wwPDB EM Validation Summary Report

Apr 28, 2026 – 01:33 PM EDT

PDB ID	:	9O5L / pdb_00009o5l
EMDB ID	:	EMD-70144
Title	:	Phosphonull (T175E) of stress-activating residues
Authors	:	Martinez-Bond, E.A.; Lopez-Ayala, I.; Qiu, L.; Garda, V.; Yu, Z.; Williams, A.H.
Deposited on	:	2025-04-10
Resolution	:	4.16 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:

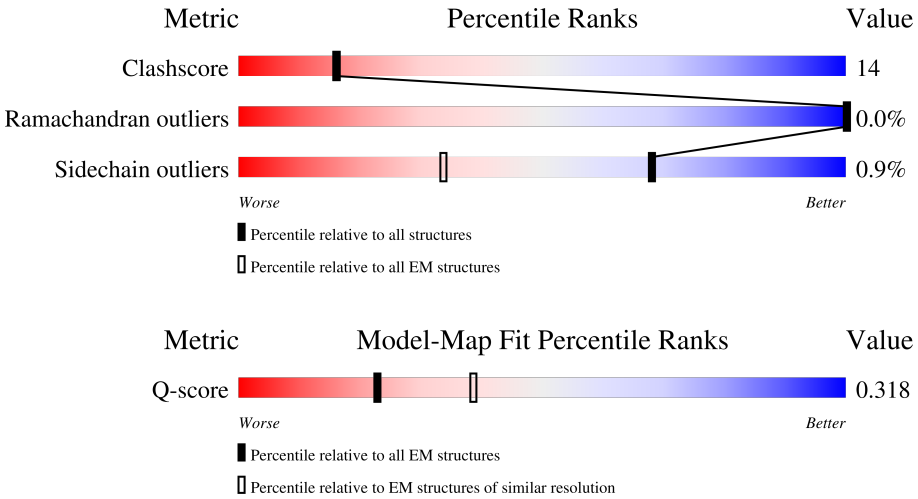
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & 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 4.16 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	5480 (3.66 - 4.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	118	70% 29%
1	ab	118	69% 31%
1	b	118	79% 21%
1	bb	118	84% 16%

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Mol	Chain	Length	Quality of chain
1	c	118	79% 21%
1	cb	118	66% 33%
1	d	118	82% 18%
1	db	118	75% 23%
1	e	118	75% 25%
1	eb	118	70% 29%
1	f	118	73% 27%
1	fb	118	78% 22%
1	g	118	70% 30%
1	gb	118	62% 38%
1	h	118	79% 21%
1	hb	118	80% 19%
1	i	118	84% 16%
1	ib	118	87% 13%
1	j	118	76% 23%
1	jb	118	76% 24%
2	A	278	29% 18% 53%
2	AB	278	34% 13% 53%
2	B	278	35% 13% 53%
2	BB	278	32% 15% 53%
2	C	278	31% 17% 53%
2	CB	278	34% 14% 53%
2	D	278	31% 17% 53%
2	DB	278	32% 15% 53%
2	E	278	32% 16% 53%

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Mol	Chain	Length	Quality of chain
2	EB	278	31% 16% 53%
2	F	278	30% 17% 53%
2	FB	278	31% 17% 53%
2	G	278	34% 14% 53%
2	GB	278	33% 15% 53%
2	H	278	29% 18% 53%
2	HB	278	28% 19% 53%
2	I	278	30% 17% 53%
2	IB	278	34% 14% 53%
2	J	278	33% 14% 53%
2	JB	278	31% 17% 53%
2	K	278	29% 18% 53%
2	KB	278	34% 13% 53%
2	L	278	28% 19% 53%
2	LB	278	31% 17% 53%
2	M	278	27% 19% 53%
2	MB	278	27% 21% 53%
2	N	278	34% 14% 53%
2	NB	278	30% 17% 53%
2	O	278	35% 13% 53%
2	OB	278	35% 12% 53%
2	P	278	28% 19% 53%
2	PB	278	28% 18% 53%
2	Q	278	30% 18% 53%
2	QB	278	29% 18% 53%

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Mol	Chain	Length	Quality of chain
2	R	278	29% 18% 53%
2	RB	278	29% 18% 53%
2	S	278	30% 17% 53%
2	SB	278	29% 18% 53%
2	T	278	33% 14% 53%
2	TB	278	36% 12% 53%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 57860 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 RsbT antagonist protein RsbS.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	ab	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	b	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	bb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	c	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	cb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	d	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	db	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	e	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	eb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	f	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	fb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	g	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	gb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	h	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	hb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	i	118	Total	C	N	O	S	0	0
			881	565	136	175	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ib	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	j	118	Total	C	N	O	S	0	0
			881	565	136	175	5		
1	jb	118	Total	C	N	O	S	0	0
			881	565	136	175	5		

- Molecule 2 is a protein called STAS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	AB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	B	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	BB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	C	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	CB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	D	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	DB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	E	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	EB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	F	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	FB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	G	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	GB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	H	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	HB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	IB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	J	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	JB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	K	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	KB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	L	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	LB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	M	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	MB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	N	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	NB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	O	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	OB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	P	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	PB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	Q	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	QB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	R	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	RB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	S	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	T	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		
2	TB	132	Total	C	N	O	S	0	0
			1006	639	171	190	6		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	ASP	ASN	variant	UNP A0AAD2RAW1
A	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
A	278	GLY	GLU	variant	UNP A0AAD2RAW1
AB	19	ASP	ASN	variant	UNP A0AAD2RAW1
AB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
AB	278	GLY	GLU	variant	UNP A0AAD2RAW1
B	19	ASP	ASN	variant	UNP A0AAD2RAW1
B	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
B	278	GLY	GLU	variant	UNP A0AAD2RAW1
BB	19	ASP	ASN	variant	UNP A0AAD2RAW1
BB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
BB	278	GLY	GLU	variant	UNP A0AAD2RAW1
C	19	ASP	ASN	variant	UNP A0AAD2RAW1
C	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
C	278	GLY	GLU	variant	UNP A0AAD2RAW1
CB	19	ASP	ASN	variant	UNP A0AAD2RAW1
CB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
CB	278	GLY	GLU	variant	UNP A0AAD2RAW1
D	19	ASP	ASN	variant	UNP A0AAD2RAW1
D	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
D	278	GLY	GLU	variant	UNP A0AAD2RAW1
DB	19	ASP	ASN	variant	UNP A0AAD2RAW1
DB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
DB	278	GLY	GLU	variant	UNP A0AAD2RAW1
E	19	ASP	ASN	variant	UNP A0AAD2RAW1
E	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
E	278	GLY	GLU	variant	UNP A0AAD2RAW1
EB	19	ASP	ASN	variant	UNP A0AAD2RAW1
EB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
EB	278	GLY	GLU	variant	UNP A0AAD2RAW1
F	19	ASP	ASN	variant	UNP A0AAD2RAW1
F	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1

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Chain	Residue	Modelled	Actual	Comment	Reference
F	278	GLY	GLU	variant	UNP A0AAD2RAW1
FB	19	ASP	ASN	variant	UNP A0AAD2RAW1
FB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
FB	278	GLY	GLU	variant	UNP A0AAD2RAW1
G	19	ASP	ASN	variant	UNP A0AAD2RAW1
G	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
G	278	GLY	GLU	variant	UNP A0AAD2RAW1
GB	19	ASP	ASN	variant	UNP A0AAD2RAW1
GB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
GB	278	GLY	GLU	variant	UNP A0AAD2RAW1
H	19	ASP	ASN	variant	UNP A0AAD2RAW1
H	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
H	278	GLY	GLU	variant	UNP A0AAD2RAW1
HB	19	ASP	ASN	variant	UNP A0AAD2RAW1
HB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
HB	278	GLY	GLU	variant	UNP A0AAD2RAW1
I	19	ASP	ASN	variant	UNP A0AAD2RAW1
I	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
I	278	GLY	GLU	variant	UNP A0AAD2RAW1
IB	19	ASP	ASN	variant	UNP A0AAD2RAW1
IB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
IB	278	GLY	GLU	variant	UNP A0AAD2RAW1
J	19	ASP	ASN	variant	UNP A0AAD2RAW1
J	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
J	278	GLY	GLU	variant	UNP A0AAD2RAW1
JB	19	ASP	ASN	variant	UNP A0AAD2RAW1
JB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
JB	278	GLY	GLU	variant	UNP A0AAD2RAW1
K	19	ASP	ASN	variant	UNP A0AAD2RAW1
K	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
K	278	GLY	GLU	variant	UNP A0AAD2RAW1
KB	19	ASP	ASN	variant	UNP A0AAD2RAW1
KB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
KB	278	GLY	GLU	variant	UNP A0AAD2RAW1
L	19	ASP	ASN	variant	UNP A0AAD2RAW1
L	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
L	278	GLY	GLU	variant	UNP A0AAD2RAW1
LB	19	ASP	ASN	variant	UNP A0AAD2RAW1
LB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
LB	278	GLY	GLU	variant	UNP A0AAD2RAW1
M	19	ASP	ASN	variant	UNP A0AAD2RAW1
M	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1

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Chain	Residue	Modelled	Actual	Comment	Reference
M	278	GLY	GLU	variant	UNP A0AAD2RAW1
MB	19	ASP	ASN	variant	UNP A0AAD2RAW1
MB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
MB	278	GLY	GLU	variant	UNP A0AAD2RAW1
N	19	ASP	ASN	variant	UNP A0AAD2RAW1
N	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
N	278	GLY	GLU	variant	UNP A0AAD2RAW1
NB	19	ASP	ASN	variant	UNP A0AAD2RAW1
NB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
NB	278	GLY	GLU	variant	UNP A0AAD2RAW1
O	19	ASP	ASN	variant	UNP A0AAD2RAW1
O	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
O	278	GLY	GLU	variant	UNP A0AAD2RAW1
OB	19	ASP	ASN	variant	UNP A0AAD2RAW1
OB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
OB	278	GLY	GLU	variant	UNP A0AAD2RAW1
P	19	ASP	ASN	variant	UNP A0AAD2RAW1
P	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
P	278	GLY	GLU	variant	UNP A0AAD2RAW1
PB	19	ASP	ASN	variant	UNP A0AAD2RAW1
PB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
PB	278	GLY	GLU	variant	UNP A0AAD2RAW1
Q	19	ASP	ASN	variant	UNP A0AAD2RAW1
Q	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
Q	278	GLY	GLU	variant	UNP A0AAD2RAW1
QB	19	ASP	ASN	variant	UNP A0AAD2RAW1
QB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
QB	278	GLY	GLU	variant	UNP A0AAD2RAW1
R	19	ASP	ASN	variant	UNP A0AAD2RAW1
R	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
R	278	GLY	GLU	variant	UNP A0AAD2RAW1
RB	19	ASP	ASN	variant	UNP A0AAD2RAW1
RB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
RB	278	GLY	GLU	variant	UNP A0AAD2RAW1
S	19	ASP	ASN	variant	UNP A0AAD2RAW1
S	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
S	278	GLY	GLU	variant	UNP A0AAD2RAW1
SB	19	ASP	ASN	variant	UNP A0AAD2RAW1
SB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
SB	278	GLY	GLU	variant	UNP A0AAD2RAW1
T	19	ASP	ASN	variant	UNP A0AAD2RAW1
T	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1

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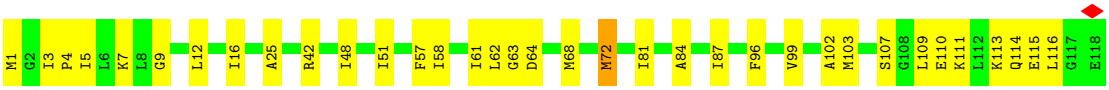
Chain	Residue	Modelled	Actual	Comment	Reference
T	278	GLY	GLU	variant	UNP A0AAD2RAW1
TB	19	ASP	ASN	variant	UNP A0AAD2RAW1
TB	175	GLU	THR	engineered mutation	UNP A0AAD2RAW1
TB	278	GLY	GLU	variant	UNP A0AAD2RAW1

3 Residue-property plots (i)

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

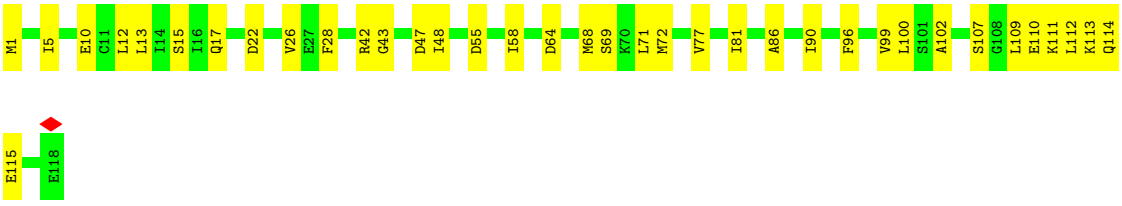
• Molecule 1: RsbT antagonist protein RsbS

Chain a:



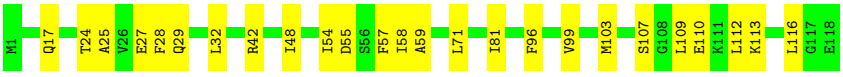
• Molecule 1: RsbT antagonist protein RsbS

Chain ab:



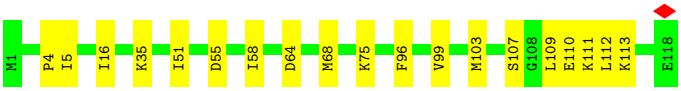
• Molecule 1: RsbT antagonist protein RsbS

Chain b:



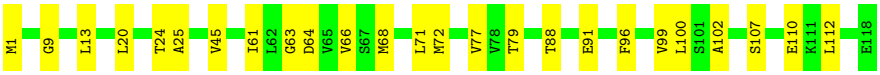
• Molecule 1: RsbT antagonist protein RsbS

Chain bb:



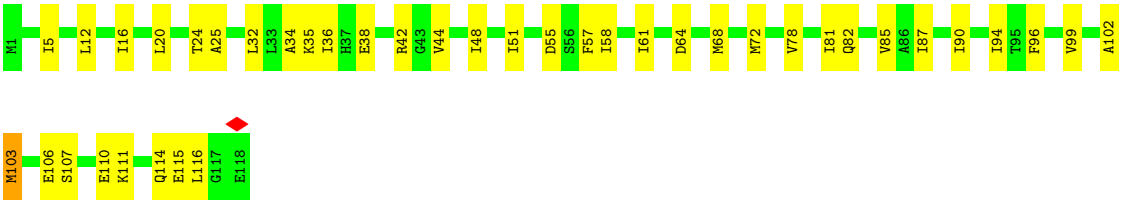
• Molecule 1: RsbT antagonist protein RsbS

Chain c:



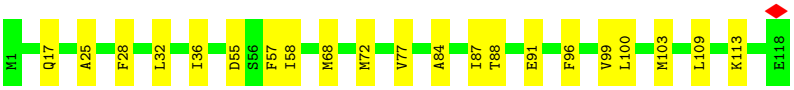
• Molecule 1: RsbT antagonist protein RsbS

Chain cb:



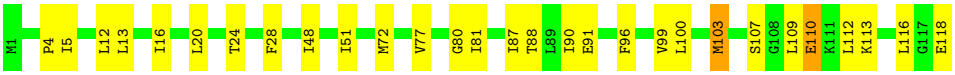
• Molecule 1: RsbT antagonist protein RsbS

Chain d:



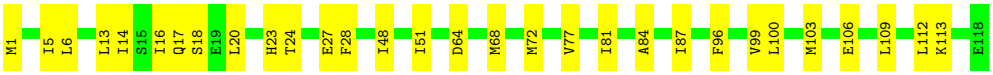
• Molecule 1: RsbT antagonist protein RsbS

Chain db:



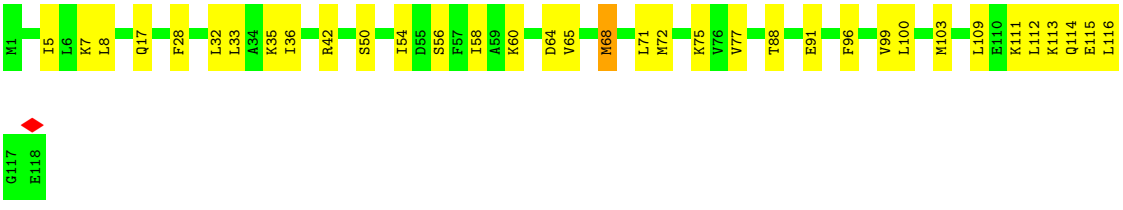
• Molecule 1: RsbT antagonist protein RsbS

Chain e:



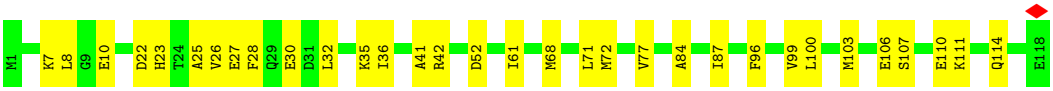
• Molecule 1: RsbT antagonist protein RsbS

Chain eb:



• Molecule 1: RsbT antagonist protein RsbS

Chain f:

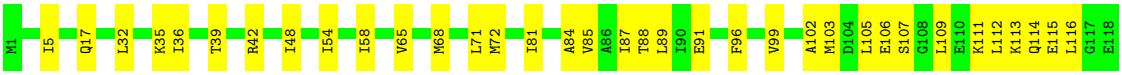


• Molecule 1: RsbT antagonist protein RsbS

Chain fb:

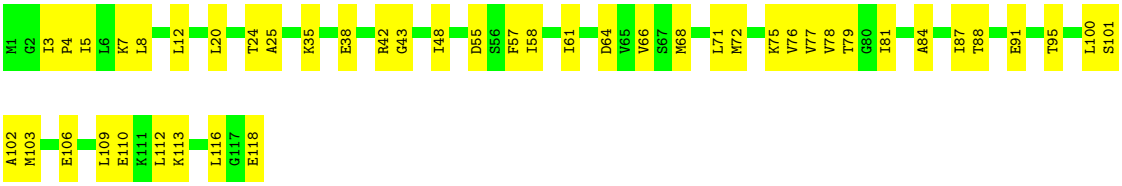
• Molecule 1: RsbT antagonist protein RsbS

Chain g:



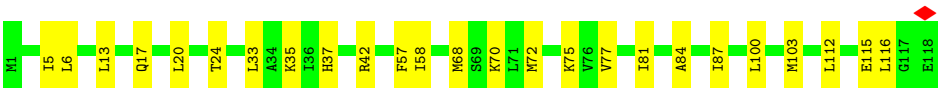
• Molecule 1: RsbT antagonist protein RsbS

Chain gb:



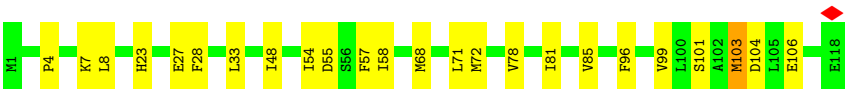
• Molecule 1: RsbT antagonist protein RsbS

Chain h:



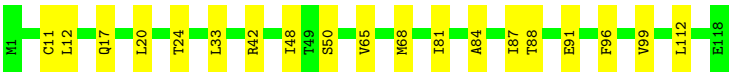
• Molecule 1: RsbT antagonist protein RsbS

Chain hb:



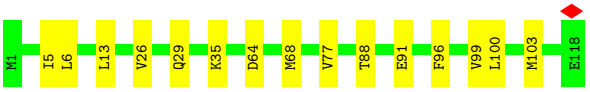
• Molecule 1: RsbT antagonist protein RsbS

Chain i:



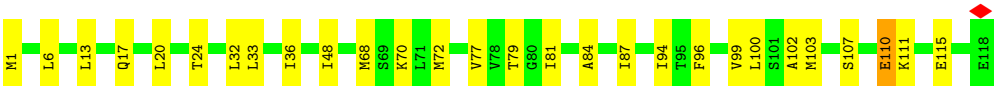
• Molecule 1: RsbT antagonist protein RsbS

Chain ib:



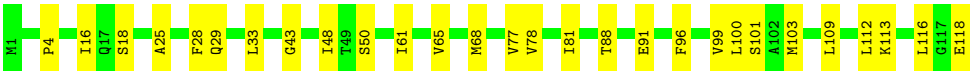
• Molecule 1: RsbT antagonist protein RsbS

Chain j:



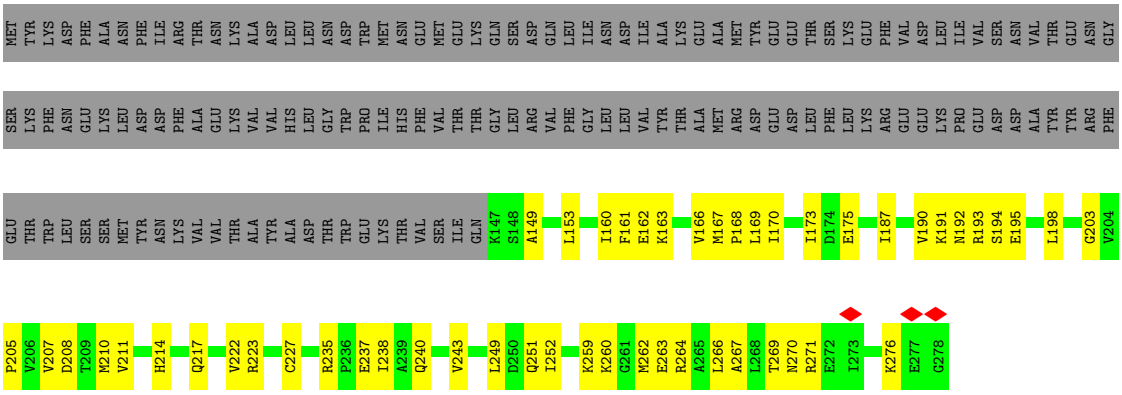
• Molecule 1: RsbT antagonist protein RsbS

Chain jb:



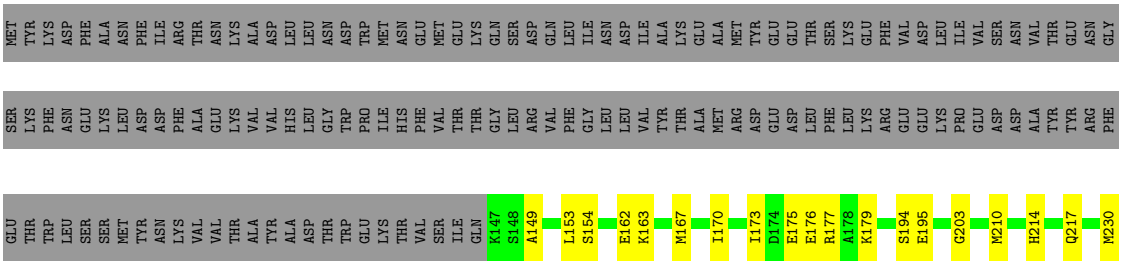
• Molecule 2: STAS domain-containing protein

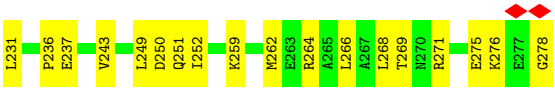
Chain A:



• Molecule 2: STAS domain-containing protein

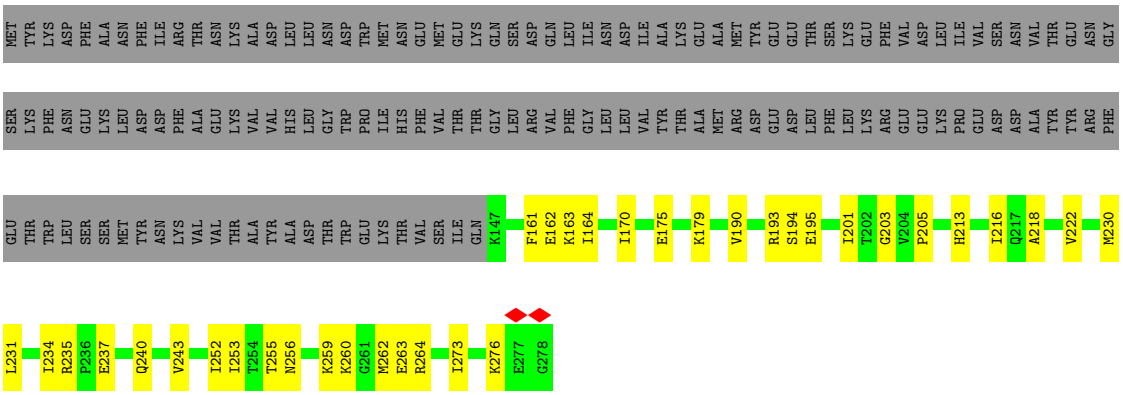
Chain AB:





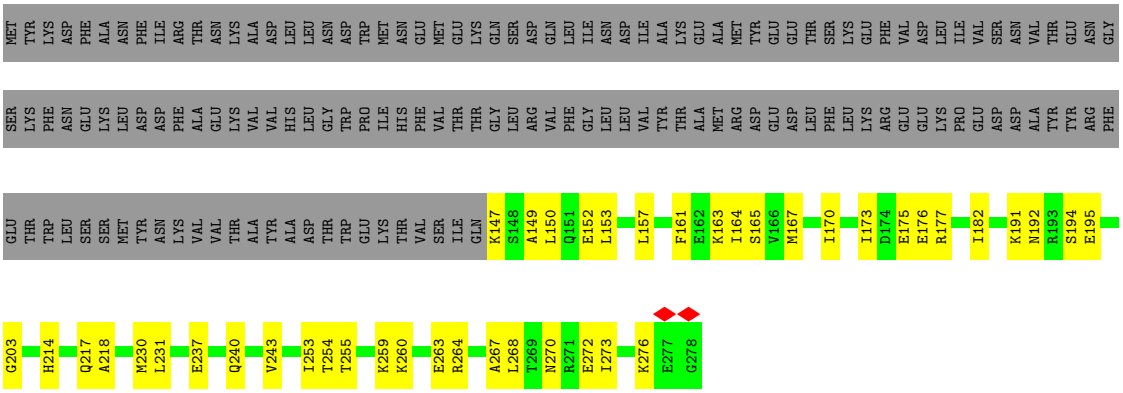
• Molecule 2: STAS domain-containing protein

Chain B:



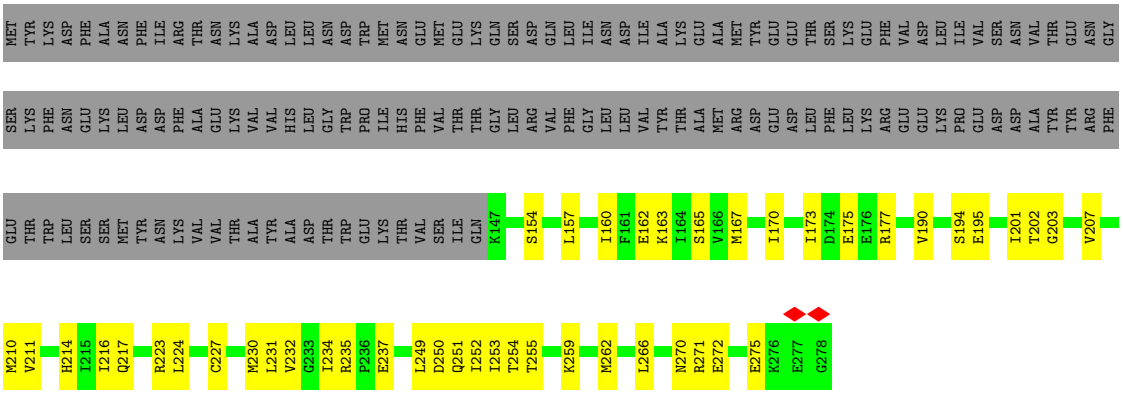
• Molecule 2: STAS domain-containing protein

Chain BB:



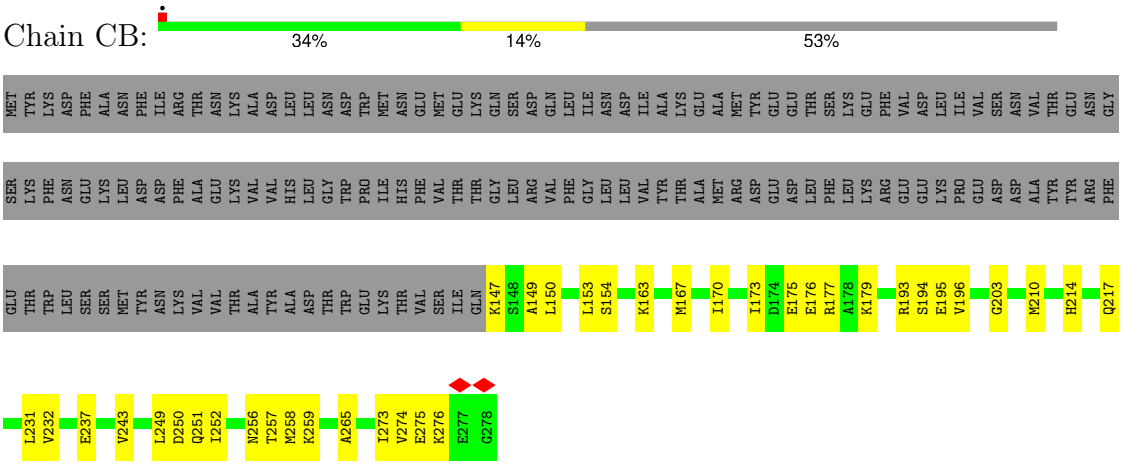
• Molecule 2: STAS domain-containing protein

Chain C:



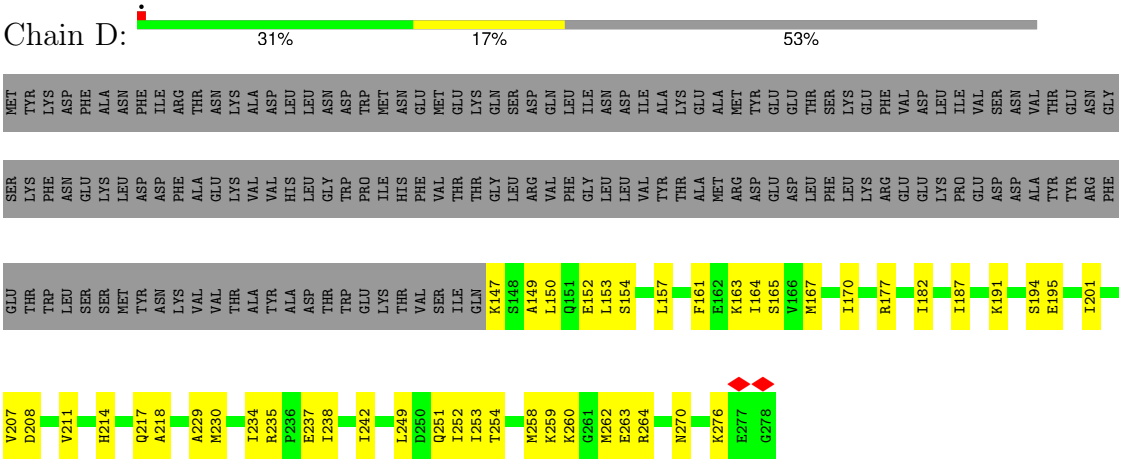
• Molecule 2: STAS domain-containing protein

Chain CB:



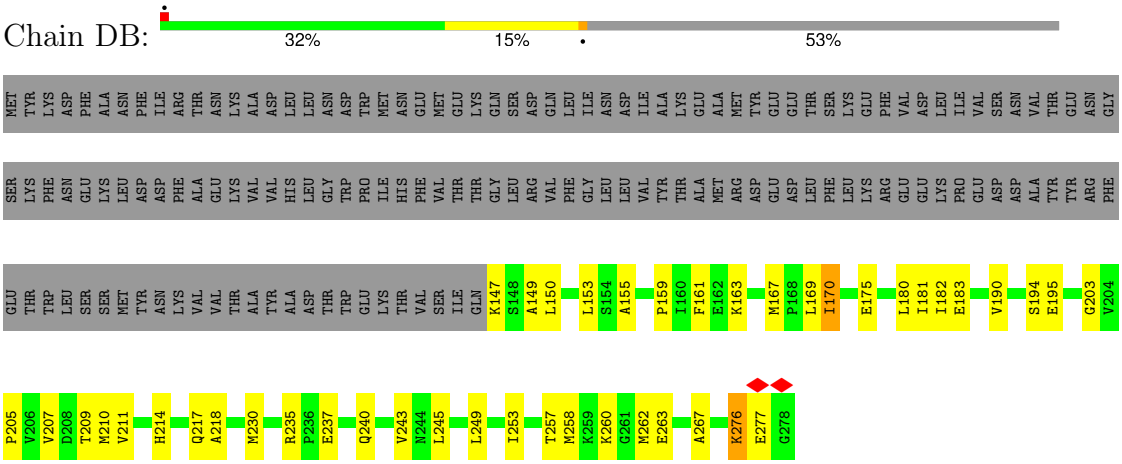
• Molecule 2: STAS domain-containing protein

Chain D:



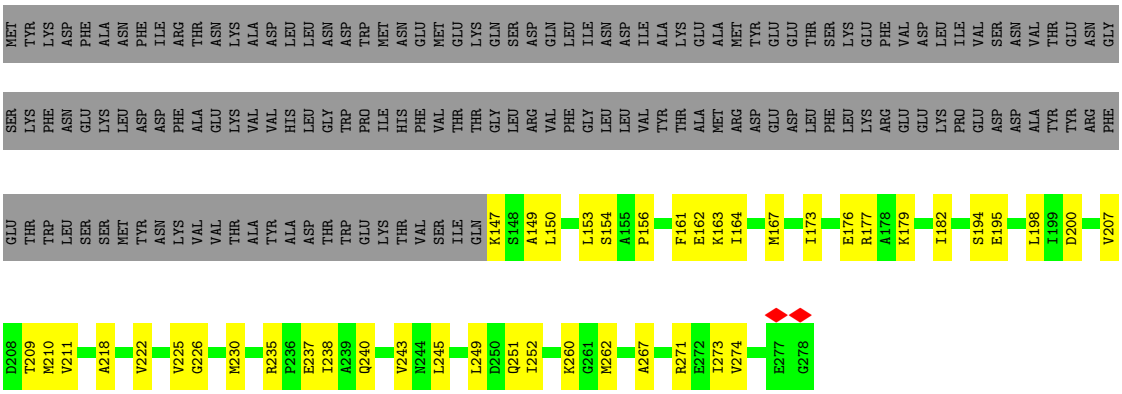
• Molecule 2: STAS domain-containing protein

Chain DB:



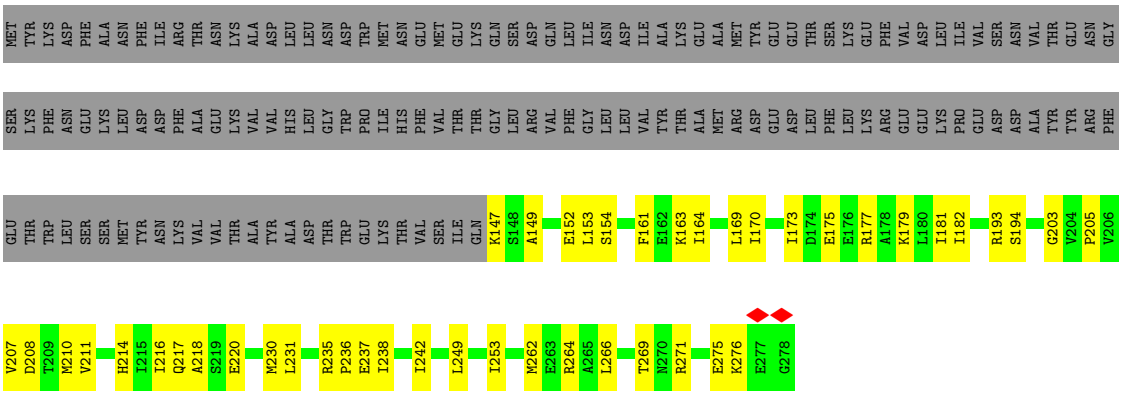
• Molecule 2: STAS domain-containing protein

Chain E:



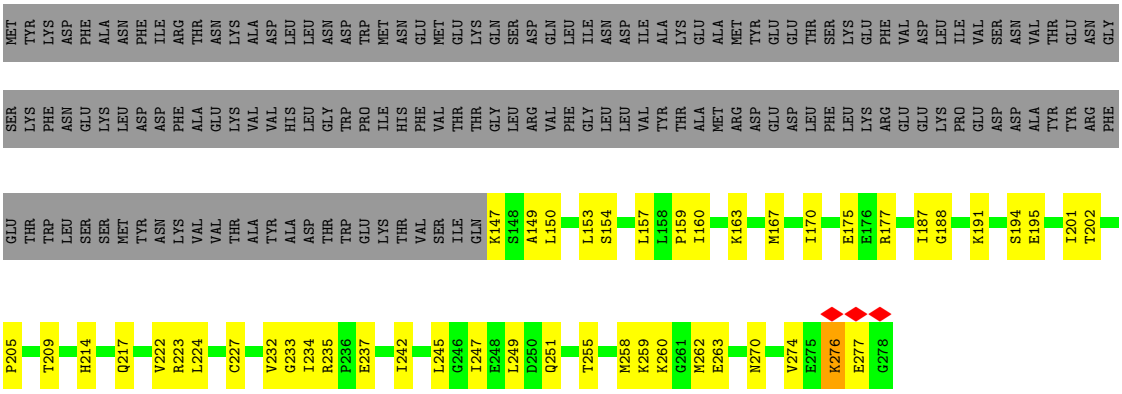
• Molecule 2: STAS domain-containing protein

Chain EB:



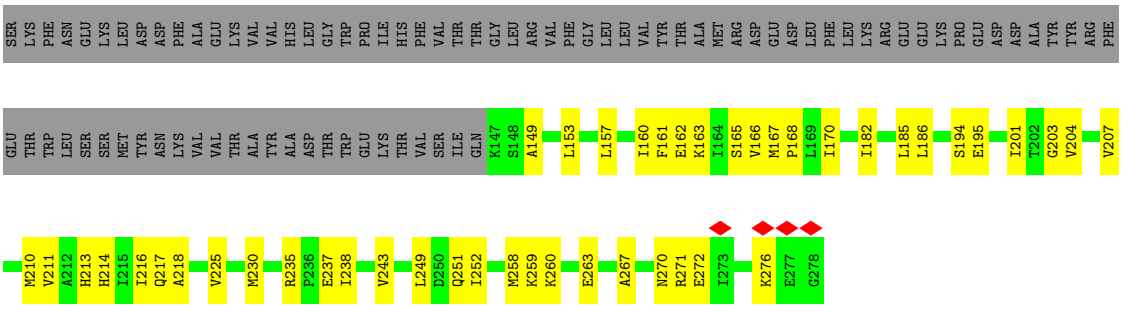
• Molecule 2: STAS domain-containing protein

Chain F:



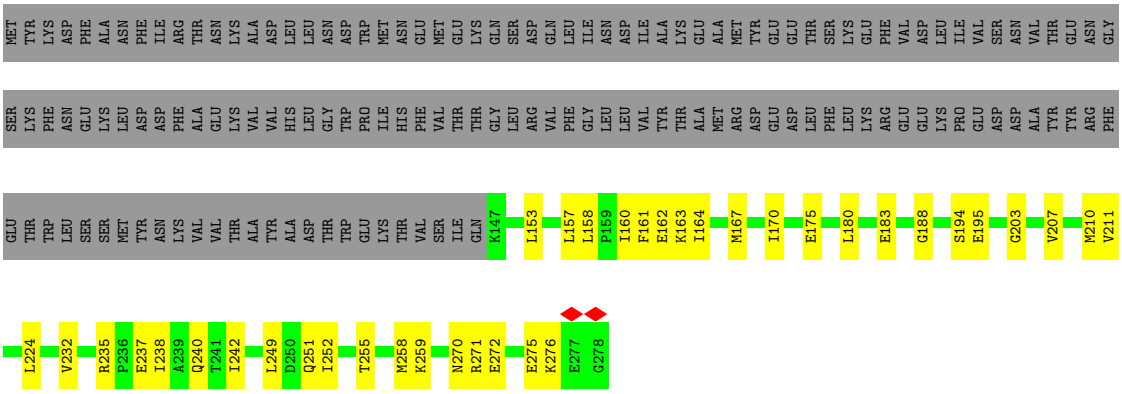
• Molecule 2: STAS domain-containing protein

Chain FB:



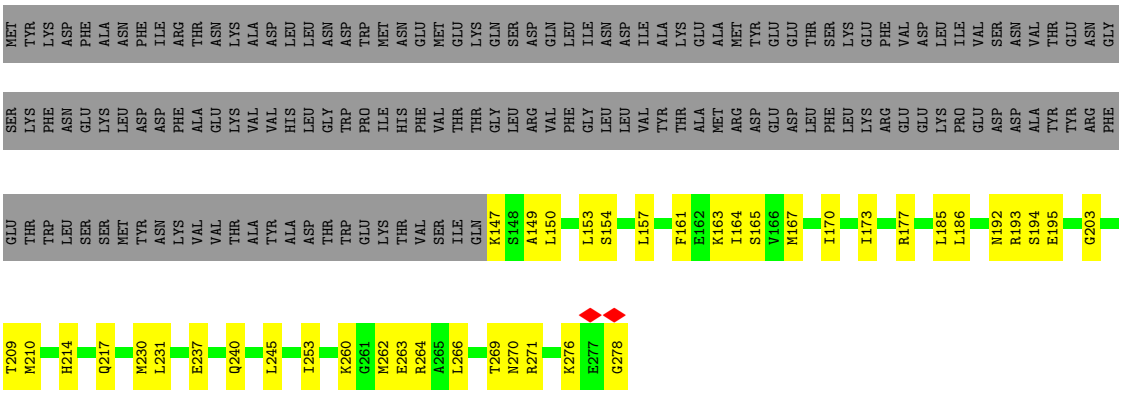
• Molecule 2: STAS domain-containing protein

Chain G:



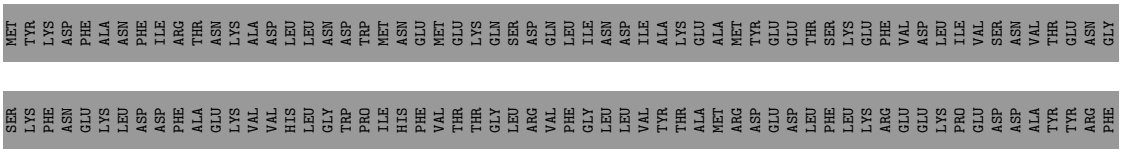
• Molecule 2: STAS domain-containing protein

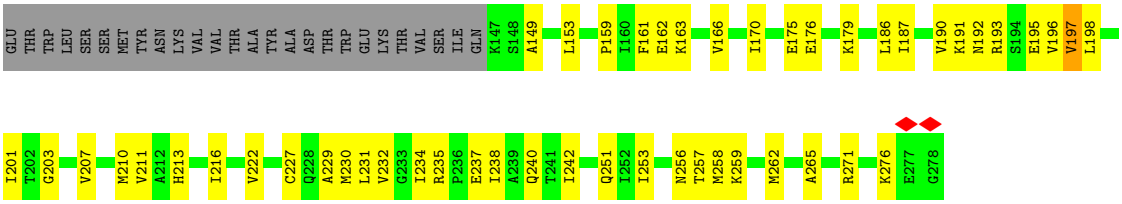
Chain GB:



• Molecule 2: STAS domain-containing protein

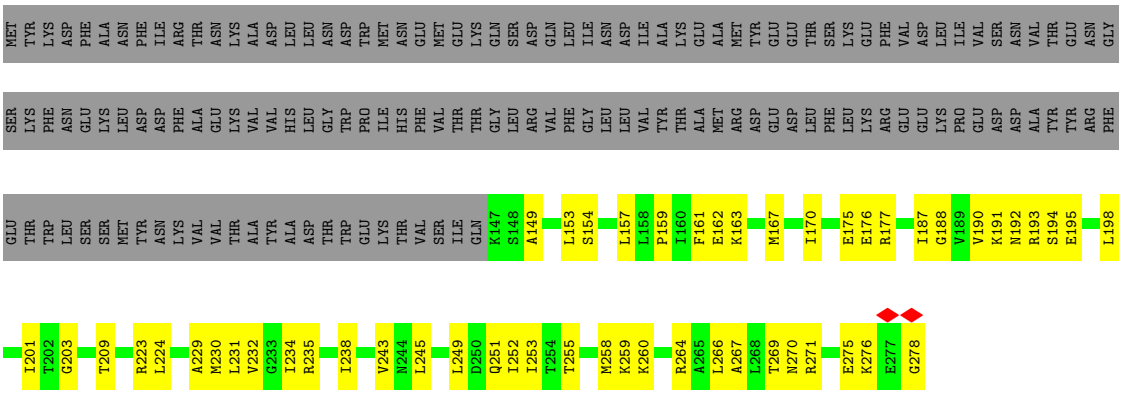
Chain H:





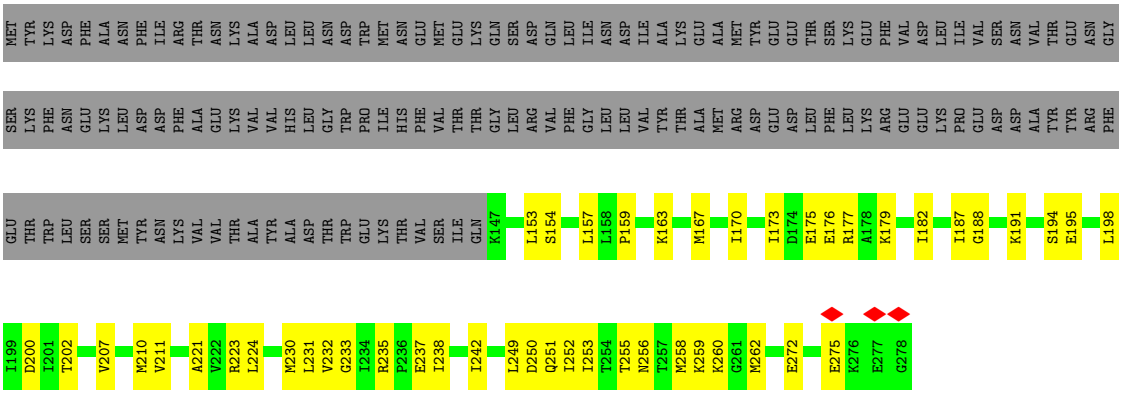
• Molecule 2: STAS domain-containing protein

Chain HB:



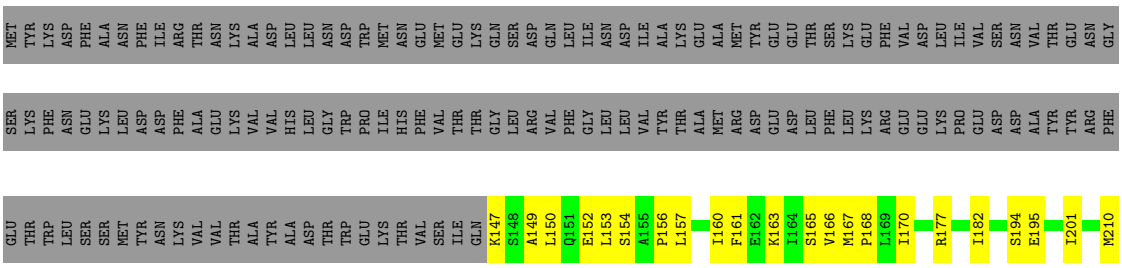
• Molecule 2: STAS domain-containing protein

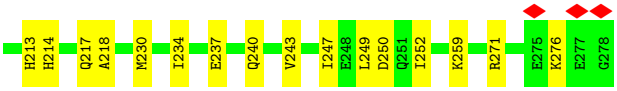
Chain I:



• Molecule 2: STAS domain-containing protein

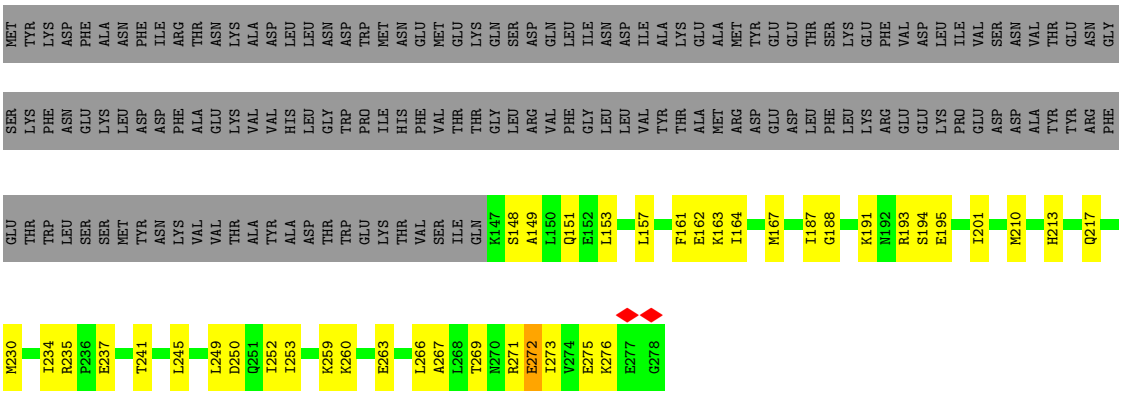
Chain IB:





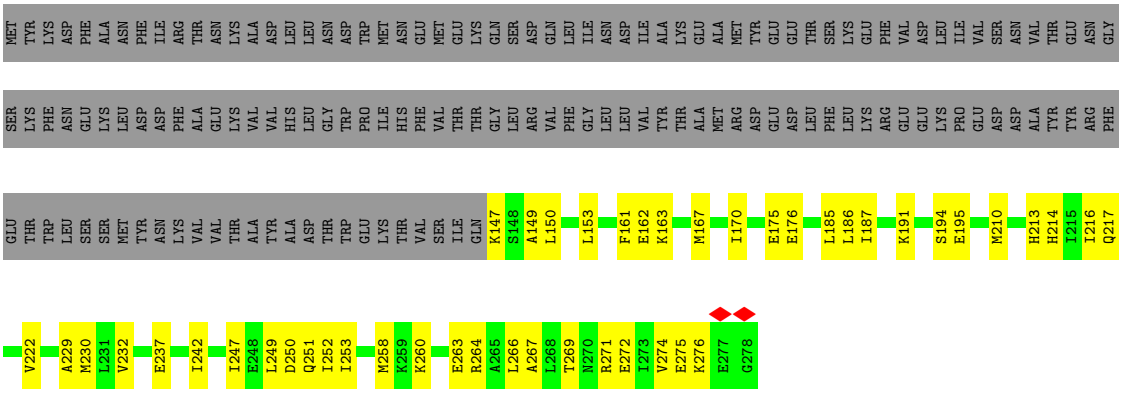
• Molecule 2: STAS domain-containing protein

Chain J:



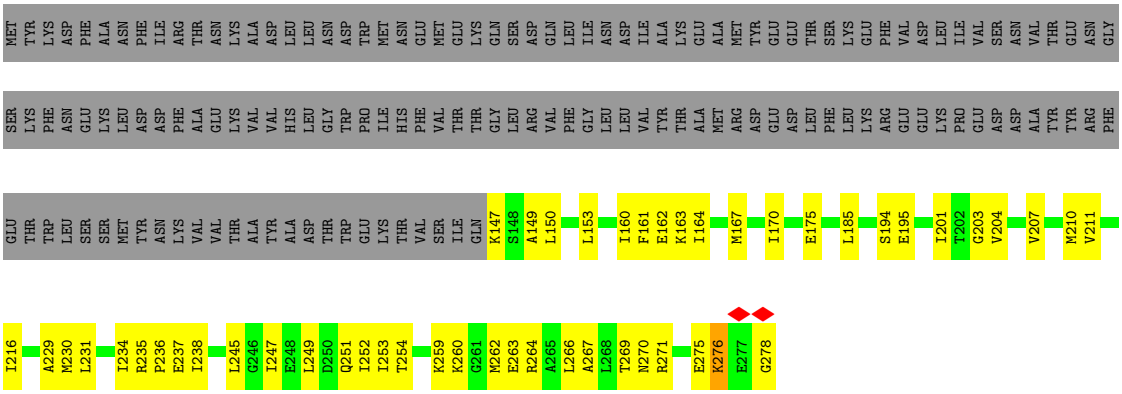
• Molecule 2: STAS domain-containing protein

Chain JB:



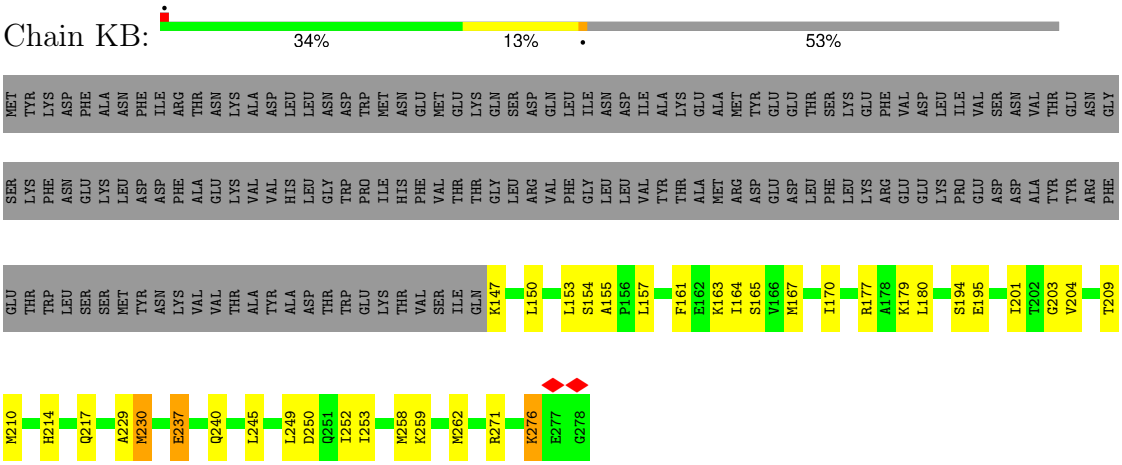
• Molecule 2: STAS domain-containing protein

Chain K:



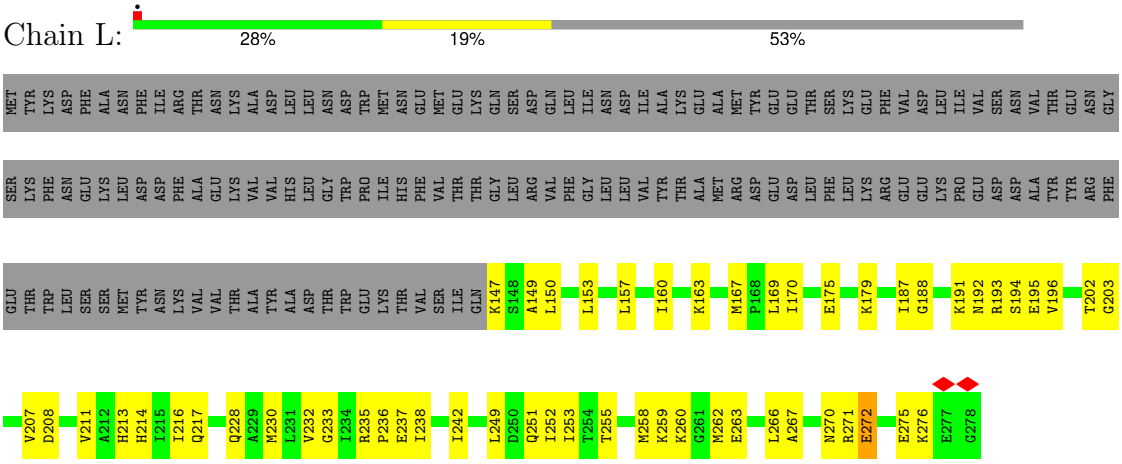
• Molecule 2: STAS domain-containing protein

Chain KB:



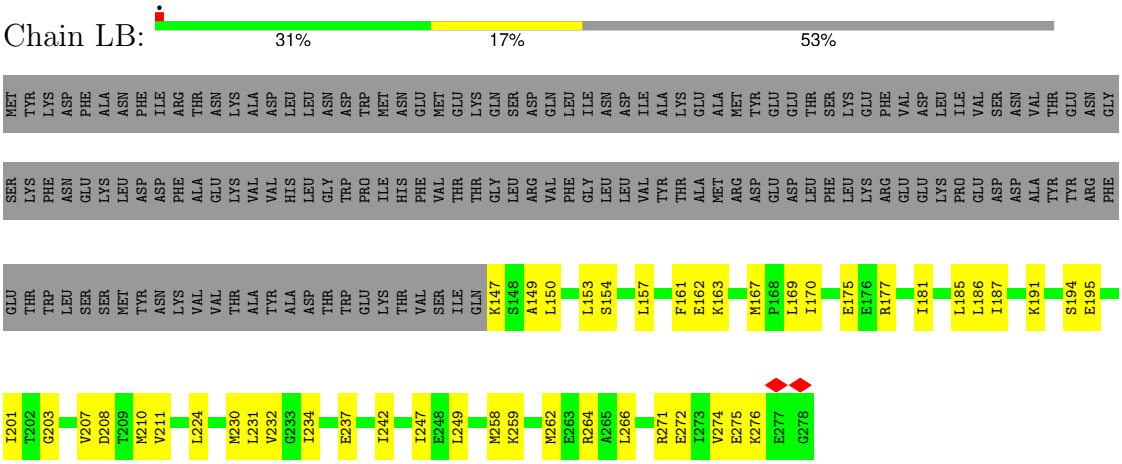
• Molecule 2: STAS domain-containing protein

Chain L:



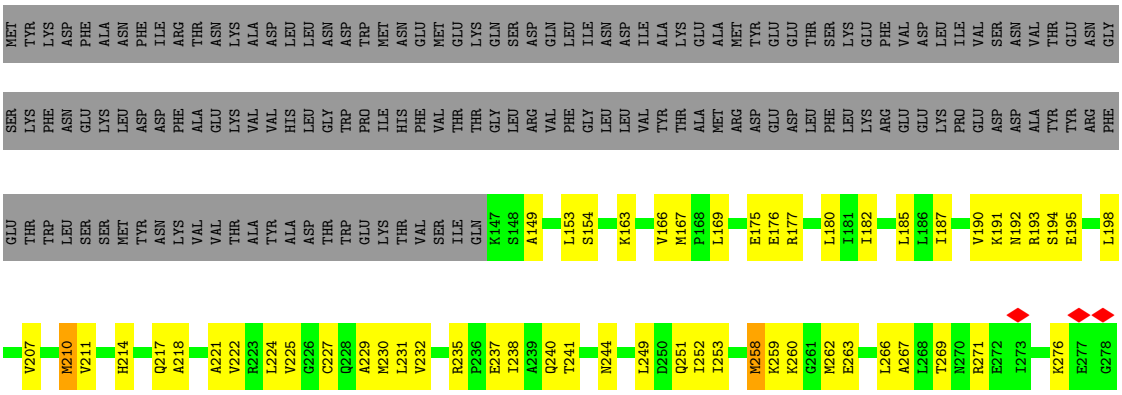
• Molecule 2: STAS domain-containing protein

Chain LB:



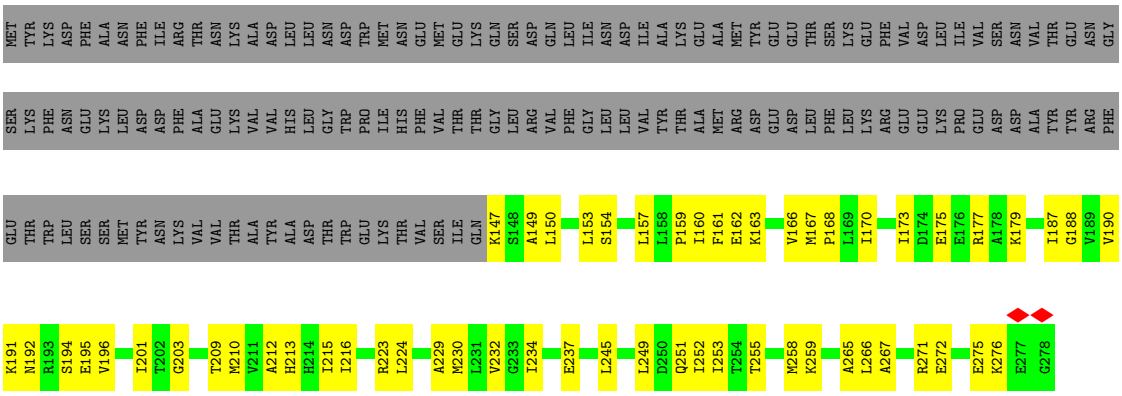
• Molecule 2: STAS domain-containing protein

Chain M:



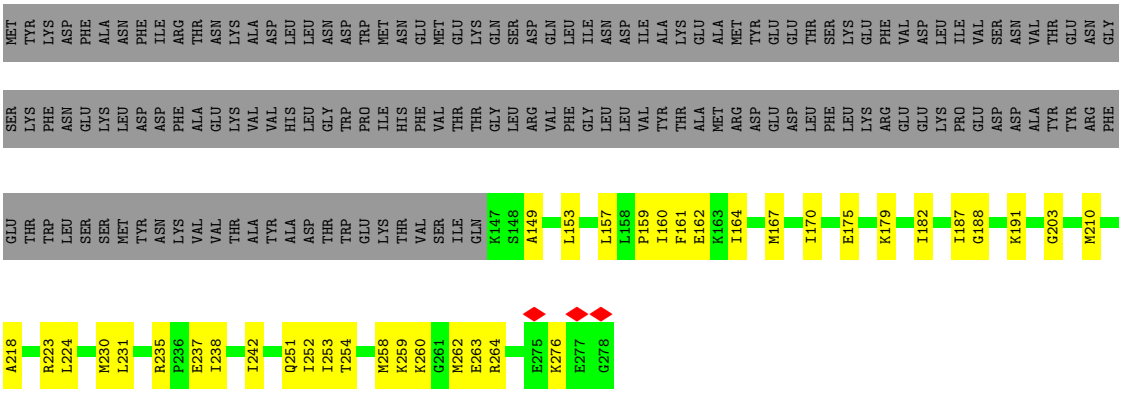
• Molecule 2: STAS domain-containing protein

Chain MB:



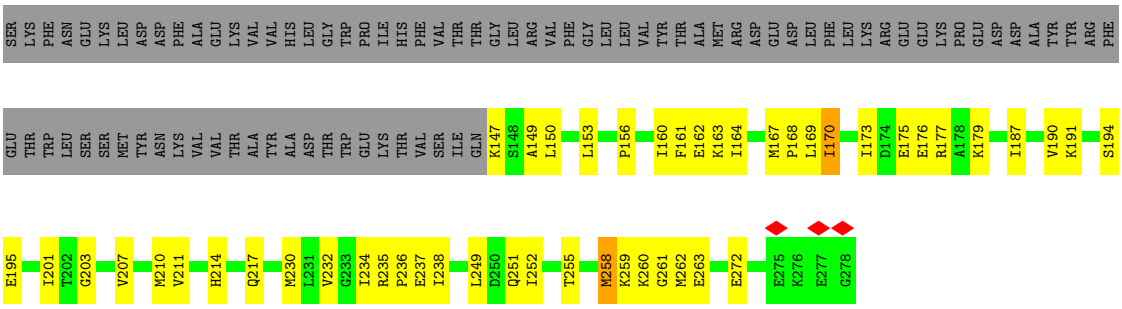
• Molecule 2: STAS domain-containing protein

Chain N:



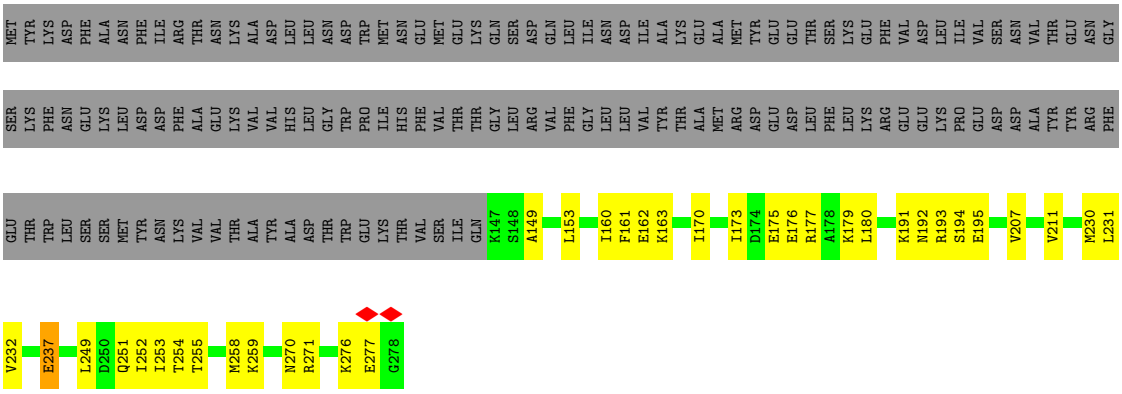
• Molecule 2: STAS domain-containing protein

Chain NB:



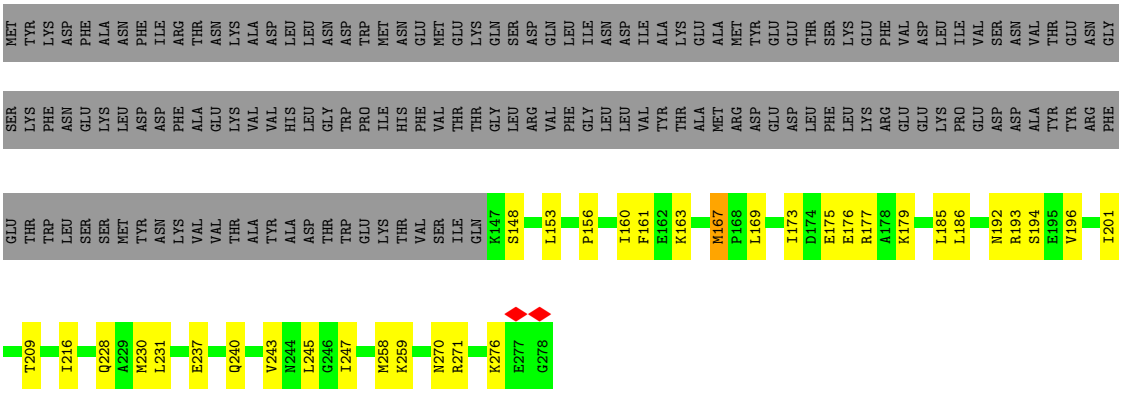
• Molecule 2: STAS domain-containing protein

Chain O:



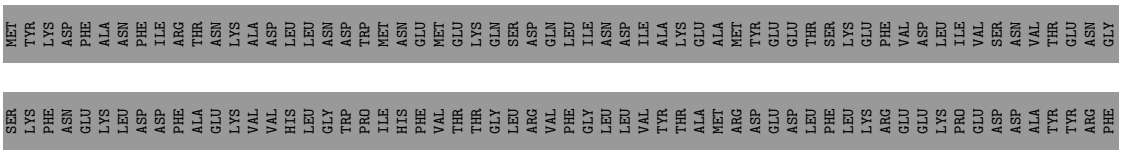
• Molecule 2: STAS domain-containing protein

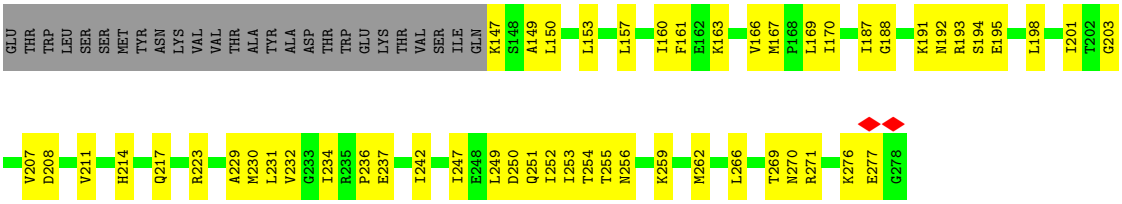
Chain OB:



• Molecule 2: STAS domain-containing protein

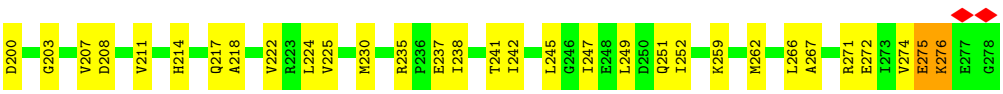
Chain P:





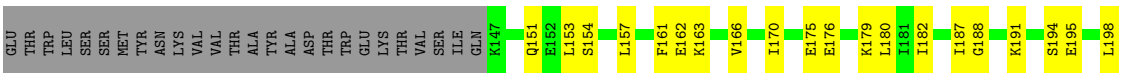
• Molecule 2: STAS domain-containing protein

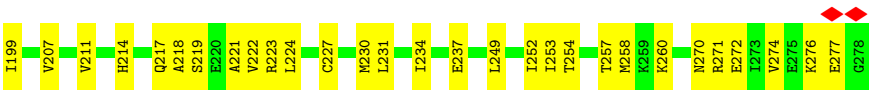
Chain PB:



• Molecule 2: STAS domain-containing protein

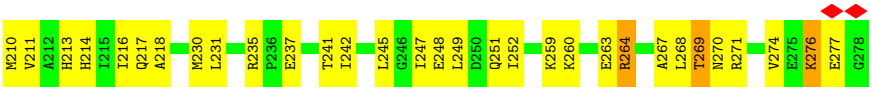
Chain Q:





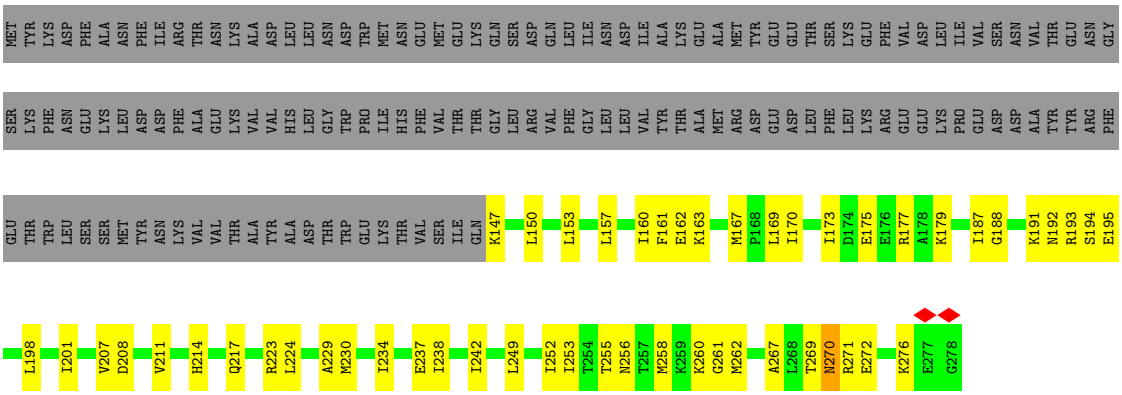
• Molecule 2: STAS domain-containing protein

Chain QB:



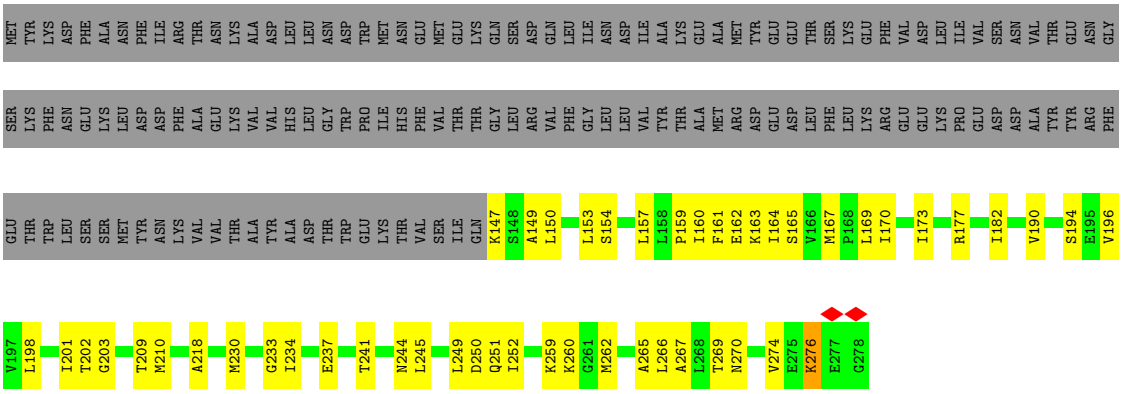
• Molecule 2: STAS domain-containing protein

Chain R:



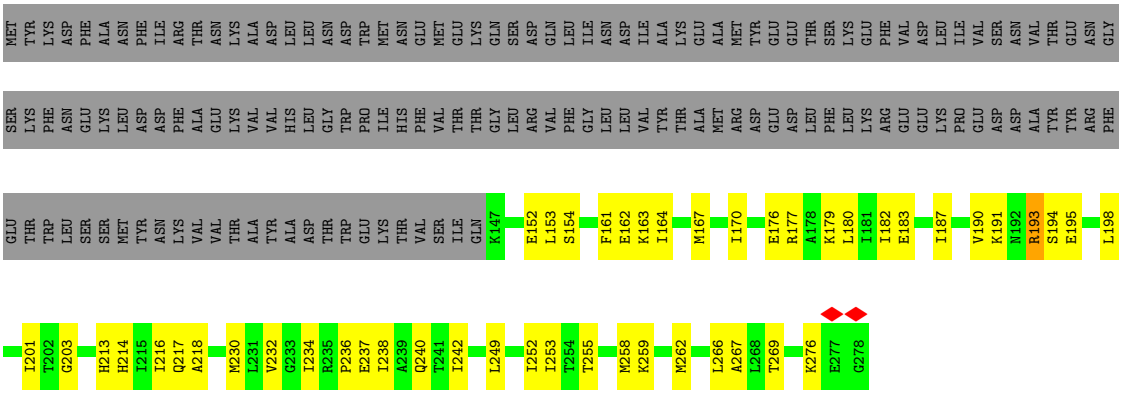
• Molecule 2: STAS domain-containing protein

Chain RB:



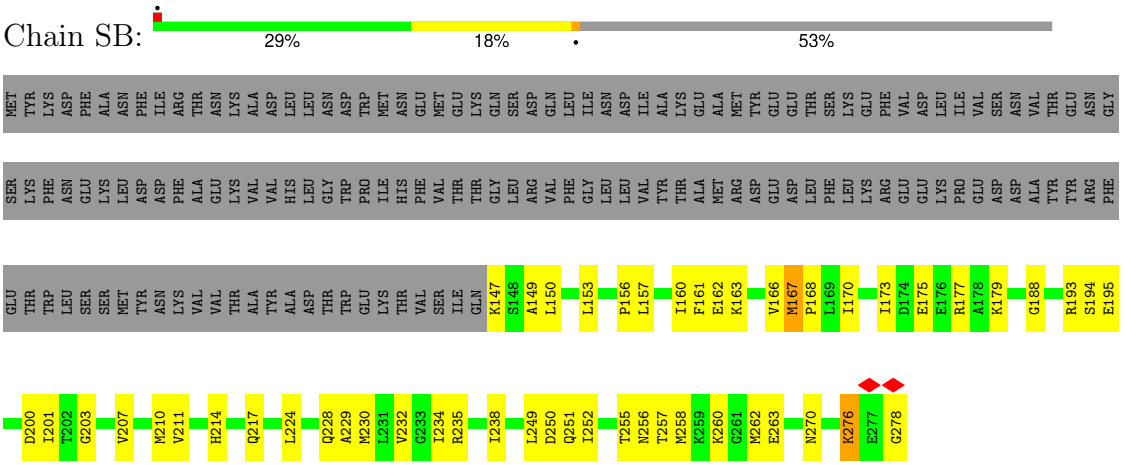
• Molecule 2: STAS domain-containing protein

Chain S:



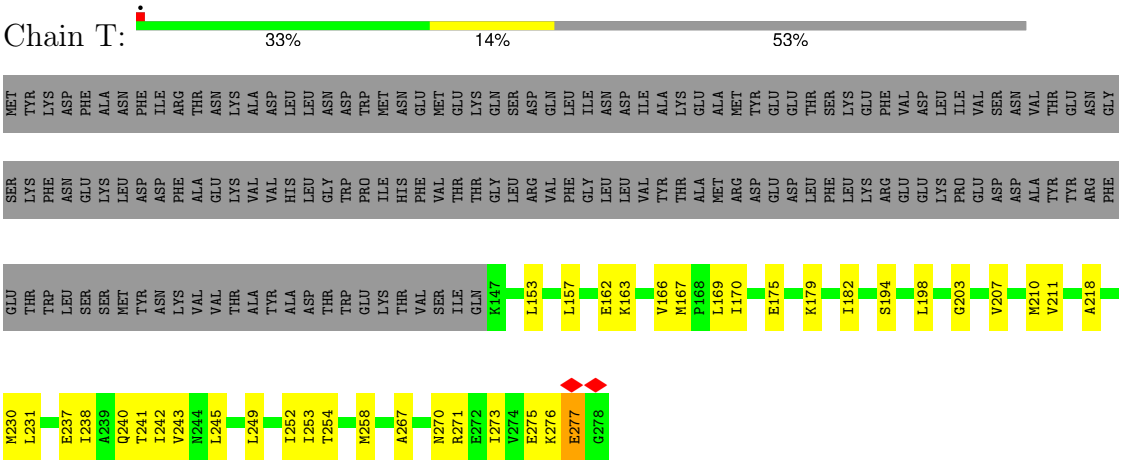
• Molecule 2: STAS domain-containing protein

Chain SB:



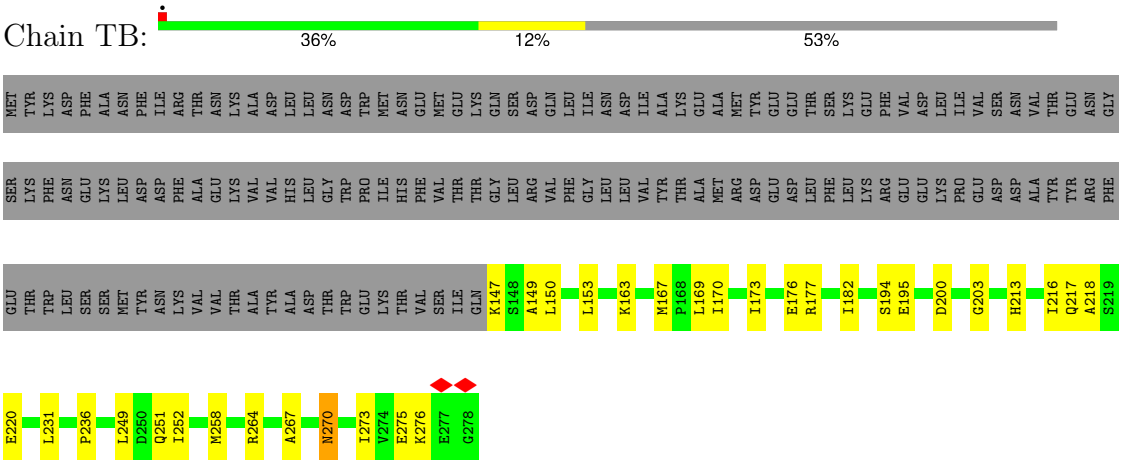
• Molecule 2: STAS domain-containing protein

Chain T:



• Molecule 2: STAS domain-containing protein

Chain TB:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58676	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.177	Depositor
Minimum map value	-0.210	Depositor
Average map value	0.017	Depositor
Map value standard deviation	0.075	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	398.4, 398.4, 398.4	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.328, 1.328, 1.328	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	0.25	0/888	0.42	0/1197
1	ab	0.25	0/888	0.38	0/1197
1	b	0.25	0/888	0.43	0/1197
1	bb	0.26	0/888	0.43	0/1197
1	c	0.24	0/888	0.38	0/1197
1	cb	0.24	0/888	0.38	0/1197
1	d	0.24	0/888	0.37	0/1197
1	db	0.24	0/888	0.40	0/1197
1	e	0.25	0/888	0.41	0/1197
1	eb	0.25	0/888	0.49	1/1197 (0.1%)
1	f	0.27	0/888	0.42	0/1197
1	fb	0.26	0/888	0.47	0/1197
1	g	0.24	0/888	0.42	0/1197
1	gb	0.25	0/888	0.39	0/1197
1	h	0.24	0/888	0.38	0/1197
1	hb	0.25	0/888	0.36	0/1197
1	i	0.25	0/888	0.39	0/1197
1	ib	0.24	0/888	0.37	0/1197
1	j	0.25	0/888	0.42	0/1197
1	jb	0.25	0/888	0.42	0/1197
2	A	0.24	0/1013	0.41	0/1370
2	AB	0.24	0/1013	0.42	0/1370
2	B	0.24	0/1013	0.46	0/1370
2	BB	0.24	0/1013	0.43	0/1370
2	C	0.25	0/1013	0.46	0/1370
2	CB	0.25	0/1013	0.41	0/1370
2	D	0.25	0/1013	0.43	0/1370
2	DB	0.24	0/1013	0.44	0/1370
2	E	0.24	0/1013	0.51	0/1370
2	EB	0.25	0/1013	0.39	0/1370
2	F	0.26	0/1013	0.43	0/1370
2	FB	0.24	0/1013	0.42	0/1370
2	G	0.26	0/1013	0.41	0/1370
2	GB	0.25	0/1013	0.41	0/1370

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
2	H	0.24	0/1013	0.40	0/1370
2	HB	0.25	0/1013	0.39	0/1370
2	I	0.25	0/1013	0.38	0/1370
2	IB	0.25	0/1013	0.42	0/1370
2	J	0.25	0/1013	0.39	0/1370
2	JB	0.25	0/1013	0.42	0/1370
2	K	0.24	0/1013	0.39	0/1370
2	KB	0.25	0/1013	0.38	0/1370
2	L	0.25	0/1013	0.43	0/1370
2	LB	0.24	0/1013	0.45	0/1370
2	M	0.25	0/1013	0.40	0/1370
2	MB	0.25	0/1013	0.41	0/1370
2	N	0.25	0/1013	0.45	0/1370
2	NB	0.24	0/1013	0.39	0/1370
2	O	0.25	0/1013	0.39	0/1370
2	OB	0.24	0/1013	0.47	0/1370
2	P	0.24	0/1013	0.44	0/1370
2	PB	0.26	0/1013	0.46	1/1370 (0.1%)
2	Q	0.25	0/1013	0.44	0/1370
2	QB	0.24	0/1013	0.41	0/1370
2	R	0.27	0/1013	0.51	0/1370
2	RB	0.25	0/1013	0.42	0/1370
2	S	0.24	0/1013	0.41	0/1370
2	SB	0.25	0/1013	0.45	0/1370
2	T	0.25	0/1013	0.40	0/1370
2	TB	0.24	0/1013	0.43	0/1370
All	All	0.25	0/58280	0.42	2/78740 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	eb	68	MET	CA-CB-CG	5.28	124.66	114.10
2	PB	275	GLU	CA-CB-CG	5.20	124.51	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	881	0	928	26	0
1	ab	881	0	928	29	0
1	b	881	0	928	21	0
1	bb	881	0	928	18	0
1	c	881	0	928	19	0
1	cb	881	0	928	26	0
1	d	881	0	928	14	0
1	db	881	0	928	19	0
1	e	881	0	928	20	0
1	eb	881	0	928	28	0
1	f	881	0	928	20	0
1	fb	881	0	928	16	0
1	g	881	0	928	25	0
1	gb	881	0	928	31	0
1	h	881	0	928	17	0
1	hb	881	0	928	16	0
1	i	881	0	928	11	0
1	ib	881	0	928	11	0
1	j	881	0	928	20	0
1	jb	881	0	928	17	0
2	A	1006	0	1084	39	0
2	AB	1006	0	1084	32	0
2	B	1006	0	1084	38	0
2	BB	1006	0	1084	37	0
2	C	1006	0	1084	40	0
2	CB	1006	0	1084	31	0
2	D	1006	0	1084	36	0
2	DB	1006	0	1084	39	0
2	E	1006	0	1084	38	0
2	EB	1006	0	1084	35	0
2	F	1006	0	1084	39	0
2	FB	1006	0	1084	38	0
2	G	1006	0	1084	30	0
2	GB	1006	0	1084	37	0
2	H	1006	0	1084	41	0
2	HB	1006	0	1084	45	0
2	I	1006	0	1084	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	IB	1006	0	1084	30	0
2	J	1006	0	1084	38	0
2	JB	1006	0	1084	43	0
2	K	1006	0	1084	44	0
2	KB	1006	0	1084	33	0
2	L	1006	0	1084	51	0
2	LB	1006	0	1084	41	0
2	M	1006	0	1084	47	0
2	MB	1006	0	1084	44	0
2	N	1006	0	1084	33	0
2	NB	1006	0	1084	43	0
2	O	1006	0	1084	39	0
2	OB	1006	0	1084	30	0
2	P	1006	0	1084	41	0
2	PB	1006	0	1084	48	0
2	Q	1006	0	1084	43	0
2	QB	1006	0	1084	46	0
2	R	1006	0	1084	49	0
2	RB	1006	0	1084	41	0
2	S	1006	0	1084	37	0
2	SB	1006	0	1084	42	0
2	T	1006	0	1084	33	0
2	TB	1006	0	1084	28	0
All	All	57860	0	61920	1711	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 14.

The worst 5 of 1711 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:A:259:LYS:HA	2:A:262:MET:HE2	1.34	1.05
2:RB:259:LYS:HA	2:RB:262:MET:HE2	1.45	0.97
2:N:259:LYS:HA	2:N:262:MET:HE2	1.59	0.85
2:HB:230:MET:HE1	2:HB:253:ILE:HB	1.60	0.83
1:j:103:MET:HE3	1:j:103:MET:H	1.44	0.82

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	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	ab	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
1	b	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
1	bb	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
1	c	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
1	cb	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	d	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
1	db	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	e	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
1	eb	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
1	f	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	fb	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	g	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
1	gb	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
1	h	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	hb	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	i	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
1	ib	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
1	j	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
1	jb	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
2	A	130/278 (47%)	128 (98%)	2 (2%)	0	100	100
2	AB	130/278 (47%)	127 (98%)	3 (2%)	0	100	100
2	B	130/278 (47%)	123 (95%)	7 (5%)	0	100	100
2	BB	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	C	130/278 (47%)	123 (95%)	6 (5%)	1 (1%)	16	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CB	130/278 (47%)	127 (98%)	3 (2%)	0	100	100
2	D	130/278 (47%)	126 (97%)	4 (3%)	0	100	100
2	DB	130/278 (47%)	121 (93%)	9 (7%)	0	100	100
2	E	130/278 (47%)	122 (94%)	8 (6%)	0	100	100
2	EB	130/278 (47%)	120 (92%)	10 (8%)	0	100	100
2	F	130/278 (47%)	123 (95%)	7 (5%)	0	100	100
2	FB	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	G	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	GB	130/278 (47%)	128 (98%)	2 (2%)	0	100	100
2	H	130/278 (47%)	122 (94%)	8 (6%)	0	100	100
2	HB	130/278 (47%)	126 (97%)	4 (3%)	0	100	100
2	I	130/278 (47%)	126 (97%)	4 (3%)	0	100	100
2	IB	130/278 (47%)	128 (98%)	2 (2%)	0	100	100
2	J	130/278 (47%)	124 (95%)	6 (5%)	0	100	100
2	JB	130/278 (47%)	127 (98%)	3 (2%)	0	100	100
2	K	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	KB	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	L	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	LB	130/278 (47%)	123 (95%)	7 (5%)	0	100	100
2	M	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	MB	130/278 (47%)	128 (98%)	2 (2%)	0	100	100
2	N	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
2	NB	130/278 (47%)	128 (98%)	2 (2%)	0	100	100
2	O	130/278 (47%)	123 (95%)	7 (5%)	0	100	100
2	OB	130/278 (47%)	124 (95%)	6 (5%)	0	100	100
2	P	130/278 (47%)	123 (95%)	7 (5%)	0	100	100
2	PB	130/278 (47%)	124 (95%)	6 (5%)	0	100	100
2	Q	130/278 (47%)	124 (95%)	6 (5%)	0	100	100
2	QB	130/278 (47%)	127 (98%)	3 (2%)	0	100	100
2	R	130/278 (47%)	121 (93%)	9 (7%)	0	100	100
2	RB	130/278 (47%)	126 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S	130/278 (47%)	126 (97%)	4 (3%)	0	100	100
2	SB	130/278 (47%)	124 (95%)	6 (5%)	0	100	100
2	T	130/278 (47%)	128 (98%)	2 (2%)	0	100	100
2	TB	130/278 (47%)	125 (96%)	5 (4%)	0	100	100
All	All	7520/13480 (56%)	7258 (96%)	261 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	275	GLU

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	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	ab	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	b	100/100 (100%)	100 (100%)	0	100	100
1	bb	100/100 (100%)	100 (100%)	0	100	100
1	c	100/100 (100%)	100 (100%)	0	100	100
1	cb	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	d	100/100 (100%)	100 (100%)	0	100	100
1	db	100/100 (100%)	97 (97%)	3 (3%)	36	57
1	e	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	eb	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	f	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	fb	100/100 (100%)	100 (100%)	0	100	100
1	g	100/100 (100%)	100 (100%)	0	100	100
1	gb	100/100 (100%)	99 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	h	100/100 (100%)	100 (100%)	0	100	100
1	hb	100/100 (100%)	97 (97%)	3 (3%)	36	57
1	i	100/100 (100%)	100 (100%)	0	100	100
1	ib	100/100 (100%)	100 (100%)	0	100	100
1	j	100/100 (100%)	99 (99%)	1 (1%)	68	75
1	jb	100/100 (100%)	99 (99%)	1 (1%)	68	75
2	A	114/247 (46%)	111 (97%)	3 (3%)	40	60
2	AB	114/247 (46%)	114 (100%)	0	100	100
2	B	114/247 (46%)	114 (100%)	0	100	100
2	BB	114/247 (46%)	114 (100%)	0	100	100
2	C	114/247 (46%)	114 (100%)	0	100	100
2	CB	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	D	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	DB	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	E	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	EB	114/247 (46%)	114 (100%)	0	100	100
2	F	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	FB	114/247 (46%)	114 (100%)	0	100	100
2	G	114/247 (46%)	114 (100%)	0	100	100
2	GB	114/247 (46%)	114 (100%)	0	100	100
2	H	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	HB	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	I	114/247 (46%)	114 (100%)	0	100	100
2	IB	114/247 (46%)	114 (100%)	0	100	100
2	J	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	JB	114/247 (46%)	114 (100%)	0	100	100
2	K	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	KB	114/247 (46%)	111 (97%)	3 (3%)	40	60
2	L	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	LB	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	M	114/247 (46%)	112 (98%)	2 (2%)	51	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	MB	114/247 (46%)	114 (100%)	0	100	100
2	N	114/247 (46%)	114 (100%)	0	100	100
2	NB	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	O	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	OB	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	P	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	PB	114/247 (46%)	111 (97%)	3 (3%)	40	60
2	Q	114/247 (46%)	114 (100%)	0	100	100
2	QB	114/247 (46%)	111 (97%)	3 (3%)	40	60
2	R	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	RB	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	S	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	SB	114/247 (46%)	112 (98%)	2 (2%)	51	66
2	T	114/247 (46%)	113 (99%)	1 (1%)	70	75
2	TB	114/247 (46%)	113 (99%)	1 (1%)	70	75
All	All	6560/11880 (55%)	6500 (99%)	60 (1%)	68	75

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	210	MET
2	S	193	ARG
2	L	272	GLU
2	RB	276	LYS
2	TB	270	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
2	KB	213	HIS
2	N	213	HIS
2	L	251	GLN
2	M	213	HIS
2	QB	151	GLN

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

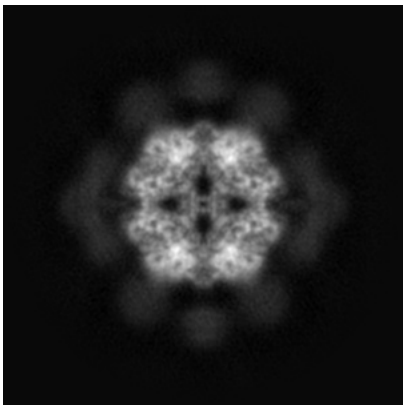
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-70144. These allow visual inspection of the internal detail of the map and identification of artifacts.

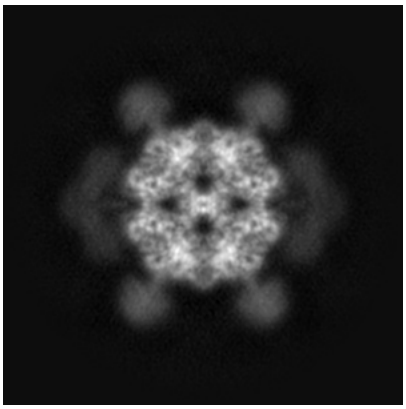
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

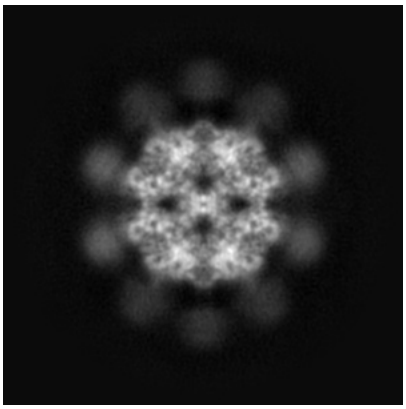
6.1.1 Primary map



X

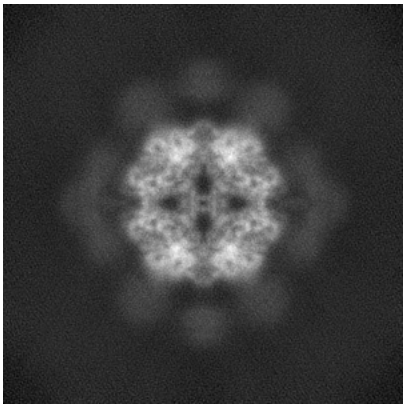


Y

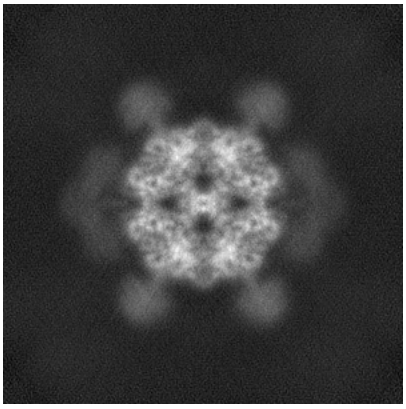


Z

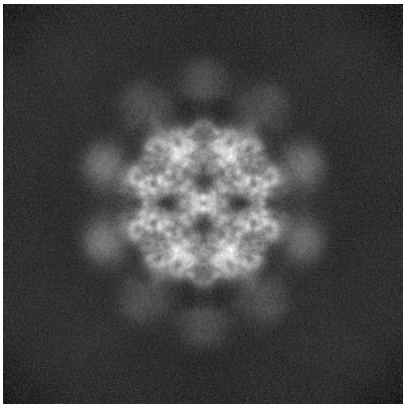
6.1.2 Raw map



X



Y

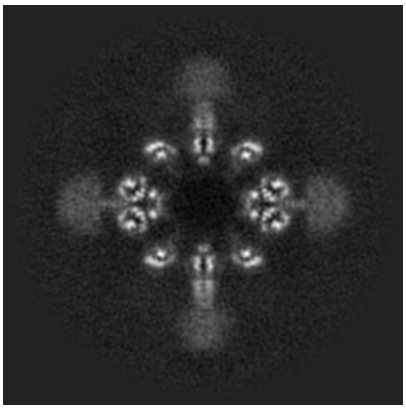


Z

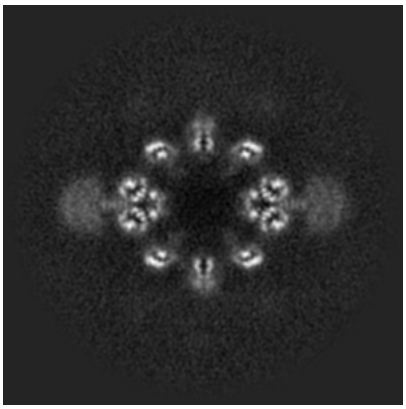
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

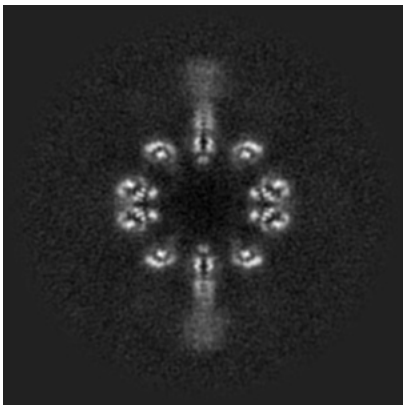
6.2.1 Primary map



X Index: 150

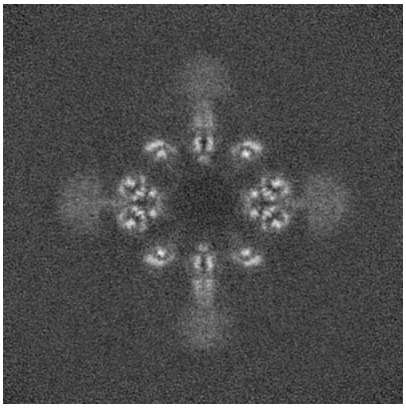


Y Index: 150

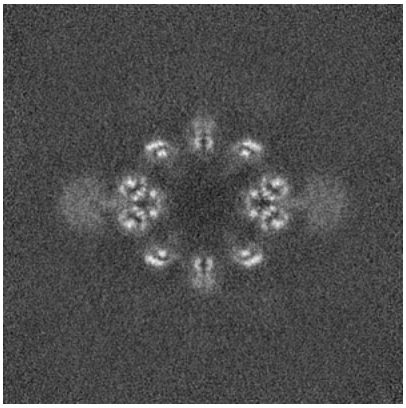


Z Index: 150

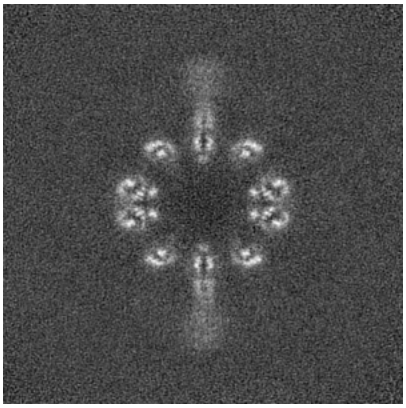
6.2.2 Raw map



X Index: 150



Y Index: 150

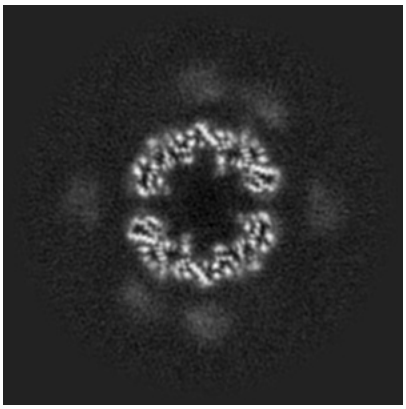


Z Index: 150

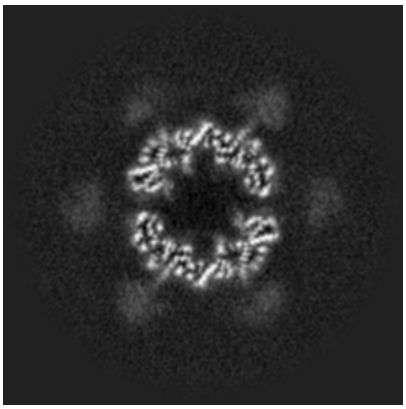
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

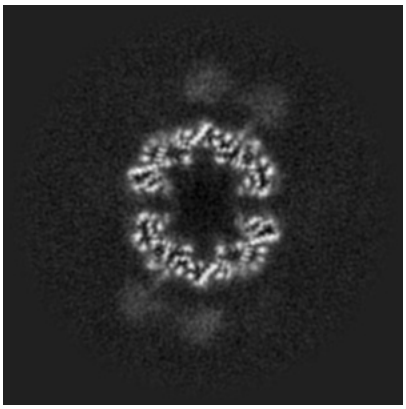
6.3.1 Primary map



X Index: 135

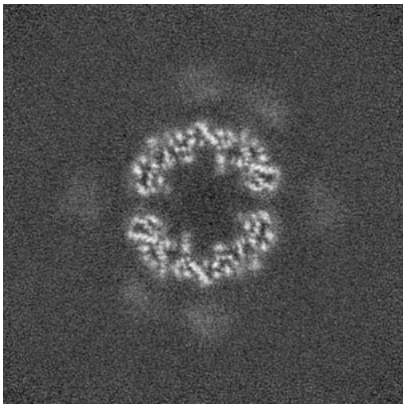


Y Index: 165

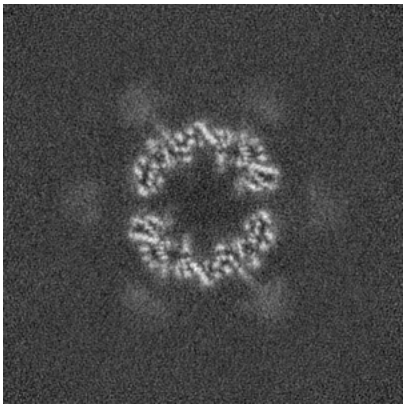


Z Index: 165

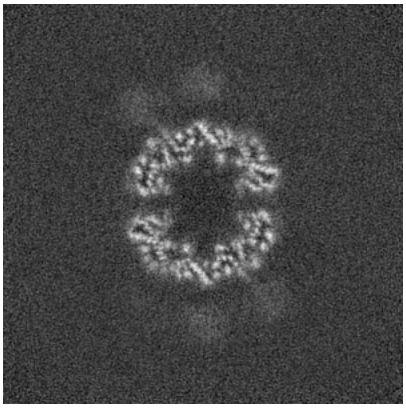
6.3.2 Raw map



X Index: 135



Y Index: 135

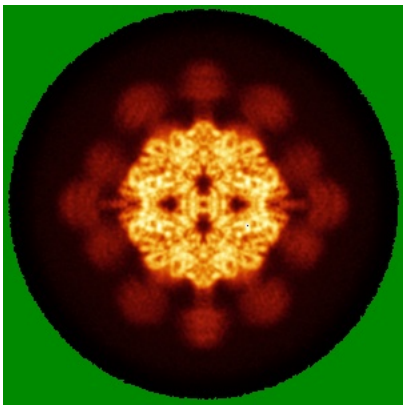


Z Index: 135

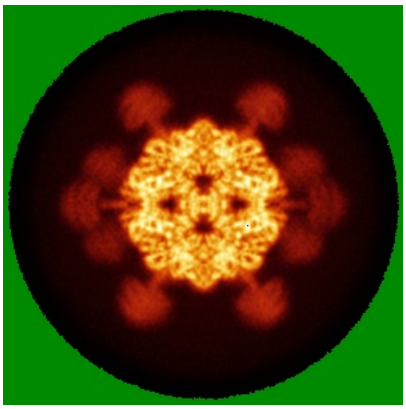
The images above show the largest variance slices of the map in three orthogonal directions.

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

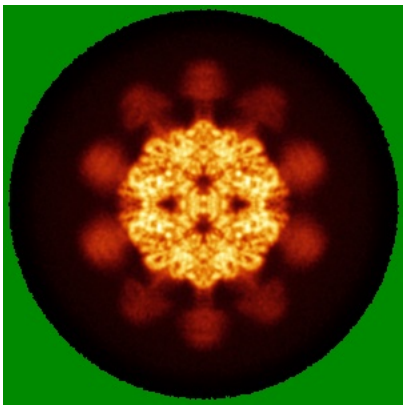
6.4.1 Primary map



X

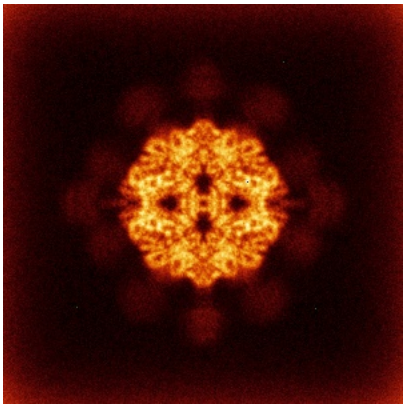


Y

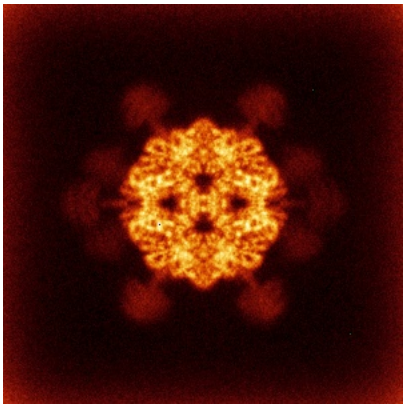


Z

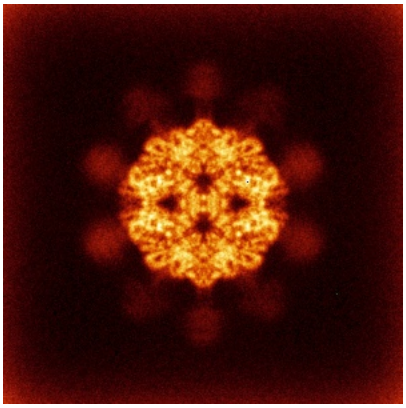
6.4.2 Raw map



X



Y

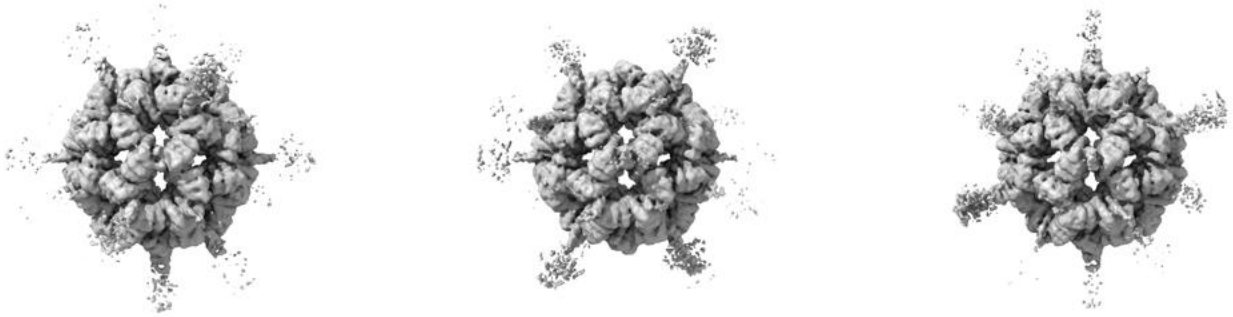


Z

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

6.5 Orthogonal surface views (i)

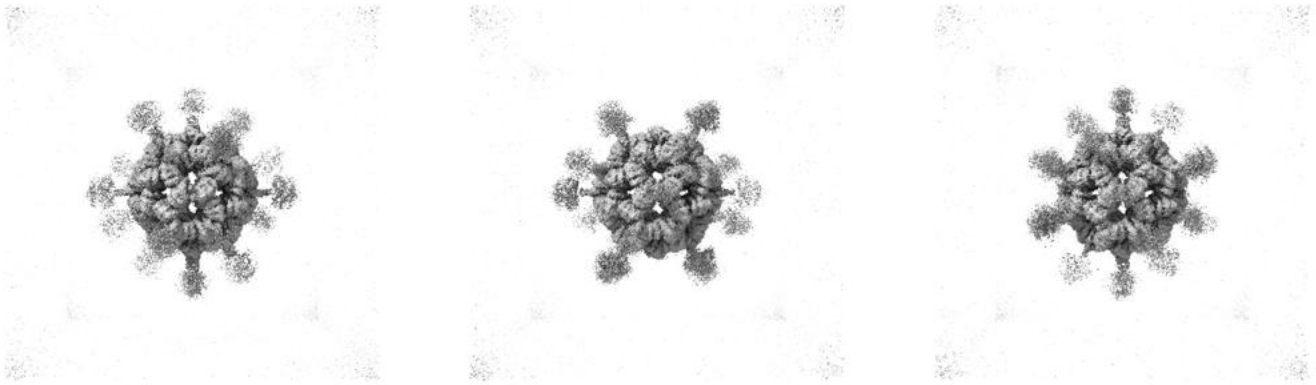
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

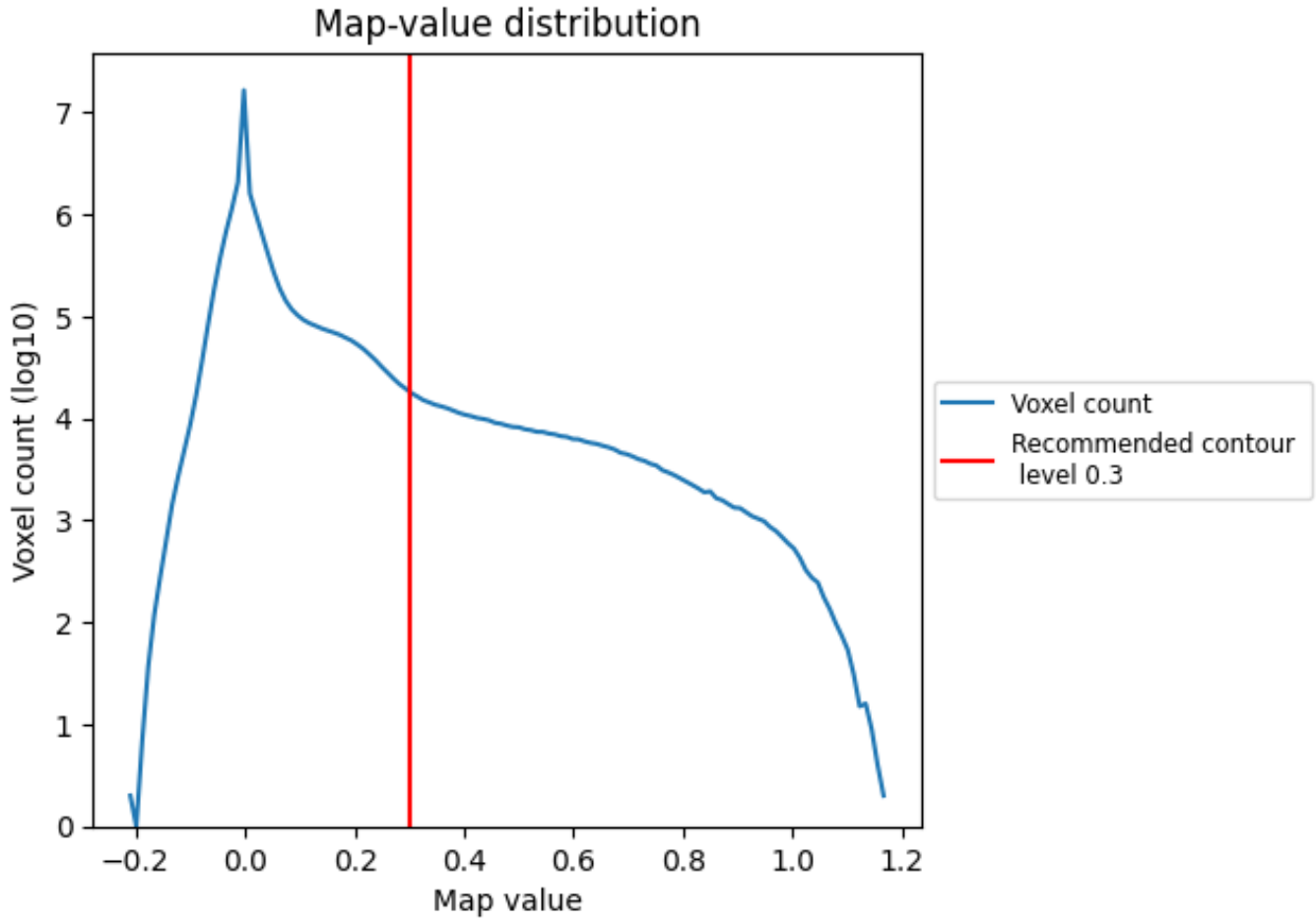
6.6 Mask visualisation (i)

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

7 Map analysis

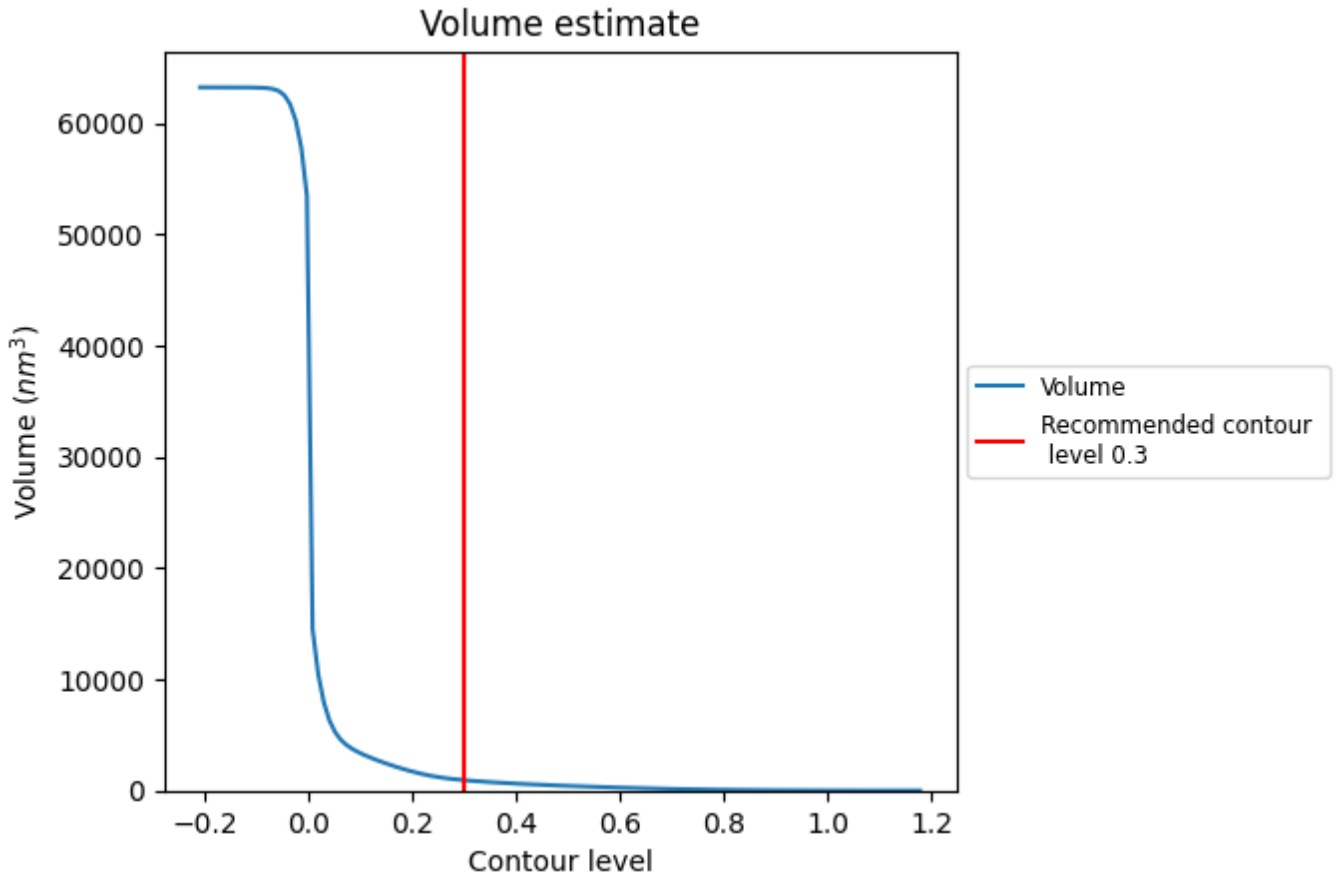
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

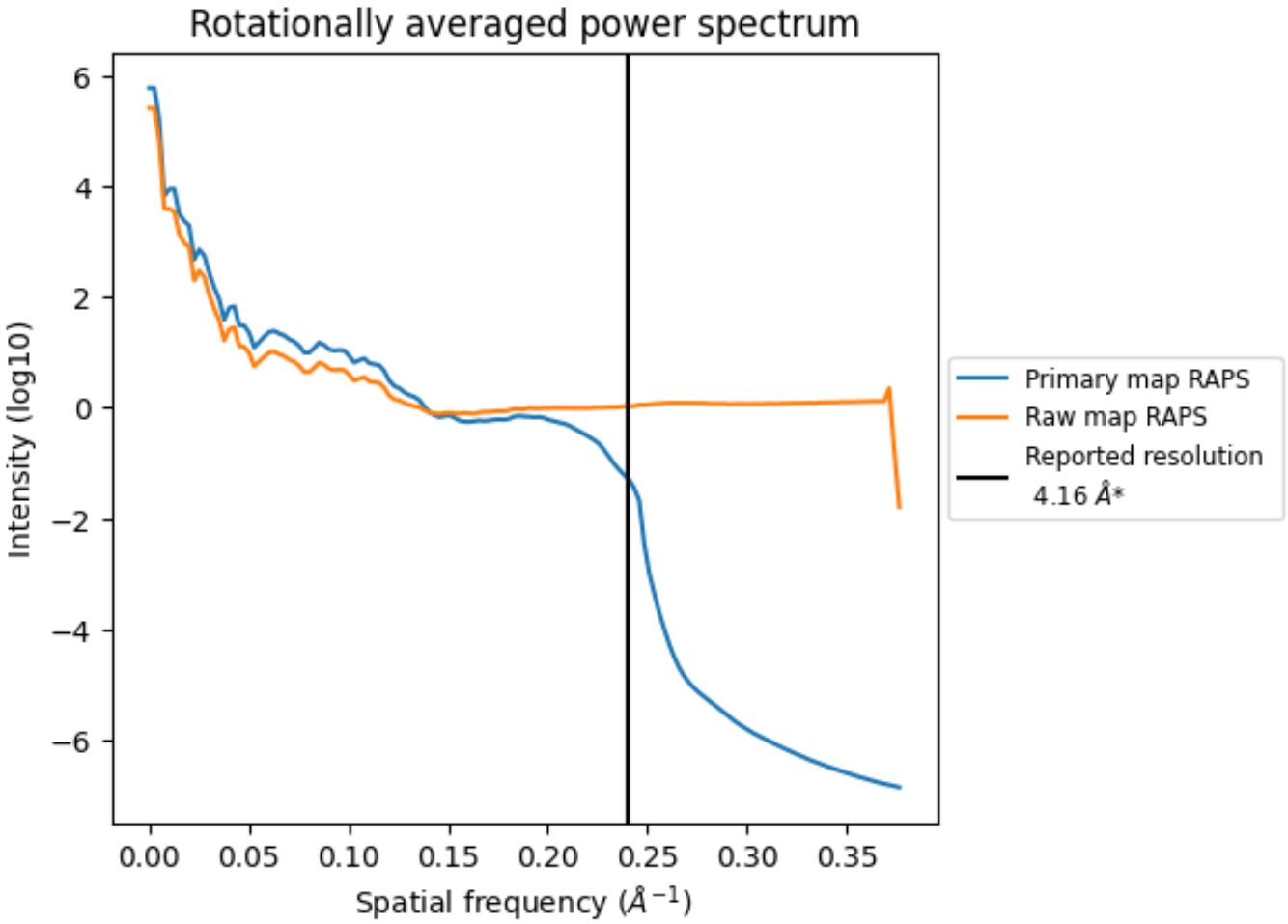
7.2 Volume estimate (i)



The volume at the recommended contour level is 929 nm^3; this corresponds to an approximate mass of 839 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)

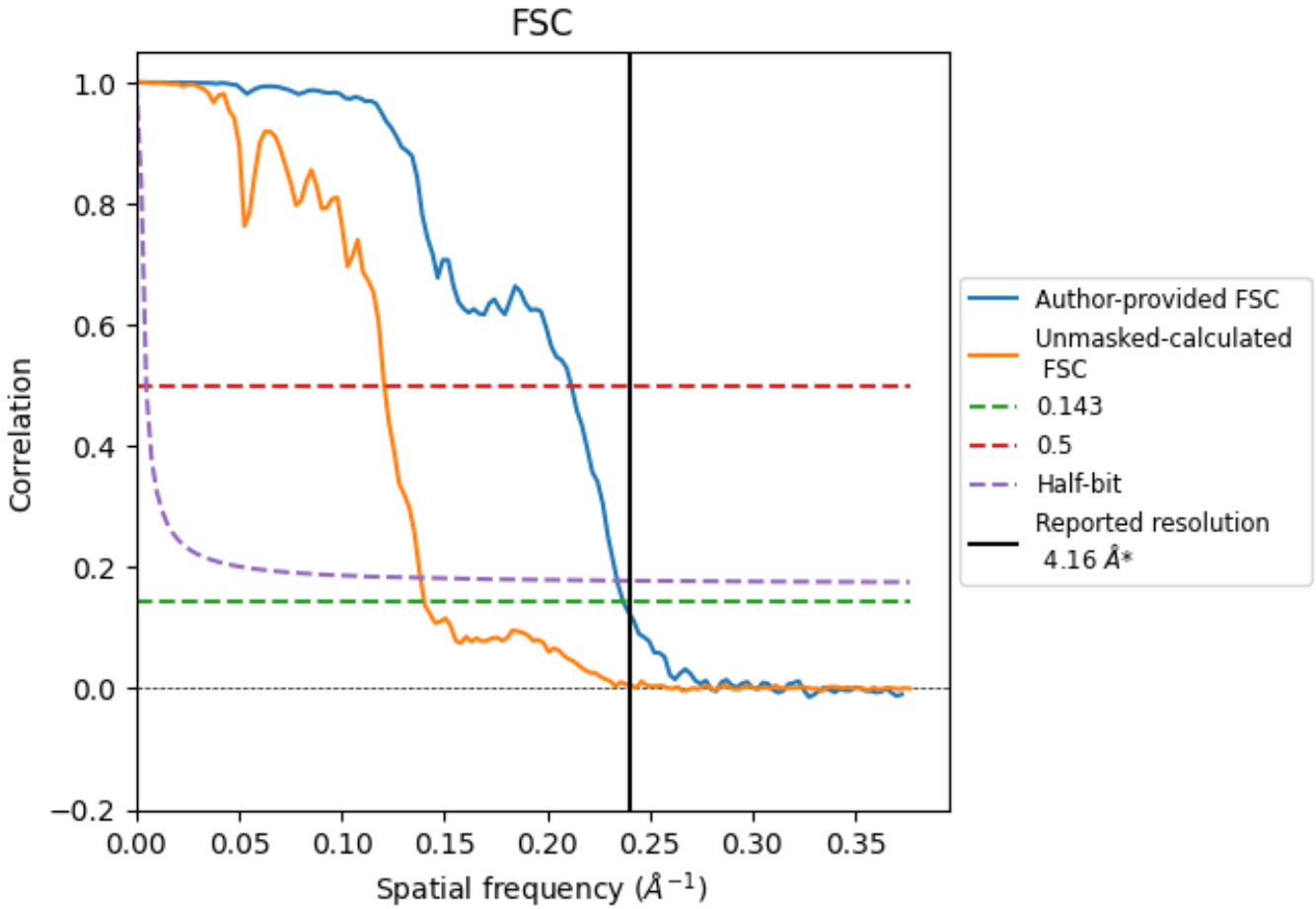


*Reported resolution corresponds to spatial frequency of 0.240 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.240 Å^{-1}

8.2 Resolution estimates (i)

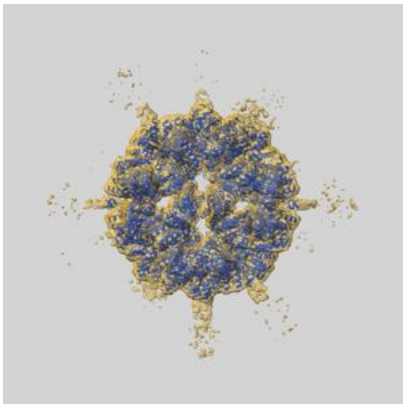
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.16	-	-
Author-provided FSC curve	4.22	4.72	4.27
Unmasked-calculated*	7.13	8.28	7.23

*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 7.13 differs from the reported value 4.16 by more than 10 %

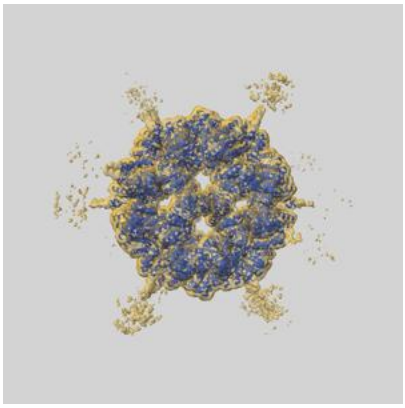
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-70144 and PDB model 9O5L. Per-residue inclusion information can be found in section 3 on page 13.

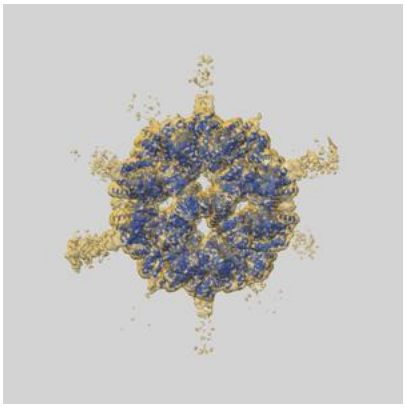
9.1 Map-model overlay



X



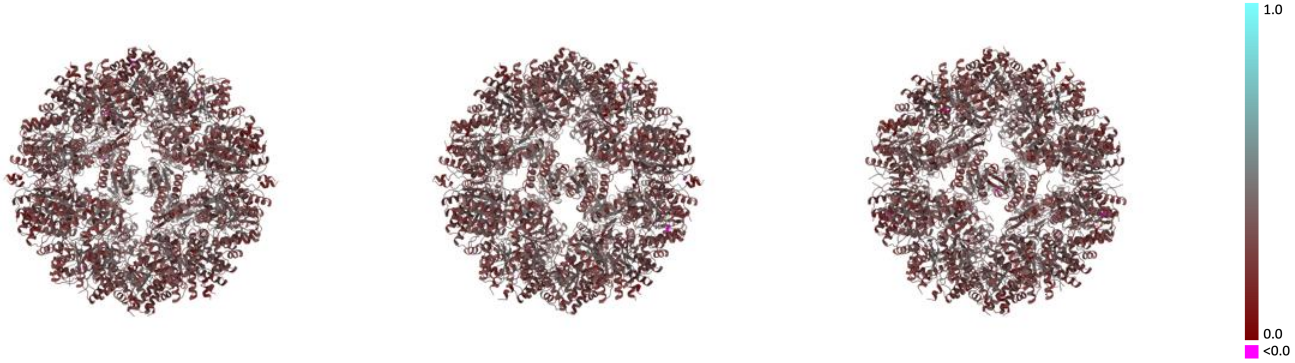
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 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.

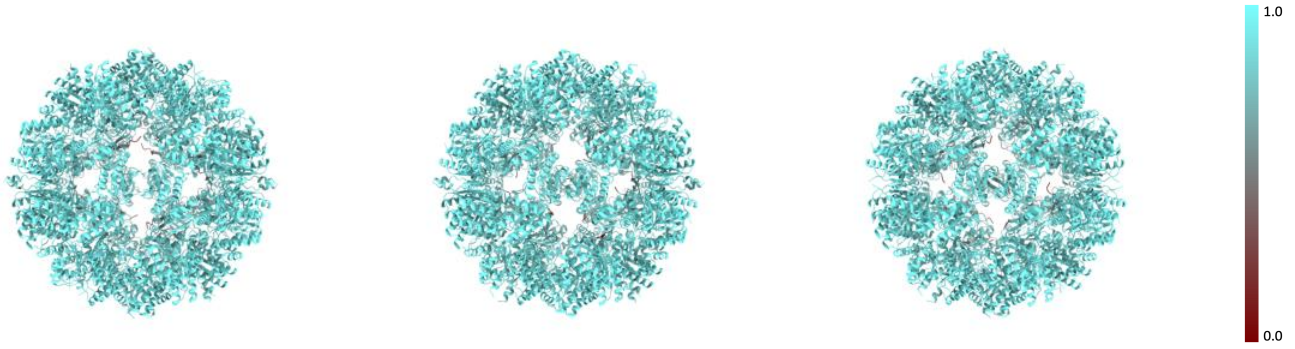
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

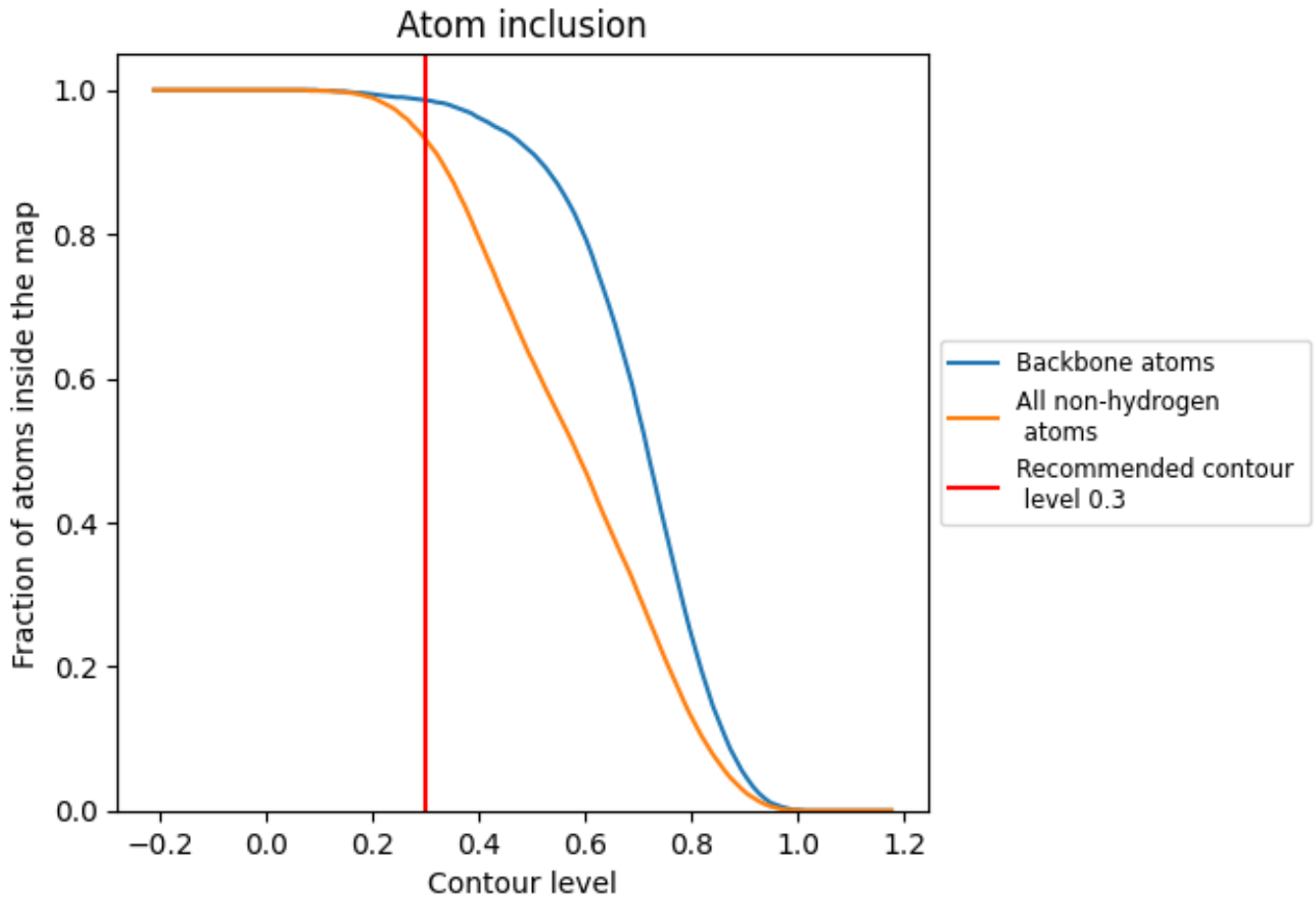
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 93% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9320	0.3180
A	0.9070	0.3070
AB	0.9180	0.3050
B	0.9330	0.3190
BB	0.9290	0.3160
C	0.9140	0.3100
CB	0.9210	0.3120
D	0.9390	0.3120
DB	0.9330	0.3230
E	0.9200	0.3120
EB	0.9330	0.3160
F	0.9120	0.2990
FB	0.9220	0.3140
G	0.9310	0.3060
GB	0.9390	0.3130
H	0.9160	0.3060
HB	0.9220	0.3020
I	0.9120	0.3090
IB	0.9180	0.3070
J	0.9260	0.3190
JB	0.9360	0.3120
K	0.9290	0.3250
KB	0.9310	0.3220
L	0.9230	0.3140
LB	0.9330	0.3190
M	0.9370	0.3130
MB	0.9210	0.3110
N	0.9220	0.3120
NB	0.9190	0.3190
O	0.9240	0.3180
OB	0.9370	0.3200
P	0.9400	0.3110
PB	0.9330	0.3110
Q	0.9220	0.3120
QB	0.9260	0.3070

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
R	0.9190	0.3130
RB	0.9080	0.3130
S	0.9260	0.3190
SB	0.9180	0.3090
T	0.9330	0.3180
TB	0.9240	0.3130
a	0.9490	0.3300
ab	0.9470	0.3250
b	0.9580	0.3310
bb	0.9510	0.3350
c	0.9410	0.3280
cb	0.9390	0.3290
d	0.9510	0.3300
db	0.9600	0.3280
e	0.9430	0.3350
eb	0.9480	0.3350
f	0.9430	0.3310
fb	0.9480	0.3330
g	0.9490	0.3350
gb	0.9560	0.3250
h	0.9480	0.3320
hb	0.9420	0.3370
i	0.9410	0.3260
ib	0.9390	0.3320
j	0.9430	0.3310
jb	0.9510	0.3300