wwPDB EM Validation Summary Report (i)

Mar 6, 2026 – 09:23 PM UTC

PDB ID	:	6NR3 / pdb_00006nr3
EMDB ID	:	EMD-0488
Title	:	Cryo-EM structure of the TRPM8 ion channel in complex with high occupancy icilin, PI(4,5)P2, and calcium
Authors	:	Yin, Y.; Le, S.C.; Hsu, A.L.; Borgnia, M.J.; Yang, H.; Lee, S.-Y.
Deposited on	:	2019-01-22
Resolution	:	3.40 Å(reported)
Based on initial model	:	6BPQ

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 (i) 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 (i)) were used in the production of this report:

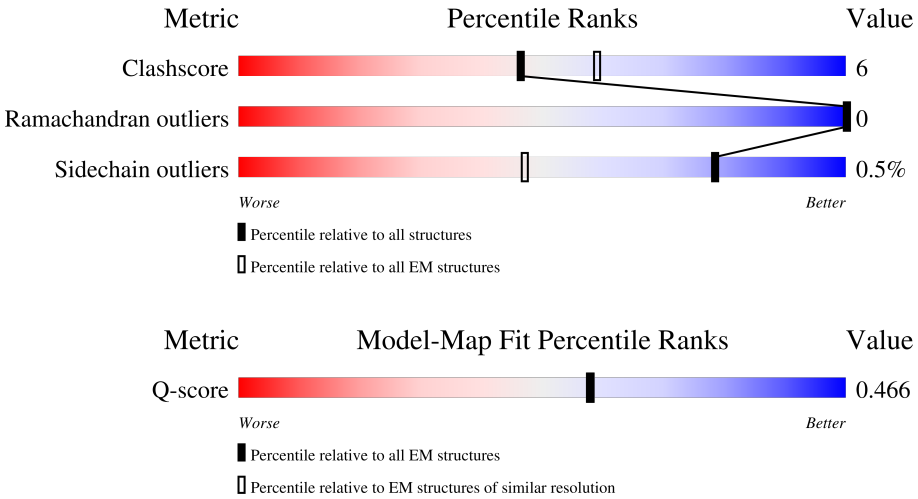
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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 3.40 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	14717 (2.90 - 3.90)

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 <=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	1135	8% 67% 8% 25%
1	B	1135	8% 67% 8% 25%
1	C	1135	8% 67% 8% 25%
1	D	1135	8% 67% 8% 25%

2 Entry composition (i)

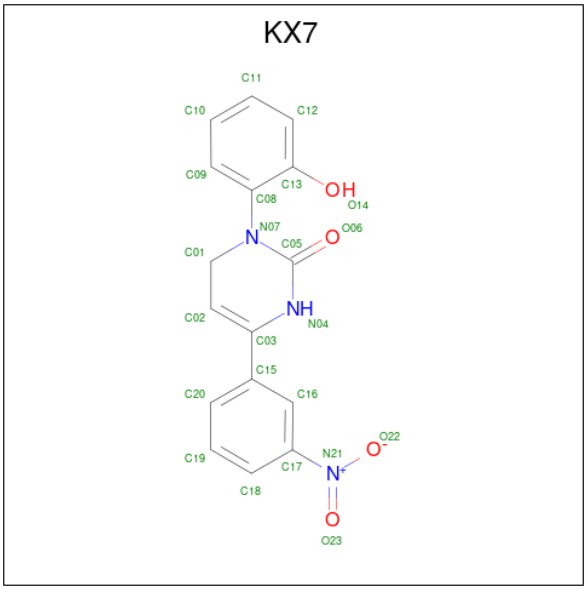
There are 4 unique types of molecules in this entry. The entry contains 25332 atoms, of which 152 are hydrogens and 0 are deuteriums.

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 M member 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	854	Total	C	N	O	S	0	0
			6232	4075	1060	1070	27		
1	B	854	Total	C	N	O	S	0	0
			6232	4075	1060	1070	27		
1	C	854	Total	C	N	O	S	0	0
			6232	4075	1060	1070	27		
1	D	854	Total	C	N	O	S	0	0
			6232	4075	1060	1070	27		

- Molecule 2 is Icilin (CCD ID: KX7) (formula: $C_{16}H_{13}N_3O_4$).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	H	N	O	0
			36	16	13	3	4	
2	B	1	Total	C	H	N	O	0
			36	16	13	3	4	

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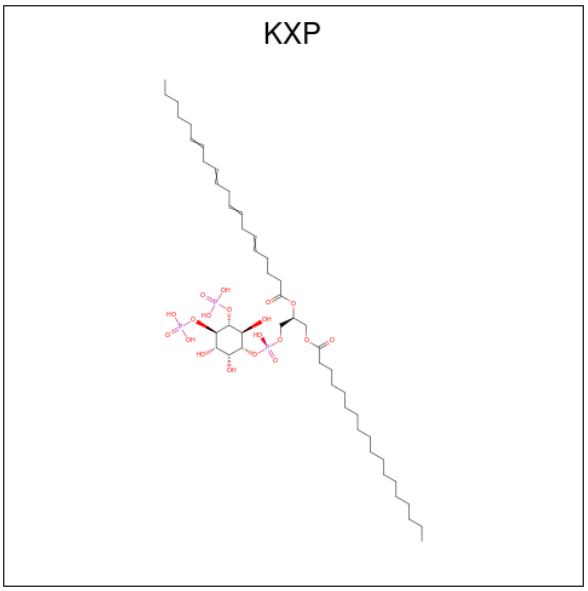
Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total	C	H	N	O	0
			36	16	13	3	4	
2	D	1	Total	C	H	N	O	0
			36	16	13	3	4	

- Molecule 3 is (2S)-1-{[(R)-hydroxy{[(1R,2R,3S,4R,5R,6S)-2,3,6-trihydroxy-4,5-bis(phosphonooxy)cyclohexyl]oxy}phosphoryl]oxy}-3-(octadecanoyloxy)propan-2-yl icosa-5,8,11,14-tetraenoate (CCD ID: KXP) (formula: $C_{47}H_{85}O_{19}P_3$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	O	P	0
			64	17	25	19	3	
3	B	1	Total	C	H	O	P	0
			64	17	25	19	3	
3	C	1	Total	C	H	O	P	0
			64	17	25	19	3	
3	D	1	Total	C	H	O	P	0
			64	17	25	19	3	

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Ca	0
			1	1	
4	B	1	Total	Ca	0
			1	1	

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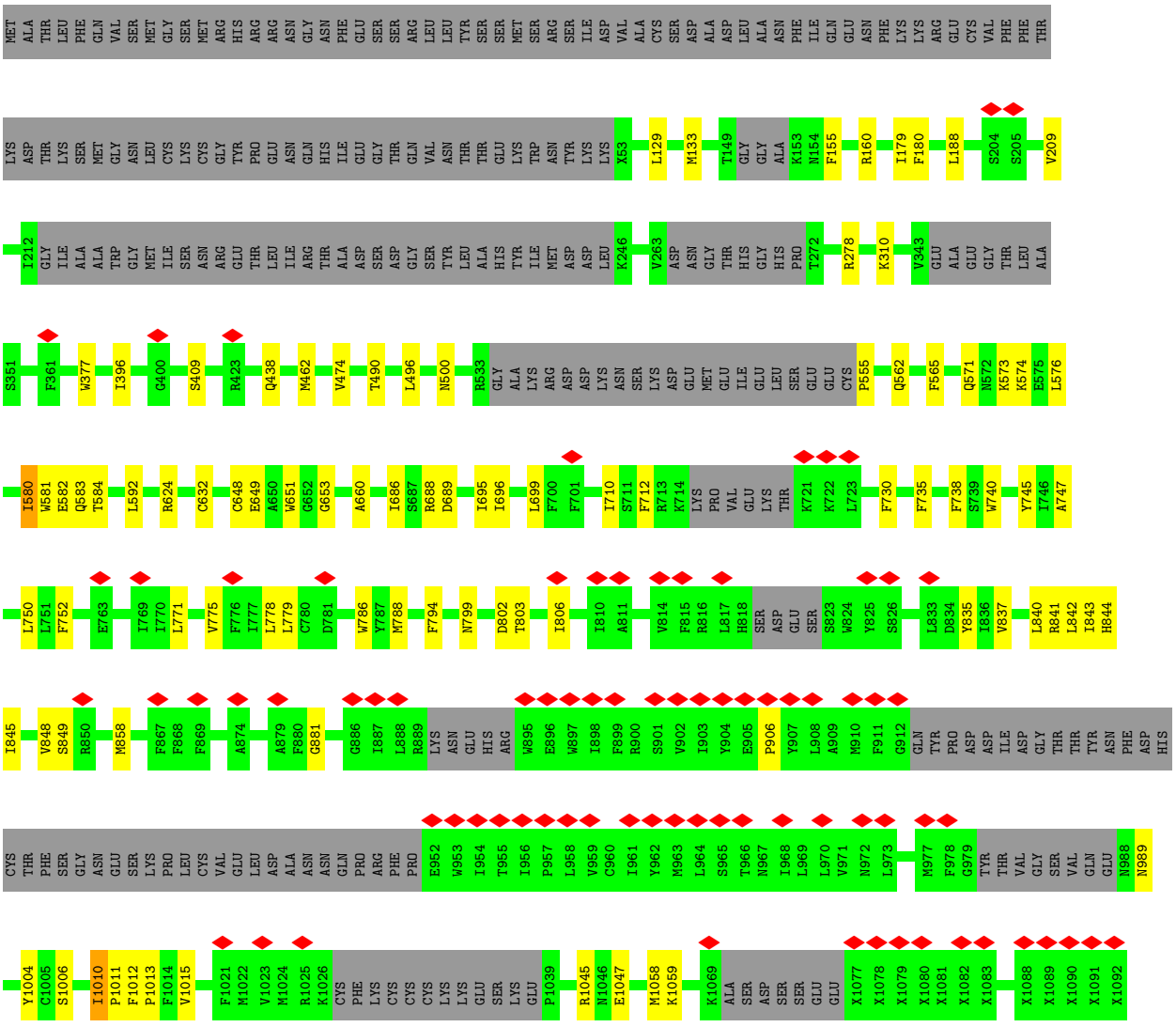
Mol	Chain	Residues	Atoms	AltConf
4	C	1	Total Ca 1 1	0
4	D	1	Total Ca 1 1	0

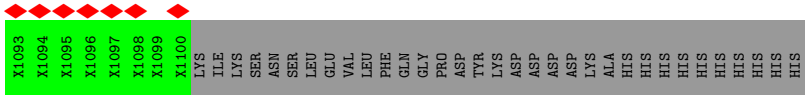
3 Residue-property plots (i)

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: Transient receptor potential cation channel subfamily M member 8

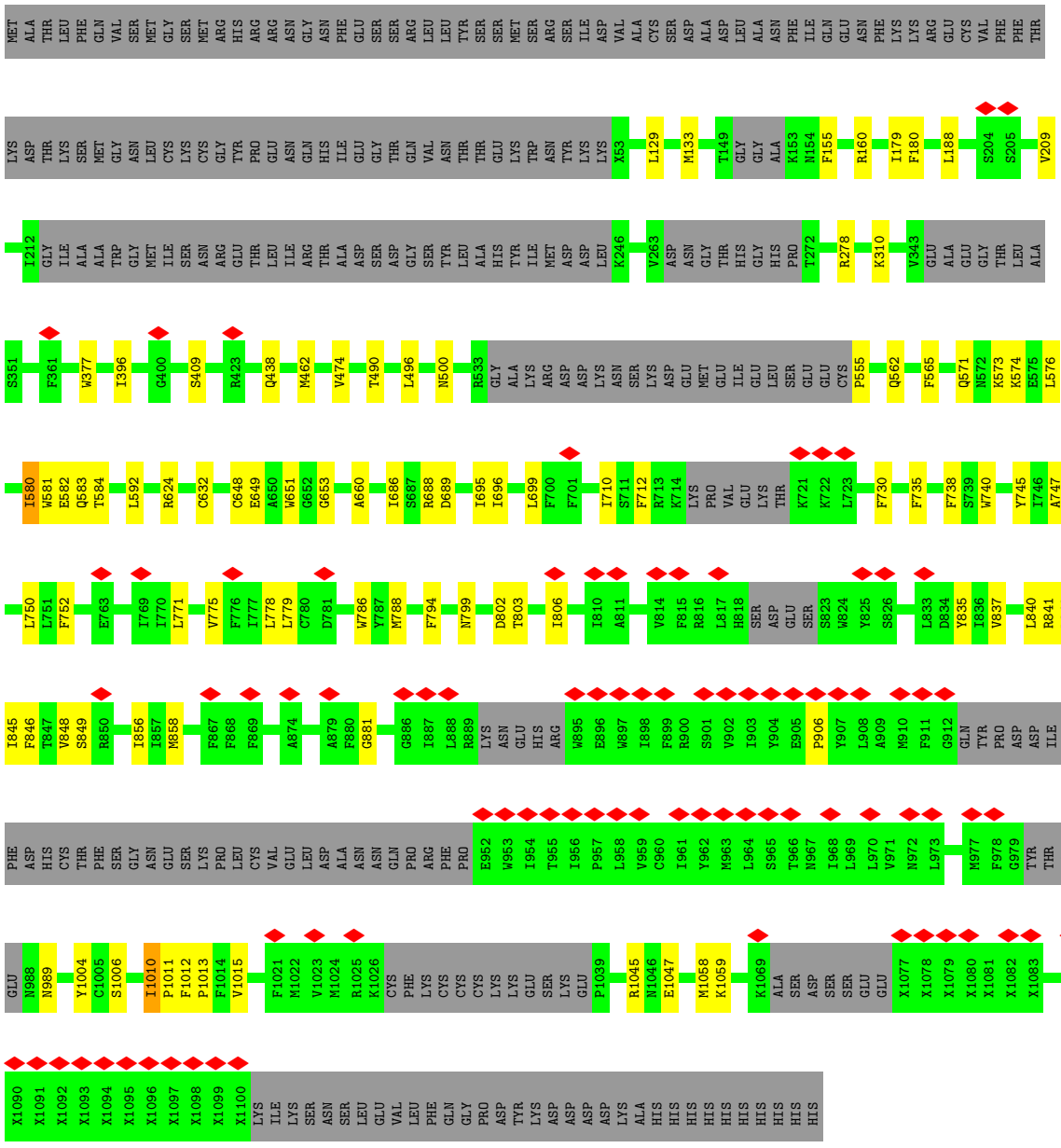
Chain A:

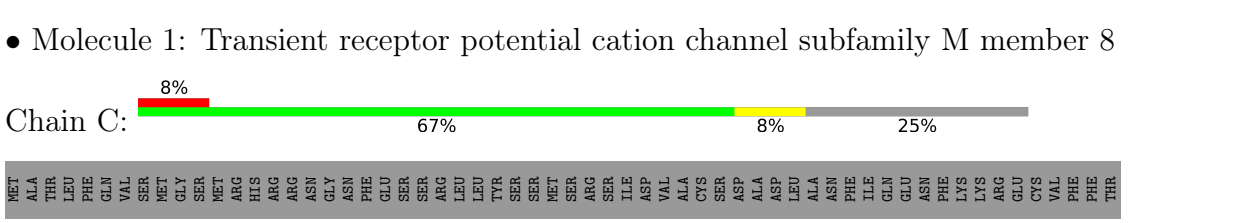


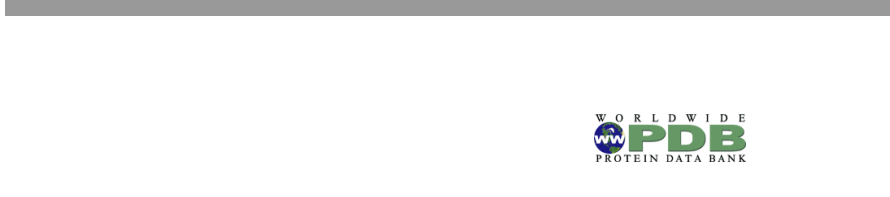


• Molecule 1: Transient receptor potential cation channel subfamily M member 8

Chain B:

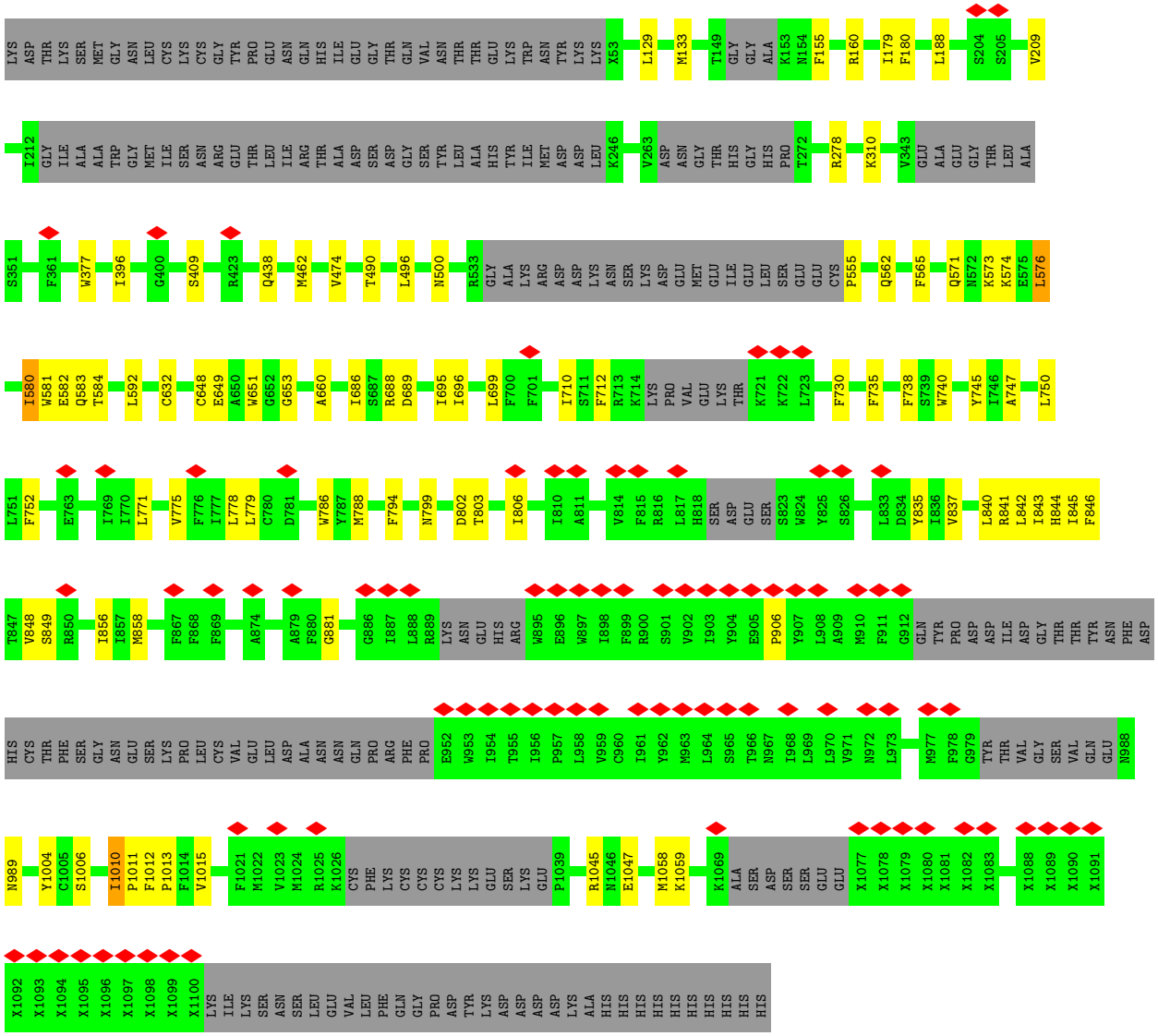






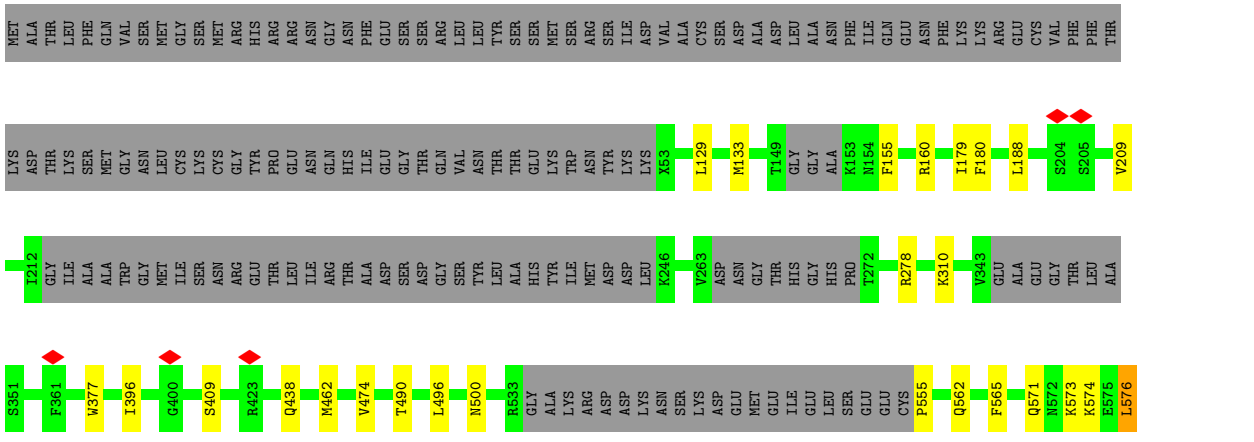
• Molecule 1: Transient receptor potential cation channel subfamily M member 8

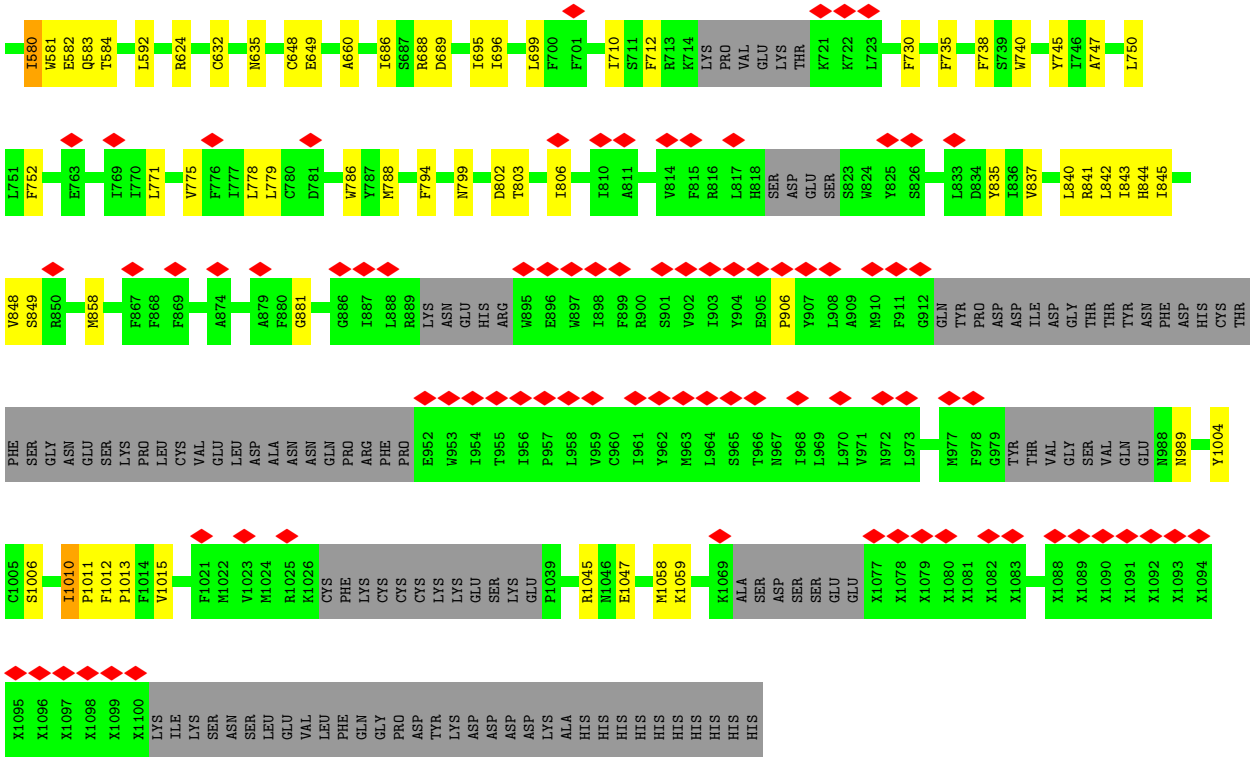
Chain C:



• Molecule 1: Transient receptor potential cation channel subfamily M member 8

Chain D:




I580 W581 E582 Q583 T584 L592 R624 C632 N635 C648 E649 A660 I686 S687 R688 D689 I695 I696 L699 F700 F701 I710 S711 F712 R713 K714 LYS PRO VAL GLU LYS THR K721 K722 L723 F730 F735 F738 S739 W740 Y745 I746 A747 L750
L751 F752 E763 I769 T770 L771 V775 F776 I777 L778 L779 C780 D781 W786 Y787 M788 F794 N799 D802 T803 I806 I810 A811 V814 F815 R816 L817 H818 SER ASP GLU SER S823 W824 Y825 S826 L833 D834 Y835 I836 V837 L840 R841 L842 I843 H844 I845
V848 S849 R850 M858 F867 F868 F869 A874 A879 F880 G881 G886 I887 L888 R889 LYS ASN GLU HIS ARG W895 E896 W897 I898 F899 R900 S901 V902 I903 Y904 E905 P906 Y907 L908 A909 M910 F911 G912 GLN TYR PRO ASP ASP ILE ASP GLY THR THR TYR ASN PHE ASP HIS CYS THR
PHE SER GLY ASN GLU SER LYS PRO LEU CYS VAL GLU LEU ASP ALA ASN ASN GLN PRO ARG PHE PRO E952 W953 I954 T955 I956 P957 L958 Y959 C960 I961 Y962 M963 L964 S965 T966 N967 I968 L969 L970 V971 N972 L973 M977 F978 G979 TYR THR VAL GLY SER VAL GLN GLU N988 N989 Y1004
C1005 S1006 I1010 P1011 F1012 P1013 F1014 V1015 F1021 M1022 V1023 M1024 R1025 K1026 CYS PHE LYS CYS CYS CYS LYS LYS GLU SER LYS GLU P1039 R1045 N1046 E1047 M1058 K1059 K1069 ALA SER ASP SER SER GLU GLU X1077 X1078 X1079 X1080 X1081 X1082 X1083 X1088 X1089 X1090 X1091 X1092 X1093 X1094
X1095 X1096 X1097 X1098 X1099 X1100 LYS ILE LYS SER ASN SER LEU GLU VAL LEU PHE GLN GLY PRO ASP TYR LYS ASP ASP ASP LYS ALA HIS HIS HIS HIS HIS HIS HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	101192	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 ($e^-/Å^2$)	42	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.228	Depositor
Minimum map value	-0.110	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KX7, CA, KXP

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	0.37	0/6136	0.67	10/8357 (0.1%)
1	B	0.37	0/6136	0.67	10/8357 (0.1%)
1	C	0.37	0/6136	0.67	10/8357 (0.1%)
1	D	0.37	0/6136	0.67	10/8357 (0.1%)
All	All	0.37	0/24544	0.67	40/33428 (0.1%)

There are no bond length outliers.

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	583	GLN	N-CA-C	10.04	122.31	111.36
1	C	583	GLN	N-CA-C	10.02	122.28	111.36
1	A	583	GLN	N-CA-C	10.02	122.28	111.36
1	B	583	GLN	N-CA-C	9.99	122.25	111.36
1	D	848	VAL	N-CA-C	8.84	119.64	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	6232	0	5619	70	0
1	B	6232	0	5619	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	6232	0	5619	72	0
1	D	6232	0	5619	72	0
2	A	23	13	0	4	0
2	B	23	13	0	4	0
2	C	23	13	0	4	0
2	D	23	13	0	4	0
3	A	39	25	0	5	0
3	B	39	25	0	5	0
3	C	39	25	0	5	0
3	D	39	25	0	5	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	25180	152	22476	289	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 6.

The worst 5 of 289 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:1012:PHE:HB3	1:D:1013:PRO:HD3	1.62	0.81
1:A:1012:PHE:HB3	1:A:1013:PRO:HD3	1.62	0.81
1:C:1012:PHE:HB3	1:C:1013:PRO:HD3	1.62	0.80
1:B:1012:PHE:HB3	1:B:1013:PRO:HD3	1.62	0.80
1:A:179:ILE:HB	1:A:209:VAL:HG23	1.67	0.77

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	784/1135 (69%)	752 (96%)	32 (4%)	0	100	100
1	B	784/1135 (69%)	752 (96%)	32 (4%)	0	100	100
1	C	784/1135 (69%)	752 (96%)	32 (4%)	0	100	100
1	D	784/1135 (69%)	752 (96%)	32 (4%)	0	100	100
All	All	3136/4540 (69%)	3008 (96%)	128 (4%)	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	551/979 (56%)	548 (100%)	3 (0%)	81	81
1	B	551/979 (56%)	548 (100%)	3 (0%)	81	81
1	C	551/979 (56%)	548 (100%)	3 (0%)	81	81
1	D	551/979 (56%)	548 (100%)	3 (0%)	81	81
All	All	2204/3916 (56%)	2192 (100%)	12 (0%)	78	81

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	580	ILE
1	C	740	TRP
1	D	740	TRP
1	D	576	LEU
1	B	576	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	500	ASN
1	D	510	GLN
1	D	666	GLN

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Mol	Chain	Res	Type
1	B	510	GLN
1	B	500	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
2	KX7	B	1201	-	24,25,25	3.76	9 (37%)	29,35,35	2.03	7 (24%)
3	KXP	D	1202	-	39,39,69	1.52	6 (15%)	52,56,87	0.98	2 (3%)
2	KX7	C	1201	-	24,25,25	3.76	9 (37%)	29,35,35	2.03	7 (24%)
2	KX7	A	1201	-	24,25,25	3.76	9 (37%)	29,35,35	2.02	7 (24%)
3	KXP	A	1202	-	39,39,69	1.52	6 (15%)	52,56,87	0.99	2 (3%)
3	KXP	C	1202	-	39,39,69	1.51	6 (15%)	52,56,87	0.99	2 (3%)
3	KXP	B	1202	-	39,39,69	1.52	6 (15%)	52,56,87	0.98	2 (3%)
2	KX7	D	1201	-	24,25,25	3.76	9 (37%)	29,35,35	2.03	7 (24%)

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	KX7	B	1201	-	-	5/10/25/25	0/3/3/3
3	KXP	D	1202	-	-	15/35/59/90	0/1/1/1
2	KX7	C	1201	-	-	5/10/25/25	0/3/3/3
2	KX7	A	1201	-	-	5/10/25/25	0/3/3/3
3	KXP	A	1202	-	-	15/35/59/90	0/1/1/1
3	KXP	C	1202	-	-	15/35/59/90	0/1/1/1
3	KXP	B	1202	-	-	15/35/59/90	0/1/1/1
2	KX7	D	1201	-	-	5/10/25/25	0/3/3/3

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	KX7	C05-N07	11.37	1.50	1.37
2	C	1201	KX7	C05-N07	11.37	1.50	1.37
2	B	1201	KX7	C05-N07	11.36	1.50	1.37
2	D	1201	KX7	C05-N07	11.35	1.50	1.37
2	A	1201	KX7	O23-N21	10.40	1.40	1.22

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1201	KX7	C01-N07-C05	-7.27	111.49	123.16
2	B	1201	KX7	C01-N07-C05	-7.27	111.50	123.16
2	A	1201	KX7	C01-N07-C05	-7.24	111.54	123.16
2	C	1201	KX7	C01-N07-C05	-7.24	111.54	123.16
3	C	1202	KXP	O48-C49-O50	-4.50	119.93	125.70

There are no chirality outliers.

5 of 80 torsion outliers are listed below:

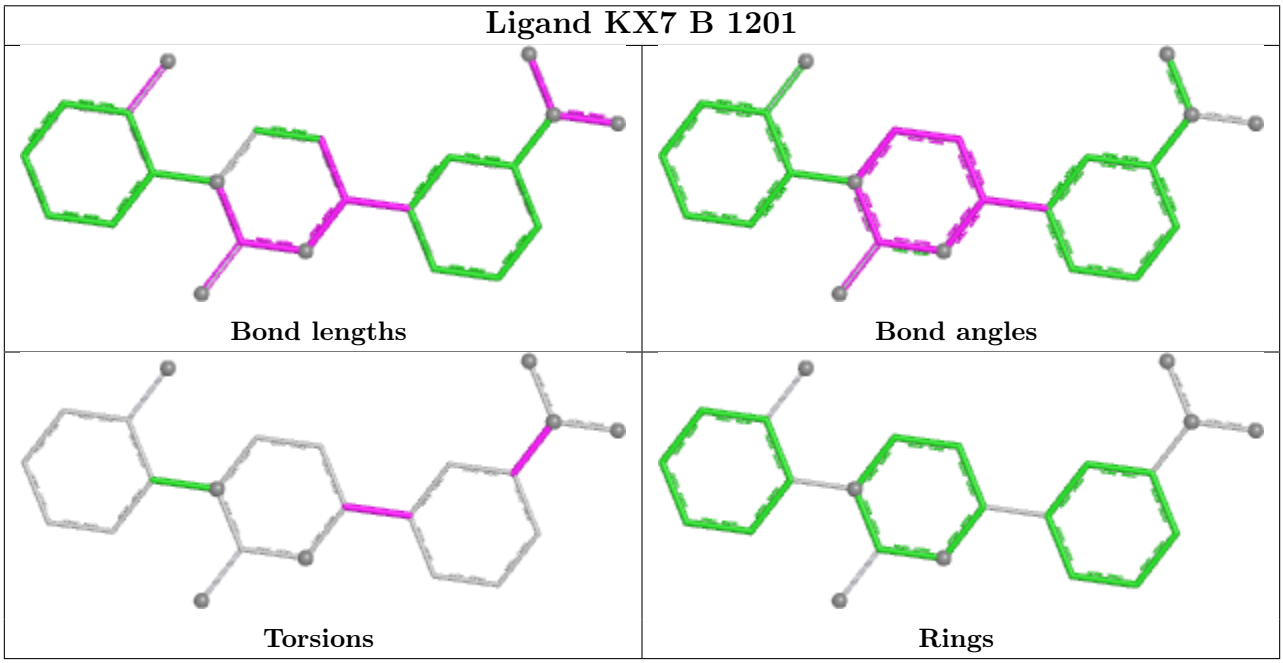
Mol	Chain	Res	Type	Atoms
2	A	1201	KX7	C16-C17-N21-O23
2	A	1201	KX7	C18-C17-N21-O23
2	B	1201	KX7	C16-C17-N21-O23
2	B	1201	KX7	C18-C17-N21-O23
2	C	1201	KX7	C16-C17-N21-O23

There are no ring outliers.

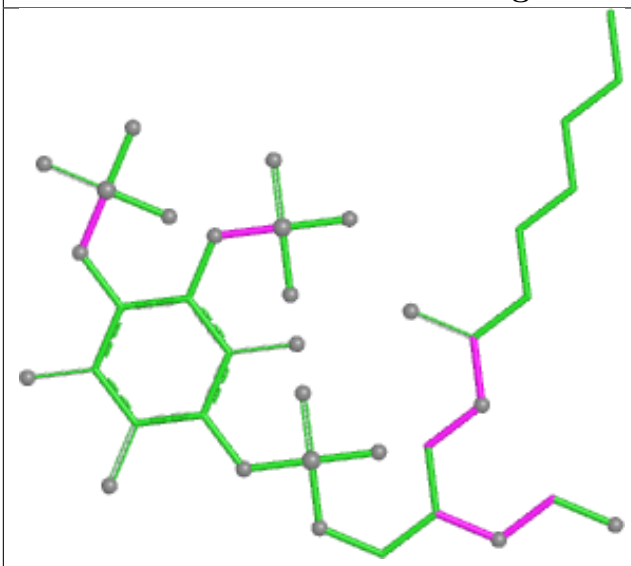
8 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1201	KX7	4	0
3	D	1202	KXP	5	0
2	C	1201	KX7	4	0
2	A	1201	KX7	4	0
3	A	1202	KXP	5	0
3	C	1202	KXP	5	0
3	B	1202	KXP	5	0
2	D	1201	KX7	4	0

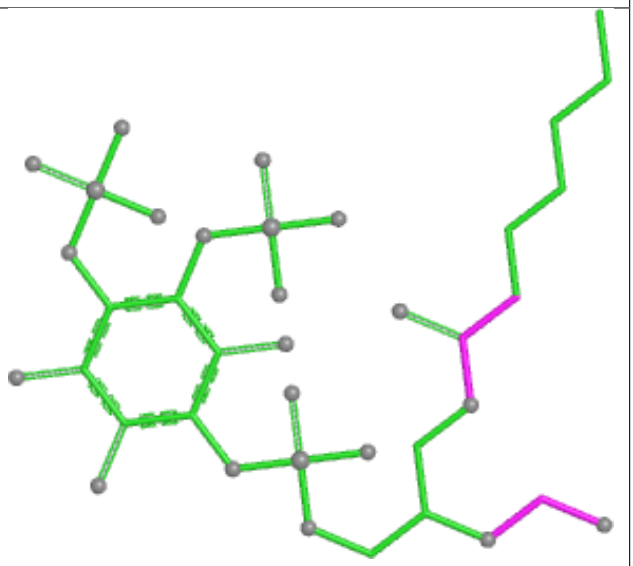
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.



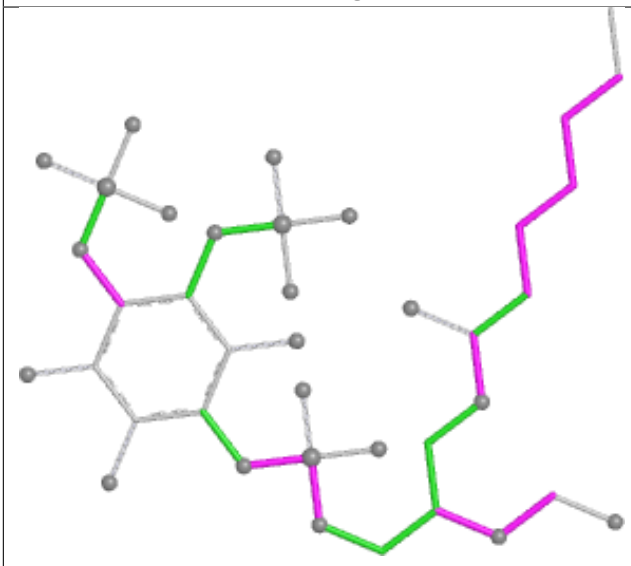
Ligand KXP D 1202



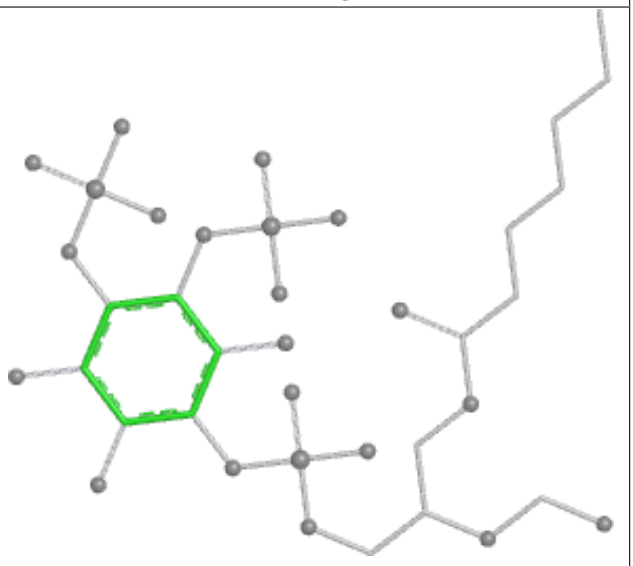
Bond lengths



Bond angles

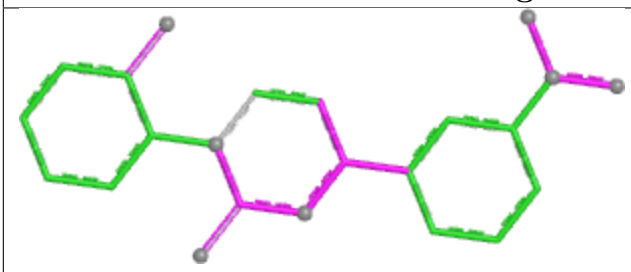


Torsions

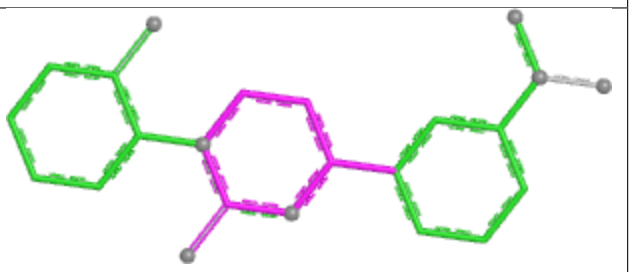


Rings

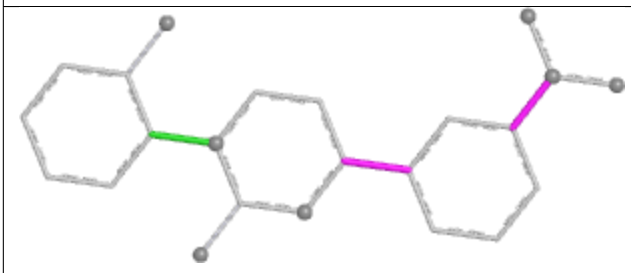
Ligand KX7 C 1201



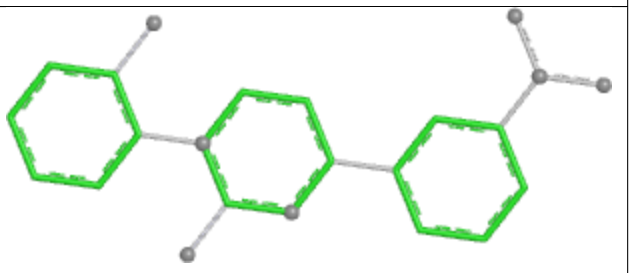
Bond lengths



Bond angles

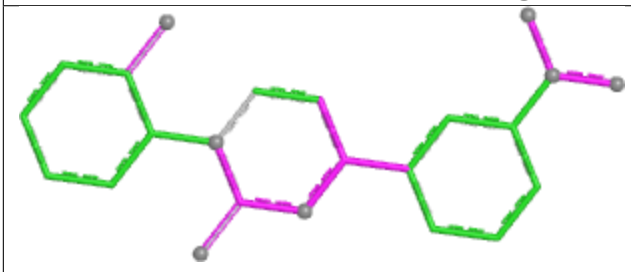


Torsions

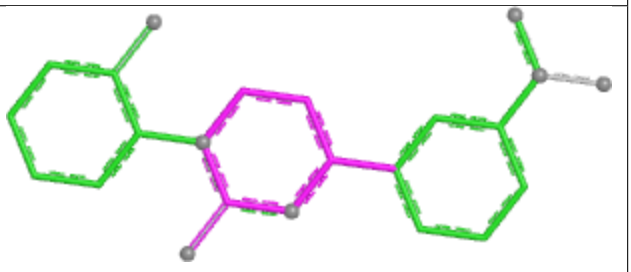


Rings

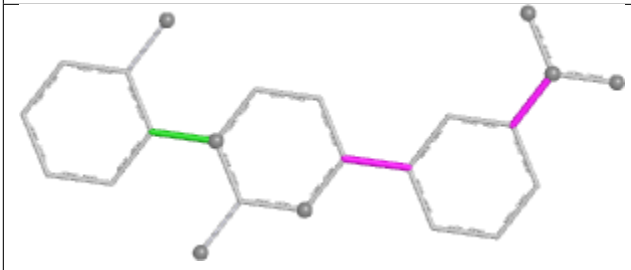
Ligand KX7 A 1201



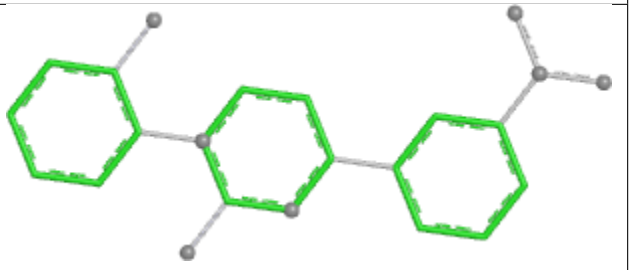
Bond lengths



Bond angles

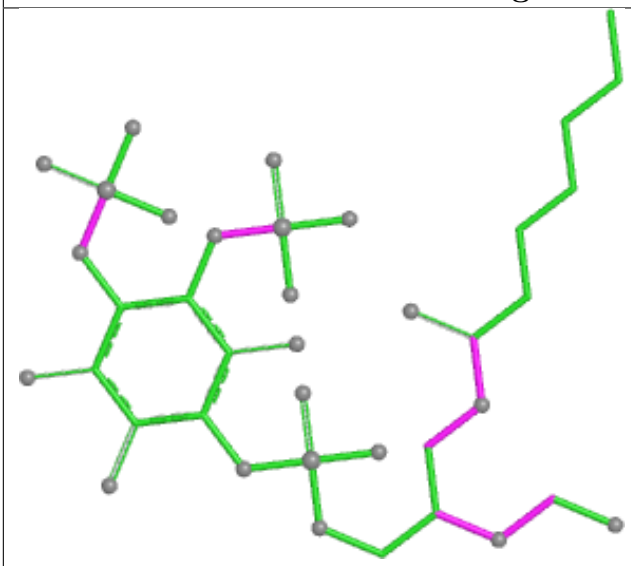


Torsions

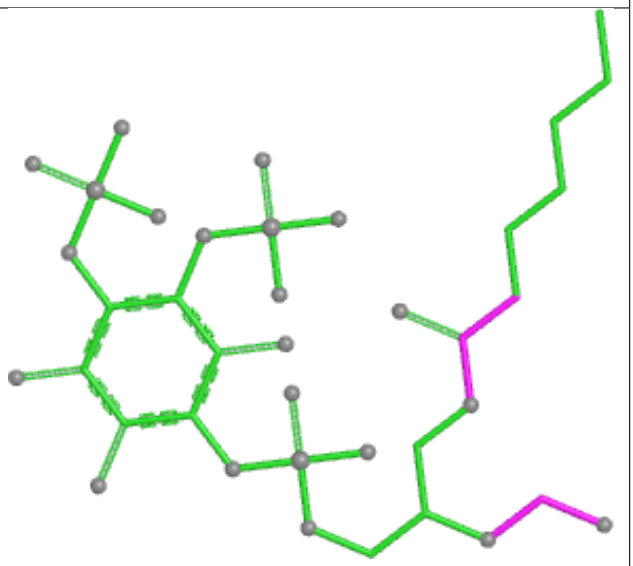


Rings

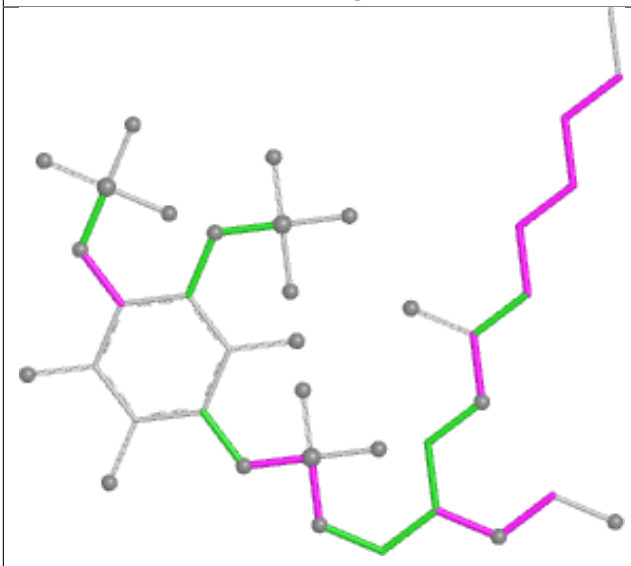
Ligand KXP A 1202



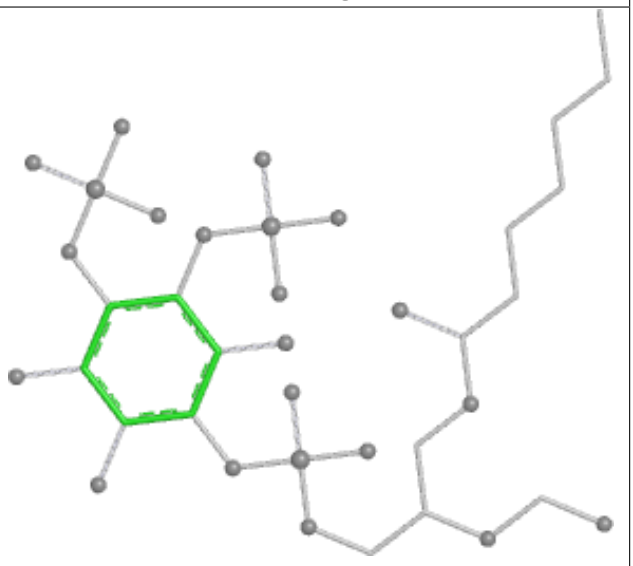
Bond lengths



Bond angles

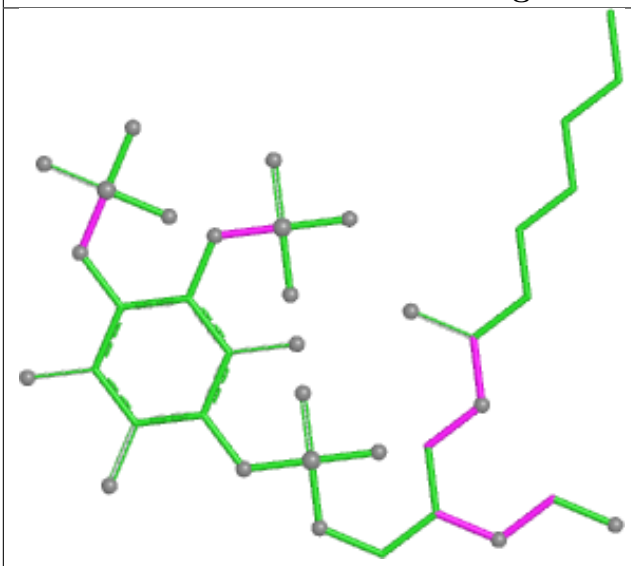


Torsions

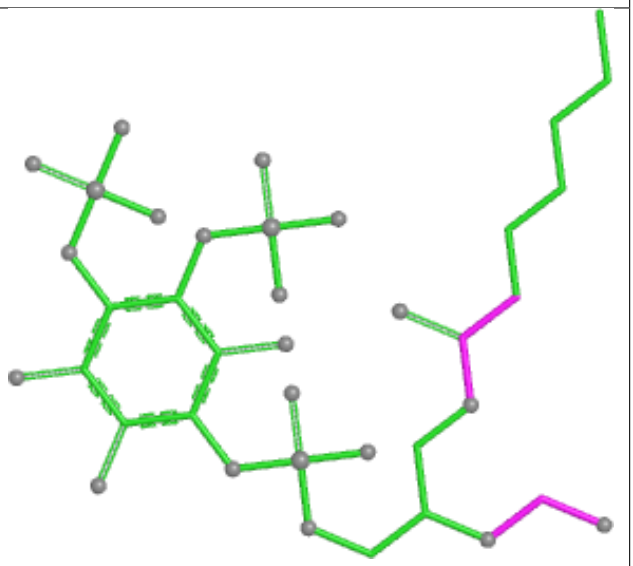


Rings

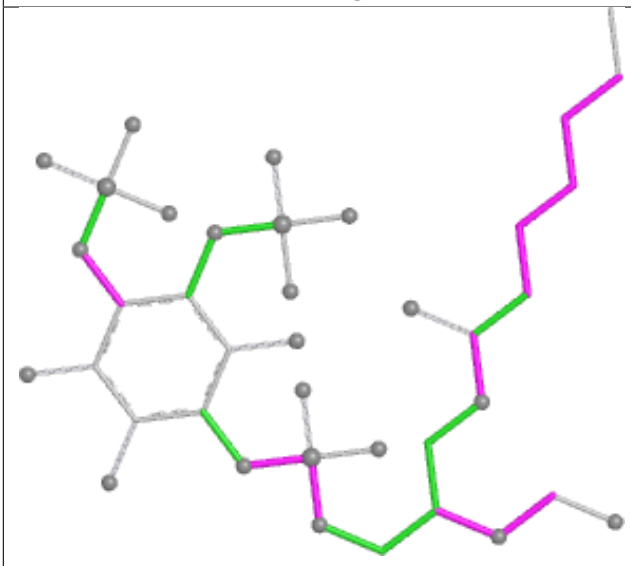
Ligand KXP C 1202



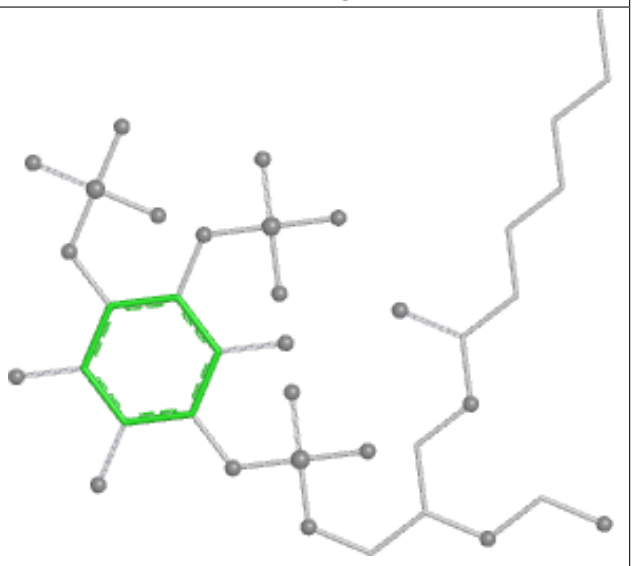
Bond lengths



Bond angles

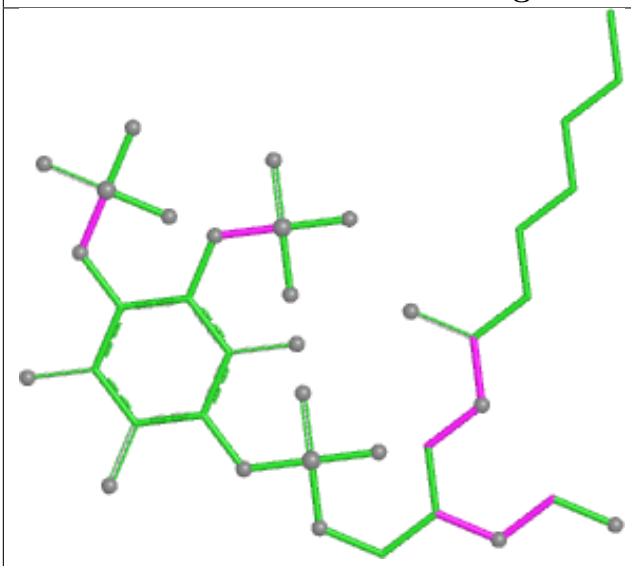


Torsions

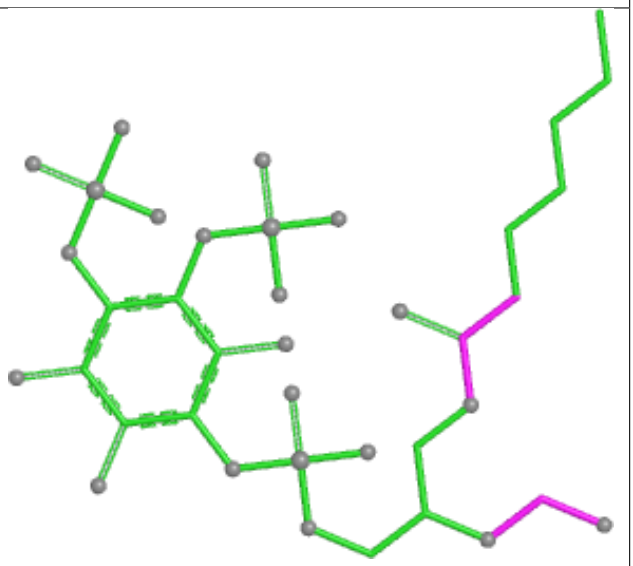


Rings

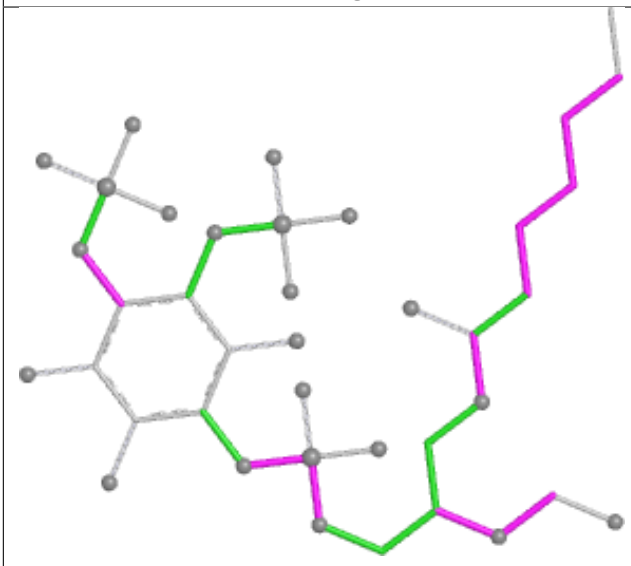
Ligand KXP B 1202



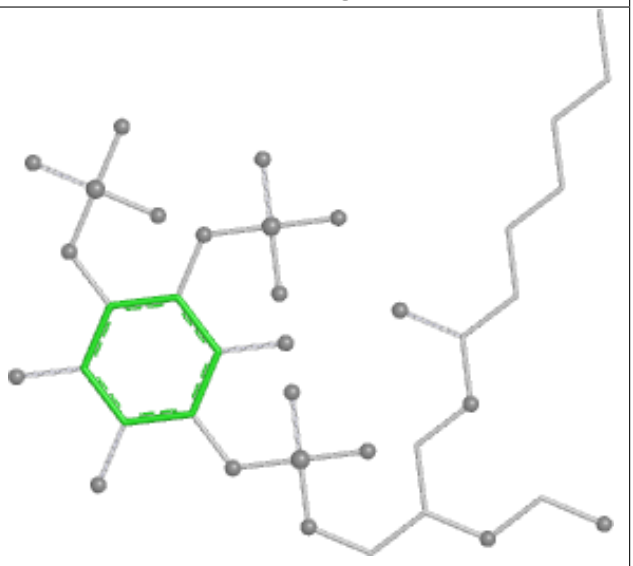
Bond lengths



Bond angles

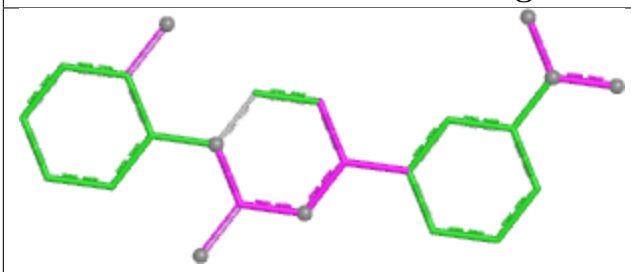


Torsions

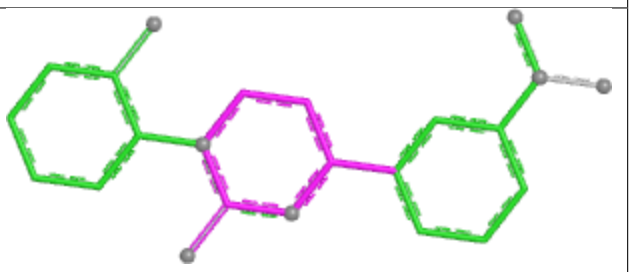


Rings

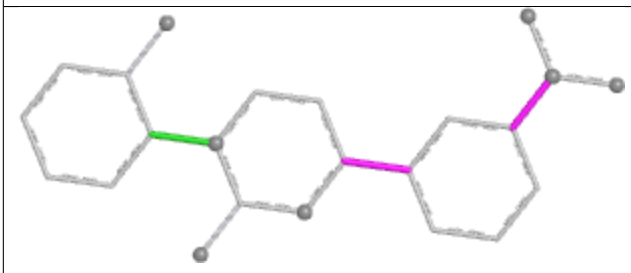
Ligand KX7 D 1201



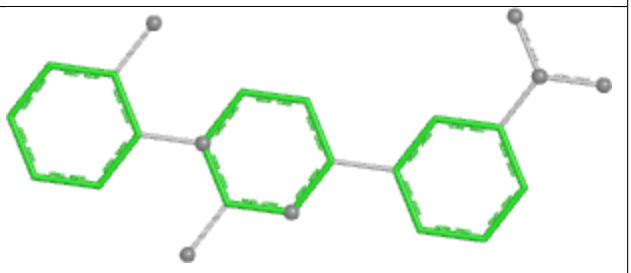
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
1	B	2
1	C	2
1	D	2

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	66:UNK	C	104:UNK	N	16.75
1	B	66:UNK	C	104:UNK	N	16.75
1	C	66:UNK	C	104:UNK	N	16.75
1	D	66:UNK	C	104:UNK	N	16.75
1	A	111:UNK	C	116:LYS	N	14.40

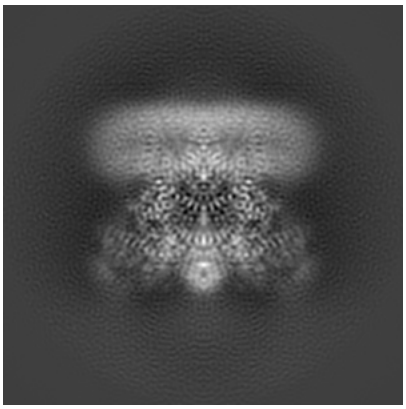
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0488. These allow visual inspection of the internal detail of the map and identification of artifacts.

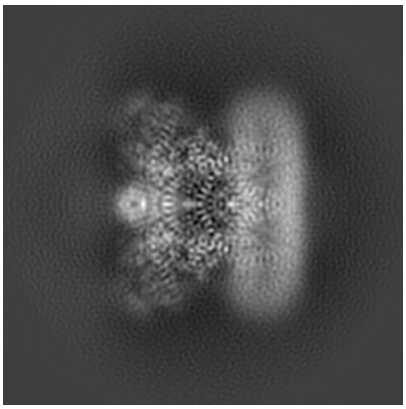
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

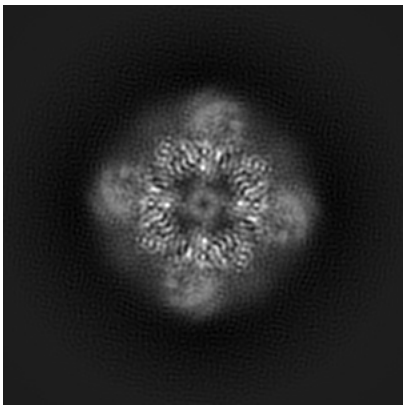
6.1.1 Primary map



X

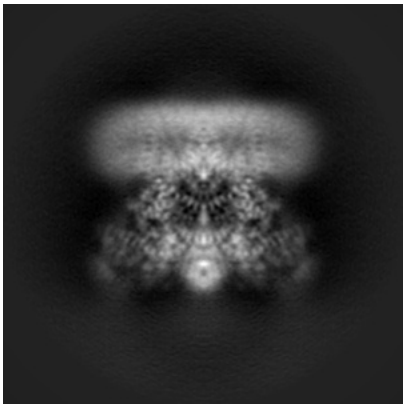


Y

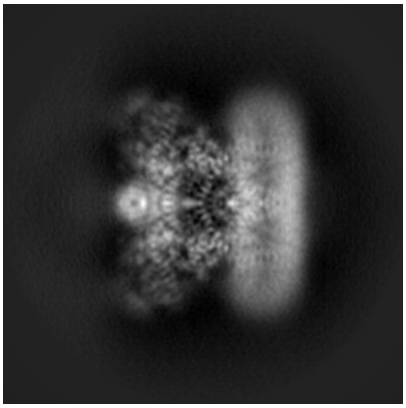


Z

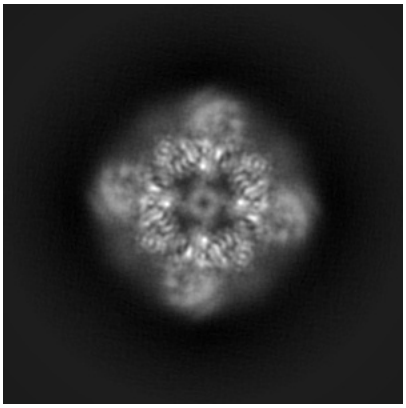
6.1.2 Raw map



X



Y

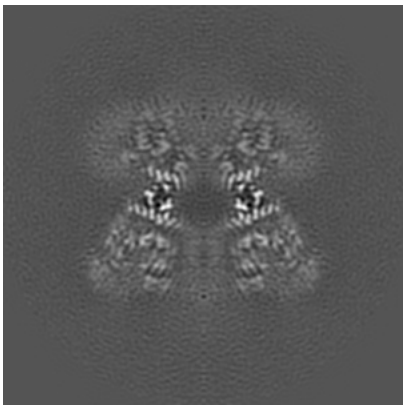


Z

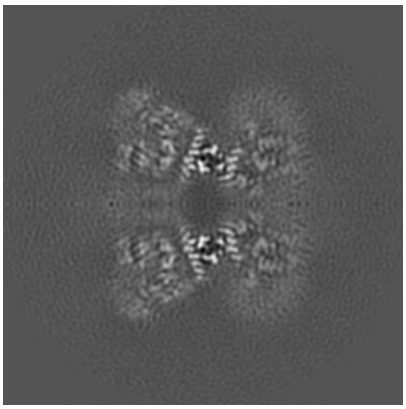
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

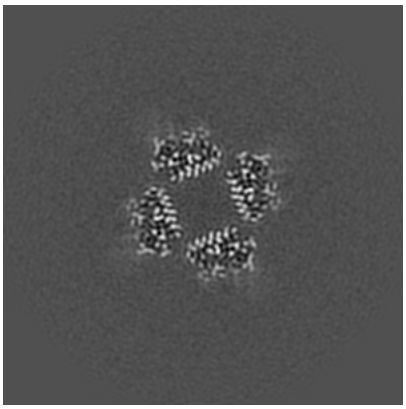
6.2.1 Primary map



X Index: 128

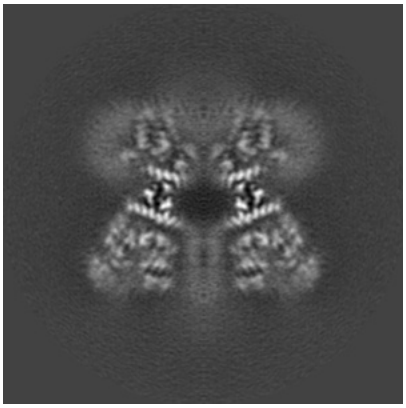


Y Index: 128

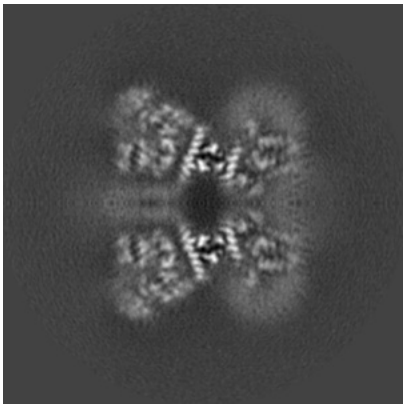


Z Index: 128

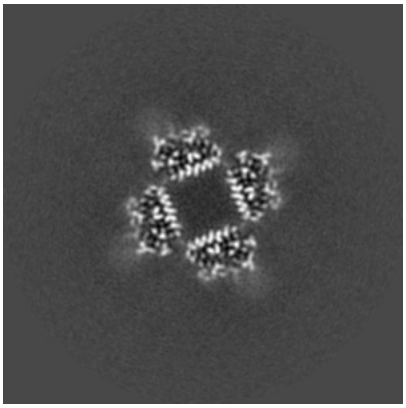
6.2.2 Raw map



X Index: 128



Y Index: 128

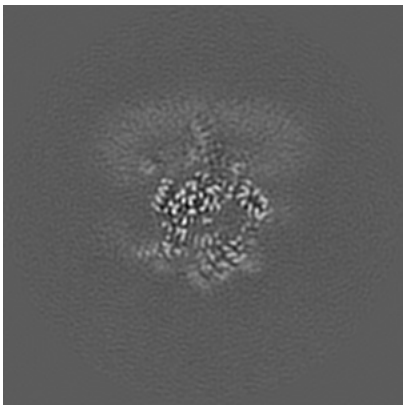


Z Index: 128

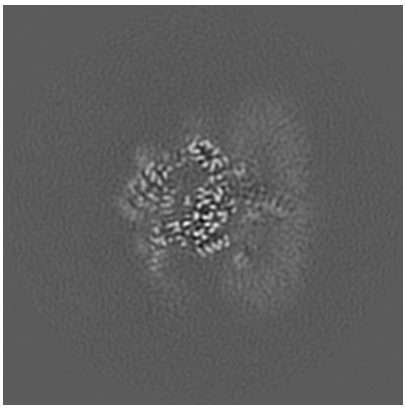
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

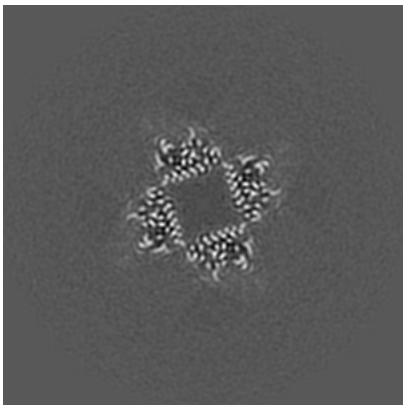
6.3.1 Primary map



X Index: 101

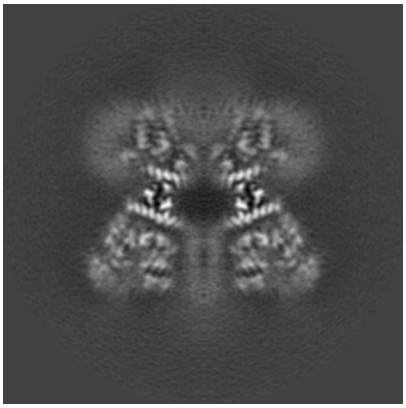


Y Index: 155

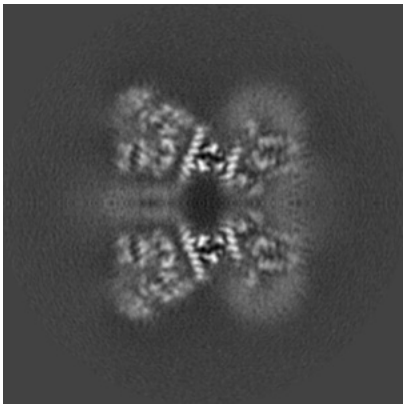


Z Index: 130

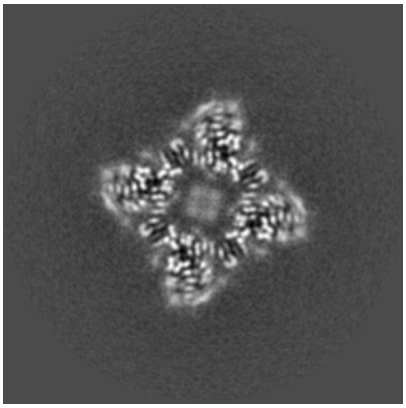
6.3.2 Raw map



X Index: 128



Y Index: 128

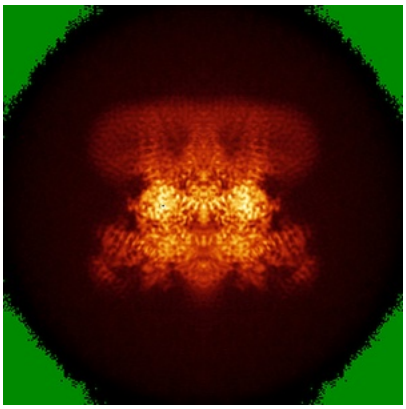


Z Index: 104

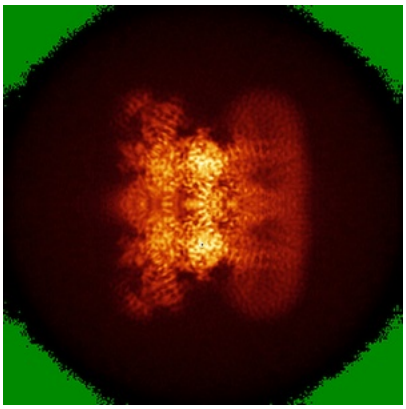
The images above show the largest variance slices of the map in three orthogonal directions.

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

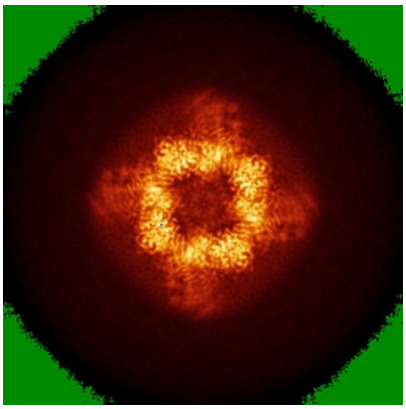
6.4.1 Primary map



X

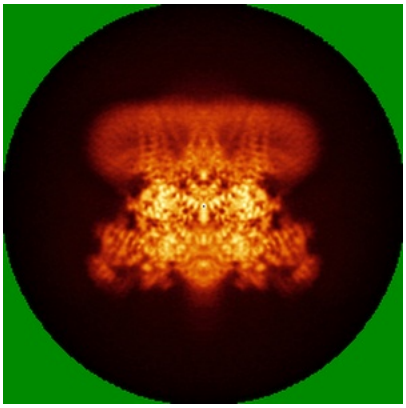


Y

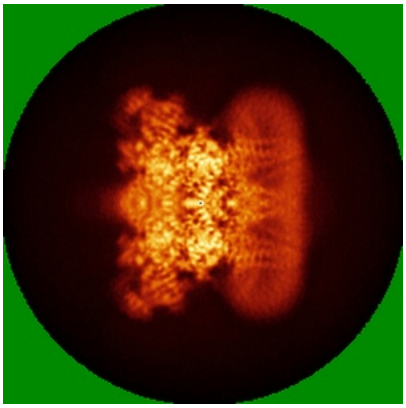


Z

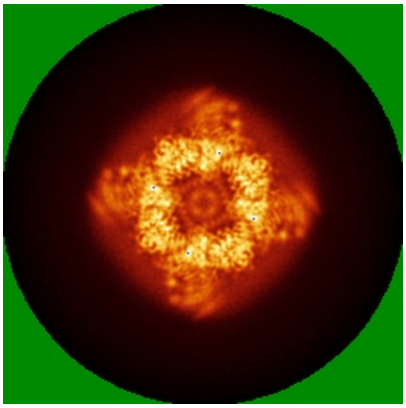
6.4.2 Raw map



X



Y

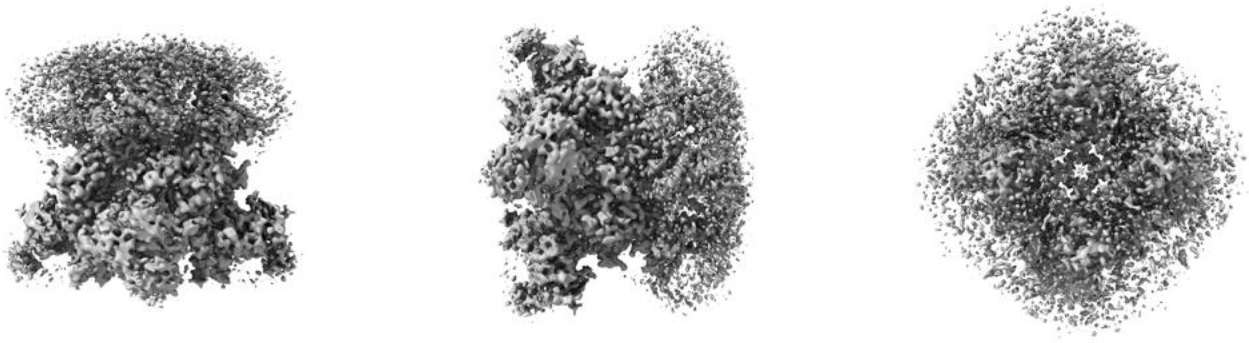


Z

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)

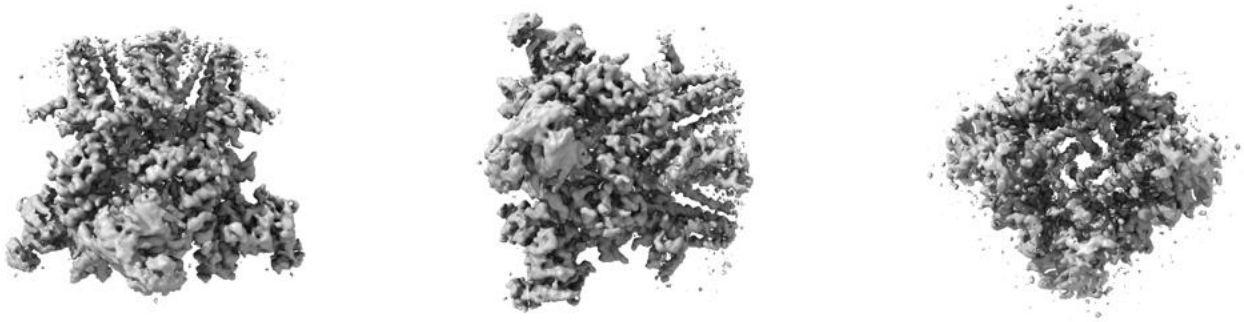
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. 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



X Y Z

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.

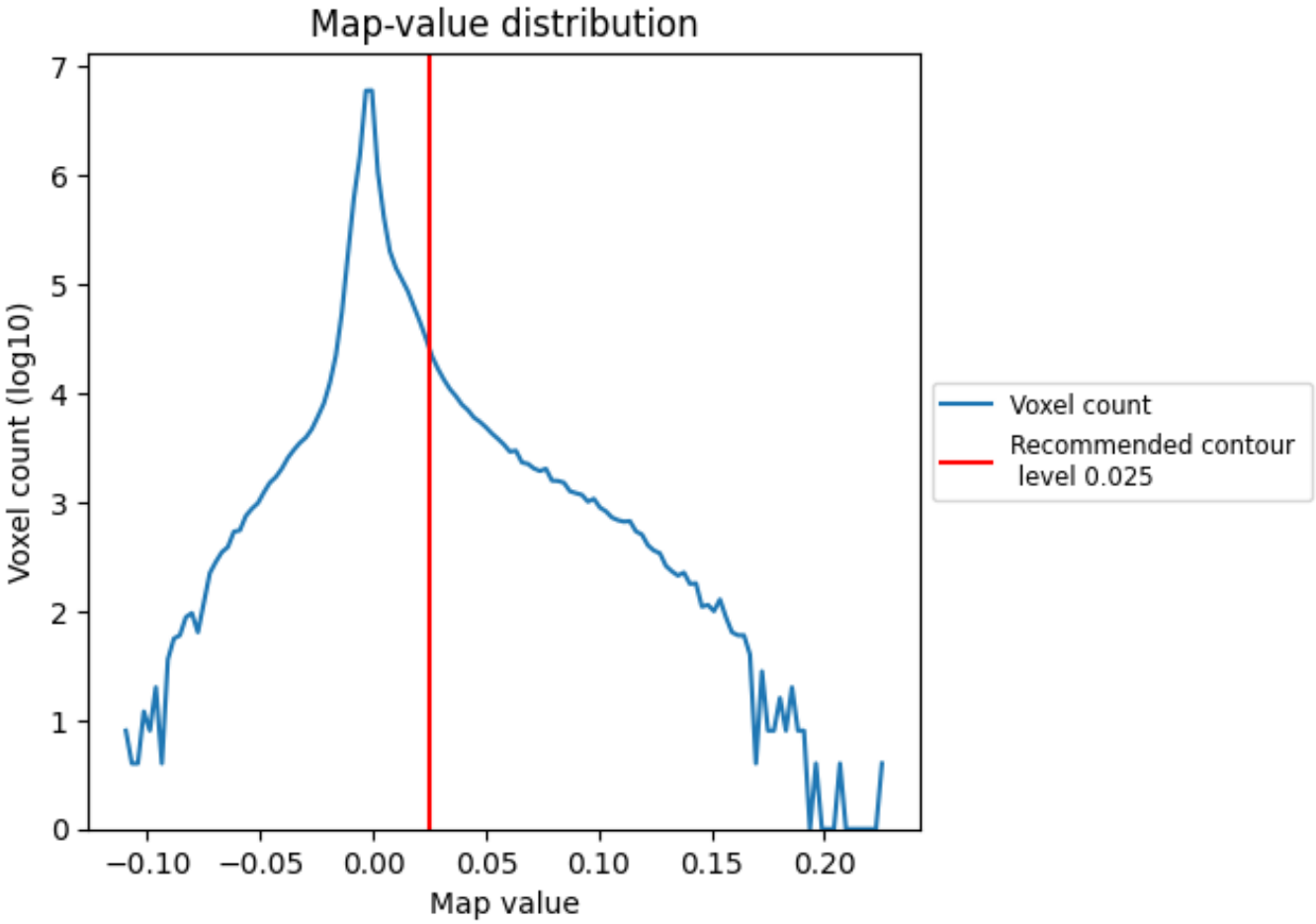
6.6 Mask visualisation (i)

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

7 Map analysis

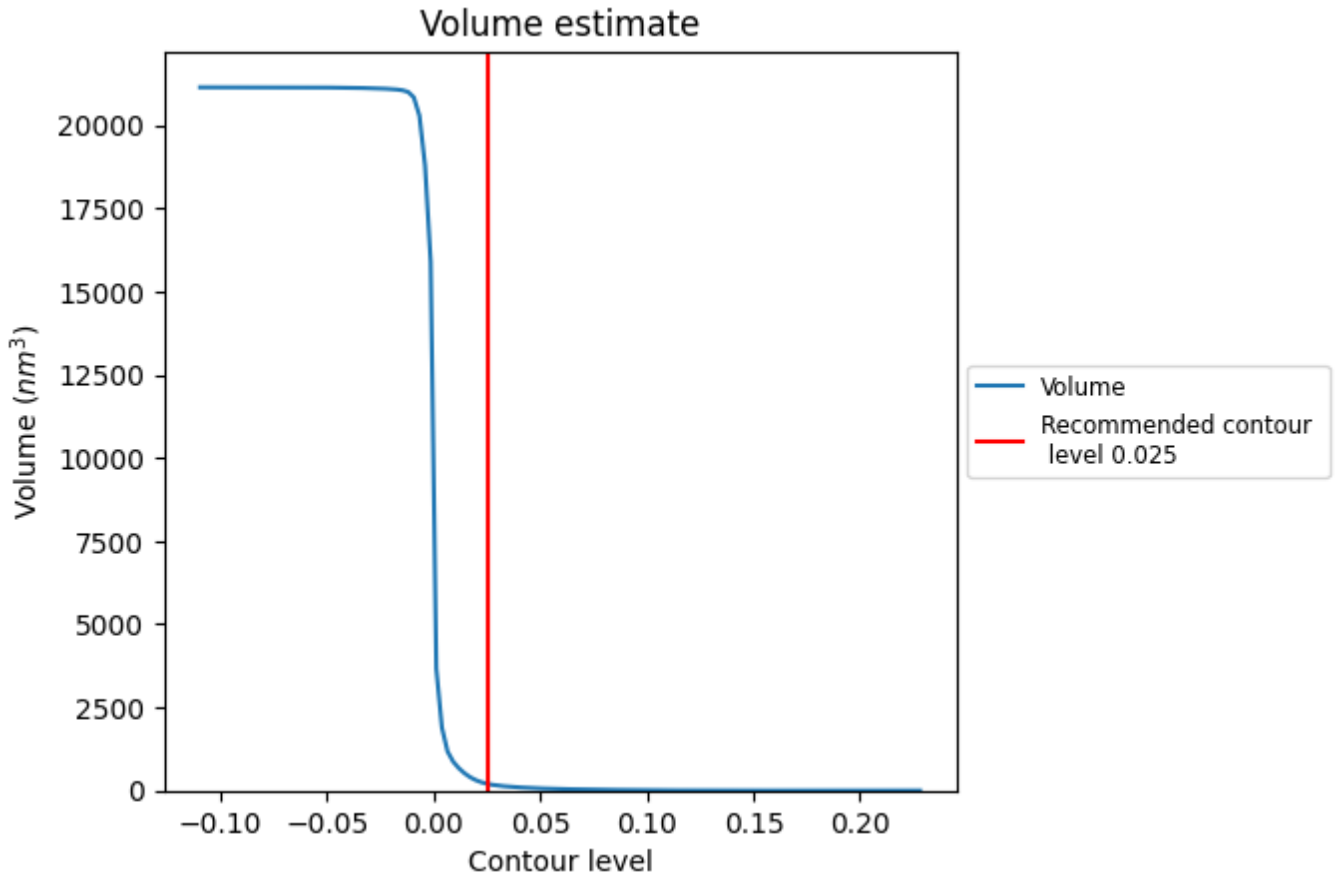
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

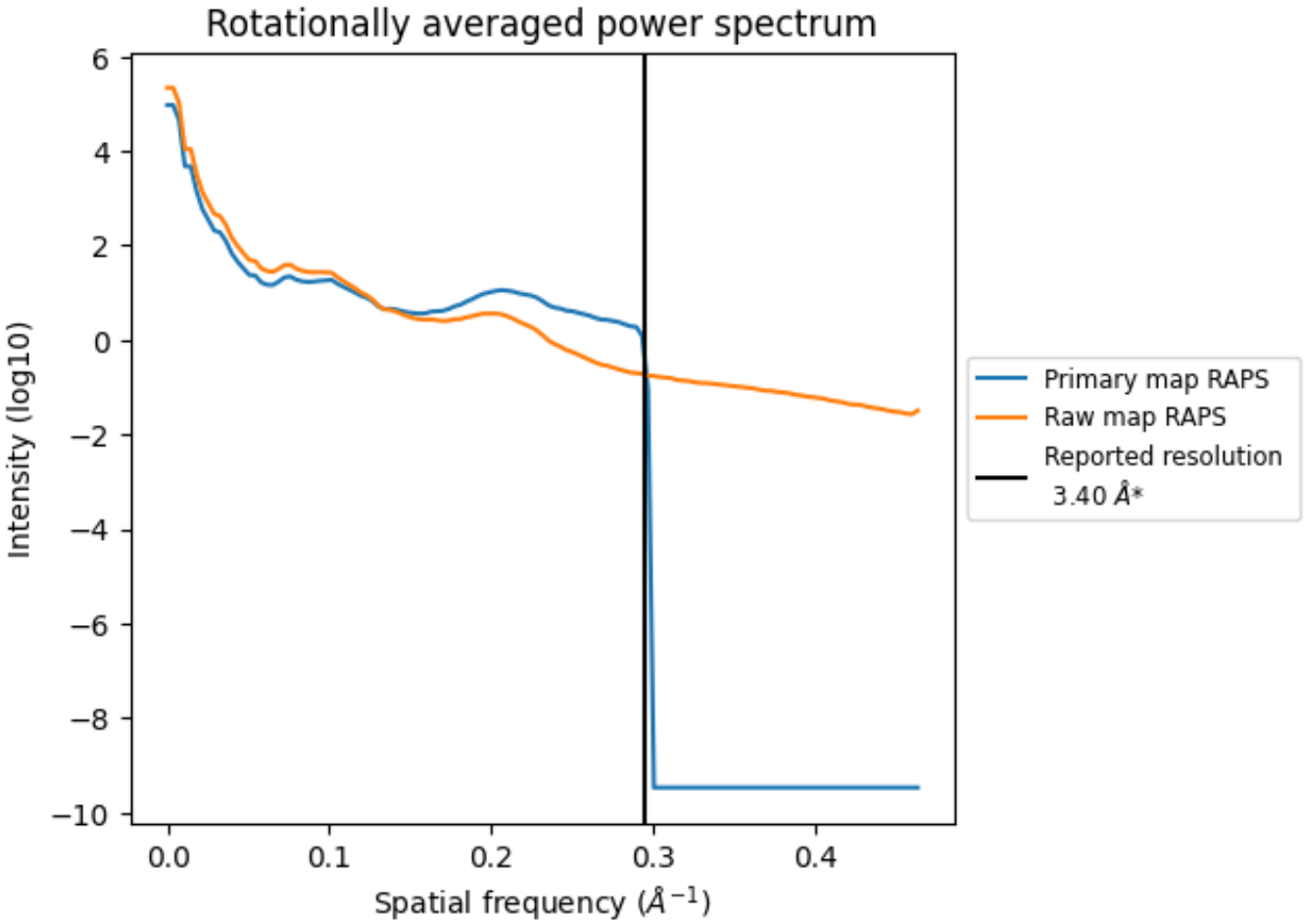
7.2 Volume estimate (i)



The volume at the recommended contour level is 205 nm^3; this corresponds to an approximate mass of 185 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)

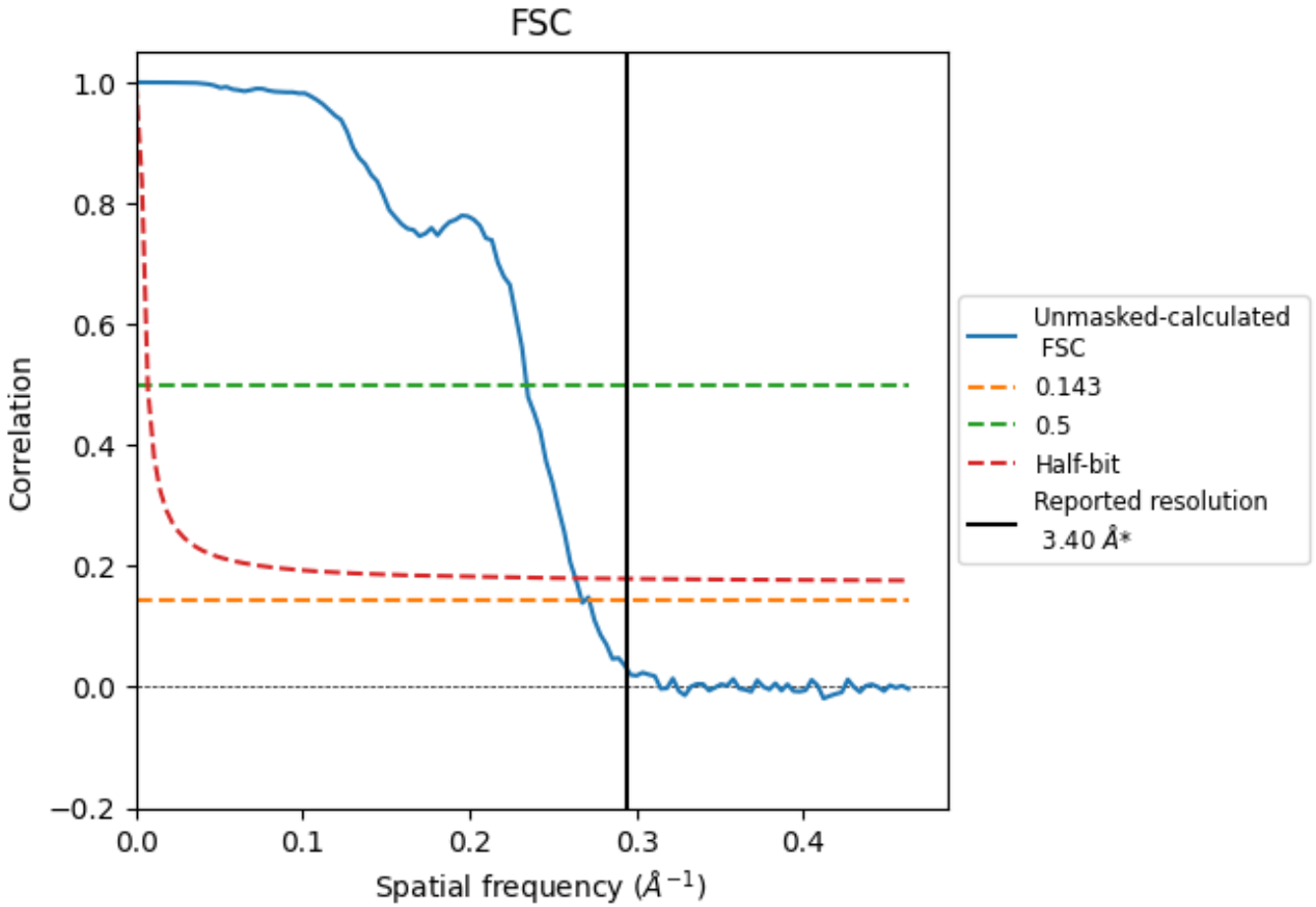


*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

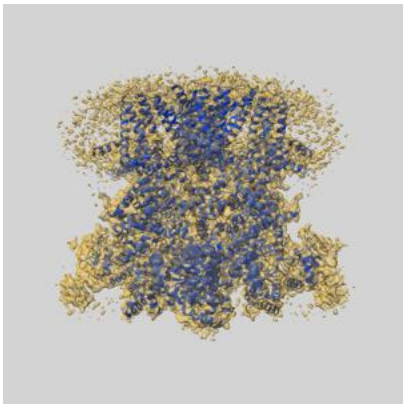
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.74	4.27	3.79

*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 3.74 differs from the reported value 3.4 by more than 10 %

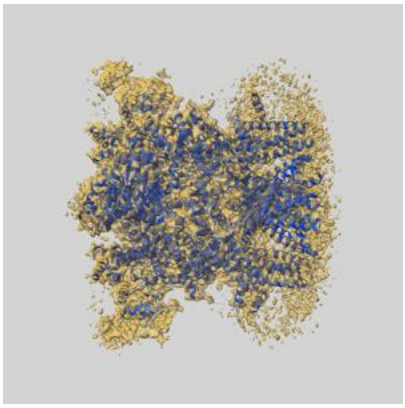
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-0488 and PDB model 6NR3. Per-residue inclusion information can be found in section 3 on page 6.

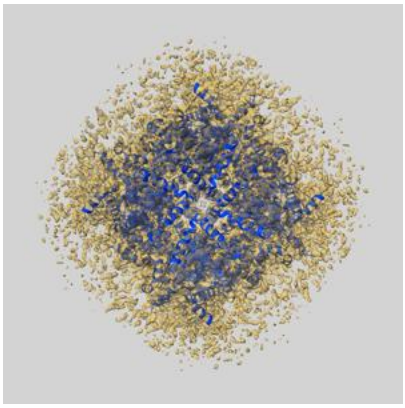
9.1 Map-model overlay



X



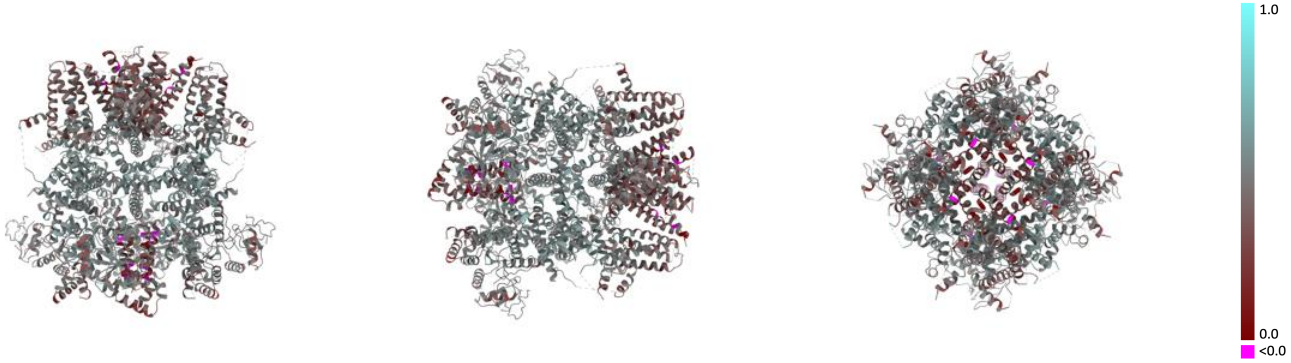
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025 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.

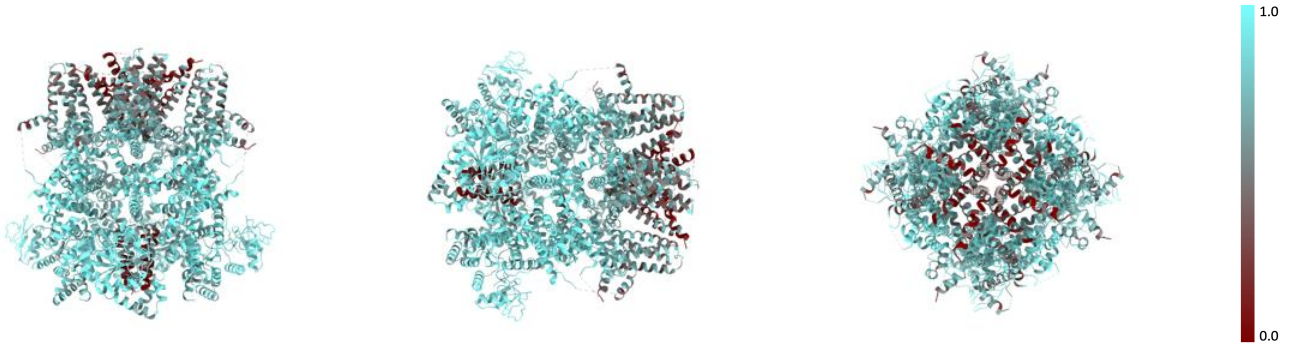
9.2 Q-score mapped to coordinate model



X Y Z

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.

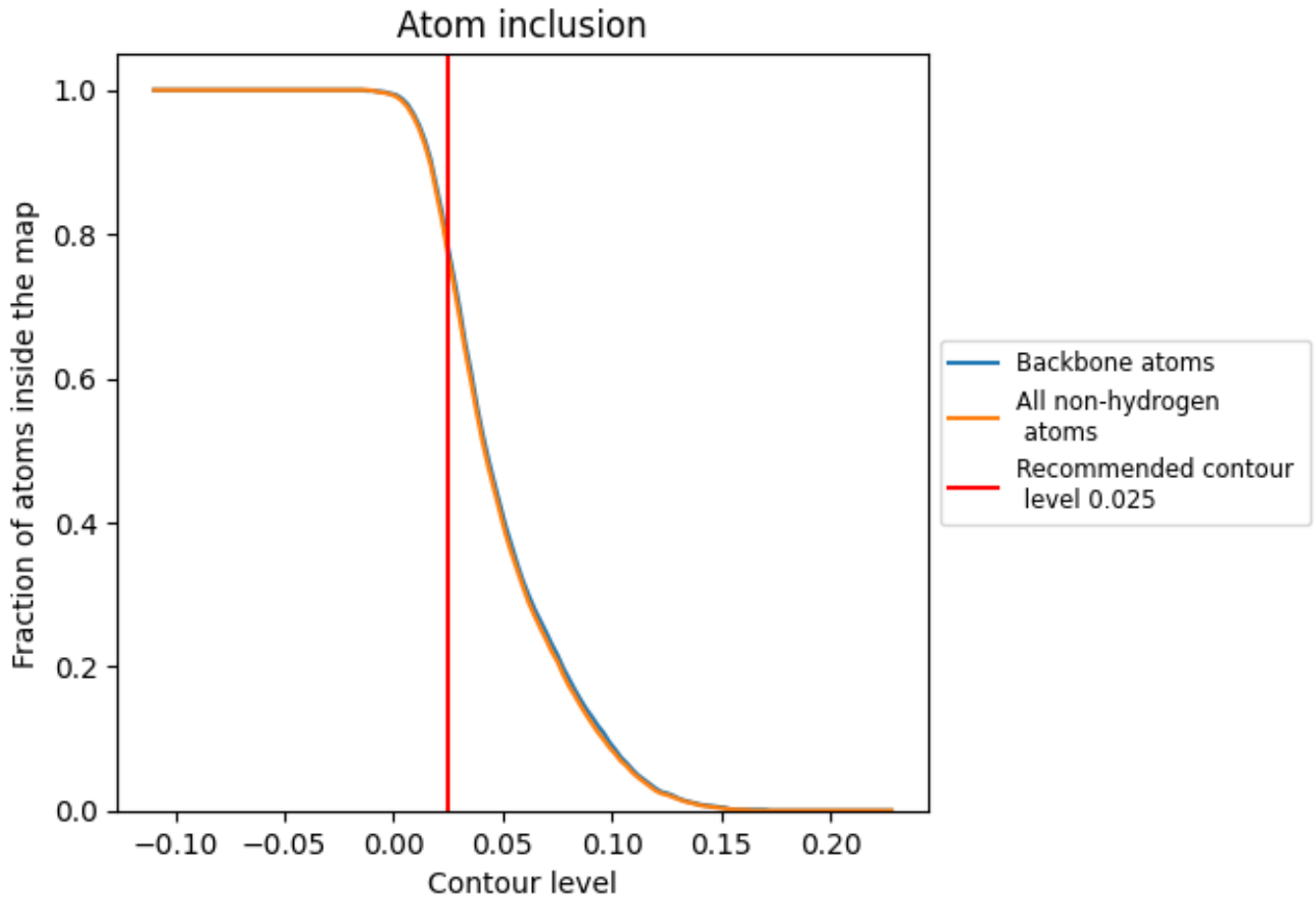
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.025).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7720	0.4660
A	0.7780	0.4660
B	0.7770	0.4660
C	0.7770	0.4660
D	0.7770	0.4660