



wwPDB EM Validation Summary Report ⓘ

Jun 27, 2026 – 09:36 AM EDT

PDB ID : 9Z6Z / pdb_00009z6z
EMDB ID : EMD-73865
Title : Structure of the resting EcDRT3 reverse transcriptase in complex with its non-coding RNA
Authors : Deng, P.; Gao, A.
Deposited on : 2025-11-14
Resolution : 2.60 Å(reported)
Based on initial model : .

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:

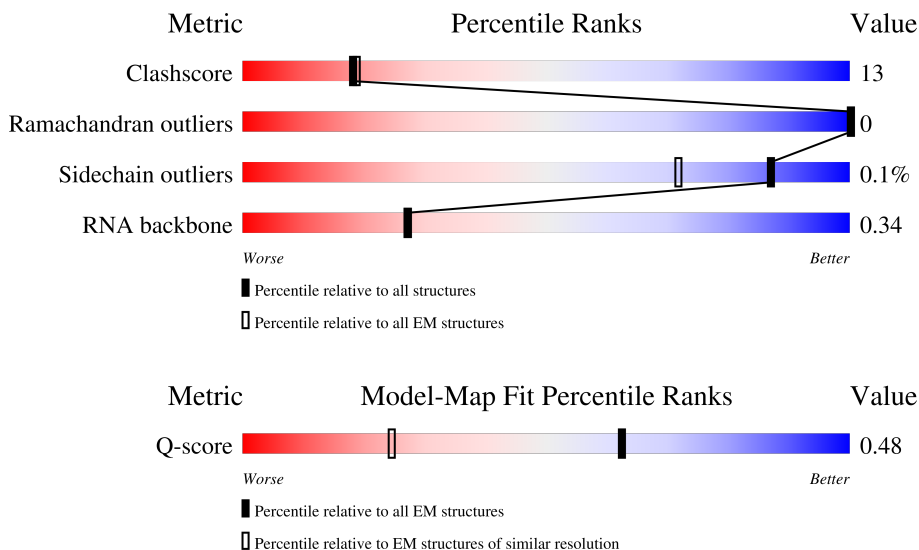
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	426	
1	B	426	
1	C	426	

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Mol	Chain	Length	Quality of chain
1	D	426	
1	E	426	
1	F	426	
2	H	650	
2	I	650	
2	J	650	
2	K	650	
2	L	650	
2	M	650	
3	R	138	
3	S	138	
3	T	138	
3	U	138	
3	V	138	
3	W	138	
4	X	12	
4	Z	12	
4	b	12	
4	d	12	
4	f	12	
4	h	12	
5	Y	17	
5	a	17	
5	c	17	
5	e	17	

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Mol	Chain	Length	Quality of chain
5	g	17	
5	i	17	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 69348 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 Drt3a reverse transcriptase protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	417	Total 3404	C 2199	N 573	O 622	S 10	0	0
1	B	417	Total 3404	C 2199	N 573	O 622	S 10	0	0
1	C	417	Total 3404	C 2199	N 573	O 622	S 10	0	0
1	D	417	Total 3404	C 2199	N 573	O 622	S 10	0	0
1	E	417	Total 3404	C 2199	N 573	O 622	S 10	0	0
1	F	417	Total 3404	C 2199	N 573	O 622	S 10	0	0

- Molecule 2 is a protein called Drt3b reverse transcriptase protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
2	H	628	Total 5197	C 3368	N 848	O 961	P 1	S 19	0	0
2	I	628	Total 5197	C 3368	N 848	O 961	P 1	S 19	0	0
2	J	628	Total 5197	C 3368	N 848	O 961	P 1	S 19	0	0
2	K	628	Total 5197	C 3368	N 848	O 961	P 1	S 19	0	0
2	L	628	Total 5197	C 3368	N 848	O 961	P 1	S 19	0	0
2	M	628	Total 5197	C 3368	N 848	O 961	P 1	S 19	0	0

- Molecule 3 is a RNA chain called non-coding RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	R	111	Total 2364	C 1058	N 424	O 771	P 111	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	111	Total 2364	C 1058	N 424	O 771	P 111	0	0
3	T	111	Total 2364	C 1058	N 424	O 771	P 111	0	0
3	U	111	Total 2364	C 1058	N 424	O 771	P 111	0	0
3	V	111	Total 2364	C 1058	N 424	O 771	P 111	0	0
3	W	111	Total 2364	C 1058	N 424	O 771	P 111	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(P*TP*GP*TP*GP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	12	Total 250	C 120	N 39	O 79	P 12	0	0
4	Z	12	Total 250	C 120	N 39	O 79	P 12	0	0
4	b	12	Total 250	C 120	N 39	O 79	P 12	0	0
4	d	12	Total 250	C 120	N 39	O 79	P 12	0	0
4	f	12	Total 250	C 120	N 39	O 79	P 12	0	0
4	h	12	Total 250	C 120	N 39	O 79	P 12	0	0

- Molecule 5 is a DNA chain called DNA (5'-D(P*AP*CP*AP*CP*AP*CP*AP*CP*AP*CP*AP*CP*AP*CP*AP*CP*A)-3').

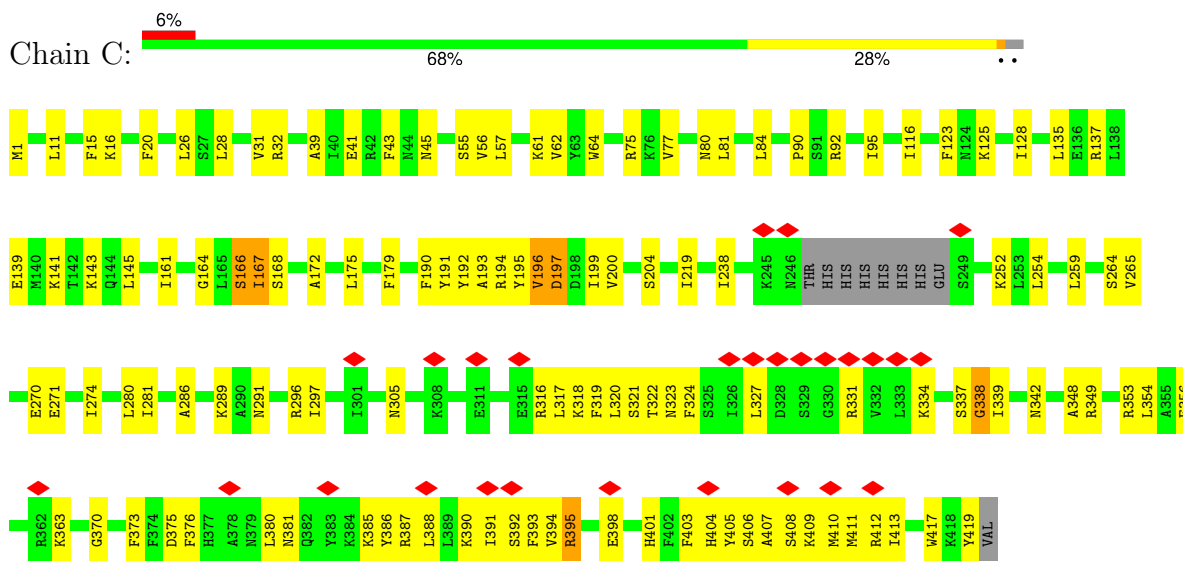
Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	17	Total 341	C 162	N 69	O 93	P 17	0	0
5	a	17	Total 341	C 162	N 69	O 93	P 17	0	0
5	c	17	Total 341	C 162	N 69	O 93	P 17	0	0
5	e	17	Total 341	C 162	N 69	O 93	P 17	0	0
5	g	17	Total 341	C 162	N 69	O 93	P 17	0	0
5	i	17	Total 341	C 162	N 69	O 93	P 17	0	0

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

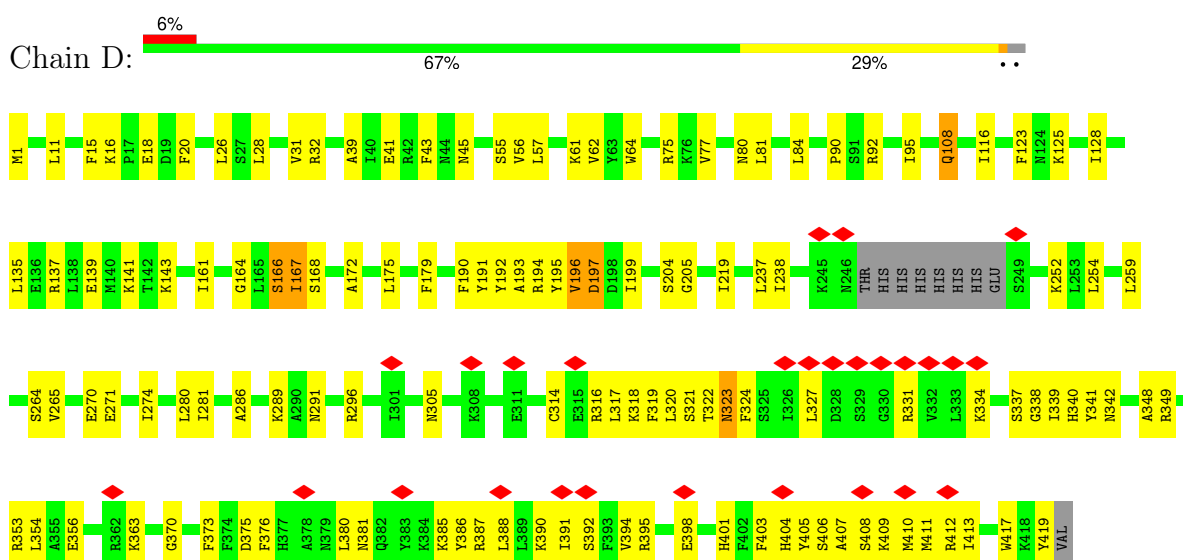
Mol	Chain	Residues	Atoms	AltConf
6	H	1	Total Mg 1 1	0
6	I	1	Total Mg 1 1	0
6	J	1	Total Mg 1 1	0
6	K	1	Total Mg 1 1	0
6	L	1	Total Mg 1 1	0
6	M	1	Total Mg 1 1	0

- Molecule 7 is water.

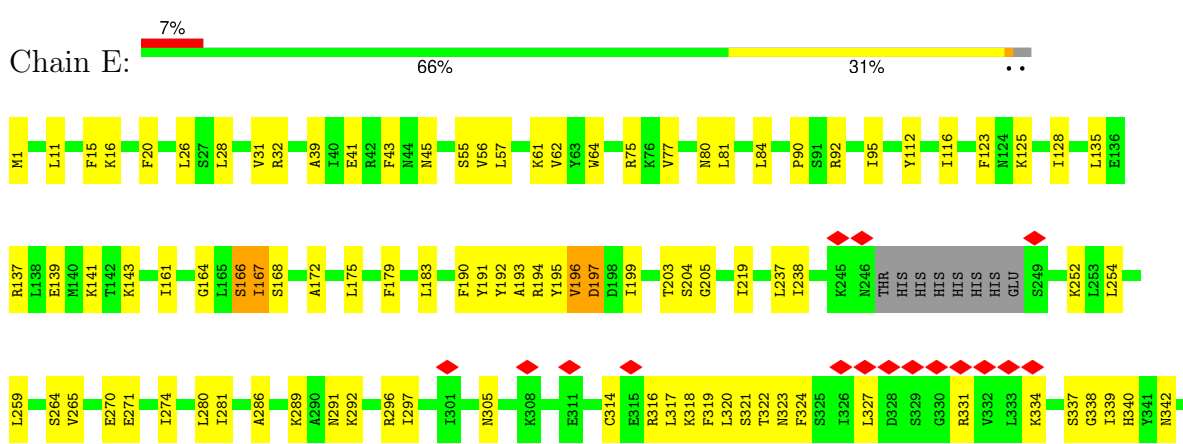
Mol	Chain	Residues	Atoms	AltConf
7	H	1	Total O 1 1	0
7	I	1	Total O 1 1	0
7	J	1	Total O 1 1	0
7	K	1	Total O 1 1	0
7	L	1	Total O 1 1	0
7	M	1	Total O 1 1	0



• Molecule 1: Drt3a reverse transcriptase protein

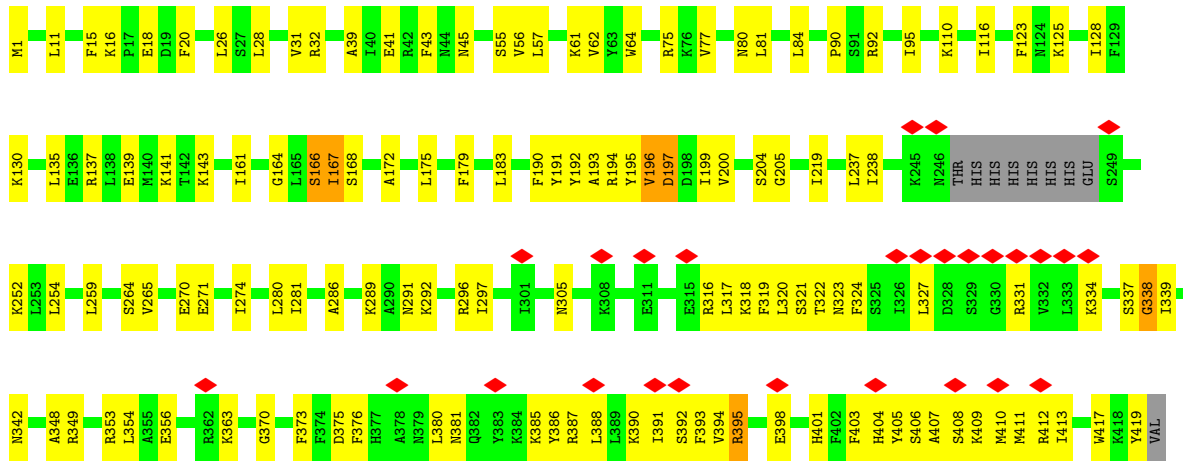


• Molecule 1: Drt3a reverse transcriptase protein

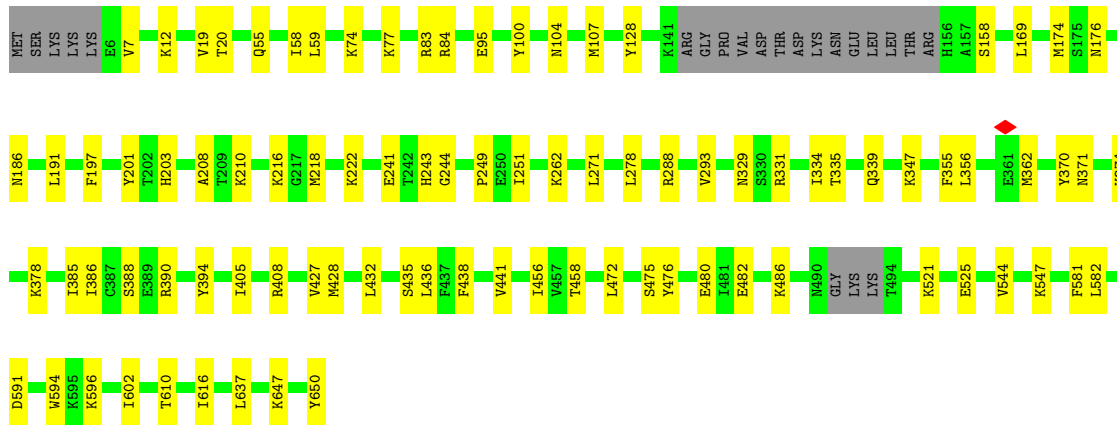
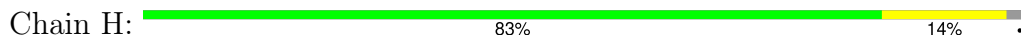




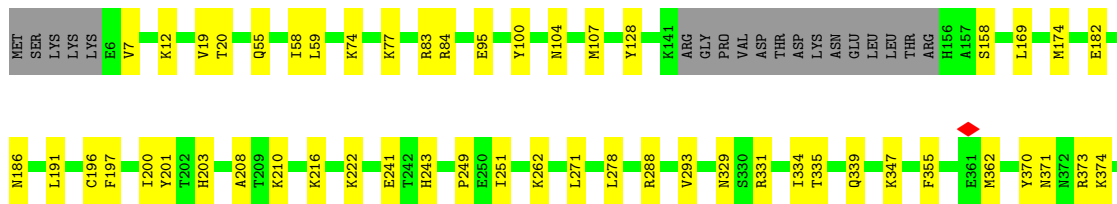
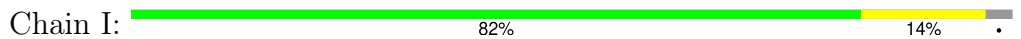
• Molecule 1: Drt3a reverse transcriptase protein

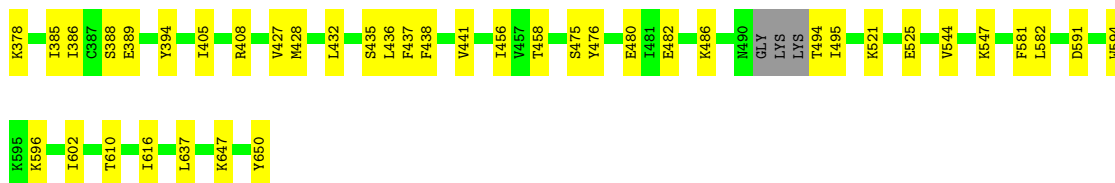


• Molecule 2: Drt3b reverse transcriptase protein

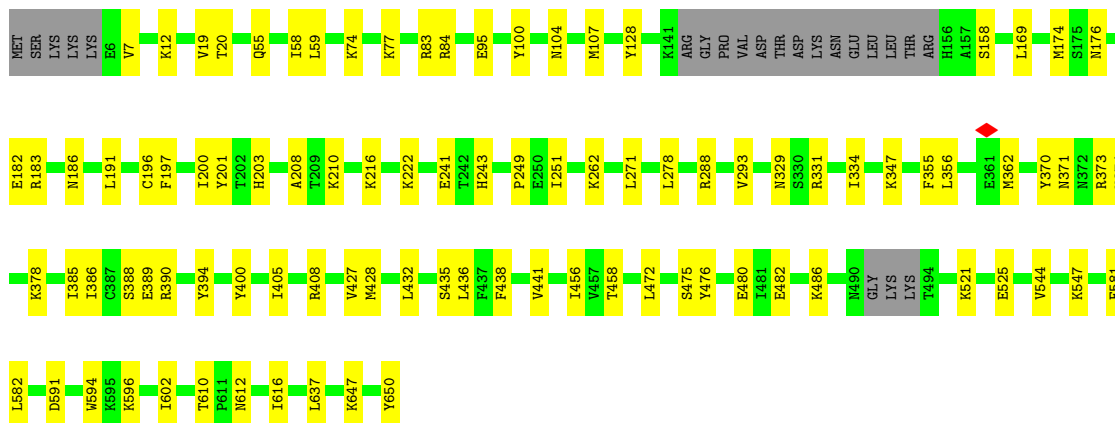
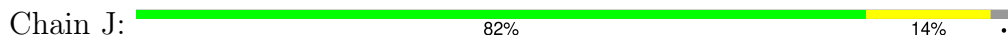


• Molecule 2: Drt3b reverse transcriptase protein

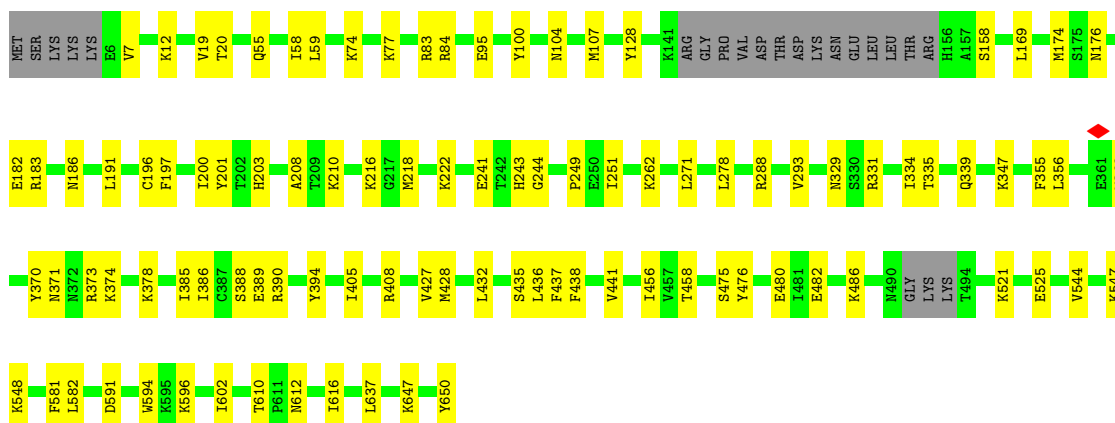
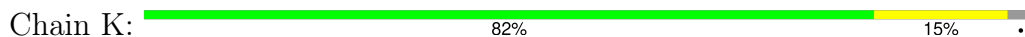




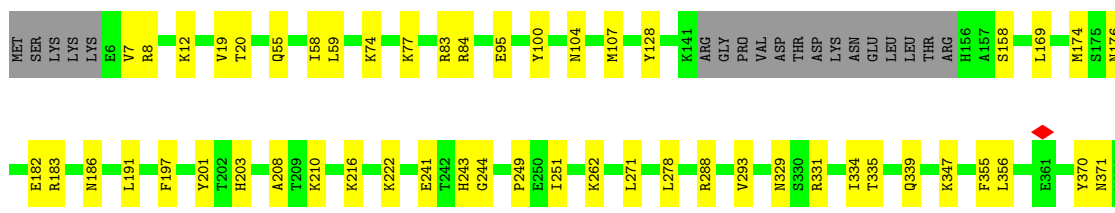
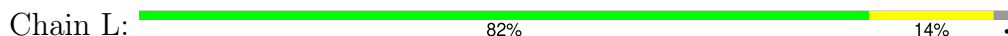
• Molecule 2: Drt3b reverse transcriptase protein

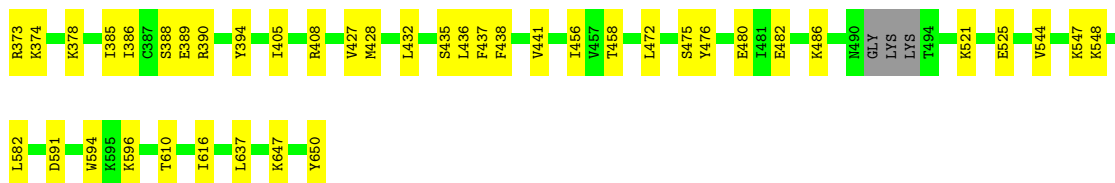


• Molecule 2: Drt3b reverse transcriptase protein

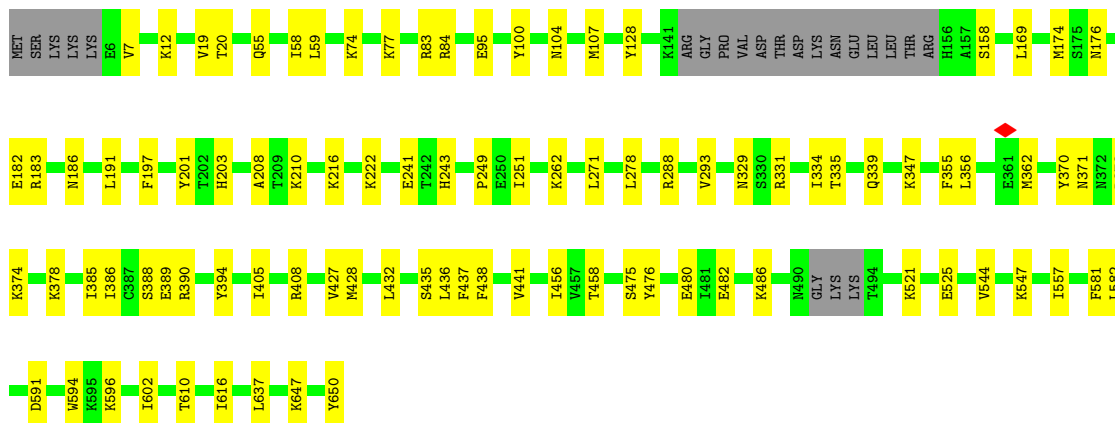
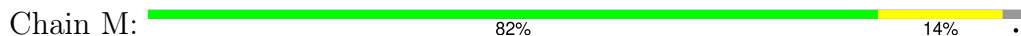


• Molecule 2: Drt3b reverse transcriptase protein

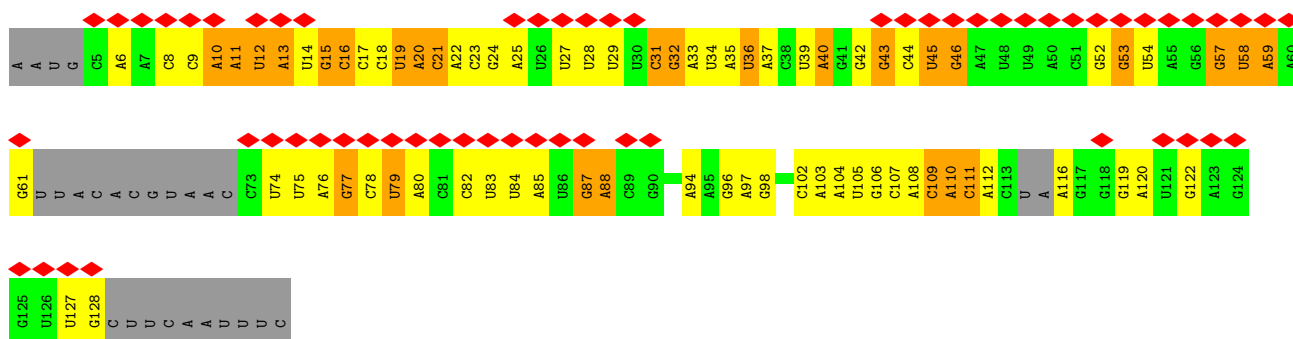
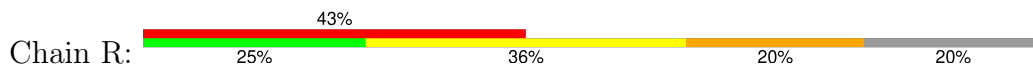




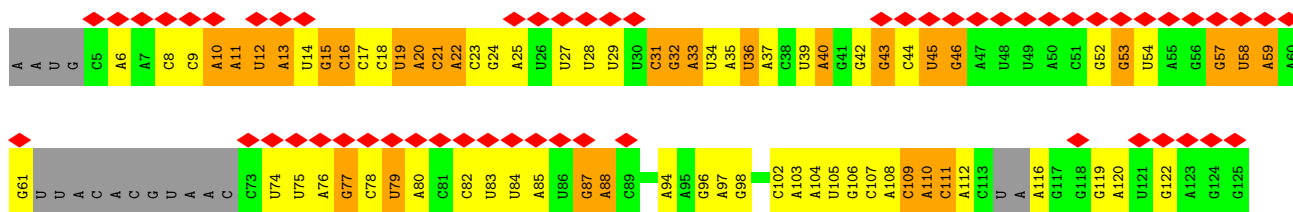
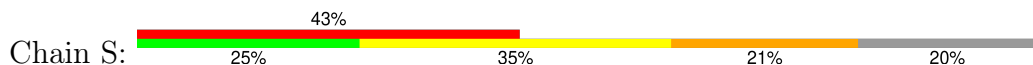
• Molecule 2: Drt3b reverse transcriptase protein



• Molecule 3: non-coding RNA

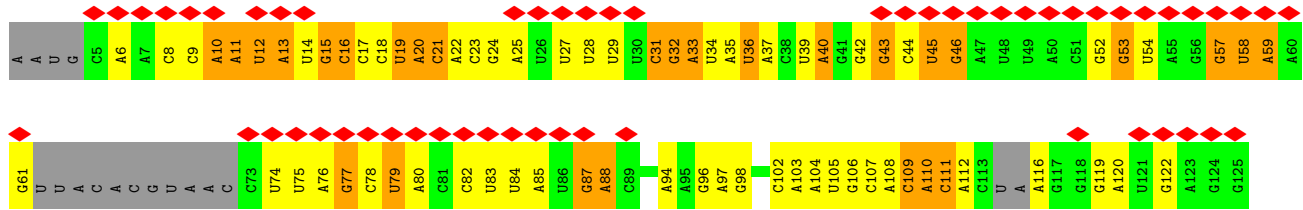
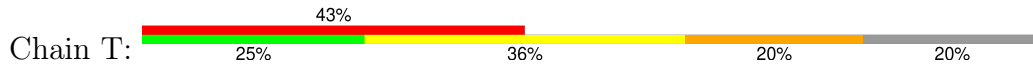


• Molecule 3: non-coding RNA

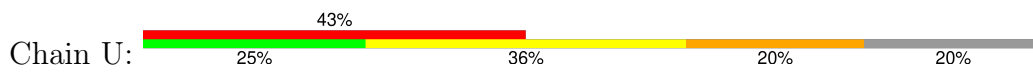




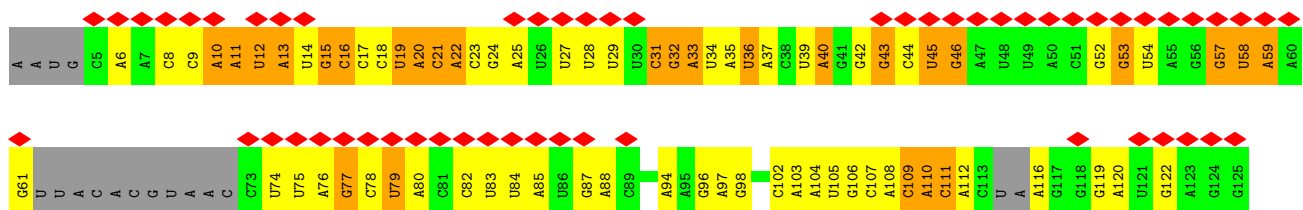
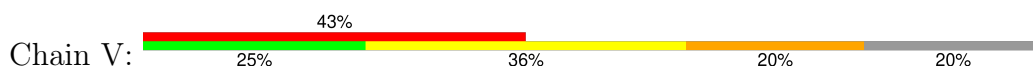
• Molecule 3: non-coding RNA



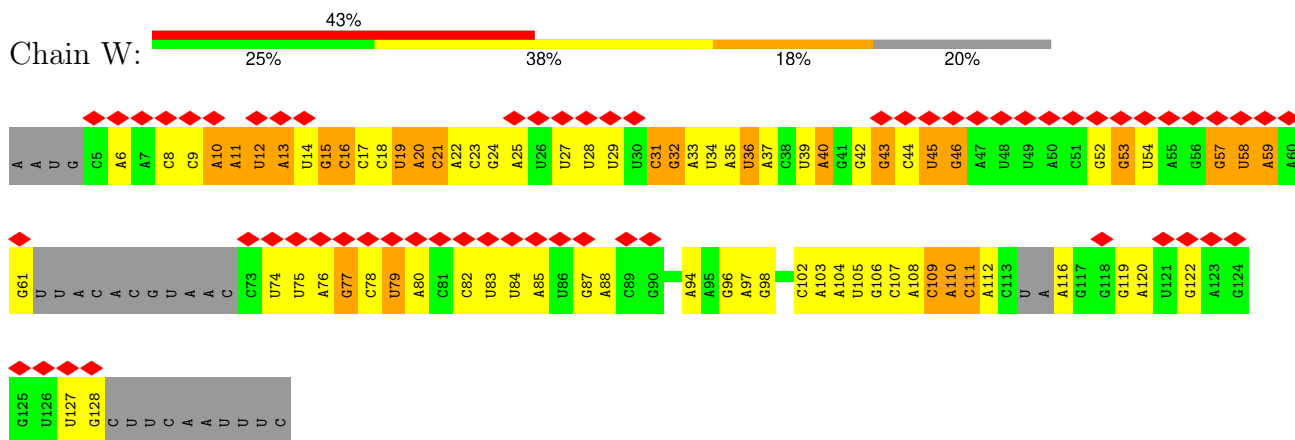
• Molecule 3: non-coding RNA



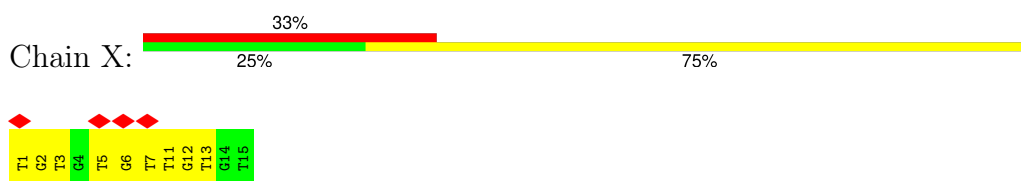
• Molecule 3: non-coding RNA



• Molecule 3: non-coding RNA



• Molecule 4: DNA (5'-D(P*TP*GP*TP*GP*T)-3')



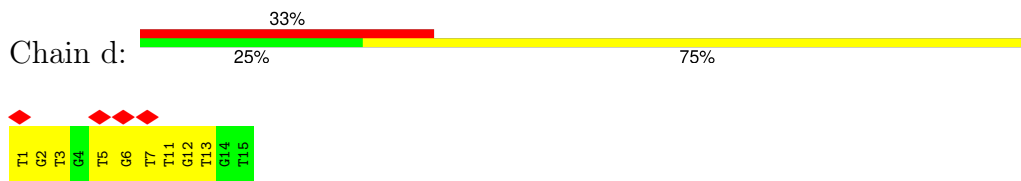
• Molecule 4: DNA (5'-D(P*TP*GP*TP*GP*T)-3')



• Molecule 4: DNA (5'-D(P*TP*GP*TP*GP*T)-3')



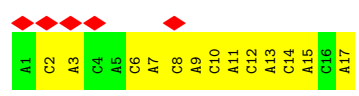
• Molecule 4: DNA (5'-D(P*TP*GP*TP*GP*T)-3')



• Molecule 4: DNA (5'-D(P*TP*GP*TP*GP*T)-3')



• Molecule 4: DNA (5'-D(P*TP*GP*TP*GP*T)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63349	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.994	Depositor
Minimum map value	-1.301	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	325.99, 325.99, 325.99	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9314, 0.9314, 0.9314	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, PTR

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	0.62	7/3480 (0.2%)	0.69	7/4689 (0.1%)
1	B	0.62	6/3480 (0.2%)	0.69	7/4689 (0.1%)
1	C	0.62	7/3480 (0.2%)	0.69	7/4689 (0.1%)
1	D	0.62	6/3480 (0.2%)	0.69	7/4689 (0.1%)
1	E	0.62	6/3480 (0.2%)	0.69	7/4689 (0.1%)
1	F	0.62	7/3480 (0.2%)	0.69	7/4689 (0.1%)
2	H	0.24	0/5295	0.36	1/7152 (0.0%)
2	I	0.24	0/5295	0.36	1/7152 (0.0%)
2	J	0.24	0/5295	0.36	1/7152 (0.0%)
2	K	0.24	0/5295	0.36	1/7152 (0.0%)
2	L	0.24	0/5295	0.36	1/7152 (0.0%)
2	M	0.24	0/5295	0.36	1/7152 (0.0%)
3	R	0.19	0/2642	0.37	0/4109
3	S	0.19	0/2642	0.37	0/4109
3	T	0.19	0/2642	0.37	0/4109
3	U	0.19	0/2642	0.37	0/4109
3	V	0.19	0/2642	0.37	0/4109
3	W	0.19	0/2642	0.37	0/4109
4	X	0.31	0/277	0.58	0/425
4	Z	0.31	0/277	0.58	0/425
4	b	0.31	0/277	0.58	0/425
4	d	0.31	0/277	0.58	0/425
4	f	0.31	0/277	0.59	0/425
4	h	0.31	0/277	0.58	0/425
5	Y	0.33	0/383	0.66	0/585
5	a	0.33	0/383	0.66	0/585
5	c	0.33	0/383	0.66	0/585
5	e	0.33	0/383	0.66	0/585
5	g	0.33	0/383	0.66	0/585
5	i	0.33	0/383	0.66	0/585
All	All	0.39	39/72462 (0.1%)	0.49	48/101760 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	F	0	1
All	All	0	3

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	195	TYR	CA-C	-6.62	1.45	1.53
1	A	195	TYR	CA-C	-6.62	1.45	1.53
1	D	195	TYR	CA-C	-6.56	1.45	1.53
1	F	195	TYR	CA-C	-6.09	1.45	1.53
1	B	195	TYR	CA-C	-6.08	1.45	1.53

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	167	ILE	N-CA-C	-9.54	99.12	111.05
1	A	167	ILE	N-CA-C	-9.51	99.16	111.05
1	D	167	ILE	N-CA-C	-9.50	99.17	111.05
1	C	167	ILE	N-CA-C	-9.47	99.21	111.05
1	F	167	ILE	N-CA-C	-9.47	99.21	111.05

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	395	ARG	Sidechain
1	C	395	ARG	Sidechain
1	F	395	ARG	Sidechain

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	3404	0	3346	119	0
1	B	3404	0	3346	114	0
1	C	3404	0	3346	111	0
1	D	3404	0	3346	113	0
1	E	3404	0	3346	113	0
1	F	3404	0	3346	117	0
2	H	5197	0	5180	104	0
2	I	5197	0	5179	108	0
2	J	5197	0	5180	109	0
2	K	5197	0	5179	117	0
2	L	5197	0	5179	113	0
2	M	5197	0	5179	112	0
3	R	2364	0	1197	69	0
3	S	2364	0	1197	68	0
3	T	2364	0	1197	70	0
3	U	2364	0	1197	69	0
3	V	2364	0	1197	69	0
3	W	2364	0	1197	69	0
4	X	250	0	141	21	0
4	Z	250	0	141	23	0
4	b	250	0	141	22	0
4	d	250	0	141	23	0
4	f	250	0	141	22	0
4	h	250	0	141	23	0
5	Y	341	0	188	42	0
5	a	341	0	188	43	0
5	c	341	0	188	47	0
5	e	341	0	188	46	0
5	g	341	0	188	45	0
5	i	341	0	188	44	0
6	H	1	0	0	0	0
6	I	1	0	0	0	0
6	J	1	0	0	0	0
6	K	1	0	0	0	0
6	L	1	0	0	0	0
6	M	1	0	0	0	0
7	H	1	0	0	0	0
7	I	1	0	0	0	0
7	J	1	0	0	0	0
7	K	1	0	0	0	0
7	L	1	0	0	0	0
7	M	1	0	0	0	0
All	All	69348	0	60308	1682	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 13.

The worst 5 of 1682 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:370:TYR:CE2	5:g:7:DA:H5'	1.08	1.60
2:I:370:TYR:CE2	5:c:7:DA:H5'	1.08	1.59
2:L:370:TYR:CE2	5:i:7:DA:H5'	1.08	1.58
2:M:370:TYR:CE2	5:e:7:DA:H5'	1.07	1.56
2:J:370:TYR:CE2	5:Y:7:DA:C5'	1.89	1.53

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	413/426 (97%)	391 (95%)	22 (5%)	0	100	100
1	B	413/426 (97%)	391 (95%)	22 (5%)	0	100	100
1	C	413/426 (97%)	391 (95%)	22 (5%)	0	100	100
1	D	413/426 (97%)	391 (95%)	22 (5%)	0	100	100
1	E	413/426 (97%)	391 (95%)	22 (5%)	0	100	100
1	F	413/426 (97%)	391 (95%)	22 (5%)	0	100	100
2	H	622/650 (96%)	609 (98%)	13 (2%)	0	100	100
2	I	622/650 (96%)	609 (98%)	13 (2%)	0	100	100
2	J	622/650 (96%)	609 (98%)	13 (2%)	0	100	100
2	K	622/650 (96%)	609 (98%)	13 (2%)	0	100	100
2	L	622/650 (96%)	609 (98%)	13 (2%)	0	100	100
2	M	622/650 (96%)	609 (98%)	13 (2%)	0	100	100
All	All	6210/6456 (96%)	6000 (97%)	210 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	366/391 (94%)	365 (100%)	1 (0%)	86	94
1	B	366/391 (94%)	364 (100%)	2 (0%)	81	92
1	C	366/391 (94%)	366 (100%)	0	100	100
1	D	366/391 (94%)	364 (100%)	2 (0%)	81	92
1	E	366/391 (94%)	365 (100%)	1 (0%)	86	94
1	F	366/391 (94%)	365 (100%)	1 (0%)	86	94
2	H	582/606 (96%)	582 (100%)	0	100	100
2	I	582/606 (96%)	582 (100%)	0	100	100
2	J	582/606 (96%)	582 (100%)	0	100	100
2	K	582/606 (96%)	582 (100%)	0	100	100
2	L	582/606 (96%)	581 (100%)	1 (0%)	87	95
2	M	582/606 (96%)	582 (100%)	0	100	100
All	All	5688/5982 (95%)	5680 (100%)	8 (0%)	87	96

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	8	ARG
1	F	292	LYS
1	D	323	ASN
1	D	108	GLN
1	E	292	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	401	HIS

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Mol	Chain	Res	Type
2	K	346	GLN
1	E	340	HIS
2	K	243	HIS
2	L	377	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	R	108/138 (78%)	44 (40%)	5 (4%)
3	S	108/138 (78%)	44 (40%)	5 (4%)
3	T	108/138 (78%)	44 (40%)	5 (4%)
3	U	108/138 (78%)	44 (40%)	5 (4%)
3	V	108/138 (78%)	44 (40%)	5 (4%)
3	W	108/138 (78%)	44 (40%)	5 (4%)
All	All	648/828 (78%)	264 (40%)	30 (4%)

5 of 264 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	R	6	A
3	R	10	A
3	R	11	A
3	R	12	U
3	R	13	A

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	T	110	A
3	W	45	U
3	U	45	U
3	W	110	A
3	V	110	A

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

6 non-standard protein/DNA/RNA residues 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	PTR	L	650	2	15,16,17	2.61	2 (13%)	17,22,24	1.24	1 (5%)
2	PTR	K	650	2	15,16,17	2.61	2 (13%)	17,22,24	1.25	2 (11%)
2	PTR	H	650	2	15,16,17	2.61	2 (13%)	17,22,24	1.25	2 (11%)
2	PTR	M	650	2	15,16,17	2.62	2 (13%)	17,22,24	1.24	2 (11%)
2	PTR	J	650	2	15,16,17	2.61	2 (13%)	17,22,24	1.25	2 (11%)
2	PTR	I	650	2	15,16,17	2.60	2 (13%)	17,22,24	1.25	2 (11%)

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	PTR	L	650	2	-	3/10/11/13	0/1/1/1
2	PTR	K	650	2	-	3/10/11/13	0/1/1/1
2	PTR	H	650	2	-	3/10/11/13	0/1/1/1
2	PTR	M	650	2	-	3/10/11/13	0/1/1/1
2	PTR	J	650	2	-	3/10/11/13	0/1/1/1
2	PTR	I	650	2	-	3/10/11/13	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	650	PTR	P-OH	9.50	1.77	1.59
2	L	650	PTR	P-OH	9.47	1.77	1.59
2	K	650	PTR	P-OH	9.46	1.77	1.59
2	H	650	PTR	P-OH	9.46	1.77	1.59
2	J	650	PTR	P-OH	9.46	1.77	1.59

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	650	PTR	O3P-P-O2P	2.19	116.03	107.80
2	I	650	PTR	O3P-P-O2P	2.19	116.02	107.80
2	K	650	PTR	O3P-P-O2P	2.19	116.00	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	650	PTR	O3P-P-O2P	2.18	115.99	107.80
2	J	650	PTR	O3P-P-O2P	2.18	115.99	107.80

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	650	PTR	O-C-CA-CB
2	H	650	PTR	N-CA-CB-CG
2	H	650	PTR	C-CA-CB-CG
2	I	650	PTR	O-C-CA-CB
2	I	650	PTR	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	X	1
4	Z	1
4	b	1
4	d	1
4	f	1
4	h	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	7:DT	O3'	11:DT	P	28.31
1	Z	7:DT	O3'	11:DT	P	28.31
1	b	7:DT	O3'	11:DT	P	28.31
1	d	7:DT	O3'	11:DT	P	28.31
1	f	7:DT	O3'	11:DT	P	28.31

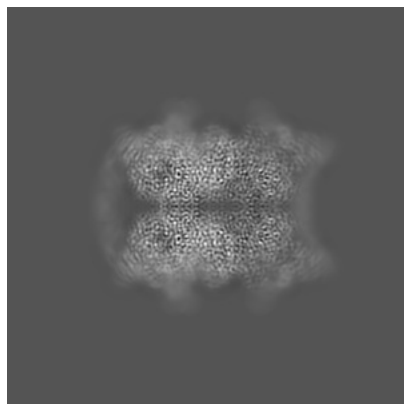
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73865. These allow visual inspection of the internal detail of the map and identification of artifacts.

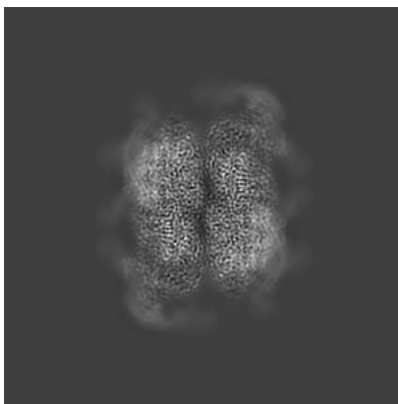
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

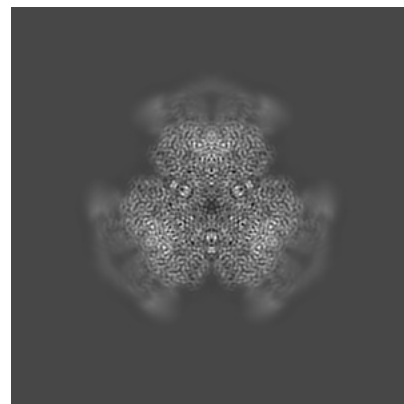
6.1.1 Primary map



X

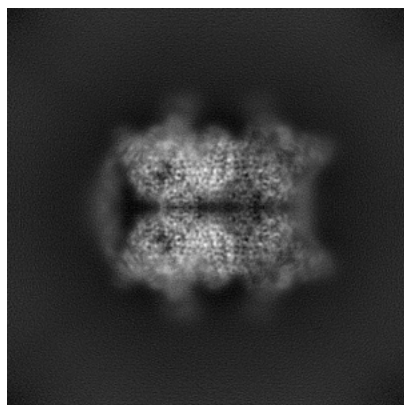


Y

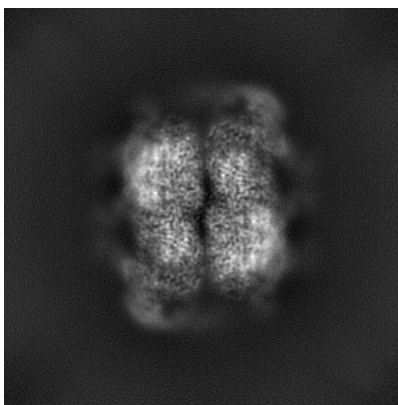


Z

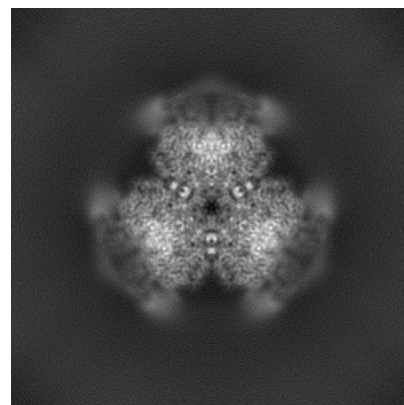
6.1.2 Raw map



X



Y

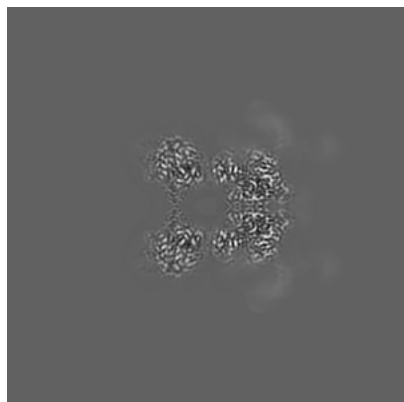


Z

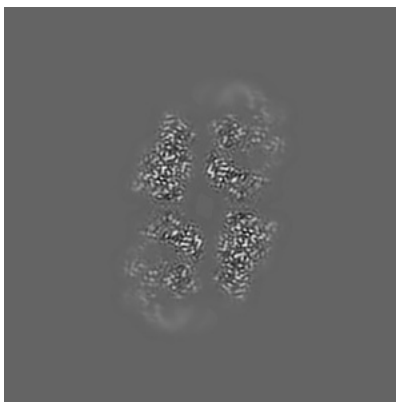
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

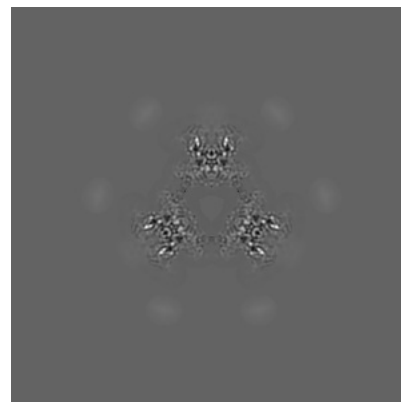
6.2.1 Primary map



X Index: 175

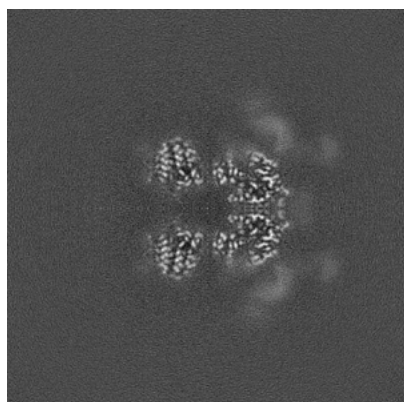


Y Index: 175

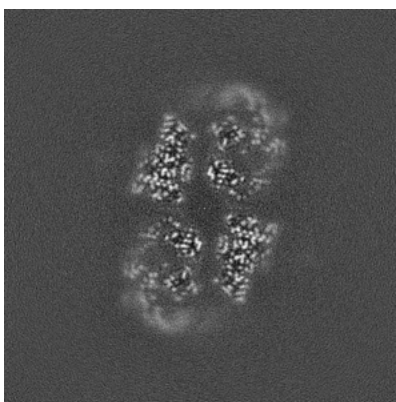


Z Index: 175

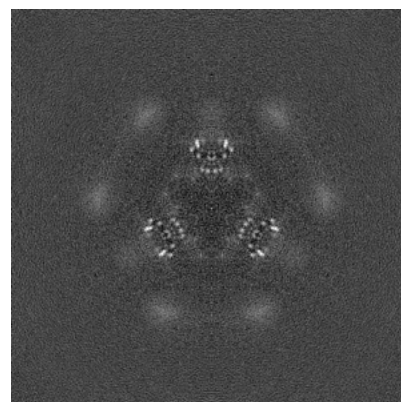
6.2.2 Raw map



X Index: 175



Y Index: 175

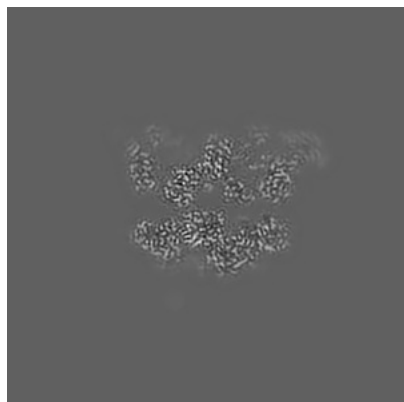


Z Index: 175

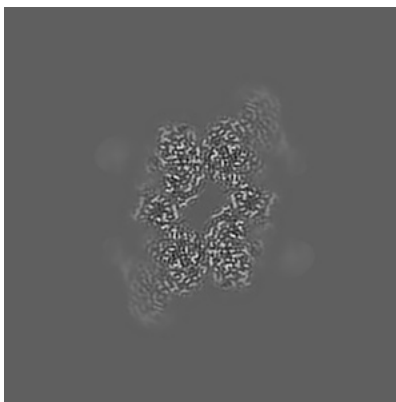
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

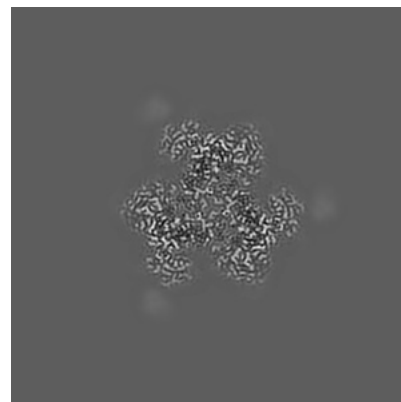
6.3.1 Primary map



X Index: 150

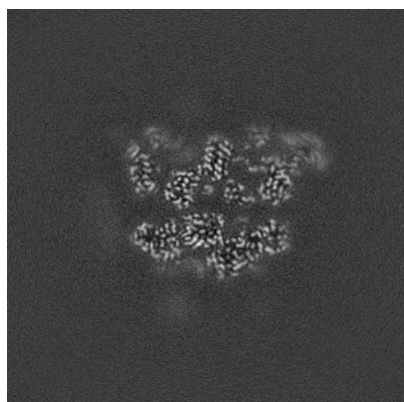


Y Index: 157

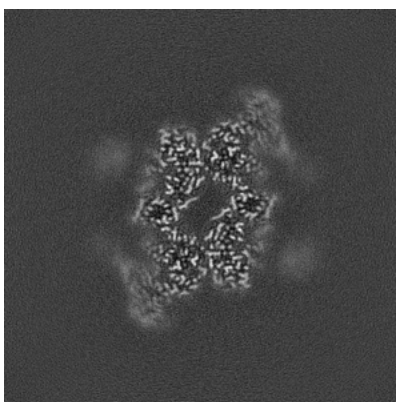


Z Index: 198

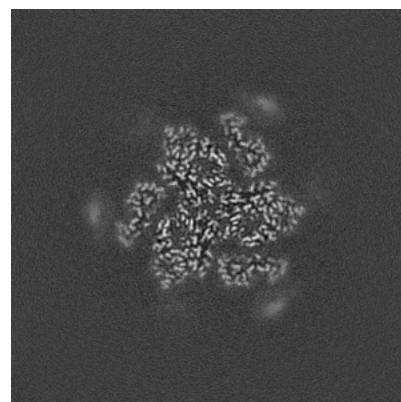
6.3.2 Raw map



X Index: 150



Y Index: 157

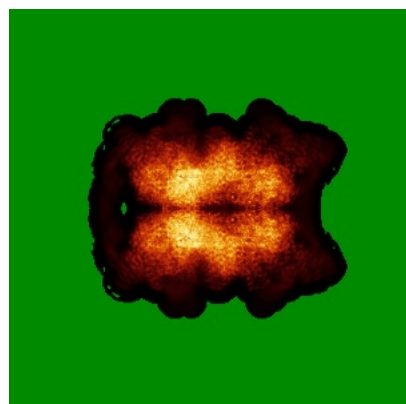


Z Index: 143

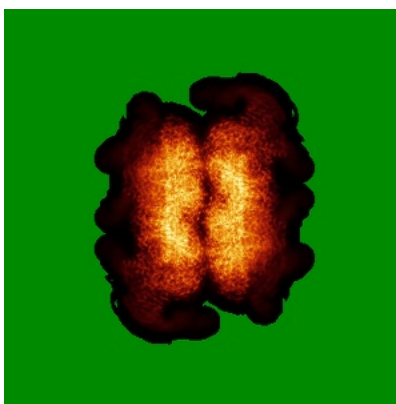
The images above show the largest variance slices of the map in three orthogonal directions.

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

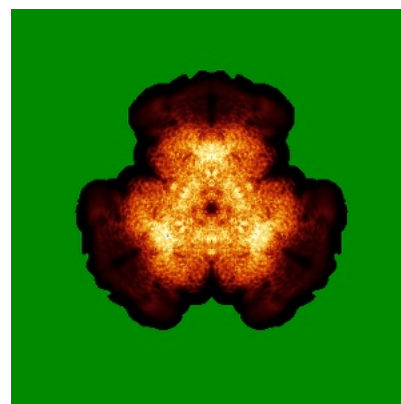
6.4.1 Primary map



X

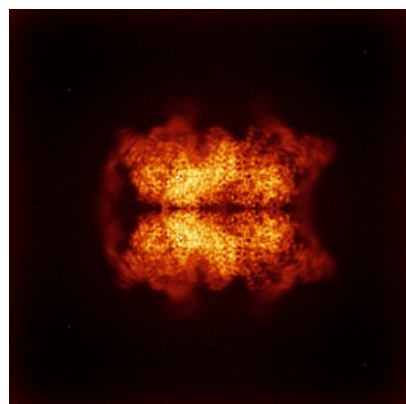


Y

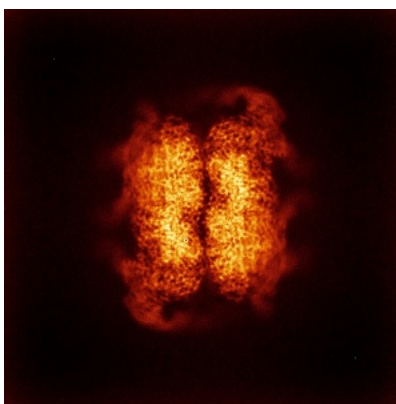


Z

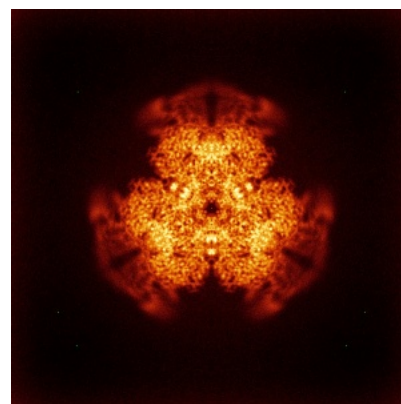
6.4.2 Raw map



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



The images above show the 3D surface view of the map at the recommended contour level 0.11. 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.

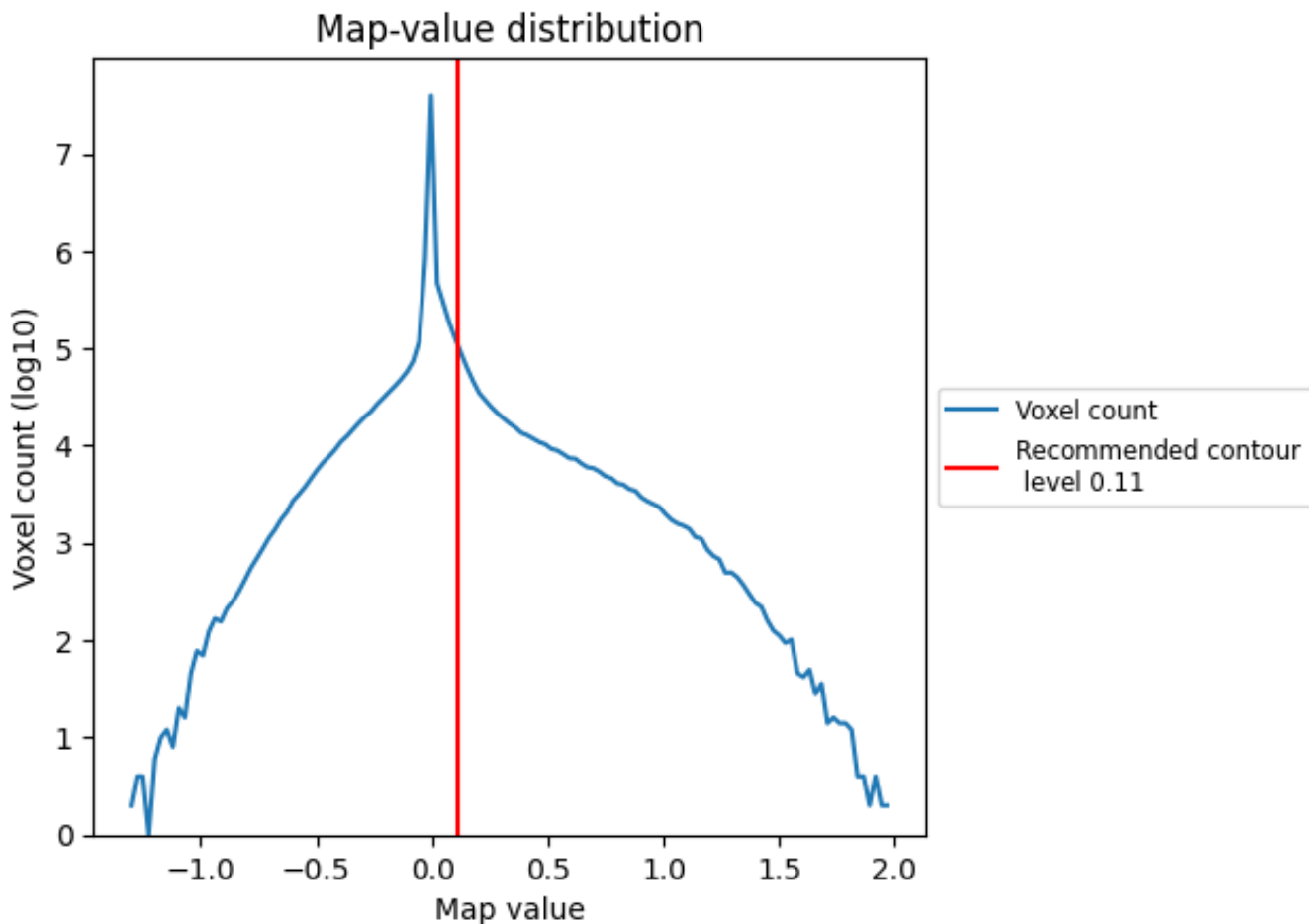
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

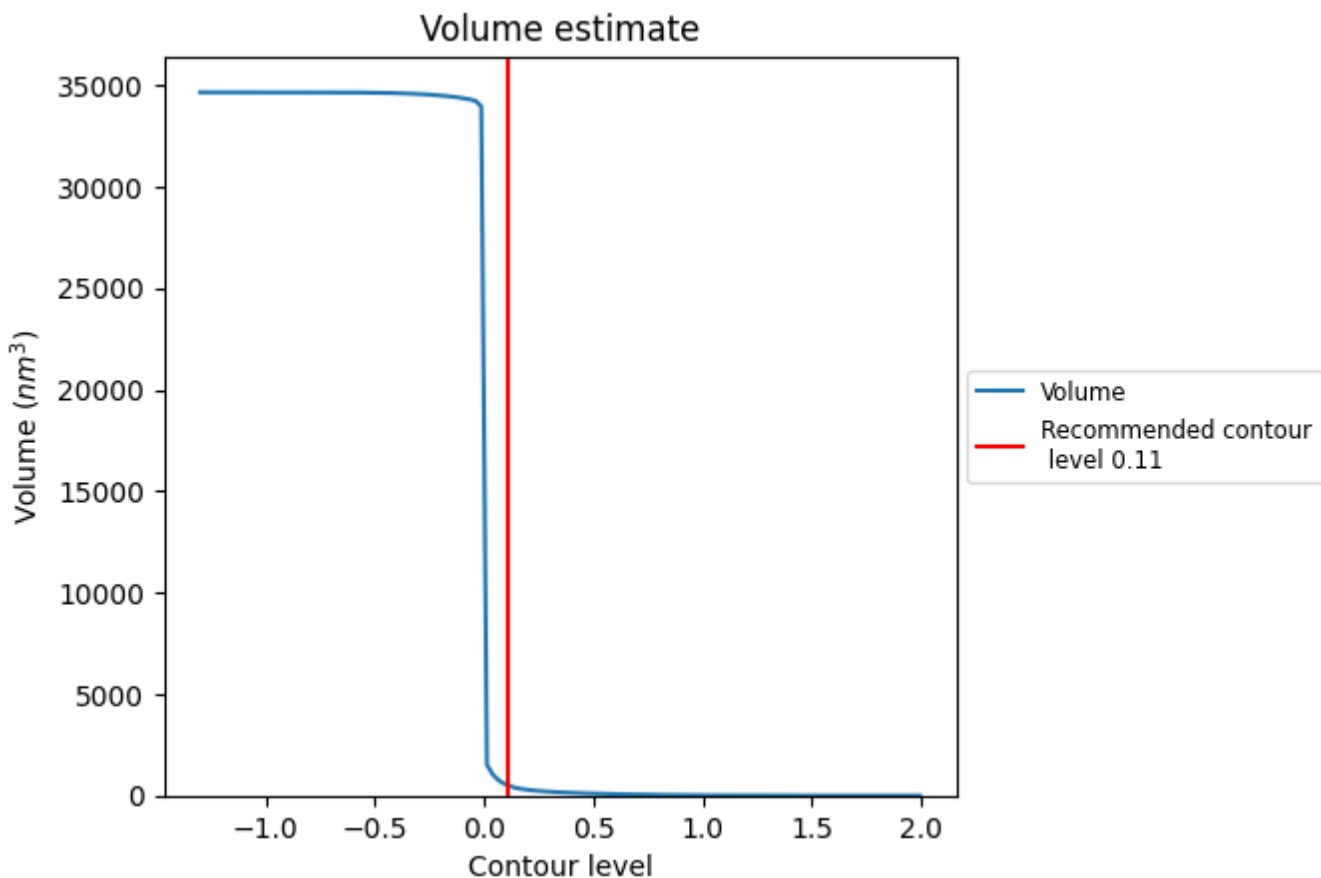
This section contains the results of statistical analysis of the map.

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.

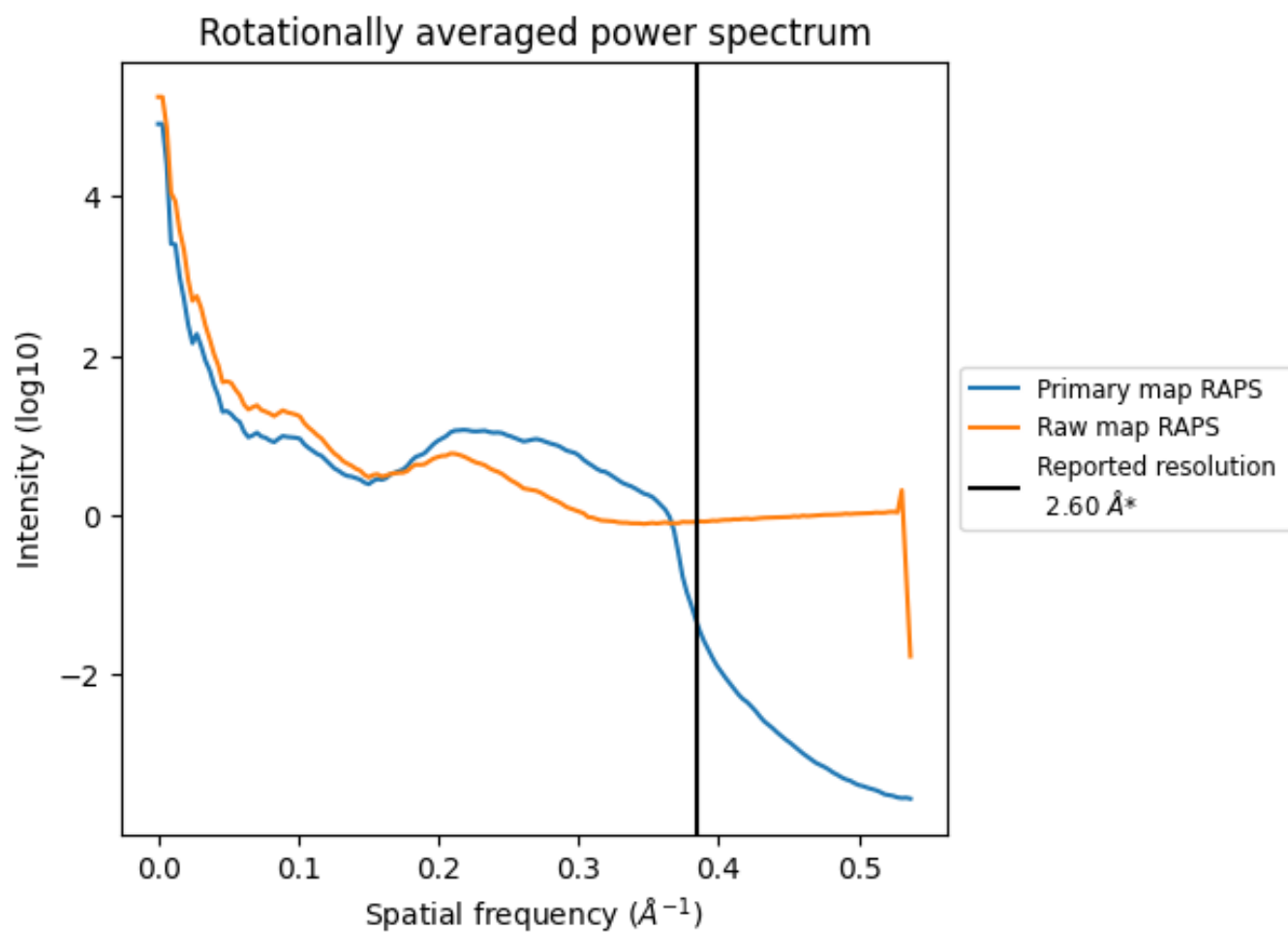
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 495 nm³; this corresponds to an approximate mass of 448 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

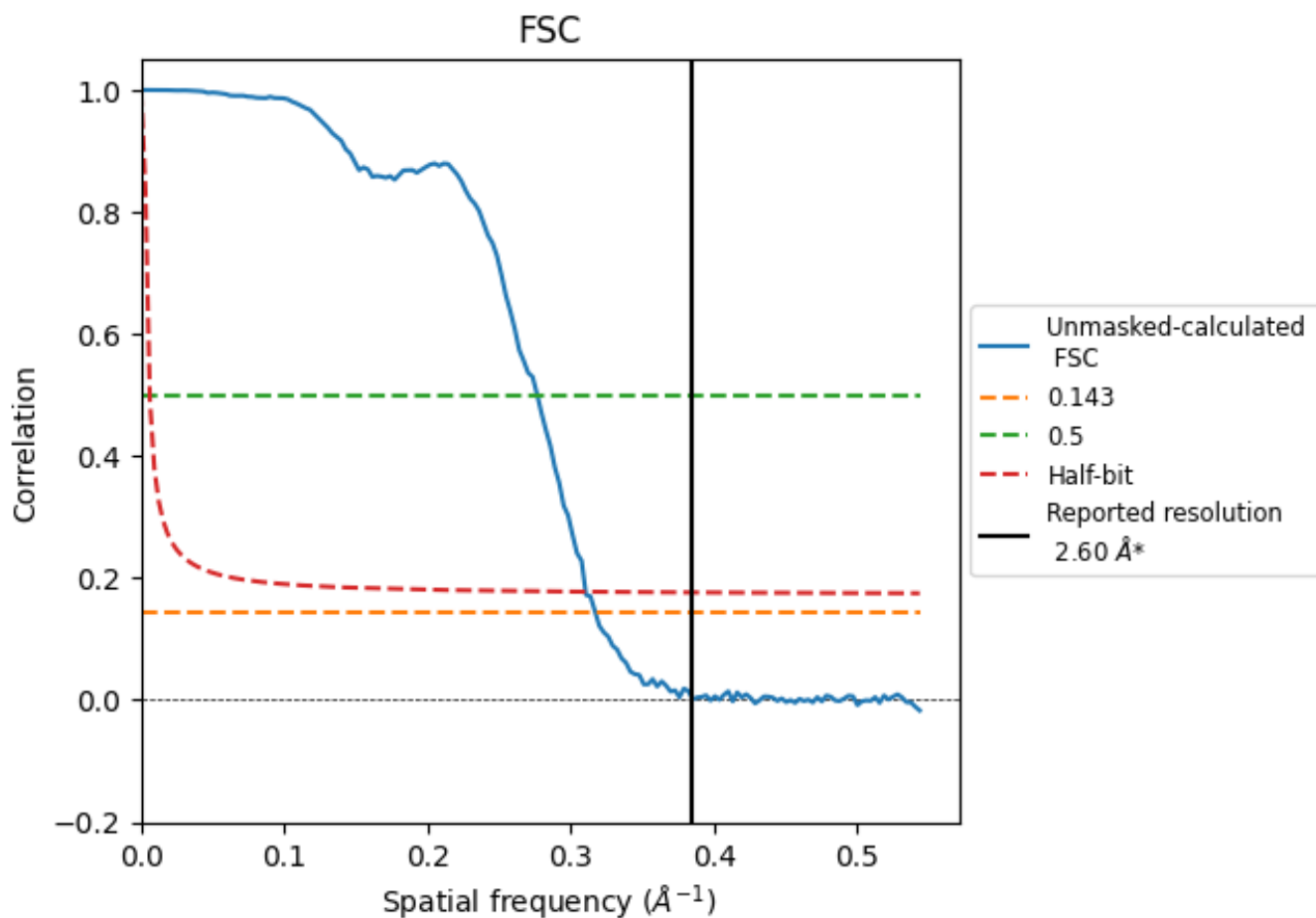


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

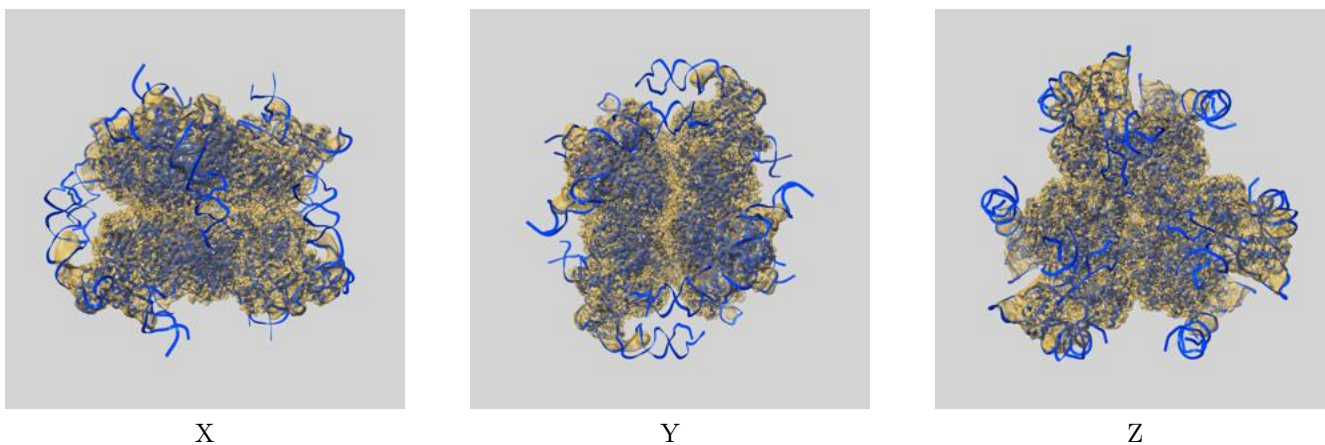
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.15	3.62	3.22

*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 3.15 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

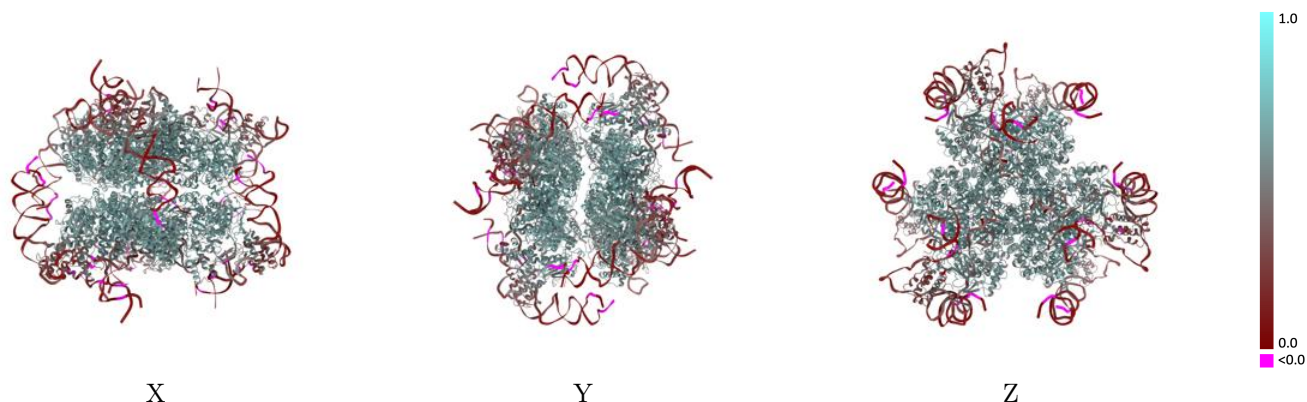
This section contains information regarding the fit between EMDB map EMD-73865 and PDB model 9Z6Z. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



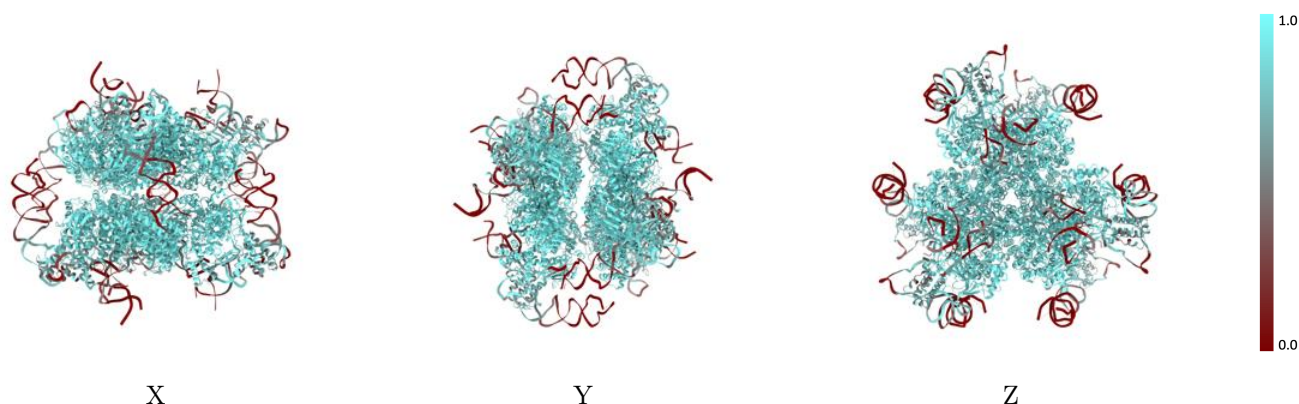
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



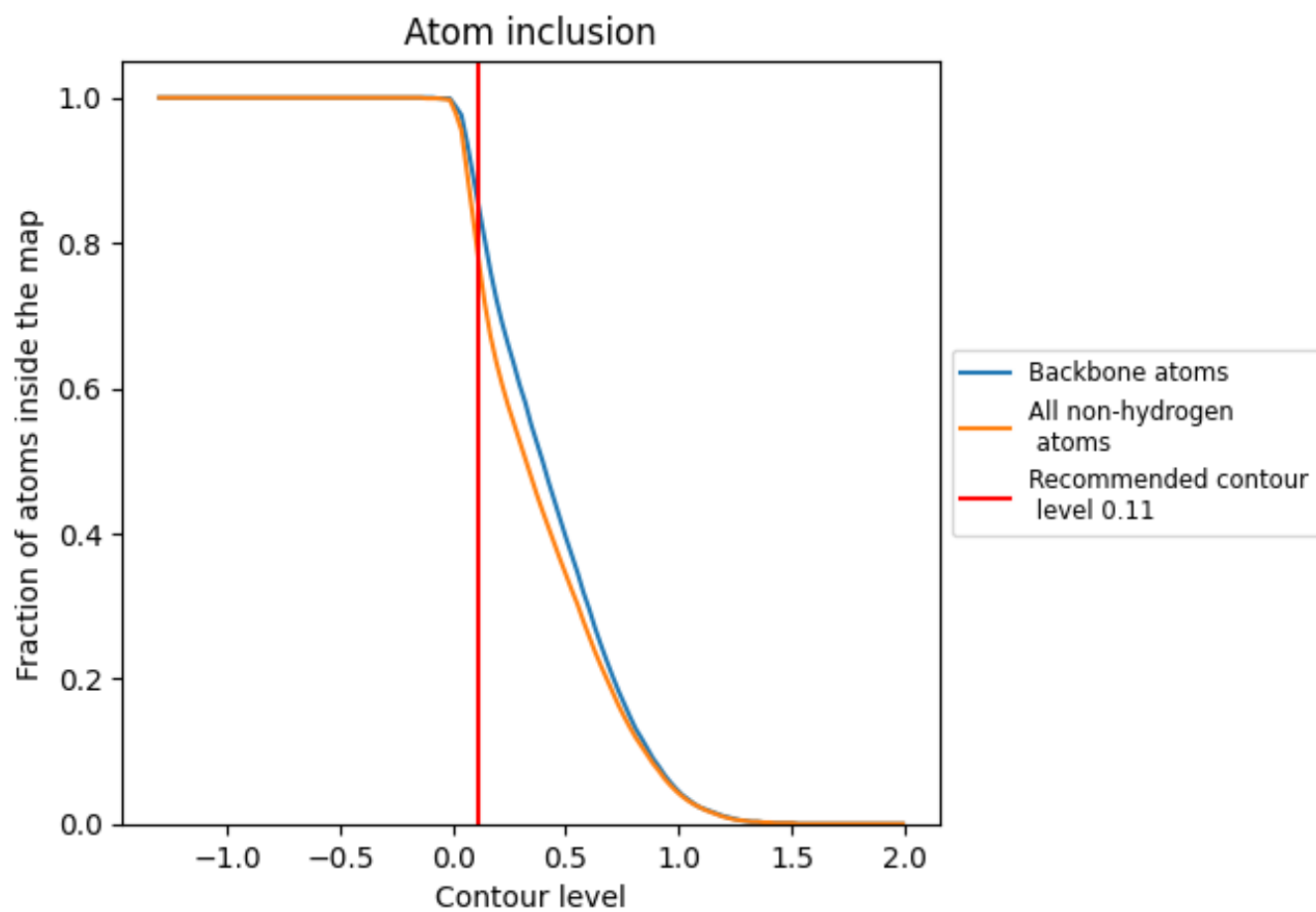
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.11).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 78% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.4800
A	 0.8260	 0.4790
B	 0.8280	 0.4860
C	 0.8300	 0.4860
D	 0.8340	 0.4860
E	 0.8300	 0.4870
F	 0.8300	 0.4860
H	 0.9590	 0.6210
I	 0.9580	 0.6200
J	 0.9580	 0.6210
K	 0.9580	 0.6220
L	 0.9580	 0.6190
M	 0.9580	 0.6200
R	 0.3870	 0.1730
S	 0.3860	 0.1740
T	 0.3870	 0.1750
U	 0.3880	 0.1750
V	 0.3860	 0.1770
W	 0.3870	 0.1760
X	 0.5800	 0.3930
Y	 0.6600	 0.4650
Z	 0.5720	 0.3950
a	 0.6510	 0.4600
b	 0.5720	 0.3970
c	 0.6540	 0.4580
d	 0.5840	 0.3960
e	 0.6570	 0.4580
f	 0.5680	 0.3940
g	 0.6510	 0.4590
h	 0.5760	 0.3960
i	 0.6540	 0.4580

