



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:40 PM UTC

PDB ID : 7XSD / pdb_00007xsd
EMDB ID : EMD-33524
Title : Cryo-EM structure of RuBisCO assembly intermediate RbcL8Raf18RbcX16
Authors : Jiang, Y.L.; Xia, L.Y.; Zhou, C.Z.
Deposited on : 2022-05-13
Resolution : 3.30 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:

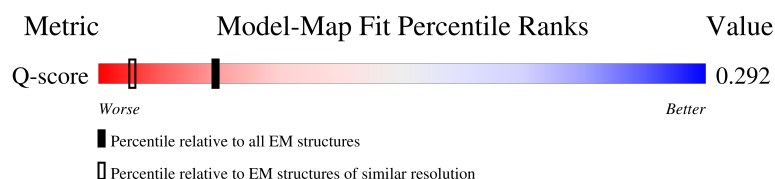
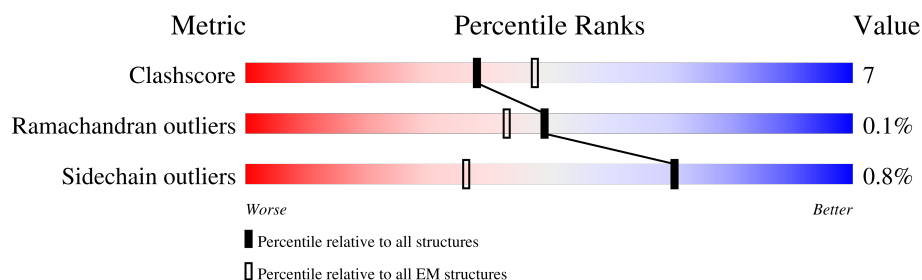
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	1	132	52% 67% 9% 23%
1	2	132	73% 77% 7% 16%
1	3	132	55% 67% 9% 23%
1	4	132	75% 80% 16%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	5	132	
1	6	132	
1	7	132	
1	8	132	
1	Q	132	
1	R	132	
1	S	132	
1	T	132	
1	U	132	
1	V	132	
1	W	132	
1	X	132	
2	I	361	
2	J	361	
2	K	361	
2	L	361	
2	M	361	
2	N	361	
2	O	361	
2	P	361	
3	A	476	
3	B	476	
3	C	476	
3	D	476	
3	E	476	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	476	7% 62% 19% 17%
3	G	476	8% 62% 19% 17%
3	H	476	7% 63% 19% 17%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 49848 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 RuBisCO chaperone RbcX.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	6	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	7	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	8	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	1	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	2	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	3	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	4	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	Q	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	R	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	S	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	T	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	U	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	V	111	Total	C	N	O	S	0	0
			897	566	159	167	5		
1	W	101	Total	C	N	O	S	0	0
			811	514	141	152	4		
1	X	111	Total	C	N	O	S	0	0
			897	566	159	167	5		

- Molecule 2 is a protein called RuBisCO accumulation factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	O	178	Total	C	N	O	0	0
			1421	892	262	267		
2	P	178	Total	C	N	O	0	0
			1421	892	262	267		
2	M	178	Total	C	N	O	0	0
			1421	892	262	267		
2	N	178	Total	C	N	O	0	0
			1421	892	262	267		
2	I	178	Total	C	N	O	0	0
			1421	892	262	267		
2	J	178	Total	C	N	O	0	0
			1421	892	262	267		
2	K	178	Total	C	N	O	0	0
			1421	892	262	267		
2	L	178	Total	C	N	O	0	0
			1421	892	262	267		

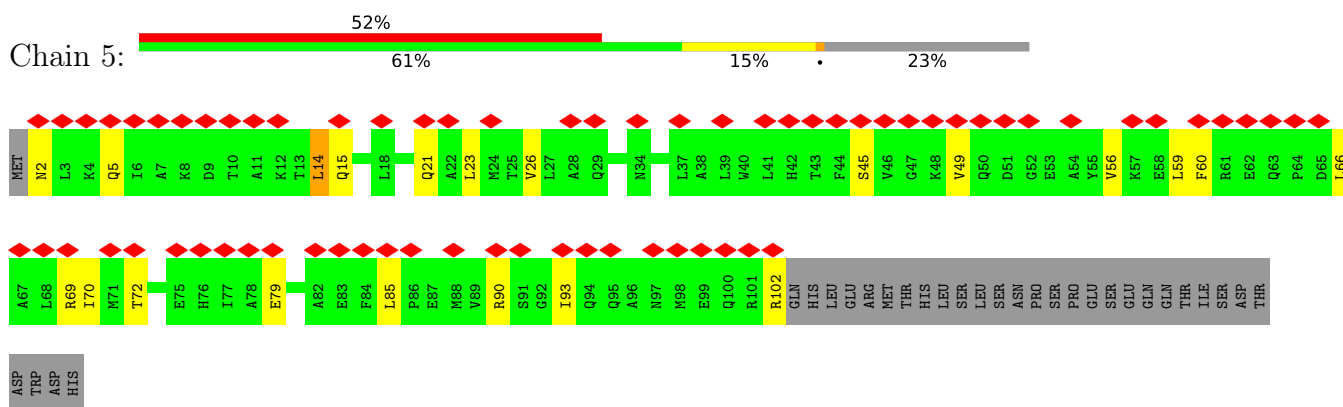
- Molecule 3 is a protein called Ribulose biphosphate carboxylase large chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	H	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	E	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	F	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	A	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	B	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	C	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		
3	D	394	Total	C	N	O	S	0	0
			3102	1977	541	572	12		

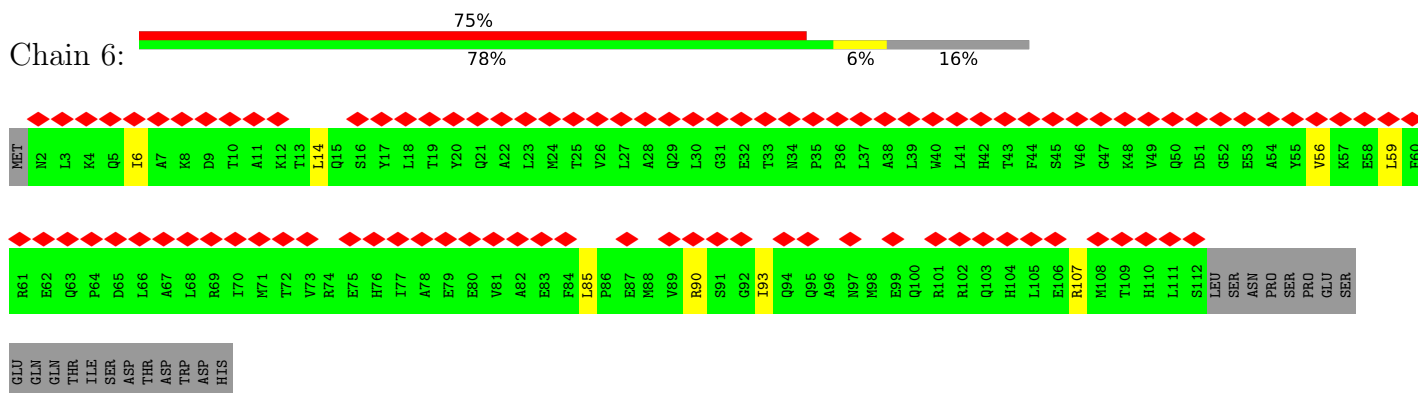
3 Residue-property plots

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.

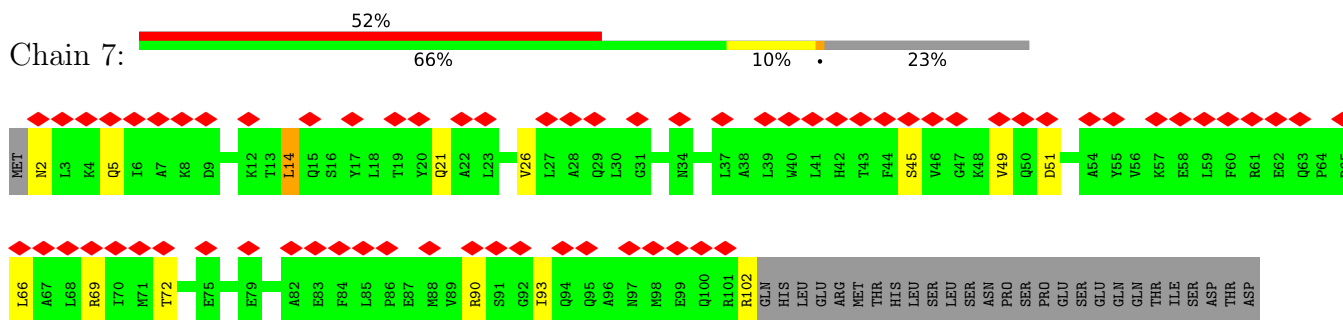
- Molecule 1: RuBisCO chaperone RbcX



- Molecule 1: RuBisCO chaperone RbcX

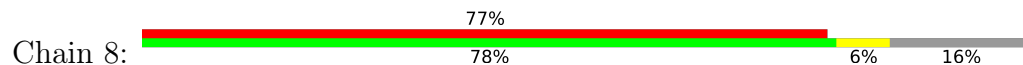


- Molecule 1: RuBisCO chaperone RbcX



TRP
ASP
HIS

● Molecule 1: RuBisCO chaperone RbcX



MET N2 L3 K4 Q5 I6 A7 R8 D9 T10 A11 K12 T13 L14 Q15 S16 Y17 Y18 L19 T20 Q21 A22 L23 M24 T25 V26 L27 A28 Q29 L30 G31 E32 T33 N34 P35 P36 L37 A38 L39 W40 L41 H42 T43 F44 S45 V46 Q47 H48 V49 Q50 D51 S52 E53 A54 Y55 V56 A57 E58 L59 F60

R61 E62 Q63 P64 D65 L66 A67 L68 R69 T70 M71 T72 V73 R74 E75 H76 T77 A78 E79 F80 Y81 A82 E83 F84 L85 P86 E87 M88 S91 Q92 I93 Q94 Q95 M98 E99 Q100 R101 A102 Q103 H104 L105 E106 R107 M108 T109 H110 S112 LEU SER ASN PRO SER PRO GLU GLN

GLN
THR
ILE
SER
ASP
THR
TRP
ASP
HIS

● Molecule 1: RuBisCO chaperone RbcX

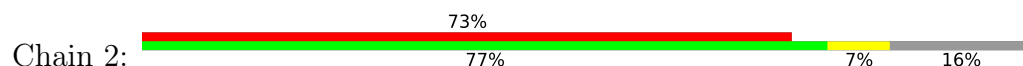


MET N2 L3 Q5 I6 A7 R8 D9 K12 T13 L14 Y17 L18 T19 Y20 Q21 A22 L23 M24 T25 V26 L27 A28 Q29 E32 L37 A38 L39 H42 T43 F44 S45 V46 Q47 K48 V49 Q50 D51 A54 Y55 V56 E58 L59 F60

R69 I70 M71 T72 V73 R74 E75 I77 E80 V81 A82 E83 L85 P86 E87 M88 R90 S91 Q92 I93 Q94 Q95 A96 N97 M98 Q100 R101 R102 GLN HIS LEU GLU ARG MET THR LEU SER LEU SER ASN PRO SER PRO GLU SER GLN THR ILE SER ASP THR ASP

TRP
ASP
HIS

● Molecule 1: RuBisCO chaperone RbcX



MET N2 L3 K4 Q5 I6 A7 R8 D9 T10 A11 K12 T13 L14 Q15 S16 Y17 Y18 T19 Y20 Q21 A22 L23 M24 T25 V26 L27 Q29 L30 G31 E32 T33 N34 P35 P36 L37 A38 L39 W40 L41 H42 T43 F44 S45 V46 Q47 H48 V49 Q50 D51 S52 E53 A54 Y55 V56 A57 E58 L59 F60

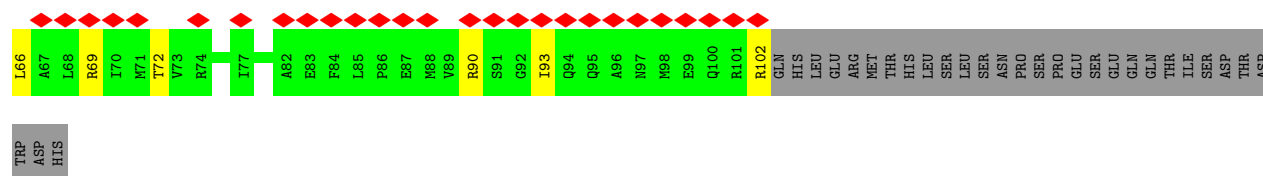
R61 E62 Q63 P64 D65 L66 A67 L68 R69 T70 M71 T72 V73 R74 E75 H76 T77 A78 E79 E80 A81 A82 E83 F84 L85 R90 S91 Q95 A96 N97 M98 E99 Q100 R101 A102 Q103 H104 L105 E106 R107 M108 T109 H110 S112 LEU SER ASN PRO SER PRO GLU GLN THR ILE

SER
ASP
THR
ASP
TRP
ASP
HIS

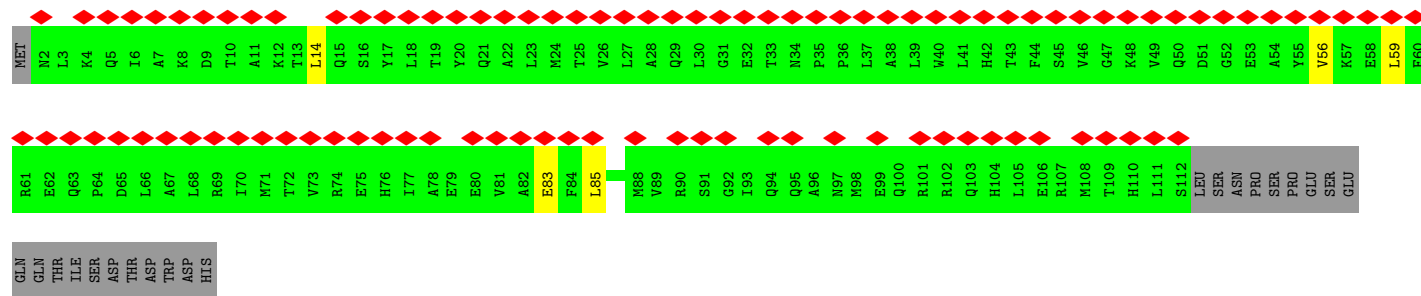
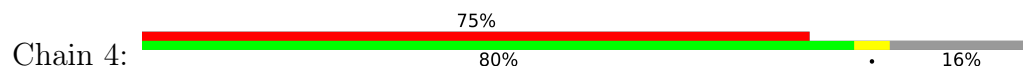
● Molecule 1: RuBisCO chaperone RbcX



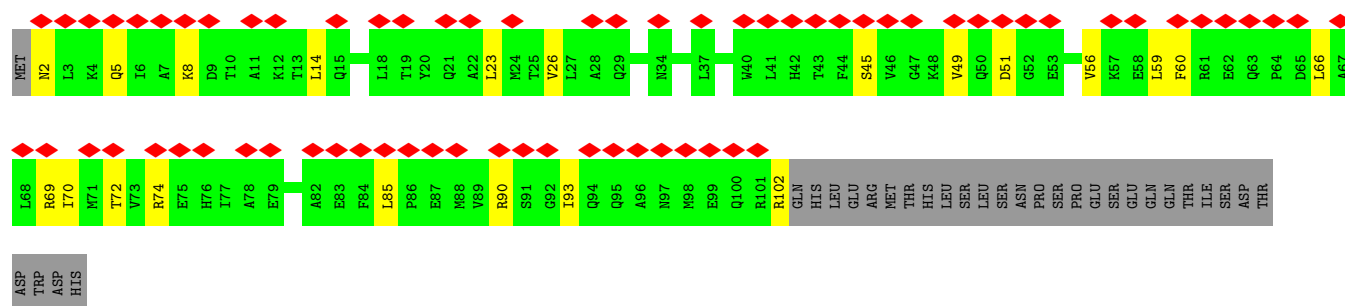
MET N2 L3 K4 Q5 I6 A7 R8 D9 K12 T13 L14 Q15 S16 Y17 L18 T19 Y20 M24 T25 V26 L27 A28 Q29 L30 G31 E32 T33 N34 L37 A38 L39 W40 L41 H42 T43 F44 S45 V46 Q47 K48 V49 Q50 D51 A54 Y55 V56 K57 E58 L59 F60 R61 E62 Q63 P64 D65



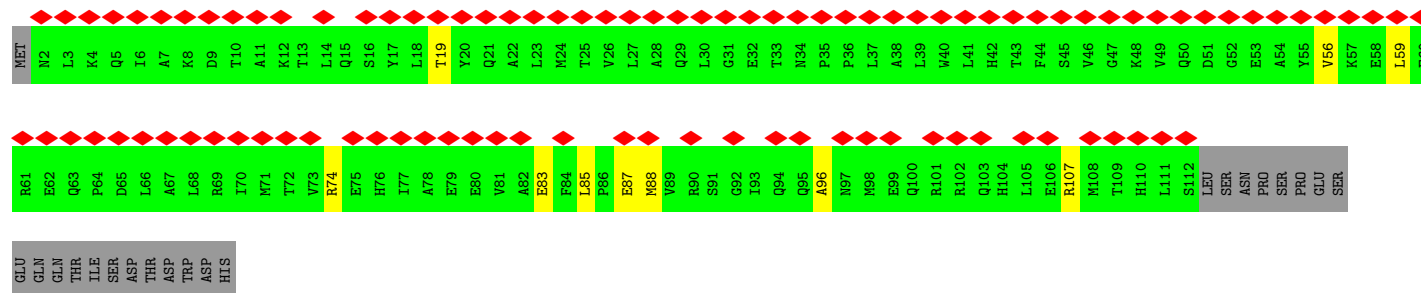
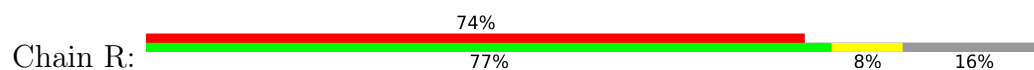
- Molecule 1: RuBisCO chaperone RbcX



- Molecule 1: RuBisCO chaperone RbcX

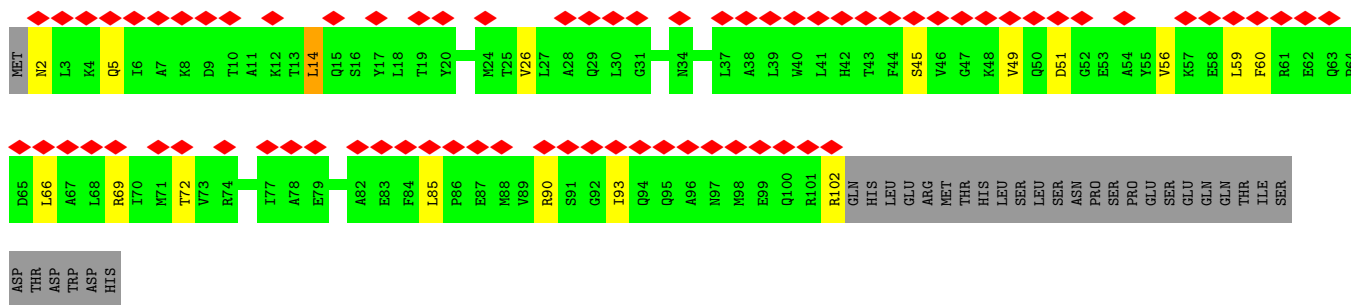


- Molecule 1: RuBisCO chaperone RbcX

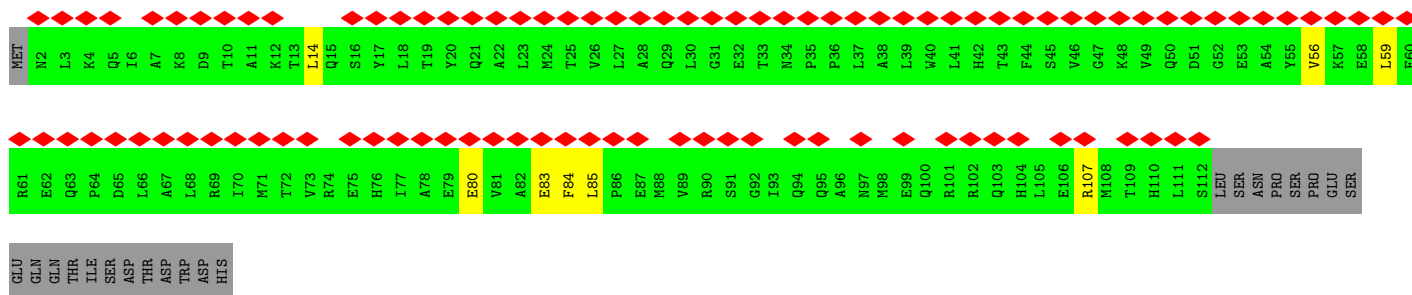
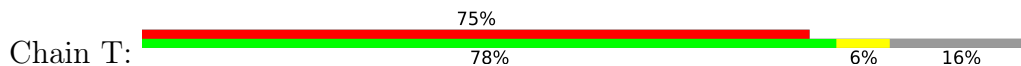


- Molecule 1: RuBisCO chaperone RbcX

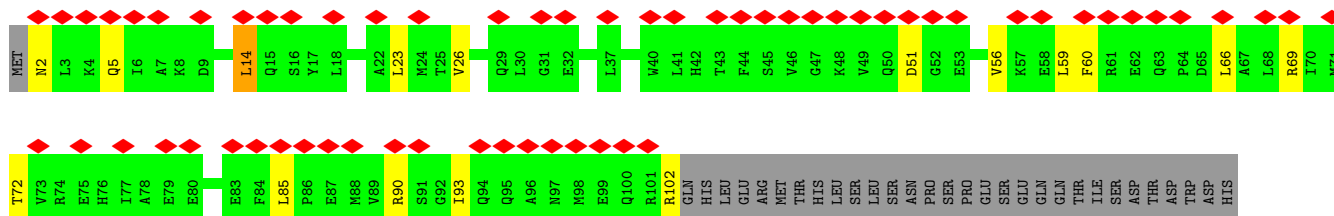




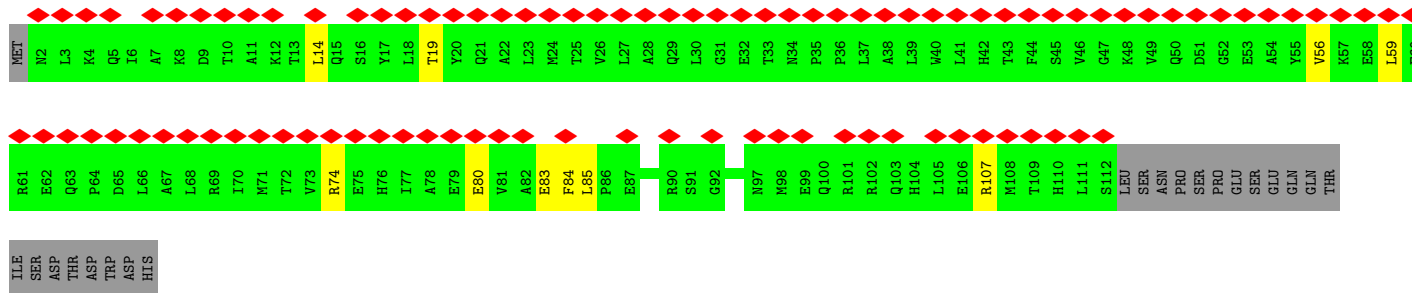
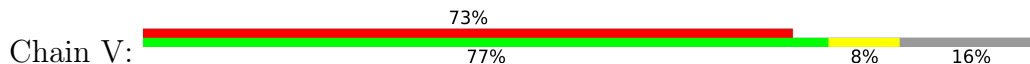
- Molecule 1: RuBisCO chaperone RbcX



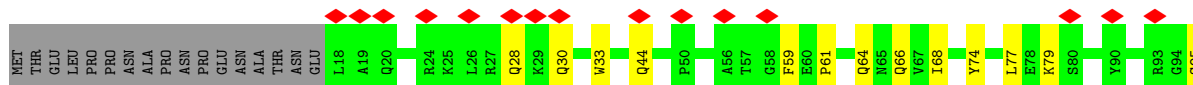
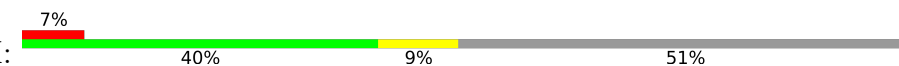
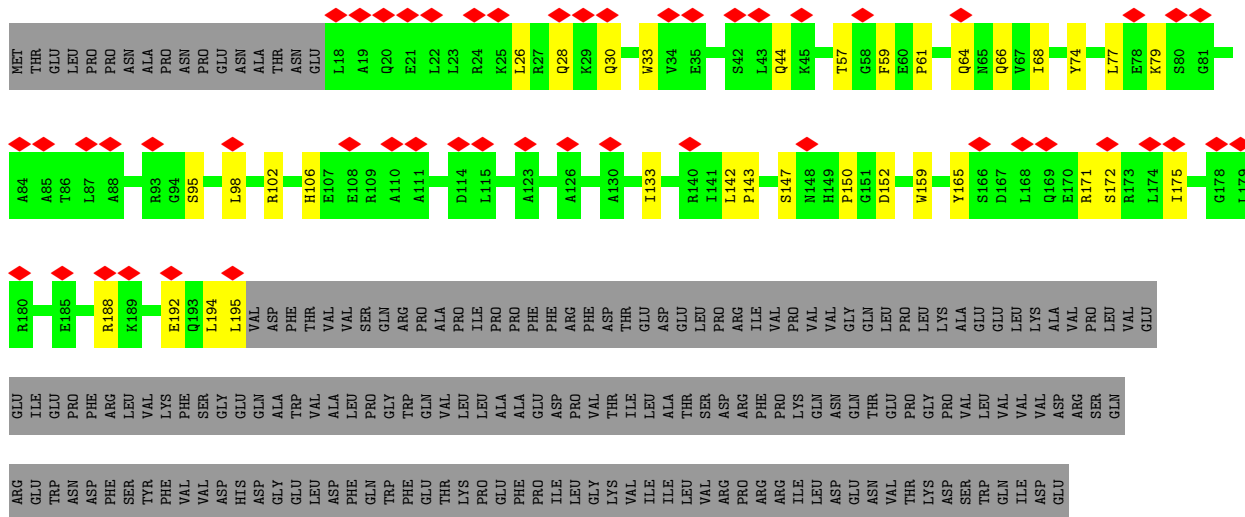
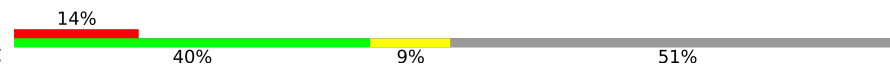
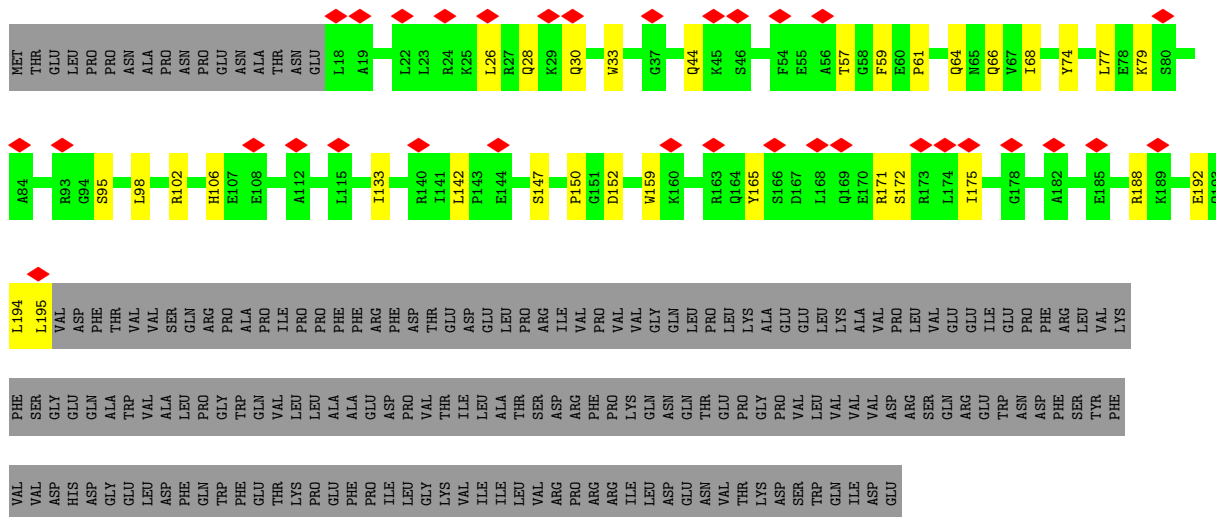
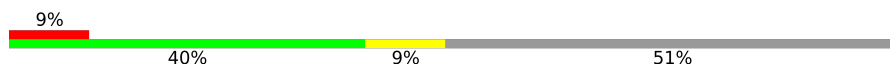
- Molecule 1: RuBisCO chaperone RbcX

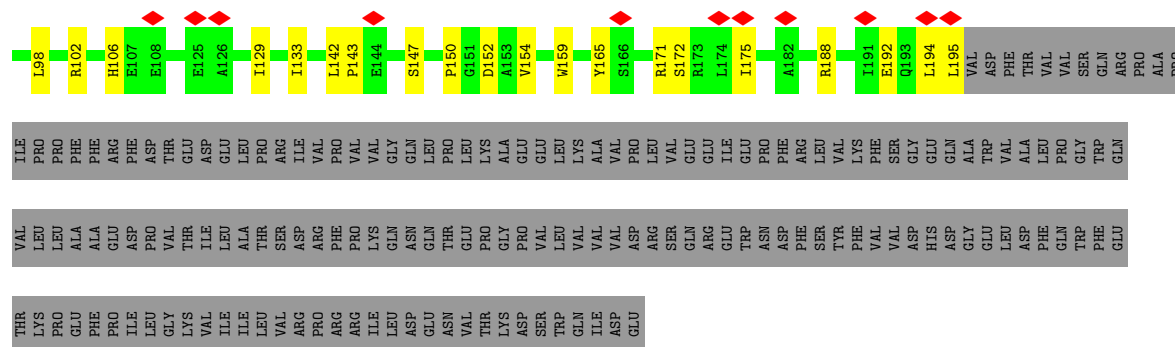


- Molecule 1: RuBisCO chaperone RbcX

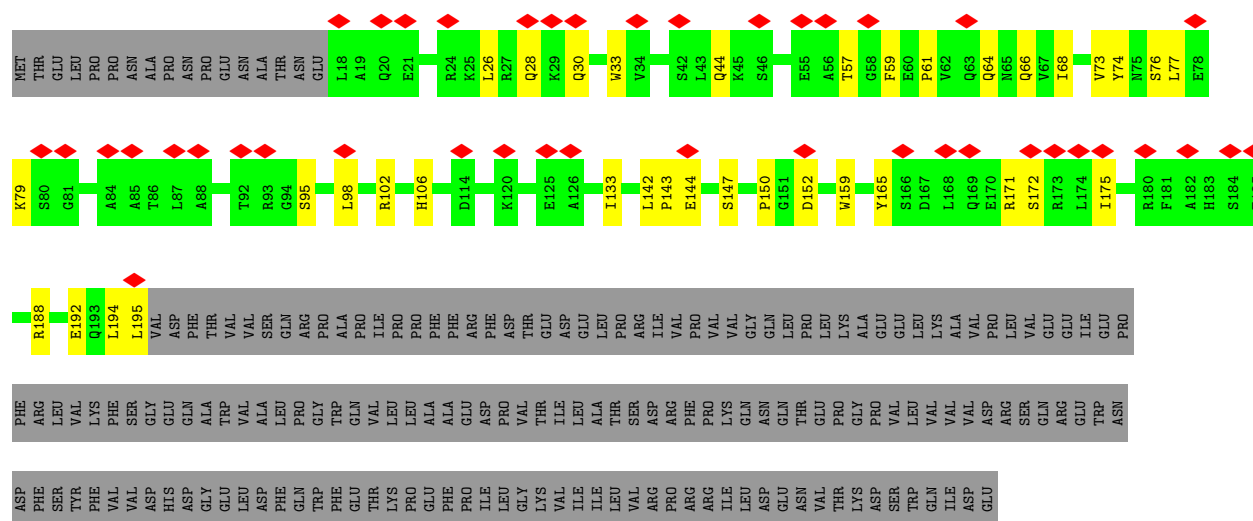
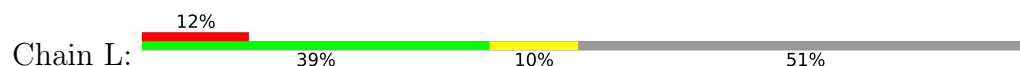


- Molecule 1: RuBisCO chaperone RbcX

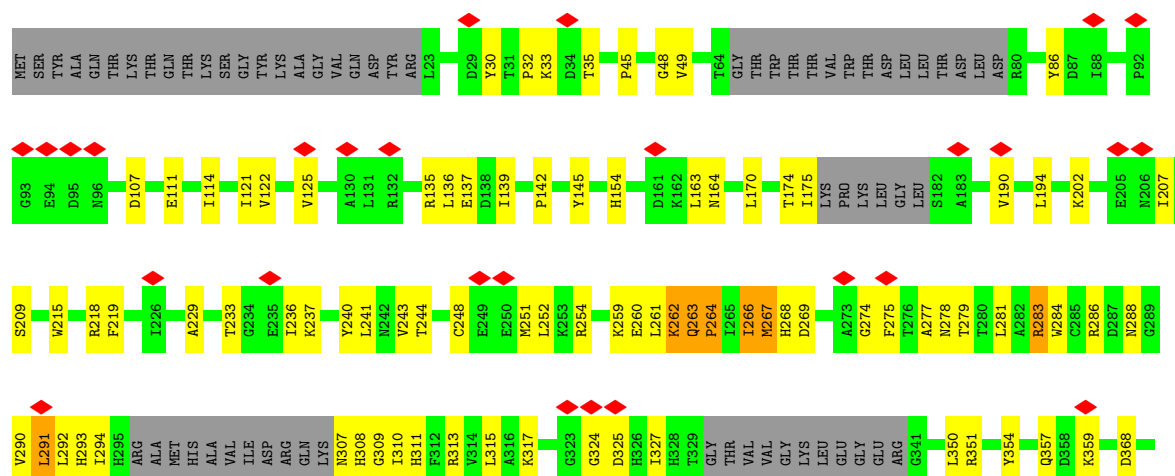


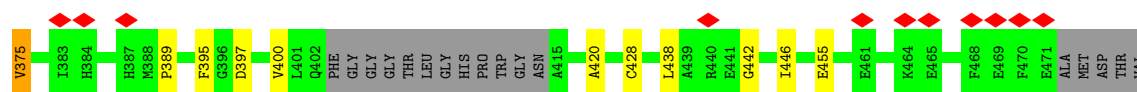


• Molecule 2: RuBisCO accumulation factor 1

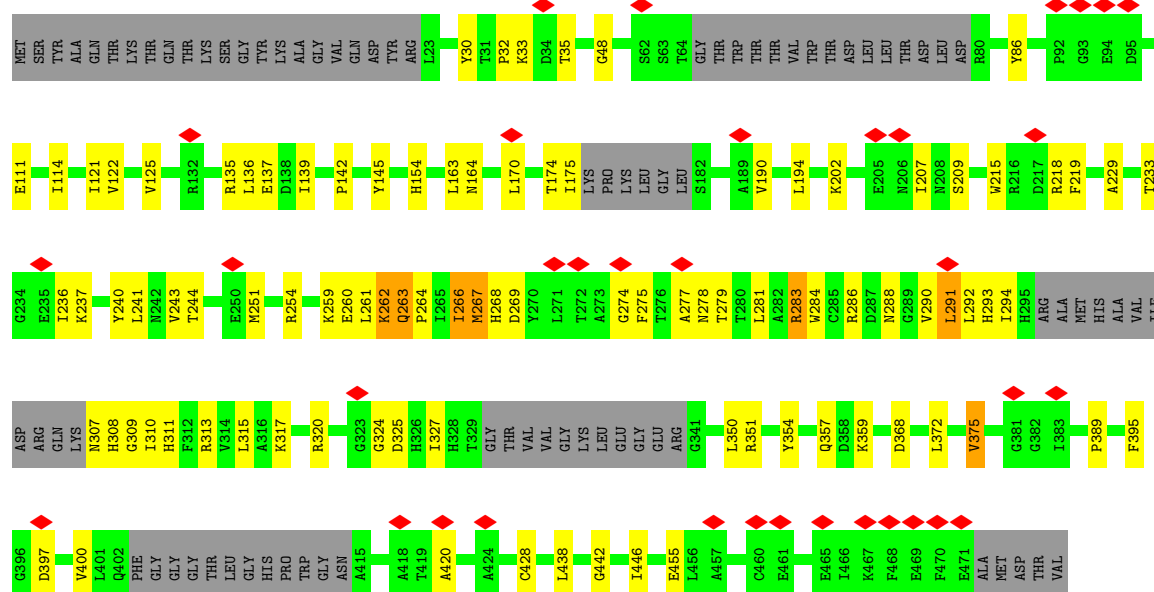


• Molecule 3: Ribulose biphosphate carboxylase large chain

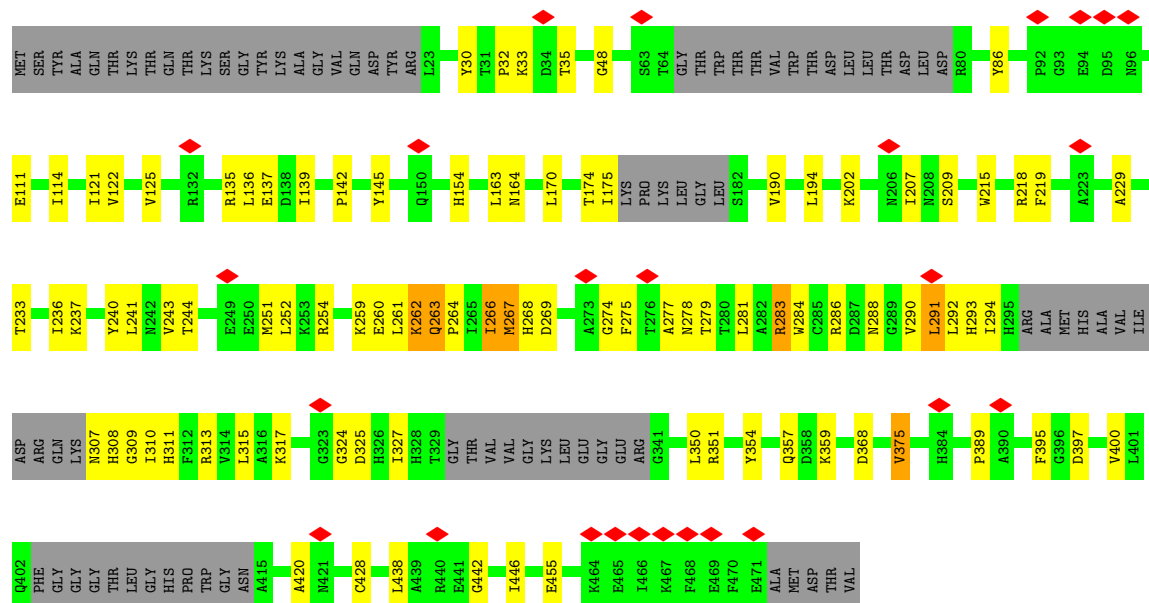




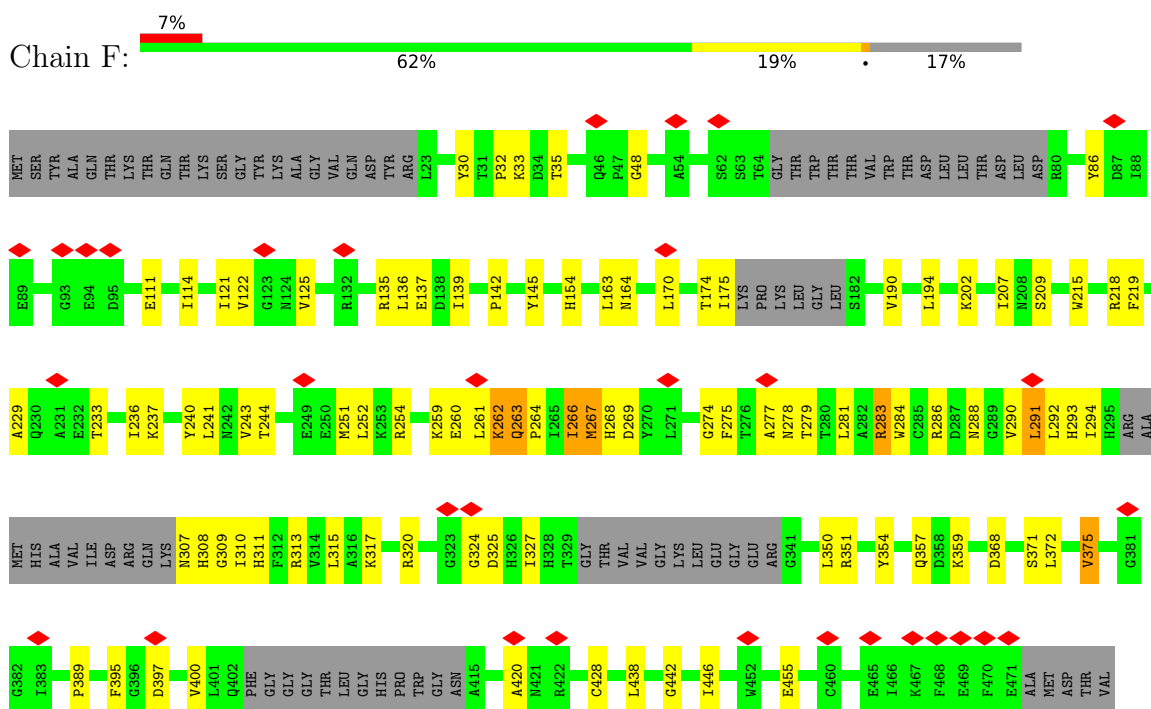
• Molecule 3: Ribulose biphosphate carboxylase large chain



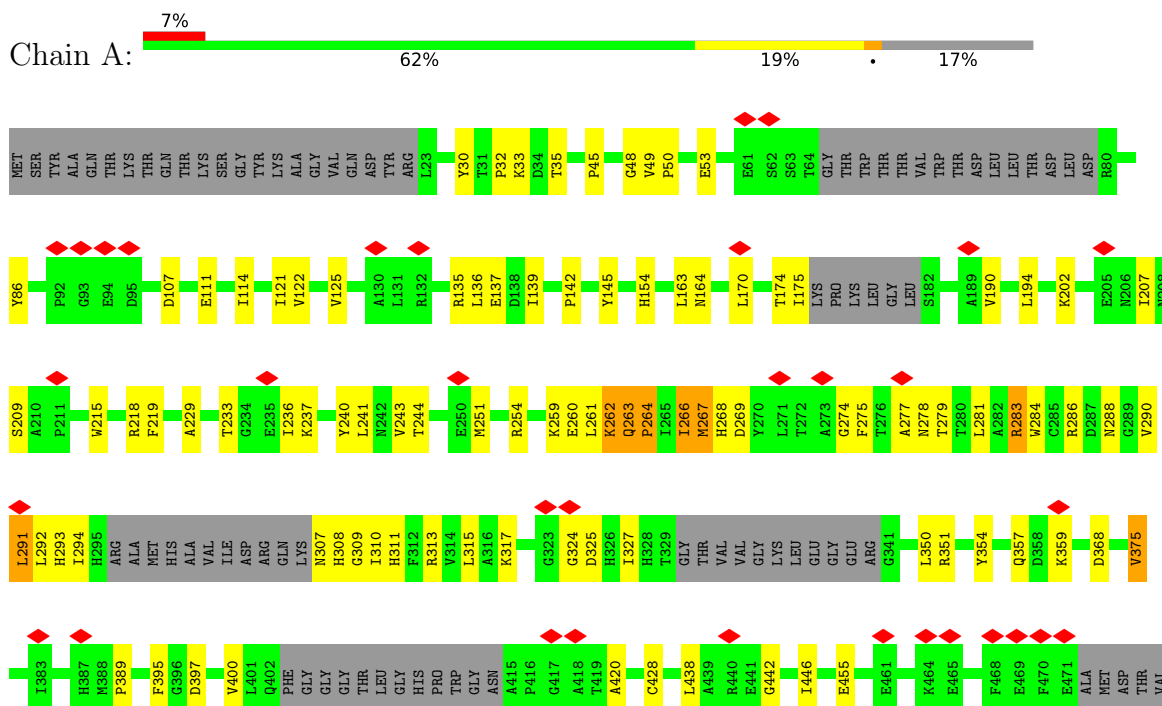
• Molecule 3: Ribulose biphosphate carboxylase large chain



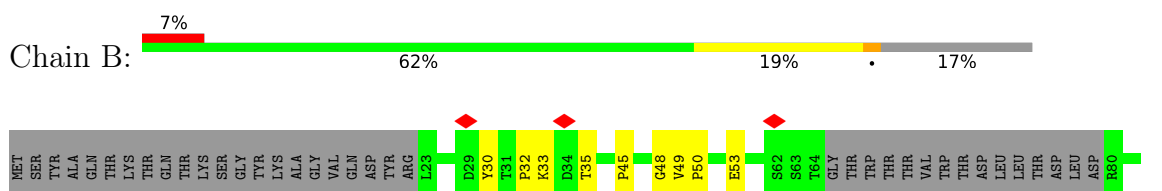
• Molecule 3: Ribulose biphosphate carboxylase large chain



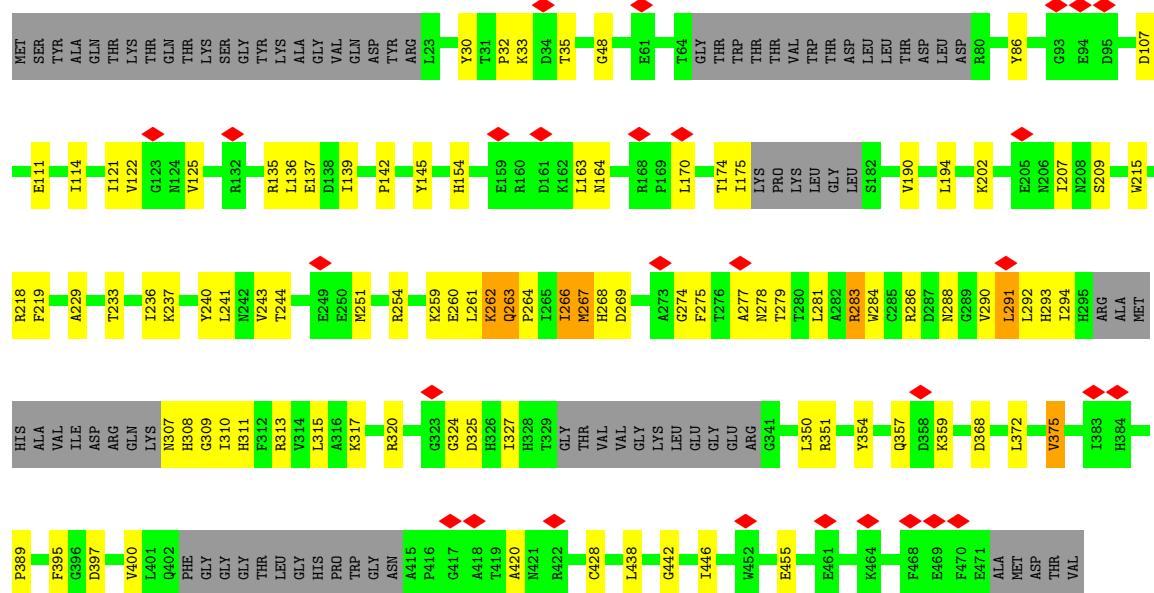
- Molecule 3: Ribulose biphosphate carboxylase large chain



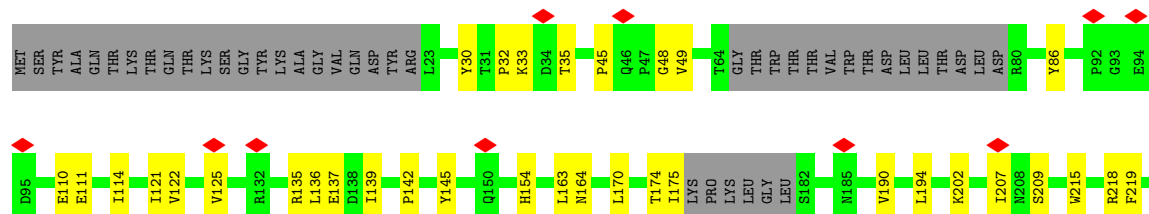
- Molecule 3: Ribulose biphosphate carboxylase large chain

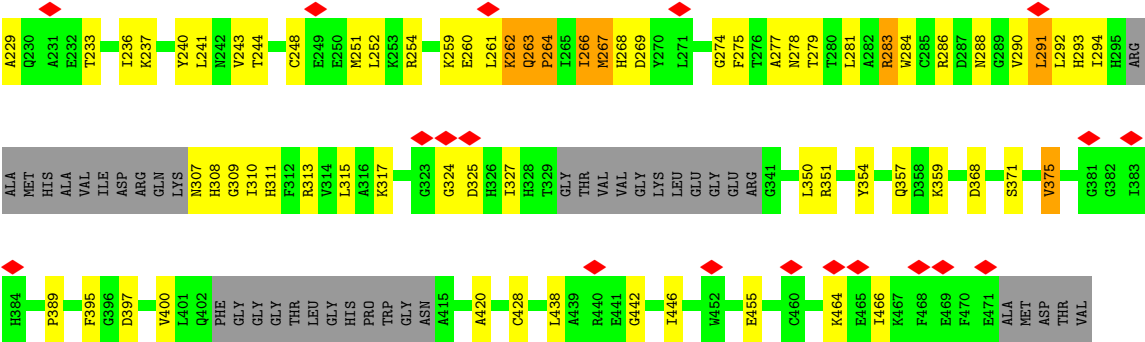


- Molecule 3: Ribulose biphosphate carboxylase large chain



- Molecule 3: Ribulose biphosphate carboxylase large chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54260	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.050	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.012	Depositor
Map size ($\text{\AA}$)	282.8, 282.8, 282.8	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.01, 1.01, 1.01	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1	0.35	0/824	0.81	1/1114 (0.1%)
1	2	0.29	0/912	0.67	0/1232
1	3	0.35	0/824	0.78	0/1114
1	4	0.30	0/912	0.70	0/1232
1	5	0.36	0/824	0.82	1/1114 (0.1%)
1	6	0.30	0/912	0.69	0/1232
1	7	0.35	0/824	0.80	1/1114 (0.1%)
1	8	0.29	0/912	0.68	0/1232
1	Q	0.35	0/824	0.82	0/1114
1	R	0.30	0/912	0.69	0/1232
1	S	0.36	0/824	0.82	1/1114 (0.1%)
1	T	0.30	0/912	0.68	0/1232
1	U	0.35	0/824	0.81	1/1114 (0.1%)
1	V	0.29	0/912	0.67	0/1232
1	W	0.36	0/824	0.80	1/1114 (0.1%)
1	X	0.29	0/912	0.68	0/1232
2	I	0.32	0/1448	0.57	0/1954
2	J	0.32	0/1448	0.57	0/1954
2	K	0.32	0/1448	0.57	0/1954
2	L	0.32	0/1448	0.57	0/1954
2	M	0.32	0/1448	0.57	0/1954
2	N	0.32	0/1448	0.57	0/1954
2	O	0.32	0/1448	0.57	0/1954
2	P	0.32	0/1448	0.57	0/1954
3	A	0.46	0/3173	0.85	7/4302 (0.2%)
3	B	0.46	0/3173	0.85	7/4302 (0.2%)
3	C	0.46	0/3173	0.85	7/4302 (0.2%)
3	D	0.46	0/3173	0.85	7/4302 (0.2%)
3	E	0.46	0/3173	0.85	7/4302 (0.2%)
3	F	0.46	0/3173	0.85	7/4302 (0.2%)
3	G	0.46	0/3173	0.85	7/4302 (0.2%)
3	H	0.46	0/3173	0.85	7/4302 (0.2%)
All	All	0.40	0/50856	0.77	62/68816 (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
3	A	0	3
3	B	0	3
3	C	0	3
3	D	0	3
3	E	0	3
3	F	0	3
3	G	0	3
3	H	0	3
All	All	0	24

There are no bond length outliers.

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	291	LEU	CA-CB-CG	5.88	136.88	116.30
3	B	291	LEU	CA-CB-CG	5.88	136.87	116.30
3	G	291	LEU	CA-CB-CG	5.88	136.86	116.30
3	A	291	LEU	CA-CB-CG	5.88	136.86	116.30
3	H	291	LEU	CA-CB-CG	5.87	136.83	116.30

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	260	GLU	Peptide
3	G	262	LYS	Peptide
3	G	266	ILE	Peptide
3	H	260	GLU	Peptide
3	H	262	LYS	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	1	811	0	822	13	0
1	2	897	0	906	7	0
1	3	811	0	822	12	0
1	4	897	0	906	4	0
1	5	811	0	822	17	0
1	6	897	0	906	7	0
1	7	811	0	822	14	0
1	8	897	0	906	6	0
1	Q	811	0	822	18	0
1	R	897	0	906	9	0
1	S	811	0	822	16	0
1	T	897	0	906	7	0
1	U	811	0	822	17	0
1	V	897	0	906	8	0
1	W	811	0	822	16	0
1	X	897	0	906	5	0
2	I	1421	0	1400	18	0
2	J	1421	0	1400	19	0
2	K	1421	0	1400	20	0
2	L	1421	0	1400	21	0
2	M	1421	0	1400	18	0
2	N	1421	0	1400	18	0
2	O	1421	0	1400	17	0
2	P	1421	0	1400	19	0
3	A	3102	0	3027	62	0
3	B	3102	0	3027	62	0
3	C	3102	0	3027	57	0
3	D	3102	0	3027	64	0
3	E	3102	0	3027	56	0
3	F	3102	0	3027	58	0
3	G	3102	0	3027	61	0
3	H	3102	0	3027	57	0
All	All	49848	0	49240	730	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 730 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:M:133:ILE:HD12	2:M:150:PRO:HB3	1.76	0.68
2:N:133:ILE:HD12	2:N:150:PRO:HB3	1.76	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:133:ILE:HD12	2:O:150:PRO:HB3	1.76	0.67
2:K:133:ILE:HD12	2:K:150:PRO:HB3	1.76	0.67
2:L:133:ILE:HD12	2:L:150:PRO:HB3	1.76	0.67

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	1	99/132 (75%)	93 (94%)	6 (6%)	0	100	100
1	2	109/132 (83%)	106 (97%)	3 (3%)	0	100	100
1	3	99/132 (75%)	93 (94%)	6 (6%)	0	100	100
1	4	109/132 (83%)	106 (97%)	3 (3%)	0	100	100
1	5	99/132 (75%)	92 (93%)	7 (7%)	0	100	100
1	6	109/132 (83%)	107 (98%)	2 (2%)	0	100	100
1	7	99/132 (75%)	93 (94%)	6 (6%)	0	100	100
1	8	109/132 (83%)	106 (97%)	3 (3%)	0	100	100
1	Q	99/132 (75%)	92 (93%)	7 (7%)	0	100	100
1	R	109/132 (83%)	107 (98%)	2 (2%)	0	100	100
1	S	99/132 (75%)	93 (94%)	6 (6%)	0	100	100
1	T	109/132 (83%)	106 (97%)	3 (3%)	0	100	100
1	U	99/132 (75%)	92 (93%)	7 (7%)	0	100	100
1	V	109/132 (83%)	106 (97%)	3 (3%)	0	100	100
1	W	99/132 (75%)	93 (94%)	6 (6%)	0	100	100
1	X	109/132 (83%)	106 (97%)	3 (3%)	0	100	100
2	I	176/361 (49%)	170 (97%)	6 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
2	K	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
2	L	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
2	M	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
2	N	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
2	O	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
2	P	176/361 (49%)	170 (97%)	6 (3%)	0	100	100
3	A	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	B	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	C	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	D	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	E	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	F	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	G	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
3	H	382/476 (80%)	341 (89%)	40 (10%)	1 (0%)	36	65
All	All	6128/8808 (70%)	5679 (93%)	441 (7%)	8 (0%)	49	75

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	264	PRO
3	H	264	PRO
3	E	264	PRO
3	F	264	PRO
3	A	264	PRO

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	1	87/118 (74%)	87 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	97/118 (82%)	97 (100%)	0	100	100
1	3	87/118 (74%)	87 (100%)	0	100	100
1	4	97/118 (82%)	97 (100%)	0	100	100
1	5	87/118 (74%)	87 (100%)	0	100	100
1	6	97/118 (82%)	97 (100%)	0	100	100
1	7	87/118 (74%)	87 (100%)	0	100	100
1	8	97/118 (82%)	97 (100%)	0	100	100
1	Q	87/118 (74%)	87 (100%)	0	100	100
1	R	97/118 (82%)	97 (100%)	0	100	100
1	S	87/118 (74%)	87 (100%)	0	100	100
1	T	97/118 (82%)	97 (100%)	0	100	100
1	U	87/118 (74%)	87 (100%)	0	100	100
1	V	97/118 (82%)	97 (100%)	0	100	100
1	W	87/118 (74%)	87 (100%)	0	100	100
1	X	97/118 (82%)	97 (100%)	0	100	100
2	I	144/311 (46%)	144 (100%)	0	100	100
2	J	144/311 (46%)	144 (100%)	0	100	100
2	K	144/311 (46%)	144 (100%)	0	100	100
2	L	144/311 (46%)	144 (100%)	0	100	100
2	M	144/311 (46%)	144 (100%)	0	100	100
2	N	144/311 (46%)	144 (100%)	0	100	100
2	O	144/311 (46%)	144 (100%)	0	100	100
2	P	144/311 (46%)	144 (100%)	0	100	100
3	A	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	B	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	C	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	D	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	E	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	F	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	G	319/386 (83%)	314 (98%)	5 (2%)	55	72
3	H	319/386 (83%)	314 (98%)	5 (2%)	55	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5176/7464 (69%)	5136 (99%)	40 (1%)	70 79

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	315	LEU
3	D	35	THR
3	B	375	VAL
3	C	267	MET
3	D	267	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 135 such sidechains are listed below:

Mol	Chain	Res	Type
1	W	21	GLN
1	X	103	GLN
3	D	185	ASN
2	N	30	GLN
2	M	106	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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](#)

There are no chain breaks in this entry.

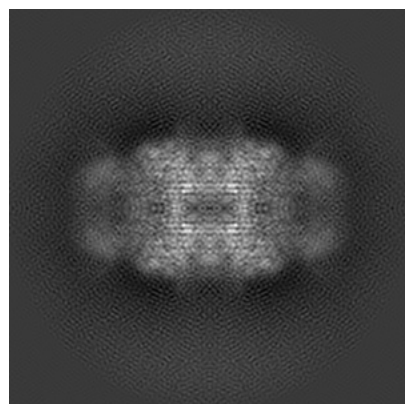
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33524. These allow visual inspection of the internal detail of the map and identification of artifacts.

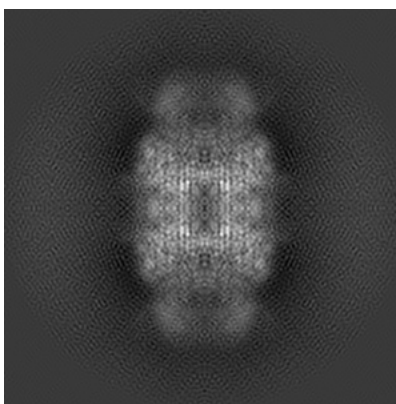
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

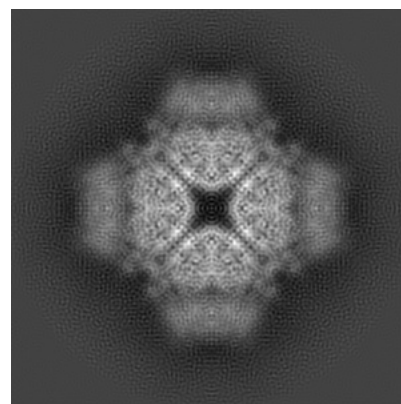
6.1.1 Primary map



X

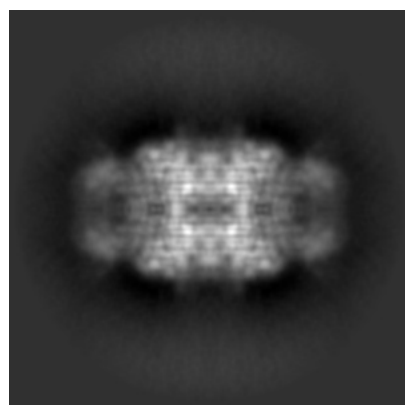


Y

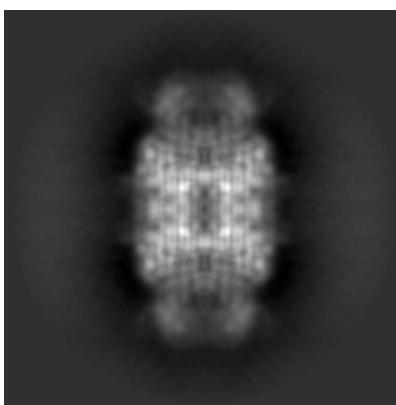


Z

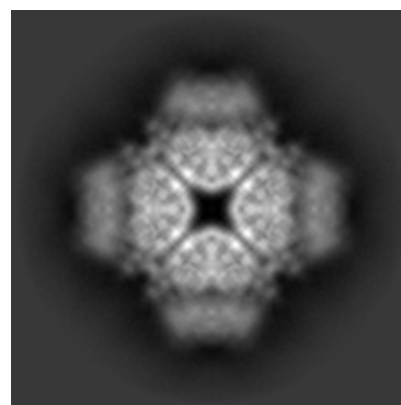
6.1.2 Raw map



X



Y

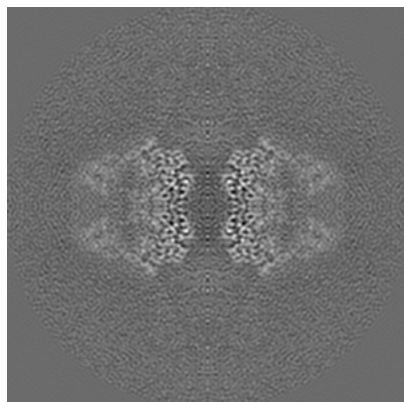


Z

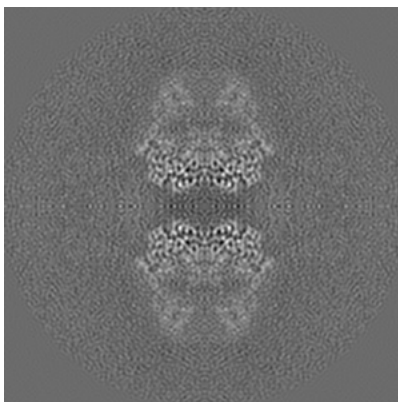
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

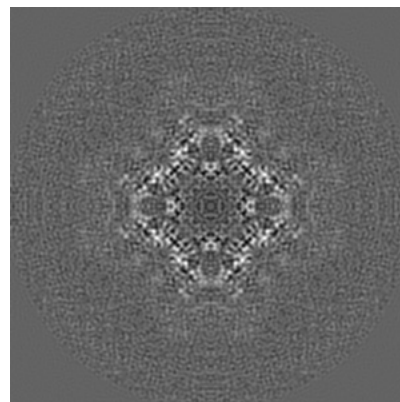
6.2.1 Primary map



X Index: 140

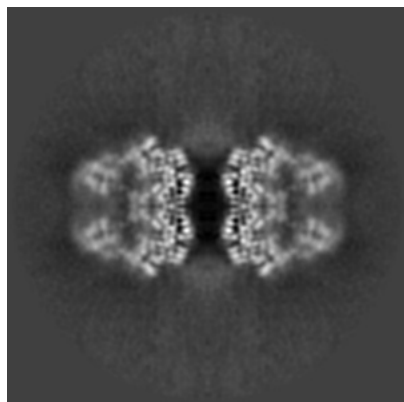


Y Index: 140

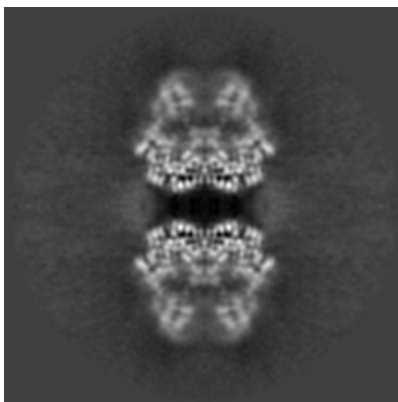


Z Index: 140

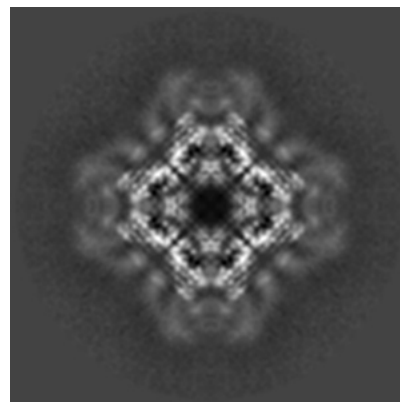
6.2.2 Raw map



X Index: 140



Y Index: 140

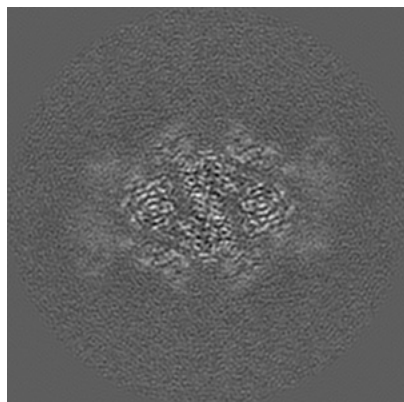


Z Index: 140

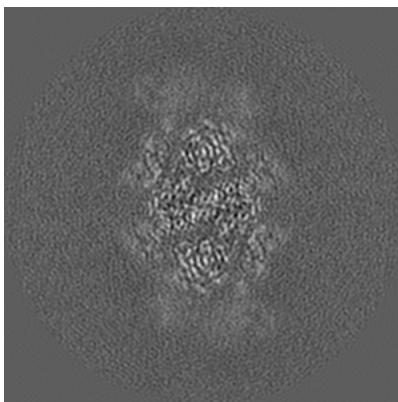
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

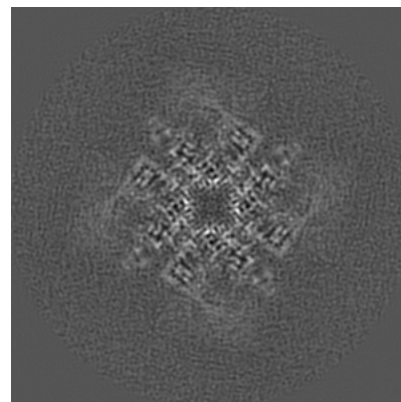
6.3.1 Primary map



X Index: 118

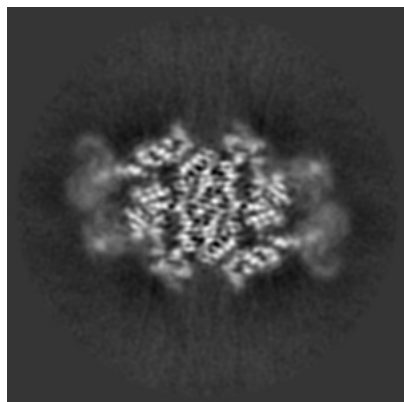


Y Index: 118

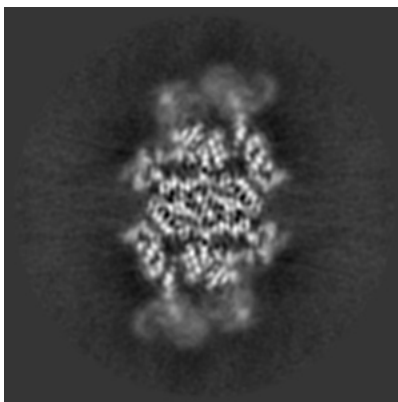


Z Index: 152

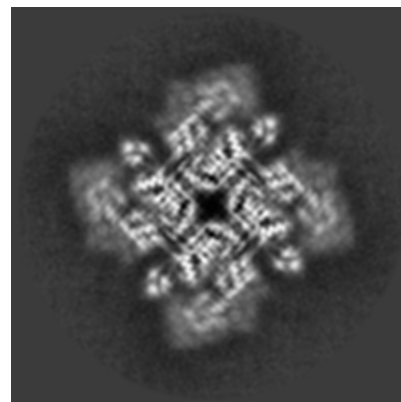
6.3.2 Raw map



X Index: 165



Y Index: 165

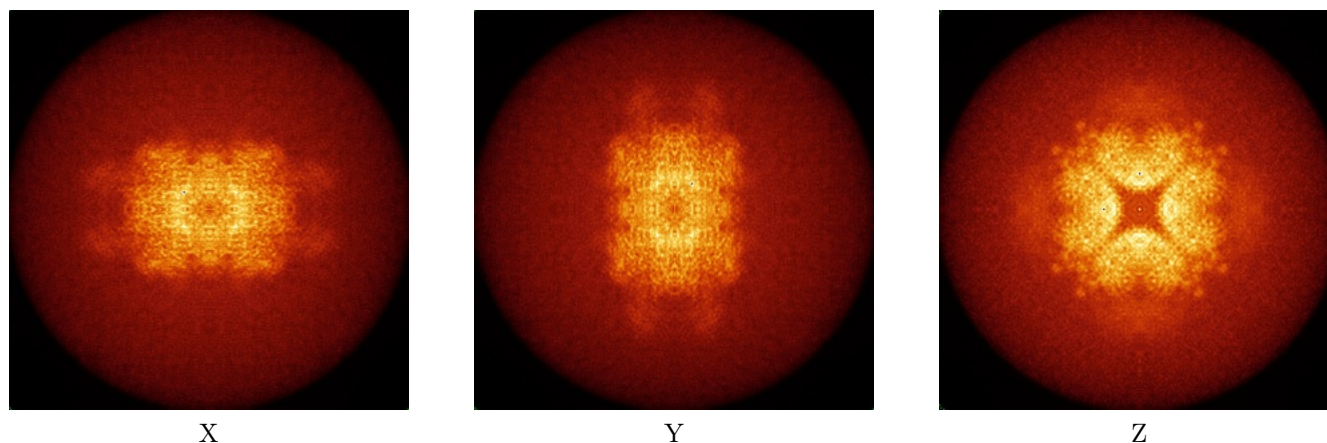


Z Index: 125

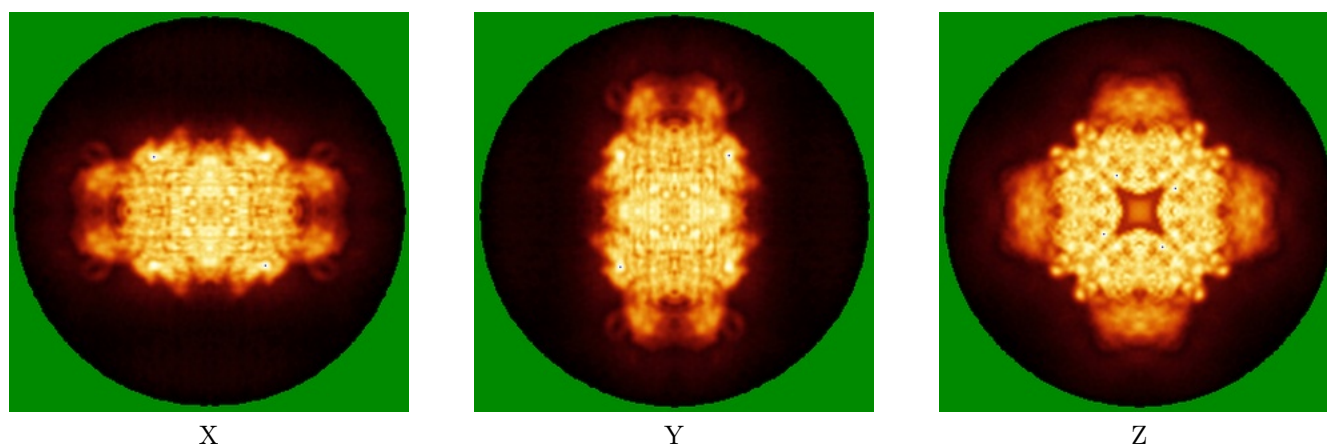
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

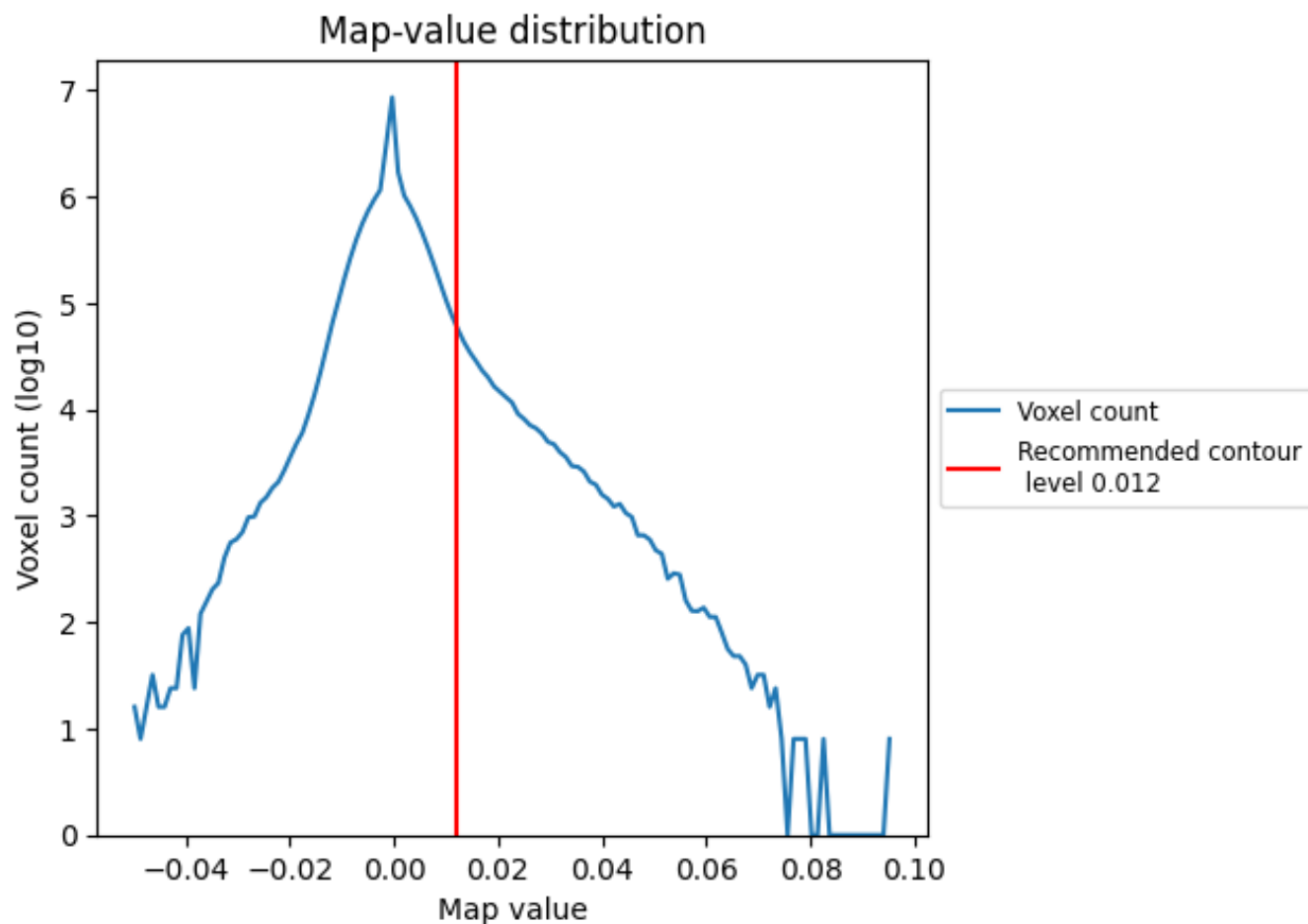
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

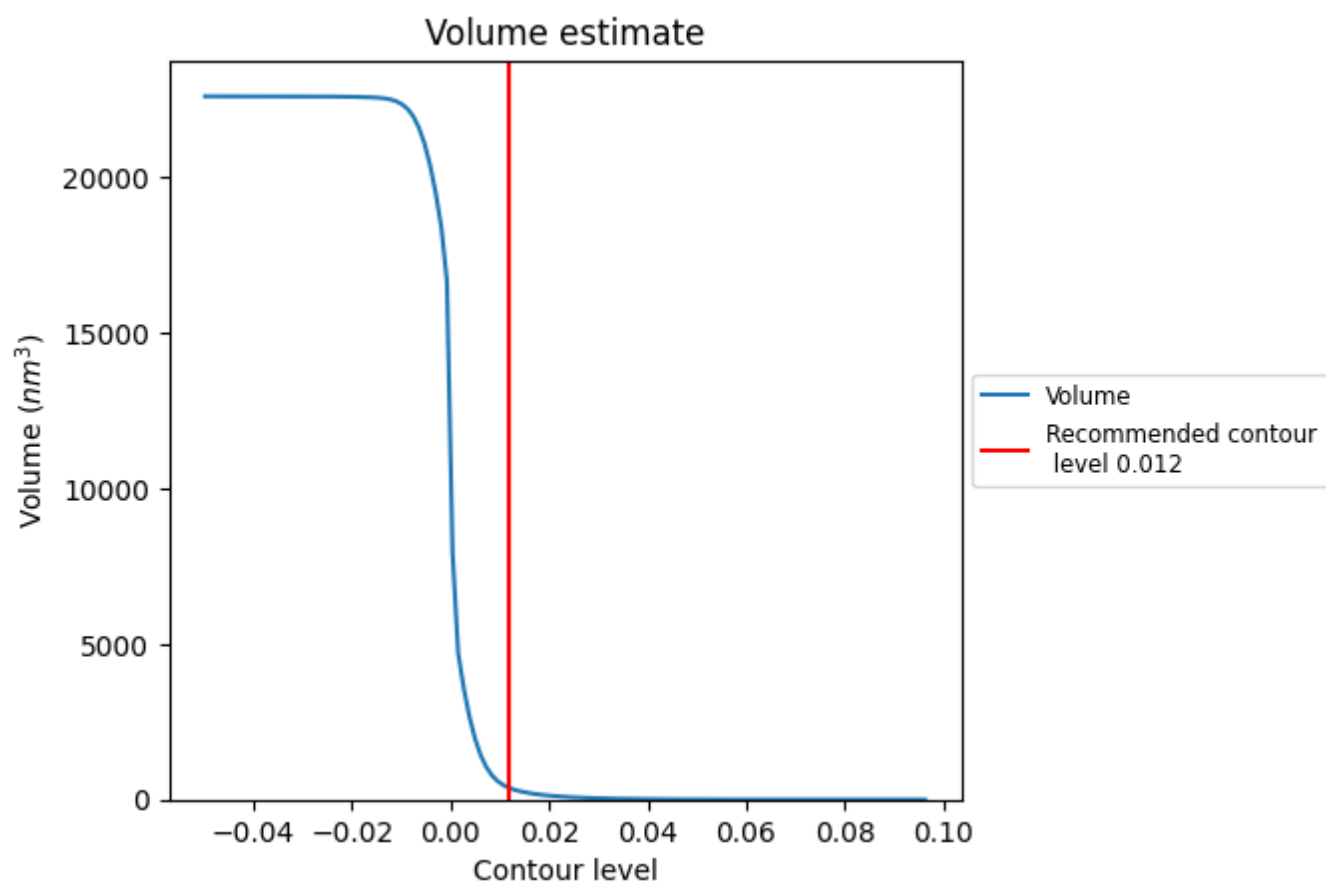
This section contains the results of statistical analysis of the map.

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.

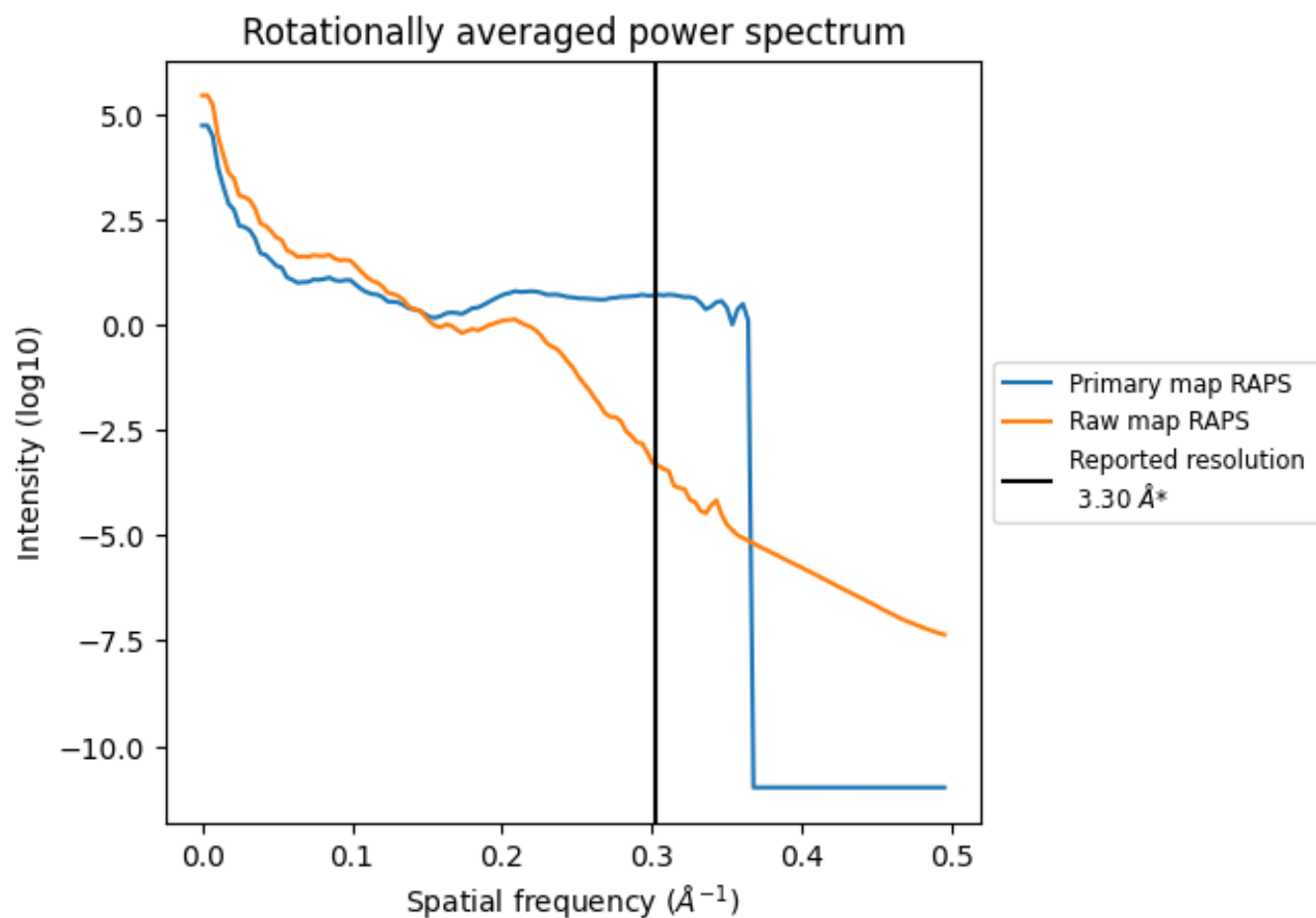
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 369 nm³; this corresponds to an approximate mass of 334 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 ⓘ

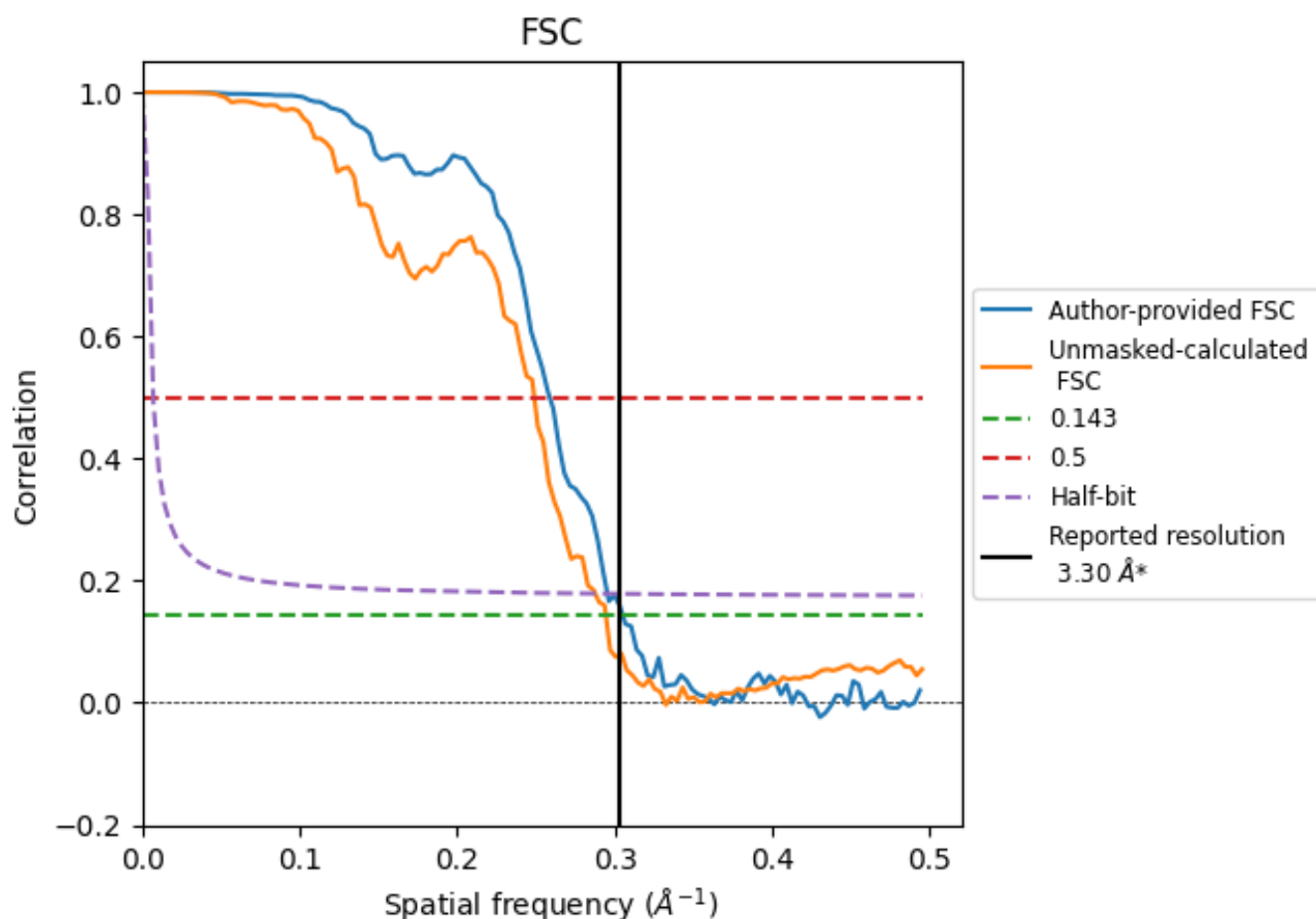


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

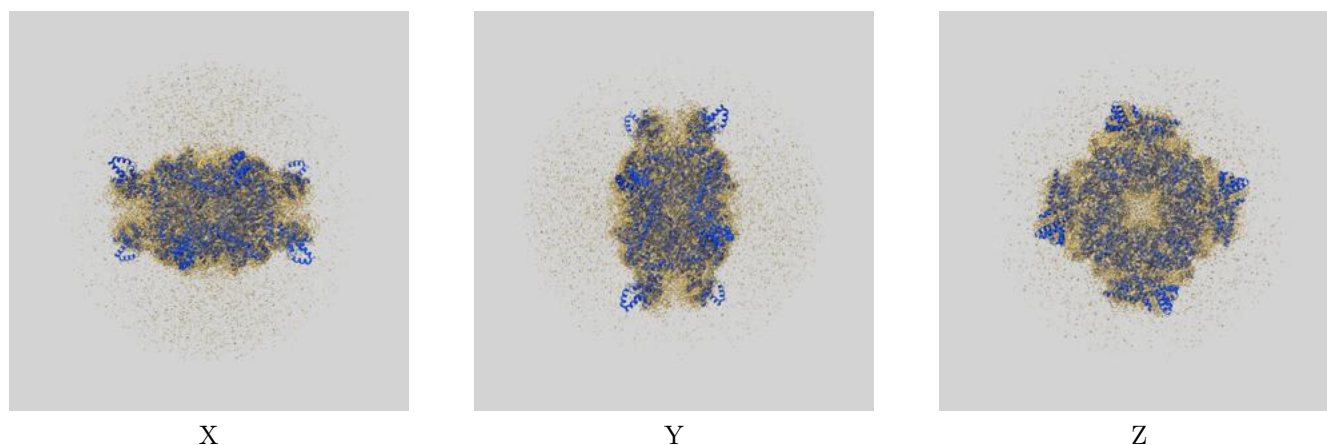
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.28	3.87	3.39
Unmasked-calculated*	3.40	4.02	3.48

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

9 Map-model fit [i](#)

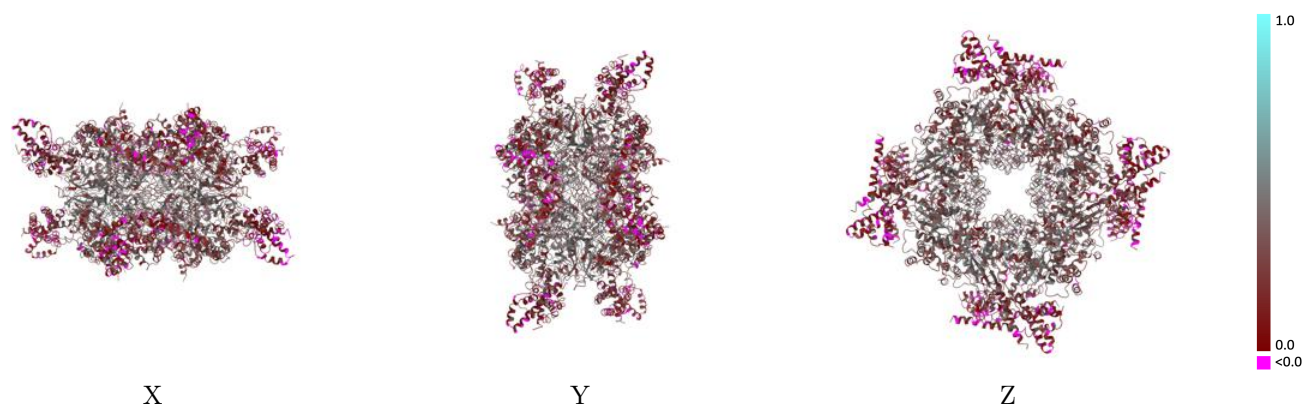
This section contains information regarding the fit between EMDB map EMD-33524 and PDB model 7XSD. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



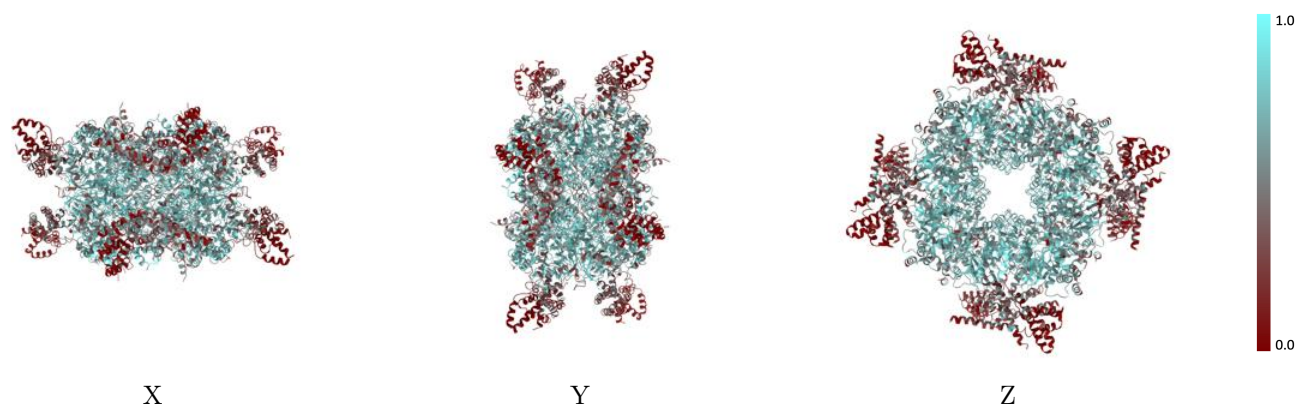
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



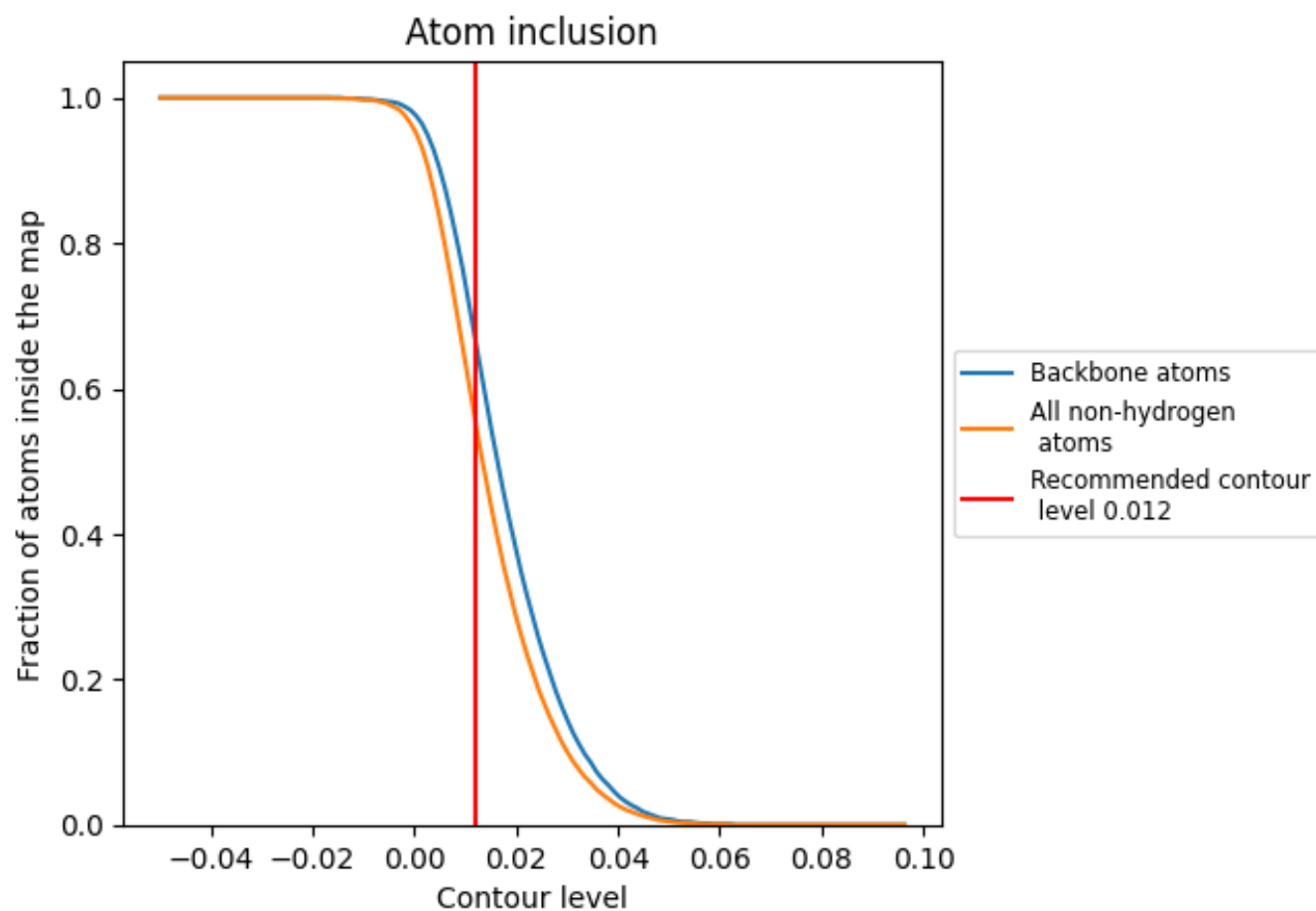
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 55% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5540	 0.2920
1	 0.3260	 0.1970
2	 0.1470	 0.1430
3	 0.2980	 0.1950
4	 0.1500	 0.1290
5	 0.2890	 0.1590
6	 0.1390	 0.1130
7	 0.2990	 0.1720
8	 0.1340	 0.0990
A	 0.7100	 0.3620
B	 0.6980	 0.3460
C	 0.7370	 0.3970
D	 0.7270	 0.3750
E	 0.7320	 0.3830
F	 0.7270	 0.3760
G	 0.7040	 0.3490
H	 0.7050	 0.3550
I	 0.6140	 0.3100
J	 0.5640	 0.2630
K	 0.6330	 0.3160
L	 0.5940	 0.2900
M	 0.6110	 0.3030
N	 0.6060	 0.3080
O	 0.5970	 0.3020
P	 0.5820	 0.2910
Q	 0.2930	 0.1610
R	 0.1380	 0.1010
S	 0.2830	 0.1620
T	 0.1410	 0.1150
U	 0.3170	 0.1970
V	 0.1580	 0.1230
W	 0.3110	 0.1860
X	 0.1500	 0.1470

