



wwPDB EM Validation Summary Report ⓘ

Jun 20, 2024 – 12:58 AM JST

PDB ID : 7W0D
EMDB ID : EMD-32239
Title : Dicer2-LoqsPD-dsRNA complex at mid-translocation state
Authors : Su, S.; Wang, J.; Wang, H.W.; Ma, J.
Deposited on : 2021-11-18
Resolution : 4.18 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.dev92
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

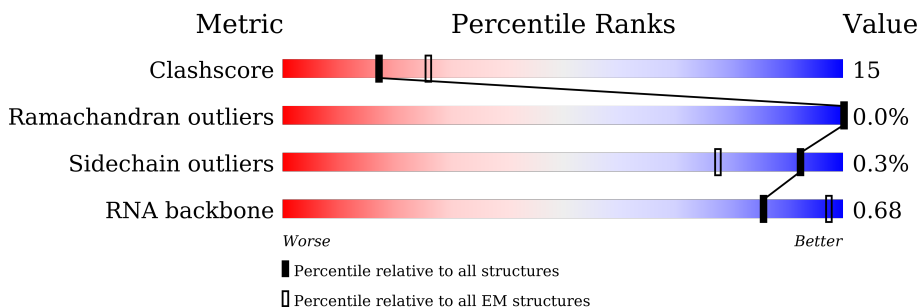
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

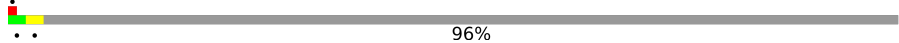
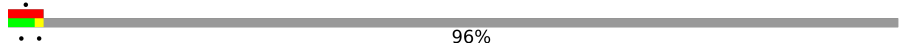




The reported resolution of this entry is 4.18 Å.

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
RNA backbone	4643	859

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	B	359	 96%
1	G	359	 96%
2	C	52	 31% 40% 60%
2	D	52	 35% 56% 44%
3	A	1722	 11% 60% 29% 10%
3	F	1722	 24% 23% 16% 62%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 20322 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 Loquacious, isoform D.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	B	16	Total	C	N	O	0	0
			144	94	22	28		
1	G	13	Total	C	N	O	0	0
			117	78	16	23		

- Molecule 2 is a RNA chain called dsRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	52	Total	C	N	O	P	0	0
			1103	493	192	366	52		
2	C	52	Total	C	N	O	P	0	0
			1100	493	192	364	51		

- Molecule 3 is a protein called Dicer-2, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1544	Total	C	N	O	S	0	0
			12490	8004	2134	2284	68		
3	F	660	Total	C	N	O	S	0	0
			5312	3385	910	983	34		

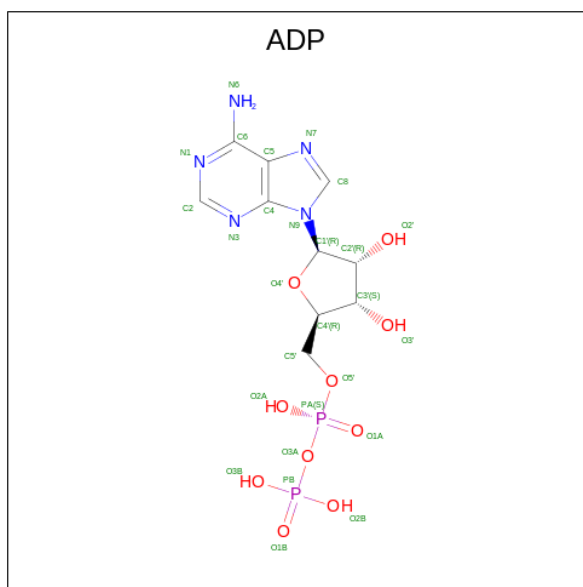
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1217	ASN	ASP	engineered mutation	UNP A1ZAW0
A	1476	ASN	ASP	engineered mutation	UNP A1ZAW0
F	1217	ASN	ASP	engineered mutation	UNP A1ZAW0
F	1476	ASN	ASP	engineered mutation	UNP A1ZAW0

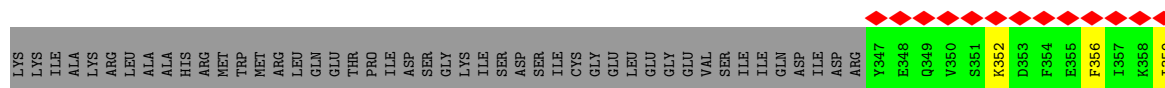
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Mg	0
			1	1	
4	F	1	Total	Mg	0
			1	1	

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



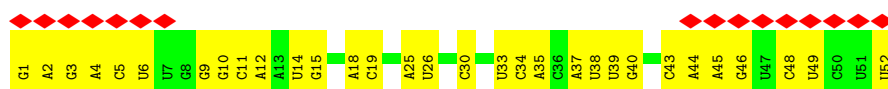
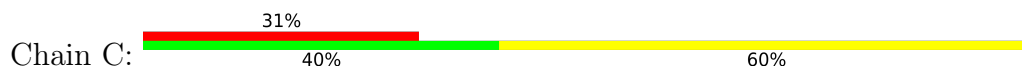
Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
5	F	1	Total	C	N	O	P	0
			27	10	5	10	2	



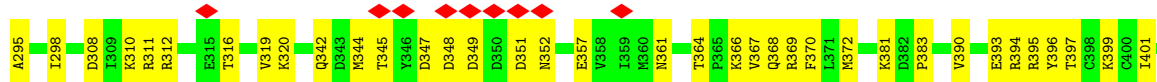
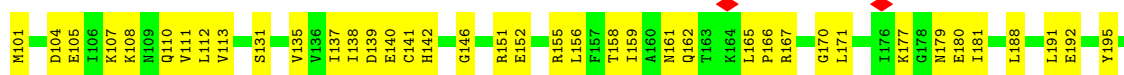
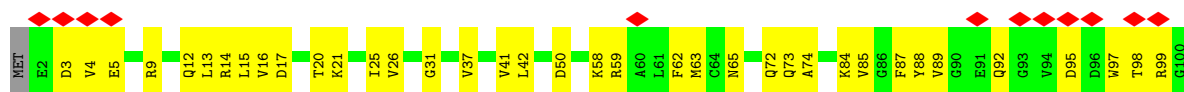
• Molecule 2: dsRNA

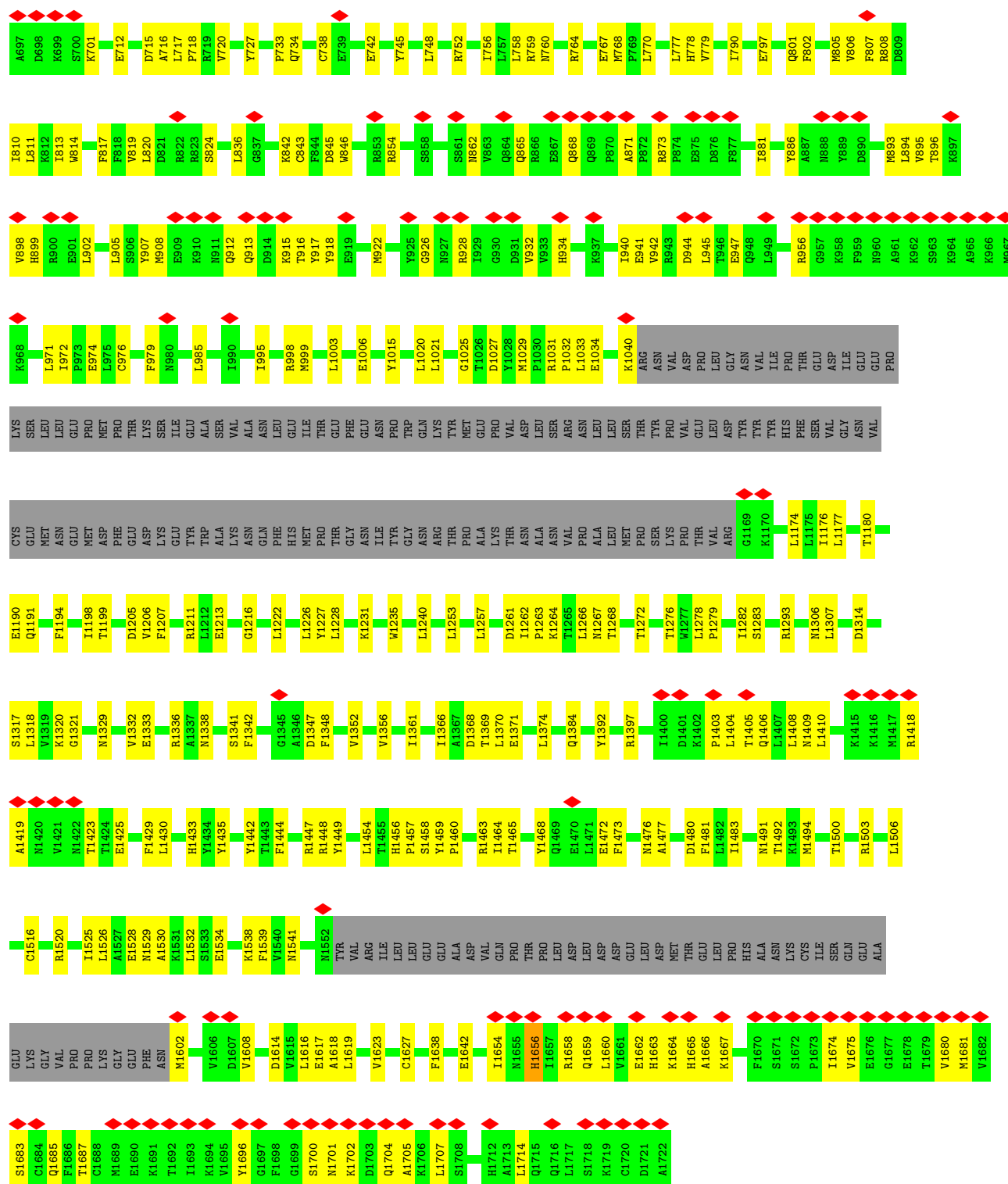


• Molecule 2: dsRNA



• Molecule 3: Dicer-2, isoform A





• Molecule 3: Dicer-2, isoform A



TYR	ASP	TYR	PRO	CYS	F647	A586	N526	L464	K399	I259	Y195	S132	M65	MET
VAL	LYS	VAL	LEU	PRO	R648	F587	D527	E465	C400	R260	R196	L133	T66	E2
VAL	PRO	VAL	GLU	GLU	A649	G588	I528	E466	G403	R261	G197	S134	V67	D3
LEU	LEU	PRO	ASN	PHE	G550	F589	E530	C467	L404	S262	N198	V135	E88	V4
ILE	VAL	LEU	GLY	ASP	R651	V590	E531	I468	L405	K263	I199	V136	L69	E5
LEU	THR	LEU	VAL	ALA	V652	L653	L532	V470	L406	S264	I200	I137	A70	I6
GLY	LYS	LEU	LYS	LEU	I591	P592	K533	Q471	Y408	L265	T201	I138	R71	K7
ALA	HIS	VAL	HIS	PRO	F594	W593	D534	A472	I409	Q266	V202	D139	M75	P8
ARG	ARG	VAL	ARG	ARG	R535	W536	R535	C473	Q410	C267	I202	E140	A76	R9
VAL	VAL	GLY	VAL	VAL	W537	V536	L537	N474	T412	L268	D204	E141	V77	G10
GLU	ALA	GLU	GLU	GLU	E681	V596	E538	H475	P413	R269	T205	H142	R78	Y11
ILE	ASN	ASN	ASN	ILE	L587	L597	E539	V476	E414	D270	K206	H143	R79	Q12
CYS	CYS	PRO	CYS	CYS	Q598	Q598	K539	F477	L415	P271	E207	G144	C80	L13
PHE	PHE	ALA	ALA	VAL	E599	E599	K539	L478	L415	K273	M208	T81	T81	R14
VAL	VAL	ALA	ALA	VAL	D600	D600	L540	L479	R416	K274	E209	N82	N82	L15
THR	THR	GLU	GLU	THR	R601	R601	P542	D480	N417	F276	N210	F150	K84	V16
LEU	LEU	VAL	VAL	LEU	B602	B602	P542	D480	N417	V277	M212	R151	K84	D17
THR	THR	LEU	THR	LEU	D603	D603	E543	V482	V418	K278	L213	E152	G86	T20
ASN	ASN	GLN	GLN	GLU	R604	R604	L544	K483	T420	Q279	Y214	F153	F87	K21
GLN	GLN	ARG	ARG	ARG	T605	T605	E546	T484	Q422	D283	A215	M154	Y88	T20
VAL	VAL	ARG	VAL	VAL	F606	F606	E547	F485	F423	K278	T216	R155	Y89	G24
ALA	ALA	ALA	ALA	ALA	G607	G607	E548	N486	N429	Y286	K217	L156	G90	G24
GLU	GLU	GLU	GLU	GLU	V608	V608	G549	N487	T430	Q287	P18	F157	E91	Y27
GLY	GLY	GLY	GLY	GLY	H550	H550	G549	V488	S431	M288	T219	T158	Q92	L28
THR	THR	THR	THR	THR	A610	A610	H550	Q490	P432	K289	E220	I159	G93	P29
THR	THR	THR	THR	THR	G611	G611	H551	S491	N428	E290	V221	A160	V94	T30
ASN	ASN	ASN	ASN	ASN	G612	G612	D553	Q492	N429	Y291	M222	N161	D95	G31
GLU	GLU	GLU	GLU	GLU	H613	H613	D554	K493	T430	Q292	H227	T163	D96	K34
GLY	GLY	GLY	GLY	GLY	H614	H614	D554	R494	S431	I293	Q228	K164	W97	T35
VAL	VAL	VAL	VAL	VAL	V615	V615	D556	A495	P432	Y294	E229	L165	T98	F36
ASN	ASN	ASN	ASN	ASN	T616	T616	D557	R496	D433	A295	Q230	G100	R99	V37
THR	THR	THR	THR	THR	S617	S617	P557	T497	F434	A296	V231	R167	M101	A38
GLN	GLN	GLN	GLN	GLN	T618	T618	F558	T498	E435	S297	L232	V168	W102	I39
GLY	GLY	GLY	GLY	GLY	N619	N619	T559	E499	S436	I298	T233	G170	D104	V41
PRO	PRO	PRO	PRO	PRO	M620	M620	N560	A500	V437	I300	H227	I106	E105	L42
ARG	ARG	ARG	ARG	ARG	P621	P621	E561	K501	L438	V305	R236	L171	K107	K43
ASN	ASN	ASN	ASN	ASN	V622	V622	N562	F502	E439	D308	L237	T172	K107	R44
THR	THR	THR	THR	THR	N623	N623	G563	N503	R440	I309	L238	G173	K108	R44
ILE	ILE	ILE	ILE	ILE	C624	C624	A564	L504	K441	K310	S239	V174	N109	F45
PHE	PHE	PHE	PHE	PHE	M625	M625	V565	F505	W442	R311	E241	L175	Q110	S46
VAL	VAL	VAL	VAL	VAL	L626	L626	L566	T506	Q443	R312	I242	I176	V111	Q47
ASP	ASP	ASP	ASP	ASP	R627	R627	L567	A507	K444	E243	E243	K177	L112	D48
LEU	LEU	LEU	LEU	LEU	D628	D628	P568	D508	F450	Q313	K244	E180	V113	F49
ARG	ARG	ARG	ARG	ARG	T629	T629	N569	K509	R451	A314	F245	I181	G114	D50
GLN	GLN	GLN	GLN	GLN	V630	V630	N570	E510	D451	E315	Y246	I181	G114	K51
THR	THR	THR	THR	THR	G631	G631	L572	R511	D452	T316	V247	T182	V118	P52
ALA	ALA	ALA	ALA	ALA	P634	P634	A573	I515	D452	L317	S248	N183	F119	I53
GLU	GLU	GLU	GLU	GLU	M635	M635	L574	Q516	G453	S318	L249	I183	F119	E54
SER	SER	SER	SER	SER	D636	D636	L575	Q517	L389	V319	D250	D121	L120	S55
THR	THR	THR	THR	THR	N637	N637	L576	I518	V390	K320	L251	M122	Q125	G56
ASN	ASN	ASN	ASN	ASN	V638	V638	R577	Y519	F391	L321	M252	K188	T126	G57
ALA	ALA	ALA	ALA	ALA	T640	T640	L578	Q520	V392	N253	I254	E190	Q125	K58
GLU	GLU	GLU	GLU	GLU	A641	A641	V578	Y521	V392	K322	G255	L191	L130	A80
GLN	GLN	GLN	GLN	GLN	R642	R642	G579	V521	V392	H323	V256	E192	S131	L61
GLN	GLN	GLN	GLN	GLN	I643	I643	T582	H525	S461	L329	T397	I193	G130	F62
GLN	GLN	GLN	GLN	GLN	A645	A645	T584	V463	C398		P258	T194	S131	M63
GLN	GLN	GLN	GLN	GLN	A646	A646	D585							C64



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71991	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.941	Depositor
Minimum map value	-0.327	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	277.12, 277.12, 277.12	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0825, 1.0825, 1.0825	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: ADP, MG

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	B	0.25	0/146	0.45	0/192
1	G	0.27	0/119	0.44	0/156
2	C	0.15	0/1228	0.66	0/1911
2	D	0.15	0/1231	0.68	0/1915
3	A	0.25	0/12759	0.49	0/17259
3	F	0.25	0/5411	0.51	0/7310
All	All	0.24	0/20894	0.52	0/28743

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	B	144	0	140	8	0
1	G	117	0	112	3	0
2	C	1100	0	560	32	0
2	D	1103	0	559	26	0
3	A	12490	0	12567	358	0
3	F	5312	0	5377	195	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	1	0	0	0	0
5	A	27	0	12	3	0
5	F	27	0	12	3	0
All	All	20322	0	19339	593	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 593 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)
3:F:34:LYS:HB2	3:F:171:LEU:HD11	1.47	0.96
3:F:618:ILE:HD11	3:F:645:ALA:HB1	1.55	0.88
3:A:62:PHE:HB3	3:A:113:VAL:HG12	1.63	0.79
3:F:495:ALA:HB1	3:F:500:ALA:HB1	1.70	0.74
3:F:290:GLU:OE2	3:F:366:LYS:NZ	2.20	0.73

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	B	14/359 (4%)	12 (86%)	2 (14%)	0	100	100
1	G	11/359 (3%)	9 (82%)	2 (18%)	0	100	100
3	A	1538/1722 (89%)	1464 (95%)	73 (5%)	1 (0%)	51	85
3	F	658/1722 (38%)	624 (95%)	34 (5%)	0	100	100
All	All	2221/4162 (53%)	2109 (95%)	111 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	1656	HIS

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	B	16/289 (6%)	16 (100%)	0	100	100
1	G	13/289 (4%)	13 (100%)	0	100	100
3	A	1386/1549 (90%)	1382 (100%)	4 (0%)	92	95
3	F	596/1549 (38%)	593 (100%)	3 (0%)	88	93
All	All	2011/3676 (55%)	2004 (100%)	7 (0%)	92	95

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	1447	ARG
3	F	217	LYS
3	F	440	ARG
3	F	427	ARG
3	A	627	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	361	ASN
3	F	410	GLN
3	F	471	GLN
3	A	1456	HIS
3	A	1659	GLN

5.3.3 RNA [i](#)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	51/52 (98%)	1 (1%)	0
2	D	51/52 (98%)	1 (1%)	0
All	All	102/104 (98%)	2 (1%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	D	23	U
2	C	52	U

There are no RNA pucker outliers to report.

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
5	ADP	A	1802	4	24,29,29	0.94	1 (4%)	29,45,45	1.48	4 (13%)
5	ADP	F	1802	4	24,29,29	0.95	1 (4%)	29,45,45	1.46	4 (13%)

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
5	ADP	A	1802	4	-	2/12/32/32	0/3/3/3
5	ADP	F	1802	4	-	1/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1802	ADP	C5-C4	2.45	1.47	1.40
5	F	1802	ADP	C5-C4	2.43	1.47	1.40

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1802	ADP	PA-O3A-PB	-3.62	120.40	132.83
5	A	1802	ADP	PA-O3A-PB	-3.51	120.79	132.83
5	F	1802	ADP	N3-C2-N1	-3.28	123.55	128.68
5	A	1802	ADP	C3'-C2'-C1'	3.17	105.76	100.98
5	A	1802	ADP	N3-C2-N1	-3.07	123.88	128.68

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	1802	ADP	C5'-O5'-PA-O1A
5	A	1802	ADP	O4'-C4'-C5'-O5'
5	A	1802	ADP	PA-O3A-PB-O1B

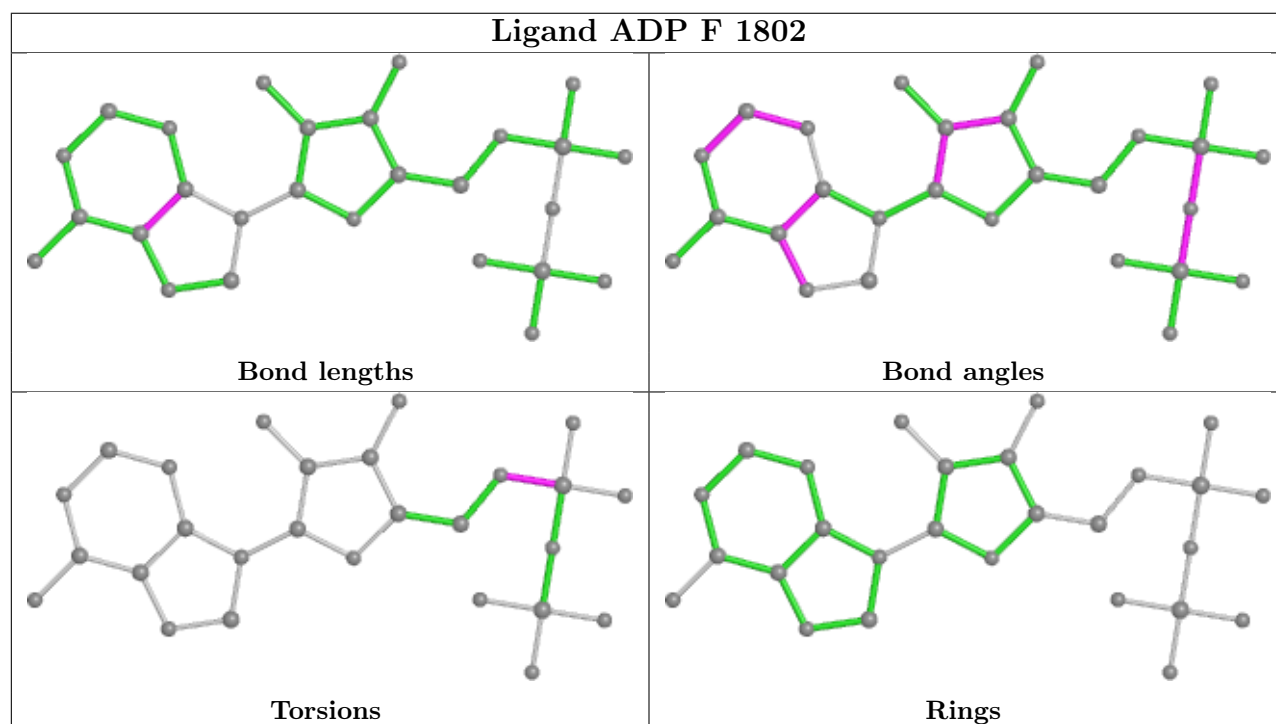
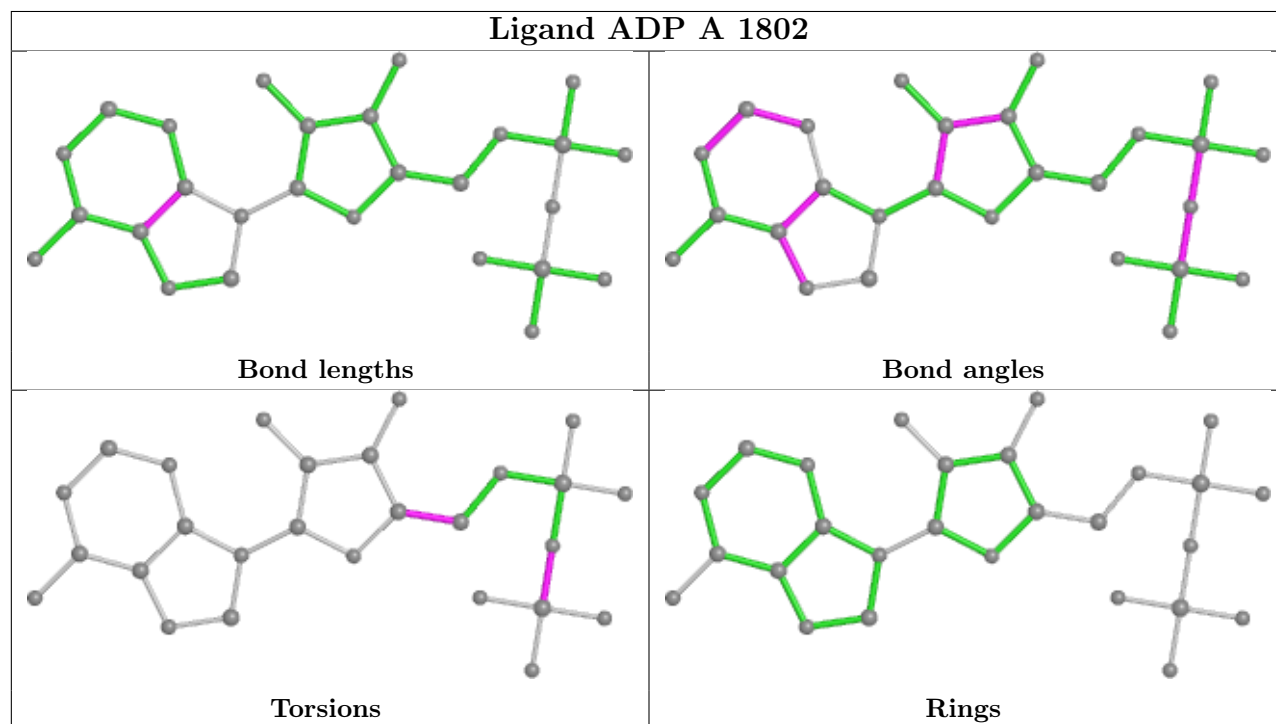
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1802	ADP	3	0
5	F	1802	ADP	3	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.

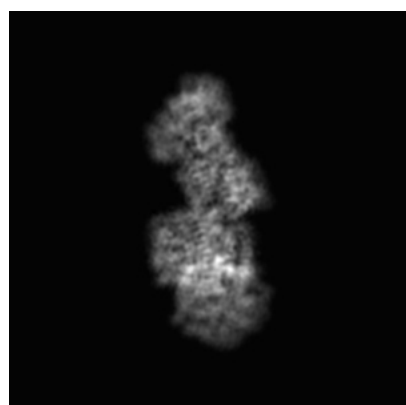
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32239. These allow visual inspection of the internal detail of the map and identification of artifacts.

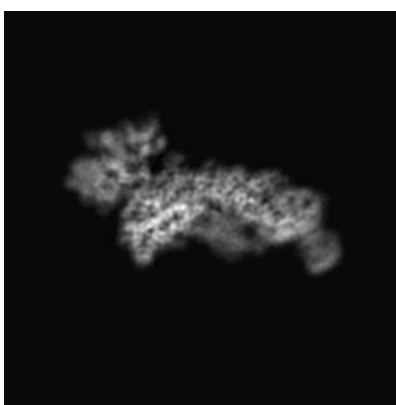
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

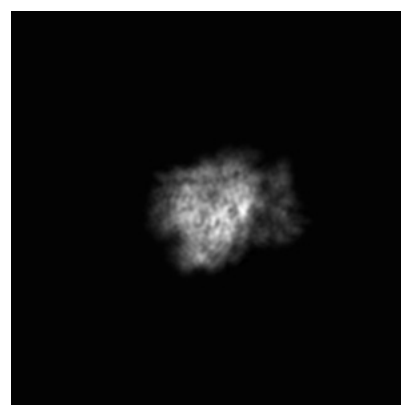
6.1.1 Primary map



X



Y

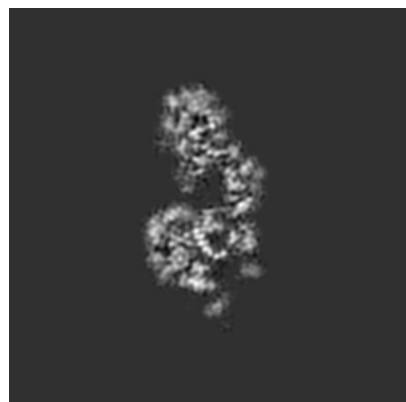


Z

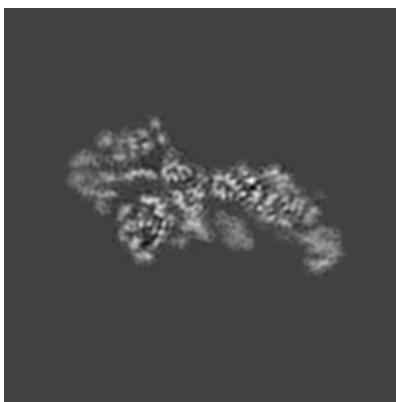
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

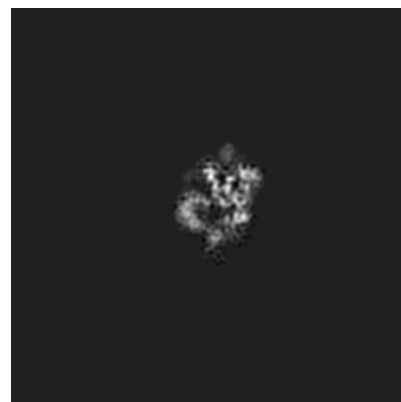
6.2.1 Primary map



X Index: 128



Y Index: 128

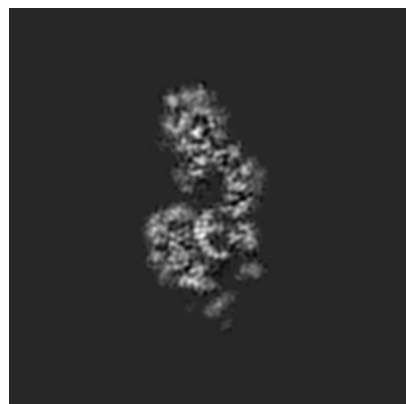


Z Index: 128

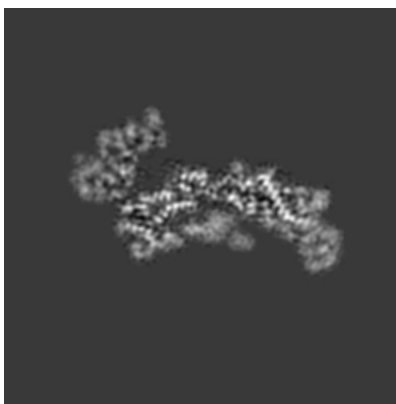
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

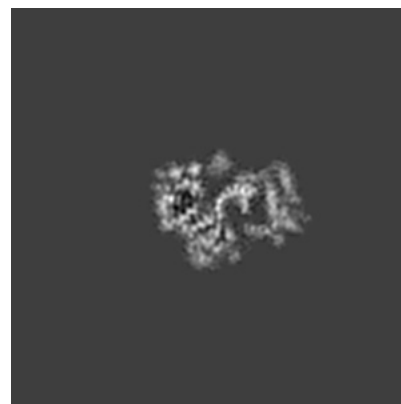
6.3.1 Primary map



X Index: 129



Y Index: 122

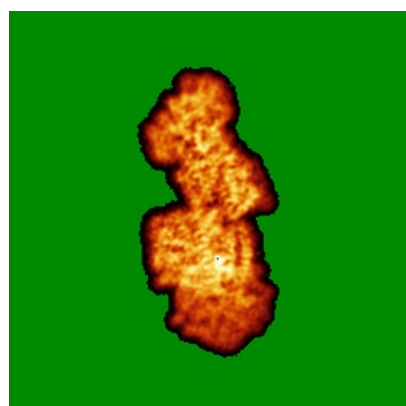


Z Index: 91

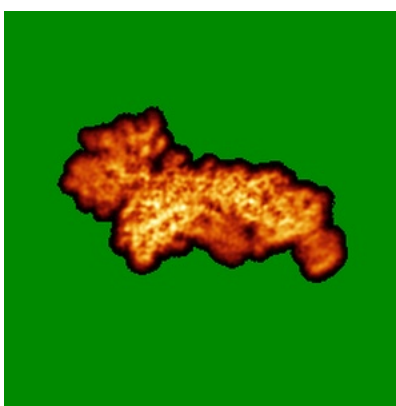
The images above show the largest variance slices of the map in three orthogonal directions.

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

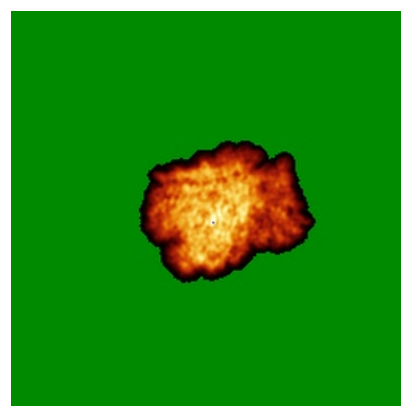
6.4.1 Primary map



X



Y

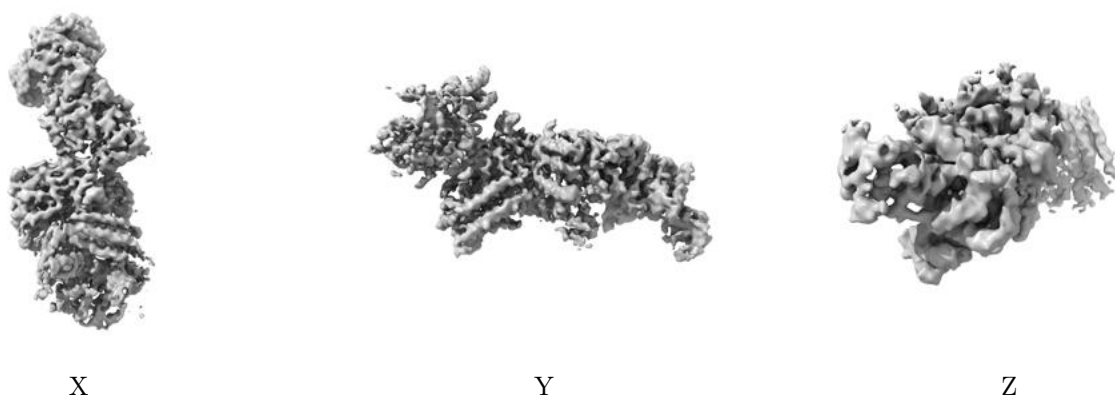


Z

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 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

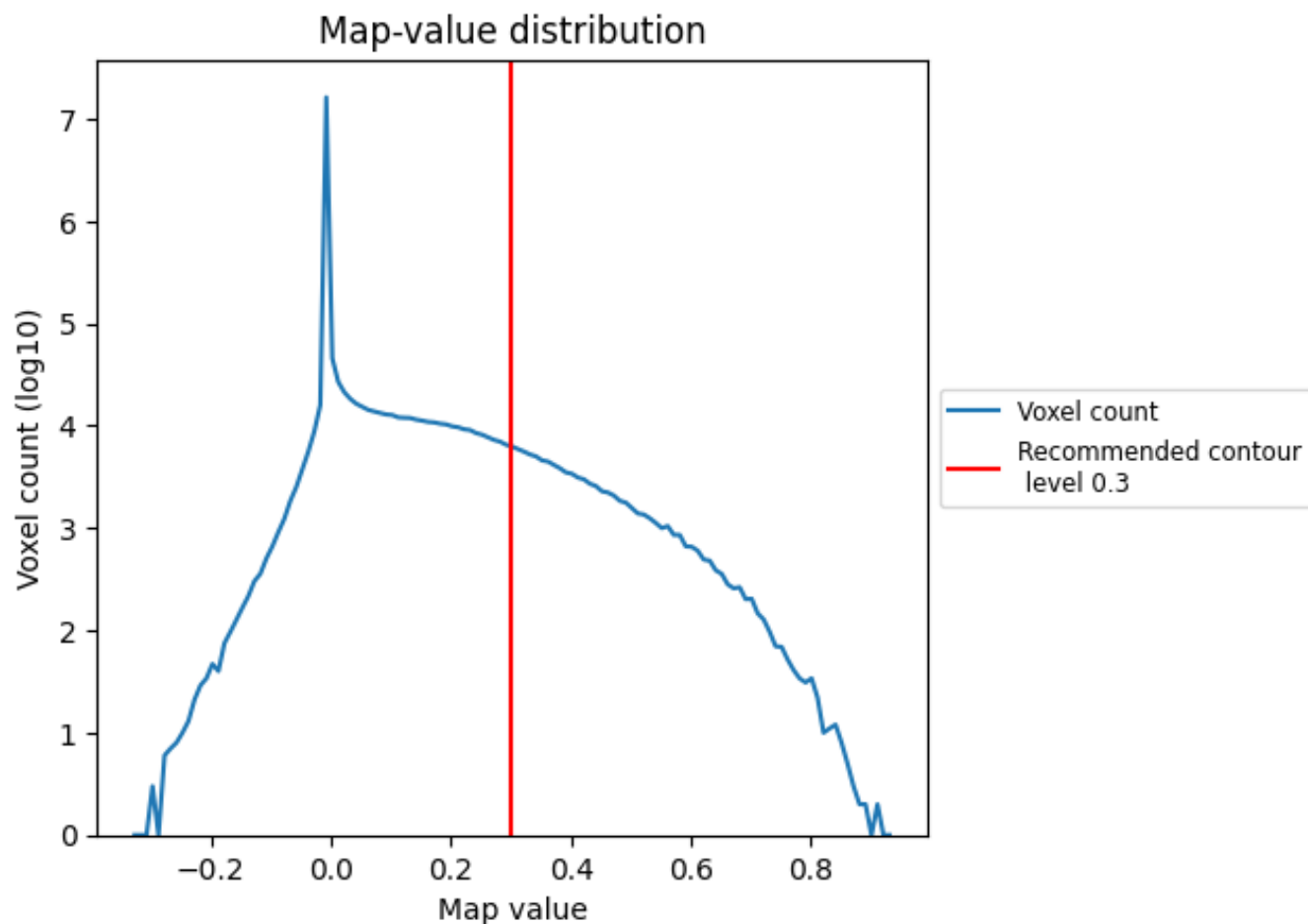
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

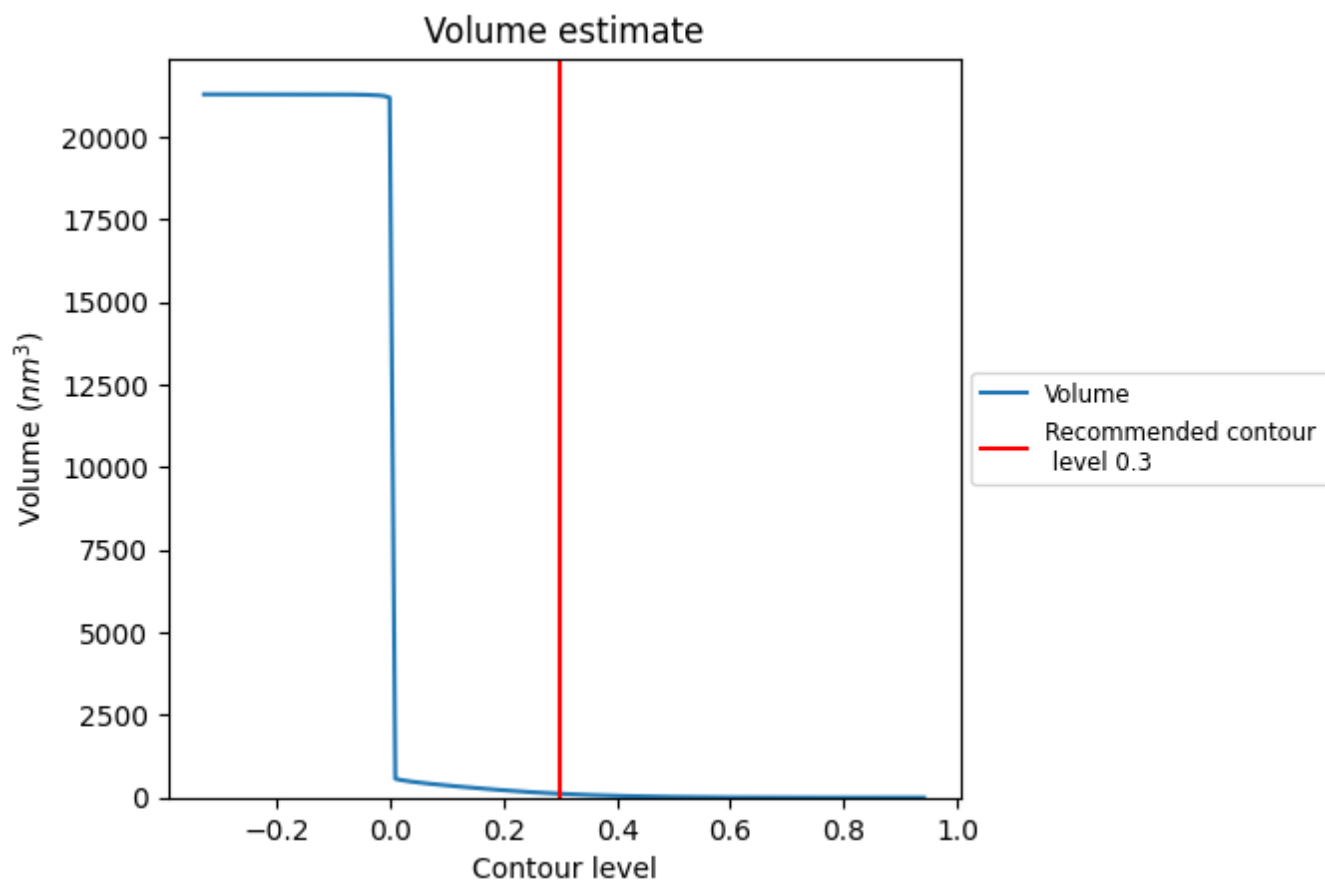
This section contains the results of statistical analysis of the map.

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.

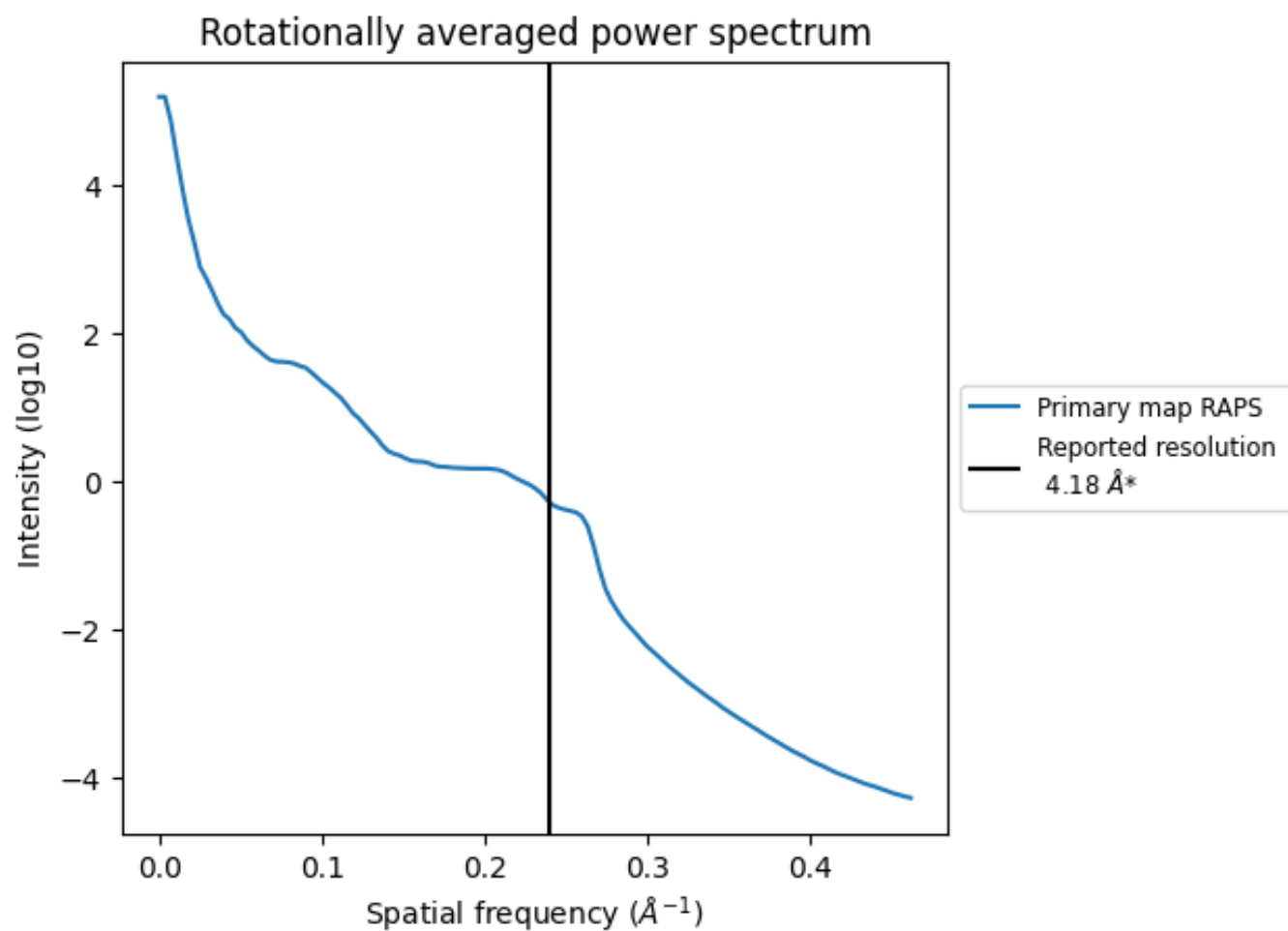
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 116 nm³; this corresponds to an approximate mass of 104 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 0.239 Å⁻¹

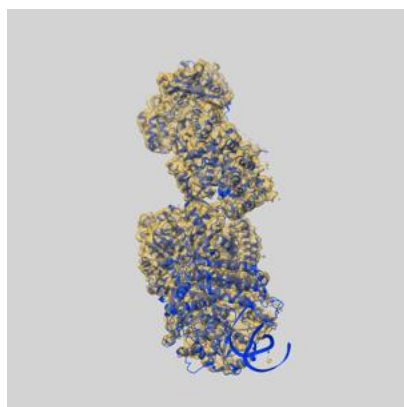
8 Fourier-Shell correlation

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

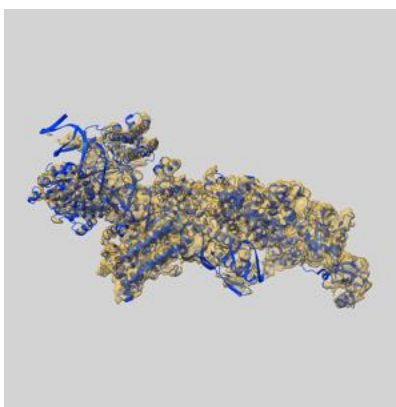
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32239 and PDB model 7W0D. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

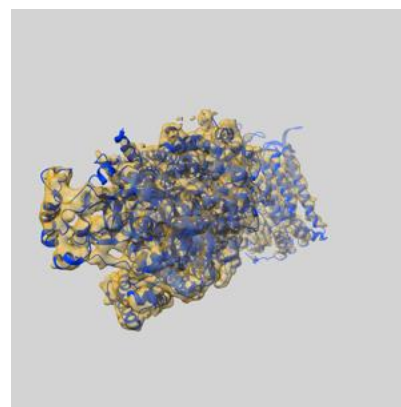
9.1 Map-model overlay [i](#)



X



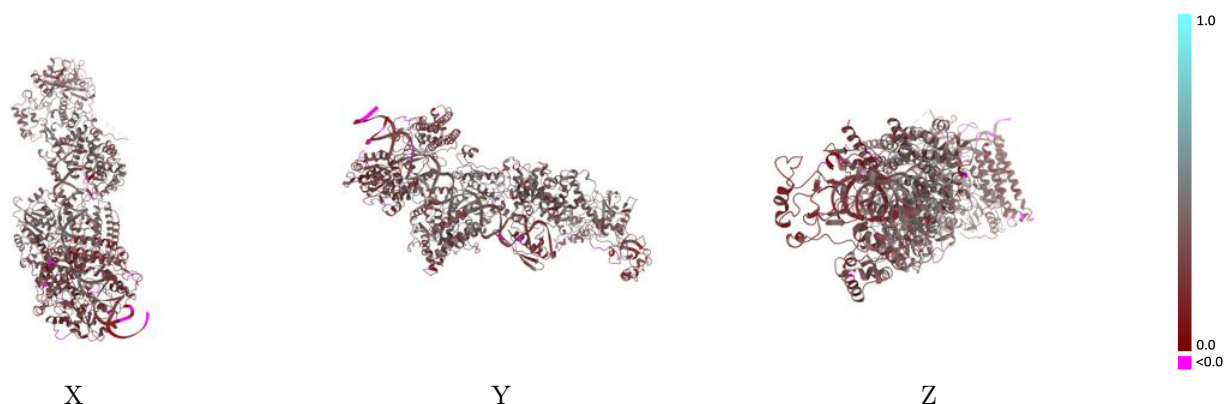
Y



Z

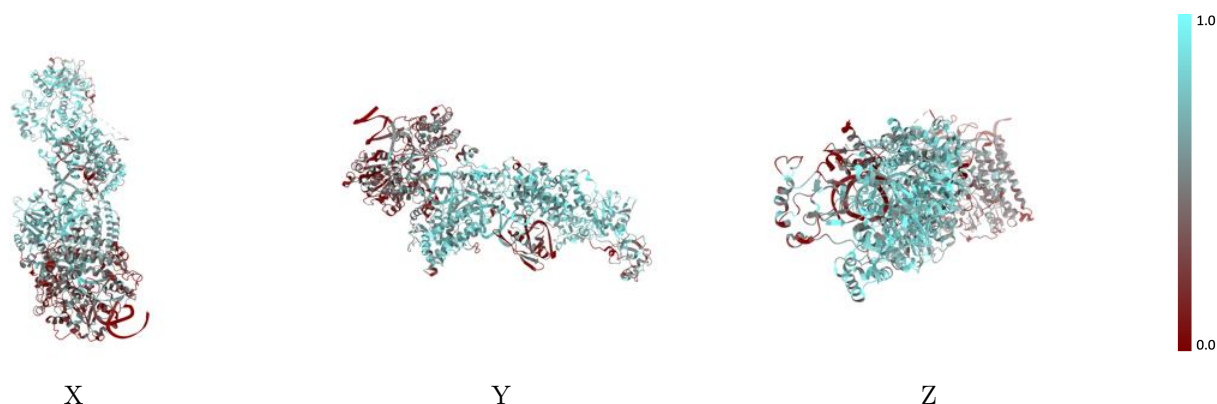
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



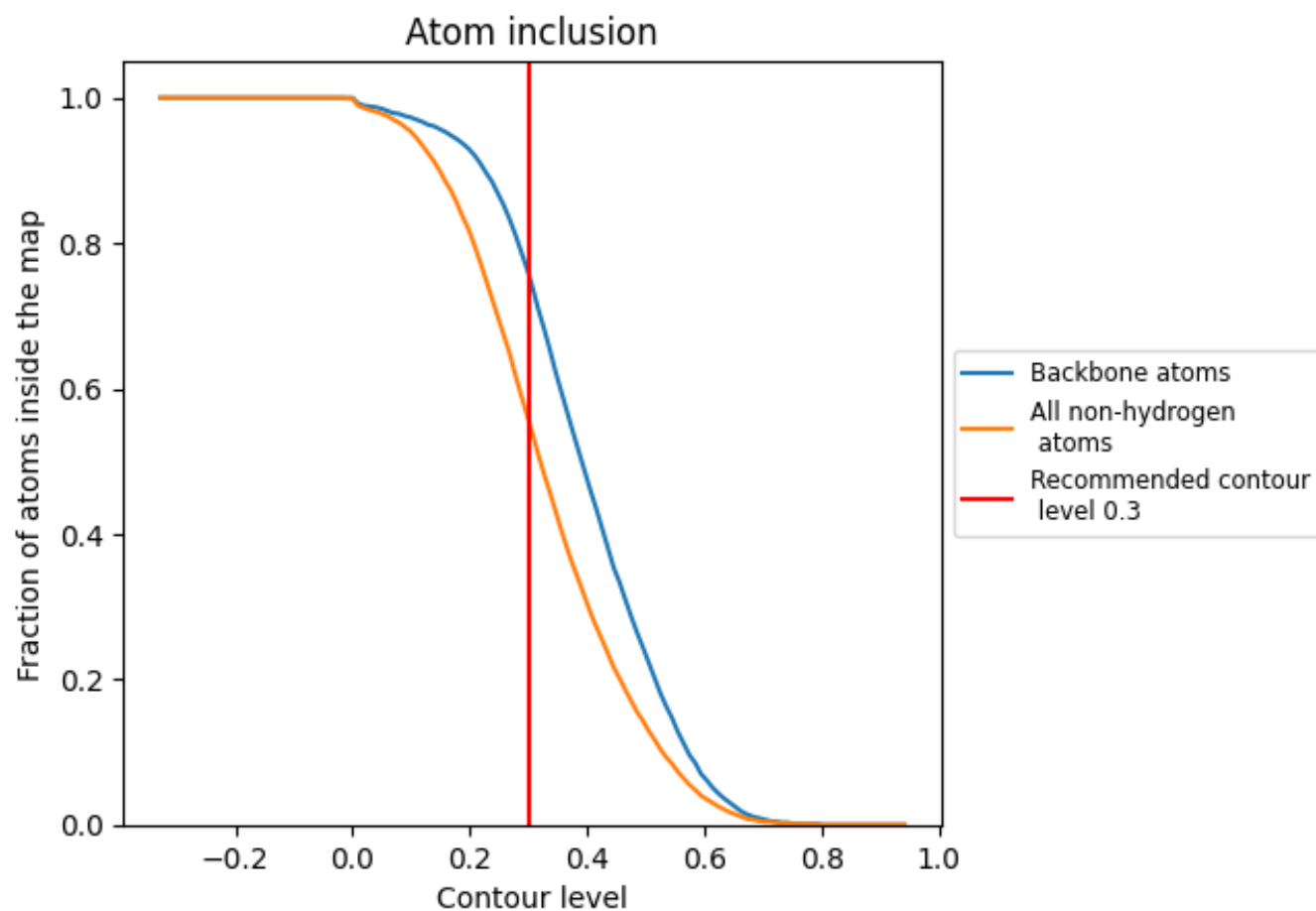
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 56% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5570	<div></div> 0.3180
A	<div></div> 0.6630	<div></div> 0.3440
B	<div></div> 0.5460	<div></div> 0.3250
C	<div></div> 0.6000	<div></div> 0.2880
D	<div></div> 0.5600	<div></div> 0.2890
F	<div></div> 0.3090	<div></div> 0.2700
G	<div></div> 0.0690	<div></div> 0.2760

