



wwPDB EM Validation Summary Report ⓘ

Jun 28, 2022 – 01:38 pm BST

PDB ID : 7PL9
EMDB ID : EMD-13485
Title : Cryo-EM structure of Bestrhodopsin (rhodopsin-rhodopsin-bestrophin) complex
Authors : Matzov, D.; Kaczmarczyk, I.; Shalev-Benami, M.
Deposited on : 2021-08-29
Resolution : 3.21 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:

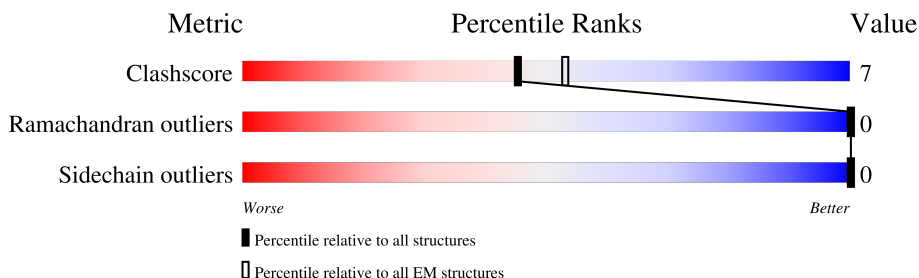
EMDB validation analysis : 0.0.1.dev8
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

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 3.21 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

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	1187	
1	B	1187	
1	C	1187	
1	D	1187	
1	E	1187	

2 Entry composition [i](#)

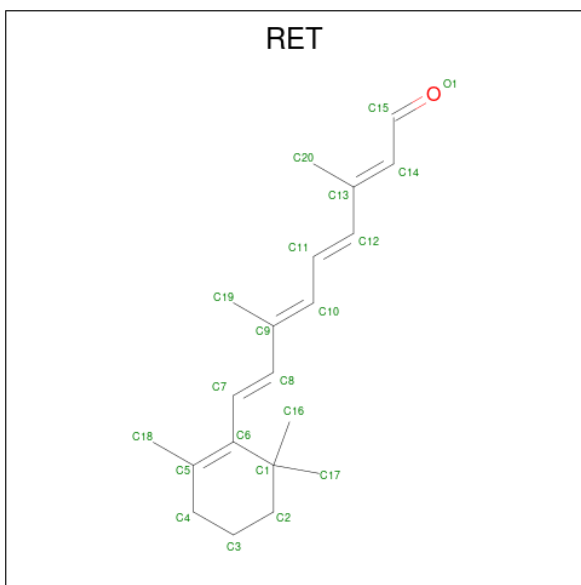
There are 2 unique types of molecules in this entry. The entry contains 37945 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Rhodopsin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	994	Total 7569	C 4978	N 1261	O 1283	S 47	0	0
1	B	994	Total 7569	C 4978	N 1261	O 1283	S 47	0	0
1	C	994	Total 7569	C 4978	N 1261	O 1283	S 47	0	0
1	D	994	Total 7569	C 4978	N 1261	O 1283	S 47	0	0
1	E	994	Total 7569	C 4978	N 1261	O 1283	S 47	0	0

- Molecule 2 is RETINAL (three-letter code: RET) (formula: C₂₀H₂₈O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total 20	C 20	0

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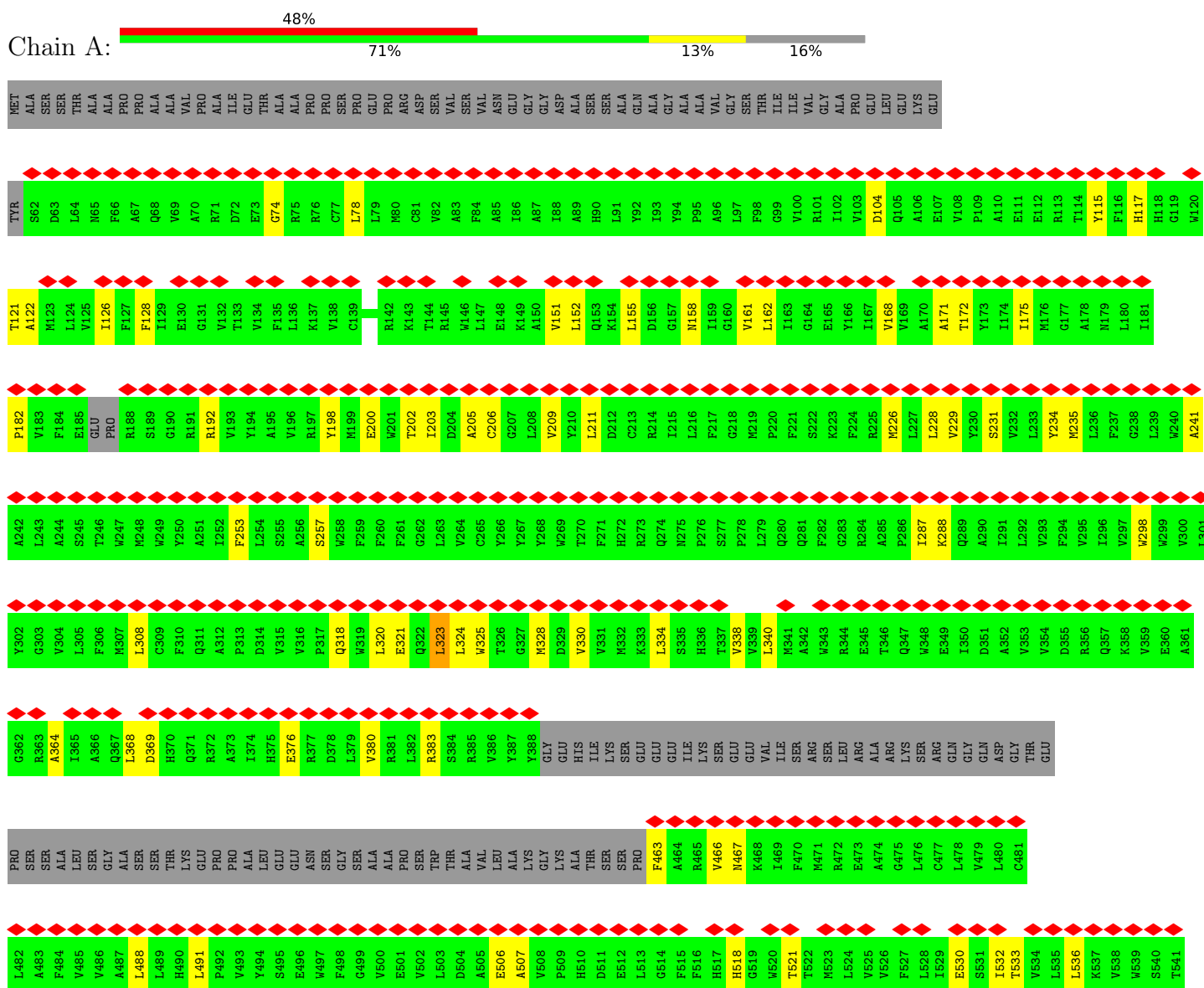
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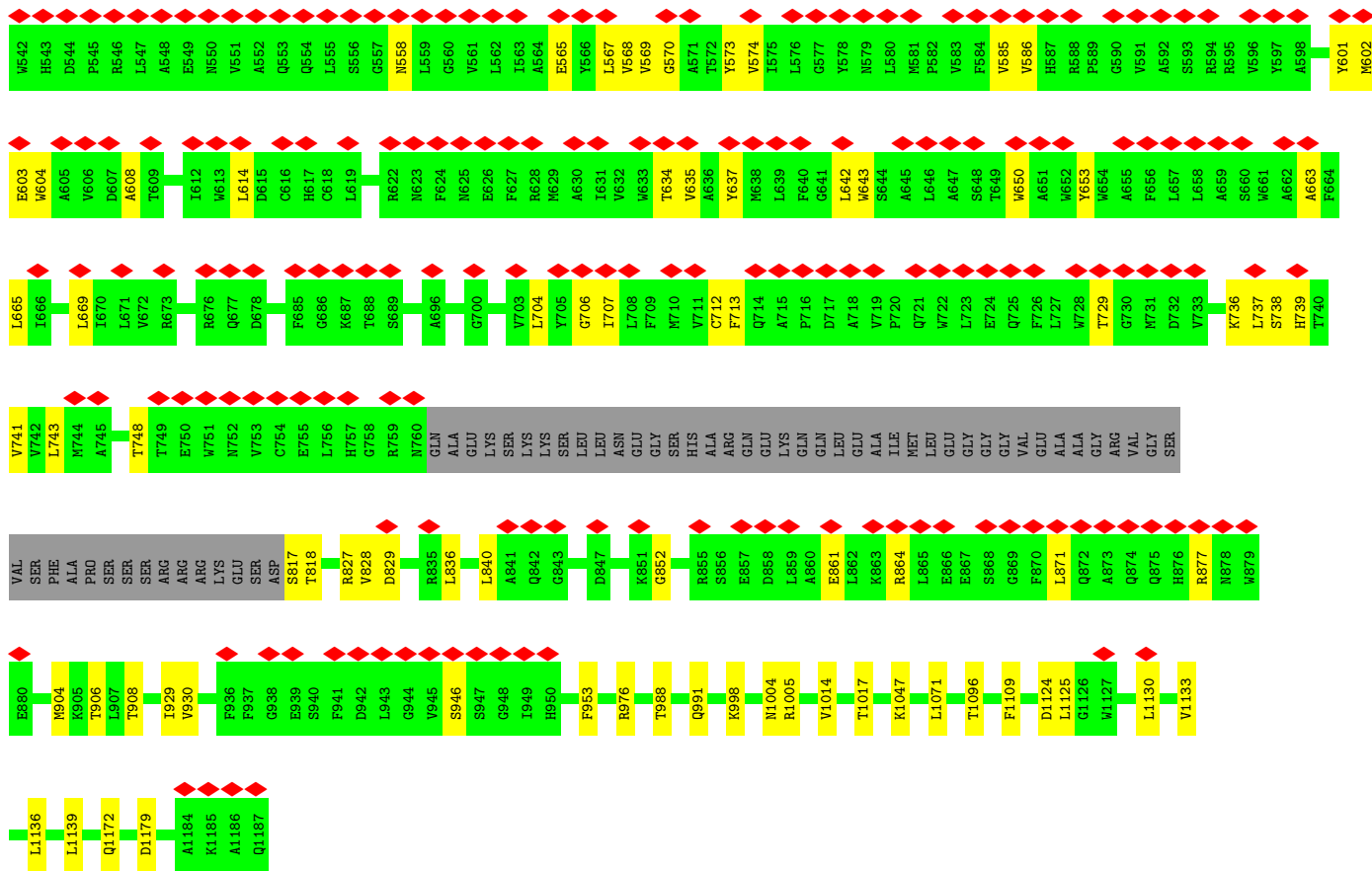
Mol	Chain	Residues	Atoms	AltConf
2	B	1	Total C 20 20	0
2	C	1	Total C 20 20	0
2	D	1	Total C 20 20	0
2	E	1	Total C 20 20	0

3 Residue-property plots

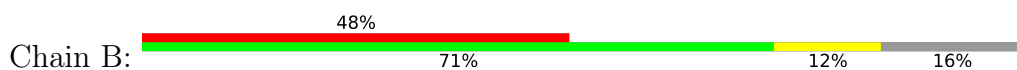
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Rhodopsin

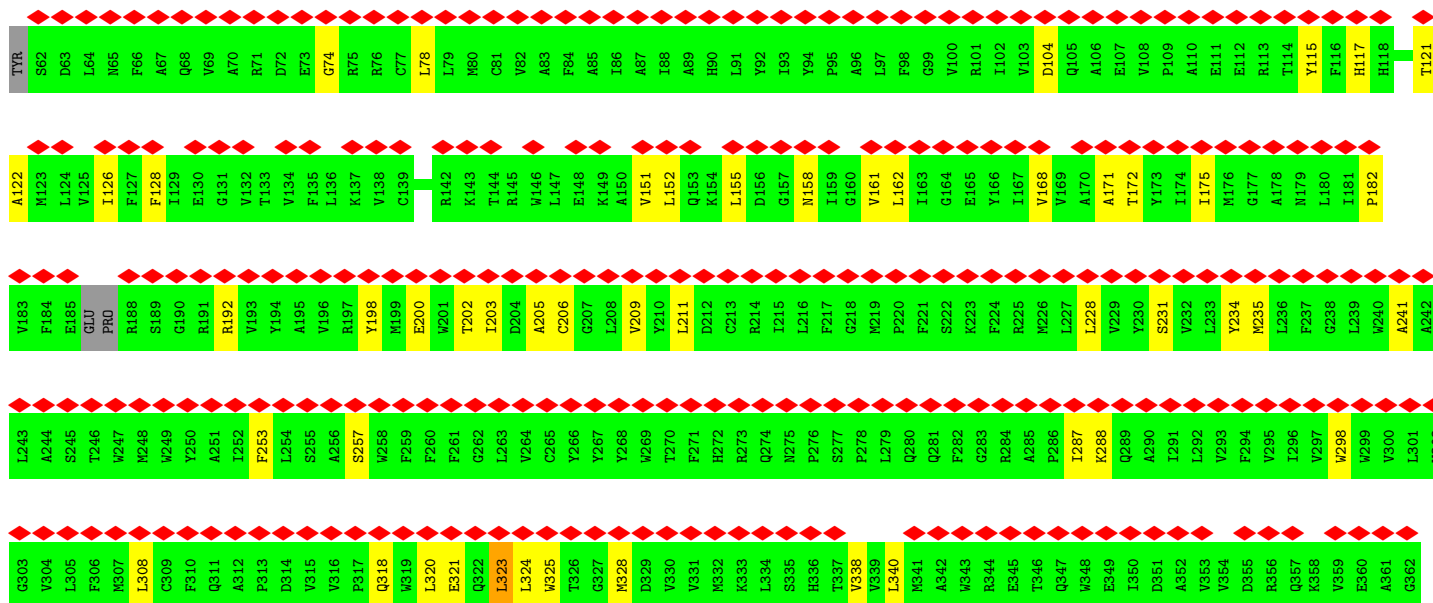


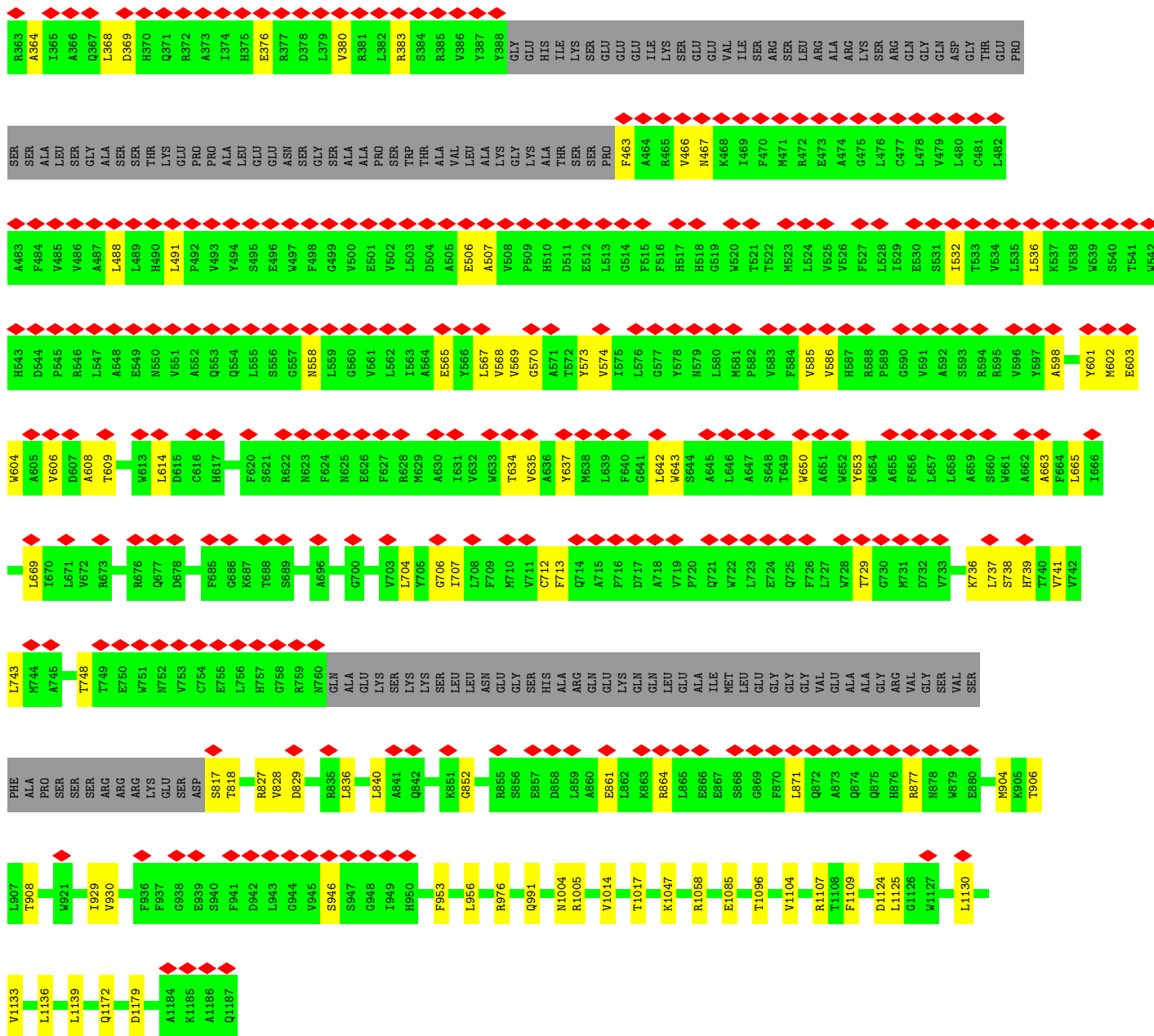


• Molecule 1: Rhodopsin

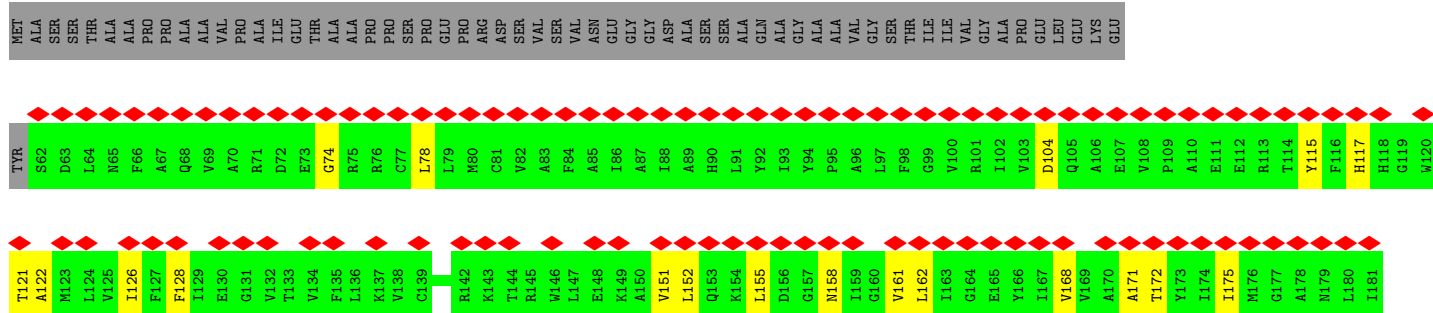
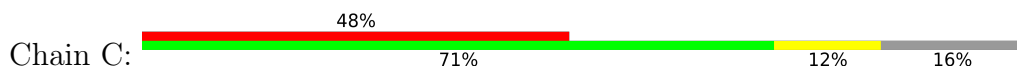


MET	ALA	SER	THR	ALA	PRO	PRO	ALA	ALA	VAL	LEU	THR	ALA	ALA	PRO	PRO	PRO	GLU	PRO	ARG	ASP	VAL	VAL	VAL	ASN	GLY	ALA	SER	SER	ALA	ALA	GLN	ALA	ALA	GLY	THR	ILE	VAL	VAL	GLY	ALA	PRO	GLU	LEU	GLY	GLU	GLU
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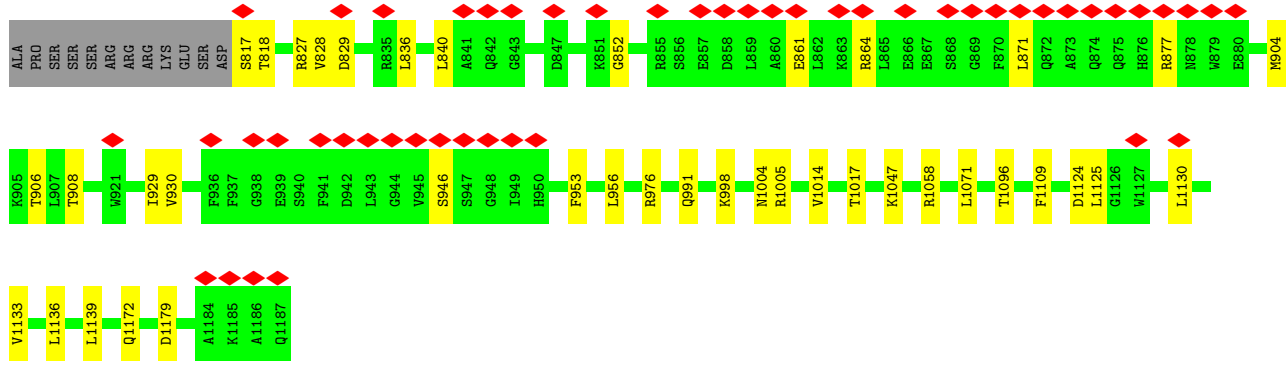


• Molecule 1: Rhodopsin

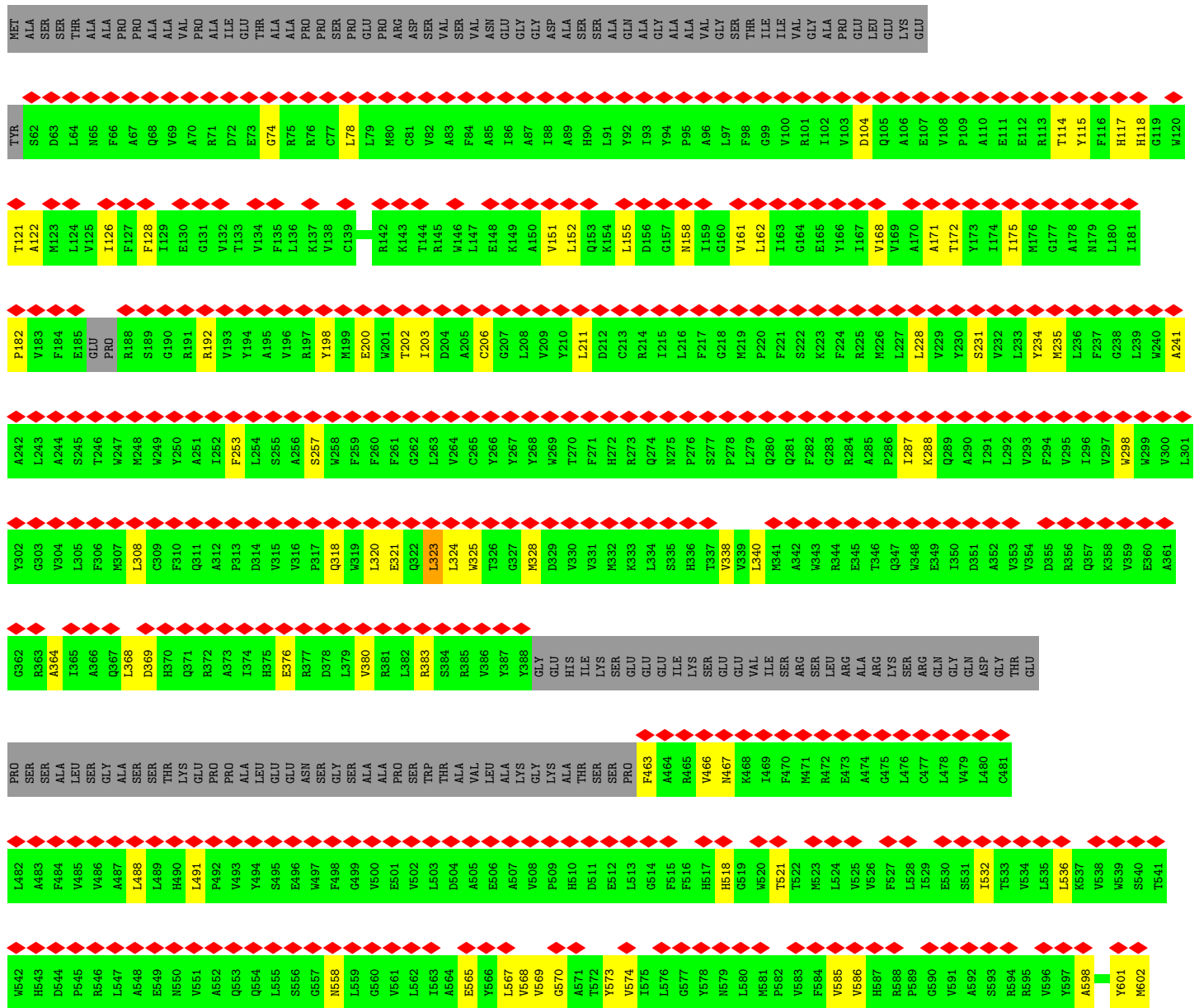
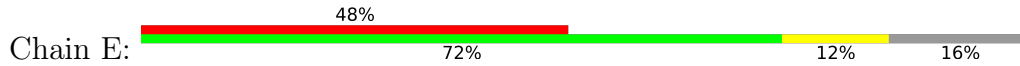


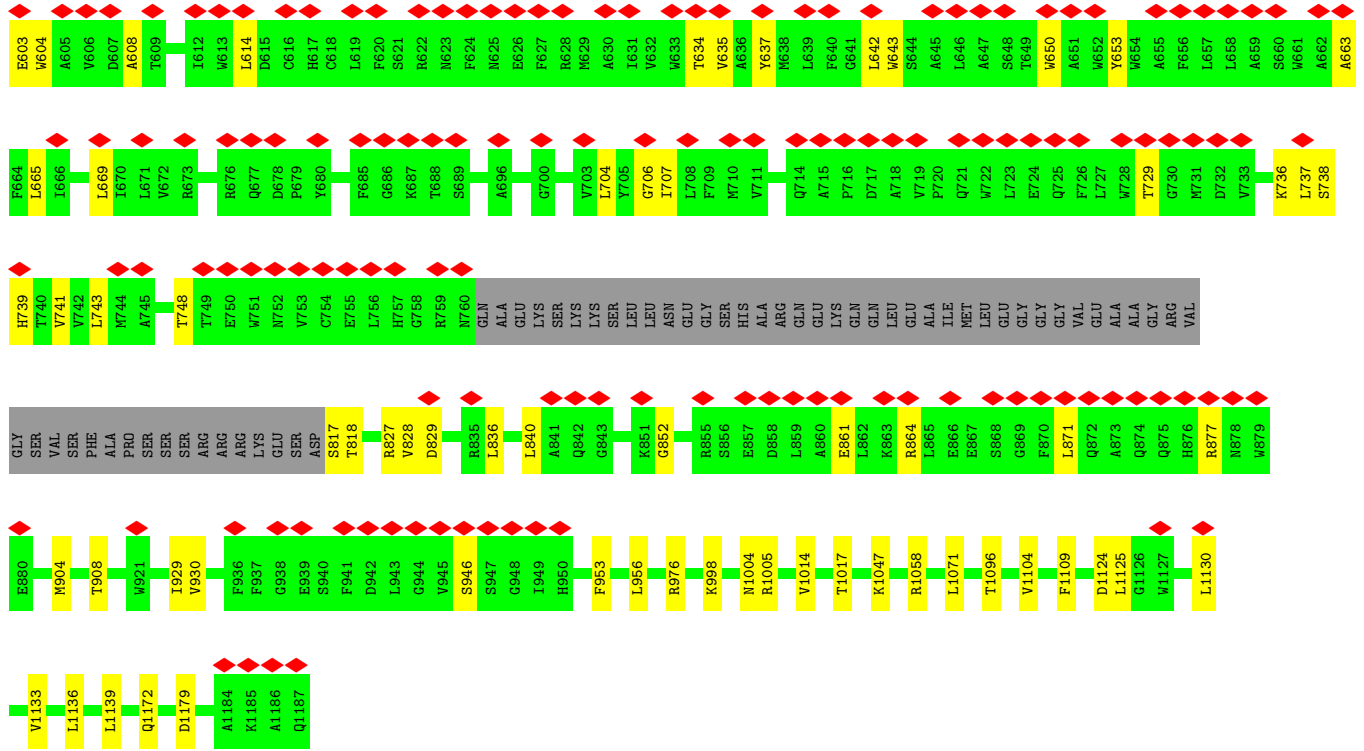
P182	A242	Y302	G362	PRO	L482	H543	E603	F684	H739	VAL	R877	L1125
V183	L243	G303	R363	SER	A483	H544	M604	L665	T740	GLY	N878	G1126
F184	A244	V304	A364	ALA	F484	D544	A605	I666	V741	SER	W879	W1127
E185	S245	L305	I365	LEU	V485	P545	V606	L669	L743	SER	E880	L1130
GLU	T246	F306	A366	SER	V486	R546	A608	I670	M744	ALA	H904	V1133
PRO	W247	M307	Q367	GLY	A487	L547	T609	V672	A745	PRO	T908	L1136
R188	M248	L308	L368	ALA	L488	A548		R673	T748	SER	W921	L1139
S189	M249	C309	D369	SER	L489	E549		R676	T749	ARG	W929	Q1172
G190	Y250	F310	H370	THR	H490	N550		Q677	E750	ARG	V930	D1179
R191	A251	Q311	Q371	LYS	L491	V551		D678	M751	ARG	F936	A1184
R192	I252	A312	R372	GLU	P492	Q553		F679	M752	ARG	F937	K1185
V193	F253	P313	A373	PRO	V493	Q554		V680	M753	GLY	G938	A1186
Y194	L254	D314	I374	ALA	Y494	Q555		F685	C754	ASP	S939	K1187
A195	L254	V315	H375	LEU	S495	L555		G686	E755	SER	E940	
V196	A256	V316	E376	GLU	S496	S556		T688	L756	SER	F941	
R197	A257	P317	R377	ASN	W497	G557		S689	H757	GLN	D942	
Y198	S257	Q318	D378	SER	F498	N558		A696	L758	ALA	L943	
H199	F259	W319	L379	GLY	G499	L559		G700	R827	GLU	G944	
E200	F260	L320	V380	SER	V500	G560			W828	LEU	V945	
W201	F261	E321	R381	ALA	E501	V561			D829	LYS	S946	
T202	G262	Q322	L382	PRO	L502	L562			R835	SER	S947	
I203	L263	L323	R383	THR	D504	I563			L836	LYS	G948	
D204	V264	L324	S384	THR	A505	A564			L840	LYS	I949	
A205	C265	W325	R385	ALA	E506	E565			A841	SER	H950	
C206	C266	T326	A386	VAL	A507	V566			Q842	LEU	F953	
C207	Y266	G327	V387	LEU	E508	L567			Q843	LEU	L956	
L208	Y267	M328	L388	LEU	V509	V568			D847	LEU	R976	
V209	Y268	M329	V389	GLY	P509	V569			R851	LEU	Q991	
Y210	W269	D330	L390	LYS	H510	G570			G852	ASN	K998	
L211	T270	V331	H391	ALA	D511	A571			R855	GLU	M1004	
D212	H271	M332	L392	THR	E512	T572			S856	ARG	R1005	
C213	H272	M333	R393	SER	L513	V573			D858	GLN	V1014	
R214	R273	K333	K394	PRO	L514	V574			L860	ALA	T1017	
L215	Q274	L334	L395	GLU	G514	L575			R862	ALA	K1047	
L216	Q275	S335	S396	GLU	F515	L576			R863	ALA	L1058	
F217	P276	H336	L397	LEU	F516	G577			L864	MET	L1071	
G218	S277	L338	V398	SER	H517	V578			L865	LEU	T1096	
M219	P278	V339	V399	GLU	H518	N579			E866	GLY	V1104	
P220	L279	V340	V400	GLU	G519	L580			E867	VAL	F1109	
F221	Q280	M341	M342	VAL	W520	L581			S868	GLY	D1124	
S222	Q281	A342	A343	ILE	T521	F582			F870	GLY		
K223	Q282	W343	W344	SER	T522	P583			L871	VAL		
F224	F283	R344	R345	LEU	N523	G584			Q872	ALA		
R225	R284	E345	E346	ARG	L524	F584			A873	ALA		
M226	A285	L346	L347	ALA	V525	V585			Q874	GLY		
L227	P286	Q347	Q348	ARG	V526	V586			H876	ARG		
L228	I287	W348	W349	LYS	H527	H587						
W229	K288	E349	E350	SER	L528	R588						
Y230	Q289	L350	L351	GLN	I529	F589						
S231	A290	D351	D352	GLY	E530	G590						
L232	I291	A352	A353	GLN	S531	V591						
L233	L292	V354	V355	THR	T532	A592						
Y234	V293	D356	D357	GLU	T533	R593						
M235	F294	R356	R357	GLU	L535	V594						
L236	V295	Q357	Q358	GLY	L536	R595						
F237	F296	V297	V298	THR	L537	V596						
G238	W299	W299	W299	GLU	K537	V597						
L239	V300	L301	L301	GLU	V538	A598						
W240					W539	Y601						
A241					S540	M602						

• Molecule 1: Rhodopsin



● Molecule 1: Rhodopsin





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27749	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 ($e^-/\text{\AA}^2$)	0.86	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.067	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	344.0, 344.0, 344.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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: RET

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	0.33	0/7779	0.45	4/10645 (0.0%)
1	B	0.33	0/7779	0.45	4/10645 (0.0%)
1	C	0.33	0/7779	0.45	4/10645 (0.0%)
1	D	0.33	0/7779	0.45	4/10645 (0.0%)
1	E	0.33	0/7779	0.45	4/10645 (0.0%)
All	All	0.33	0/38895	0.45	20/53225 (0.0%)

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	871	LEU	CB-CG-CD2	6.06	121.30	111.00
1	B	871	LEU	CB-CG-CD2	6.05	121.29	111.00
1	C	871	LEU	CB-CG-CD2	6.05	121.29	111.00
1	A	871	LEU	CB-CG-CD2	6.05	121.28	111.00
1	E	871	LEU	CB-CG-CD2	6.04	121.26	111.00

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	7569	0	7216	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	7569	0	7216	110	0
1	C	7569	0	7216	109	0
1	D	7569	0	7216	109	0
1	E	7569	0	7216	106	0
2	A	20	0	27	5	0
2	B	20	0	27	5	0
2	C	20	0	27	5	0
2	D	20	0	27	5	0
2	E	20	0	27	5	0
All	All	37945	0	36215	499	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 7.

The worst 5 of 499 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:D:704:LEU:HD12	1:D:707:ILE:HD11	1.66	0.78
1:C:704:LEU:HD12	1:C:707:ILE:HD11	1.66	0.77
1:E:704:LEU:HD12	1:E:707:ILE:HD11	1.66	0.77
1:B:704:LEU:HD12	1:B:707:ILE:HD11	1.66	0.76
1:A:704:LEU:HD12	1:A:707:ILE:HD11	1.66	0.76

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	986/1187 (83%)	934 (95%)	52 (5%)	0	100 100
1	B	986/1187 (83%)	933 (95%)	53 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	986/1187 (83%)	933 (95%)	53 (5%)	0	100	100
1	D	986/1187 (83%)	934 (95%)	52 (5%)	0	100	100
1	E	986/1187 (83%)	933 (95%)	53 (5%)	0	100	100
All	All	4930/5935 (83%)	4667 (95%)	263 (5%)	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	726/999 (73%)	726 (100%)	0	100	100
1	B	726/999 (73%)	726 (100%)	0	100	100
1	C	726/999 (73%)	726 (100%)	0	100	100
1	D	726/999 (73%)	726 (100%)	0	100	100
1	E	726/999 (73%)	726 (100%)	0	100	100
All	All	3630/4995 (73%)	3630 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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
2	RET	C	1201	1	20,20,21	0.69	1 (5%)	27,27,28	0.38	0
2	RET	B	1201	1	20,20,21	0.69	1 (5%)	27,27,28	0.38	0
2	RET	A	1201	1	20,20,21	0.68	1 (5%)	27,27,28	0.38	0
2	RET	D	1201	1	20,20,21	0.67	1 (5%)	27,27,28	0.38	0
2	RET	E	1201	1	20,20,21	0.69	1 (5%)	27,27,28	0.39	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
2	RET	C	1201	1	-	7/13/30/31	0/1/1/1
2	RET	B	1201	1	-	7/13/30/31	0/1/1/1
2	RET	A	1201	1	-	7/13/30/31	0/1/1/1
2	RET	D	1201	1	-	7/13/30/31	0/1/1/1
2	RET	E	1201	1	-	7/13/30/31	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	RET	C14-C13	2.66	1.35	1.33
2	E	1201	RET	C14-C13	2.65	1.35	1.33
2	C	1201	RET	C14-C13	2.63	1.35	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	RET	C14-C13	2.61	1.35	1.33
2	D	1201	RET	C14-C13	2.57	1.35	1.33

There are no bond angle outliers.

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

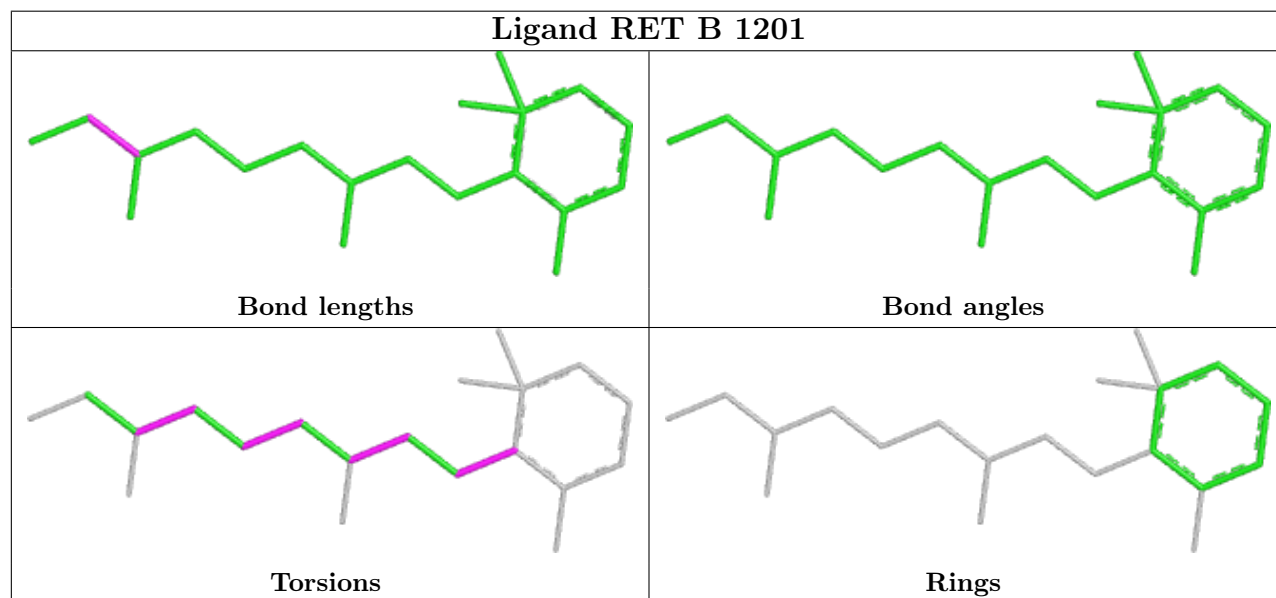
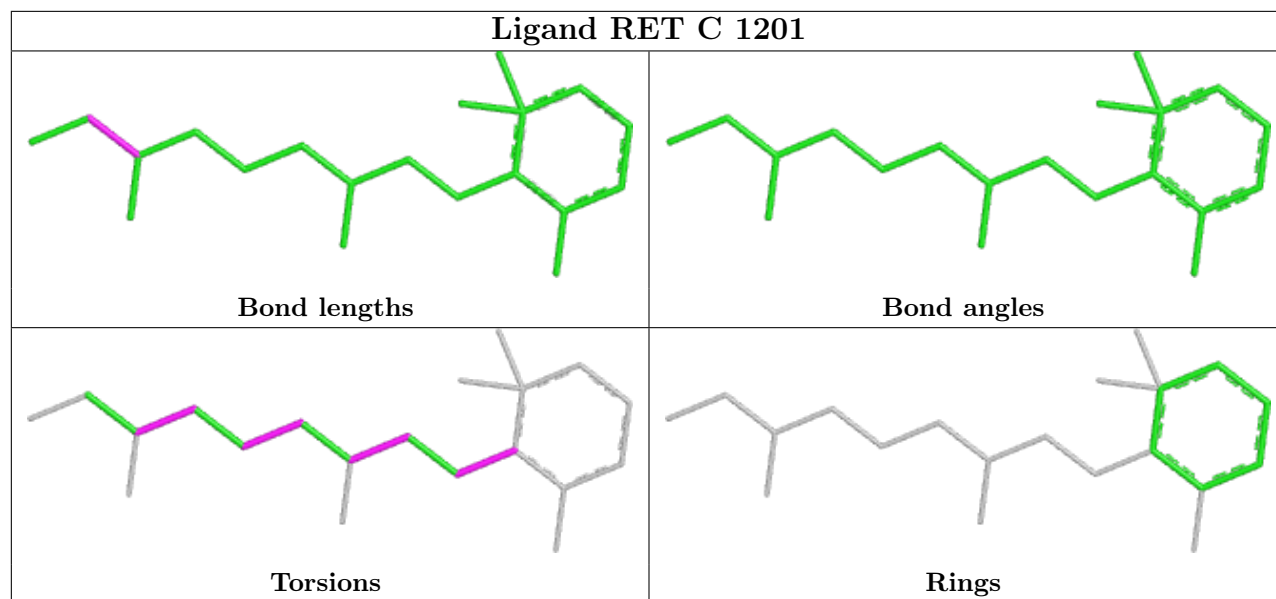
Mol	Chain	Res	Type	Atoms
2	A	1201	RET	C1-C6-C7-C8
2	A	1201	RET	C5-C6-C7-C8
2	A	1201	RET	C7-C8-C9-C10
2	A	1201	RET	C7-C8-C9-C19
2	B	1201	RET	C1-C6-C7-C8

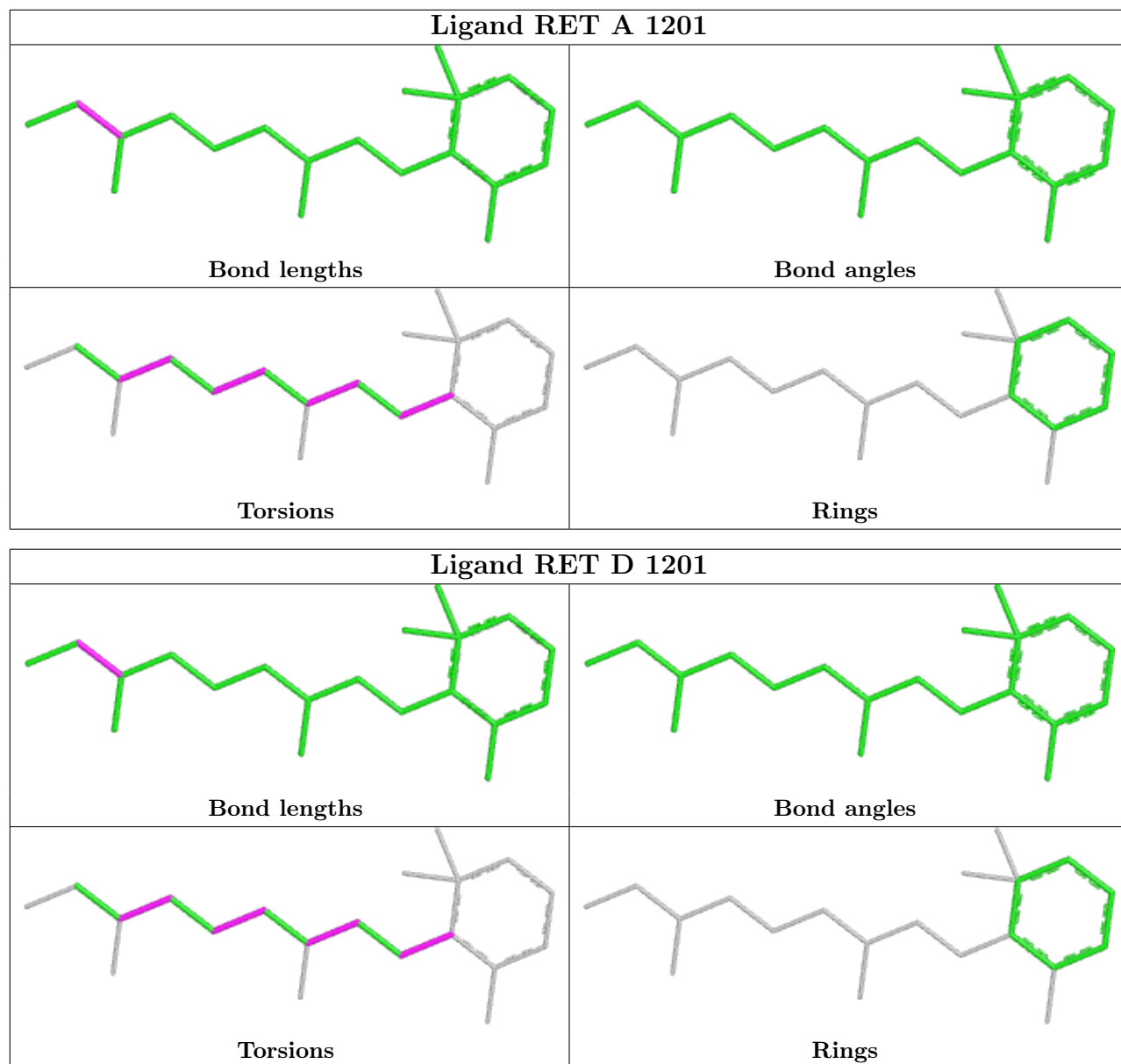
There are no ring outliers.

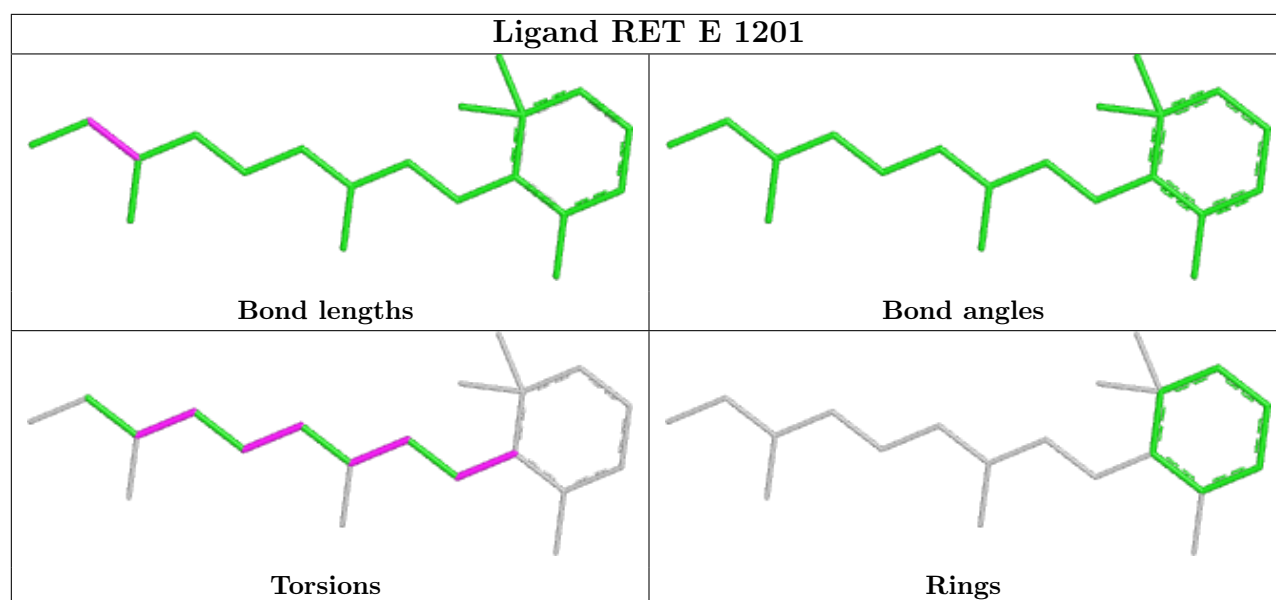
5 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1201	RET	5	0
2	B	1201	RET	5	0
2	A	1201	RET	5	0
2	D	1201	RET	5	0
2	E	1201	RET	5	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.

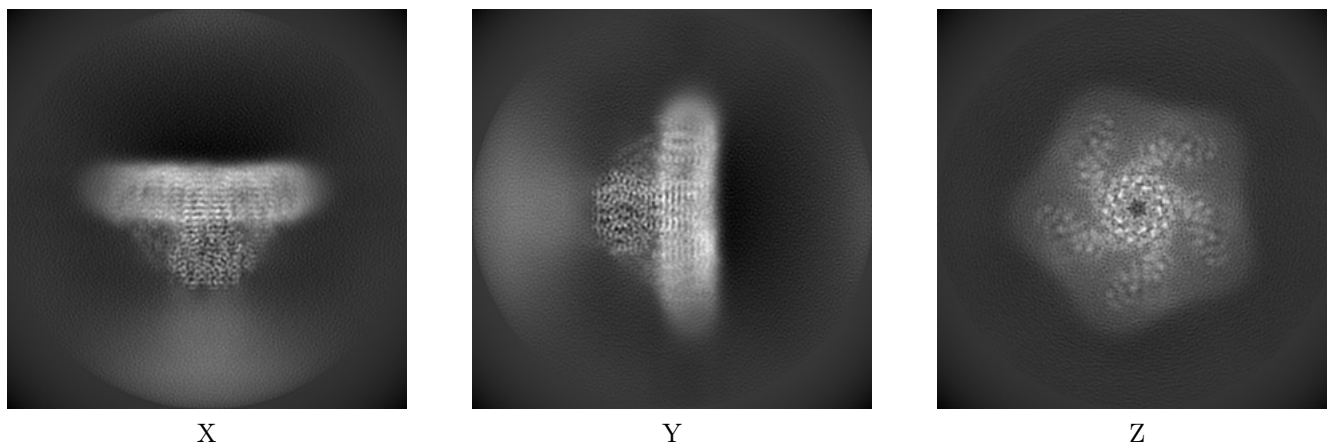
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13485. These allow visual inspection of the internal detail of the map and identification of artifacts.

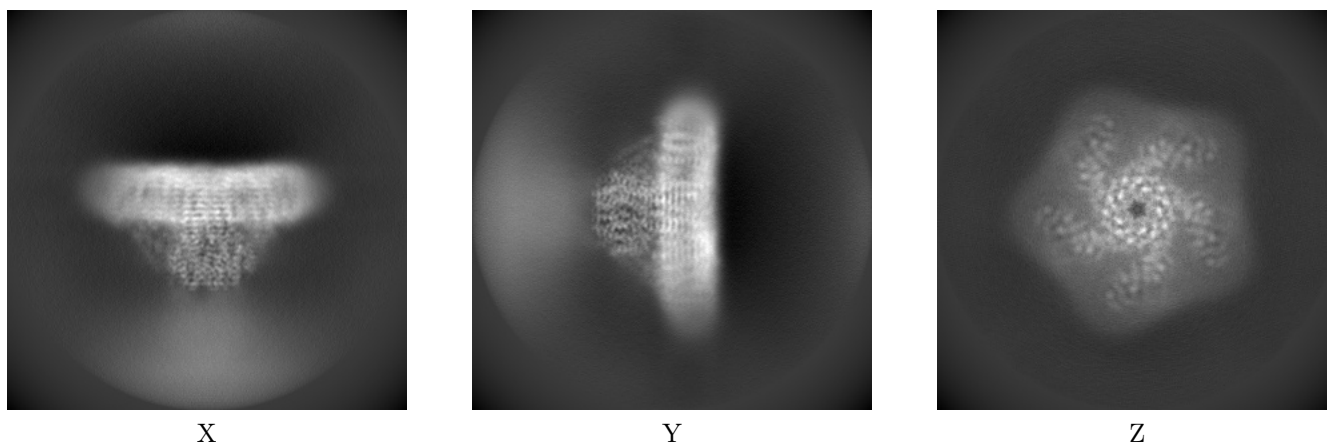
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



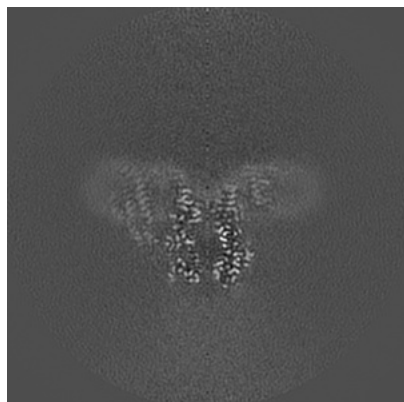
6.1.2 Raw map



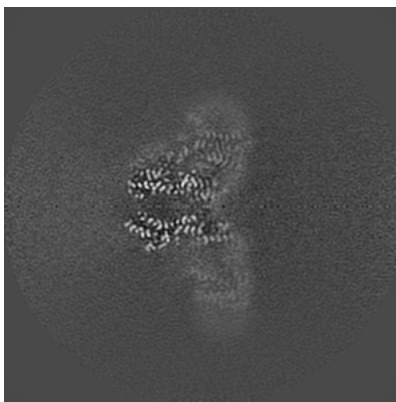
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

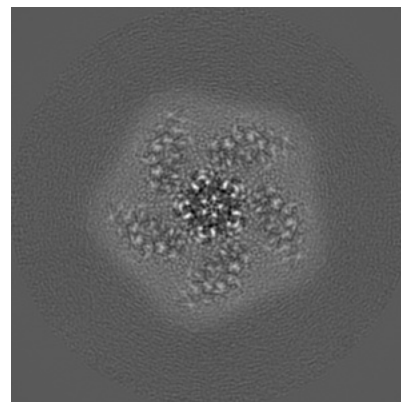
6.2.1 Primary map



X Index: 200

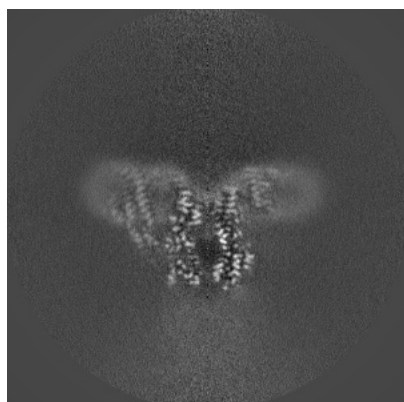


Y Index: 200

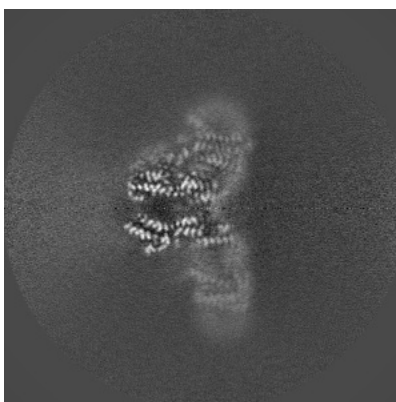


Z Index: 200

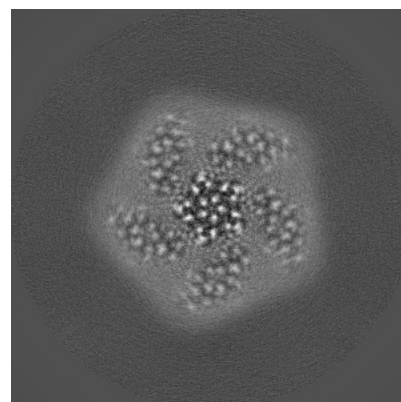
6.2.2 Raw map



X Index: 200



Y Index: 200

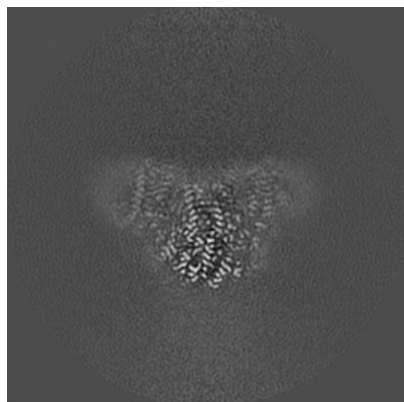


Z Index: 200

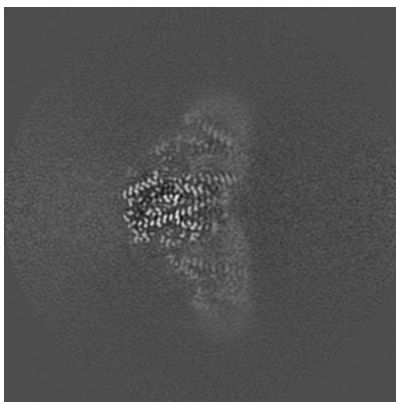
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

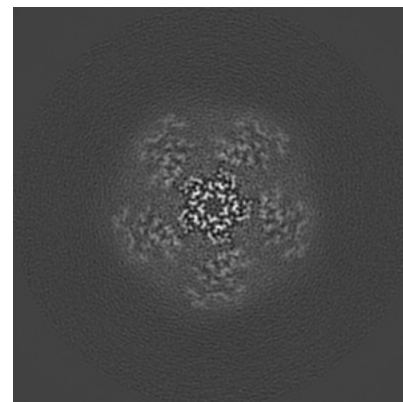
6.3.1 Primary map



X Index: 218

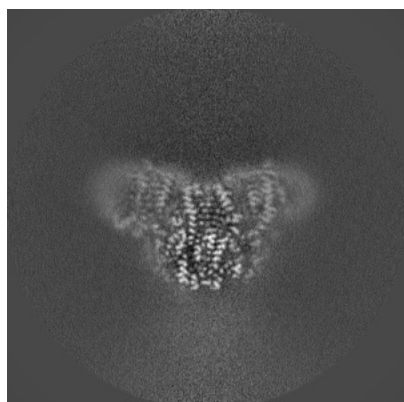


Y Index: 186

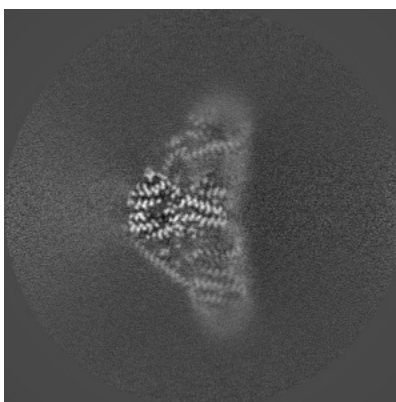


Z Index: 191

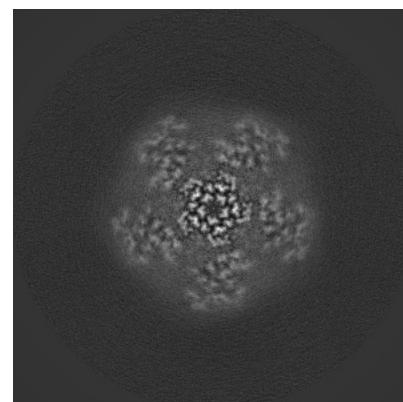
6.3.2 Raw map



X Index: 215



Y Index: 178

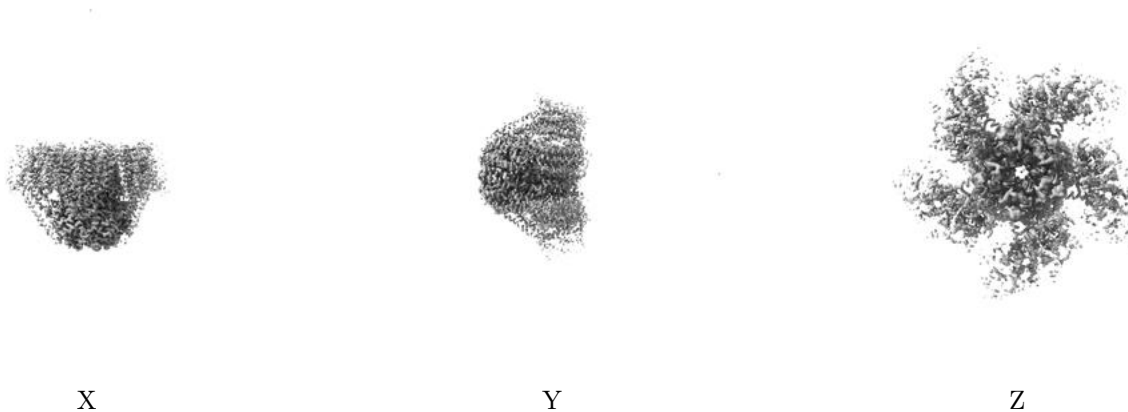


Z Index: 191

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

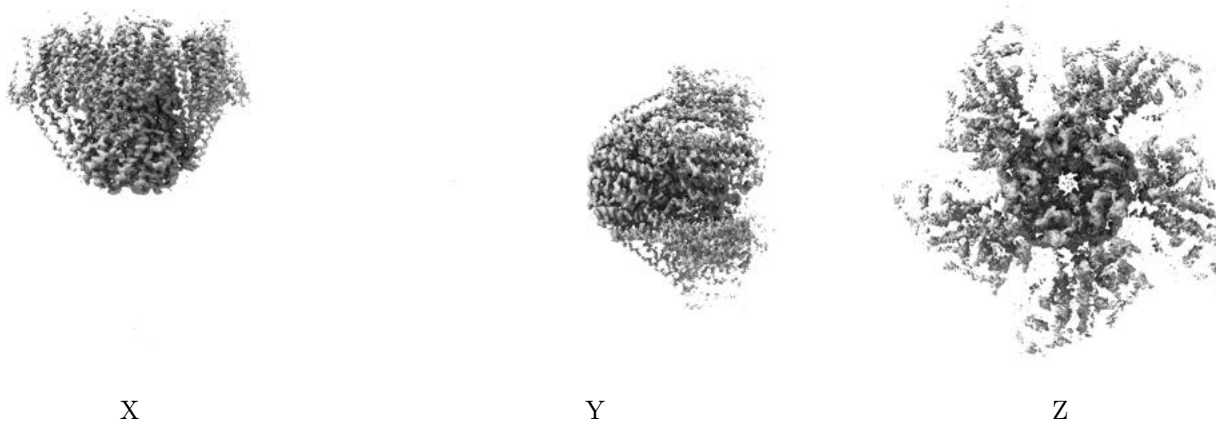
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

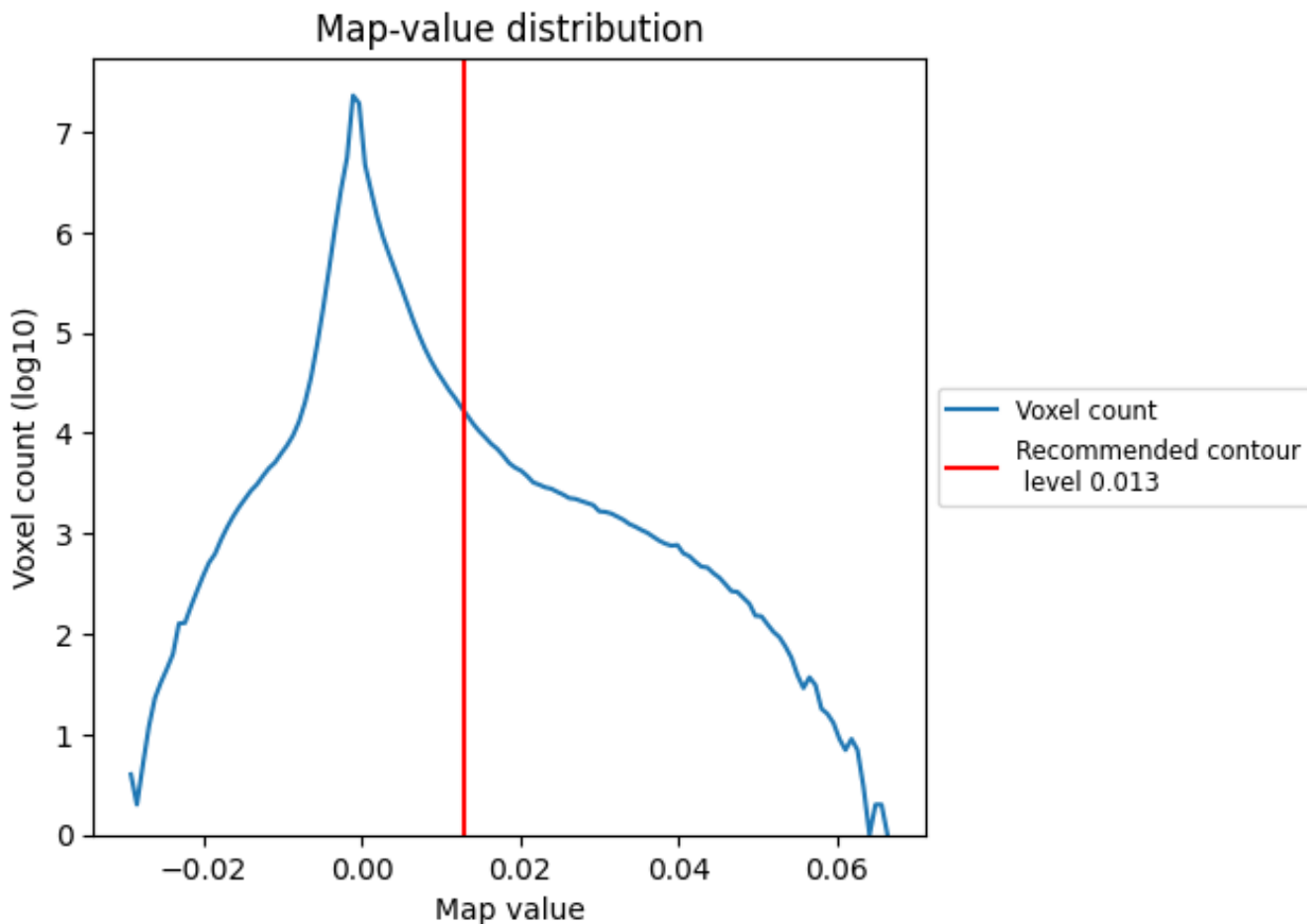
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

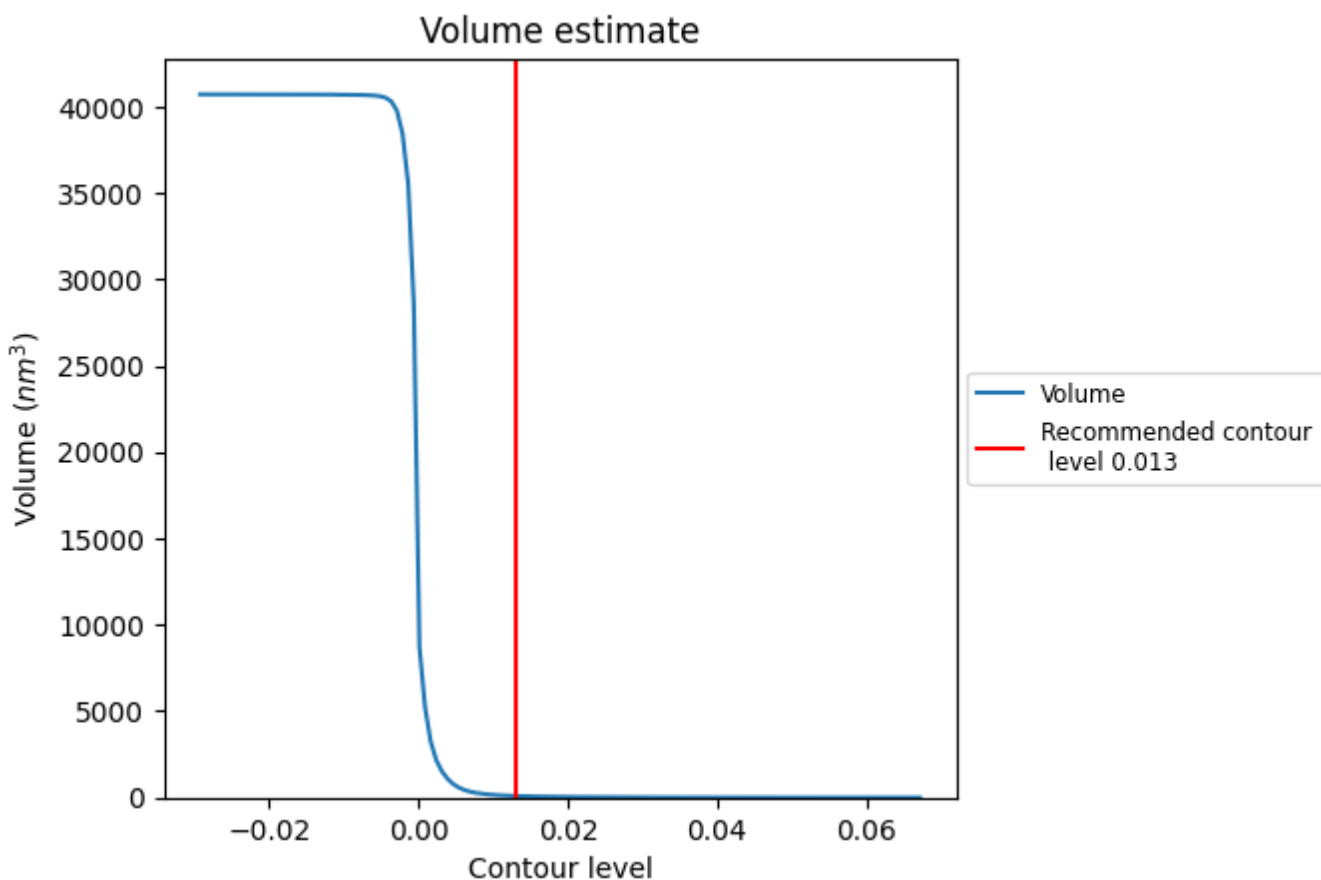
This section contains the results of statistical analysis of the map.

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.

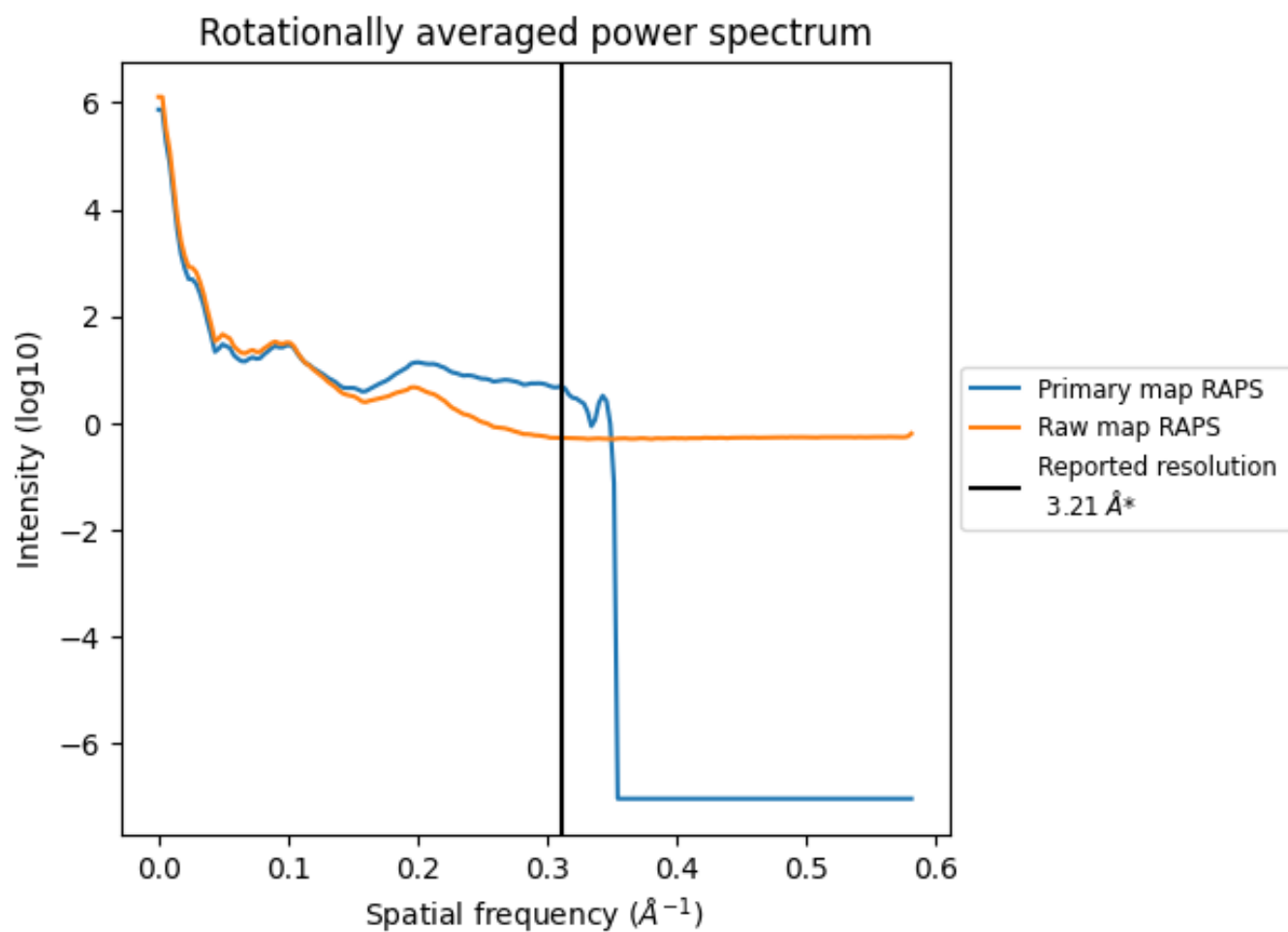
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 90 nm^3 ; this corresponds to an approximate mass of 81 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

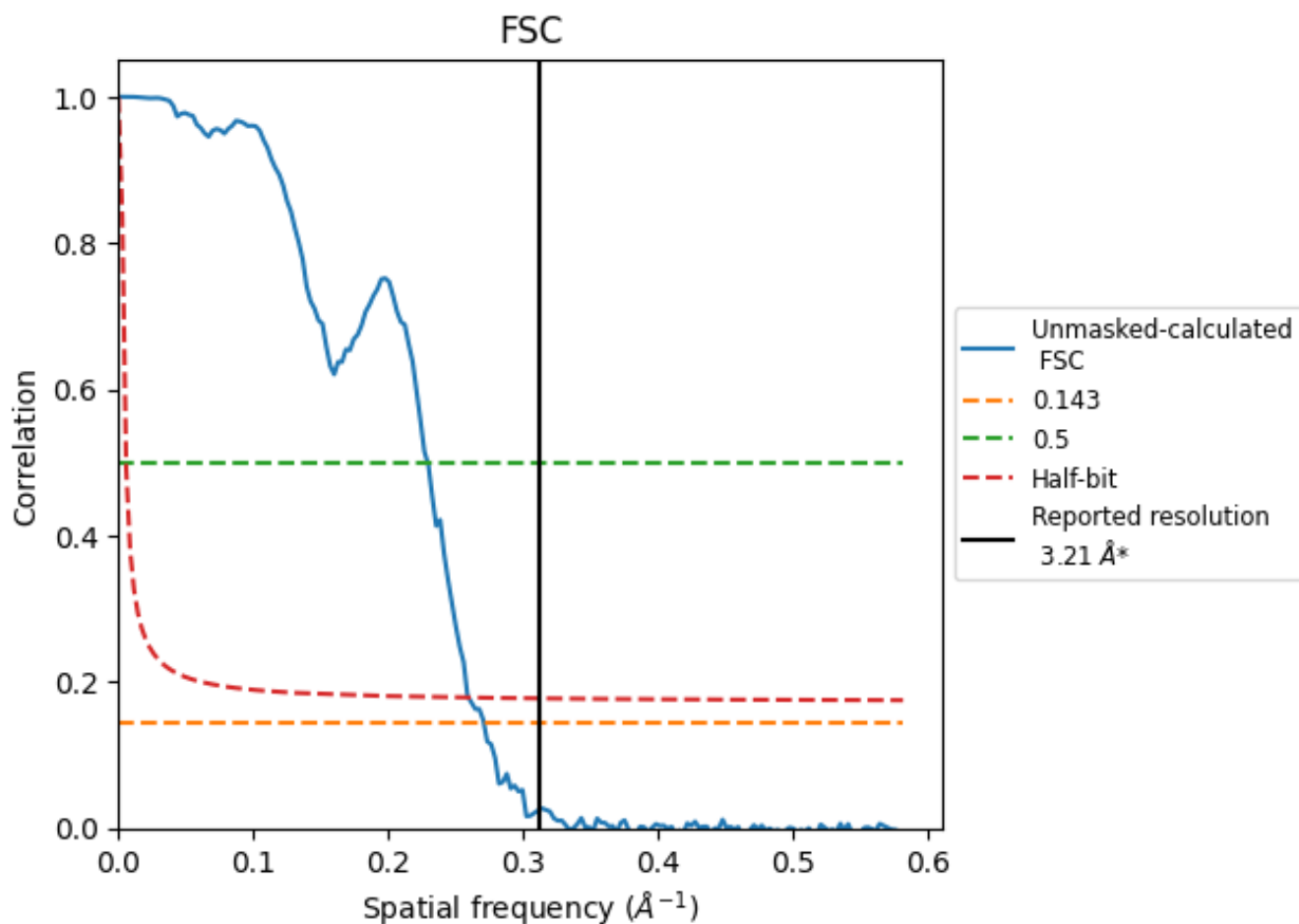


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

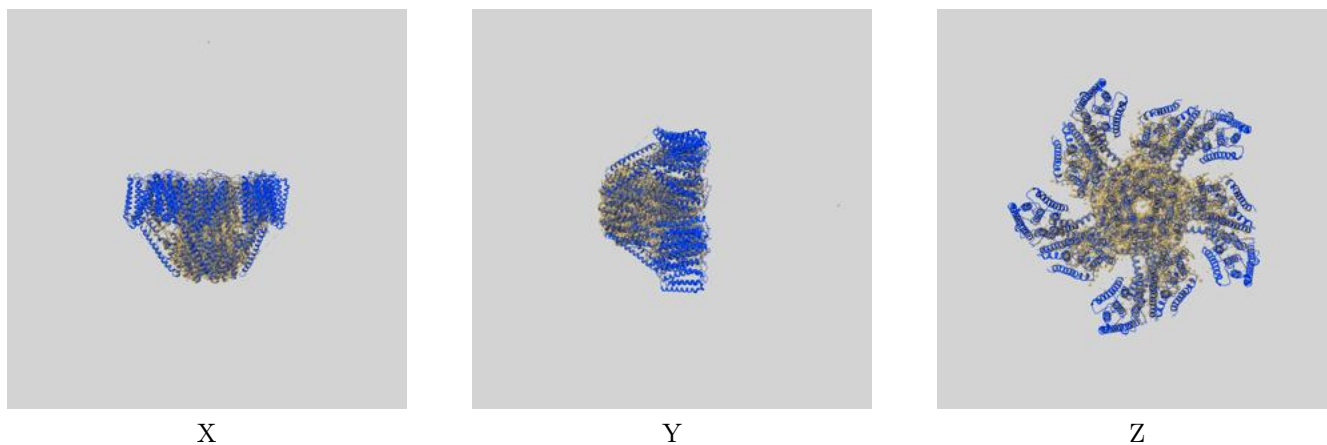
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.69	4.36	3.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.69 differs from the reported value 3.21 by more than 10 %

9 Map-model fit [i](#)

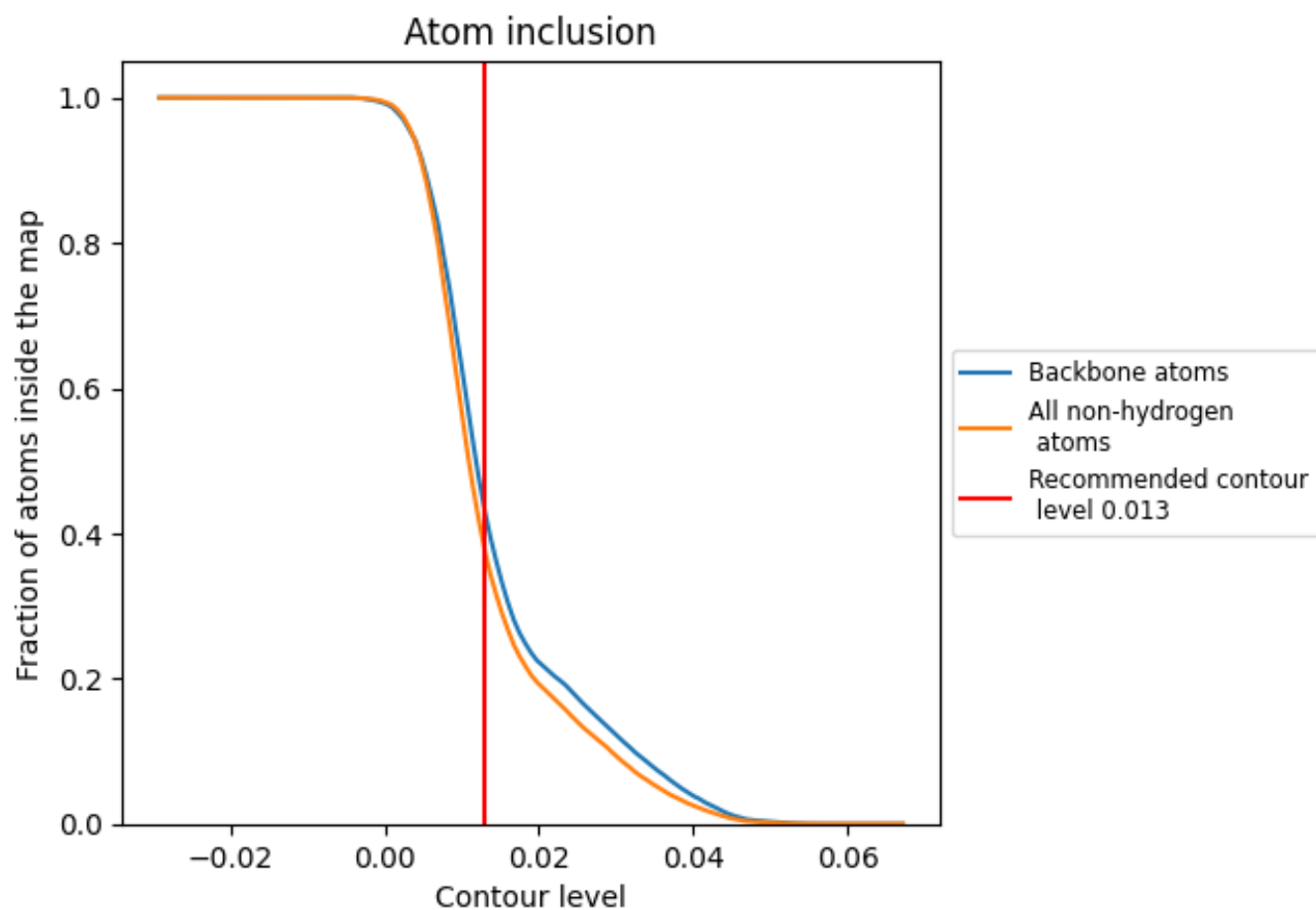
This section contains information regarding the fit between EMDB map EMD-13485 and PDB model 7PL9. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.013 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 Atom inclusion [i](#)



At the recommended contour level, 43% of all backbone atoms, 38% of all non-hydrogen atoms, are inside the map.