



Full wwPDB EM Validation Report ⓘ

May 13, 2025 – 04:36 PM EDT

PDB ID : 8FC9 / pdb_00008fc9
EMDB ID : EMD-28977
Title : Cryo-EM structure of the human TRPV4 - RhoA, apo condition
Authors : Kwon, D.H.; Lee, S.-Y.; Zhang, F.
Deposited on : 2022-12-01
Resolution : 3.75 Å(reported)

This is a Full wwPDB EM Validation 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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

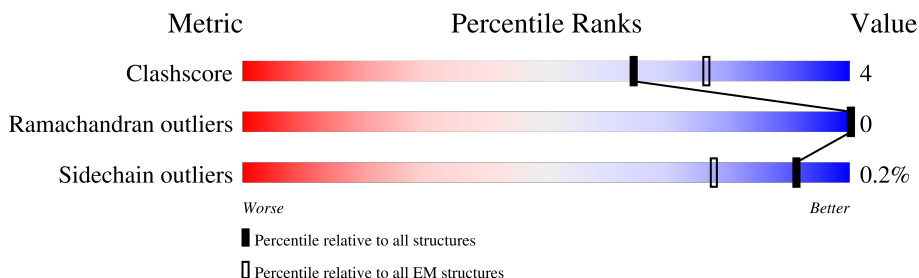
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	901	<div> <div>5%</div> <div>59%</div> <div>6%</div> <div>35%</div> </div>
1	B	901	<div> <div>5%</div> <div>59%</div> <div>6%</div> <div>35%</div> </div>
1	C	901	<div> <div>5%</div> <div>59%</div> <div>6%</div> <div>35%</div> </div>
1	D	901	<div> <div>5%</div> <div>59%</div> <div>6%</div> <div>35%</div> </div>
2	E	193	<div> <div>80%</div> <div>93%</div> <div>6%</div> <div>.</div> </div>
2	F	193	<div> <div>80%</div> <div>93%</div> <div>6%</div> <div>.</div> </div>
2	G	193	<div> <div>82%</div> <div>92%</div> <div>7%</div> <div>.</div> </div>
2	H	193	<div> <div>78%</div> <div>91%</div> <div>7%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 41172 atoms, of which 19360 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 Transient receptor potential cation channel subfamily V member 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	583	Total	C	H	N	O	S	0	0
			7676	2608	3595	720	736	17		
1	B	583	Total	C	H	N	O	S	0	0
			7676	2608	3595	720	736	17		
1	C	583	Total	C	H	N	O	S	0	0
			7676	2608	3595	720	736	17		
1	D	583	Total	C	H	N	O	S	0	0
			7676	2608	3595	720	736	17		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	872	GLU	-	expression tag	UNP Q9HBA0
A	873	ASN	-	expression tag	UNP Q9HBA0
A	874	SER	-	expression tag	UNP Q9HBA0
A	875	LEU	-	expression tag	UNP Q9HBA0
A	876	GLU	-	expression tag	UNP Q9HBA0
A	877	VAL	-	expression tag	UNP Q9HBA0
A	878	LEU	-	expression tag	UNP Q9HBA0
A	879	PHE	-	expression tag	UNP Q9HBA0
A	880	GLN	-	expression tag	UNP Q9HBA0
A	881	GLY	-	expression tag	UNP Q9HBA0
A	882	PRO	-	expression tag	UNP Q9HBA0
A	883	ASP	-	expression tag	UNP Q9HBA0
A	884	TYR	-	expression tag	UNP Q9HBA0
A	885	LYS	-	expression tag	UNP Q9HBA0
A	886	ASP	-	expression tag	UNP Q9HBA0
A	887	ASP	-	expression tag	UNP Q9HBA0
A	888	ASP	-	expression tag	UNP Q9HBA0
A	889	ASP	-	expression tag	UNP Q9HBA0
A	890	LYS	-	expression tag	UNP Q9HBA0
A	891	ALA	-	expression tag	UNP Q9HBA0
A	892	HIS	-	expression tag	UNP Q9HBA0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	893	HIS	-	expression tag	UNP Q9HBA0
A	894	HIS	-	expression tag	UNP Q9HBA0
A	895	HIS	-	expression tag	UNP Q9HBA0
A	896	HIS	-	expression tag	UNP Q9HBA0
A	897	HIS	-	expression tag	UNP Q9HBA0
A	898	HIS	-	expression tag	UNP Q9HBA0
A	899	HIS	-	expression tag	UNP Q9HBA0
A	900	HIS	-	expression tag	UNP Q9HBA0
A	901	HIS	-	expression tag	UNP Q9HBA0
B	872	GLU	-	expression tag	UNP Q9HBA0
B	873	ASN	-	expression tag	UNP Q9HBA0
B	874	SER	-	expression tag	UNP Q9HBA0
B	875	LEU	-	expression tag	UNP Q9HBA0
B	876	GLU	-	expression tag	UNP Q9HBA0
B	877	VAL	-	expression tag	UNP Q9HBA0
B	878	LEU	-	expression tag	UNP Q9HBA0
B	879	PHE	-	expression tag	UNP Q9HBA0
B	880	GLN	-	expression tag	UNP Q9HBA0
B	881	GLY	-	expression tag	UNP Q9HBA0
B	882	PRO	-	expression tag	UNP Q9HBA0
B	883	ASP	-	expression tag	UNP Q9HBA0
B	884	TYR	-	expression tag	UNP Q9HBA0
B	885	LYS	-	expression tag	UNP Q9HBA0
B	886	ASP	-	expression tag	UNP Q9HBA0
B	887	ASP	-	expression tag	UNP Q9HBA0
B	888	ASP	-	expression tag	UNP Q9HBA0
B	889	ASP	-	expression tag	UNP Q9HBA0
B	890	LYS	-	expression tag	UNP Q9HBA0
B	891	ALA	-	expression tag	UNP Q9HBA0
B	892	HIS	-	expression tag	UNP Q9HBA0
B	893	HIS	-	expression tag	UNP Q9HBA0
B	894	HIS	-	expression tag	UNP Q9HBA0
B	895	HIS	-	expression tag	UNP Q9HBA0
B	896	HIS	-	expression tag	UNP Q9HBA0
B	897	HIS	-	expression tag	UNP Q9HBA0
B	898	HIS	-	expression tag	UNP Q9HBA0
B	899	HIS	-	expression tag	UNP Q9HBA0
B	900	HIS	-	expression tag	UNP Q9HBA0
B	901	HIS	-	expression tag	UNP Q9HBA0
C	872	GLU	-	expression tag	UNP Q9HBA0
C	873	ASN	-	expression tag	UNP Q9HBA0
C	874	SER	-	expression tag	UNP Q9HBA0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	875	LEU	-	expression tag	UNP Q9HBA0
C	876	GLU	-	expression tag	UNP Q9HBA0
C	877	VAL	-	expression tag	UNP Q9HBA0
C	878	LEU	-	expression tag	UNP Q9HBA0
C	879	PHE	-	expression tag	UNP Q9HBA0
C	880	GLN	-	expression tag	UNP Q9HBA0
C	881	GLY	-	expression tag	UNP Q9HBA0
C	882	PRO	-	expression tag	UNP Q9HBA0
C	883	ASP	-	expression tag	UNP Q9HBA0
C	884	TYR	-	expression tag	UNP Q9HBA0
C	885	LYS	-	expression tag	UNP Q9HBA0
C	886	ASP	-	expression tag	UNP Q9HBA0
C	887	ASP	-	expression tag	UNP Q9HBA0
C	888	ASP	-	expression tag	UNP Q9HBA0
C	889	ASP	-	expression tag	UNP Q9HBA0
C	890	LYS	-	expression tag	UNP Q9HBA0
C	891	ALA	-	expression tag	UNP Q9HBA0
C	892	HIS	-	expression tag	UNP Q9HBA0
C	893	HIS	-	expression tag	UNP Q9HBA0
C	894	HIS	-	expression tag	UNP Q9HBA0
C	895	HIS	-	expression tag	UNP Q9HBA0
C	896	HIS	-	expression tag	UNP Q9HBA0
C	897	HIS	-	expression tag	UNP Q9HBA0
C	898	HIS	-	expression tag	UNP Q9HBA0
C	899	HIS	-	expression tag	UNP Q9HBA0
C	900	HIS	-	expression tag	UNP Q9HBA0
C	901	HIS	-	expression tag	UNP Q9HBA0
D	872	GLU	-	expression tag	UNP Q9HBA0
D	873	ASN	-	expression tag	UNP Q9HBA0
D	874	SER	-	expression tag	UNP Q9HBA0
D	875	LEU	-	expression tag	UNP Q9HBA0
D	876	GLU	-	expression tag	UNP Q9HBA0
D	877	VAL	-	expression tag	UNP Q9HBA0
D	878	LEU	-	expression tag	UNP Q9HBA0
D	879	PHE	-	expression tag	UNP Q9HBA0
D	880	GLN	-	expression tag	UNP Q9HBA0
D	881	GLY	-	expression tag	UNP Q9HBA0
D	882	PRO	-	expression tag	UNP Q9HBA0
D	883	ASP	-	expression tag	UNP Q9HBA0
D	884	TYR	-	expression tag	UNP Q9HBA0
D	885	LYS	-	expression tag	UNP Q9HBA0
D	886	ASP	-	expression tag	UNP Q9HBA0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	887	ASP	-	expression tag	UNP Q9HBA0
D	888	ASP	-	expression tag	UNP Q9HBA0
D	889	ASP	-	expression tag	UNP Q9HBA0
D	890	LYS	-	expression tag	UNP Q9HBA0
D	891	ALA	-	expression tag	UNP Q9HBA0
D	892	HIS	-	expression tag	UNP Q9HBA0
D	893	HIS	-	expression tag	UNP Q9HBA0
D	894	HIS	-	expression tag	UNP Q9HBA0
D	895	HIS	-	expression tag	UNP Q9HBA0
D	896	HIS	-	expression tag	UNP Q9HBA0
D	897	HIS	-	expression tag	UNP Q9HBA0
D	898	HIS	-	expression tag	UNP Q9HBA0
D	899	HIS	-	expression tag	UNP Q9HBA0
D	900	HIS	-	expression tag	UNP Q9HBA0
D	901	HIS	-	expression tag	UNP Q9HBA0

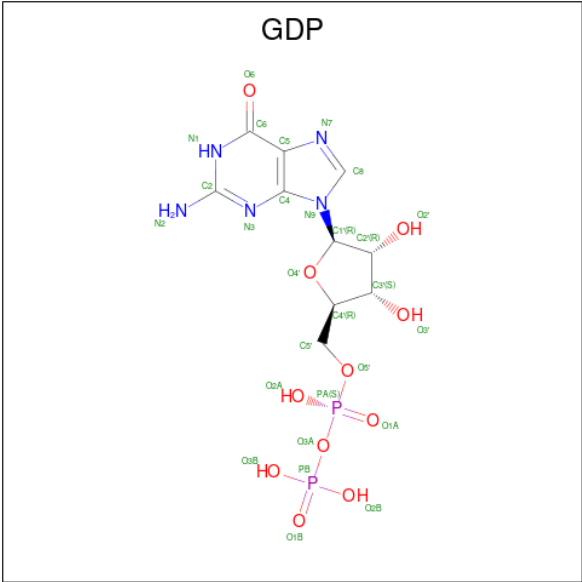
- Molecule 2 is a protein called Transforming protein RhoA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	E	190	Total	C	H	N	O	S	0	0
			2576	855	1233	234	245	9		
2	F	190	Total	C	H	N	O	S	0	0
			2576	855	1233	234	245	9		
2	G	190	Total	C	H	N	O	S	0	0
			2576	855	1233	234	245	9		
2	H	190	Total	C	H	N	O	S	0	0
			2576	855	1233	234	245	9		

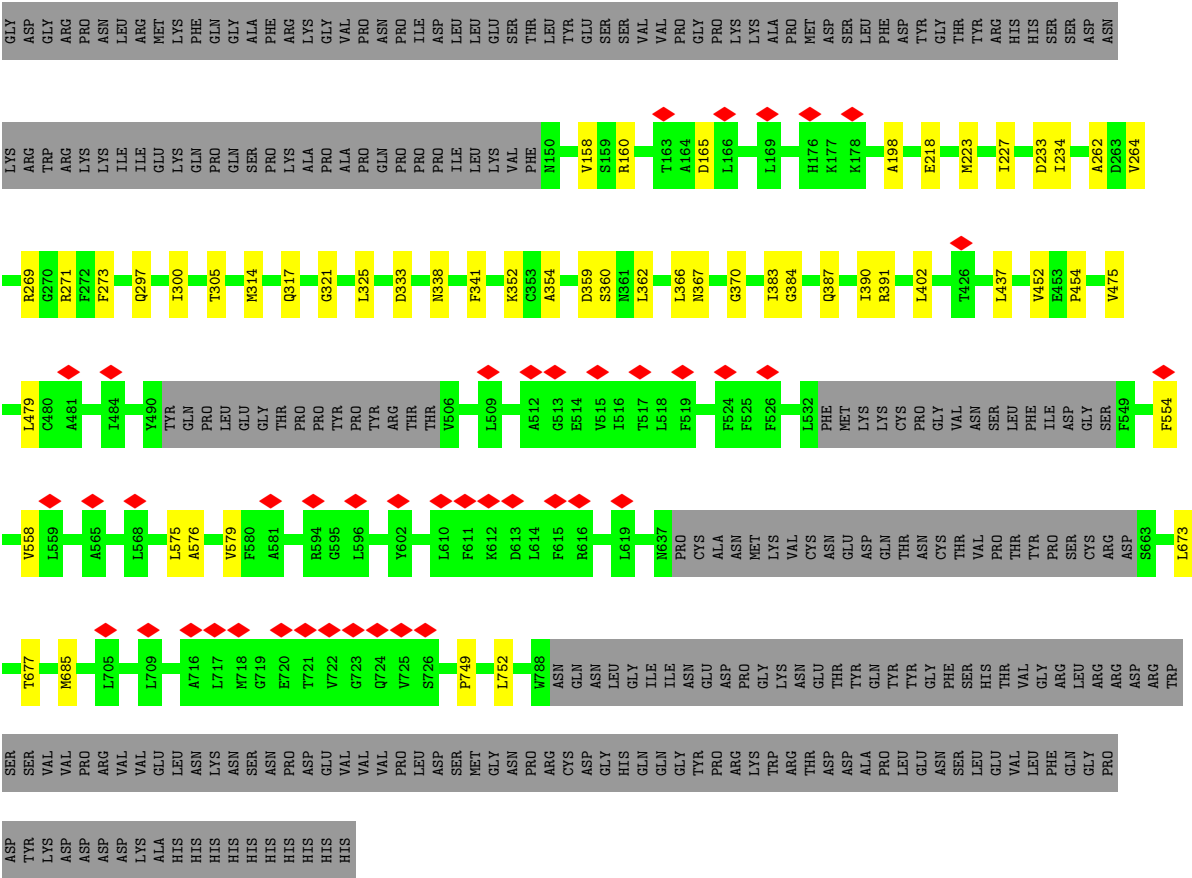
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	E	1	Total	Mg	0
			1	1	
3	F	1	Total	Mg	0
			1	1	
3	G	1	Total	Mg	0
			1	1	
3	H	1	Total	Mg	0
			1	1	

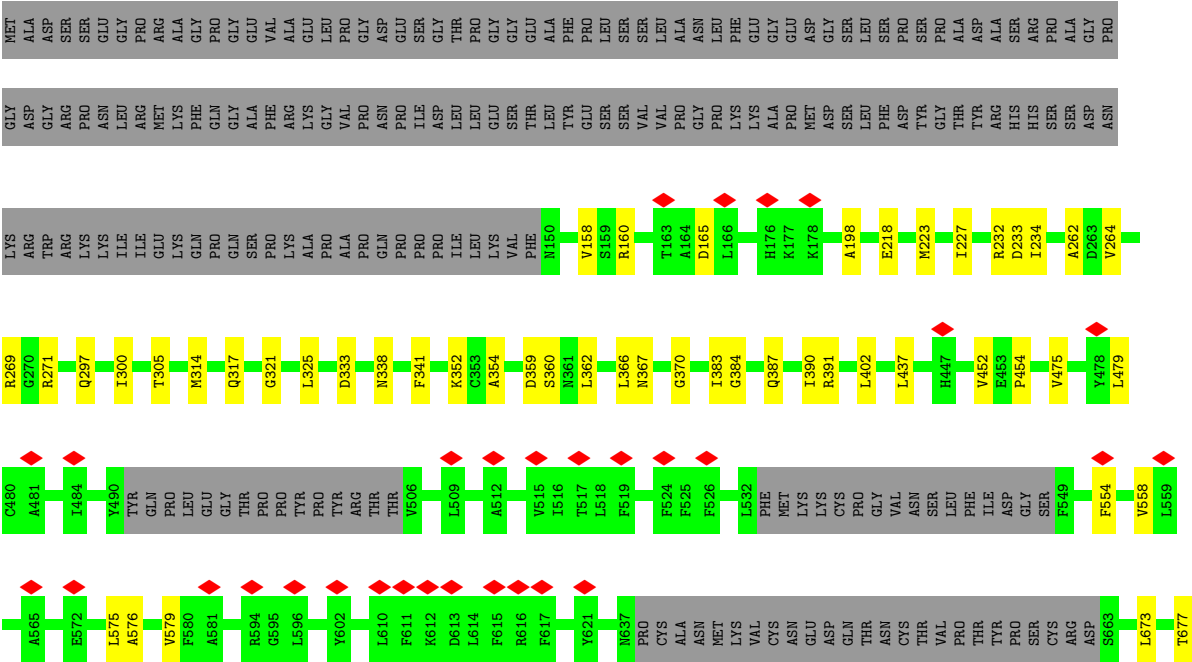
- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



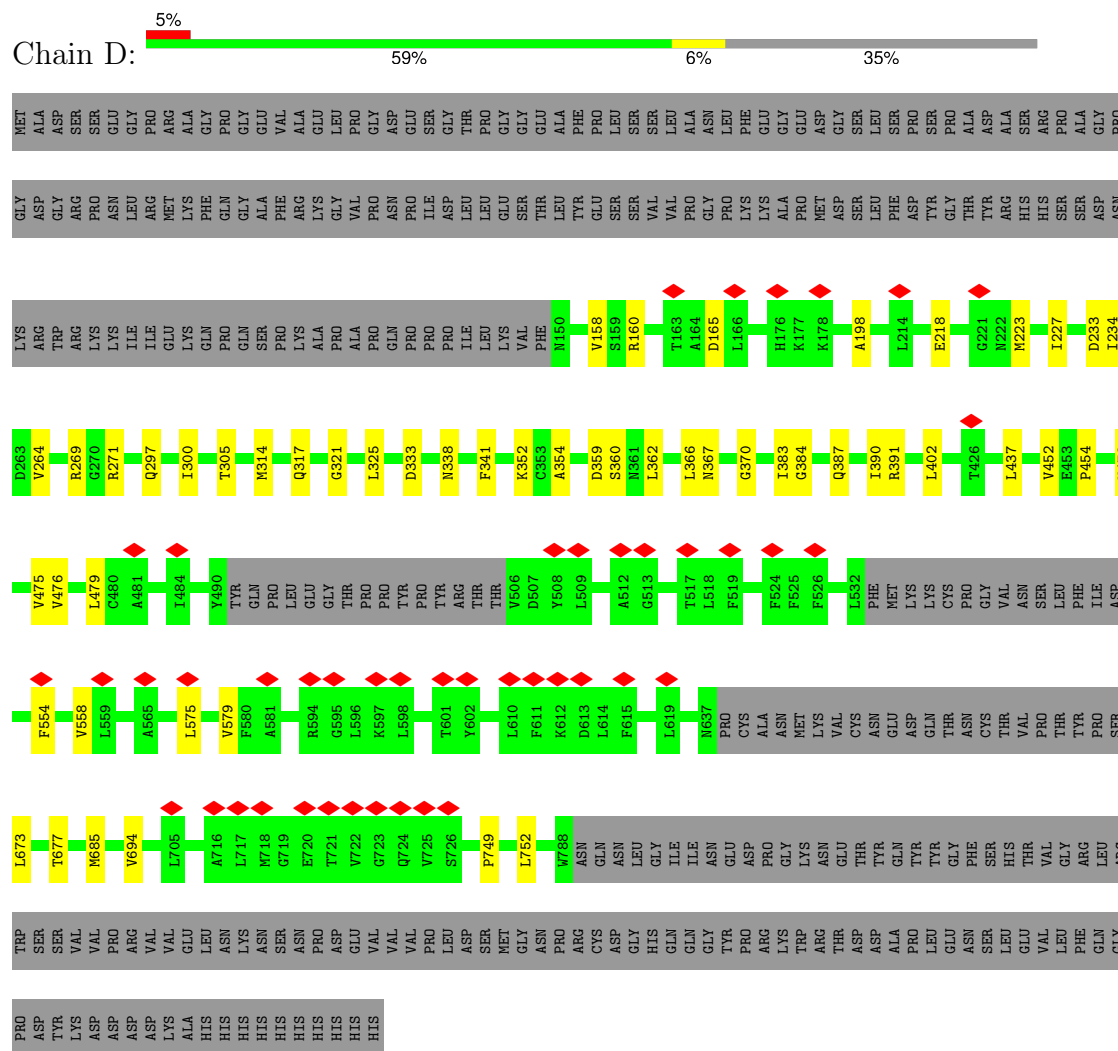
Mol	Chain	Residues	Atoms						AltConf
4	E	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	
4	F	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	
4	G	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	
4	H	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	



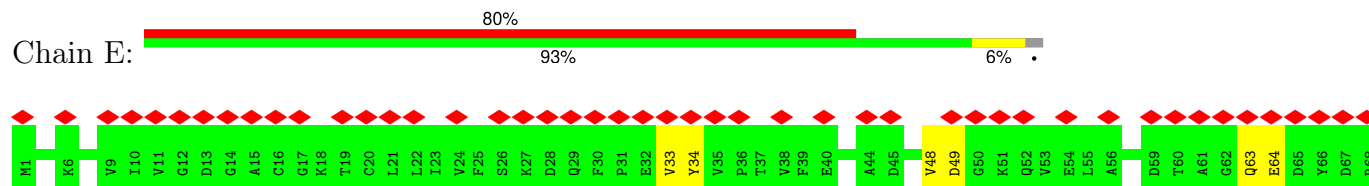
● Molecule 1: Transient receptor potential cation channel subfamily V member 4

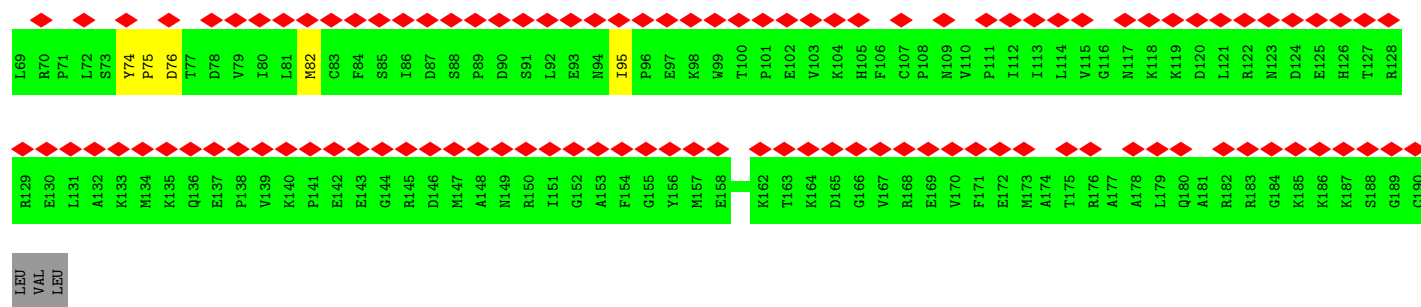


- Molecule 1: Transient receptor potential cation channel subfamily V member 4

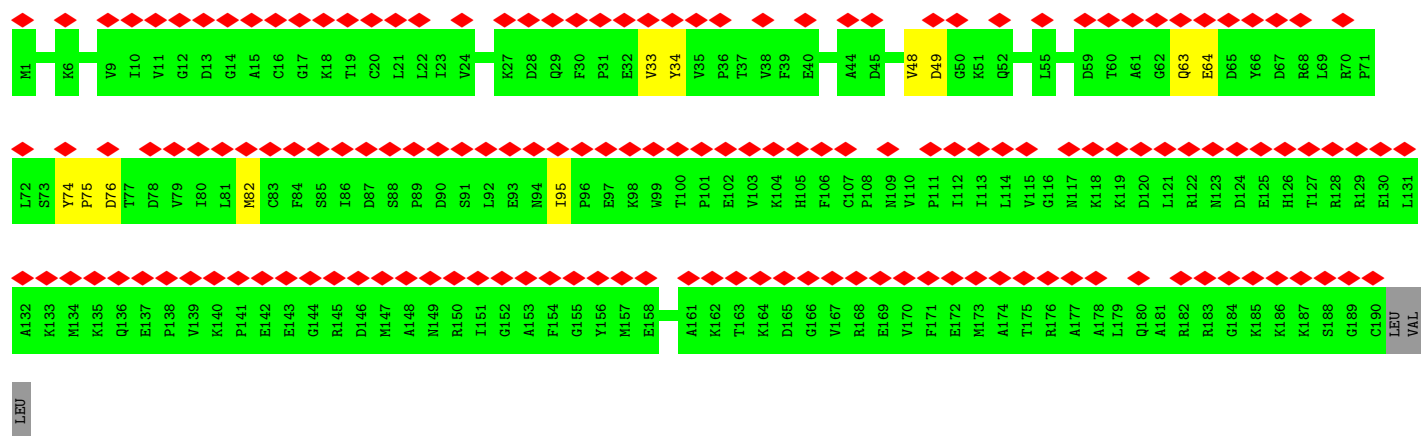
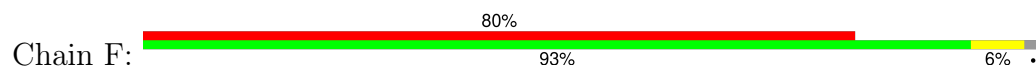


- Molecule 2: Transforming protein RhoA

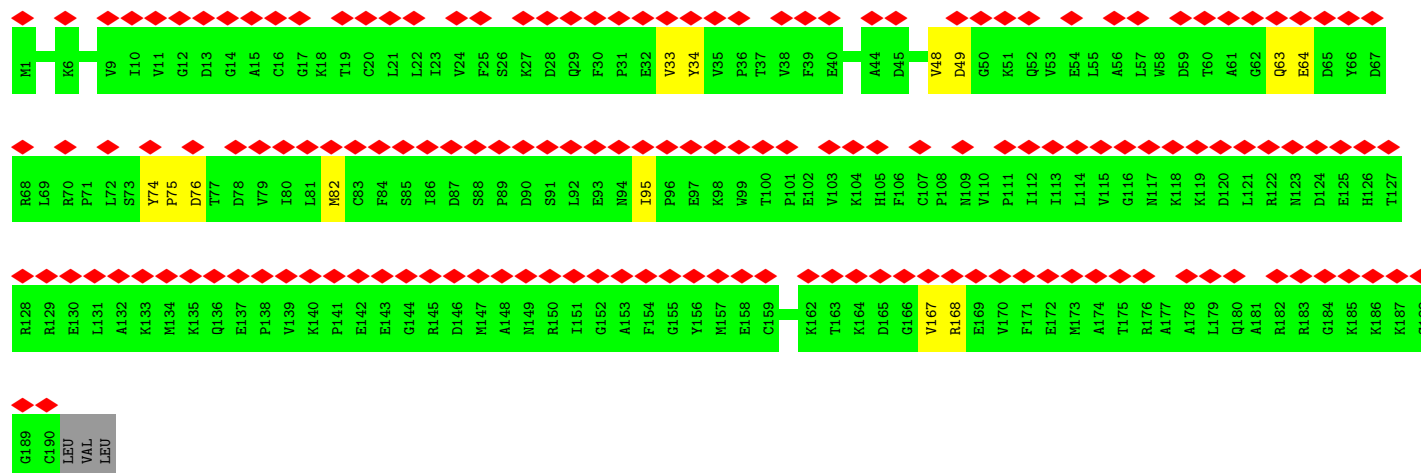
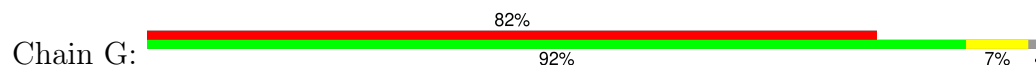




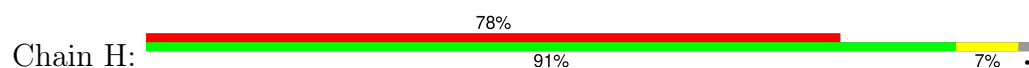
• Molecule 2: Transforming protein RhoA



• Molecule 2: Transforming protein RhoA



• Molecule 2: Transforming protein RhoA



K1										K6										V9										K27										V33										V48										V56										D59										D65										D71									
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G12										G13										G14										Q29										Y35										D50										A57										D60										D66										D72									
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A15										C16										E32										Y36										D52										A59										D62										D68										D74																			
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M94										M95										M96										M97										M98										M99										N00										N01																													
I95										I96										I97										I98										I99										J00										J01										J02																													
P96										P97										P98										P99										Q00										Q01										Q02										Q03																													
K98										K99										L00										L01										L02										L03										L04										L05																													
W99										W00										W01										W02										W03										W04										W05										W06																													
T100										T101										T102										T103										T104										T105										T106										T107																													
P101										P102										P103										P104										P105										P106										P107										P108																													
E102										E103										E104										E105										E106										E107										E108										E109																													
V103										V104										V105										V106										V107										V108										V109										V110																													
K104										K105										K106										K107										K108										K109										K110										K111																													
H105										H106										H107										H108										H109										H110										H111										H112																													
F106										F107										F108										F109										F110										F111										F112										F113																													
C107										C108										C109										C110										C111										C112										C113										C114																													
P111										P112										P113										P114										P115										P116										P117										P118																													
I112										I113										I114										I115										I116										I117										I118										I119																													
L114										L115										L116										L117										L118										L119										L120										L121																													
V115										V116										V117										V118										V119										V120										V121										V122																													
G116										G117										G118										G119										G120										G121										G122										G123																													
N117										N118										N119										N120										N121										N122										N123										N124																													
K118										K119										K120										K121										K122										K123										K124										K125																													
K119										K120										K121										K122										K123										K124										K125										K126																													
D120										D121										D122										D123										D124										D125										D126										D127																													
L121										L122										L123										L124										L125										L126										L127										L128																													
A61										A62										A63										A64										A65										A66										A67										A68																													
G62										G63										G64										G65										G66										G67										G68										G69																													
D63										D64										D65										D66										D67										D68										D69										D70																													
E64										E65										E66										E67										E68										E69										E70										E71																													
D65										D66										D67										D68										D69										D70										D71										D72																													
Y66										Y67										Y68										Y69										Y70										Y71										Y72										Y73																													
D67										D68										D69										D70										D71										D72										D73										D74																													
R68										R69										R70										R71										R72										R73										R74										R75																													
L69										L70										L71										L72										L73										L74										L75										L76																													
R70										R71										R72										R73										R74										R75										R76										R77																													
R71										R72										R73										R74										R75										R76										R77										R78																													
P71										P72										P73										P74										P75										P76										P77										P78																													
I72										I73										I74										I75										I76										I77										I78										I79																													
S73										S74										S75										S76										S77										S78										S79										S80																													
Y74										Y75										Y76										Y77										Y78										Y79										Y80										Y81																													
P75										P76										P77										P78										P79										P80										P81										P82																													
D76										D77										D78										D79										D80										D81										D82										D83																													
I78										I79										I80										I81										I82										I83										I84										I85																													
C83										C84										C85										C86										C87										C88										C89										C90																													
F84										F85										F86										F87										F88										F89										F90										F91																													
S85										S86										S87										S88										S89										S90										S91										S92																													
I86										I87										I88										I89										I90										I91										I92										I93																													
D87										D88										D89										D90										D91										D92										D93										D94																													
S88										S89										S90										S91										S92										S93										S94										S95																													
P89										P90										P91										P92										P93										P94										P95										P96																													
D90										D91										D92										D93										D94										D95										D96										D97																													
S91										S92										S93										S94										S95										S96										S97										S98																													
L92										L93										L94										L95										L96										L97										L98										L99																													
E93										E94										E95										E96										E97										E98										E99										F00																													
M94										M95										M96										M97										M98										M99										N00										N01																													
I95										I96										I97										I98										I99										J00										J01										J02																													
P96										P97										P98										P99										Q00										Q01										Q02										Q03																													
K98										K99										L00										L01										L02										L03										L04										L05																													
W99										W00										W01										W02										W03										W04										W05										W06																													
T100										T101										T102										T103										T104										T105										T106										T107																													
P101										P102										P103										P104										P105										P106										P107										P108																													
E102										E103										E104										E105										E106										E107										E108										E109																													
V103										V104										V105										V106										V107										V108										V109										V110																													
K104										K105										K106										K107										K108										K109										K110										K111																													
H105										H106										H107										H108										H109										H110										H111										H112																													
F106										F107										F108										F109										F110																																																											

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	172225	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.356	Depositor
Minimum map value	-2.290	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.209	Depositor
Map size (Å)	276.48, 276.48, 276.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, GDP

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	0.15	0/4158	0.32	0/5683
1	B	0.16	0/4158	0.32	0/5683
1	C	0.16	0/4158	0.32	0/5683
1	D	0.16	0/4158	0.32	0/5683
2	E	0.13	0/1370	0.31	0/1872
2	F	0.13	0/1370	0.31	0/1872
2	G	0.13	0/1370	0.31	0/1872
2	H	0.13	0/1370	0.31	0/1872
All	All	0.15	0/22112	0.32	0/30220

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	4081	3595	3592	33	0
1	B	4081	3595	3592	33	0
1	C	4081	3595	3592	33	0
1	D	4081	3595	3592	33	0
2	E	1343	1233	1233	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1343	1233	1233	8	0
2	G	1343	1233	1233	9	0
2	H	1343	1233	1233	10	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	E	28	12	12	0	0
4	F	28	12	12	0	0
4	G	28	12	12	0	0
4	H	28	12	12	0	0
All	All	21812	19360	19348	159	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 4.

All (159) 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:390:ILE:HG23	1:C:391:ARG:HG3	1.74	0.69
1:A:390:ILE:HG23	1:A:391:ARG:HG3	1.74	0.69
1:D:390:ILE:HG23	1:D:391:ARG:HG3	1.74	0.68
1:B:314:MET:HE1	1:B:352:LYS:HB3	1.76	0.68
1:D:314:MET:HE1	1:D:352:LYS:HB3	1.76	0.68
1:B:390:ILE:HG23	1:B:391:ARG:HG3	1.74	0.67
1:C:314:MET:HE1	1:C:352:LYS:HB3	1.76	0.66
1:A:314:MET:HE1	1:A:352:LYS:HB3	1.76	0.65
1:C:305:THR:HG21	1:C:314:MET:HE2	1.78	0.65
1:A:305:THR:HG21	1:A:314:MET:HE2	1.78	0.65
1:B:305:THR:HG21	1:B:314:MET:HE2	1.78	0.65
2:G:76:ASP:OD2	1:D:269:ARG:NE	2.29	0.64
1:D:305:THR:HG21	1:D:314:MET:HE2	1.78	0.64
2:H:76:ASP:OD2	1:C:269:ARG:NE	2.29	0.62
1:D:387:GLN:O	1:D:390:ILE:HG22	2.00	0.62
1:C:387:GLN:O	1:C:390:ILE:HG22	2.00	0.62
1:A:387:GLN:O	1:A:390:ILE:HG22	2.00	0.62
1:B:387:GLN:O	1:B:390:ILE:HG22	2.00	0.60
1:A:269:ARG:NE	2:E:76:ASP:OD2	2.29	0.58
2:F:76:ASP:OD2	1:B:269:ARG:NE	2.29	0.56
1:D:227:ILE:HG21	1:D:262:ALA:HB2	1.90	0.54
1:A:354:ALA:HB2	1:A:402:LEU:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:PHE:O	1:A:558:VAL:HG23	2.08	0.54
1:C:354:ALA:HB2	1:C:402:LEU:HD11	1.90	0.53
1:C:554:PHE:O	1:C:558:VAL:HG23	2.08	0.53
1:B:227:ILE:HG21	1:B:262:ALA:HB2	1.90	0.53
1:B:452:VAL:HG12	1:B:454:PRO:HD2	1.91	0.53
1:C:452:VAL:HG12	1:C:454:PRO:HD2	1.91	0.53
1:D:554:PHE:O	1:D:558:VAL:HG23	2.08	0.53
1:D:354:ALA:HB2	1:D:402:LEU:HD11	1.90	0.53
1:D:452:VAL:HG12	1:D:454:PRO:HD2	1.91	0.53
1:A:452:VAL:HG12	1:A:454:PRO:HD2	1.91	0.53
1:A:227:ILE:HG21	1:A:262:ALA:HB2	1.90	0.53
1:B:325:LEU:HD11	1:B:362:LEU:HD23	1.91	0.53
1:C:227:ILE:HG21	1:C:262:ALA:HB2	1.90	0.53
1:B:554:PHE:O	1:B:558:VAL:HG23	2.08	0.53
1:D:325:LEU:HD11	1:D:362:LEU:HD23	1.91	0.53
1:A:694:VAL:HG21	1:C:576:ALA:HB2	1.90	0.52
1:B:354:ALA:HB2	1:B:402:LEU:HD11	1.90	0.52
1:C:367:ASN:OD1	1:C:370:GLY:N	2.43	0.52
1:A:367:ASN:OD1	1:A:370:GLY:N	2.43	0.52
1:A:575:LEU:O	1:A:579:VAL:HG23	2.11	0.51
1:B:367:ASN:OD1	1:B:370:GLY:N	2.43	0.51
1:C:575:LEU:O	1:C:579:VAL:HG23	2.11	0.51
1:D:575:LEU:O	1:D:579:VAL:HG23	2.11	0.51
2:F:74:TYR:N	2:F:75:PRO:HD2	2.26	0.51
1:C:325:LEU:HD11	1:C:362:LEU:HD23	1.91	0.51
1:D:317:GLN:NE2	1:D:366:LEU:O	2.43	0.51
1:D:367:ASN:OD1	1:D:370:GLY:N	2.43	0.51
1:A:325:LEU:HD11	1:A:362:LEU:HD23	1.91	0.51
1:B:575:LEU:O	1:B:579:VAL:HG23	2.11	0.51
1:D:160:ARG:NH2	1:D:165:ASP:OD2	2.44	0.51
2:E:74:TYR:N	2:E:75:PRO:HD2	2.26	0.50
1:B:297:GLN:HB3	1:B:300:ILE:HD13	1.94	0.50
1:A:317:GLN:NE2	1:A:366:LEU:O	2.43	0.50
2:G:74:TYR:N	2:G:75:PRO:HD2	2.26	0.50
1:B:160:ARG:NH2	1:B:165:ASP:OD2	2.44	0.50
1:D:297:GLN:HB3	1:D:300:ILE:HD13	1.94	0.50
1:B:317:GLN:NE2	1:B:366:LEU:O	2.43	0.50
1:C:160:ARG:NH2	1:C:165:ASP:OD2	2.44	0.50
1:A:160:ARG:NH2	1:A:165:ASP:OD2	2.44	0.50
2:F:48:VAL:HG23	2:F:49:ASP:N	2.27	0.50
2:G:48:VAL:HG23	2:G:49:ASP:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:317:GLN:NE2	1:C:366:LEU:O	2.43	0.50
2:E:48:VAL:HG23	2:E:49:ASP:N	2.27	0.49
1:D:233:ASP:OD1	1:D:234:ILE:N	2.45	0.49
2:H:48:VAL:HG23	2:H:49:ASP:N	2.27	0.49
1:A:233:ASP:OD1	1:A:234:ILE:N	2.45	0.49
2:H:74:TYR:N	2:H:75:PRO:HD2	2.26	0.49
1:B:233:ASP:OD1	1:B:234:ILE:N	2.45	0.49
1:C:233:ASP:OD1	1:C:234:ILE:N	2.45	0.49
1:C:685:MET:SD	1:C:685:MET:N	2.86	0.49
1:D:685:MET:SD	1:D:685:MET:N	2.86	0.49
1:A:685:MET:SD	1:A:685:MET:N	2.86	0.49
1:A:297:GLN:HB3	1:A:300:ILE:HD13	1.94	0.49
1:C:297:GLN:HB3	1:C:300:ILE:HD13	1.94	0.49
1:B:685:MET:SD	1:B:685:MET:N	2.86	0.48
1:B:576:ALA:HB2	1:D:694:VAL:HG21	1.96	0.48
2:E:48:VAL:HG23	2:E:49:ASP:H	1.79	0.48
2:F:48:VAL:HG23	2:F:49:ASP:H	1.79	0.48
2:H:48:VAL:HG23	2:H:49:ASP:H	1.79	0.48
2:G:48:VAL:HG23	2:G:49:ASP:H	1.79	0.47
1:D:475:VAL:O	1:D:479:LEU:HG	2.15	0.47
1:A:475:VAL:O	1:A:479:LEU:HG	2.15	0.46
1:C:475:VAL:O	1:C:479:LEU:HG	2.15	0.46
2:G:63:GLN:HG3	2:G:64:GLU:N	2.31	0.46
2:E:63:GLN:HG3	2:E:64:GLU:N	2.31	0.46
2:F:63:GLN:HG3	2:F:64:GLU:N	2.31	0.46
1:B:475:VAL:O	1:B:479:LEU:HG	2.15	0.46
1:B:158:VAL:HG13	1:B:198:ALA:HB2	1.98	0.46
1:C:158:VAL:HG13	1:C:198:ALA:HB2	1.98	0.45
1:A:158:VAL:HG13	1:A:198:ALA:HB2	1.98	0.45
2:H:63:GLN:HG3	2:H:64:GLU:N	2.31	0.45
1:C:218:GLU:CB	1:C:223:MET:HE3	2.47	0.45
1:D:218:GLU:CB	1:D:223:MET:HE3	2.47	0.45
1:B:218:GLU:CB	1:B:223:MET:HE3	2.47	0.45
1:A:218:GLU:CB	1:A:223:MET:HE3	2.47	0.45
1:D:158:VAL:HG13	1:D:198:ALA:HB2	1.98	0.45
1:A:749:PRO:HG2	1:A:752:LEU:HD23	1.99	0.45
1:C:749:PRO:HG2	1:C:752:LEU:HD23	1.99	0.44
1:C:264:VAL:HG12	1:C:264:VAL:O	2.17	0.44
1:D:333:ASP:N	1:D:338:ASN:OD1	2.46	0.44
1:C:234:ILE:HG22	1:C:271:ARG:HG2	1.99	0.44
1:D:264:VAL:O	1:D:264:VAL:HG12	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ILE:HG22	1:A:271:ARG:HG2	1.99	0.44
1:B:390:ILE:HG21	1:B:452:VAL:HG11	2.00	0.44
1:A:264:VAL:HG12	1:A:264:VAL:O	2.17	0.44
1:A:411:TYR:HH	1:B:273:PHE:HE2	1.64	0.43
1:B:749:PRO:HG2	1:B:752:LEU:HD23	1.99	0.43
1:C:390:ILE:HG21	1:C:452:VAL:HG11	2.00	0.43
1:A:317:GLN:NE2	1:A:321:GLY:O	2.52	0.43
1:D:234:ILE:HG22	1:D:271:ARG:HG2	1.99	0.43
1:D:390:ILE:HG21	1:D:452:VAL:HG11	2.00	0.43
1:B:264:VAL:HG12	1:B:264:VAL:O	2.18	0.43
1:D:749:PRO:HG2	1:D:752:LEU:HD23	1.99	0.43
1:D:437:LEU:HD23	1:D:437:LEU:O	2.19	0.43
1:B:234:ILE:HG22	1:B:271:ARG:HG2	1.99	0.43
1:B:317:GLN:NE2	1:B:321:GLY:O	2.52	0.43
2:E:82:MET:SD	2:E:95:ILE:HG23	2.59	0.43
2:F:33:VAL:HG23	2:F:34:TYR:N	2.34	0.43
1:C:437:LEU:HD23	1:C:437:LEU:O	2.19	0.43
1:A:390:ILE:HG21	1:A:452:VAL:HG11	2.00	0.42
2:E:33:VAL:HG23	2:E:34:TYR:N	2.34	0.42
2:H:82:MET:SD	2:H:95:ILE:HG23	2.59	0.42
1:A:437:LEU:HD23	1:A:437:LEU:O	2.19	0.42
2:G:82:MET:SD	2:G:95:ILE:HG23	2.59	0.42
1:C:317:GLN:NE2	1:C:321:GLY:O	2.52	0.42
1:D:317:GLN:NE2	1:D:321:GLY:O	2.52	0.42
2:F:82:MET:SD	2:F:95:ILE:HG23	2.59	0.42
1:B:333:ASP:N	1:B:338:ASN:OD1	2.46	0.42
2:G:33:VAL:HG23	2:G:34:TYR:N	2.34	0.42
2:H:33:VAL:HG23	2:H:34:TYR:N	2.34	0.42
1:B:437:LEU:O	1:B:437:LEU:HD23	2.19	0.42
1:D:673:LEU:O	1:D:677:THR:HG23	2.20	0.42
1:B:359:ASP:OD1	1:B:360:SER:N	2.53	0.41
1:C:359:ASP:OD1	1:C:360:SER:N	2.53	0.41
1:C:391:ARG:NH1	1:C:391:ARG:HB3	2.36	0.41
2:E:74:TYR:N	2:E:75:PRO:CD	2.84	0.41
2:G:74:TYR:N	2:G:75:PRO:CD	2.84	0.41
1:A:391:ARG:HB3	1:A:391:ARG:NH1	2.36	0.41
1:B:673:LEU:O	1:B:677:THR:HG23	2.20	0.41
1:D:391:ARG:HB3	1:D:391:ARG:NH1	2.36	0.41
2:F:74:TYR:N	2:F:75:PRO:CD	2.84	0.41
1:A:359:ASP:OD1	1:A:360:SER:N	2.53	0.41
2:H:74:TYR:N	2:H:75:PRO:CD	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:359:ASP:OD1	1:D:360:SER:N	2.53	0.41
1:C:673:LEU:O	1:C:677:THR:HG23	2.20	0.41
1:B:391:ARG:HB3	1:B:391:ARG:NH1	2.36	0.41
1:C:333:ASP:N	1:C:338:ASN:OD1	2.46	0.41
1:D:383:ILE:HG23	1:D:384:GLY:N	2.36	0.41
1:C:383:ILE:HG23	1:C:384:GLY:N	2.36	0.41
1:A:673:LEU:O	1:A:677:THR:HG23	2.20	0.41
1:B:383:ILE:HG23	1:B:384:GLY:N	2.36	0.41
1:A:574:TYR:CE2	1:A:575:LEU:CD1	3.05	0.40
2:G:167:VAL:HG23	2:G:168:ARG:N	2.37	0.40
2:H:69:LEU:HD22	1:C:232:ARG:HE	1.87	0.40
1:A:383:ILE:HG23	1:A:384:GLY:N	2.36	0.40
2:H:167:VAL:HG23	2:H:168:ARG:N	2.37	0.40
1:D:472:TYR:O	1:D:476:VAL:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	575/901 (64%)	567 (99%)	8 (1%)	0	100	100
1	B	575/901 (64%)	567 (99%)	8 (1%)	0	100	100
1	C	575/901 (64%)	567 (99%)	8 (1%)	0	100	100
1	D	575/901 (64%)	567 (99%)	8 (1%)	0	100	100
2	E	188/193 (97%)	184 (98%)	4 (2%)	0	100	100
2	F	188/193 (97%)	184 (98%)	4 (2%)	0	100	100
2	G	188/193 (97%)	184 (98%)	4 (2%)	0	100	100
2	H	188/193 (97%)	184 (98%)	4 (2%)	0	100	100
All	All	3052/4376 (70%)	3004 (98%)	48 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	342/789 (43%)	341 (100%)	1 (0%)	91	94
1	B	342/789 (43%)	341 (100%)	1 (0%)	91	94
1	C	342/789 (43%)	341 (100%)	1 (0%)	91	94
1	D	342/789 (43%)	341 (100%)	1 (0%)	91	94
2	E	122/167 (73%)	122 (100%)	0	100	100
2	F	122/167 (73%)	122 (100%)	0	100	100
2	G	122/167 (73%)	122 (100%)	0	100	100
2	H	122/167 (73%)	122 (100%)	0	100	100
All	All	1856/3824 (48%)	1852 (100%)	4 (0%)	91	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	341	PHE
1	B	341	PHE
1	C	341	PHE
1	D	341	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	322	ASN
2	E	63	GLN
2	F	63	GLN
2	G	63	GLN
2	H	63	GLN
1	B	322	ASN
1	D	322	ASN

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 ⓘ

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	$\# Z > 2$
4	GDP	H	302	3	25,30,30	1.00	2 (8%)	30,47,47	1.30	3 (10%)
4	GDP	E	302	3	25,30,30	1.01	2 (8%)	30,47,47	1.30	3 (10%)
4	GDP	F	302	3	25,30,30	1.01	2 (8%)	30,47,47	1.30	3 (10%)
4	GDP	G	302	3	25,30,30	1.01	2 (8%)	30,47,47	1.30	3 (10%)

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	GDP	H	302	3	-	5/12/32/32	0/3/3/3
4	GDP	E	302	3	-	5/12/32/32	0/3/3/3
4	GDP	F	302	3	-	5/12/32/32	0/3/3/3
4	GDP	G	302	3	-	5/12/32/32	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	302	GDP	O4'-C1'	2.27	1.43	1.40
4	G	302	GDP	O4'-C1'	2.26	1.43	1.40
4	E	302	GDP	O4'-C1'	2.25	1.43	1.40
4	H	302	GDP	O4'-C1'	2.20	1.43	1.40
4	G	302	GDP	C6-N1	-2.18	1.34	1.37
4	F	302	GDP	C6-N1	-2.15	1.34	1.37
4	E	302	GDP	C6-N1	-2.15	1.34	1.37
4	H	302	GDP	C6-N1	-2.13	1.34	1.37

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	302	GDP	O4'-C1'-N9	3.36	113.20	108.75
4	F	302	GDP	O4'-C1'-N9	3.36	113.20	108.75
4	G	302	GDP	O4'-C1'-N9	3.34	113.17	108.75
4	E	302	GDP	O4'-C1'-N9	3.33	113.17	108.75
4	E	302	GDP	C8-N7-C5	3.12	107.86	102.55
4	G	302	GDP	C8-N7-C5	3.11	107.85	102.55
4	F	302	GDP	C8-N7-C5	3.11	107.84	102.55
4	H	302	GDP	C8-N7-C5	3.10	107.83	102.55
4	E	302	GDP	C5-C6-N1	2.25	118.35	114.07
4	H	302	GDP	C5-C6-N1	2.24	118.34	114.07
4	G	302	GDP	C5-C6-N1	2.24	118.33	114.07
4	F	302	GDP	C5-C6-N1	2.23	118.33	114.07

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	302	GDP	C5'-O5'-PA-O3A
4	E	302	GDP	C5'-O5'-PA-O1A
4	E	302	GDP	C5'-O5'-PA-O2A
4	F	302	GDP	C5'-O5'-PA-O3A
4	F	302	GDP	C5'-O5'-PA-O1A
4	F	302	GDP	C5'-O5'-PA-O2A
4	G	302	GDP	C5'-O5'-PA-O3A
4	G	302	GDP	C5'-O5'-PA-O1A
4	G	302	GDP	C5'-O5'-PA-O2A
4	H	302	GDP	C5'-O5'-PA-O3A
4	H	302	GDP	C5'-O5'-PA-O1A
4	H	302	GDP	C5'-O5'-PA-O2A

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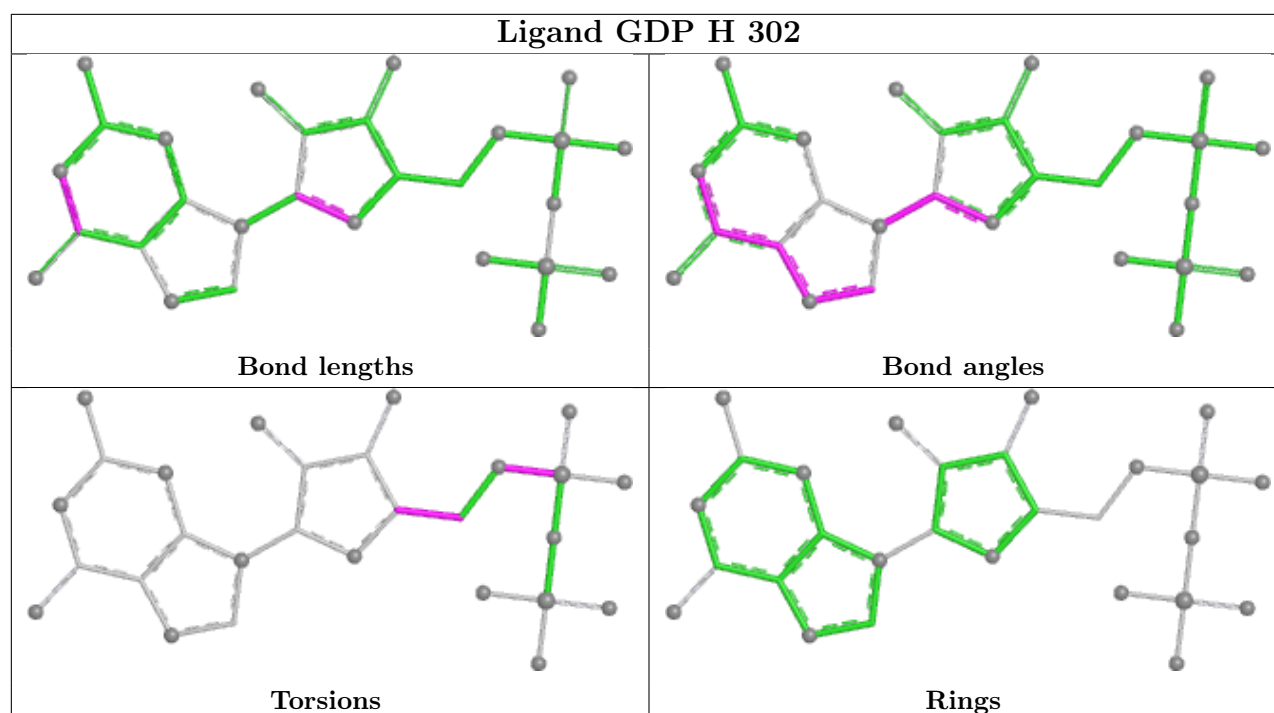
Continued from previous page...

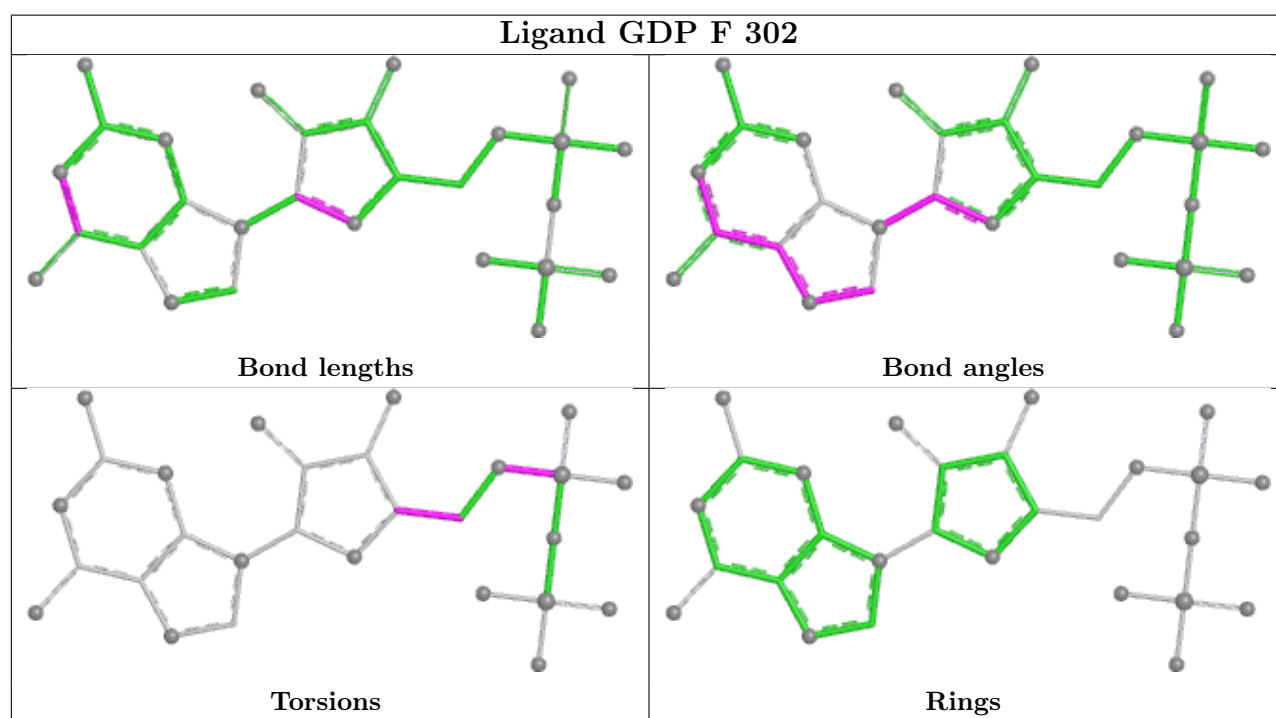
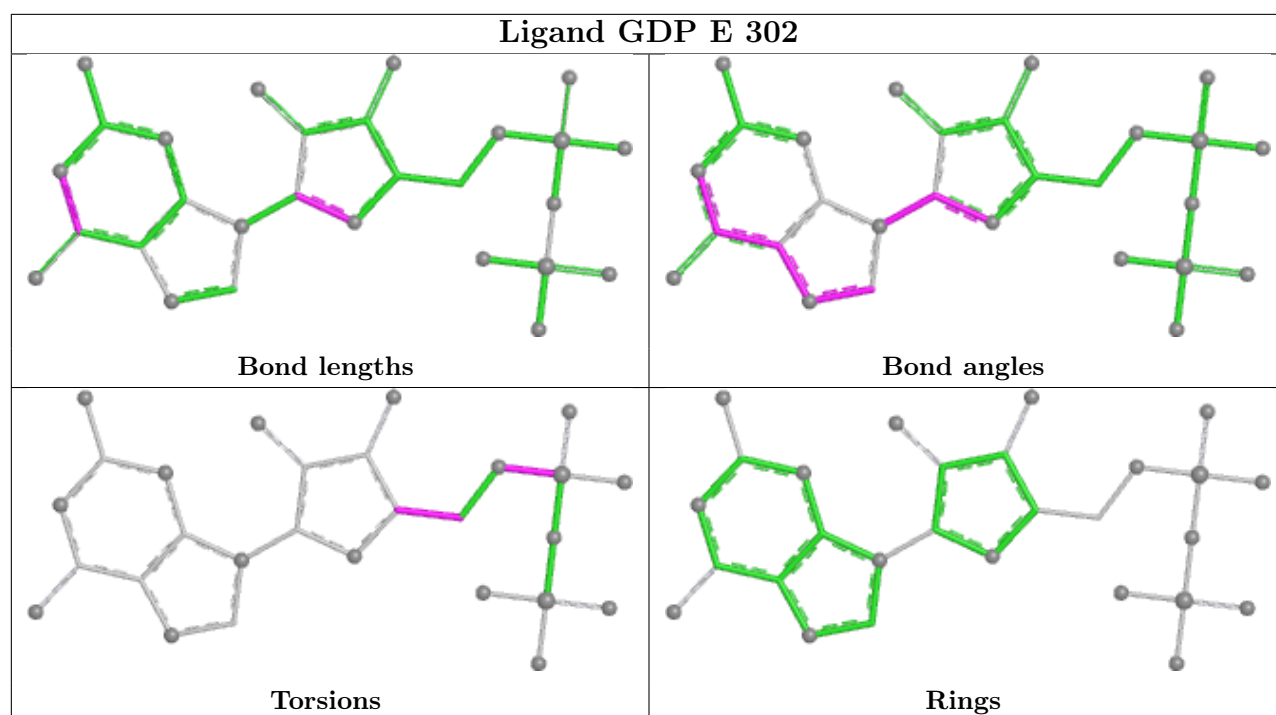
Mol	Chain	Res	Type	Atoms
4	E	302	GDP	O4'-C4'-C5'-O5'
4	F	302	GDP	O4'-C4'-C5'-O5'
4	G	302	GDP	O4'-C4'-C5'-O5'
4	H	302	GDP	O4'-C4'-C5'-O5'
4	E	302	GDP	C3'-C4'-C5'-O5'
4	F	302	GDP	C3'-C4'-C5'-O5'
4	G	302	GDP	C3'-C4'-C5'-O5'
4	H	302	GDP	C3'-C4'-C5'-O5'

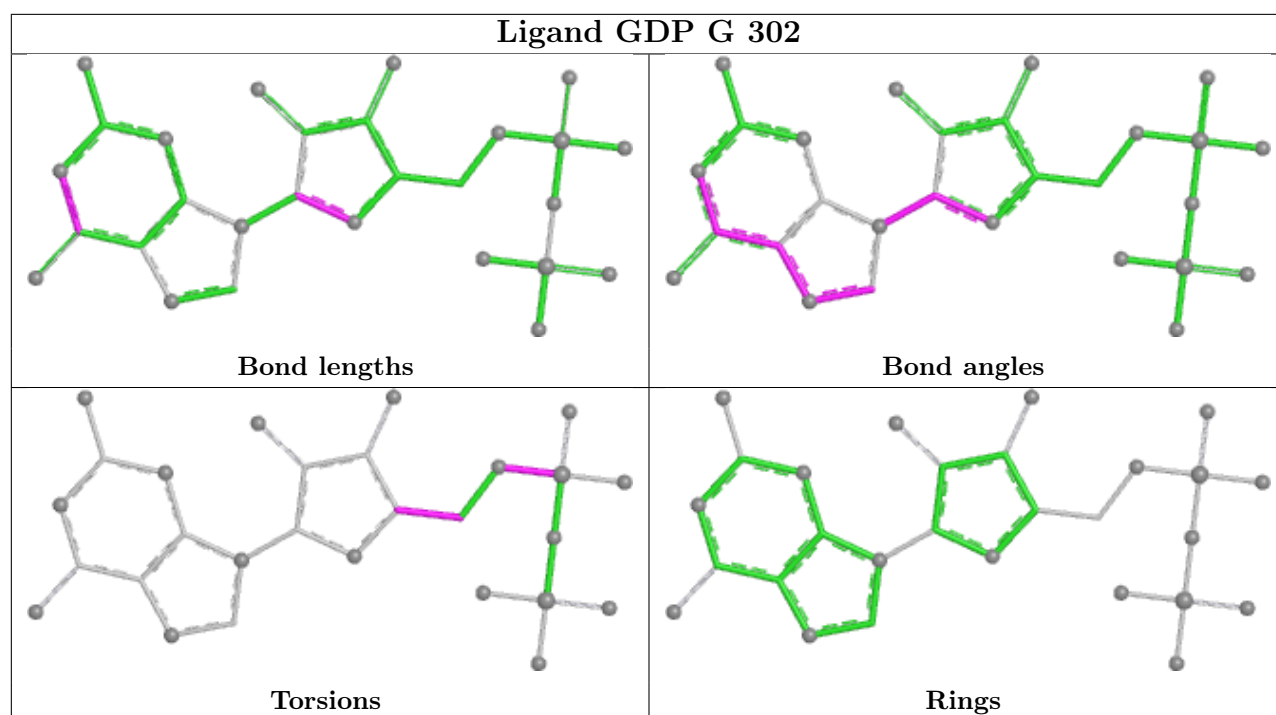
There are no ring outliers.

No monomer is involved in short contacts.

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.

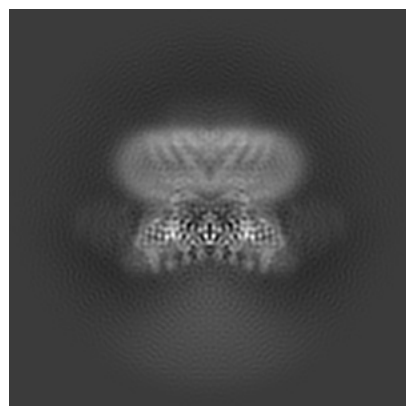
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28977. These allow visual inspection of the internal detail of the map and identification of artifacts.

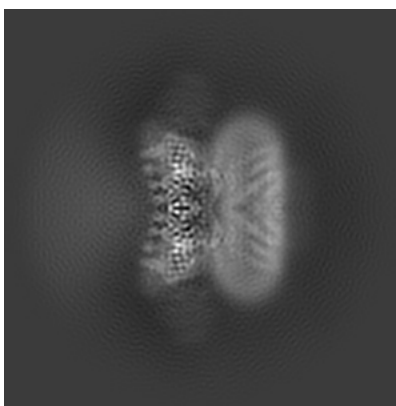
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

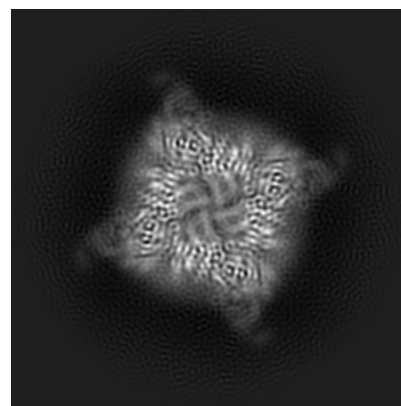
6.1.1 Primary map



X

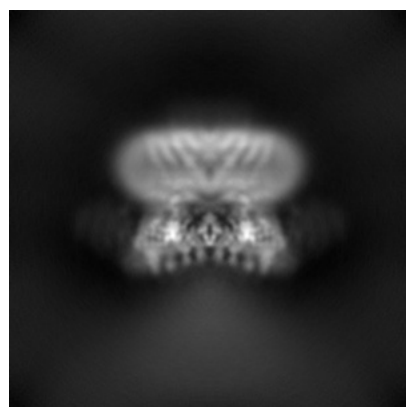


Y

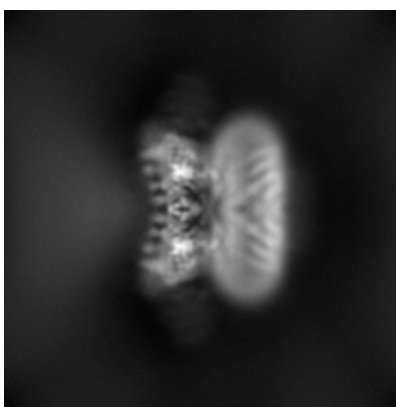


Z

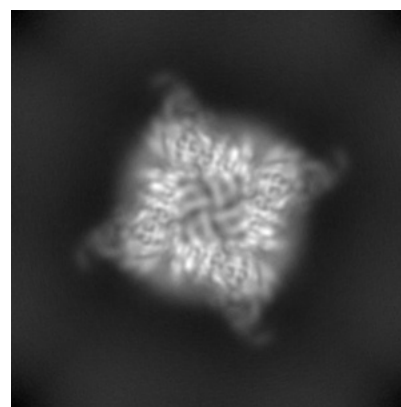
6.1.2 Raw map



X



Y

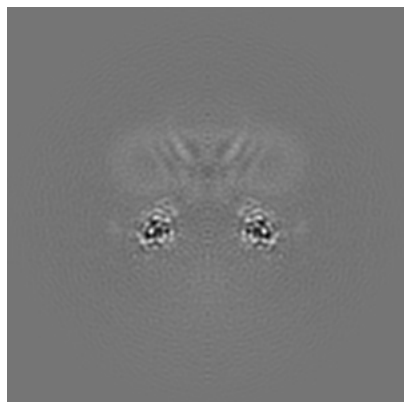


Z

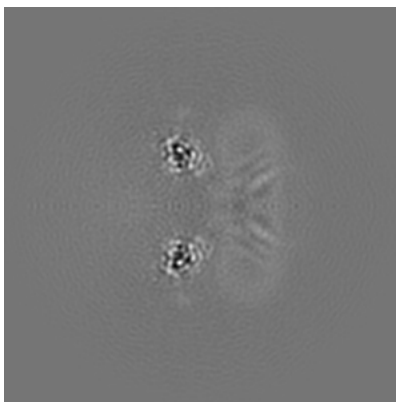
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

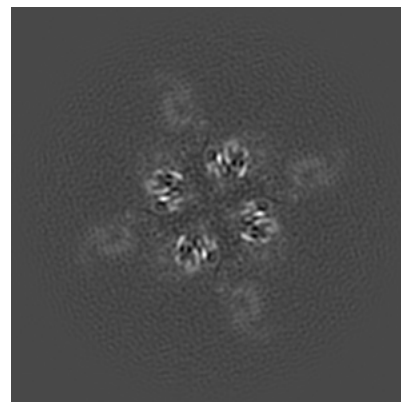
6.2.1 Primary map



X Index: 128

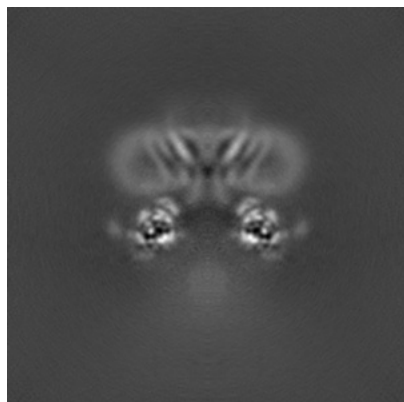


Y Index: 128

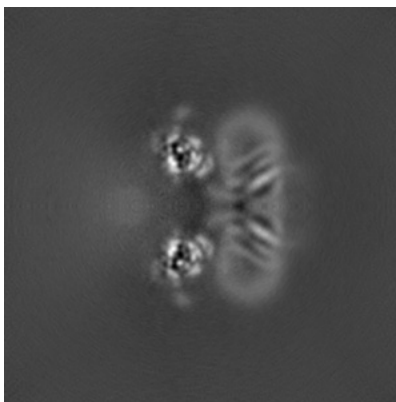


Z Index: 128

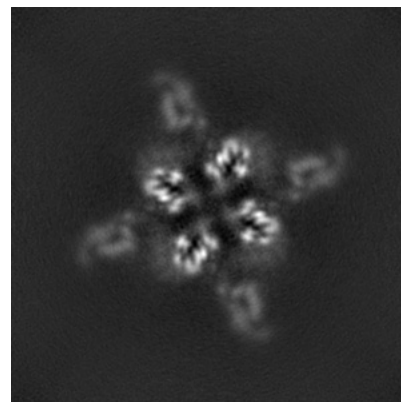
6.2.2 Raw map



X Index: 128



Y Index: 128

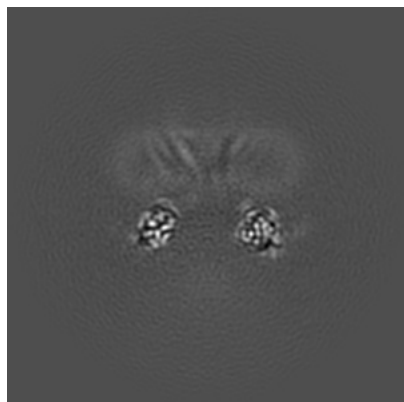


Z Index: 128

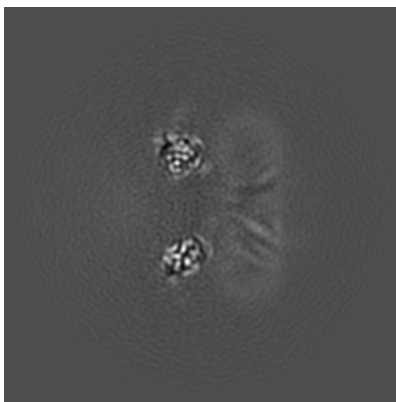
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

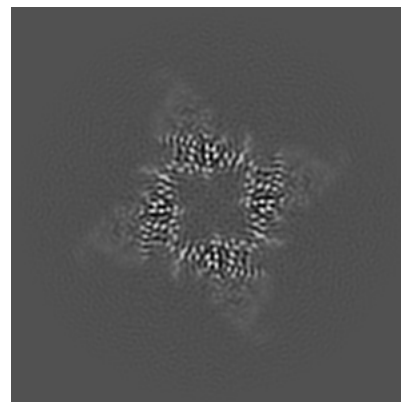
6.3.1 Primary map



X Index: 126

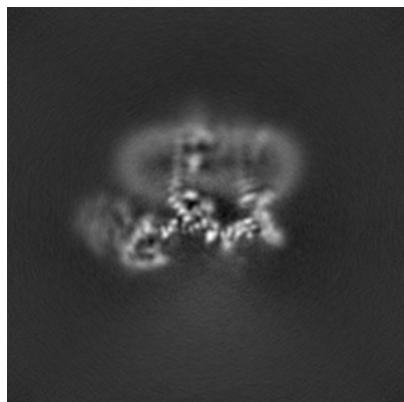


Y Index: 130

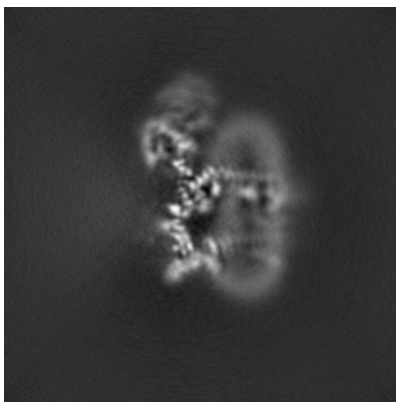


Z Index: 111

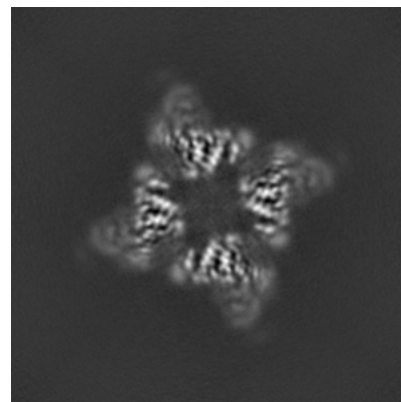
6.3.2 Raw map



X Index: 151



Y Index: 151

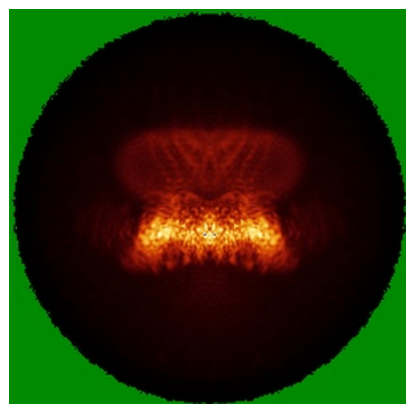


Z Index: 106

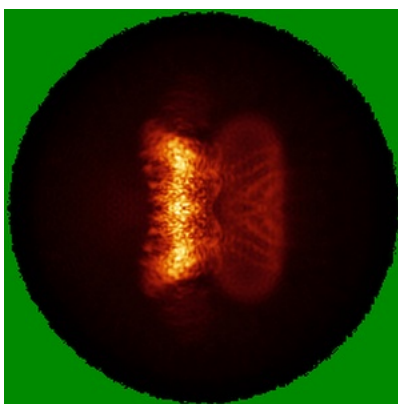
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

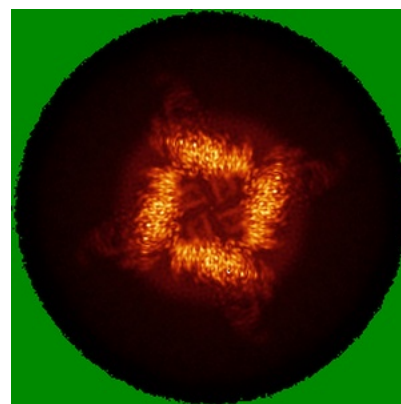
6.4.1 Primary map



X

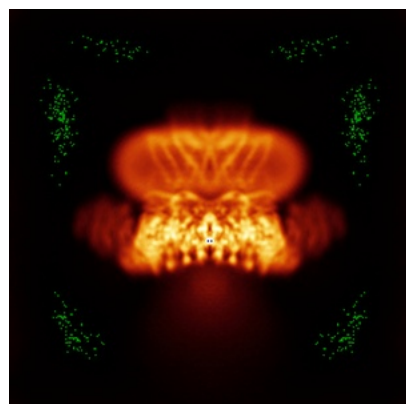


Y

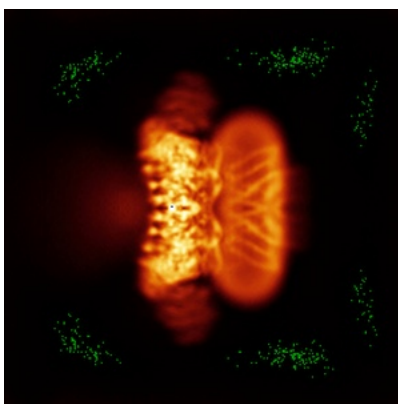


Z

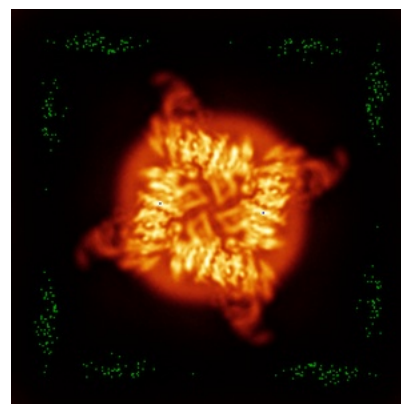
6.4.2 Raw map



X



Y

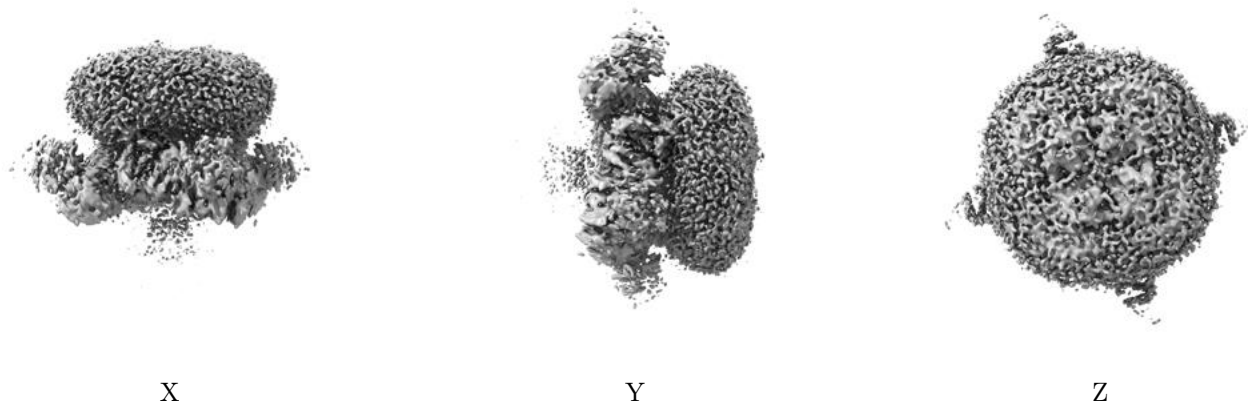


Z

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.

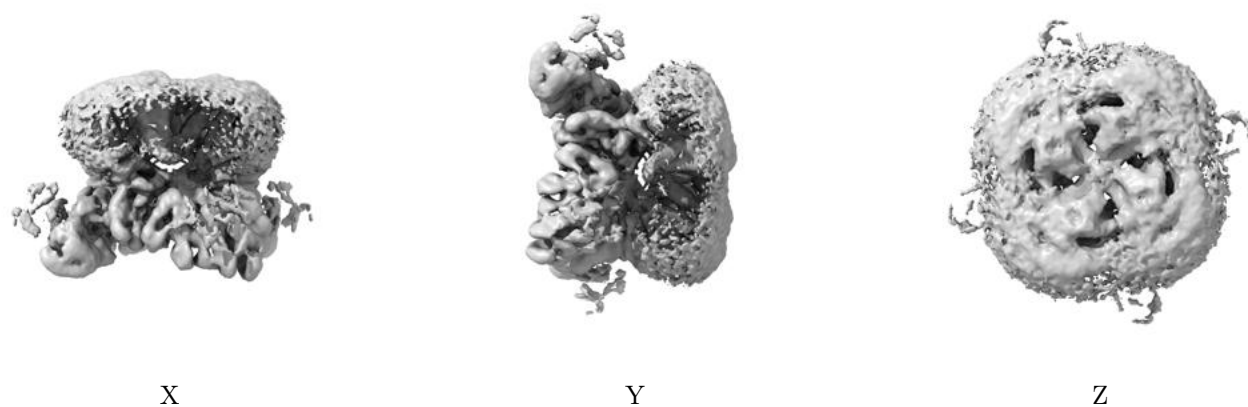
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.209. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

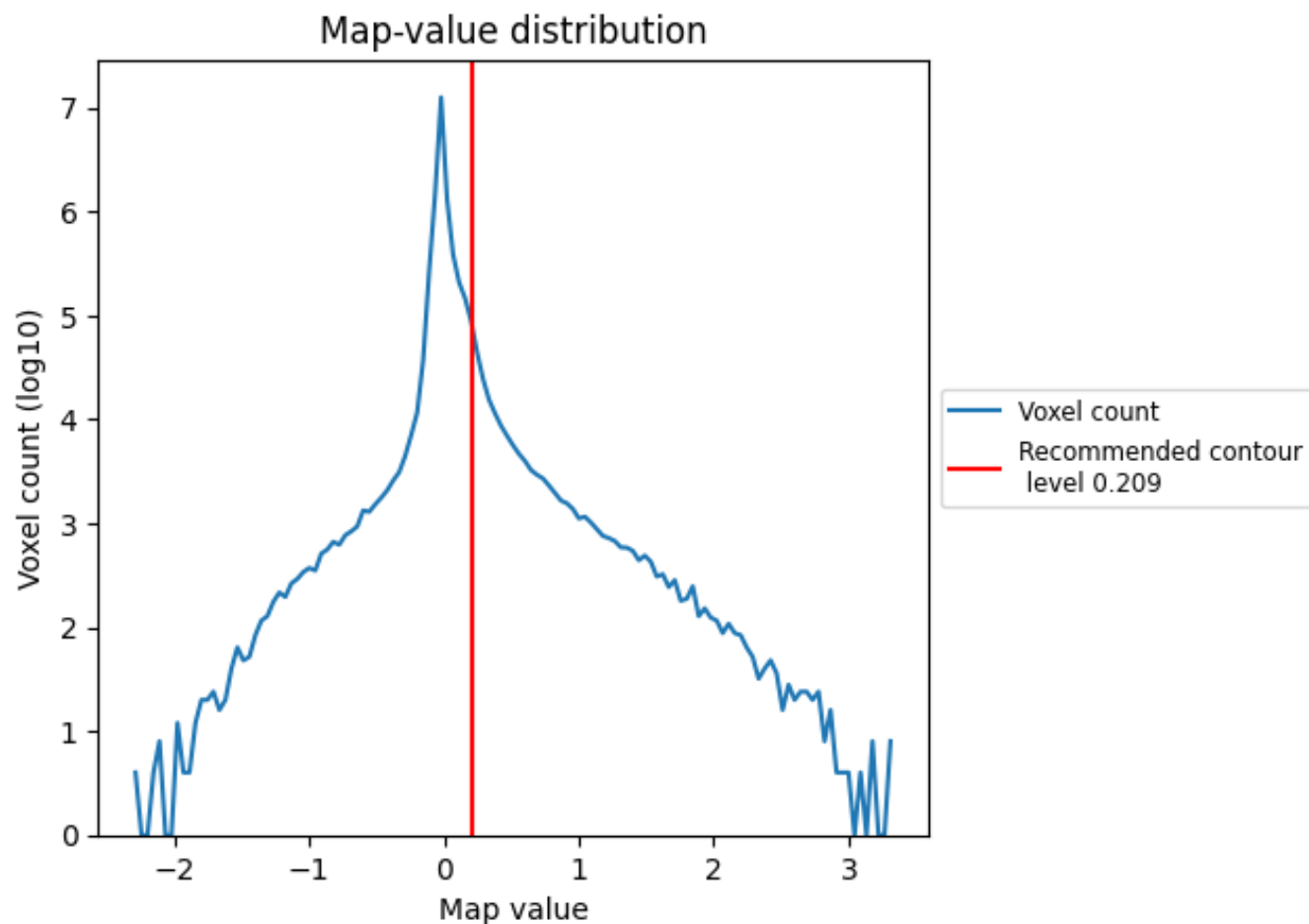
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

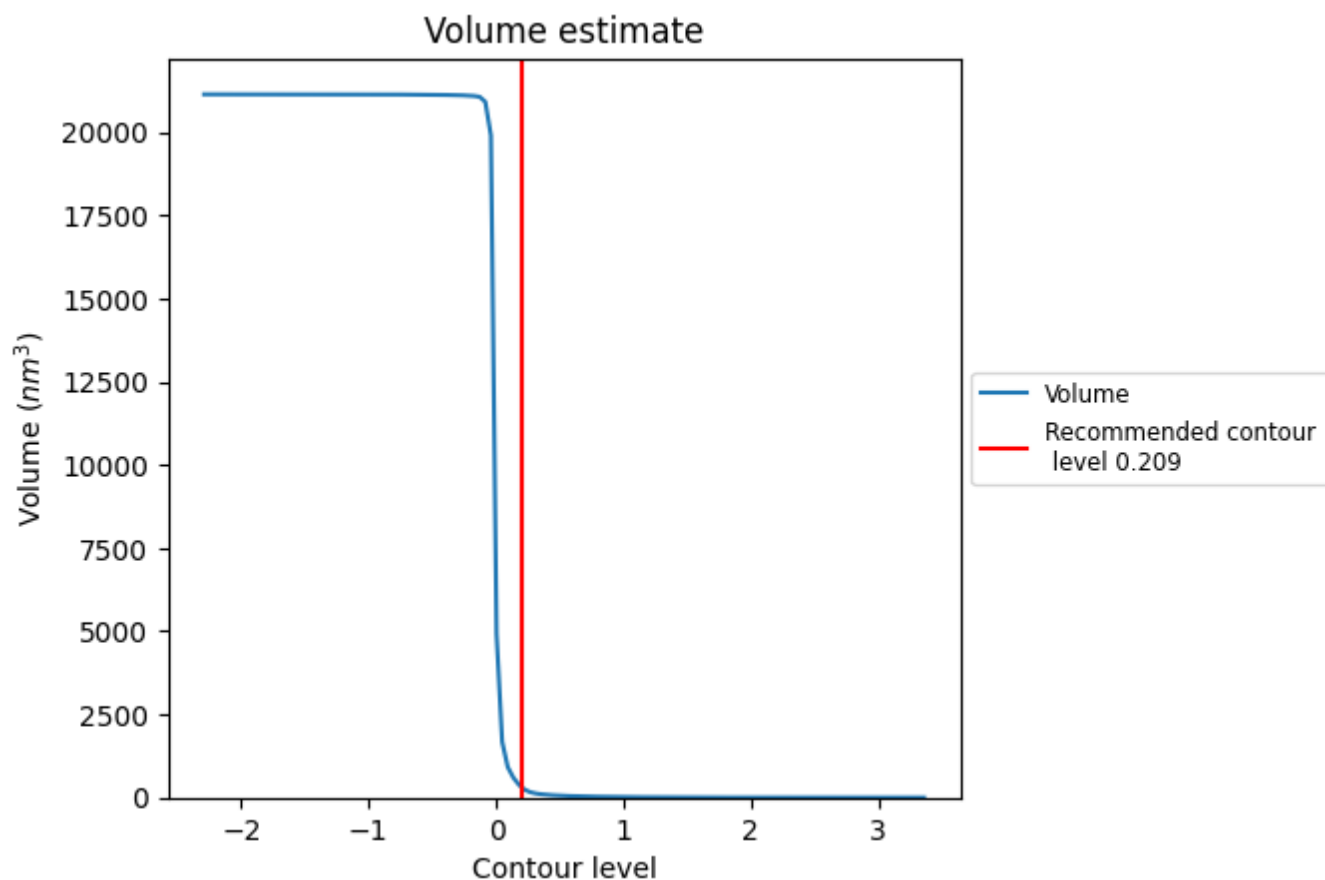
This section contains the results of statistical analysis of the map.

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.

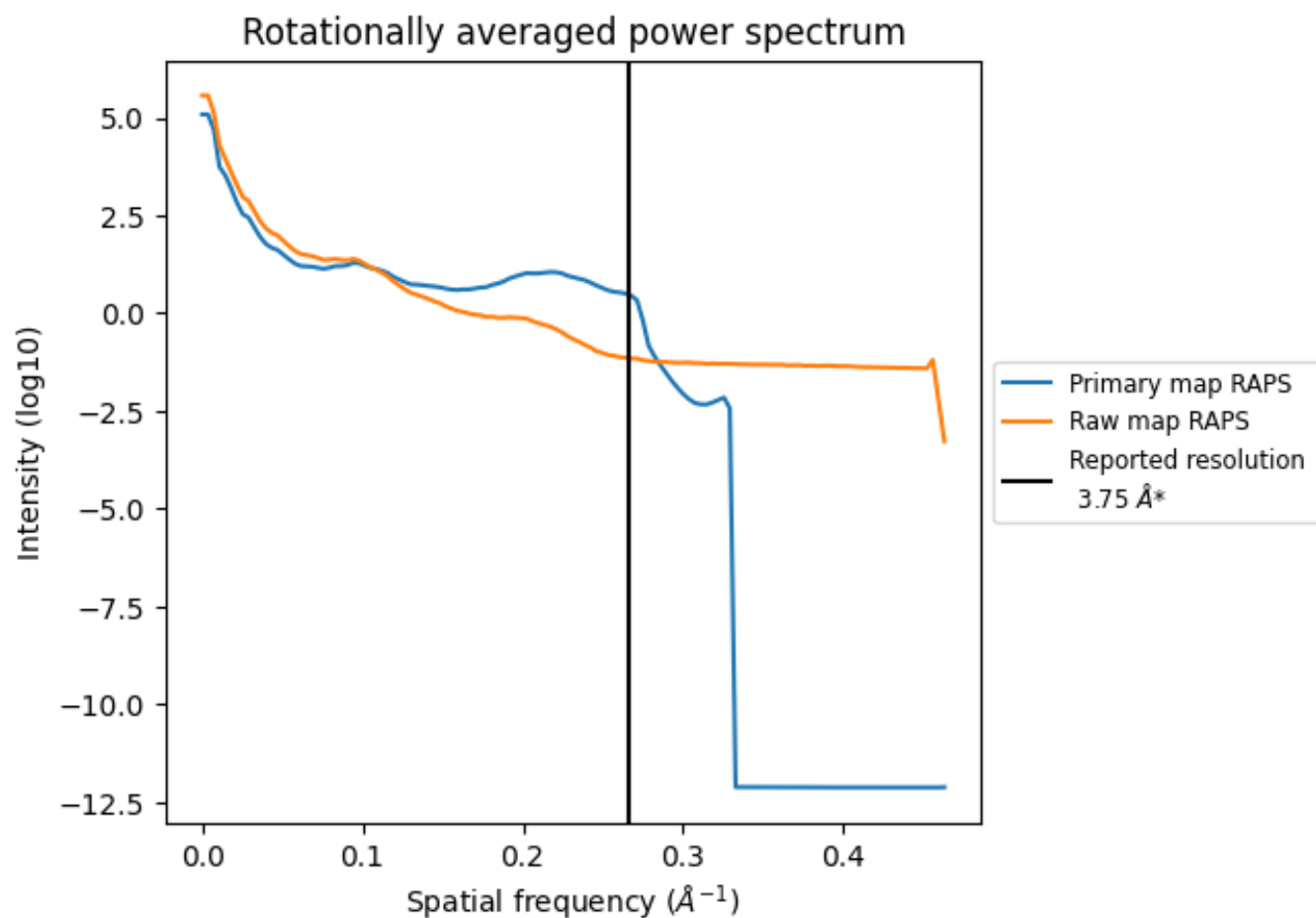
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 287 nm^3 ; this corresponds to an approximate mass of 259 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 ⓘ

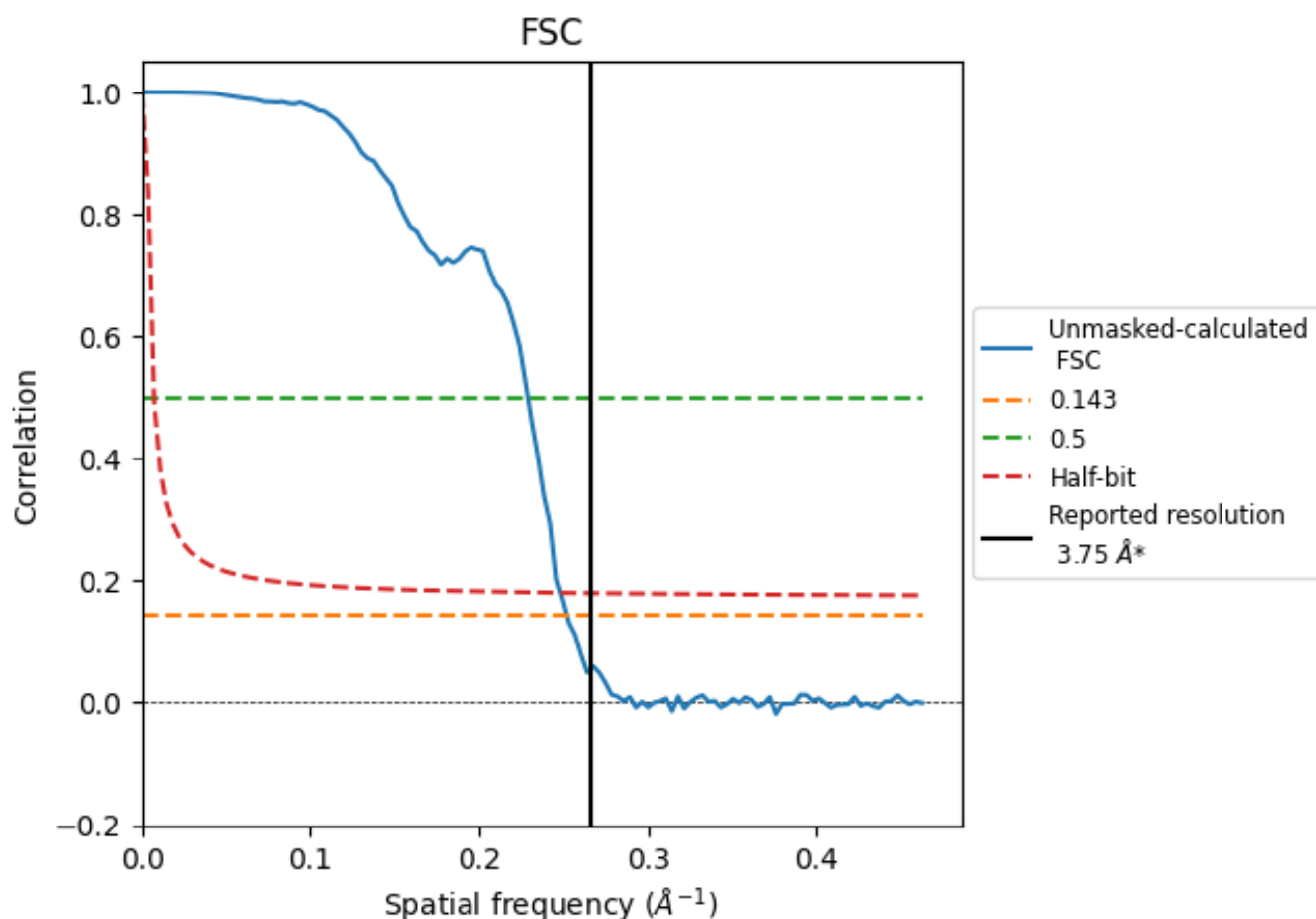


*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

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 0.267 \AA^{-1}

8.2 Resolution estimates [i](#)

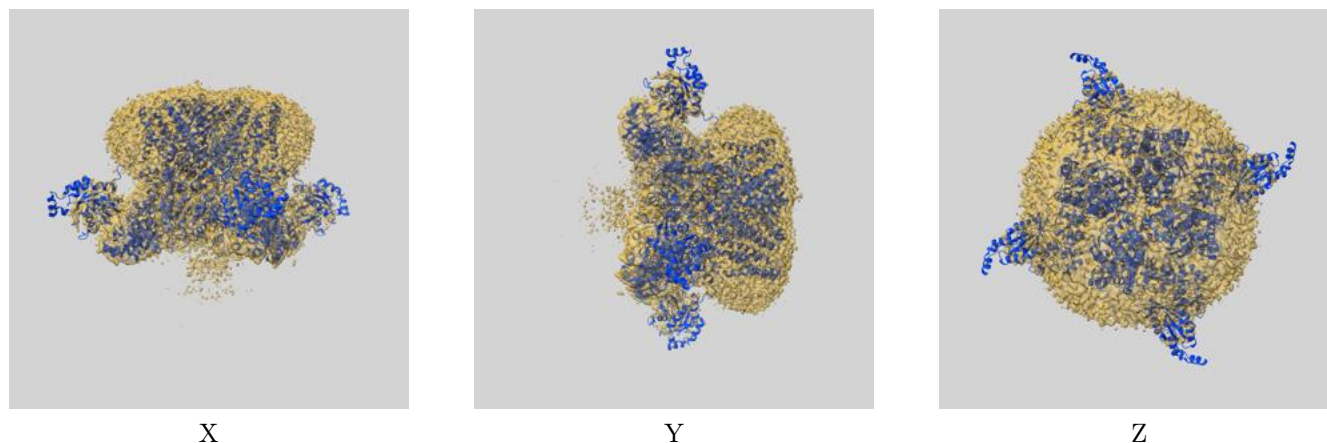
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.75	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.97	4.36	4.03

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

9 Map-model fit [i](#)

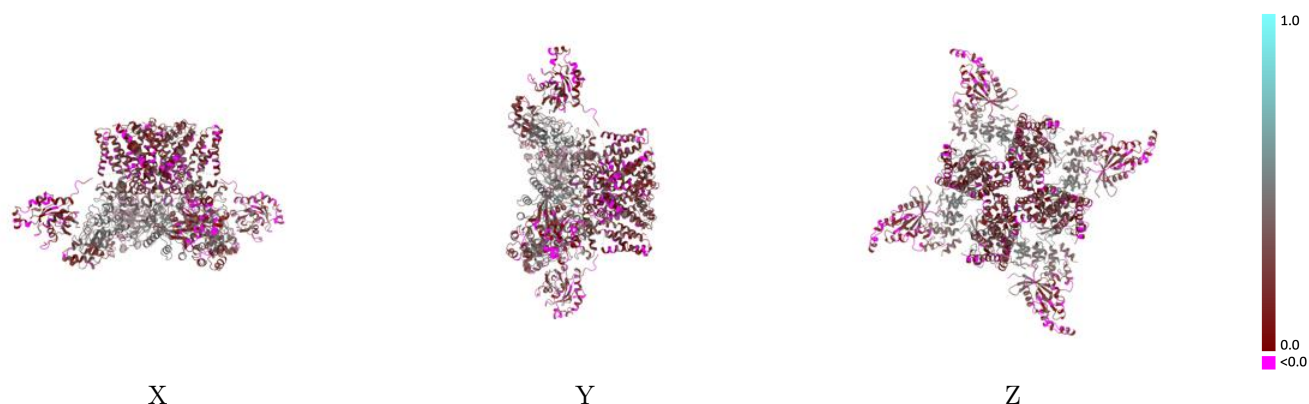
This section contains information regarding the fit between EMDB map EMD-28977 and PDB model 8FC9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



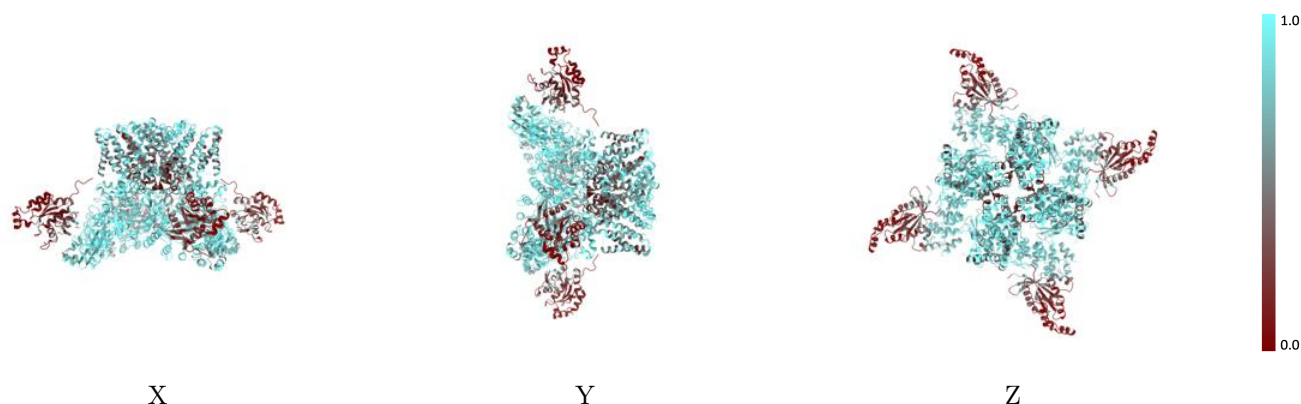
The images above show the 3D surface view of the map at the recommended contour level 0.209 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



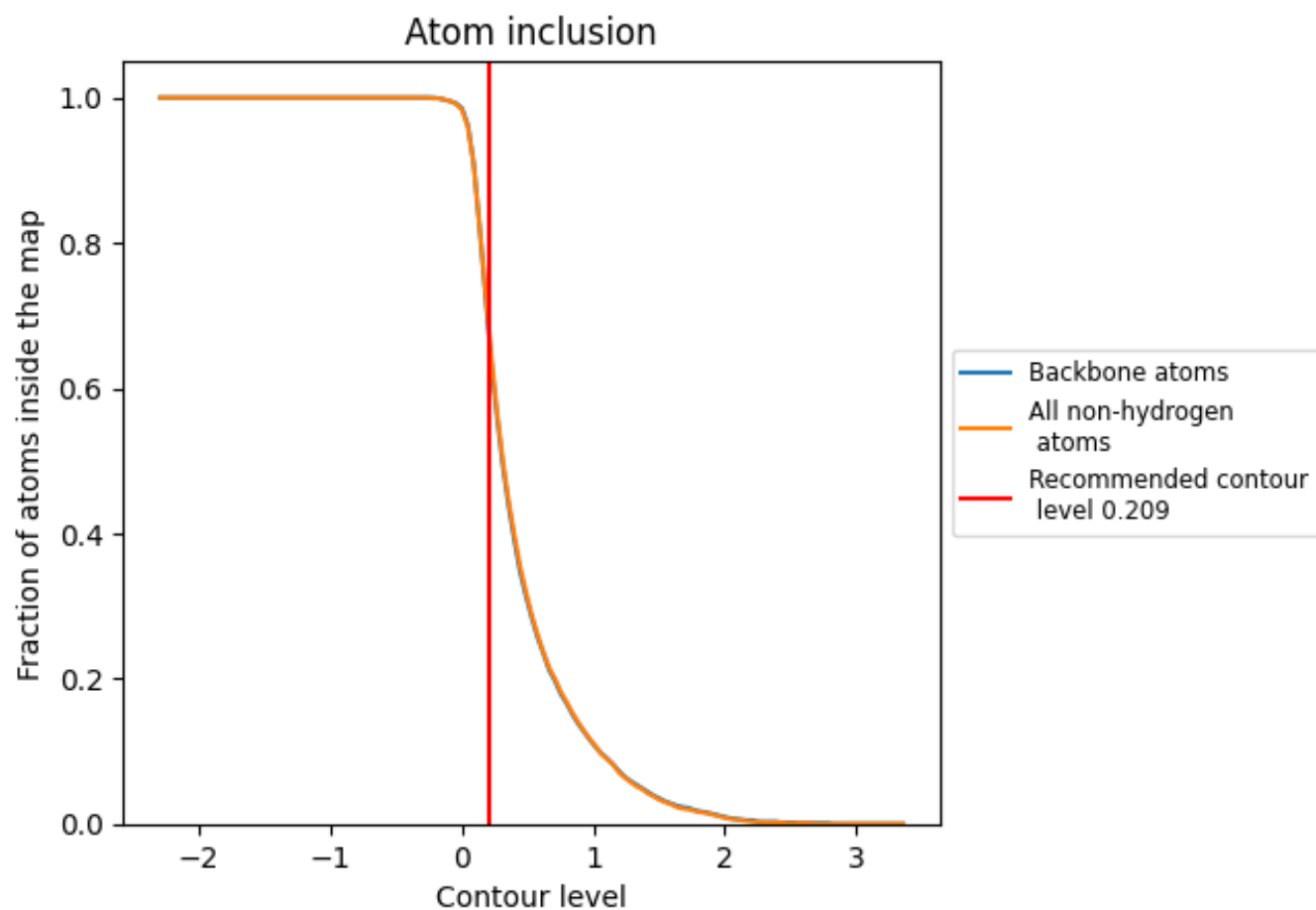
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.209).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 68% 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 (0.209) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6770	<div></div> 0.2820
A	<div></div> 0.8370	<div></div> 0.3290
B	<div></div> 0.8420	<div></div> 0.3320
C	<div></div> 0.8380	<div></div> 0.3270
D	<div></div> 0.8360	<div></div> 0.3280
E	<div></div> 0.2260	<div></div> 0.1420
F	<div></div> 0.2310	<div></div> 0.1490
G	<div></div> 0.2220	<div></div> 0.1390
H	<div></div> 0.2310	<div></div> 0.1450

1.0

0.0

<0.0