C7-C6-C18	-5.47	110.86	118.36

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

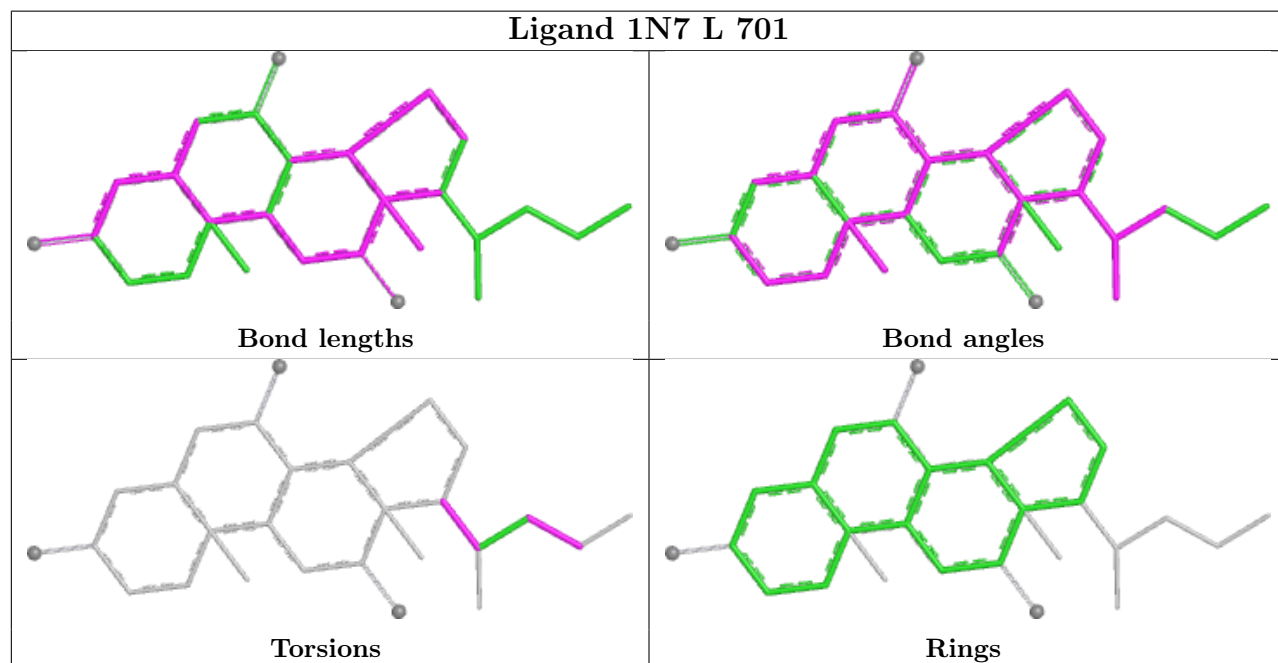
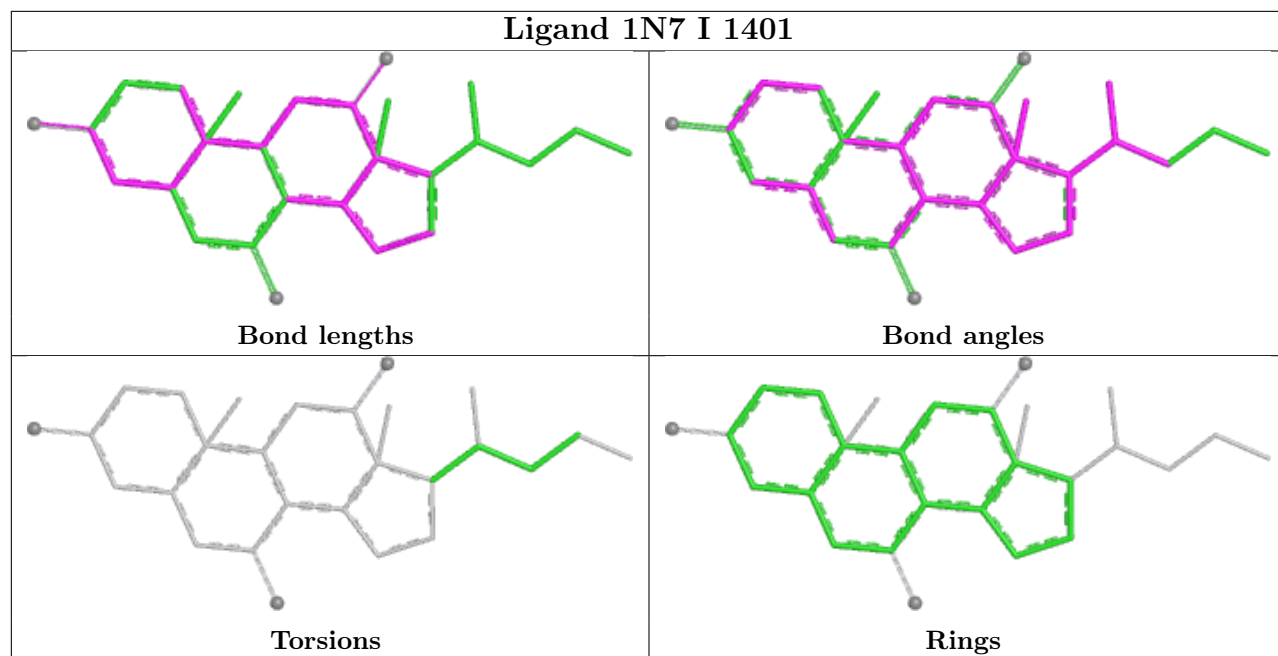
Mol	Chain	Res	Type	Atoms
10	N	102	1N7	C9-C20-C22-C23
10	N	102	1N7	C21-C20-C22-C23
10	L	701	1N7	C22-C20-C9-C5
10	L	701	1N7	C20-C22-C23-C24
10	L	701	1N7	C21-C20-C9-C5

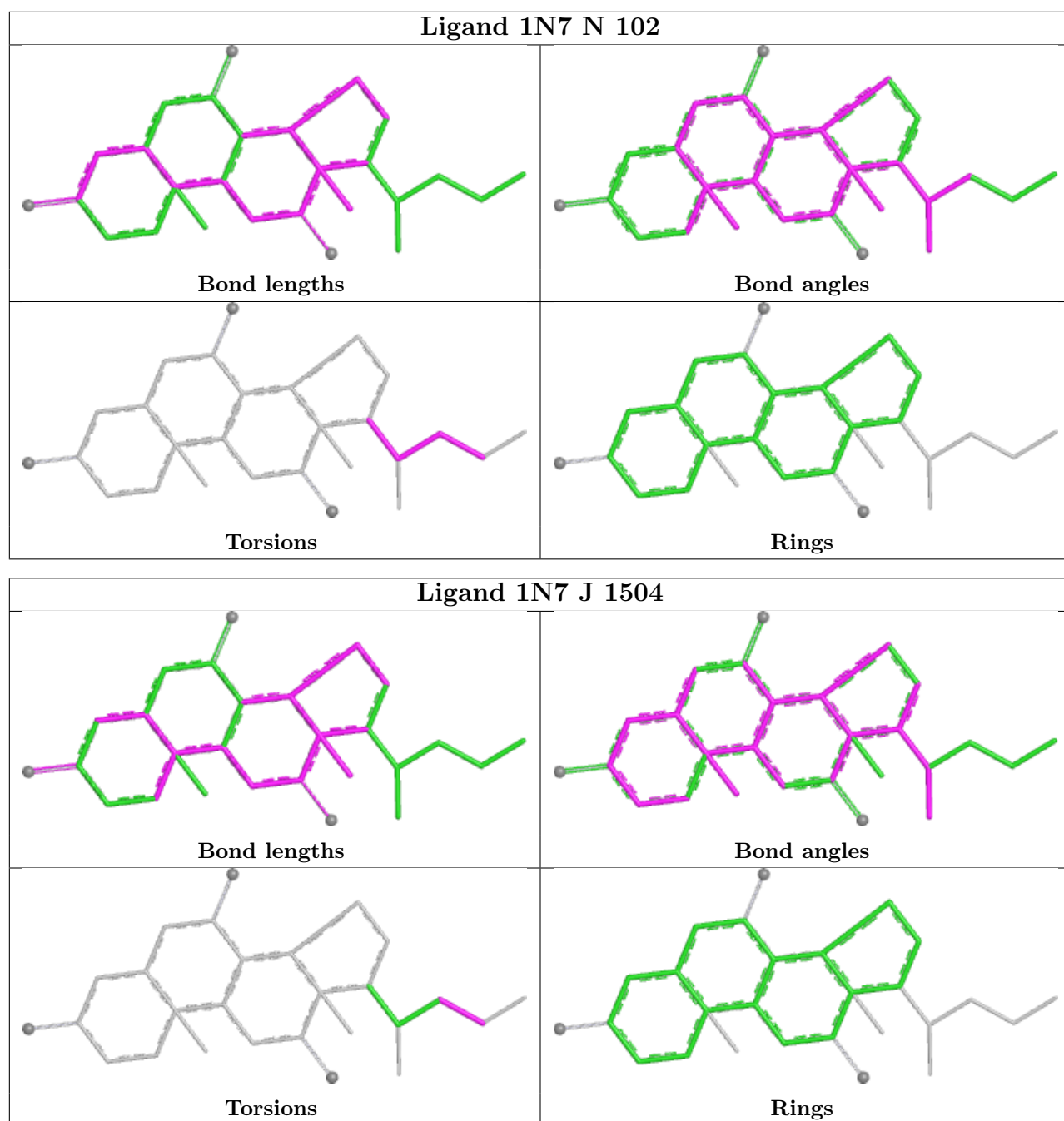
There are no ring outliers.

4 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	I	1401	1N7	7	0
10	L	701	1N7	3	0
10	N	102	1N7	4	0
10	J	1504	1N7	4	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

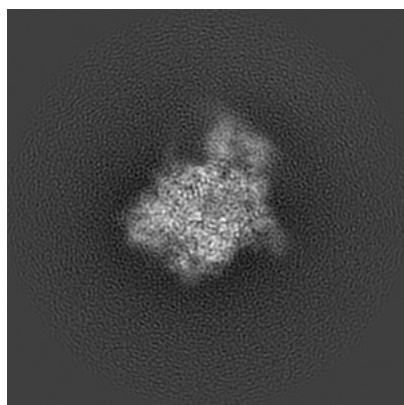
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20464. These allow visual inspection of the internal detail of the map and identification of artifacts.

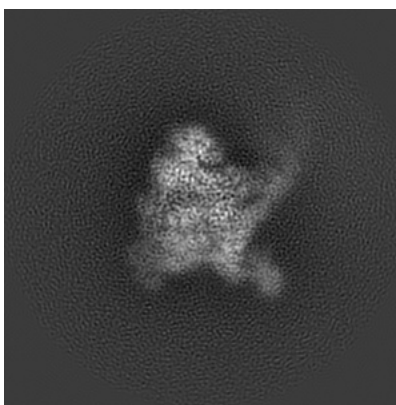
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

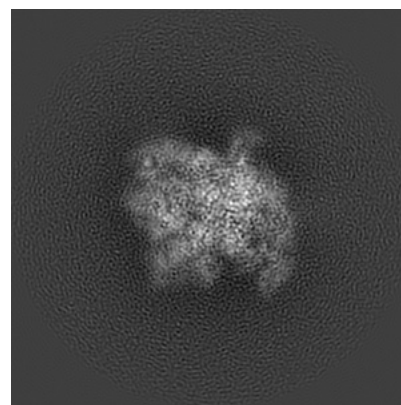
6.1.1 Primary map



X



Y

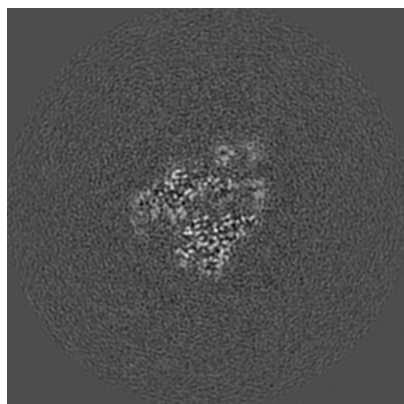


Z

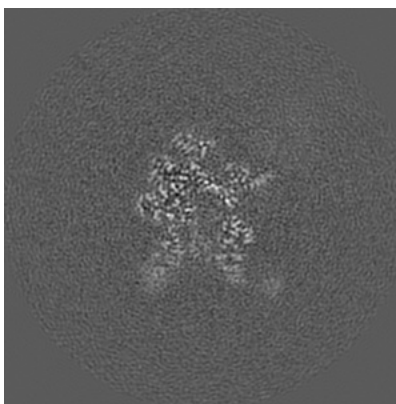
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

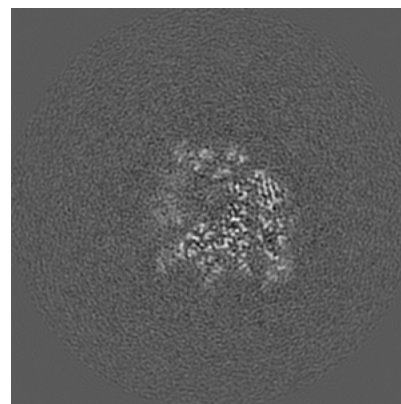
6.2.1 Primary map



X Index: 128



Y Index: 128

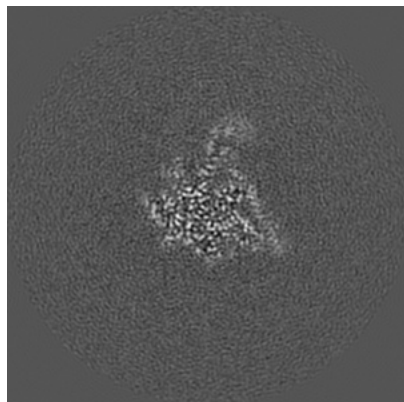


Z Index: 128

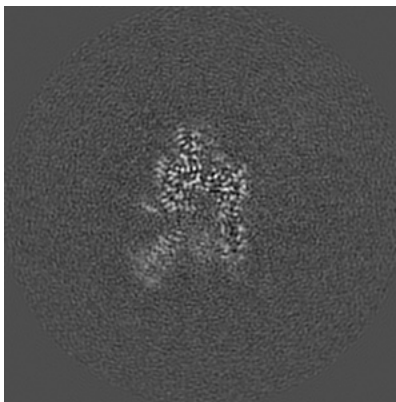
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

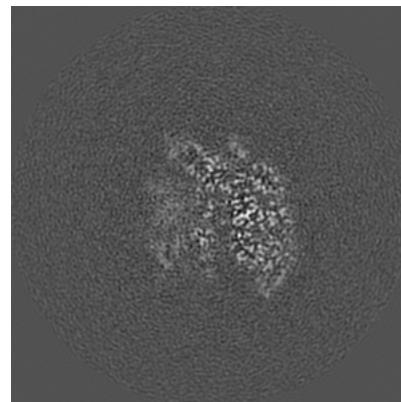
6.3.1 Primary map



X Index: 146



Y Index: 123

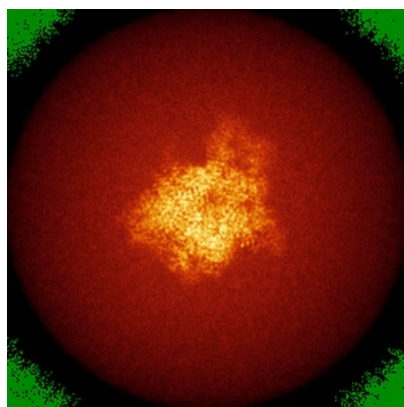


Z Index: 121

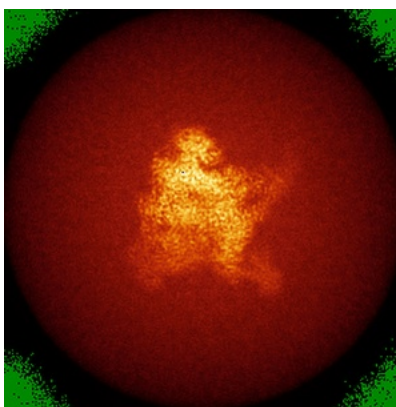
The images above show the largest variance slices of the map in three orthogonal directions.

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

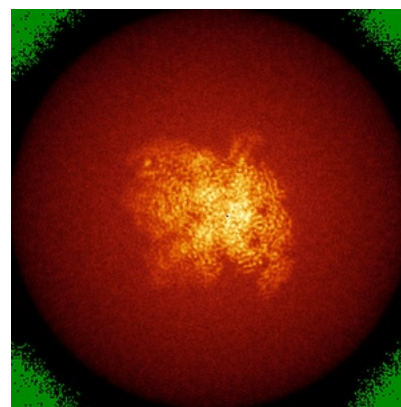
6.4.1 Primary map



X



Y

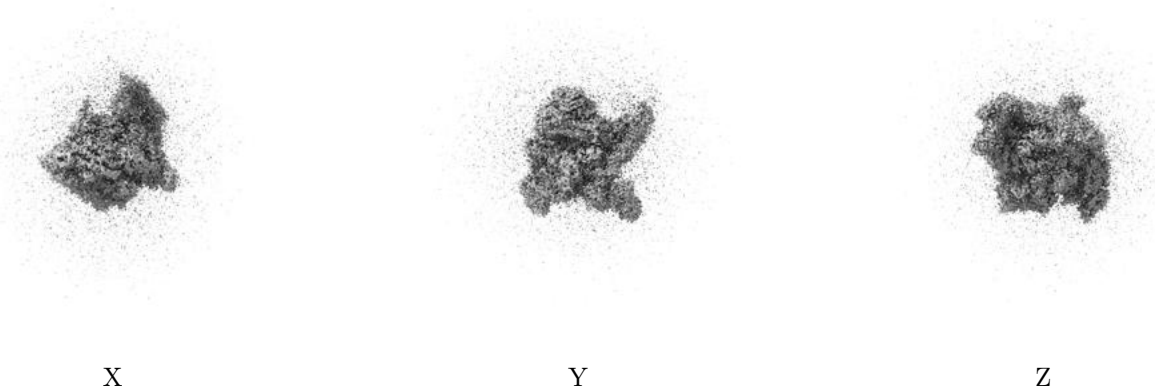


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

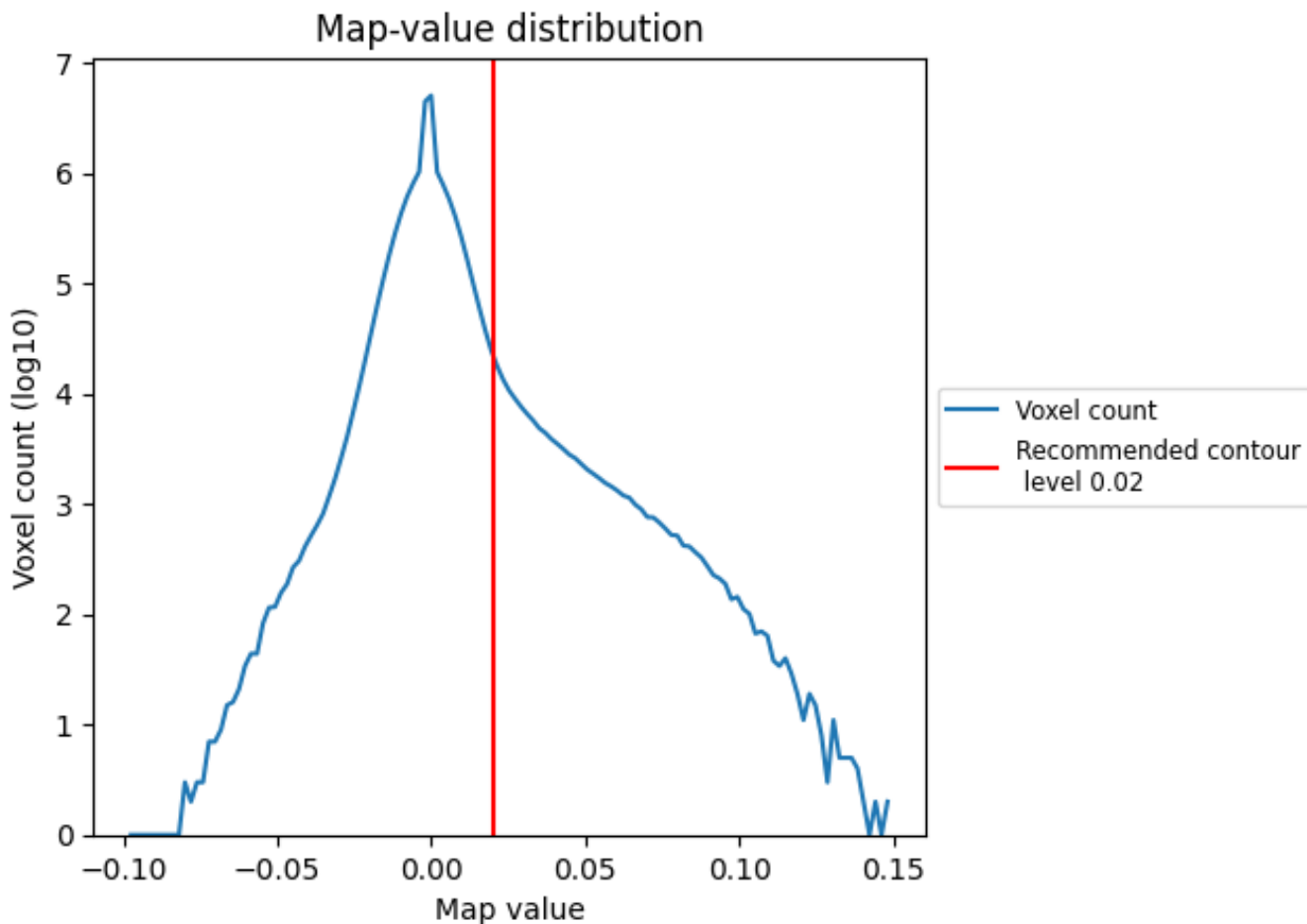
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

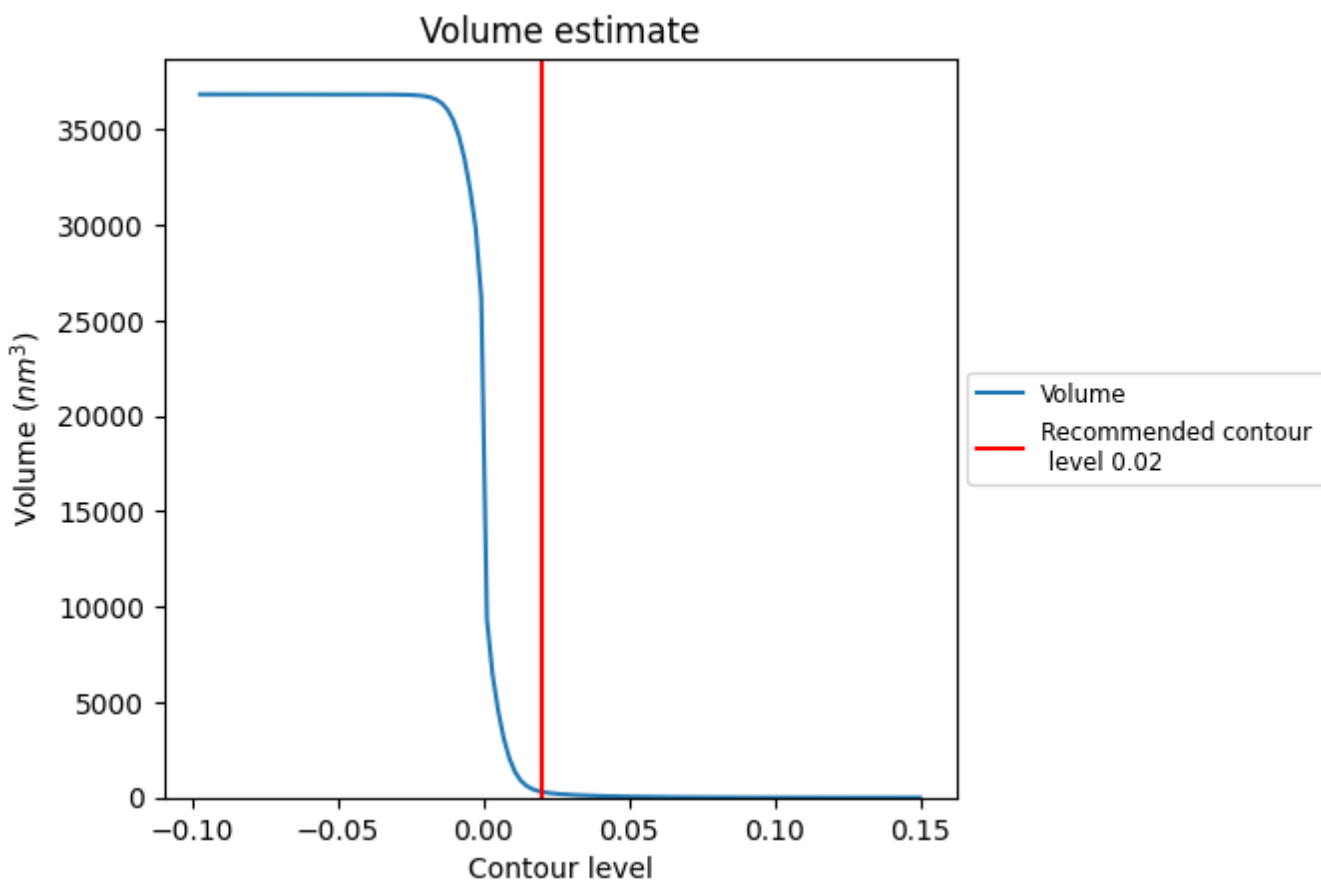
This section contains the results of statistical analysis of the map.

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.

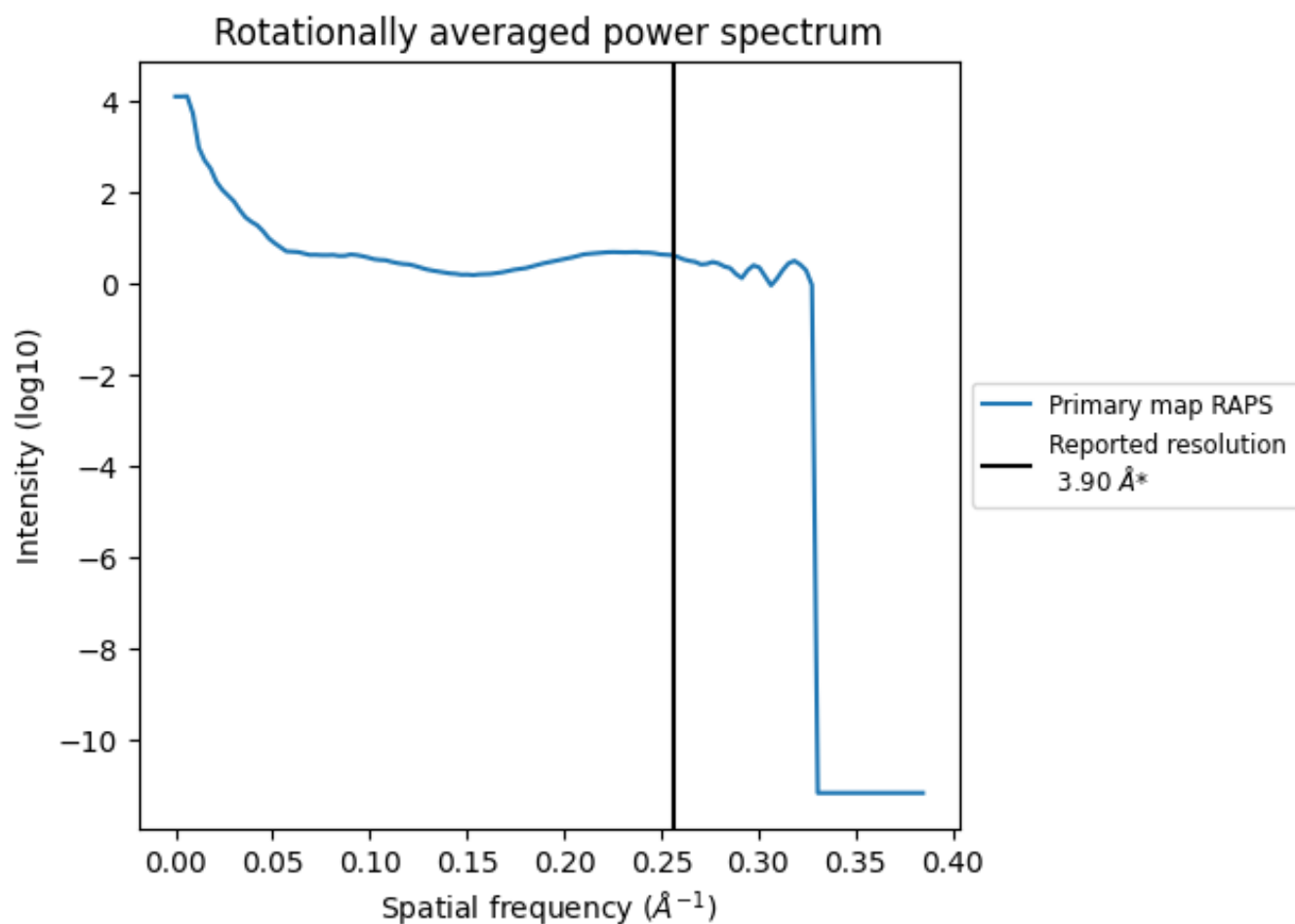
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 302 nm³; this corresponds to an approximate mass of 273 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 [\(i\)](#)

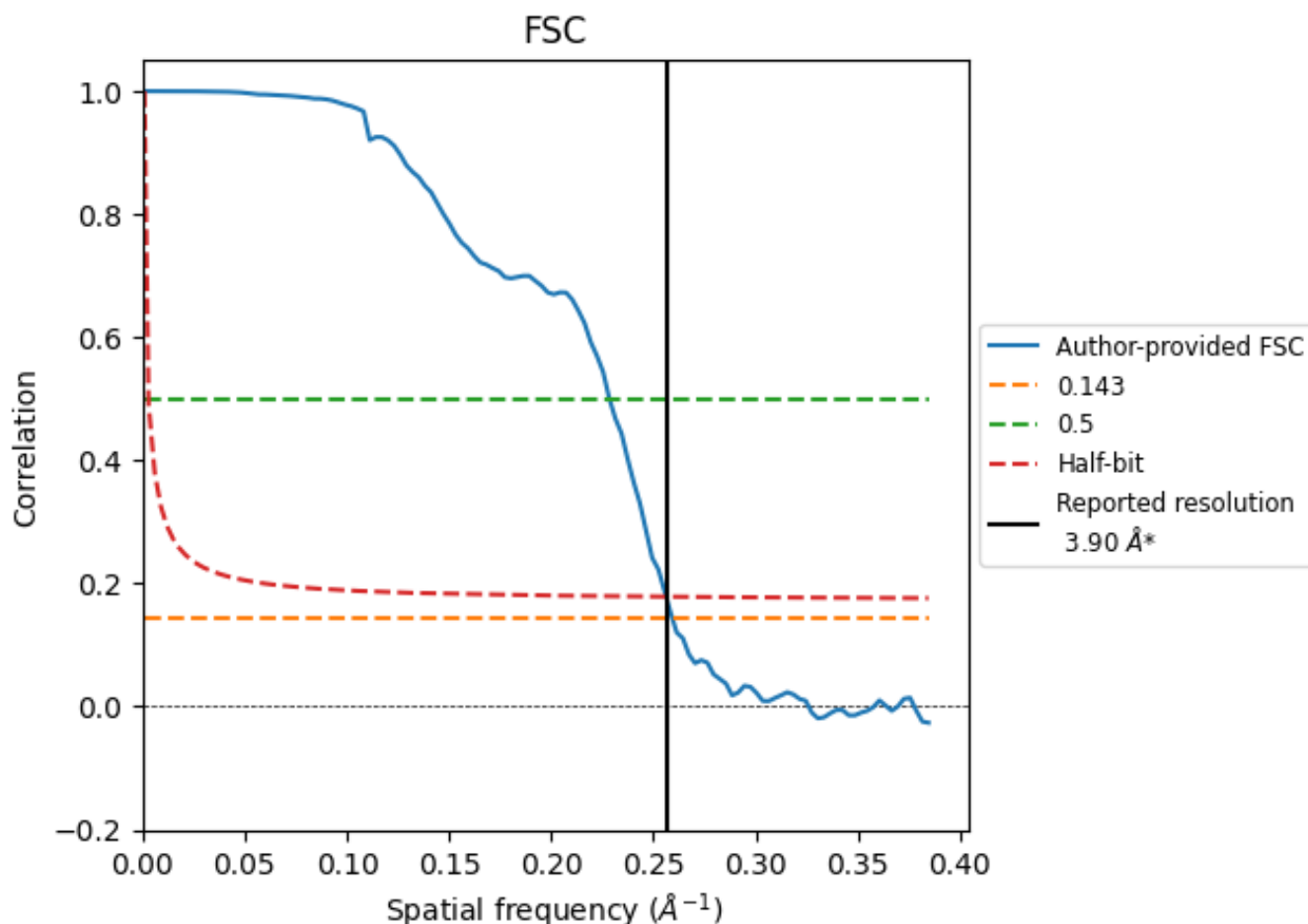


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.86	4.38	3.90
Unmasked-calculated*	-	-	-

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

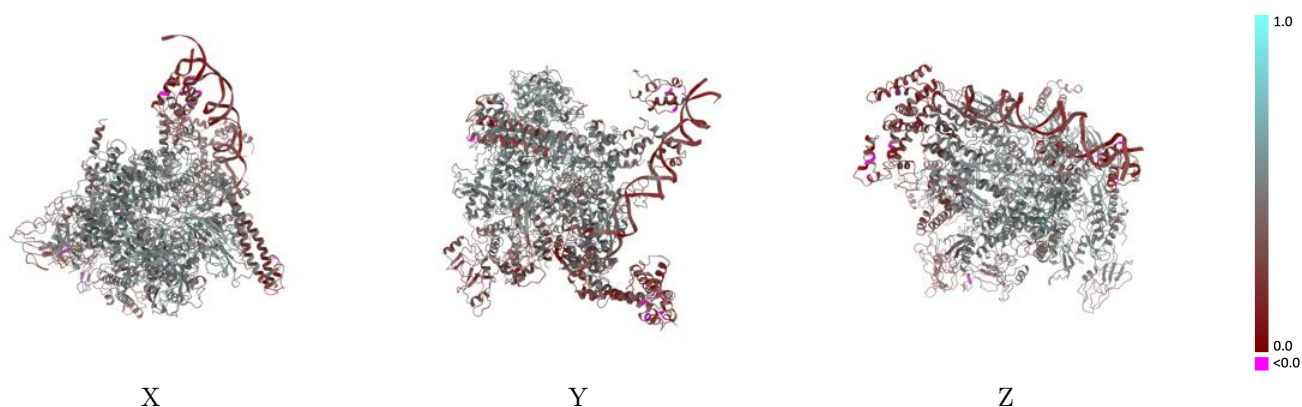
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20464 and PDB model 6PSU. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

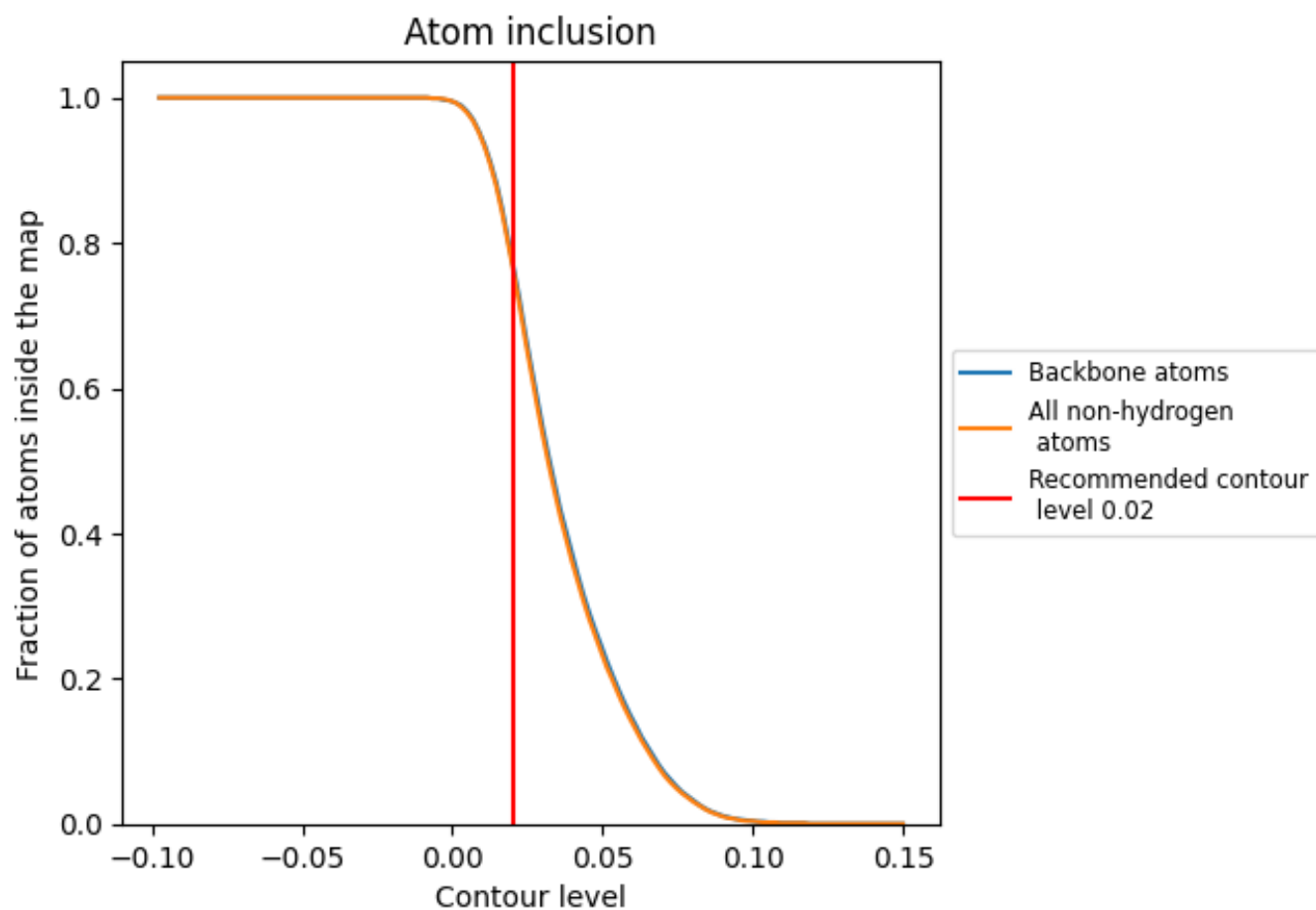


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.























9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.4260
G	 0.8540	 0.4910
H	 0.8310	 0.4540
I	 0.8310	 0.4600
J	 0.8070	 0.4510
K	 0.6990	 0.4460
L	 0.6740	 0.3370
M	 0.0520	 0.2280
N	 0.8300	 0.4370
O	 0.5680	 0.2450
P	 0.5250	 0.2260

