



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:17 PM UTC

PDB ID : 5NSS / pdb_00005nss
EMDB ID : EMD-3696
Title : Cryo-EM structure of RNA polymerase-sigma54 holoenzyme with promoter
DNA and transcription activator PspF intermediate complex
Authors : Glyde, R.; Ye, F.Z.; Darbari, V.C.; Zhang, N.; Buck, M.; Zhang, X.D.
Deposited on : 2017-04-26
Resolution : 5.80 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:

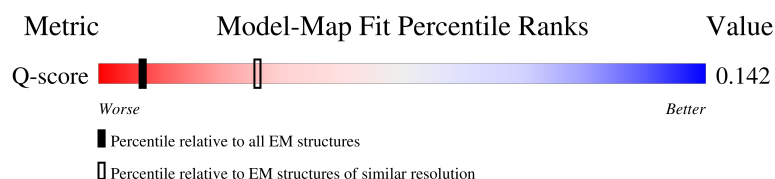
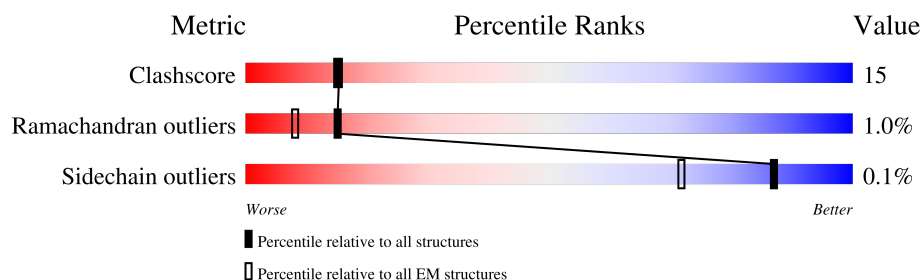
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 5.80 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	511 (5.30 - 6.30)

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	329	
1	B	329	
2	C	1342	
3	D	1449	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	E	91	 8% 58% 23% 19%
5	F	295	 1% 74% 11% 16%
5	G	295	 1% 75% 9% 15%
5	J	295	 74% 11% 15%
5	K	295	 1% 76% 8% 16%
5	L	295	 75% 9% 15%
5	N	295	 76% 9% 15%
6	H	63	 10% 10% 38% 8% 44%
7	M	581	 9% 60% 6% 33%
8	I	63	 6% 5% 40% 5% 51%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 32252 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	238	Total	C	N	O	S	0	0
			1691	1057	301	327	6		
1	B	235	Total	C	N	O	S	0	0
			1665	1040	295	325	5		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0
			9347	5862	1629	1823	33		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta',DNA-directed RNA polymerase subunit beta',DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1352	Total	C	N	O	S	0	0
			8312	5137	1533	1616	26		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	74	Total	C	N	O	S	0	0
			520	320	98	101	1		

- Molecule 5 is a protein called Psp operon transcriptional activator.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	248	Total	C	N	O		0	0
			1222	726	248	248			
5	G	251	Total	C	N	O		0	0
			1237	735	251	251			
5	J	251	Total	C	N	O		0	0
			1237	735	251	251			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
5	K	248	Total	C	N	O	0	0
			1222	726	248	248		
5	L	250	Total	C	N	O	0	0
			1232	732	250	250		
5	N	251	Total	C	N	O	0	0
			1237	735	251	251		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	MET	-	initiating methionine	UNP P37344
F	-18	GLY	-	expression tag	UNP P37344
F	-17	SER	-	expression tag	UNP P37344
F	-16	SER	-	expression tag	UNP P37344
F	-15	HIS	-	expression tag	UNP P37344
F	-14	HIS	-	expression tag	UNP P37344
F	-13	HIS	-	expression tag	UNP P37344
F	-12	HIS	-	expression tag	UNP P37344
F	-11	HIS	-	expression tag	UNP P37344
F	-10	HIS	-	expression tag	UNP P37344
F	-9	SER	-	expression tag	UNP P37344
F	-8	SER	-	expression tag	UNP P37344
F	-7	GLY	-	expression tag	UNP P37344
F	-6	LEU	-	expression tag	UNP P37344
F	-5	VAL	-	expression tag	UNP P37344
F	-4	PRO	-	expression tag	UNP P37344
F	-3	ARG	-	expression tag	UNP P37344
F	-2	GLY	-	expression tag	UNP P37344
F	-1	SER	-	expression tag	UNP P37344
F	0	HIS	-	expression tag	UNP P37344
G	-19	MET	-	initiating methionine	UNP P37344
G	-18	GLY	-	expression tag	UNP P37344
G	-17	SER	-	expression tag	UNP P37344
G	-16	SER	-	expression tag	UNP P37344
G	-15	HIS	-	expression tag	UNP P37344
G	-14	HIS	-	expression tag	UNP P37344
G	-13	HIS	-	expression tag	UNP P37344
G	-12	HIS	-	expression tag	UNP P37344
G	-11	HIS	-	expression tag	UNP P37344
G	-10	HIS	-	expression tag	UNP P37344
G	-9	SER	-	expression tag	UNP P37344
G	-8	SER	-	expression tag	UNP P37344

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	-7	GLY	-	expression tag	UNP P37344
G	-6	LEU	-	expression tag	UNP P37344
G	-5	VAL	-	expression tag	UNP P37344
G	-4	PRO	-	expression tag	UNP P37344
G	-3	ARG	-	expression tag	UNP P37344
G	-2	GLY	-	expression tag	UNP P37344
G	-1	SER	-	expression tag	UNP P37344
G	0	HIS	-	expression tag	UNP P37344
J	-19	MET	-	initiating methionine	UNP P37344
J	-18	GLY	-	expression tag	UNP P37344
J	-17	SER	-	expression tag	UNP P37344
J	-16	SER	-	expression tag	UNP P37344
J	-15	HIS	-	expression tag	UNP P37344
J	-14	HIS	-	expression tag	UNP P37344
J	-13	HIS	-	expression tag	UNP P37344
J	-12	HIS	-	expression tag	UNP P37344
J	-11	HIS	-	expression tag	UNP P37344
J	-10	HIS	-	expression tag	UNP P37344
J	-9	SER	-	expression tag	UNP P37344
J	-8	SER	-	expression tag	UNP P37344
J	-7	GLY	-	expression tag	UNP P37344
J	-6	LEU	-	expression tag	UNP P37344
J	-5	VAL	-	expression tag	UNP P37344
J	-4	PRO	-	expression tag	UNP P37344
J	-3	ARG	-	expression tag	UNP P37344
J	-2	GLY	-	expression tag	UNP P37344
J	-1	SER	-	expression tag	UNP P37344
J	0	HIS	-	expression tag	UNP P37344
K	-19	MET	-	initiating methionine	UNP P37344
K	-18	GLY	-	expression tag	UNP P37344
K	-17	SER	-	expression tag	UNP P37344
K	-16	SER	-	expression tag	UNP P37344
K	-15	HIS	-	expression tag	UNP P37344
K	-14	HIS	-	expression tag	UNP P37344
K	-13	HIS	-	expression tag	UNP P37344
K	-12	HIS	-	expression tag	UNP P37344
K	-11	HIS	-	expression tag	UNP P37344
K	-10	HIS	-	expression tag	UNP P37344
K	-9	SER	-	expression tag	UNP P37344
K	-8	SER	-	expression tag	UNP P37344
K	-7	GLY	-	expression tag	UNP P37344
K	-6	LEU	-	expression tag	UNP P37344

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
K	-5	VAL	-	expression tag	UNP P37344
K	-4	PRO	-	expression tag	UNP P37344
K	-3	ARG	-	expression tag	UNP P37344
K	-2	GLY	-	expression tag	UNP P37344
K	-1	SER	-	expression tag	UNP P37344
K	0	HIS	-	expression tag	UNP P37344
L	-19	MET	-	initiating methionine	UNP P37344
L	-18	GLY	-	expression tag	UNP P37344
L	-17	SER	-	expression tag	UNP P37344
L	-16	SER	-	expression tag	UNP P37344
L	-15	HIS	-	expression tag	UNP P37344
L	-14	HIS	-	expression tag	UNP P37344
L	-13	HIS	-	expression tag	UNP P37344
L	-12	HIS	-	expression tag	UNP P37344
L	-11	HIS	-	expression tag	UNP P37344
L	-10	HIS	-	expression tag	UNP P37344
L	-9	SER	-	expression tag	UNP P37344
L	-8	SER	-	expression tag	UNP P37344
L	-7	GLY	-	expression tag	UNP P37344
L	-6	LEU	-	expression tag	UNP P37344
L	-5	VAL	-	expression tag	UNP P37344
L	-4	PRO	-	expression tag	UNP P37344
L	-3	ARG	-	expression tag	UNP P37344
L	-2	GLY	-	expression tag	UNP P37344
L	-1	SER	-	expression tag	UNP P37344
L	0	HIS	-	expression tag	UNP P37344
N	-19	MET	-	initiating methionine	UNP P37344
N	-18	GLY	-	expression tag	UNP P37344
N	-17	SER	-	expression tag	UNP P37344
N	-16	SER	-	expression tag	UNP P37344
N	-15	HIS	-	expression tag	UNP P37344
N	-14	HIS	-	expression tag	UNP P37344
N	-13	HIS	-	expression tag	UNP P37344
N	-12	HIS	-	expression tag	UNP P37344
N	-11	HIS	-	expression tag	UNP P37344
N	-10	HIS	-	expression tag	UNP P37344
N	-9	SER	-	expression tag	UNP P37344
N	-8	SER	-	expression tag	UNP P37344
N	-7	GLY	-	expression tag	UNP P37344
N	-6	LEU	-	expression tag	UNP P37344
N	-5	VAL	-	expression tag	UNP P37344
N	-4	PRO	-	expression tag	UNP P37344

Continued on next page...

Chain	Residue	Modelled	Actual	Comment	Reference
N	-3	ARG	-	expression tag	UNP P37344
N	-2	GLY	-	expression tag	UNP P37344
N	-1	SER	-	expression tag	UNP P37344
N	0	HIS	-	expression tag	UNP P37344

- | Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|---------|---------|-------|
| 6 | H | 35 | Total
719 | C
340 | N
134 | O
210 | P
35 | 0 | 0 |

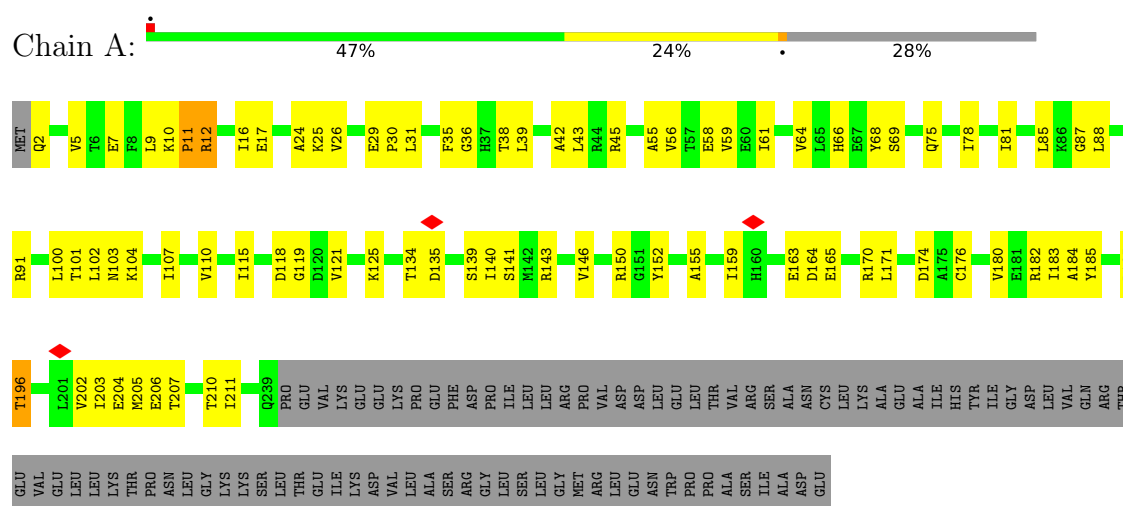
- | Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|---------|-------|
| 7 | M | 388 | Total
1977 | C
1191 | N
388 | O
398 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | | | | AltConf | Trace | |
|-----|-------|----------|--------------|----------|----------|----------|---------|-------|---|
| 8 | I | 31 | Total
634 | C
300 | N
117 | O
186 | P
31 | 0 | 0 |

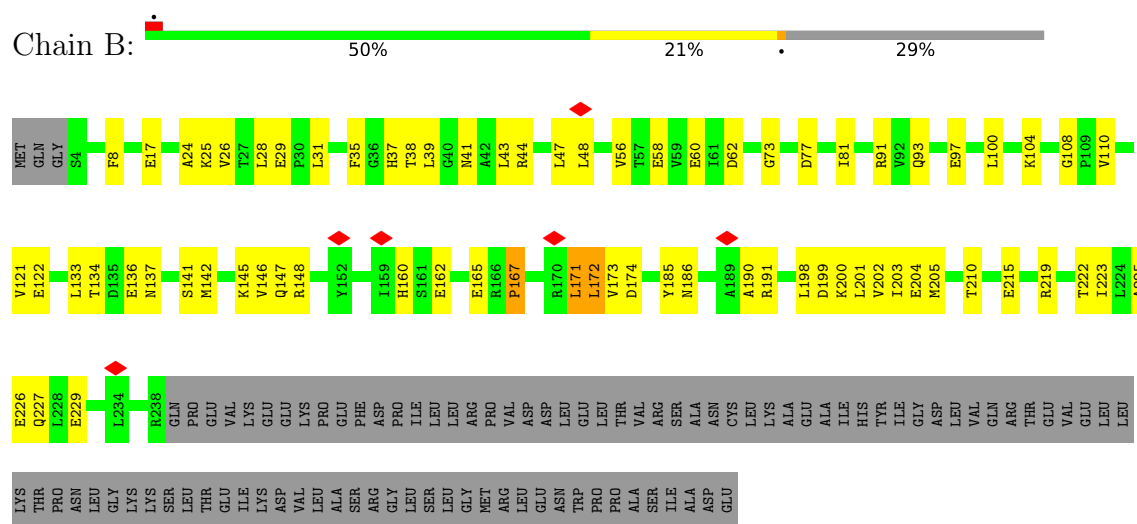
3 Residue-property plots

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: DNA-directed RNA polymerase subunit alpha

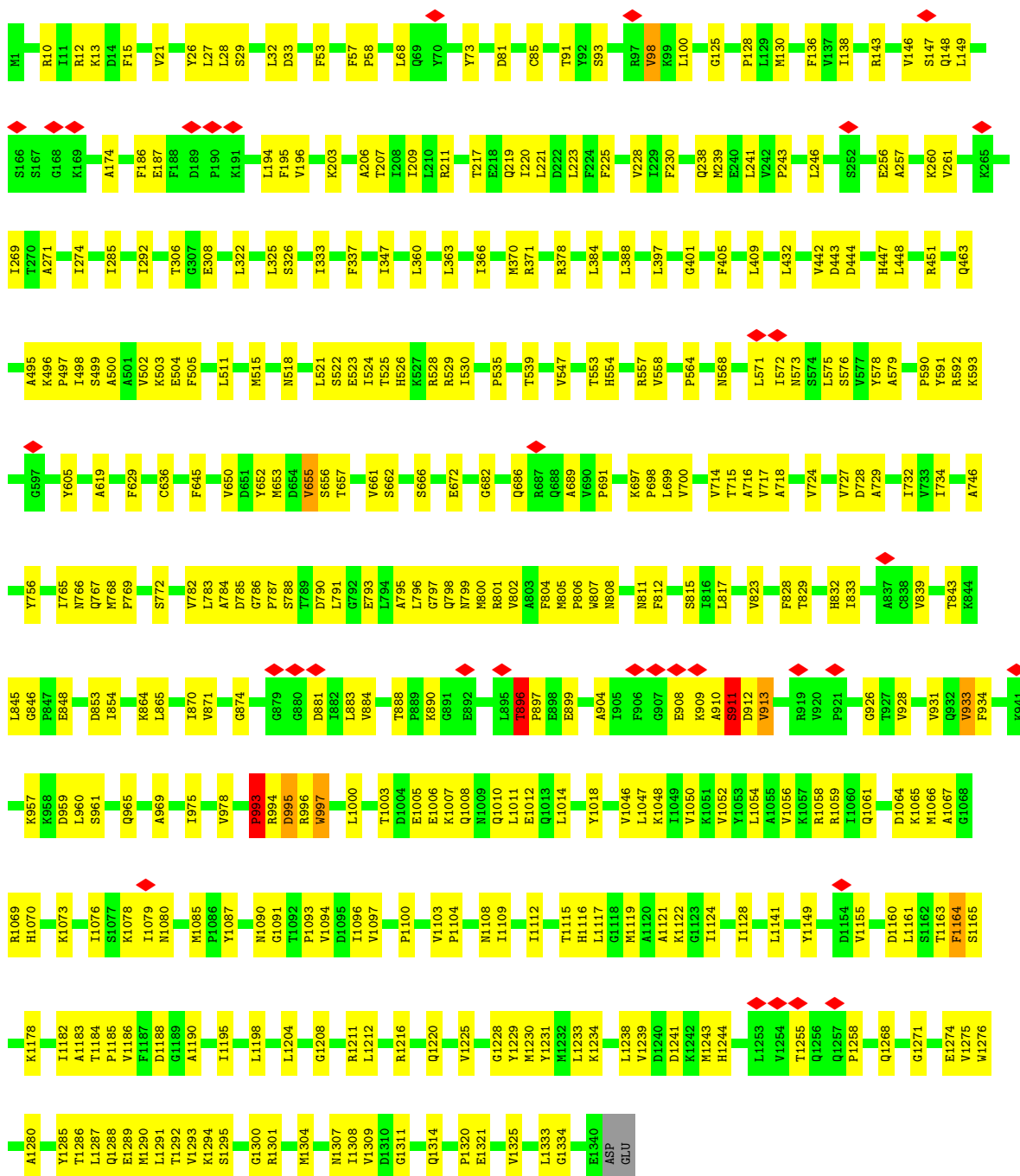


• Molecule 1: DNA-directed RNA polymerase subunit alpha

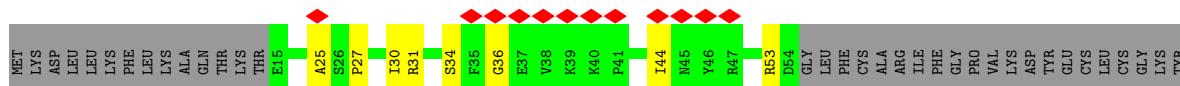


• Molecule 2: DNA-directed RNA polymerase subunit beta

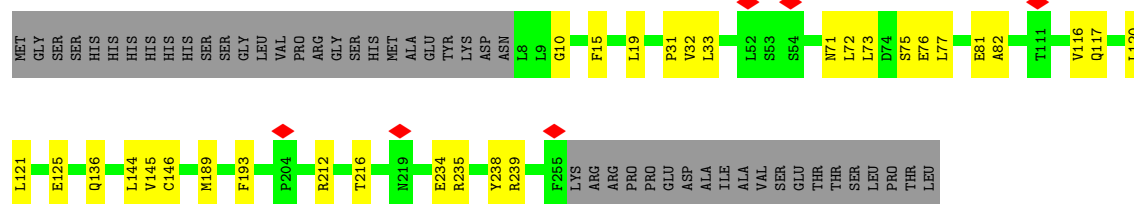




- Molecule 3: DNA-directed RNA polymerase subunit beta',DNA-directed RNA polymerase subunit beta',DNA-directed RNA polymerase subunit beta'

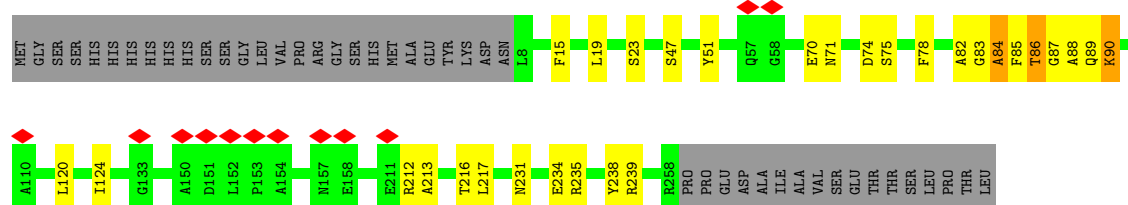


Chain F:  74% 11% 16%



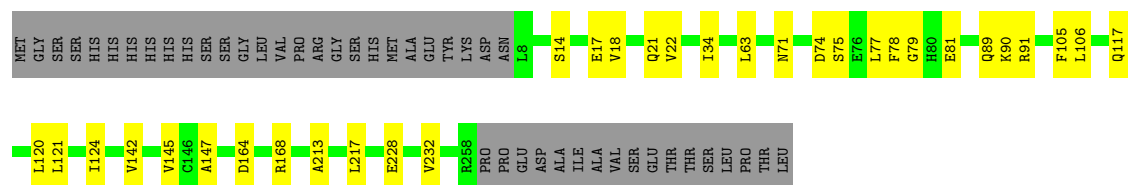
- Molecule 5: Psp operon transcriptional activator

Chain G:  75% 9% 15%



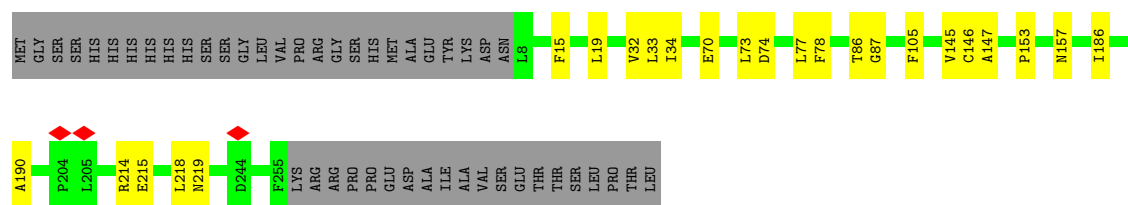
- Molecule 5: Psp operon transcriptional activator

Chain J:  74% 11% 15%



- Molecule 5: Psp operon transcriptional activator

Chain K:  76% 8% 16%



- Molecule 5: Psp operon transcriptional activator

Chain L:  75% 9% 15%





- Molecule 8: Template promoter DNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	79355	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 ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.002	Depositor
Map size (Å)	285.59998, 285.59998, 285.59998	wwPDB
Map dimensions	272, 272, 272	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.13	0/1708	0.38	0/2328
1	B	0.13	0/1680	0.39	1/2291 (0.0%)
2	C	0.13	0/9475	0.40	6/12931 (0.0%)
3	D	0.15	0/8180	0.44	3/11220 (0.0%)
4	E	0.11	0/521	0.34	0/711
5	F	0.12	0/1221	0.36	0/1697
5	G	0.12	0/1236	0.39	3/1718 (0.2%)
5	J	0.12	0/1236	0.43	3/1718 (0.2%)
5	K	0.09	0/1221	0.23	0/1697
5	L	0.12	0/1231	0.39	3/1711 (0.2%)
5	N	0.09	0/1236	0.29	1/1718 (0.1%)
6	H	1.59	2/806 (0.2%)	1.35	11/1242 (0.9%)
7	M	0.22	0/1459	0.80	2/2034 (0.1%)
8	I	0.64	2/709 (0.3%)	0.75	4/1089 (0.4%)
All	All	0.30	4/31919 (0.0%)	0.49	37/44105 (0.1%)

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
2	C	0	1
3	D	0	3
7	M	0	1
All	All	0	5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	68	DT	O3'-P	-32.46	1.12	1.61
6	H	83	DC	O3'-P	-26.63	1.21	1.61
8	I	-22	DC	O3'-P	-8.33	1.48	1.61

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	I	-21	DG	O3'-P	6.68	1.71	1.61

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	83	DC	P-O3'-C3'	29.70	164.75	120.20
6	H	69	DG	P-O3'-C3'	-19.45	91.02	120.20
6	H	83	DC	C5'-C4'-O4'	13.98	130.37	109.40
3	D	180	MET	N-CA-C	10.81	123.06	111.28
8	I	-13	DC	P-O3'-C3'	9.94	135.11	120.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	896	THR	Peptide
3	D	1183	SER	Peptide
3	D	250	ARG	Peptide
3	D	614	LEU	Peptide
7	M	133	PHE	Peptide

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	1691	0	1625	57	0
1	B	1665	0	1603	57	0
2	C	9347	0	8545	280	0
3	D	8312	0	6467	228	0
4	E	520	0	493	16	0
5	F	1222	0	556	16	0
5	G	1237	0	562	18	0
5	J	1237	0	562	18	0
5	K	1222	0	556	12	0
5	L	1232	0	560	18	0
5	N	1237	0	562	16	0
6	H	719	0	395	63	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	M	1977	0	888	36	0
8	I	634	0	349	45	0
All	All	32252	0	23723	827	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 15.

The worst 5 of 827 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)
6:H:68:DT:O3'	6:H:69:DG:P	1.12	1.51
6:H:72:DC:H41	7:M:13:UNK:CB	1.33	1.42
6:H:74:DT:H2''	6:H:75:DG:C5'	1.52	1.40
3:D:366:CYS:SG	3:D:437:PHE:HB2	1.70	1.32
6:H:72:DC:N4	7:M:13:UNK:CB	1.92	1.31

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	234/329 (71%)	211 (90%)	18 (8%)	5 (2%)	5	29
1	B	233/329 (71%)	212 (91%)	17 (7%)	4 (2%)	7	36
2	C	1338/1342 (100%)	1221 (91%)	103 (8%)	14 (1%)	12	48
3	D	1304/1449 (90%)	1161 (89%)	135 (10%)	8 (1%)	21	59
4	E	72/91 (79%)	68 (94%)	4 (6%)	0	100	100
5	F	246/295 (83%)	231 (94%)	14 (6%)	1 (0%)	30	67
5	G	249/295 (84%)	236 (95%)	11 (4%)	2 (1%)	16	54
5	J	249/295 (84%)	232 (93%)	15 (6%)	2 (1%)	16	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	K	246/295 (83%)	229 (93%)	15 (6%)	2 (1%)	16	54
5	L	248/295 (84%)	236 (95%)	10 (4%)	2 (1%)	16	54
5	N	249/295 (84%)	235 (94%)	13 (5%)	1 (0%)	30	67
7	M	276/581 (48%)	233 (84%)	37 (13%)	6 (2%)	5	28
All	All	4944/5891 (84%)	4505 (91%)	392 (8%)	47 (1%)	15	48

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	10	LYS
1	A	11	PRO
1	A	12	ARG
1	A	196	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	166/286 (58%)	166 (100%)	0	100	100
1	B	162/286 (57%)	161 (99%)	1 (1%)	78	82
2	C	857/1157 (74%)	857 (100%)	0	100	100
3	D	509/1168 (44%)	508 (100%)	1 (0%)	87	86
4	E	48/75 (64%)	48 (100%)	0	100	100
7	M	23/423 (5%)	23 (100%)	0	100	100
All	All	1765/3395 (52%)	1763 (100%)	2 (0%)	87	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	172	LEU
3	D	685	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1136	GLN
4	E	43	ASN
3	D	364	HIS
4	E	7	GLN
2	C	1288	GLN

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](#)

There are no ligands in this entry.

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
7	M	3
6	H	2
1	A	1
3	D	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	49:UNK	C	120:LEU	N	59.90
1	M	413:UNK	C	415:ALA	N	4.42
1	A	237:VAL	C	238:ARG	N	3.50
1	M	304:UNK	C	306:MET	N	3.31
1	D	97:UNK	C	99:ARG	N	3.04

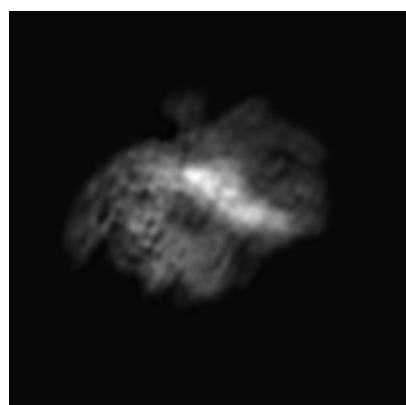
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3696. These allow visual inspection of the internal detail of the map and identification of artifacts.

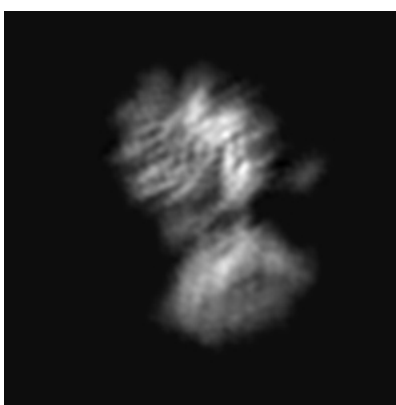
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

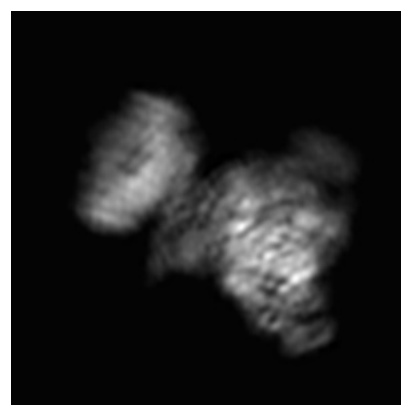
6.1.1 Primary map



X



Y



Z

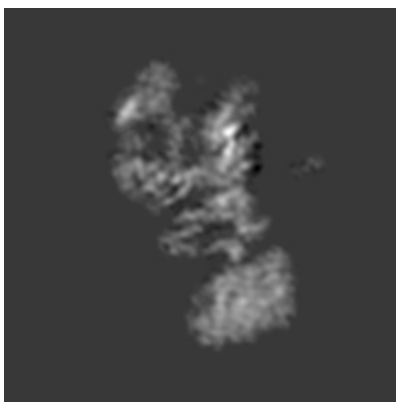
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

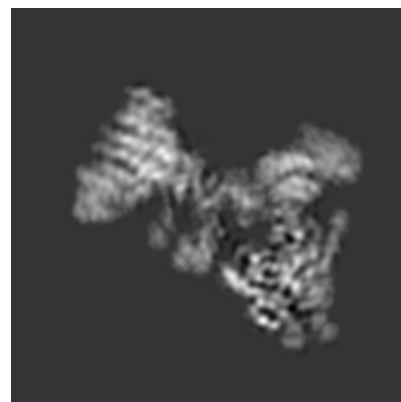
6.2.1 Primary map



X Index: 136



Y Index: 136



Z Index: 136

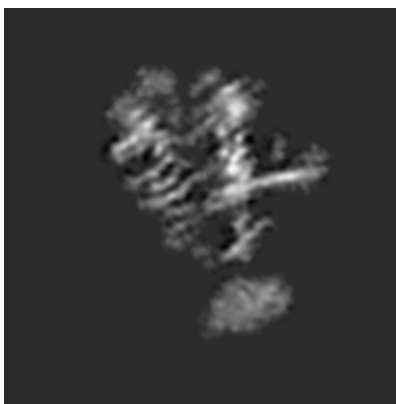
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

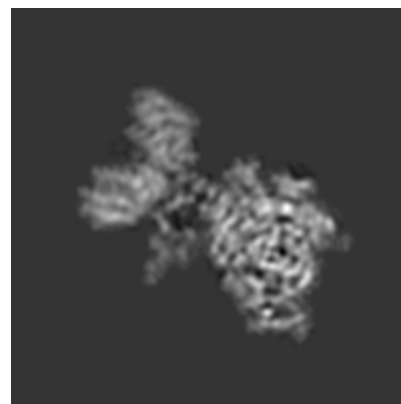
6.3.1 Primary map



X Index: 193



Y Index: 125

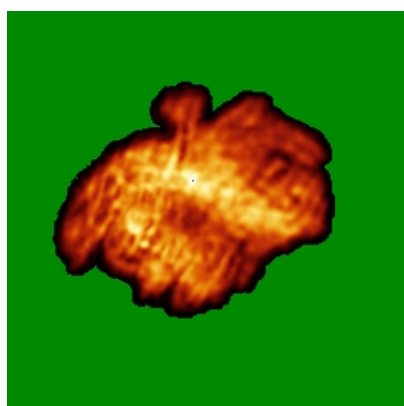


Z Index: 152

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

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

6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.002. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

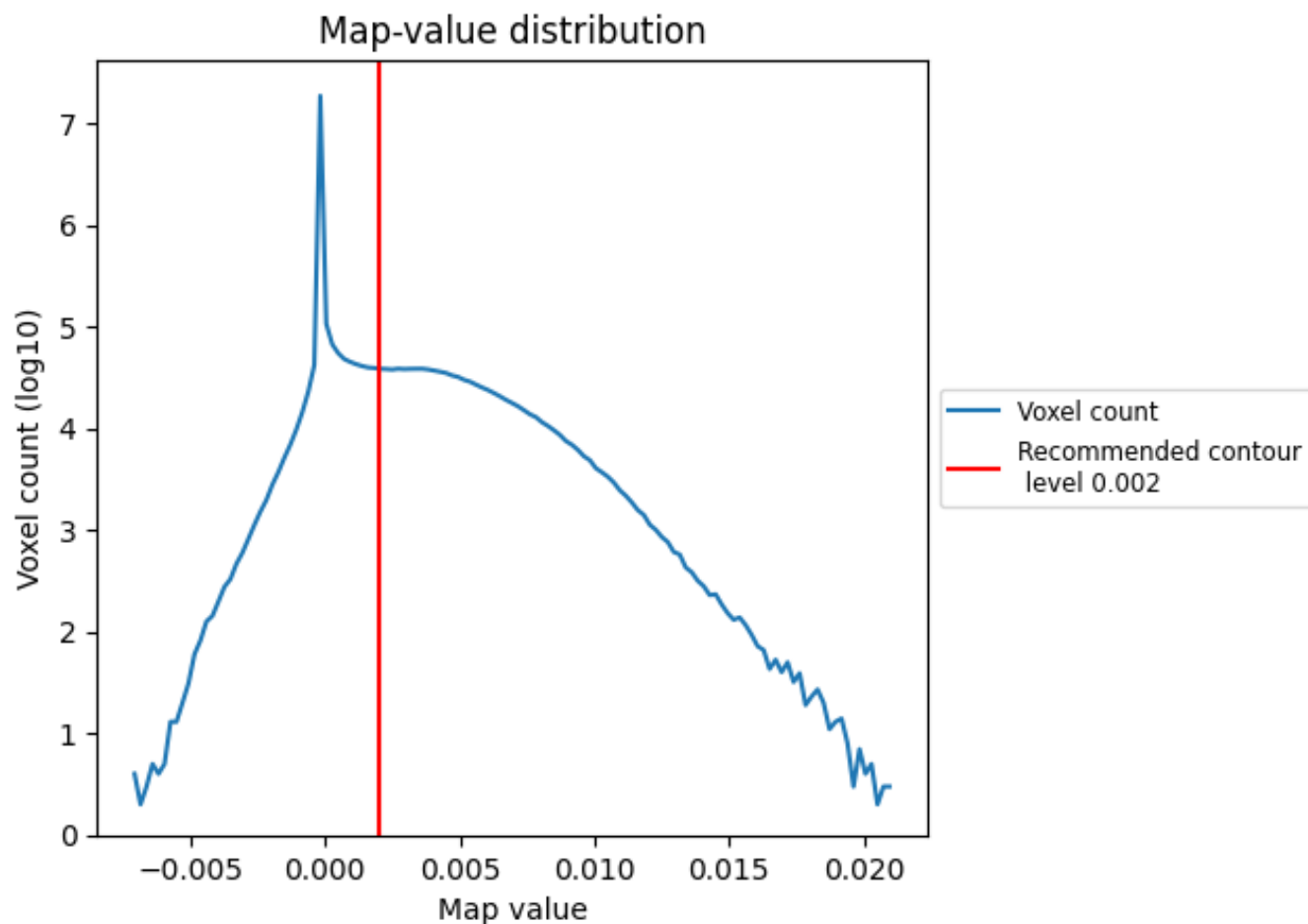
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

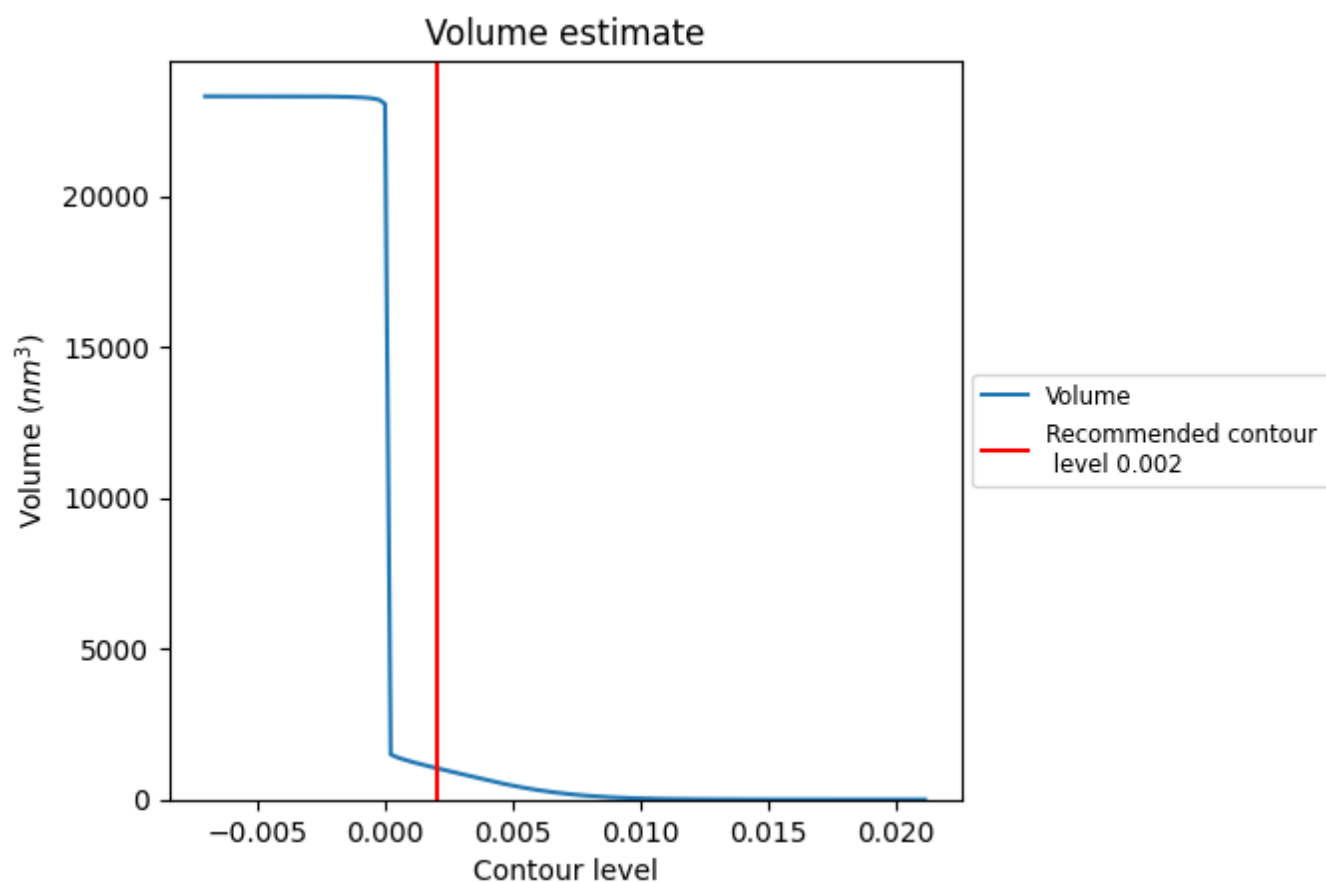
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

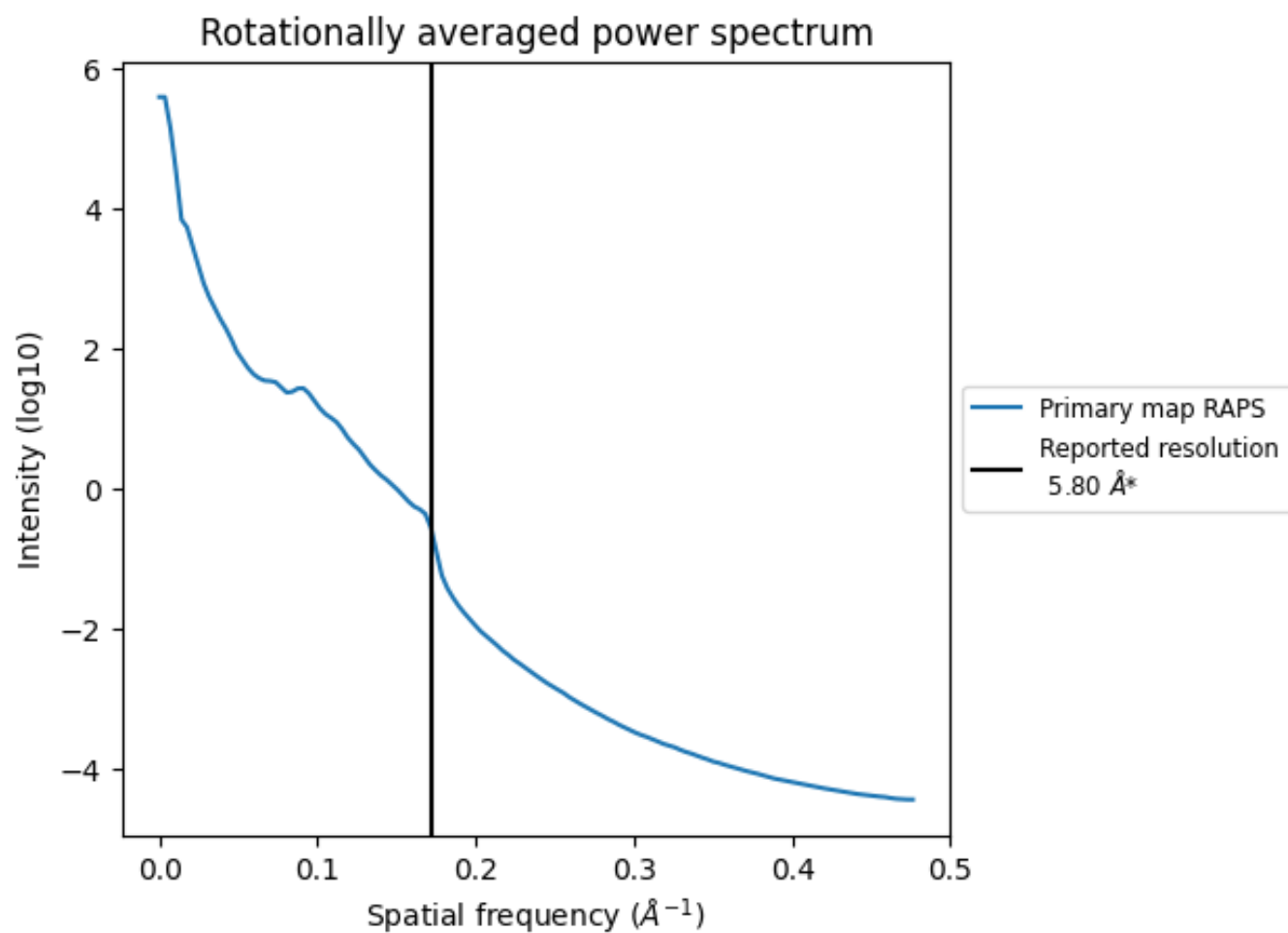
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1044 nm³; this corresponds to an approximate mass of 943 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.172 Å⁻¹

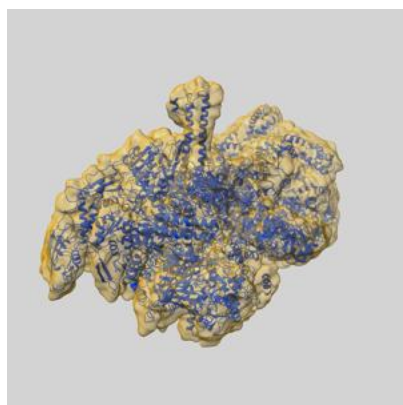
8 Fourier-Shell correlation ⓘ

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

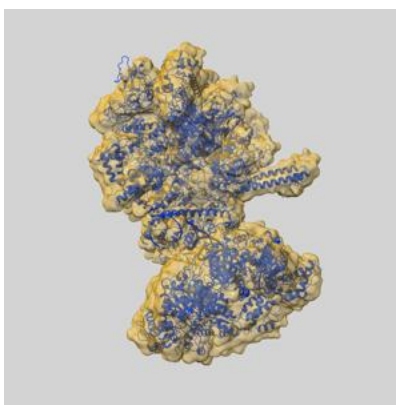
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3696 and PDB model 5NSS. Per-residue inclusion information can be found in section [3](#) on page [9](#).

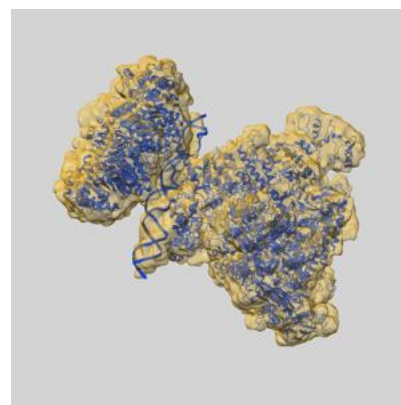
9.1 Map-model overlay [i](#)



X



Y



Z

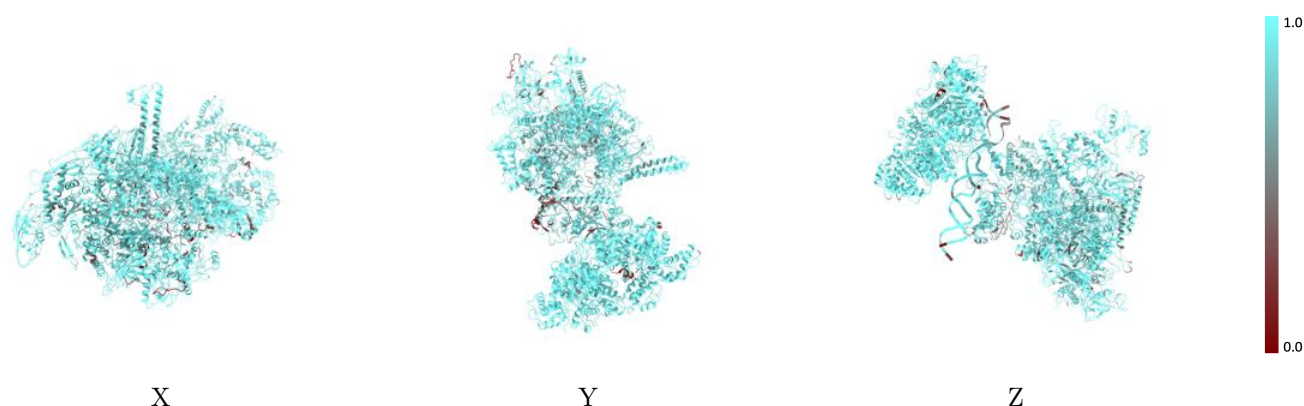
The images above show the 3D surface view of the map at the recommended contour level 0.002 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



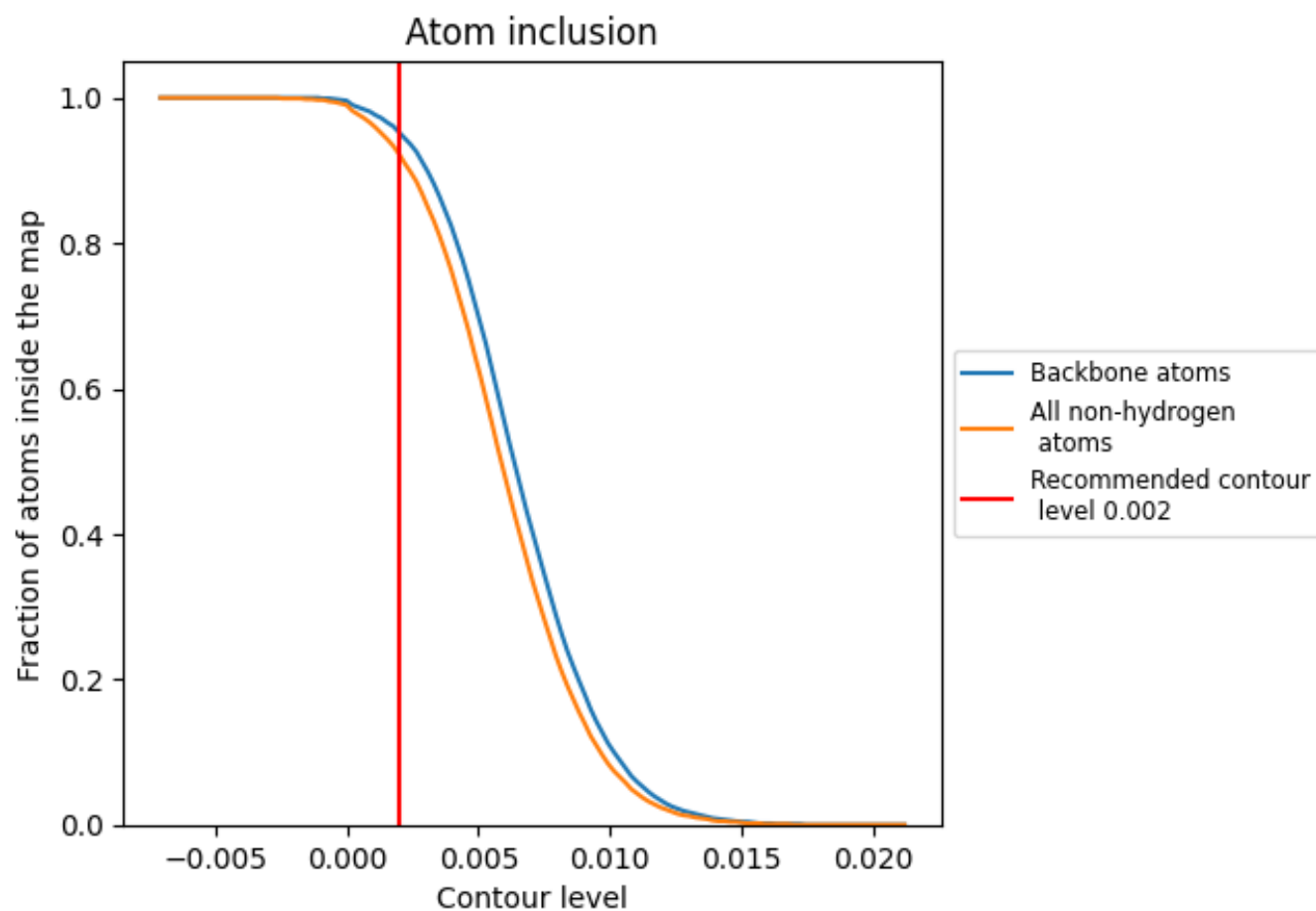
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.002).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.002) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9220	 0.1420
A	 0.9480	 0.1480
B	 0.9140	 0.1500
C	 0.9340	 0.1390
D	 0.9020	 0.1400
E	 0.8610	 0.1320
F	 0.9680	 0.1410
G	 0.9500	 0.1470
H	 0.7270	 0.0970
I	 0.8030	 0.1090
J	 0.9970	 0.1640
K	 0.9890	 0.1730
L	 0.9980	 0.1820
M	 0.8280	 0.1050
N	 0.9940	 0.1700

