



wwPDB EM Validation Summary Report ⓘ

Jun 3, 2025 – 06:55 PM JST

PDB ID : 8ZUK / pdb_00008zuk
EMDB ID : EMD-60486
Title : Cluster structure of the BAFF-BAFFR-TRAF3 complex
Authors : Lim, C.S.; Lee, J.O.
Deposited on : 2024-06-09
Resolution : 2.83 Å(reported)
Based on initial models : 8T5P, 2GKW

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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

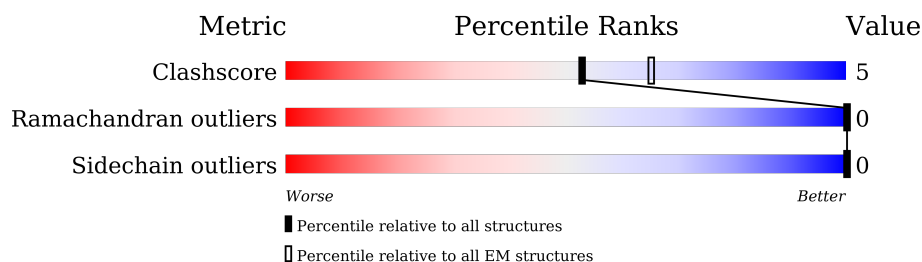
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	A	310	
1	B	310	
1	C	310	
1	G	310	
1	H	310	
1	I	310	
1	M	310	
1	N	310	










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Mol	Chain	Length	Quality of chain
1	O	310	
1	S	310	
1	T	310	
1	U	310	
1	Y	310	
1	Z	310	
1	a	310	
1	e	310	
1	f	310	
1	g	310	
1	k	310	
1	l	310	
1	m	310	
2	D	193	
2	E	193	
2	F	193	
2	J	193	
2	K	193	
2	L	193	
2	P	193	
2	Q	193	
2	R	193	
2	V	193	
2	W	193	
2	X	193	

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Mol	Chain	Length	Quality of chain
2	b	193	 8% 91%
2	c	193	 8% 91%
2	d	193	 7% 91%
2	h	193	 8% 91%
2	i	193	 7% 91%
2	j	193	 8% 91%
2	n	193	 8% 91%
2	o	193	 5% 8% 91%
2	p	193	 7% 91%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 32550 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 TNF receptor-associated factor 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	B	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	C	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	G	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	H	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	I	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	M	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	N	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	O	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	S	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	T	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	U	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	Y	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	Z	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	a	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	e	179	Total 1432	C 920	N 241	O 260	S 11	0	0
1	f	179	Total 1432	C 920	N 241	O 260	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	179	Total	C	N	O	S	0	0
			1432	920	241	260	11		
1	k	179	Total	C	N	O	S	0	0
			1432	920	241	260	11		
1	l	179	Total	C	N	O	S	0	0
			1432	920	241	260	11		
1	m	179	Total	C	N	O	S	0	0
			1432	920	241	260	11		

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	265	MET	-	initiating methionine	UNP Q13114
A	568	GLY	-	expression tag	UNP Q13114
A	569	GLY	-	expression tag	UNP Q13114
A	570	SER	-	expression tag	UNP Q13114
A	571	LEU	-	expression tag	UNP Q13114
A	572	VAL	-	expression tag	UNP Q13114
A	573	PRO	-	expression tag	UNP Q13114
A	574	ARG	-	expression tag	UNP Q13114
B	265	MET	-	initiating methionine	UNP Q13114
B	568	GLY	-	expression tag	UNP Q13114
B	569	GLY	-	expression tag	UNP Q13114
B	570	SER	-	expression tag	UNP Q13114
B	571	LEU	-	expression tag	UNP Q13114
B	572	VAL	-	expression tag	UNP Q13114
B	573	PRO	-	expression tag	UNP Q13114
B	574	ARG	-	expression tag	UNP Q13114
C	265	MET	-	initiating methionine	UNP Q13114
C	568	GLY	-	expression tag	UNP Q13114
C	569	GLY	-	expression tag	UNP Q13114
C	570	SER	-	expression tag	UNP Q13114
C	571	LEU	-	expression tag	UNP Q13114
C	572	VAL	-	expression tag	UNP Q13114
C	573	PRO	-	expression tag	UNP Q13114
C	574	ARG	-	expression tag	UNP Q13114
G	265	MET	-	initiating methionine	UNP Q13114
G	568	GLY	-	expression tag	UNP Q13114
G	569	GLY	-	expression tag	UNP Q13114
G	570	SER	-	expression tag	UNP Q13114
G	571	LEU	-	expression tag	UNP Q13114
G	572	VAL	-	expression tag	UNP Q13114
G	573	PRO	-	expression tag	UNP Q13114

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Chain	Residue	Modelled	Actual	Comment	Reference
G	574	ARG	-	expression tag	UNP Q13114
H	265	MET	-	initiating methionine	UNP Q13114
H	568	GLY	-	expression tag	UNP Q13114
H	569	GLY	-	expression tag	UNP Q13114
H	570	SER	-	expression tag	UNP Q13114
H	571	LEU	-	expression tag	UNP Q13114
H	572	VAL	-	expression tag	UNP Q13114
H	573	PRO	-	expression tag	UNP Q13114
H	574	ARG	-	expression tag	UNP Q13114
I	265	MET	-	initiating methionine	UNP Q13114
I	568	GLY	-	expression tag	UNP Q13114
I	569	GLY	-	expression tag	UNP Q13114
I	570	SER	-	expression tag	UNP Q13114
I	571	LEU	-	expression tag	UNP Q13114
I	572	VAL	-	expression tag	UNP Q13114
I	573	PRO	-	expression tag	UNP Q13114
I	574	ARG	-	expression tag	UNP Q13114
M	265	MET	-	initiating methionine	UNP Q13114
M	568	GLY	-	expression tag	UNP Q13114
M	569	GLY	-	expression tag	UNP Q13114
M	570	SER	-	expression tag	UNP Q13114
M	571	LEU	-	expression tag	UNP Q13114
M	572	VAL	-	expression tag	UNP Q13114
M	573	PRO	-	expression tag	UNP Q13114
M	574	ARG	-	expression tag	UNP Q13114
N	265	MET	-	initiating methionine	UNP Q13114
N	568	GLY	-	expression tag	UNP Q13114
N	569	GLY	-	expression tag	UNP Q13114
N	570	SER	-	expression tag	UNP Q13114
N	571	LEU	-	expression tag	UNP Q13114
N	572	VAL	-	expression tag	UNP Q13114
N	573	PRO	-	expression tag	UNP Q13114
N	574	ARG	-	expression tag	UNP Q13114
O	265	MET	-	initiating methionine	UNP Q13114
O	568	GLY	-	expression tag	UNP Q13114
O	569	GLY	-	expression tag	UNP Q13114
O	570	SER	-	expression tag	UNP Q13114
O	571	LEU	-	expression tag	UNP Q13114
O	572	VAL	-	expression tag	UNP Q13114
O	573	PRO	-	expression tag	UNP Q13114
O	574	ARG	-	expression tag	UNP Q13114
S	265	MET	-	initiating methionine	UNP Q13114

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Chain	Residue	Modelled	Actual	Comment	Reference
S	568	GLY	-	expression tag	UNP Q13114
S	569	GLY	-	expression tag	UNP Q13114
S	570	SER	-	expression tag	UNP Q13114
S	571	LEU	-	expression tag	UNP Q13114
S	572	VAL	-	expression tag	UNP Q13114
S	573	PRO	-	expression tag	UNP Q13114
S	574	ARG	-	expression tag	UNP Q13114
T	265	MET	-	initiating methionine	UNP Q13114
T	568	GLY	-	expression tag	UNP Q13114
T	569	GLY	-	expression tag	UNP Q13114
T	570	SER	-	expression tag	UNP Q13114
T	571	LEU	-	expression tag	UNP Q13114
T	572	VAL	-	expression tag	UNP Q13114
T	573	PRO	-	expression tag	UNP Q13114
T	574	ARG	-	expression tag	UNP Q13114
U	265	MET	-	initiating methionine	UNP Q13114
U	568	GLY	-	expression tag	UNP Q13114
U	569	GLY	-	expression tag	UNP Q13114
U	570	SER	-	expression tag	UNP Q13114
U	571	LEU	-	expression tag	UNP Q13114
U	572	VAL	-	expression tag	UNP Q13114
U	573	PRO	-	expression tag	UNP Q13114
U	574	ARG	-	expression tag	UNP Q13114
Y	265	MET	-	initiating methionine	UNP Q13114
Y	568	GLY	-	expression tag	UNP Q13114
Y	569	GLY	-	expression tag	UNP Q13114
Y	570	SER	-	expression tag	UNP Q13114
Y	571	LEU	-	expression tag	UNP Q13114
Y	572	VAL	-	expression tag	UNP Q13114
Y	573	PRO	-	expression tag	UNP Q13114
Y	574	ARG	-	expression tag	UNP Q13114
Z	265	MET	-	initiating methionine	UNP Q13114
Z	568	GLY	-	expression tag	UNP Q13114
Z	569	GLY	-	expression tag	UNP Q13114
Z	570	SER	-	expression tag	UNP Q13114
Z	571	LEU	-	expression tag	UNP Q13114
Z	572	VAL	-	expression tag	UNP Q13114
Z	573	PRO	-	expression tag	UNP Q13114
Z	574	ARG	-	expression tag	UNP Q13114
a	265	MET	-	initiating methionine	UNP Q13114
a	568	GLY	-	expression tag	UNP Q13114
a	569	GLY	-	expression tag	UNP Q13114

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Chain	Residue	Modelled	Actual	Comment	Reference
a	570	SER	-	expression tag	UNP Q13114
a	571	LEU	-	expression tag	UNP Q13114
a	572	VAL	-	expression tag	UNP Q13114
a	573	PRO	-	expression tag	UNP Q13114
a	574	ARG	-	expression tag	UNP Q13114
e	265	MET	-	initiating methionine	UNP Q13114
e	568	GLY	-	expression tag	UNP Q13114
e	569	GLY	-	expression tag	UNP Q13114
e	570	SER	-	expression tag	UNP Q13114
e	571	LEU	-	expression tag	UNP Q13114
e	572	VAL	-	expression tag	UNP Q13114
e	573	PRO	-	expression tag	UNP Q13114
e	574	ARG	-	expression tag	UNP Q13114
f	265	MET	-	initiating methionine	UNP Q13114
f	568	GLY	-	expression tag	UNP Q13114
f	569	GLY	-	expression tag	UNP Q13114
f	570	SER	-	expression tag	UNP Q13114
f	571	LEU	-	expression tag	UNP Q13114
f	572	VAL	-	expression tag	UNP Q13114
f	573	PRO	-	expression tag	UNP Q13114
f	574	ARG	-	expression tag	UNP Q13114
g	265	MET	-	initiating methionine	UNP Q13114
g	568	GLY	-	expression tag	UNP Q13114
g	569	GLY	-	expression tag	UNP Q13114
g	570	SER	-	expression tag	UNP Q13114
g	571	LEU	-	expression tag	UNP Q13114
g	572	VAL	-	expression tag	UNP Q13114
g	573	PRO	-	expression tag	UNP Q13114
g	574	ARG	-	expression tag	UNP Q13114
k	265	MET	-	initiating methionine	UNP Q13114
k	568	GLY	-	expression tag	UNP Q13114
k	569	GLY	-	expression tag	UNP Q13114
k	570	SER	-	expression tag	UNP Q13114
k	571	LEU	-	expression tag	UNP Q13114
k	572	VAL	-	expression tag	UNP Q13114
k	573	PRO	-	expression tag	UNP Q13114
k	574	ARG	-	expression tag	UNP Q13114
l	265	MET	-	initiating methionine	UNP Q13114
l	568	GLY	-	expression tag	UNP Q13114
l	569	GLY	-	expression tag	UNP Q13114
l	570	SER	-	expression tag	UNP Q13114
l	571	LEU	-	expression tag	UNP Q13114

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Chain	Residue	Modelled	Actual	Comment	Reference
l	572	VAL	-	expression tag	UNP Q13114
l	573	PRO	-	expression tag	UNP Q13114
l	574	ARG	-	expression tag	UNP Q13114
m	265	MET	-	initiating methionine	UNP Q13114
m	568	GLY	-	expression tag	UNP Q13114
m	569	GLY	-	expression tag	UNP Q13114
m	570	SER	-	expression tag	UNP Q13114
m	571	LEU	-	expression tag	UNP Q13114
m	572	VAL	-	expression tag	UNP Q13114
m	573	PRO	-	expression tag	UNP Q13114
m	574	ARG	-	expression tag	UNP Q13114

- Molecule 2 is a protein called Tumor necrosis factor receptor superfamily member 13C.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	17	Total 118	C 74	N 17	O 27	0	0
2	E	17	Total 118	C 74	N 17	O 27	0	0
2	F	17	Total 118	C 74	N 17	O 27	0	0
2	J	17	Total 118	C 74	N 17	O 27	0	0
2	K	17	Total 118	C 74	N 17	O 27	0	0
2	L	17	Total 118	C 74	N 17	O 27	0	0
2	P	17	Total 118	C 74	N 17	O 27	0	0
2	Q	17	Total 118	C 74	N 17	O 27	0	0
2	R	17	Total 118	C 74	N 17	O 27	0	0
2	V	17	Total 118	C 74	N 17	O 27	0	0
2	W	17	Total 118	C 74	N 17	O 27	0	0
2	X	17	Total 118	C 74	N 17	O 27	0	0
2	b	17	Total 118	C 74	N 17	O 27	0	0
2	c	17	Total 118	C 74	N 17	O 27	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	d	17	Total 118	C 74	N 17	O 27	0	0
2	h	17	Total 118	C 74	N 17	O 27	0	0
2	i	17	Total 118	C 74	N 17	O 27	0	0
2	j	17	Total 118	C 74	N 17	O 27	0	0
2	n	17	Total 118	C 74	N 17	O 27	0	0
2	o	17	Total 118	C 74	N 17	O 27	0	0
2	p	17	Total 118	C 74	N 17	O 27	0	0

There are 189 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	185	SER	-	expression tag	UNP Q96RJ3
D	186	ASN	-	expression tag	UNP Q96RJ3
D	187	SER	-	expression tag	UNP Q96RJ3
D	188	LEU	-	expression tag	UNP Q96RJ3
D	189	GLU	-	expression tag	UNP Q96RJ3
D	190	VAL	-	expression tag	UNP Q96RJ3
D	191	LEU	-	expression tag	UNP Q96RJ3
D	192	PHE	-	expression tag	UNP Q96RJ3
D	193	GLN	-	expression tag	UNP Q96RJ3
E	185	SER	-	expression tag	UNP Q96RJ3
E	186	ASN	-	expression tag	UNP Q96RJ3
E	187	SER	-	expression tag	UNP Q96RJ3
E	188	LEU	-	expression tag	UNP Q96RJ3
E	189	GLU	-	expression tag	UNP Q96RJ3
E	190	VAL	-	expression tag	UNP Q96RJ3
E	191	LEU	-	expression tag	UNP Q96RJ3
E	192	PHE	-	expression tag	UNP Q96RJ3
E	193	GLN	-	expression tag	UNP Q96RJ3
F	185	SER	-	expression tag	UNP Q96RJ3
F	186	ASN	-	expression tag	UNP Q96RJ3
F	187	SER	-	expression tag	UNP Q96RJ3
F	188	LEU	-	expression tag	UNP Q96RJ3
F	189	GLU	-	expression tag	UNP Q96RJ3
F	190	VAL	-	expression tag	UNP Q96RJ3
F	191	LEU	-	expression tag	UNP Q96RJ3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	192	PHE	-	expression tag	UNP Q96RJ3
F	193	GLN	-	expression tag	UNP Q96RJ3
J	185	SER	-	expression tag	UNP Q96RJ3
J	186	ASN	-	expression tag	UNP Q96RJ3
J	187	SER	-	expression tag	UNP Q96RJ3
J	188	LEU	-	expression tag	UNP Q96RJ3
J	189	GLU	-	expression tag	UNP Q96RJ3
J	190	VAL	-	expression tag	UNP Q96RJ3
J	191	LEU	-	expression tag	UNP Q96RJ3
J	192	PHE	-	expression tag	UNP Q96RJ3
J	193	GLN	-	expression tag	UNP Q96RJ3
K	185	SER	-	expression tag	UNP Q96RJ3
K	186	ASN	-	expression tag	UNP Q96RJ3
K	187	SER	-	expression tag	UNP Q96RJ3
K	188	LEU	-	expression tag	UNP Q96RJ3
K	189	GLU	-	expression tag	UNP Q96RJ3
K	190	VAL	-	expression tag	UNP Q96RJ3
K	191	LEU	-	expression tag	UNP Q96RJ3
K	192	PHE	-	expression tag	UNP Q96RJ3
K	193	GLN	-	expression tag	UNP Q96RJ3
L	185	SER	-	expression tag	UNP Q96RJ3
L	186	ASN	-	expression tag	UNP Q96RJ3
L	187	SER	-	expression tag	UNP Q96RJ3
L	188	LEU	-	expression tag	UNP Q96RJ3
L	189	GLU	-	expression tag	UNP Q96RJ3
L	190	VAL	-	expression tag	UNP Q96RJ3
L	191	LEU	-	expression tag	UNP Q96RJ3
L	192	PHE	-	expression tag	UNP Q96RJ3
L	193	GLN	-	expression tag	UNP Q96RJ3
P	185	SER	-	expression tag	UNP Q96RJ3
P	186	ASN	-	expression tag	UNP Q96RJ3
P	187	SER	-	expression tag	UNP Q96RJ3
P	188	LEU	-	expression tag	UNP Q96RJ3
P	189	GLU	-	expression tag	UNP Q96RJ3
P	190	VAL	-	expression tag	UNP Q96RJ3
P	191	LEU	-	expression tag	UNP Q96RJ3
P	192	PHE	-	expression tag	UNP Q96RJ3
P	193	GLN	-	expression tag	UNP Q96RJ3
Q	185	SER	-	expression tag	UNP Q96RJ3
Q	186	ASN	-	expression tag	UNP Q96RJ3
Q	187	SER	-	expression tag	UNP Q96RJ3
Q	188	LEU	-	expression tag	UNP Q96RJ3

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	189	GLU	-	expression tag	UNP Q96RJ3
Q	190	VAL	-	expression tag	UNP Q96RJ3
Q	191	LEU	-	expression tag	UNP Q96RJ3
Q	192	PHE	-	expression tag	UNP Q96RJ3
Q	193	GLN	-	expression tag	UNP Q96RJ3
R	185	SER	-	expression tag	UNP Q96RJ3
R	186	ASN	-	expression tag	UNP Q96RJ3
R	187	SER	-	expression tag	UNP Q96RJ3
R	188	LEU	-	expression tag	UNP Q96RJ3
R	189	GLU	-	expression tag	UNP Q96RJ3
R	190	VAL	-	expression tag	UNP Q96RJ3
R	191	LEU	-	expression tag	UNP Q96RJ3
R	192	PHE	-	expression tag	UNP Q96RJ3
R	193	GLN	-	expression tag	UNP Q96RJ3
V	185	SER	-	expression tag	UNP Q96RJ3
V	186	ASN	-	expression tag	UNP Q96RJ3
V	187	SER	-	expression tag	UNP Q96RJ3
V	188	LEU	-	expression tag	UNP Q96RJ3
V	189	GLU	-	expression tag	UNP Q96RJ3
V	190	VAL	-	expression tag	UNP Q96RJ3
V	191	LEU	-	expression tag	UNP Q96RJ3
V	192	PHE	-	expression tag	UNP Q96RJ3
V	193	GLN	-	expression tag	UNP Q96RJ3
W	185	SER	-	expression tag	UNP Q96RJ3
W	186	ASN	-	expression tag	UNP Q96RJ3
W	187	SER	-	expression tag	UNP Q96RJ3
W	188	LEU	-	expression tag	UNP Q96RJ3
W	189	GLU	-	expression tag	UNP Q96RJ3
W	190	VAL	-	expression tag	UNP Q96RJ3
W	191	LEU	-	expression tag	UNP Q96RJ3
W	192	PHE	-	expression tag	UNP Q96RJ3
W	193	GLN	-	expression tag	UNP Q96RJ3
X	185	SER	-	expression tag	UNP Q96RJ3
X	186	ASN	-	expression tag	UNP Q96RJ3
X	187	SER	-	expression tag	UNP Q96RJ3
X	188	LEU	-	expression tag	UNP Q96RJ3
X	189	GLU	-	expression tag	UNP Q96RJ3
X	190	VAL	-	expression tag	UNP Q96RJ3
X	191	LEU	-	expression tag	UNP Q96RJ3
X	192	PHE	-	expression tag	UNP Q96RJ3
X	193	GLN	-	expression tag	UNP Q96RJ3
b	185	SER	-	expression tag	UNP Q96RJ3

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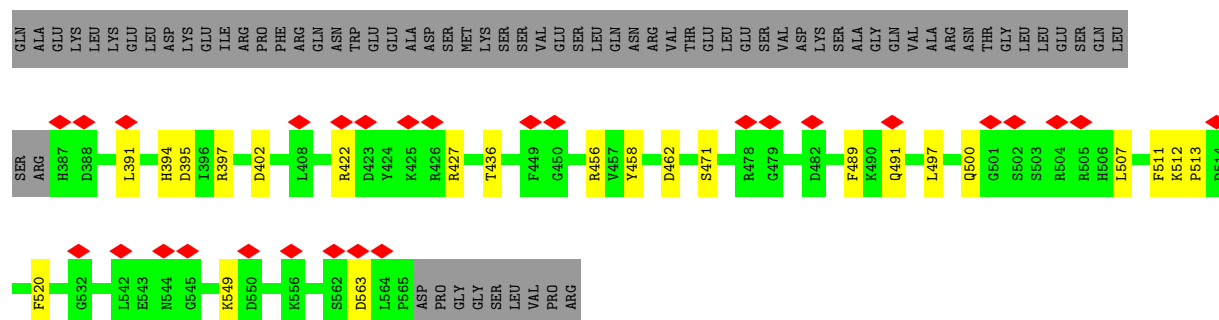
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b	187	SER	-	expression tag	UNP Q96RJ3
b	188	LEU	-	expression tag	UNP Q96RJ3
b	189	GLU	-	expression tag	UNP Q96RJ3
b	190	VAL	-	expression tag	UNP Q96RJ3
b	191	LEU	-	expression tag	UNP Q96RJ3
b	192	PHE	-	expression tag	UNP Q96RJ3
b	193	GLN	-	expression tag	UNP Q96RJ3
c	185	SER	-	expression tag	UNP Q96RJ3
c	186	ASN	-	expression tag	UNP Q96RJ3
c	187	SER	-	expression tag	UNP Q96RJ3
c	188	LEU	-	expression tag	UNP Q96RJ3
c	189	GLU	-	expression tag	UNP Q96RJ3
c	190	VAL	-	expression tag	UNP Q96RJ3
c	191	LEU	-	expression tag	UNP Q96RJ3
c	192	PHE	-	expression tag	UNP Q96RJ3
c	193	GLN	-	expression tag	UNP Q96RJ3
d	185	SER	-	expression tag	UNP Q96RJ3
d	186	ASN	-	expression tag	UNP Q96RJ3
d	187	SER	-	expression tag	UNP Q96RJ3
d	188	LEU	-	expression tag	UNP Q96RJ3
d	189	GLU	-	expression tag	UNP Q96RJ3
d	190	VAL	-	expression tag	UNP Q96RJ3
d	191	LEU	-	expression tag	UNP Q96RJ3
d	192	PHE	-	expression tag	UNP Q96RJ3
d	193	GLN	-	expression tag	UNP Q96RJ3
h	185	SER	-	expression tag	UNP Q96RJ3
h	186	ASN	-	expression tag	UNP Q96RJ3
h	187	SER	-	expression tag	UNP Q96RJ3
h	188	LEU	-	expression tag	UNP Q96RJ3
h	189	GLU	-	expression tag	UNP Q96RJ3
h	190	VAL	-	expression tag	UNP Q96RJ3
h	191	LEU	-	expression tag	UNP Q96RJ3
h	192	PHE	-	expression tag	UNP Q96RJ3
h	193	GLN	-	expression tag	UNP Q96RJ3
i	185	SER	-	expression tag	UNP Q96RJ3
i	186	ASN	-	expression tag	UNP Q96RJ3
i	187	SER	-	expression tag	UNP Q96RJ3
i	188	LEU	-	expression tag	UNP Q96RJ3
i	189	GLU	-	expression tag	UNP Q96RJ3
i	190	VAL	-	expression tag	UNP Q96RJ3
i	191	LEU	-	expression tag	UNP Q96RJ3

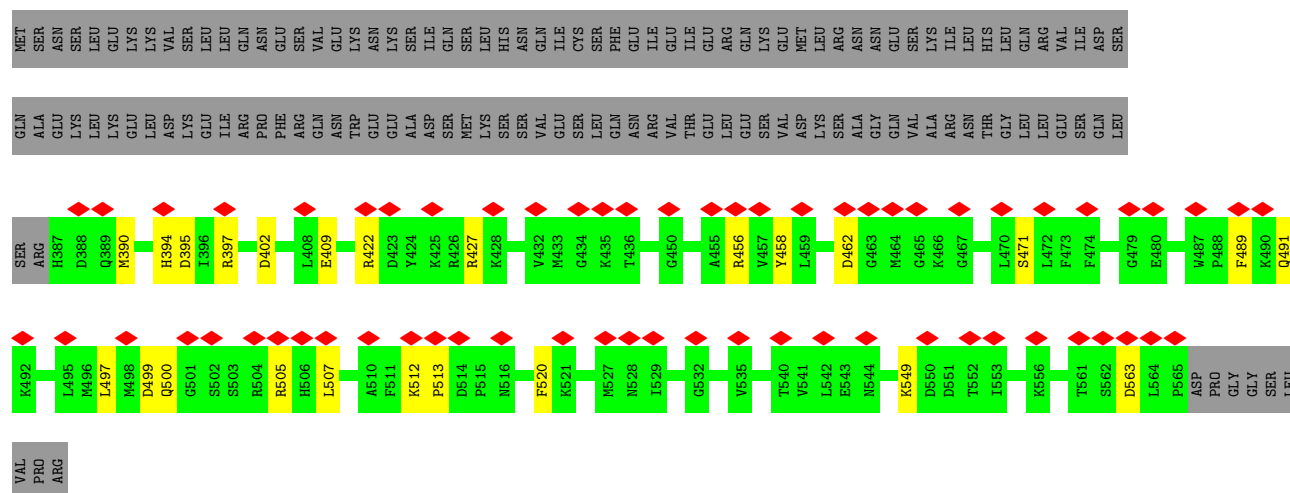
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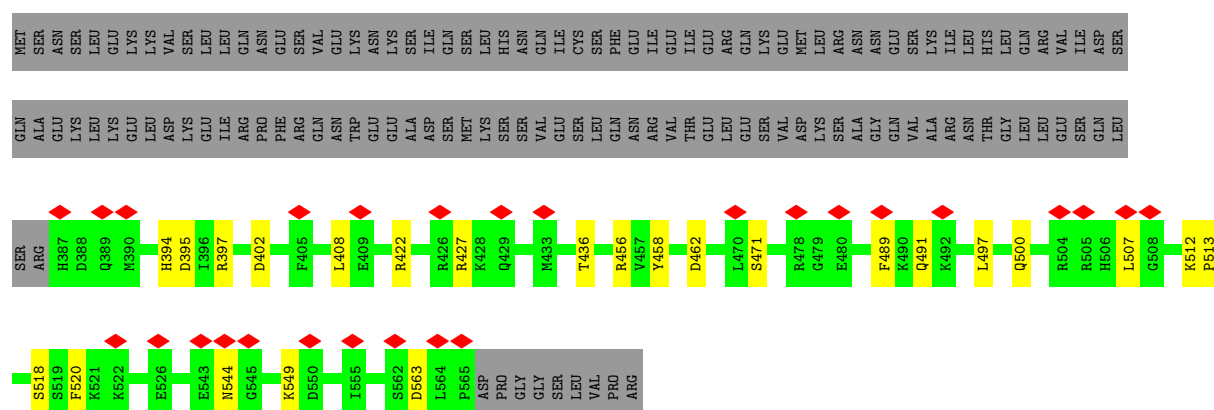
Chain	Residue	Modelled	Actual	Comment	Reference
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i	193	GLN	-	expression tag	UNP Q96RJ3
j	185	SER	-	expression tag	UNP Q96RJ3
j	186	ASN	-	expression tag	UNP Q96RJ3
j	187	SER	-	expression tag	UNP Q96RJ3
j	188	LEU	-	expression tag	UNP Q96RJ3
j	189	GLU	-	expression tag	UNP Q96RJ3
j	190	VAL	-	expression tag	UNP Q96RJ3
j	191	LEU	-	expression tag	UNP Q96RJ3
j	192	PHE	-	expression tag	UNP Q96RJ3
j	193	GLN	-	expression tag	UNP Q96RJ3
n	185	SER	-	expression tag	UNP Q96RJ3
n	186	ASN	-	expression tag	UNP Q96RJ3
n	187	SER	-	expression tag	UNP Q96RJ3
n	188	LEU	-	expression tag	UNP Q96RJ3
n	189	GLU	-	expression tag	UNP Q96RJ3
n	190	VAL	-	expression tag	UNP Q96RJ3
n	191	LEU	-	expression tag	UNP Q96RJ3
n	192	PHE	-	expression tag	UNP Q96RJ3
n	193	GLN	-	expression tag	UNP Q96RJ3
o	185	SER	-	expression tag	UNP Q96RJ3
o	186	ASN	-	expression tag	UNP Q96RJ3
o	187	SER	-	expression tag	UNP Q96RJ3
o	188	LEU	-	expression tag	UNP Q96RJ3
o	189	GLU	-	expression tag	UNP Q96RJ3
o	190	VAL	-	expression tag	UNP Q96RJ3
o	191	LEU	-	expression tag	UNP Q96RJ3
o	192	PHE	-	expression tag	UNP Q96RJ3
o	193	GLN	-	expression tag	UNP Q96RJ3
p	185	SER	-	expression tag	UNP Q96RJ3
p	186	ASN	-	expression tag	UNP Q96RJ3
p	187	SER	-	expression tag	UNP Q96RJ3
p	188	LEU	-	expression tag	UNP Q96RJ3
p	189	GLU	-	expression tag	UNP Q96RJ3
p	190	VAL	-	expression tag	UNP Q96RJ3
p	191	LEU	-	expression tag	UNP Q96RJ3
p	192	PHE	-	expression tag	UNP Q96RJ3
p	193	GLN	-	expression tag	UNP Q96RJ3



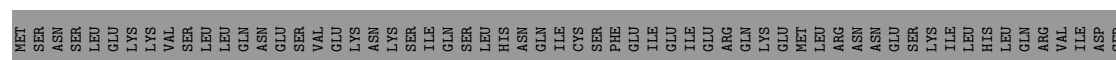
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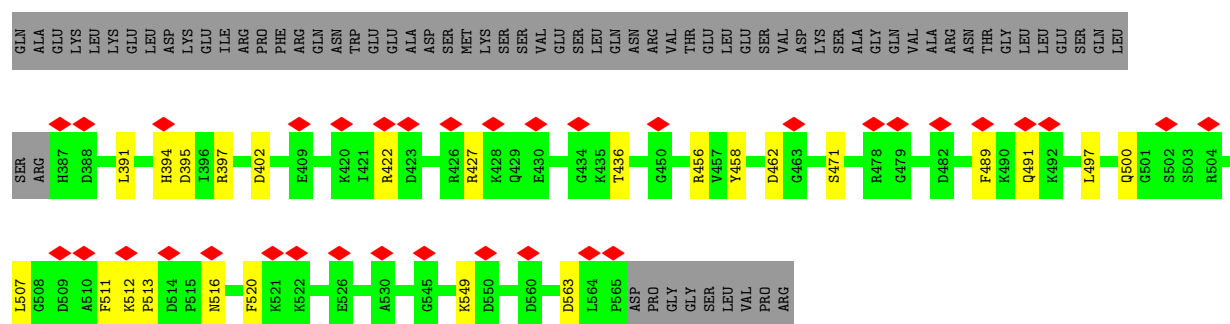


• Molecule 1: TNF receptor-associated factor 3

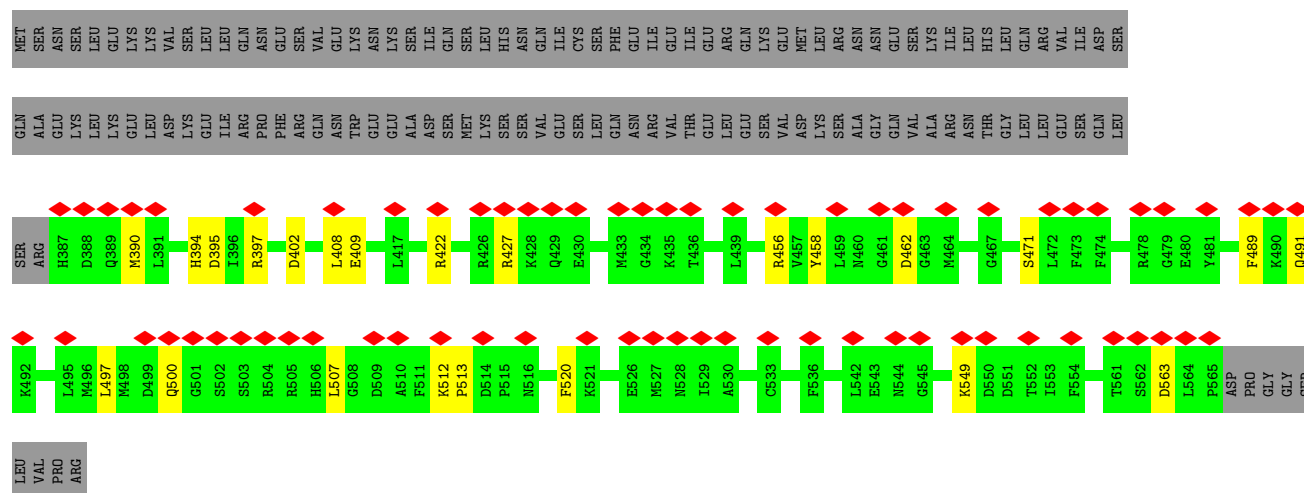


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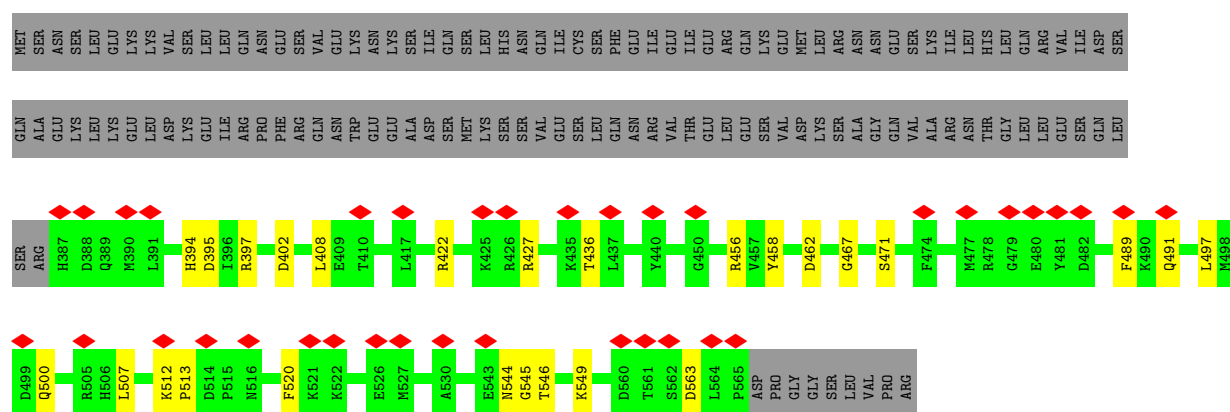




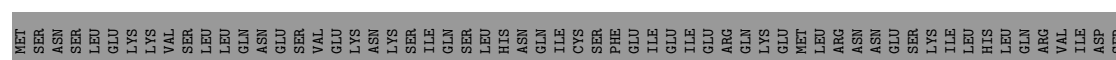
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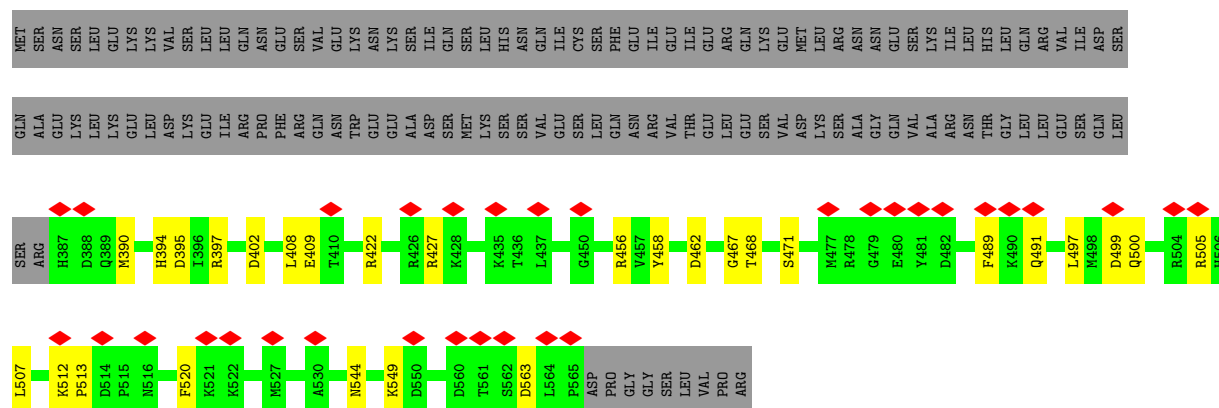
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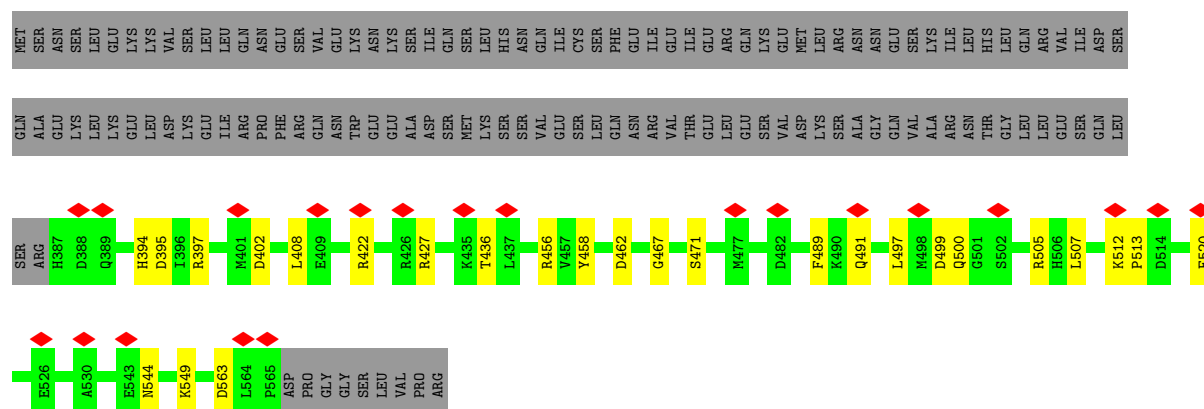
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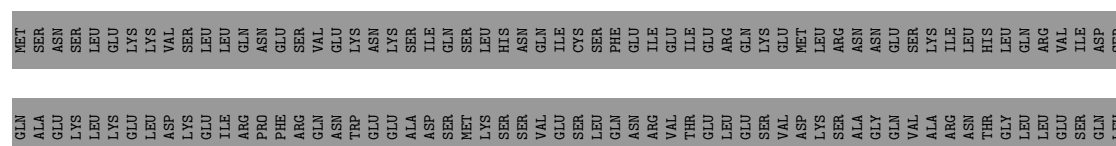
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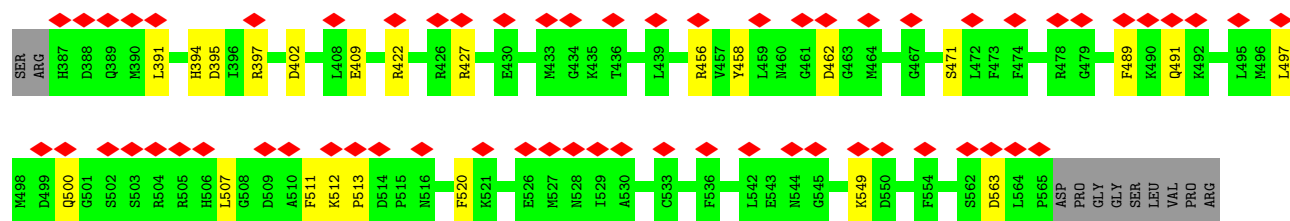


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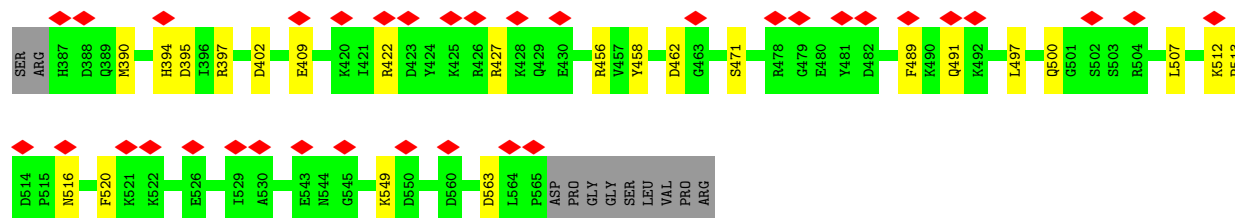
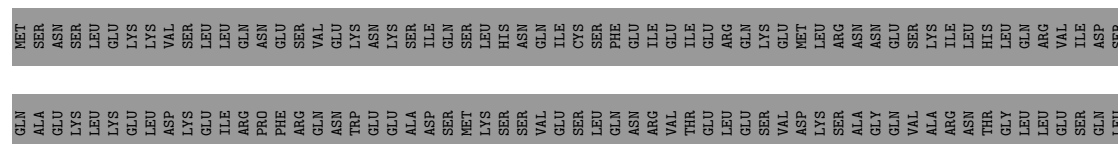


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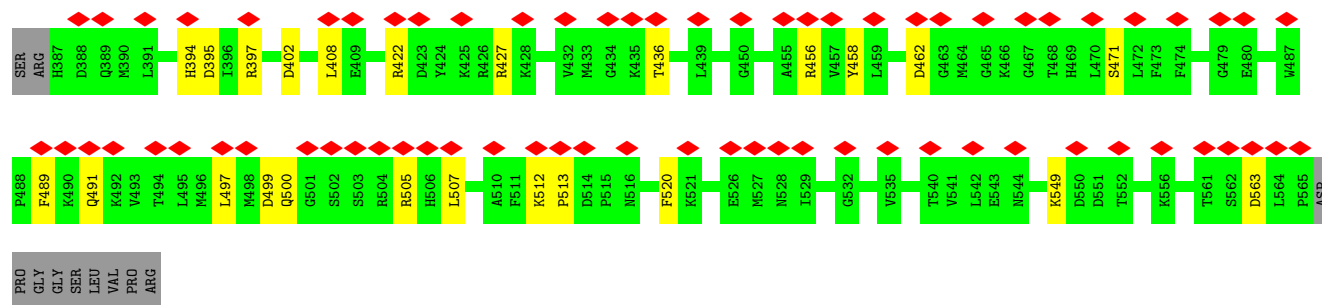
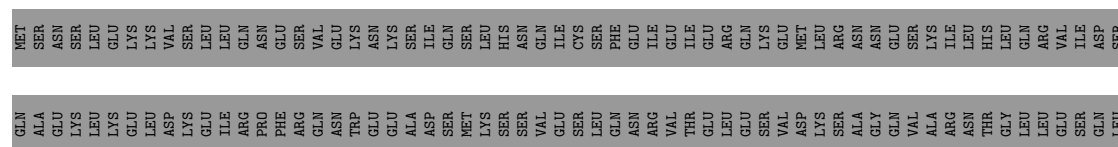




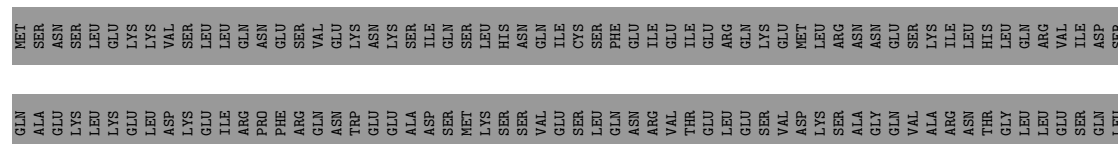
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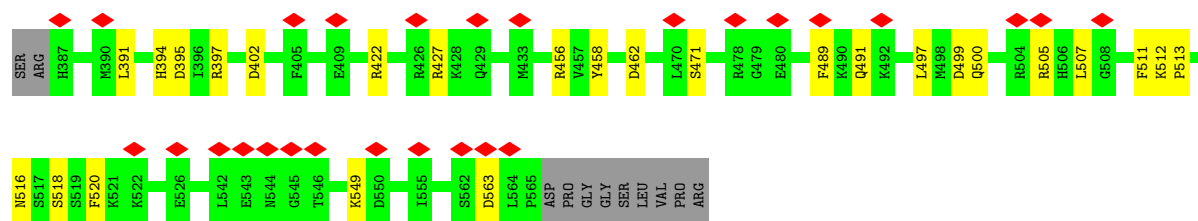


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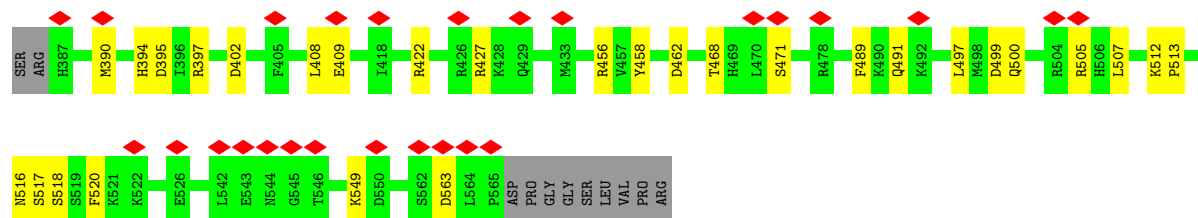
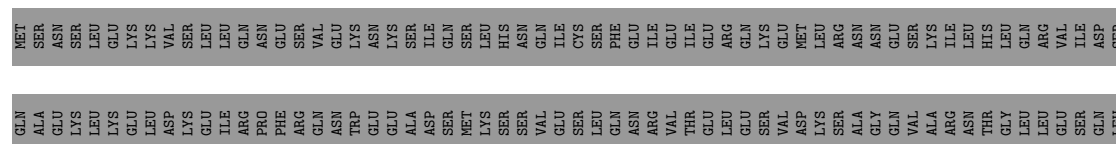


• Molecule 1: TNF receptor-associated factor 3

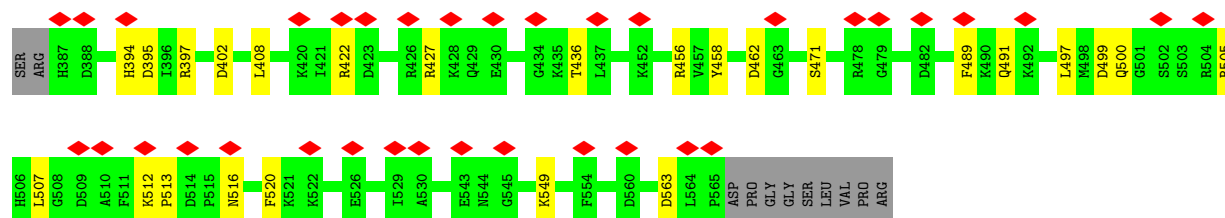
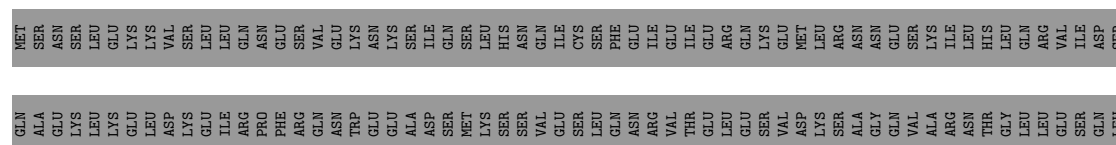




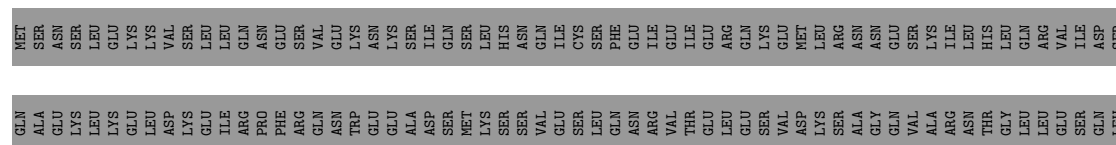
• Molecule 1: TNF receptor-associated factor 3

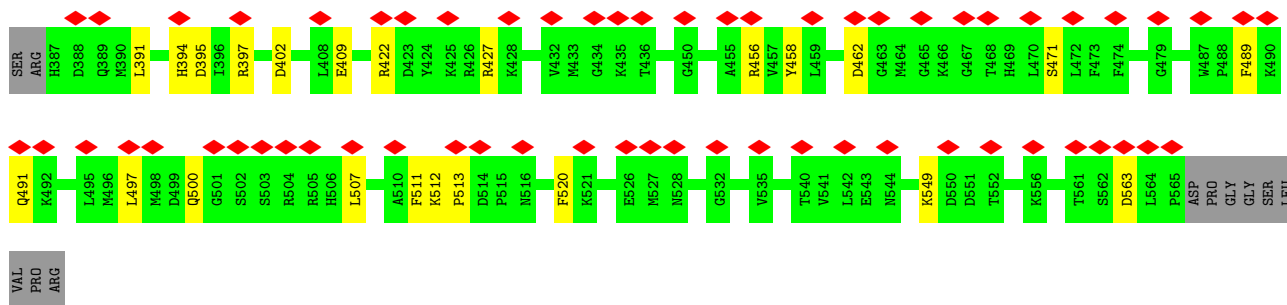


• Molecule 1: TNF receptor-associated factor 3

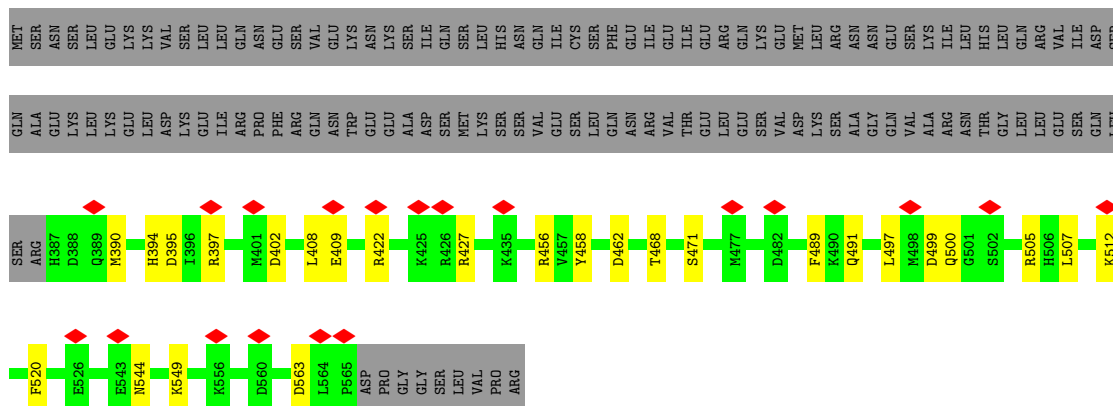


• Molecule 1: TNF receptor-associated factor 3

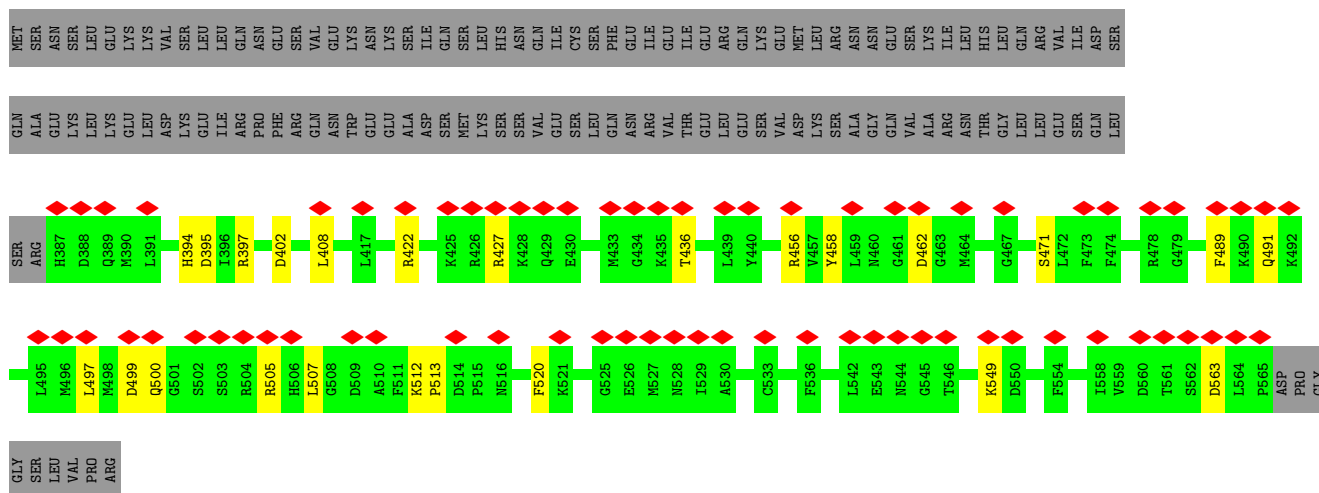




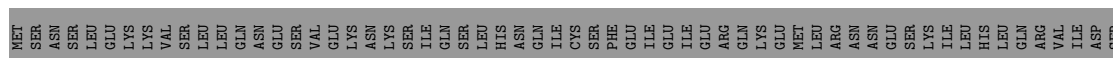
- Molecule 1: TNF receptor-associated factor 3

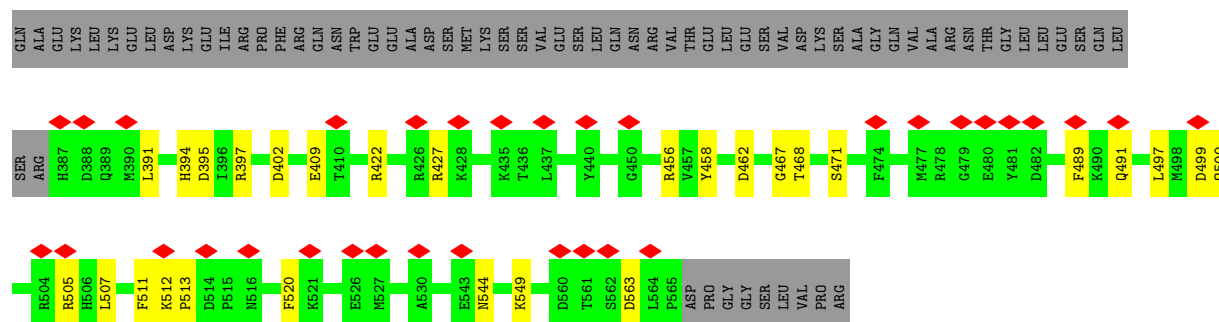


- Molecule 1: TNF receptor-associated factor 3

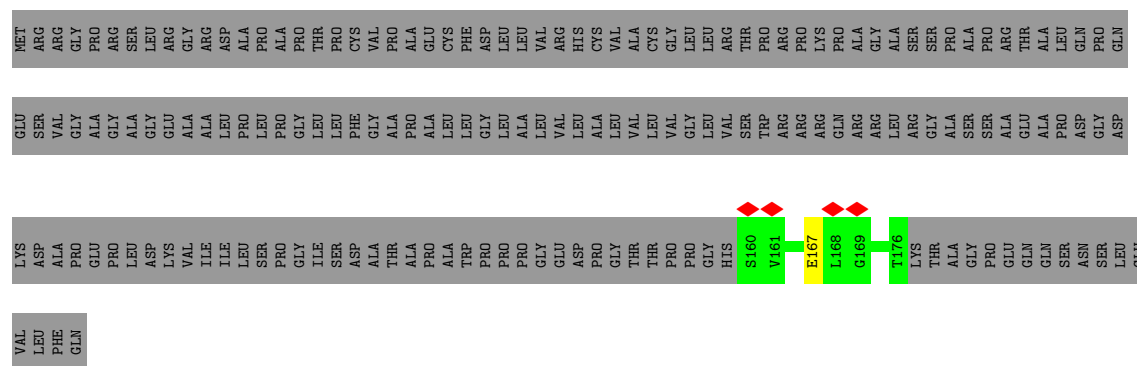


- Molecule 1: TNF receptor-associated factor 3

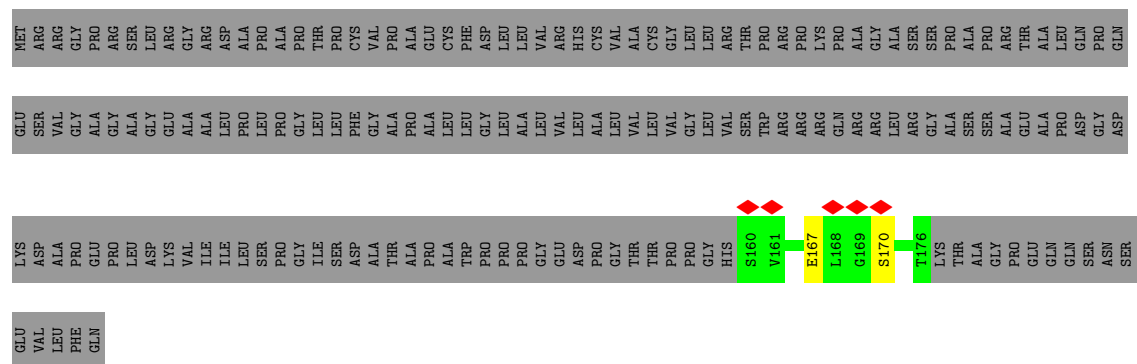




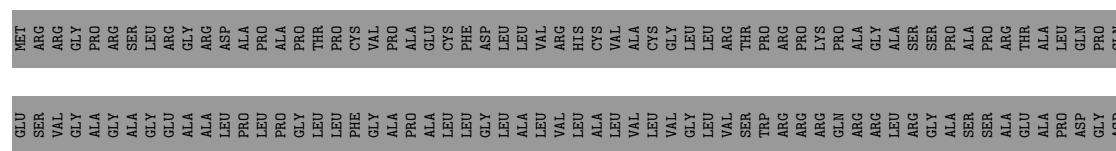
- Molecule 2: Tumor necrosis factor receptor superfamily member 13C

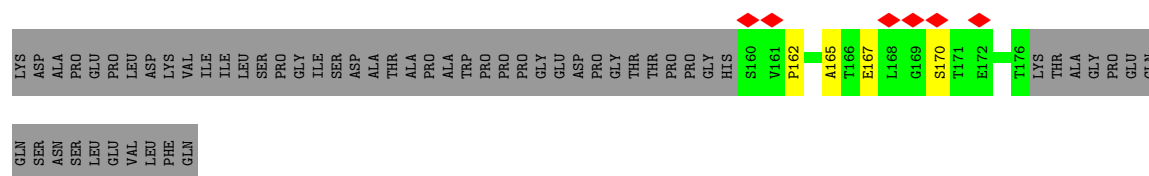


- Molecule 2: Tumor necrosis factor receptor superfamily member 13C

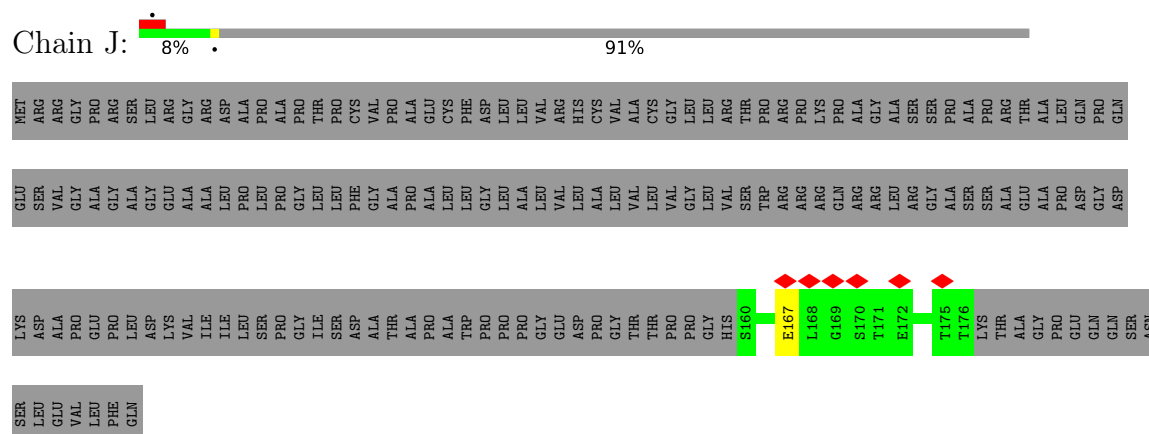


- Molecule 2: Tumor necrosis factor receptor superfamily member 13C

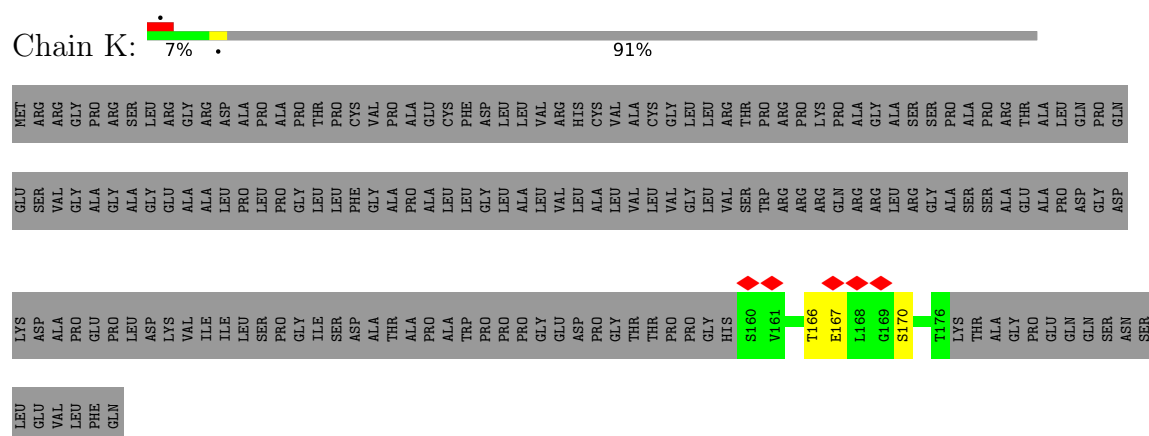




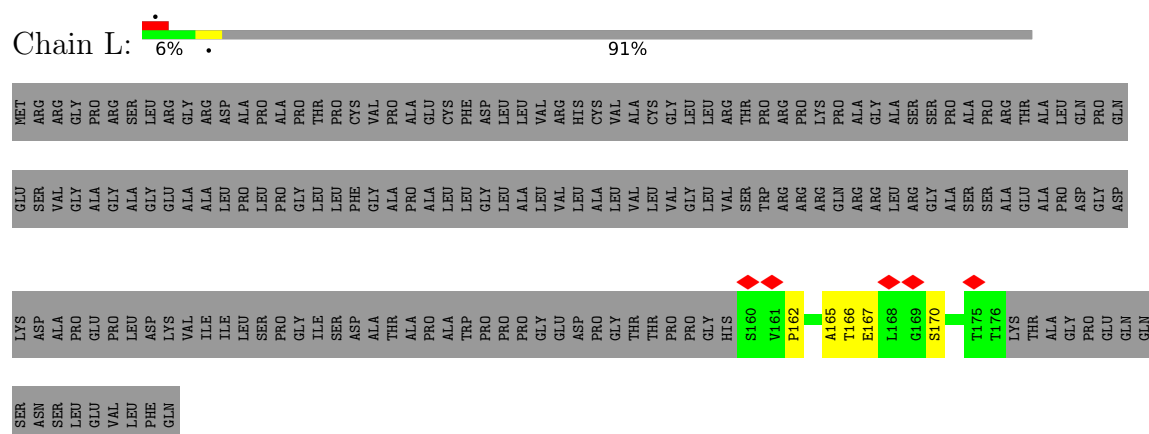
- Molecule 2: Tumor necrosis factor receptor superfamily member 13C

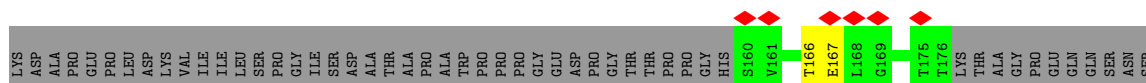


- Molecule 2: Tumor necrosis factor receptor superfamily member 13C



- Molecule 2: Tumor necrosis factor receptor superfamily member 13C





LEU
GLU
VAL
LEU
PHE
GLN

• Molecule 2: Tumor necrosis factor receptor superfamily member 13C

Chain c:  8% 91%

MET ARG ARG GLY VAL ARG ARG ARG ARG ASP ALA PRO PRO GLY THR PRO CYS VAL PRO ALA GLU CYS LEU PHE ASP LEU LEU LEU LEU ARG THR PRO ARG PRO LYS PRO ALA ARG GLY ALA SER SER ALA PRO ARG THR ALA LEU GLN ASP

LYS ASP ALA PRO GLU LEU ASP VAL ILE ILE SER PRO ILE SER ASP ALA THR PRO ALA CYS TRP PRO PRO GLY THR PRO GLY HIS S160 E167 L168 G169 S170 T171 E172 L173 V174 T175 LYS THR ALA PRO GLY PRO GLN SER

ASN
SER
LEU
GLU
VAL
PHE
GLN

• Molecule 2: Tumor necrosis factor receptor superfamily member 13C

Chain d:  7% 91%

MET ARG ARG GLY VAL ARG ARG ARG ASP ALA PRO PRO GLY THR PRO CYS VAL PRO ALA GLU CYS LEU PHE ASP LEU LEU LEU LEU ARG THR PRO ARG PRO LYS PRO ALA ARG GLY ALA SER SER ALA PRO ARG THR ALA LEU GLN ASP

LYS ASP ALA PRO GLU LEU ASP VAL ILE ILE SER PRO ILE SER ASP ALA THR PRO ALA CYS TRP PRO PRO GLY THR PRO GLY HIS S160 V161 P162 A165 T166 E167 L168 G169 S170 T171 E172 T176 LYS THR ALA PRO GLY PRO GLN

GLN
SER
ASN
LEU
VAL
PHE
GLN

• Molecule 2: Tumor necrosis factor receptor superfamily member 13C

Chain h:  8% 91%

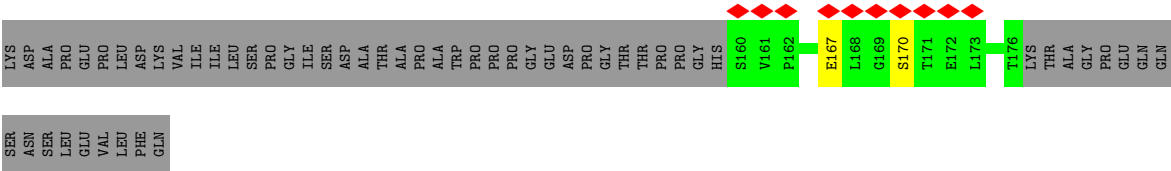
MET ARG ARG GLY VAL ARG ARG ARG ASP ALA PRO PRO GLY THR PRO CYS VAL PRO ALA GLU CYS LEU PHE ASP LEU LEU LEU LEU ARG THR PRO ARG PRO LYS PRO ALA ARG GLY ALA SER SER ALA PRO ARG THR ALA LEU GLN ASP

LYS ASP ALA PRO GLU LEU ASP VAL ILE ILE SER PRO ILE SER ASP ALA THR PRO ALA CYS TRP PRO PRO GLY THR PRO GLY HIS S160 V161 T166 E167 L168 G169 S170 T175 T176 LYS THR ALA PRO GLY PRO ASN

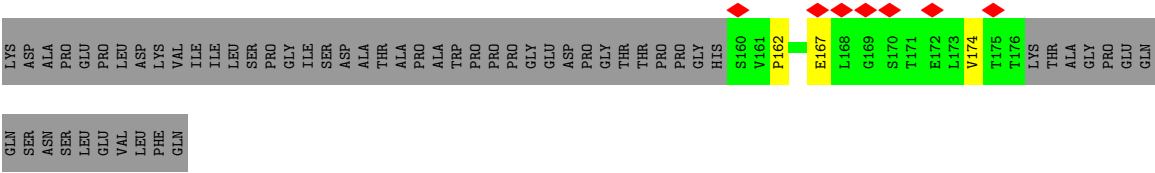
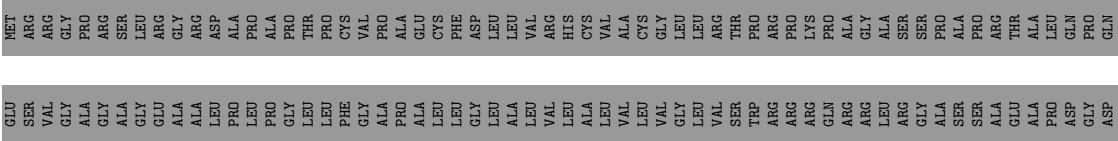
SER
LEU
GLU
VAL
PHE
GLN

• Molecule 2: Tumor necrosis factor receptor superfamily member 13C

Chain i:  7% 91%



● Molecule 2: Tumor necrosis factor receptor superfamily member 13C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	205165	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.864	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.222	Depositor
Map size (Å)	338.4, 338.4, 338.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.94, 0.94, 0.94	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	0.09	0/1466	0.24	0/1977
1	B	0.09	0/1466	0.24	0/1977
1	C	0.09	0/1466	0.24	0/1977
1	G	0.08	0/1466	0.24	0/1977
1	H	0.09	0/1466	0.24	0/1977
1	I	0.09	0/1466	0.24	0/1977
1	M	0.09	0/1466	0.24	0/1977
1	N	0.09	0/1466	0.24	0/1977
1	O	0.09	0/1466	0.24	0/1977
1	S	0.08	0/1466	0.24	0/1977
1	T	0.09	0/1466	0.24	0/1977
1	U	0.09	0/1466	0.24	0/1977
1	Y	0.08	0/1466	0.24	0/1977
1	Z	0.09	0/1466	0.24	0/1977
1	a	0.09	0/1466	0.24	0/1977
1	e	0.08	0/1466	0.24	0/1977
1	f	0.09	0/1466	0.24	0/1977
1	g	0.09	0/1466	0.24	0/1977
1	k	0.09	0/1466	0.24	0/1977
1	l	0.09	0/1466	0.24	0/1977
1	m	0.09	0/1466	0.24	0/1977
2	D	0.12	0/119	0.34	0/165
2	E	0.13	0/119	0.34	0/165
2	F	0.12	0/119	0.34	0/165
2	J	0.13	0/119	0.34	0/165
2	K	0.12	0/119	0.34	0/165
2	L	0.12	0/119	0.34	0/165
2	P	0.12	0/119	0.34	0/165
2	Q	0.12	0/119	0.34	0/165
2	R	0.12	0/119	0.34	0/165
2	V	0.12	0/119	0.34	0/165
2	W	0.13	0/119	0.34	0/165
2	X	0.12	0/119	0.34	0/165
2	b	0.12	0/119	0.34	0/165

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	c	0.12	0/119	0.34	0/165
2	d	0.13	0/119	0.34	0/165
2	h	0.12	0/119	0.34	0/165
2	i	0.13	0/119	0.34	0/165
2	j	0.12	0/119	0.34	0/165
2	n	0.12	0/119	0.34	0/165
2	o	0.12	0/119	0.34	0/165
2	p	0.12	0/119	0.34	0/165
All	All	0.09	0/33285	0.25	0/44982

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1432	0	1429	20	0
1	B	1432	0	1429	18	0
1	C	1432	0	1429	17	0
1	G	1432	0	1429	17	0
1	H	1432	0	1429	18	0
1	I	1432	0	1429	19	0
1	M	1432	0	1429	16	0
1	N	1432	0	1429	20	0
1	O	1432	0	1429	24	0
1	S	1432	0	1429	21	0
1	T	1432	0	1429	21	0
1	U	1432	0	1429	18	0
1	Y	1432	0	1429	18	0
1	Z	1432	0	1429	17	0
1	a	1432	0	1429	19	0
1	e	1432	0	1429	22	0
1	f	1432	0	1429	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	g	1432	0	1429	17	0
1	k	1432	0	1429	23	0
1	l	1432	0	1429	17	0
1	m	1432	0	1429	23	0
2	D	118	0	120	1	0
2	E	118	0	120	2	0
2	F	118	0	120	4	0
2	J	118	0	120	1	0
2	K	118	0	120	4	0
2	L	118	0	120	5	0
2	P	118	0	120	1	0
2	Q	118	0	120	2	0
2	R	118	0	120	5	0
2	V	118	0	120	1	0
2	W	118	0	120	2	0
2	X	118	0	120	3	0
2	b	118	0	120	2	0
2	c	118	0	120	2	0
2	d	118	0	120	4	0
2	h	118	0	120	2	0
2	i	118	0	120	4	0
2	j	118	0	120	2	0
2	n	118	0	120	1	0
2	o	118	0	120	2	0
2	p	118	0	120	3	0
All	All	32550	0	32529	329	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 5.

The worst 5 of 329 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:422:ARG:O	1:B:427:ARG:NH1	2.26	0.69
1:U:422:ARG:O	1:U:427:ARG:NH1	2.26	0.69
1:A:422:ARG:O	1:A:427:ARG:NH1	2.26	0.69
1:a:422:ARG:O	1:a:427:ARG:NH1	2.26	0.69
1:m:422:ARG:O	1:m:427:ARG:NH1	2.26	0.69

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	B	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	C	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	G	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	H	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	I	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	M	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	N	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	O	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	S	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	T	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	U	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	Y	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	Z	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	a	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	e	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	f	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	g	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	k	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	l	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
1	m	177/310 (57%)	174 (98%)	3 (2%)	0	100	100
2	D	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	E	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	F	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	J	15/193 (8%)	12 (80%)	3 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	L	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	P	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	Q	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	R	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	V	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	W	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	X	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	b	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	c	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	d	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	h	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	i	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	j	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	n	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	o	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
2	p	15/193 (8%)	12 (80%)	3 (20%)	0	100	100
All	All	4032/10563 (38%)	3906 (97%)	126 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	157/280 (56%)	157 (100%)	0	100	100
1	B	157/280 (56%)	157 (100%)	0	100	100
1	C	157/280 (56%)	157 (100%)	0	100	100
1	G	157/280 (56%)	157 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	157/280 (56%)	157 (100%)	0	100	100
1	I	157/280 (56%)	157 (100%)	0	100	100
1	M	157/280 (56%)	157 (100%)	0	100	100
1	N	157/280 (56%)	157 (100%)	0	100	100
1	O	157/280 (56%)	157 (100%)	0	100	100
1	S	157/280 (56%)	157 (100%)	0	100	100
1	T	157/280 (56%)	157 (100%)	0	100	100
1	U	157/280 (56%)	157 (100%)	0	100	100
1	Y	157/280 (56%)	157 (100%)	0	100	100
1	Z	157/280 (56%)	157 (100%)	0	100	100
1	a	157/280 (56%)	157 (100%)	0	100	100
1	e	157/280 (56%)	157 (100%)	0	100	100
1	f	157/280 (56%)	157 (100%)	0	100	100
1	g	157/280 (56%)	157 (100%)	0	100	100
1	k	157/280 (56%)	157 (100%)	0	100	100
1	l	157/280 (56%)	157 (100%)	0	100	100
1	m	157/280 (56%)	157 (100%)	0	100	100
2	D	15/149 (10%)	15 (100%)	0	100	100
2	E	15/149 (10%)	15 (100%)	0	100	100
2	F	15/149 (10%)	15 (100%)	0	100	100
2	J	15/149 (10%)	15 (100%)	0	100	100
2	K	15/149 (10%)	15 (100%)	0	100	100
2	L	15/149 (10%)	15 (100%)	0	100	100
2	P	15/149 (10%)	15 (100%)	0	100	100
2	Q	15/149 (10%)	15 (100%)	0	100	100
2	R	15/149 (10%)	15 (100%)	0	100	100
2	V	15/149 (10%)	15 (100%)	0	100	100
2	W	15/149 (10%)	15 (100%)	0	100	100
2	X	15/149 (10%)	15 (100%)	0	100	100
2	b	15/149 (10%)	15 (100%)	0	100	100
2	c	15/149 (10%)	15 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	d	15/149 (10%)	15 (100%)	0	100	100
2	h	15/149 (10%)	15 (100%)	0	100	100
2	i	15/149 (10%)	15 (100%)	0	100	100
2	j	15/149 (10%)	15 (100%)	0	100	100
2	n	15/149 (10%)	15 (100%)	0	100	100
2	o	15/149 (10%)	15 (100%)	0	100	100
2	p	15/149 (10%)	15 (100%)	0	100	100
All	All	3612/9009 (40%)	3612 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	g	544	ASN
1	l	544	ASN
1	U	544	ASN
1	Y	544	ASN
1	Z	544	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

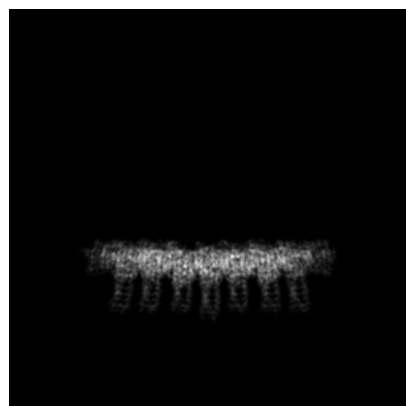
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60486. These allow visual inspection of the internal detail of the map and identification of artifacts.

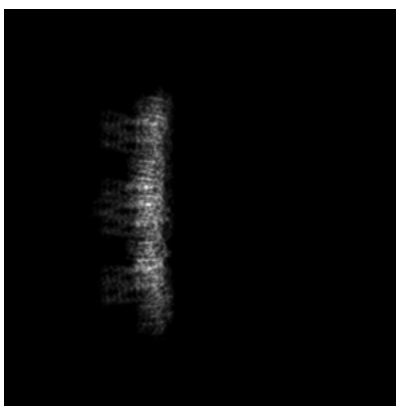
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

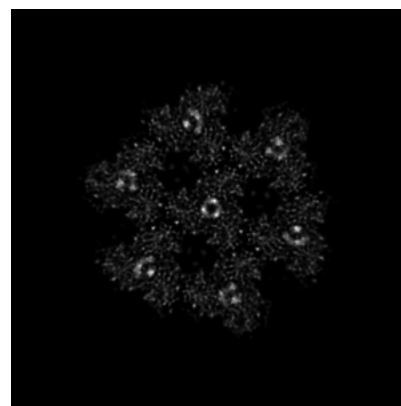
6.1.1 Primary map



X

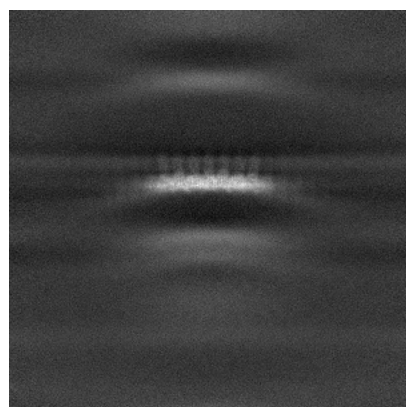


Y

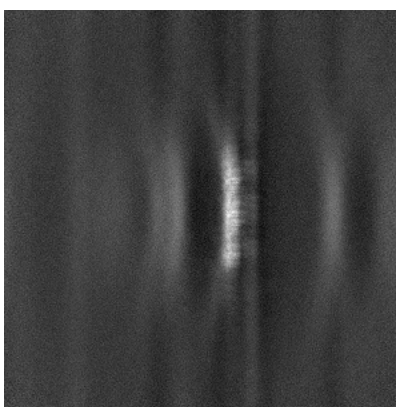


Z

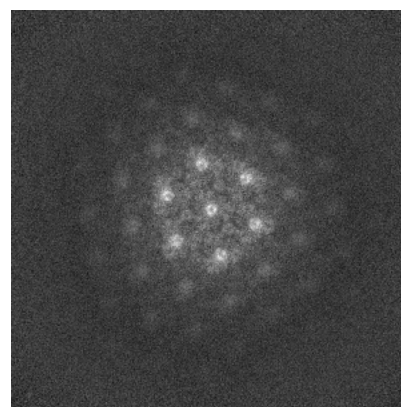
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

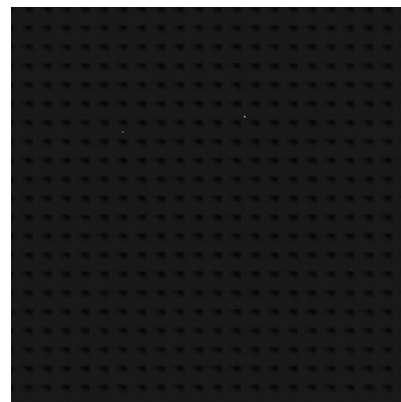
6.2.1 Primary map



X Index: 180



Y Index: 180

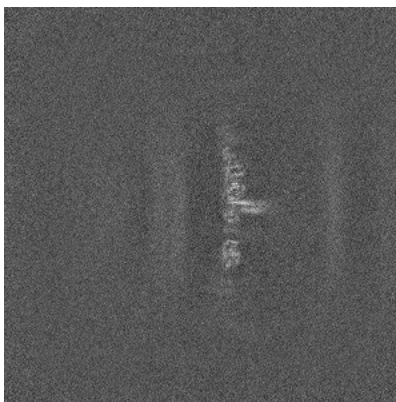


Z Index: 180

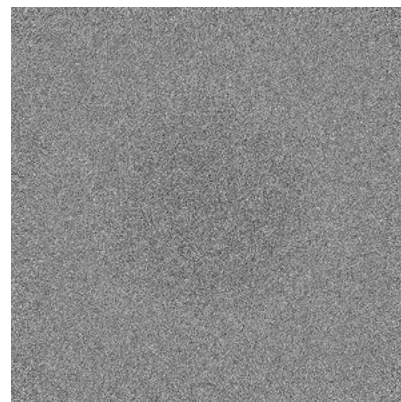
6.2.2 Raw map



X Index: 350



Y Index: 350



Z Index: 350

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: 184

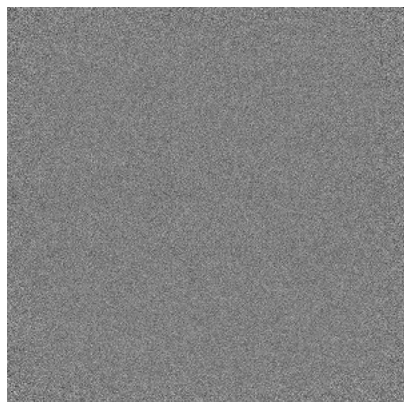


Y Index: 201

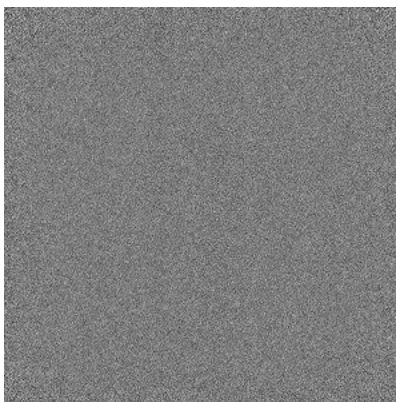


Z Index: 134

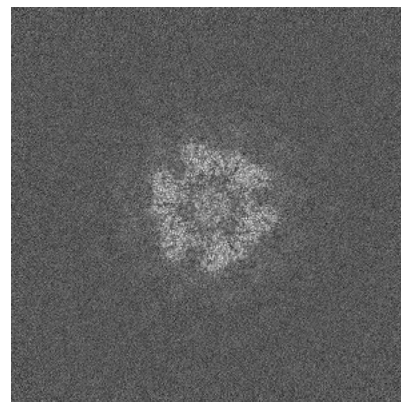
6.3.2 Raw map



X Index: 0



Y Index: 0

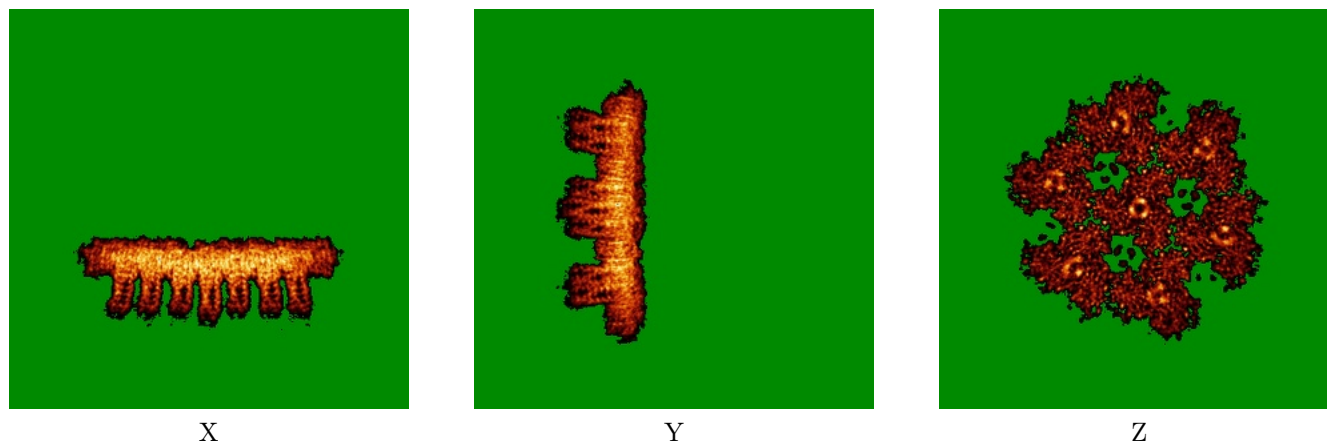


Z Index: 394

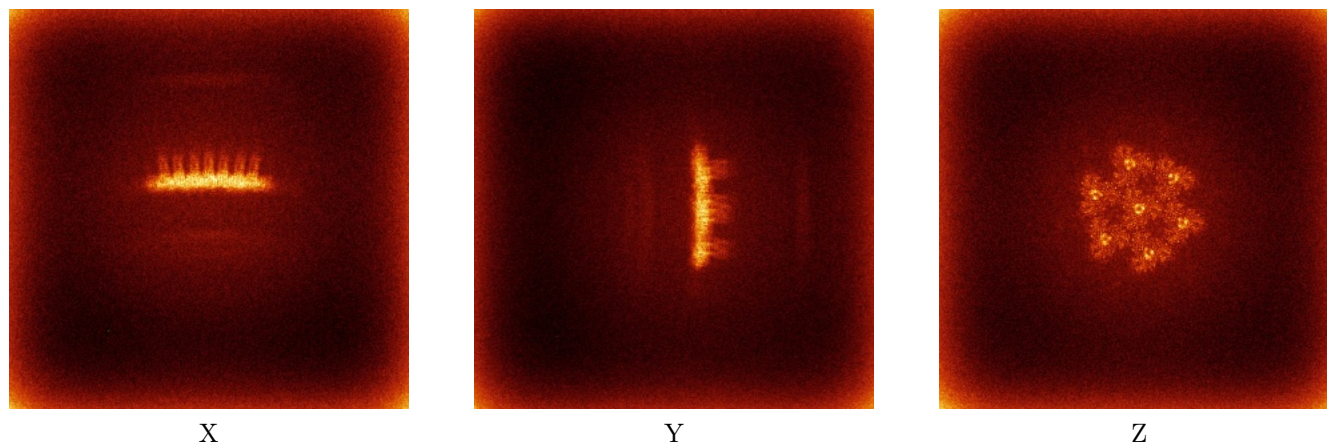
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



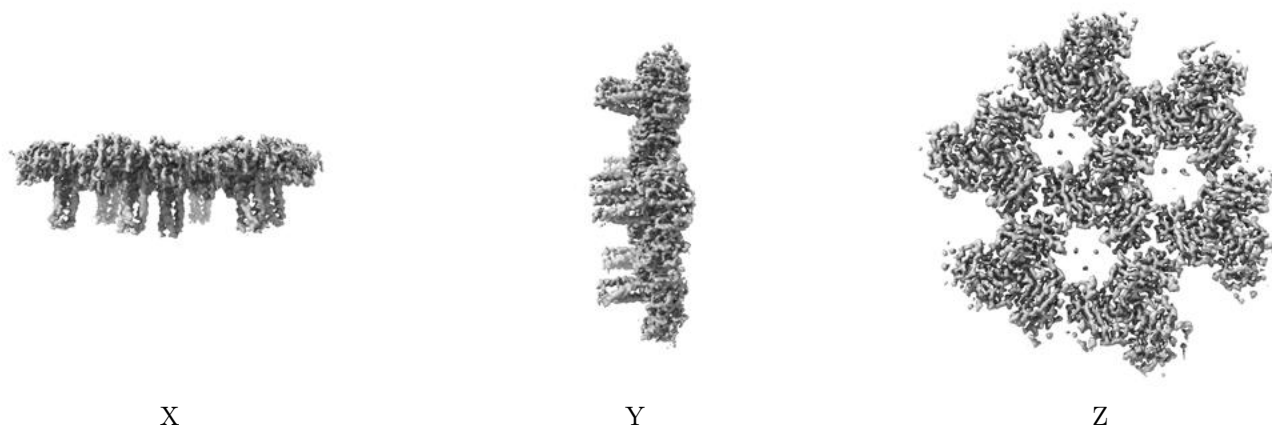
6.4.2 Raw map



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.

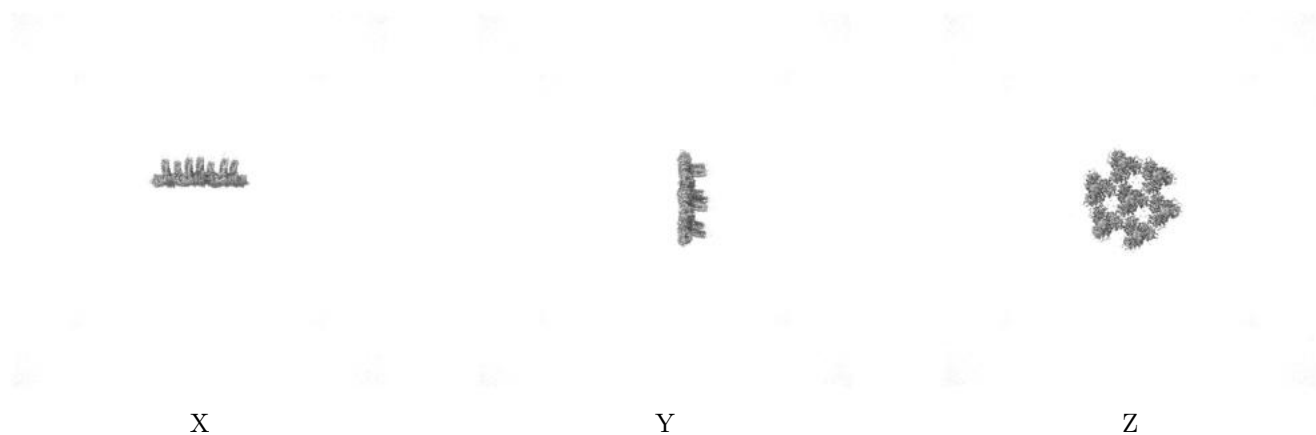
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.222. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

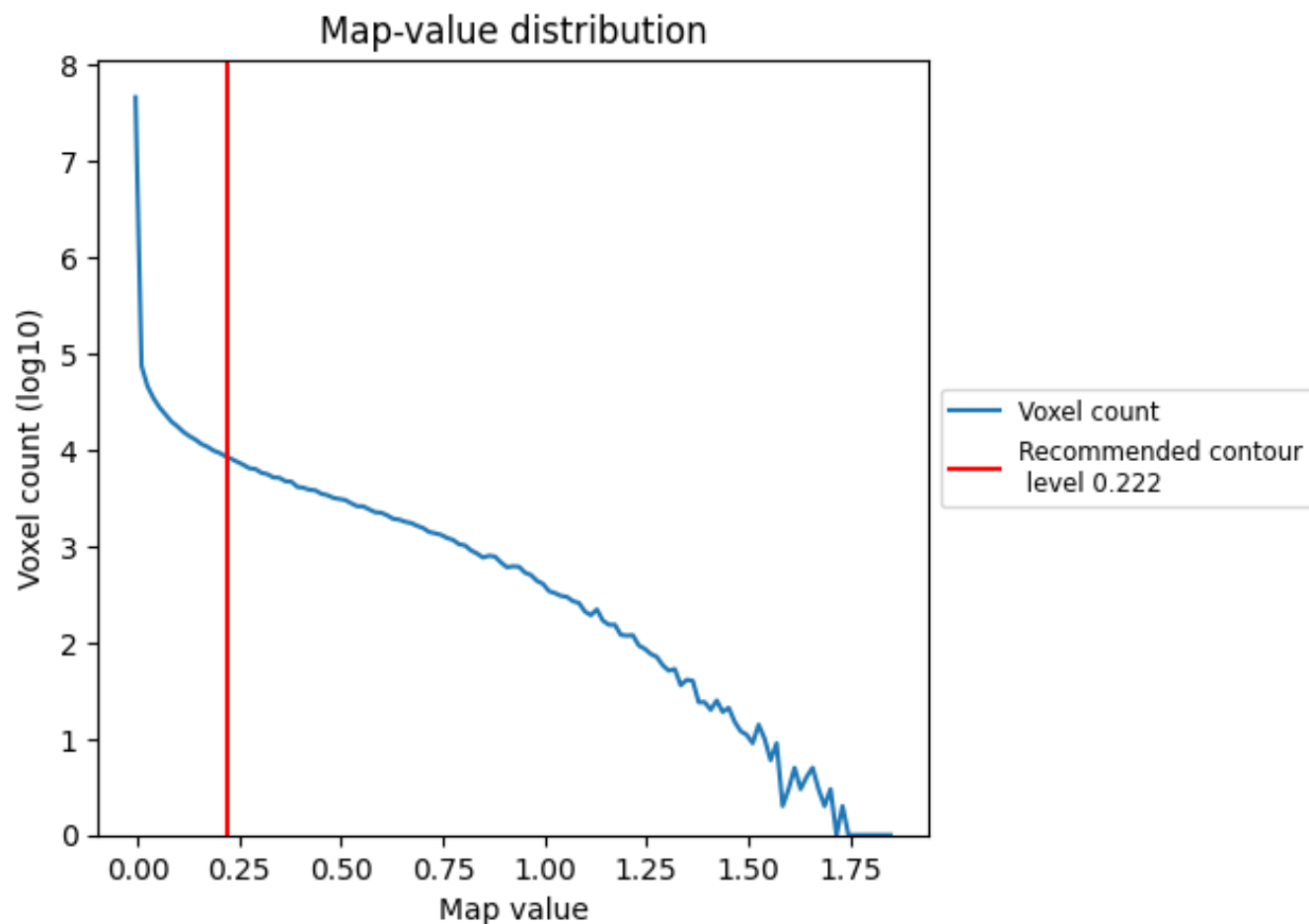
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

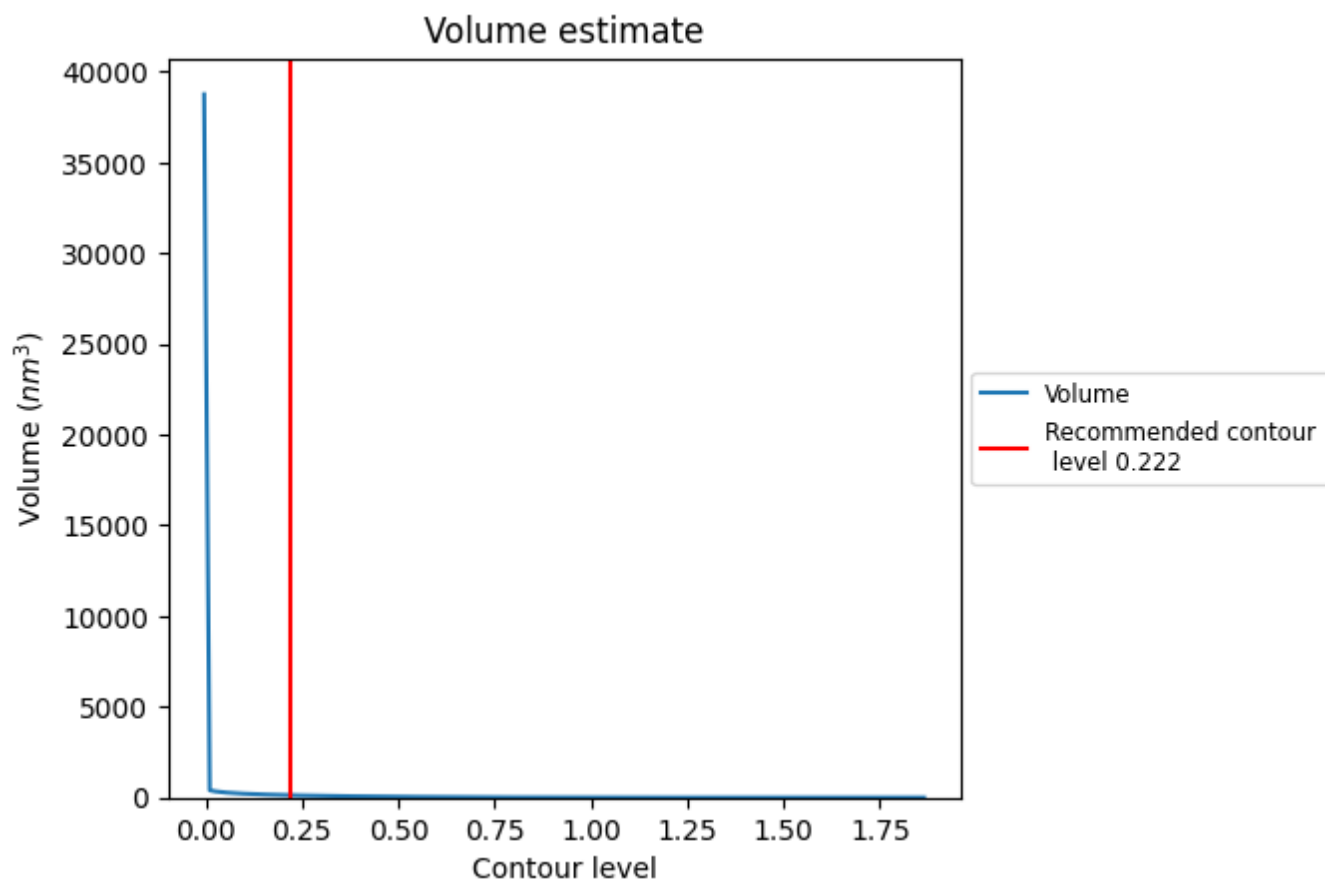
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

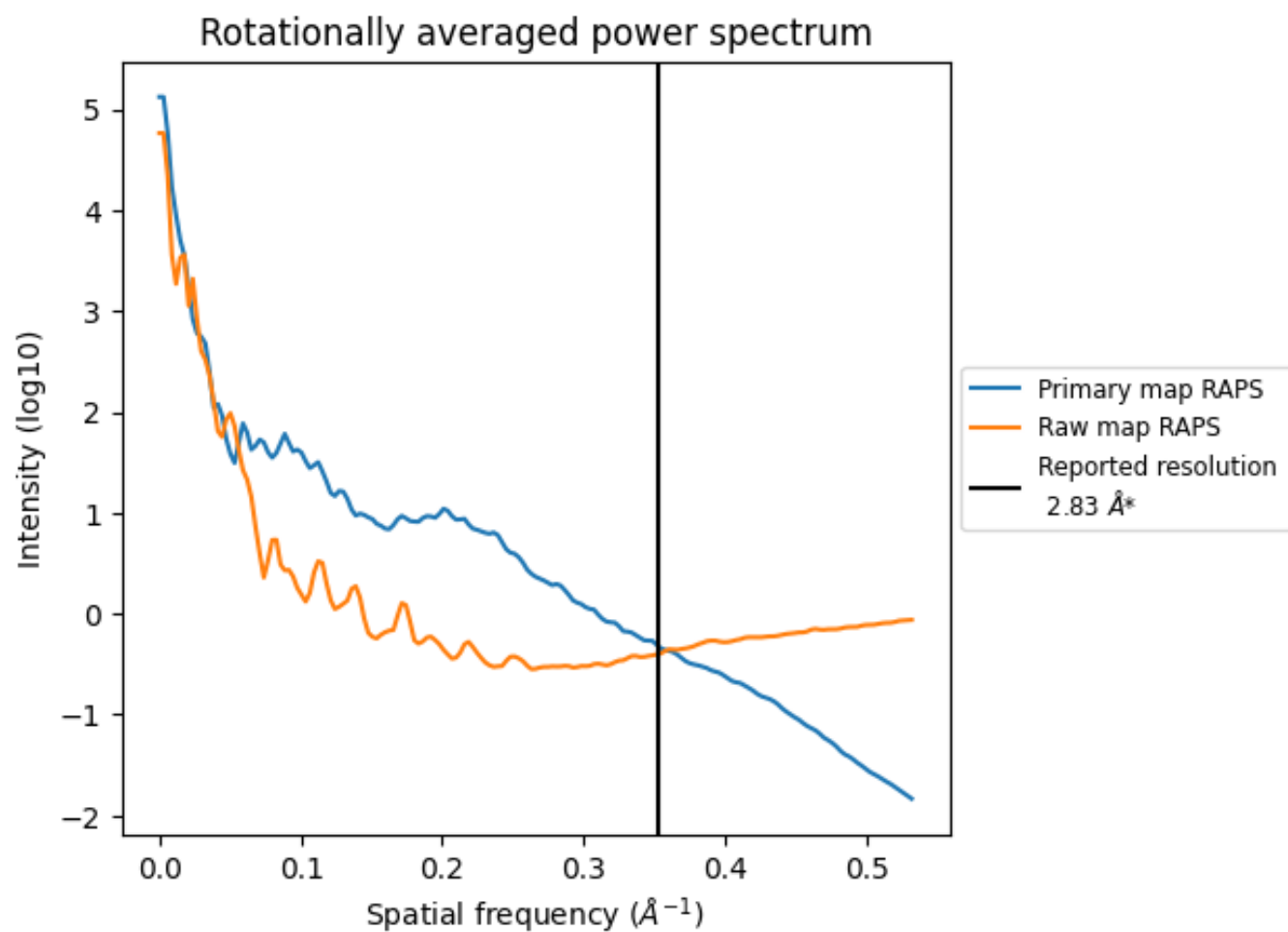
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 127 nm³; this corresponds to an approximate mass of 115 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 ⓘ

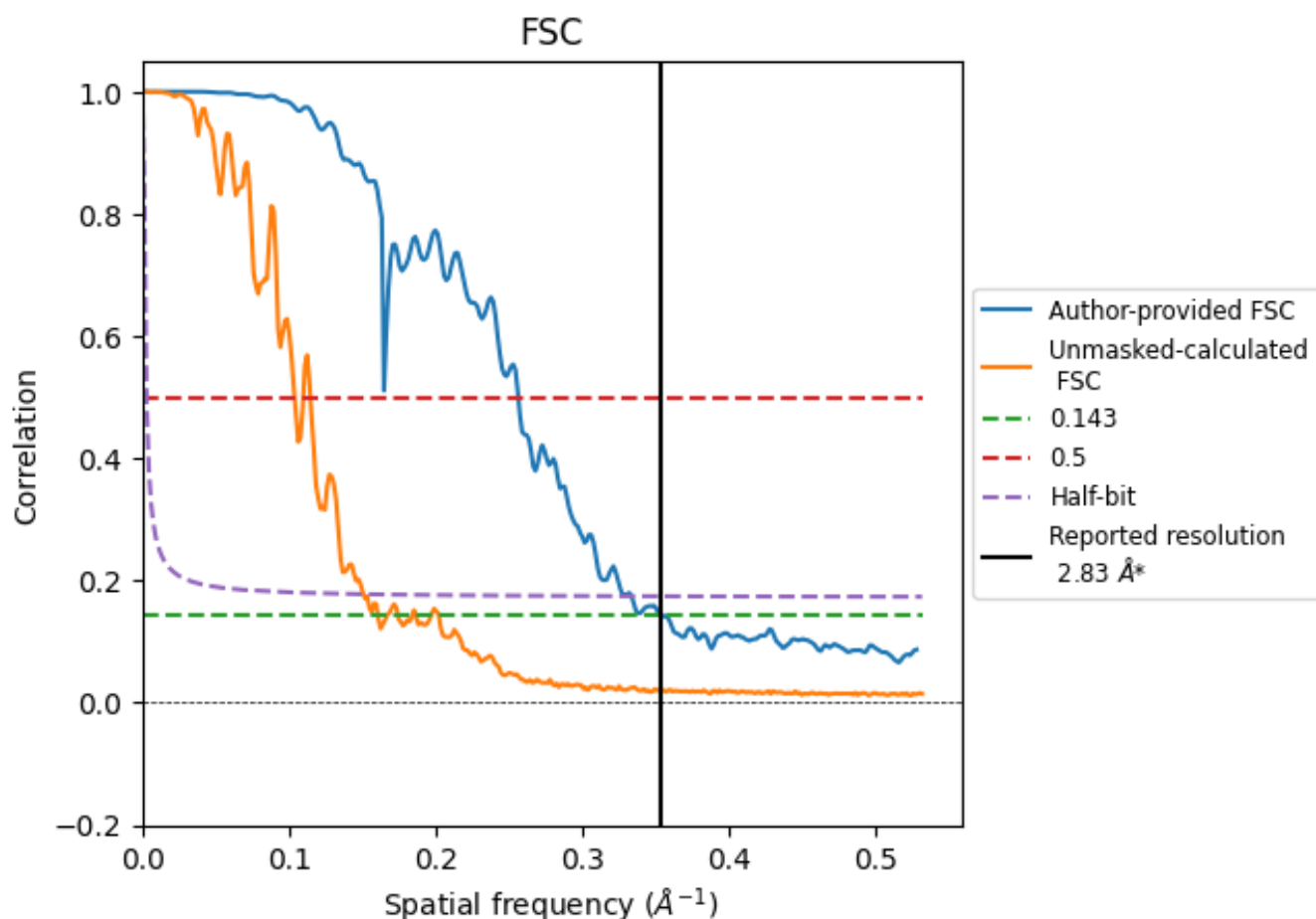


*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

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 0.353 \AA^{-1}

8.2 Resolution estimates [i](#)

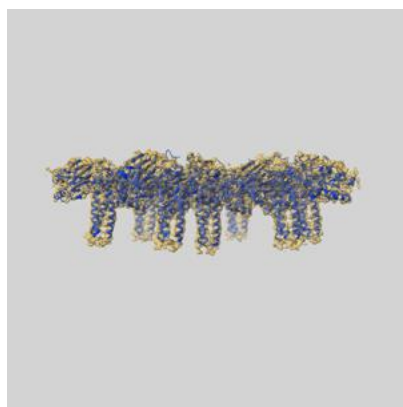
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.83	3.90	3.00
Unmasked-calculated*	6.22	9.62	6.63

*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 6.22 differs from the reported value 2.83 by more than 10 %

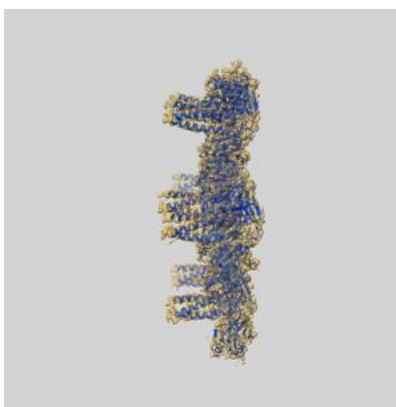
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60486 and PDB model 8ZUK. Per-residue inclusion information can be found in section 3 on page 16.

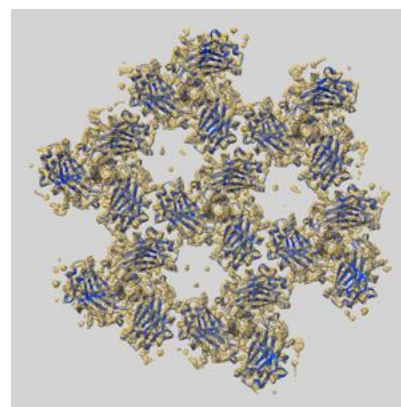
9.1 Map-model overlay [i](#)



X



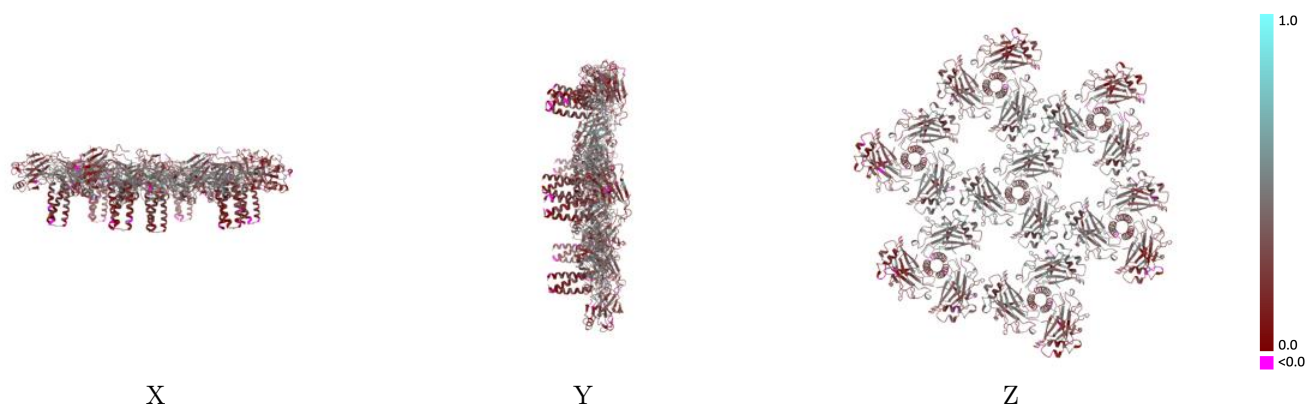
Y



Z

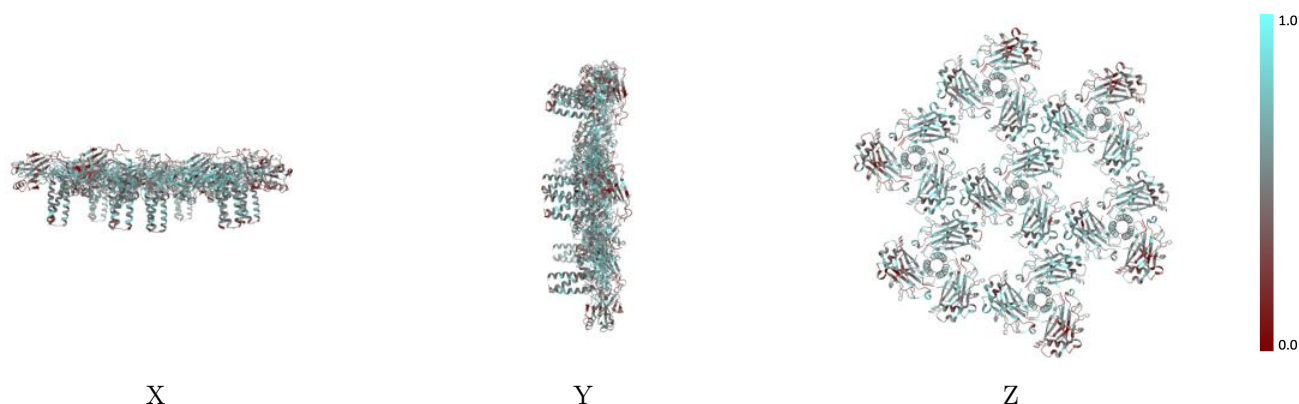
The images above show the 3D surface view of the map at the recommended contour level 0.222 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



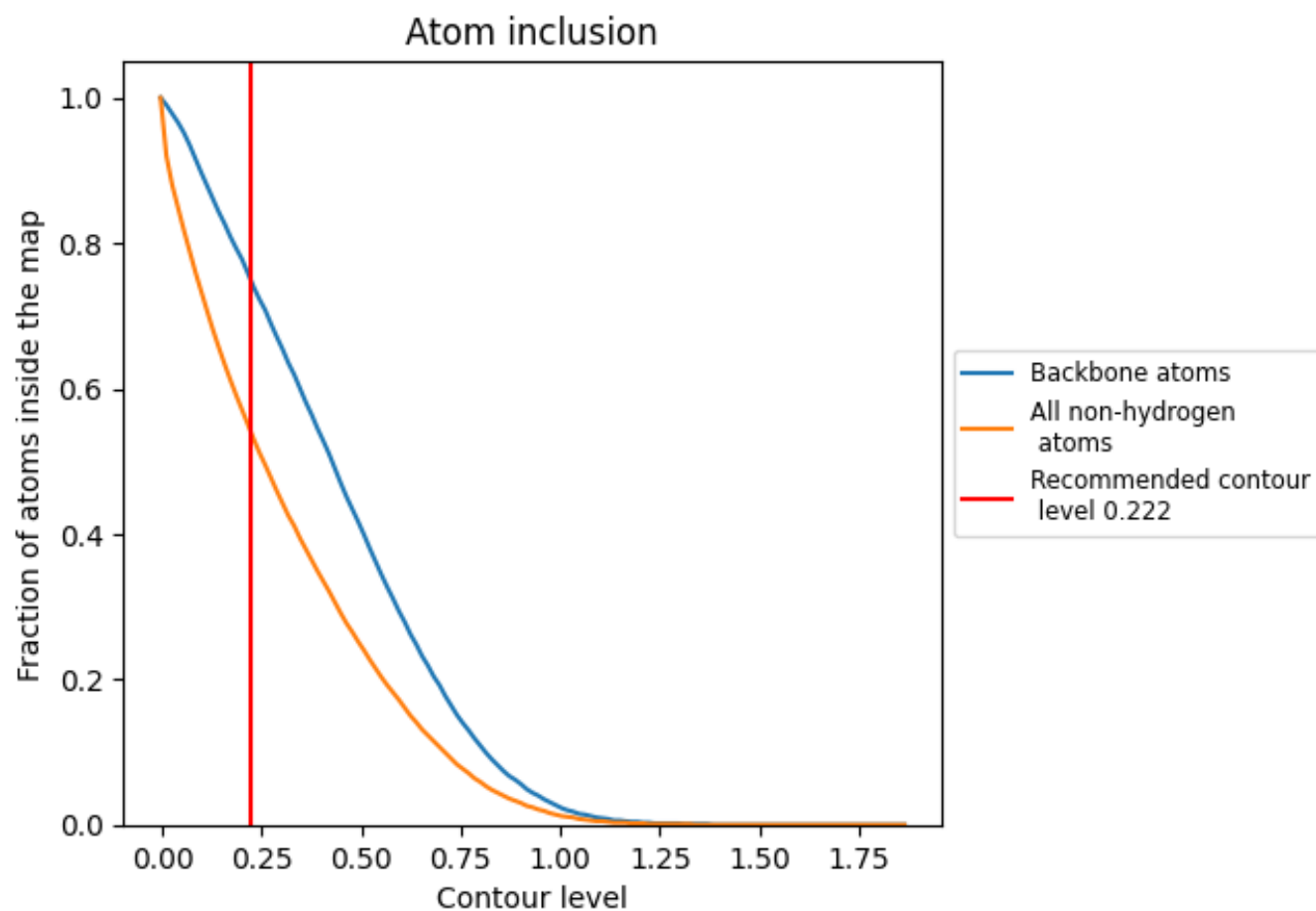
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.222).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 54% 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 (0.222) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5410	 0.3340
A	 0.5940	 0.4020
B	 0.5950	 0.4060
C	 0.5760	 0.4020
D	 0.5080	 0.3030
E	 0.4750	 0.3060
F	 0.4750	 0.3140
G	 0.5000	 0.2640
H	 0.5850	 0.3760
I	 0.5480	 0.3360
J	 0.4240	 0.1810
K	 0.4910	 0.3120
L	 0.4580	 0.2590
M	 0.4630	 0.2750
N	 0.5570	 0.3420
O	 0.6050	 0.3890
P	 0.3310	 0.1630
Q	 0.4410	 0.2310
R	 0.5080	 0.2880
S	 0.5610	 0.3440
T	 0.6030	 0.3860
U	 0.4800	 0.2730
V	 0.4750	 0.2260
W	 0.5000	 0.2790
X	 0.2970	 0.1470
Y	 0.5400	 0.3380
Z	 0.4700	 0.2670
a	 0.5820	 0.3770
b	 0.4490	 0.2480
c	 0.4070	 0.2160
d	 0.4490	 0.3170
e	 0.5940	 0.3820
f	 0.5510	 0.3380
g	 0.4970	 0.2630
h	 0.4660	 0.2860



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Chain	Atom inclusion	Q-score
i	 0.5080	 0.2790
j	 0.4410	 0.2010
k	 0.5970	 0.3910
l	 0.4660	 0.2760
m	 0.5570	 0.3400
n	 0.5000	 0.2590
o	 0.3050	 0.1650
p	 0.4660	 0.2450