



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 04:50 AM UTC

PDB ID : 7CKW / pdb_00007ckw
EMDB ID : EMD-30392
Title : Cryo-EM structure of Fenoldopam bound dopamine receptor DRD1-Gs signaling complex
Authors : Yan, W.; Shao, W.
Deposited on : 2020-07-20
Resolution : 3.22 Å(reported)
Based on initial model : 3SN6

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

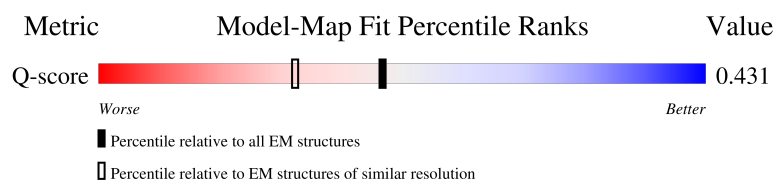
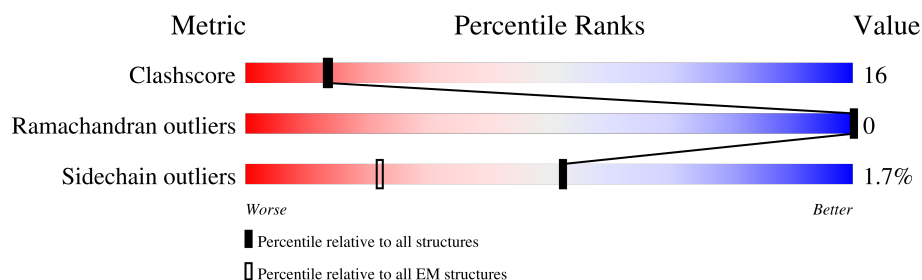
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.22 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	14612 (2.72 - 3.72)

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	394	15% 44% 16% 40%
2	B	356	13% 59% 36% • •
3	G	71	41% 69% 13% 18%
4	N	156	10% 45% 36% • 18%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	R	453	15%44%16%40%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8103 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 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	236	1906	1204	347	348	7	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	THR	SER	engineered mutation	UNP P63092
A	226	ALA	GLY	engineered mutation	UNP P63092
A	366	SER	ALA	engineered mutation	UNP P63092

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	340	2587	1597	462	507	21	0	0

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	initiating methionine	UNP P62873
B	-14	HIS	-	expression tag	UNP P62873
B	-13	HIS	-	expression tag	UNP P62873
B	-12	HIS	-	expression tag	UNP P62873
B	-11	HIS	-	expression tag	UNP P62873
B	-10	LEU	-	expression tag	UNP P62873
B	-9	GLU	-	expression tag	UNP P62873
B	-8	VAL	-	expression tag	UNP P62873
B	-7	LEU	-	expression tag	UNP P62873
B	-6	PHE	-	expression tag	UNP P62873
B	-5	GLN	-	expression tag	UNP P62873
B	-4	GLY	-	expression tag	UNP P62873

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PRO	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	58	Total	C	N	O	S	0	0
			438	274	76	85	3		

- Molecule 4 is a protein called nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	128	Total	C	N	O	S	0	0
			970	604	170	190	6		

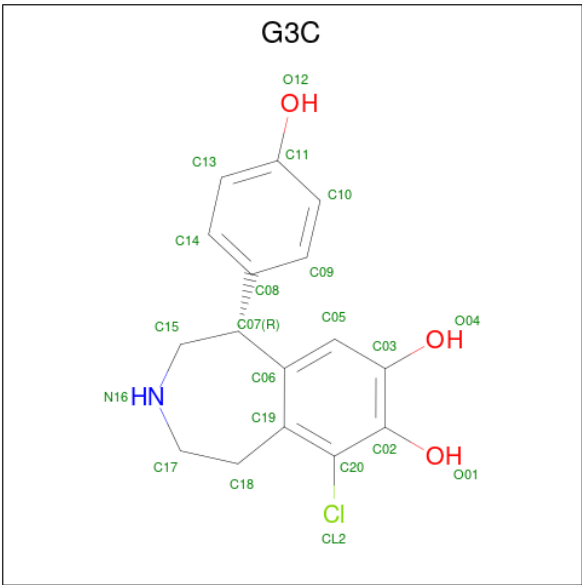
- Molecule 5 is a protein called D(1A) dopamine receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	273	Total	C	N	O	S	0	0
			2153	1436	347	354	16		

There are 7 discrepancies between the modelled and reference sequences:

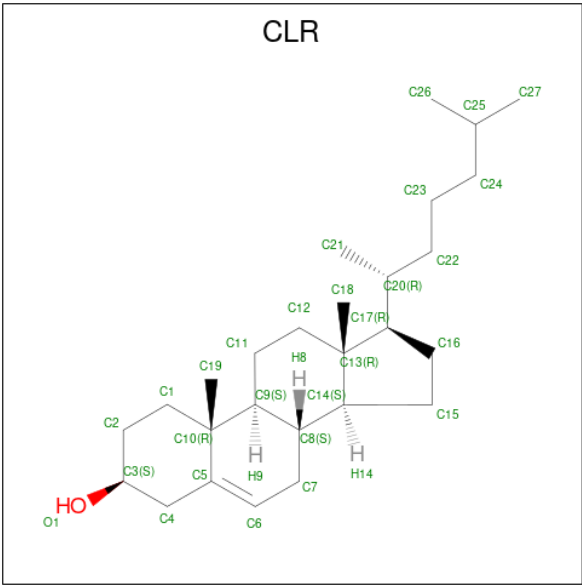
Chain	Residue	Modelled	Actual	Comment	Reference
R	-6	ASP	-	expression tag	UNP P21728
R	-5	TYR	-	expression tag	UNP P21728
R	-4	ASP	-	expression tag	UNP P21728
R	-3	ASP	-	expression tag	UNP P21728
R	-2	ASP	-	expression tag	UNP P21728
R	-1	LYS	-	expression tag	UNP P21728
R	0	ALA	-	expression tag	UNP P21728

- Molecule 6 is (1R)-6-chloranyl-1-(4-hydroxyphenyl)-2,3,4,5-tetrahydro-1H-3-benzazepine-7,8-diol (CCD ID: G3C) (formula: C₁₆H₁₆ClNO₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
6	R	1	Total	C	Cl	N	O	0
			21	16	1	1	3	

- Molecule 7 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).

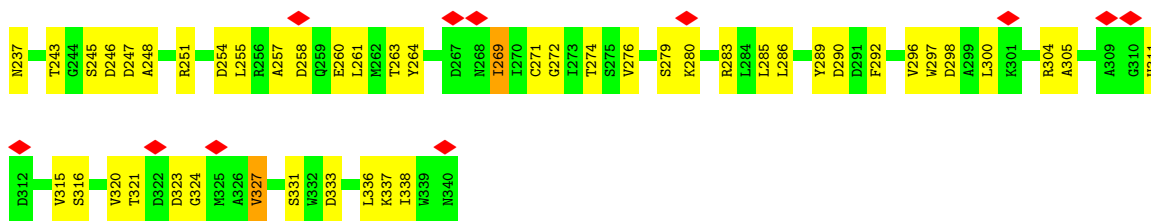


Mol	Chain	Residues	Atoms			AltConf
7	R	1	Total	C	O	0
			28	27	1	

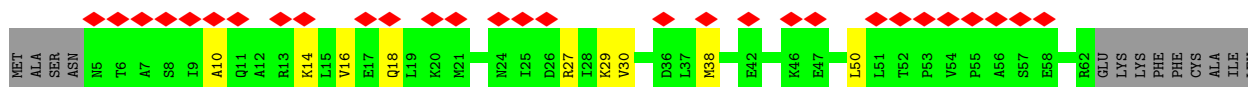
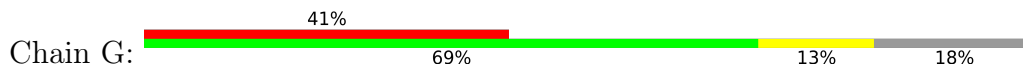
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

- Chain A:
-
- 15%
44%
16%
40%
- 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
- ALA ARG ARG ARG
PHE PHE PHE
PRO PRO
GLU GLU
THR THR
PHE PHE
GLU GLU
HIS HIS
ALA ALA
LYS LYS
VAL VAL
LEU LEU
TRP TRP
GLU GLU
ASP ASP
GLY GLY
VAL VAL
ARG ARG
ALA ALA
CYS CYS
TYR TYR
GLU GLU
ARG ARG
SER SER
ASN ASN
GLU GLU
TYR TYR
ALA ALA
MET MET
LEU LEU
VAL VAL
CYS CYS
ALA ALA
GLN GLN
TYR TYR
PHE PHE
LEU LEU
ASP ASP
LYS LYS
ILE ILE
ASP ASP
VAL VAL
GLN GLN
PRO PRO
TYR TYR
ILE ILE
LEU LEU
SER SER
VAL VAL
ASP ASP
GLN GLN
PHE PHE
ARG ARG
ALA ALA
ASP ASP
TYR TYR
VAL VAL
PRO PRO
SER SER
VAL VAL
MET MET
ASN ASN
GLY GLY
VAL VAL
PRO PRO
ASP ASP
- CYS
ARG
VAL
THR
T205
G206
N218
F219
H220
M221
F222
D223
V224
G225
A226
Q227
R228
D229
E230
C231
R232
K233
W234
N239
D240
V241
T244
I245
V248
S251
S252
Y253
N254
W255
VAL
ILE
ARG
GLU
ASP
ASN
GLN
T263
N264
R265
L266
Q267
E268
A269
L270
T276
W277
N278
- W281
L282
L283
T284
L285
S286
L289
F290
L291
N292
K293
Q294
T295
L296
L297
A298
E299
K300
V301
L302
A303
G304
K305
S306
K307
L308
E309
D310
Y311
F312
P313
E314
F315
A316
R317
E322
D323
E327
F328
G329
E330
D331
P332
R333
R336
I341
R342
D343
E344
F345
L346
S349
T350
- G353
D354
G355
R356
H357
Y358
P361
T364
C365
S366
V367
D368
T369
E370
C379
R380
D381
I382
T383
Q384
L388
L394

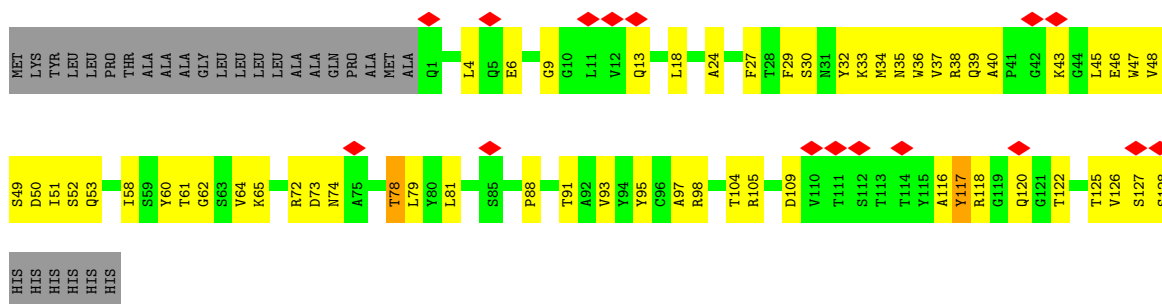
- Chain B:
-
- 13%
- 59%
- 36%
-
- Chain B:
- 13%
- 59%
- 36%
-



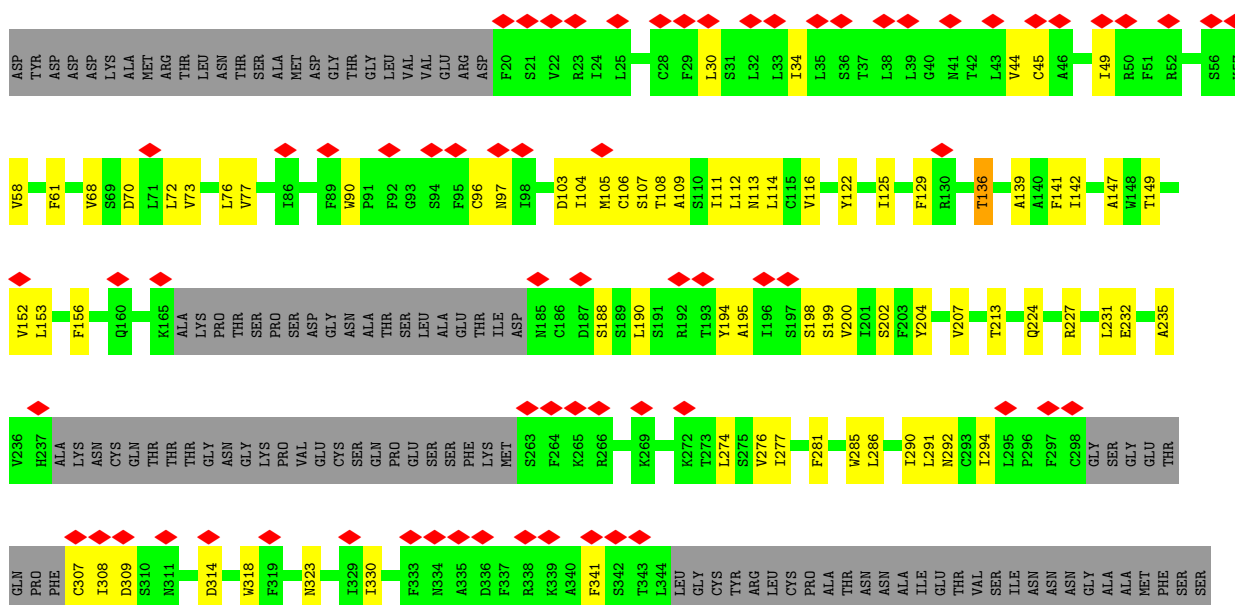
- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



- Molecule 4: nanobody 35



- Molecule 5: D(1A) dopamine receptor



HIS
HIS
GLU
PRO
ILE
ARG
GLY
SER
ILE
SER
LYS
GLU
CYS
ASN
LEU
VAL
TYR
LEU
ILE
PRO
HIS
ALA
VAL
GLY
SER
SER
GLU
ASP
LEU
LYS
LYS
GLU
GLU
ALA
ALA
GLY
ILE
ALA
ARG
PRO
LEU
GLU
LYS
LEU
SER
PRO
ALA
LEU
SER
VAL
ILE
LEU
TYR
ASP
THR
ASP
VAL
SER
LEU
GLU

LYS
ILE
GLN
PRO
ILE
THR
GLN
ASN
GLY
GLN
HIS
PRO
THR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	539327	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 ($e^-/\text{\AA}^2$)	64	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	0.178	Depositor
Minimum map value	-0.115	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0251	Depositor
Map size (Å)	216.0, 216.0, 216.0	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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: CLR, G3C

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	0.13	0/1942	0.28	0/2616
2	B	0.12	0/2634	0.31	0/3573
3	G	0.08	0/444	0.20	0/601
4	N	0.10	0/990	0.30	0/1341
5	R	0.12	0/2210	0.30	0/3012
All	All	0.12	0/8220	0.29	0/11143

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	A	1906	0	1842	59	0
2	B	2587	0	2480	116	0
3	G	438	0	443	8	0
4	N	970	0	930	51	0
5	R	2153	0	2193	56	0
6	R	21	0	0	2	0
7	R	28	0	46	12	0
All	All	8103	0	7934	255	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 16.

The worst 5 of 255 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)
2:B:200:VAL:HG12	2:B:234:PHE:CE2	1.71	1.26
2:B:200:VAL:CG1	2:B:234:PHE:CE2	2.20	1.24
4:N:91:THR:OG1	4:N:126:VAL:HG22	1.37	1.19
2:B:200:VAL:HB	2:B:234:PHE:CE2	1.77	1.18
2:B:200:VAL:CB	2:B:234:PHE:CE2	2.27	1.16

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	230/394 (58%)	223 (97%)	7 (3%)	0	100	100
2	B	338/356 (95%)	328 (97%)	10 (3%)	0	100	100
3	G	56/71 (79%)	54 (96%)	2 (4%)	0	100	100
4	N	126/156 (81%)	119 (94%)	7 (6%)	0	100	100
5	R	265/453 (58%)	261 (98%)	4 (2%)	0	100	100
All	All	1015/1430 (71%)	985 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	197/351 (56%)	195 (99%)	2 (1%)	68	78
2	B	277/296 (94%)	272 (98%)	5 (2%)	51	72
3	G	46/58 (79%)	45 (98%)	1 (2%)	45	69
4	N	104/126 (82%)	100 (96%)	4 (4%)	29	60
5	R	236/395 (60%)	233 (99%)	3 (1%)	61	75
All	All	860/1226 (70%)	845 (98%)	15 (2%)	52	72

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	50	LEU
5	R	114	LEU
4	N	4	LEU
5	R	136	THR
4	N	117	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
4	N	123	GLN
5	R	323	ASN
5	R	292	ASN
2	B	266	HIS
4	N	120	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 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	$\# Z > 2$
7	CLR	R	502	-	31,31,31	0.28	0	48,48,48	0.33	0
6	G3C	R	501	-	23,23,23	1.48	3 (13%)	25,33,33	0.72	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
7	CLR	R	502	-	-	8/10/68/68	0/4/4/4
6	G3C	R	501	-	-	0/4/15/15	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	501	G3C	C18-C19	4.18	1.55	1.51
6	R	501	G3C	C20-CL2	2.86	1.78	1.72
6	R	501	G3C	O04-C03	2.04	1.40	1.36

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

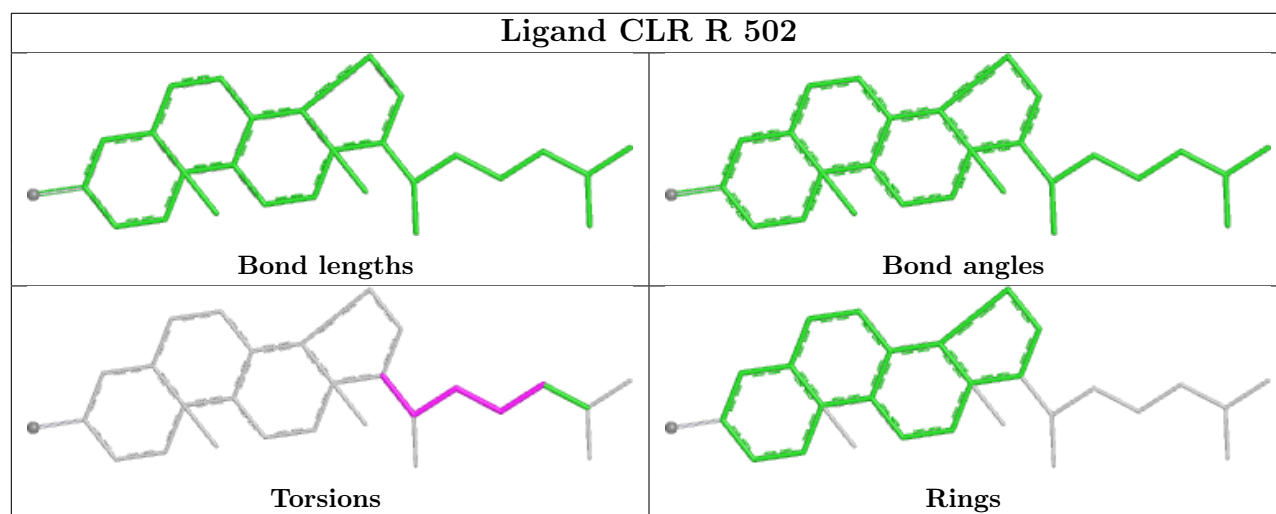
Mol	Chain	Res	Type	Atoms
7	R	502	CLR	C21-C20-C22-C23
7	R	502	CLR	C22-C23-C24-C25
7	R	502	CLR	C16-C17-C20-C21
7	R	502	CLR	C13-C17-C20-C22
7	R	502	CLR	C13-C17-C20-C21

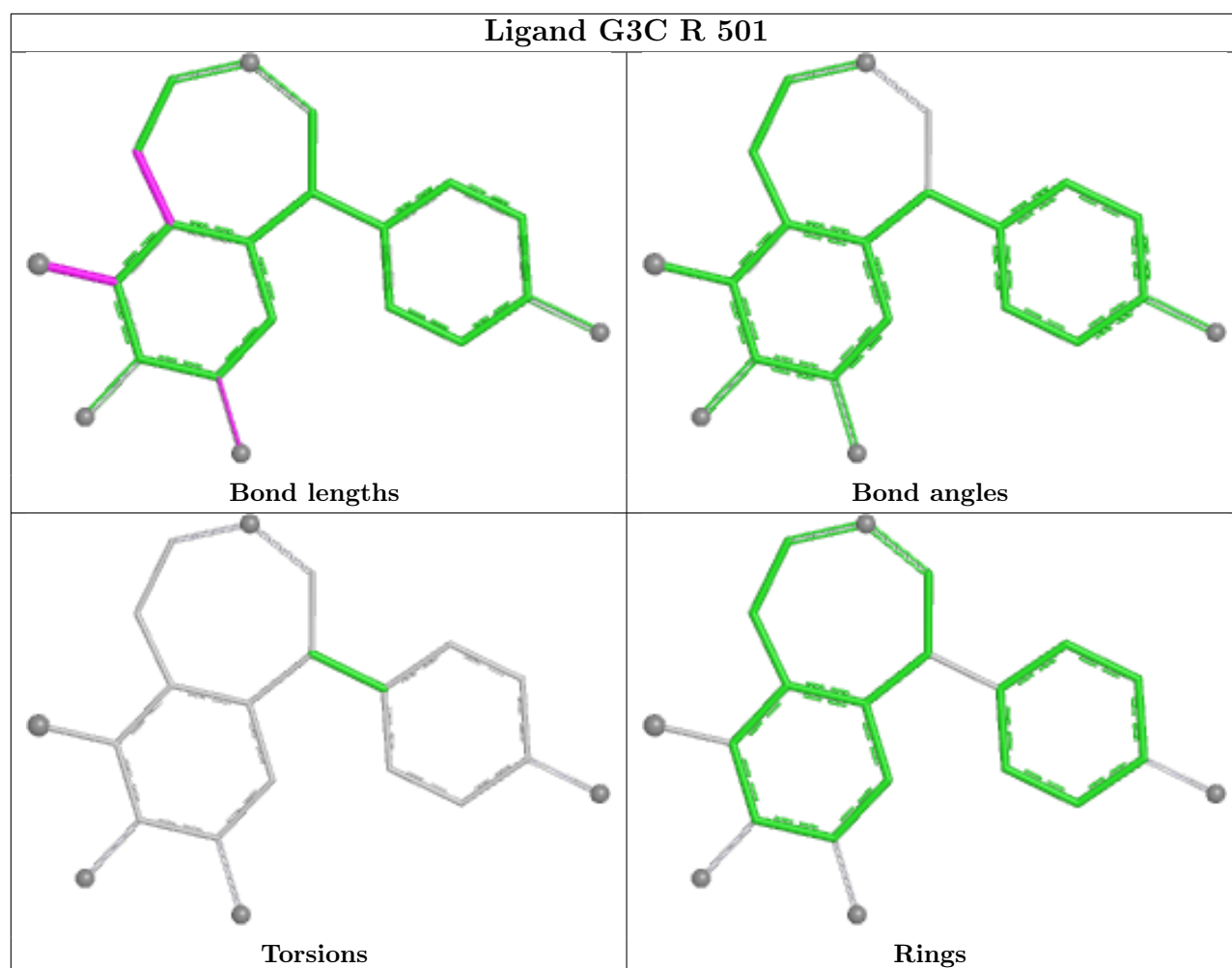
There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	R	502	CLR	12	0
6	R	501	G3C	2	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.

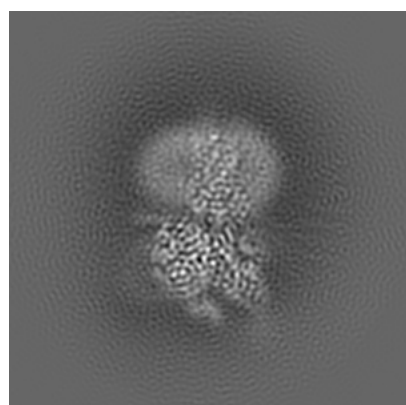
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30392. These allow visual inspection of the internal detail of the map and identification of artifacts.

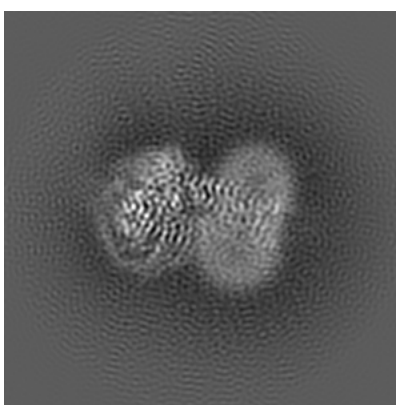
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

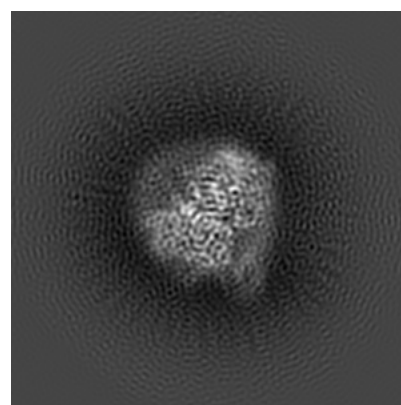
6.1.1 Primary map



X



Y

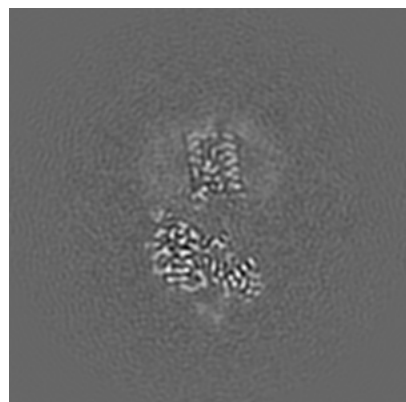


Z

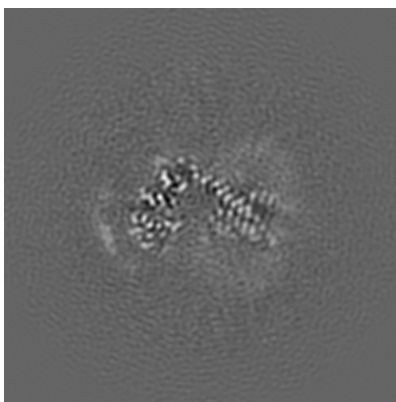
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

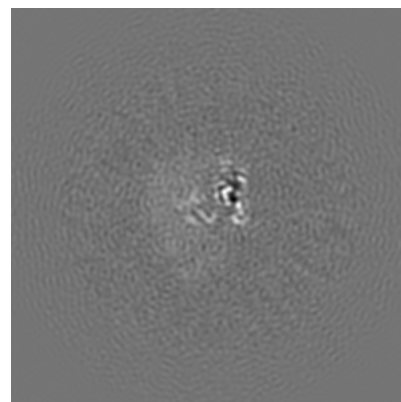
6.2.1 Primary map



X Index: 108



Y Index: 108

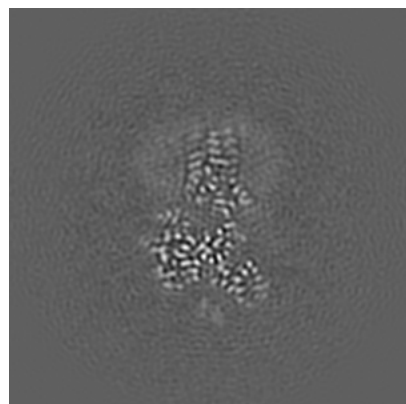


Z Index: 108

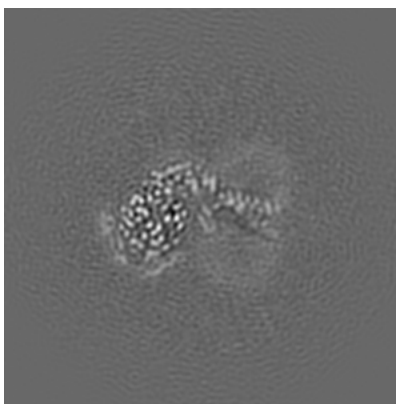
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

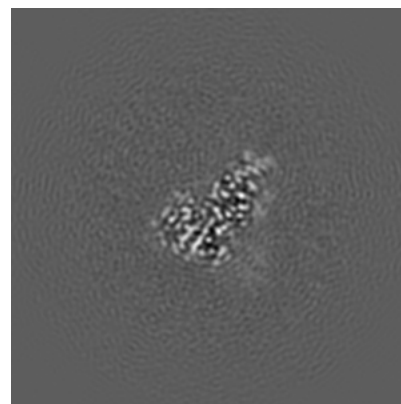
6.3.1 Primary map



X Index: 112



Y Index: 100

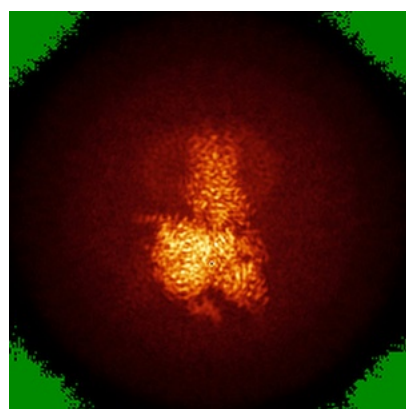


Z Index: 86

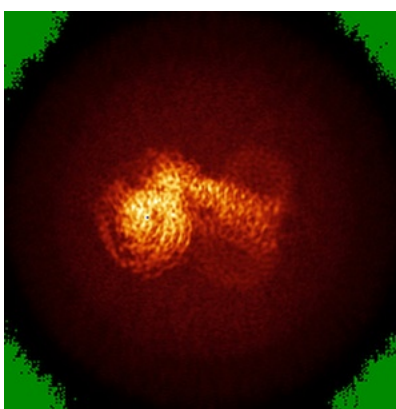
The images above show the largest variance slices of the map in three orthogonal directions.

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

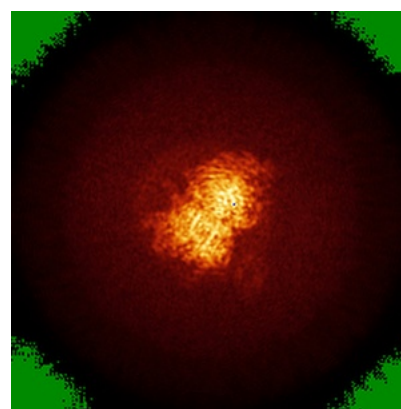
6.4.1 Primary map



X



Y

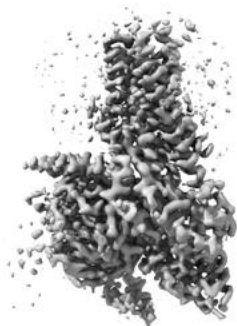


Z

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 0.0251. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

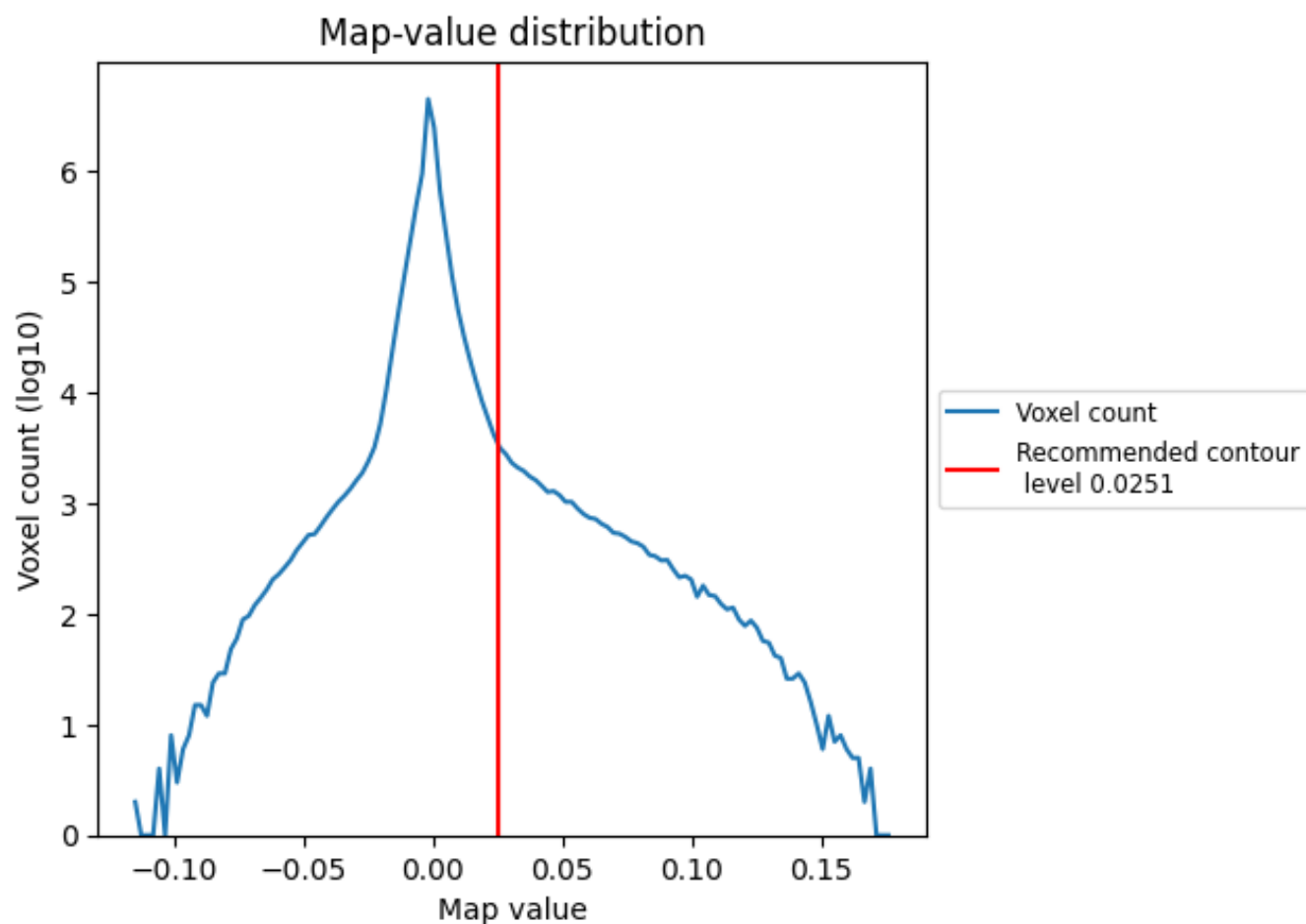
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

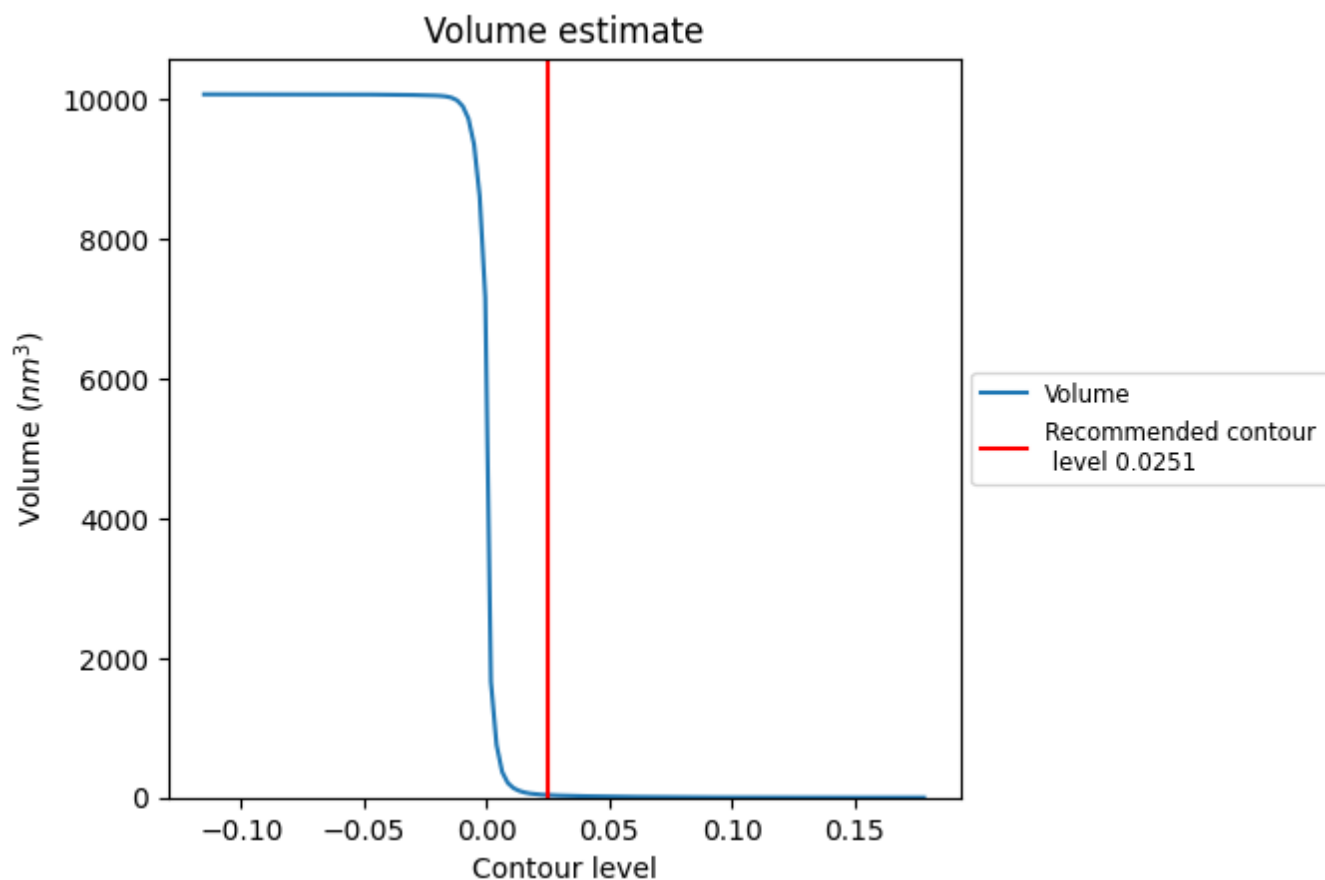
This section contains the results of statistical analysis of the map.

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.

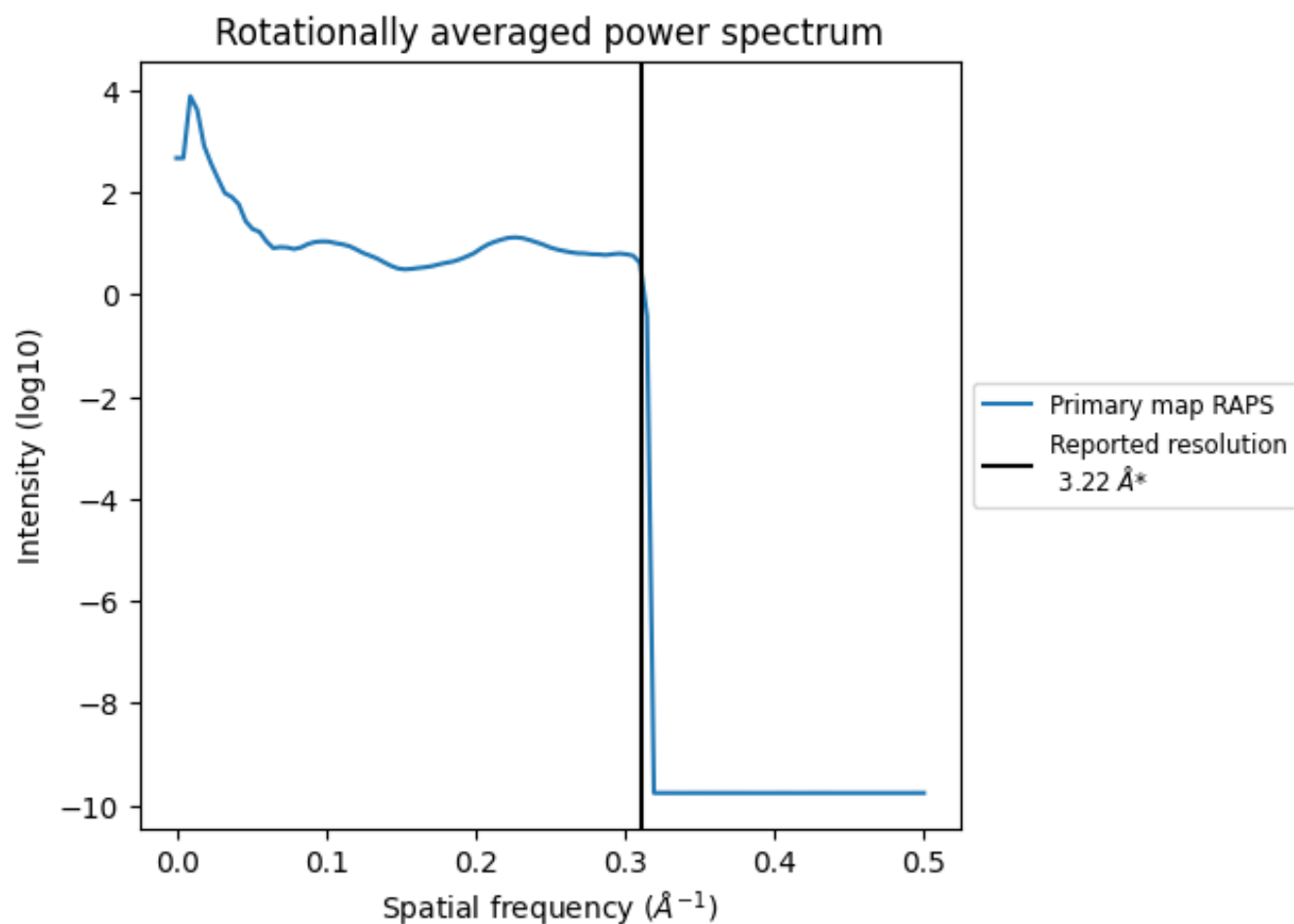
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 35 nm³; this corresponds to an approximate mass of 32 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 0.311 $\text{\AA}^{-1}$

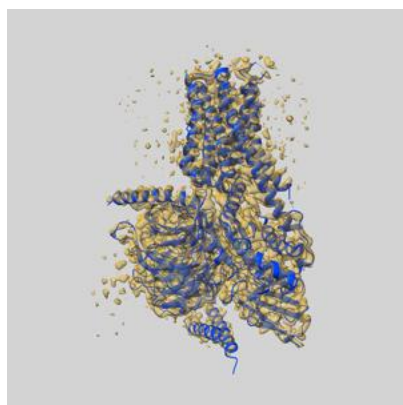
8 Fourier-Shell correlation ⓘ

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

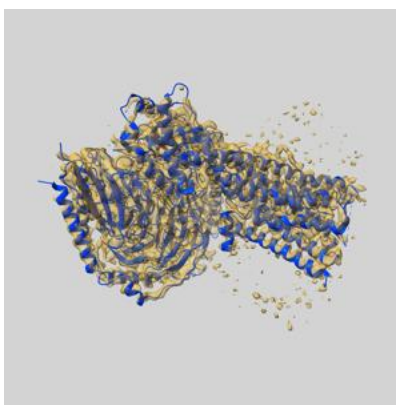
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30392 and PDB model 7CKW. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

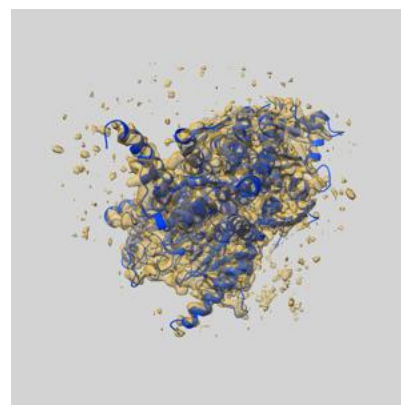
9.1 Map-model overlay [i](#)



X



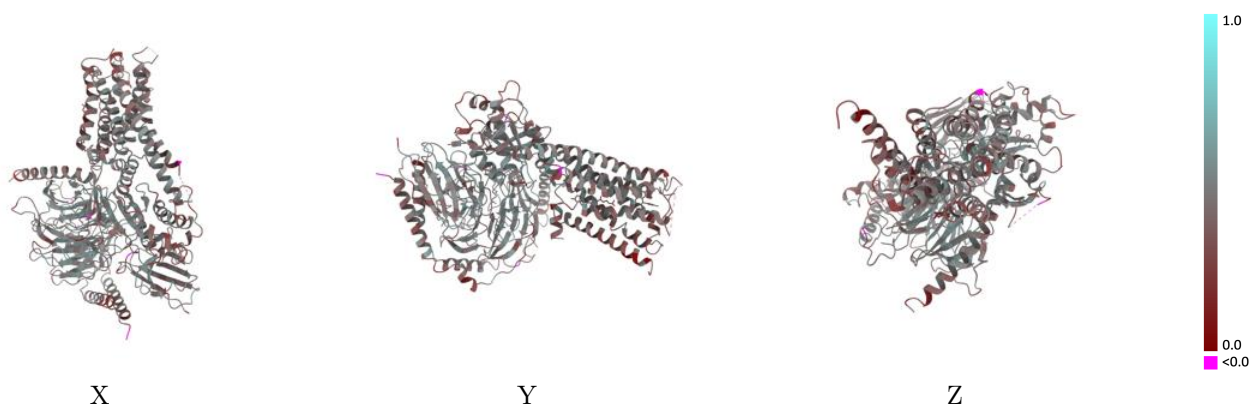
Y



Z

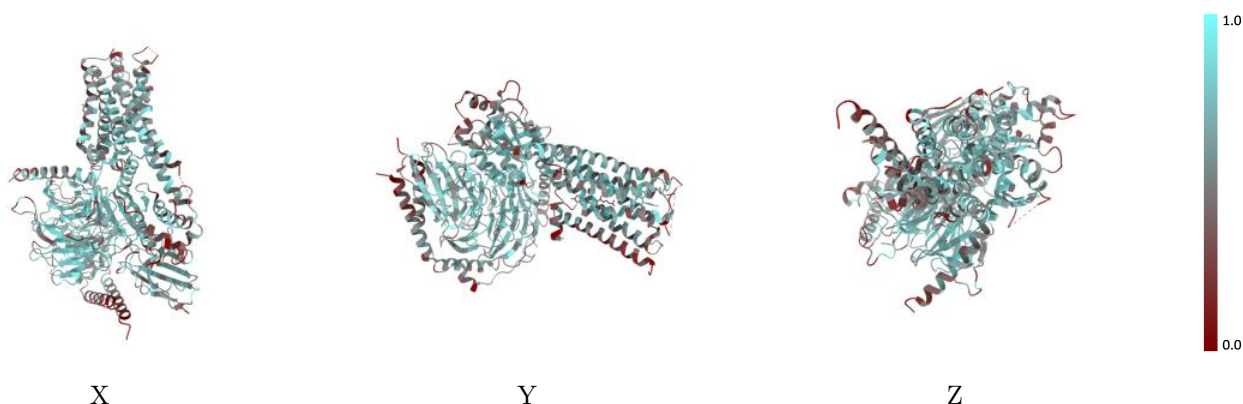
The images above show the 3D surface view of the map at the recommended contour level 0.0251 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



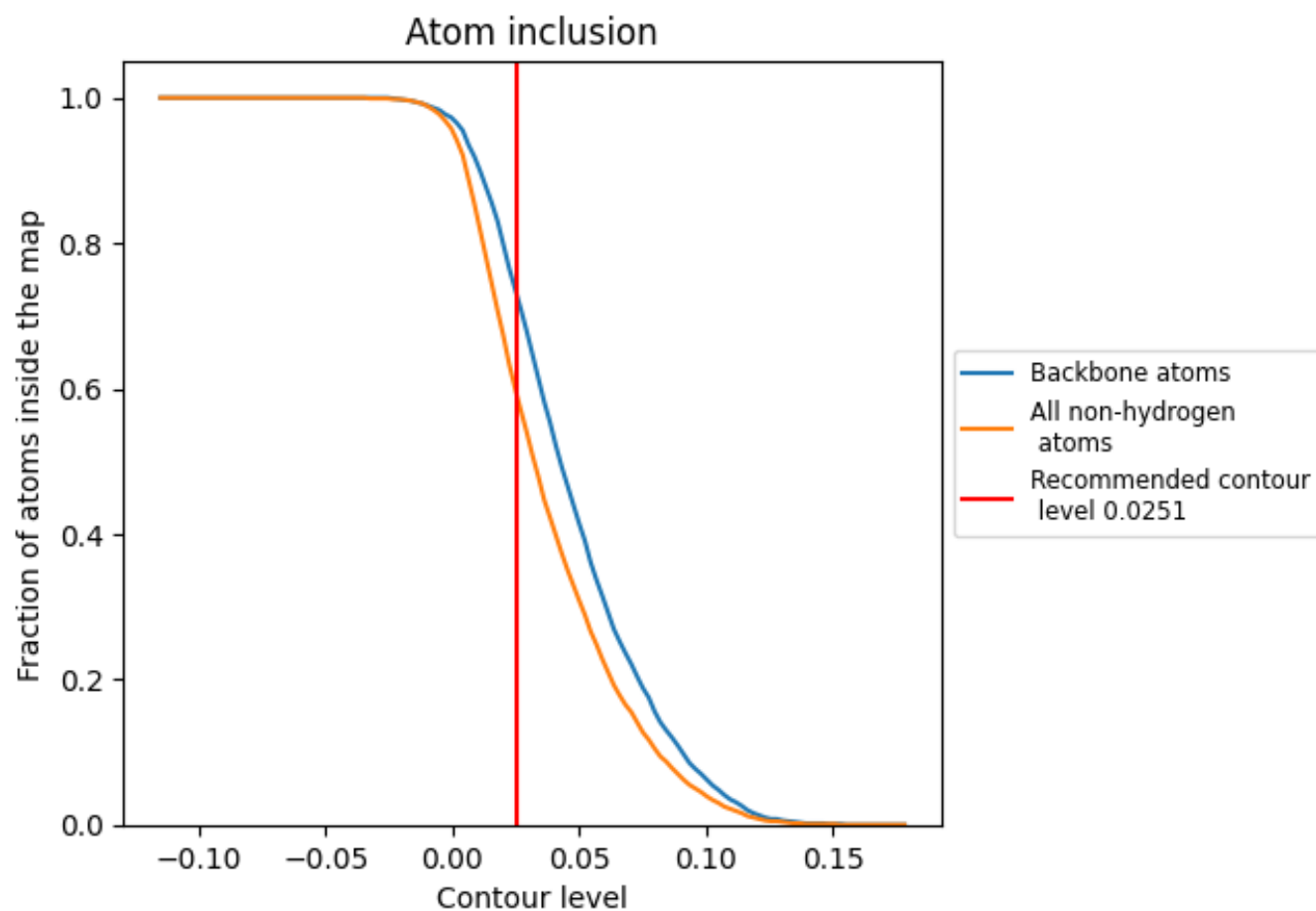
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0251).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 59% 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 (0.0251) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5940	0.4310
A	0.5950	0.4380
B	0.6470	0.4540
G	0.4270	0.3920
N	0.6400	0.4530
R	0.5430	0.3970

