



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:02 PM UTC

PDB ID : 6Q14 / pdb_00006q14
EMDB ID : EMD-20310
Title : Structure of the Salmonella SPI-1 injectisome NC-base
Authors : Hu, J.; Worrall, L.J.; Strynadka, N.C.J.
Deposited on : 2019-08-02
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

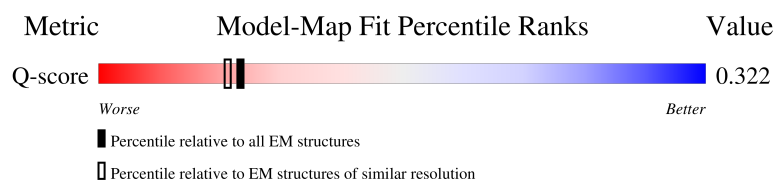
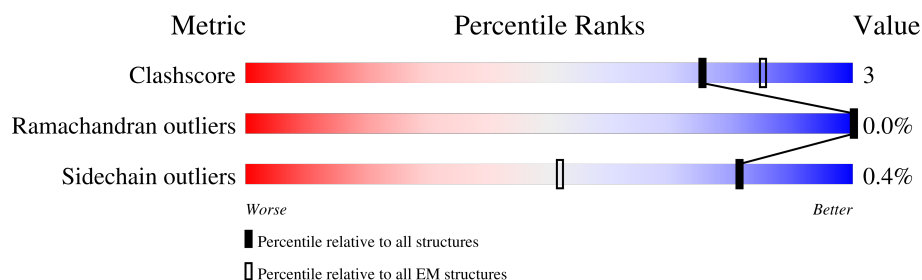
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



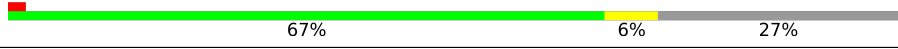
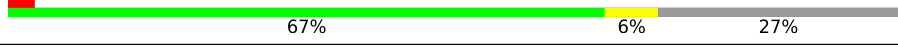
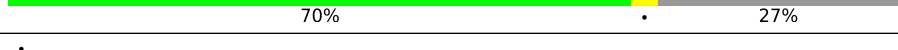
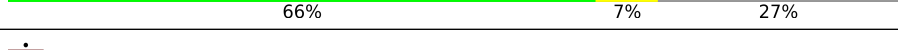
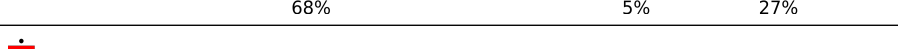
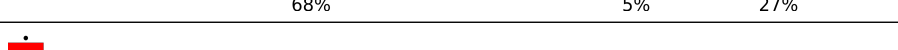
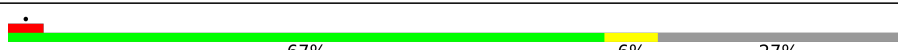
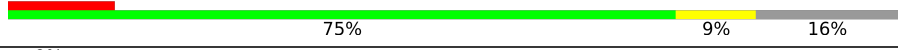
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	AA	252	
1	AB	252	
1	AC	252	
1	AD	252	

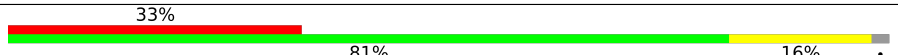
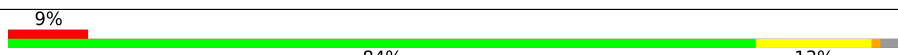
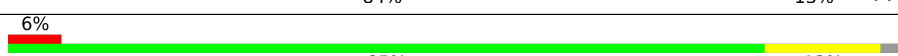
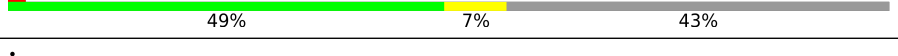
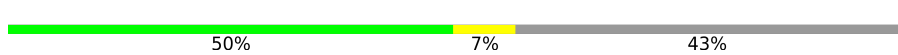
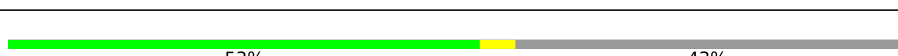
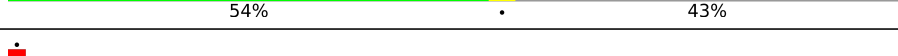
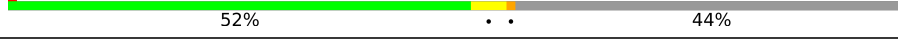
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Mol	Chain	Length	Quality of chain
1	AE	252	
1	AF	252	
1	AG	252	
1	AH	252	
1	AI	252	
1	AJ	252	
1	AK	252	
1	AL	252	
1	o	252	
1	p	252	
1	q	252	
1	r	252	
1	s	252	
1	t	252	
1	u	252	
1	v	252	
1	w	252	
1	x	252	
1	y	252	
1	z	252	
2	0	224	
2	1	224	
2	2	224	
2	3	224	
2	4	224	

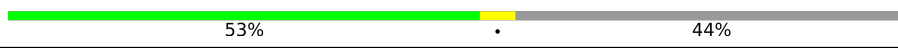
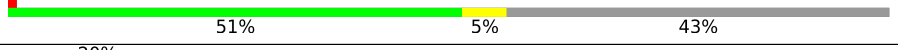
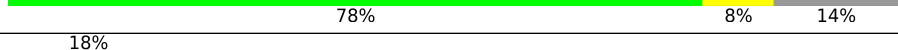
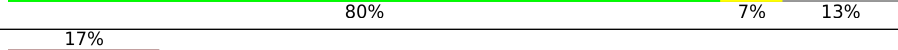
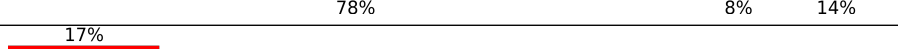
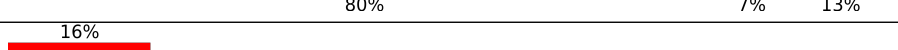
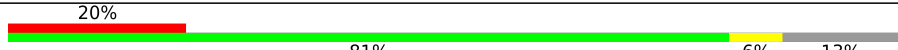
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Mol	Chain	Length	Quality of chain
3	5	263	
4	6	86	
4	7	86	
4	8	86	
4	9	86	
5	E	392	
5	R	392	
5	S	392	
5	T	392	
5	U	392	
5	V	392	
5	W	392	
5	X	392	
5	Y	392	
5	Z	392	
5	a	392	
5	b	392	
5	c	392	
5	d	392	
5	e	392	
5	f	392	
5	g	392	
5	h	392	
5	i	392	
5	j	392	

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Mol	Chain	Length	Quality of chain
5	k	392	
5	l	392	
5	m	392	
5	n	392	
6	A	562	
6	B	562	
6	C	562	
6	D	562	
6	F	562	
6	G	562	
6	H	562	
6	I	562	
6	J	562	
6	K	562	
6	L	562	
6	M	562	
6	N	562	
6	O	562	
6	P	562	
6	Q	562	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 147873 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 Lipoprotein PrgK.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AB	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AC	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AD	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AE	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AF	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AG	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AH	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AI	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AL	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	o	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	p	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	q	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	r	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	s	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	t	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	u	184	Total 1431	C 901	N 250	O 277	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	v	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		
1	w	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		
1	x	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		
1	y	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		
1	z	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		
1	AJ	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		
1	AK	184	Total	C	N	O	S	0	0
			1431	901	250	277	3		

- Molecule 2 is a protein called Surface presentation of antigens protein SpaP.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	189	Total	C	N	O	S	0	0
			1468	982	219	256	11		
2	1	189	Total	C	N	O	S	0	0
			1475	988	220	256	11		
2	2	187	Total	C	N	O	S	0	0
			1464	981	219	253	11		
2	3	194	Total	C	N	O	S	0	0
			1520	1016	227	266	11		
2	4	211	Total	C	N	O	S	1	0
			1672	1108	255	298	11		

- Molecule 3 is a protein called Surface presentation of antigens protein SpaR.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	228	Total	C	N	O	S	0	0
			1718	1136	276	293	13		

- Molecule 4 is a protein called Surface presentation of antigens protein SpaQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	53	Total	C	N	O	S	0	0
			405	276	61	67	1		
4	7	84	Total	C	N	O	S	0	0
			644	436	97	109	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	84	Total	C	N	O	S	0	0
			644	436	97	109	2		
4	9	84	Total	C	N	O	S	0	0
			647	438	97	109	3		

- Molecule 5 is a protein called Protein PrgH.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	R	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	S	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	T	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	U	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	V	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	W	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	X	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	Y	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	Z	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	a	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	b	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	c	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	d	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	e	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	f	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	g	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	i	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	j	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	k	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		
5	l	222	Total	C	N	O	S	0	0
			1836	1170	326	335	5		
5	m	221	Total	C	N	O	S	0	0
			1827	1164	325	333	5		
5	n	222	Total	C	N	O	S	0	0
			1831	1167	326	333	5		

- Molecule 6 is a protein called Protein InvG.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	144	Total	C	N	O	S	1	0
			1154	741	198	209	6		
6	A	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		
6	B	489	Total	C	N	O	S	1	0
			3810	2415	665	718	12		
6	C	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		
6	D	489	Total	C	N	O	S	0	0
			3802	2410	662	718	12		
6	F	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		
6	G	489	Total	C	N	O	S	1	0
			3810	2415	665	718	12		
6	H	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		
6	I	489	Total	C	N	O	S	1	0
			3810	2415	665	718	12		
6	J	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		
6	K	489	Total	C	N	O	S	1	0
			3810	2415	665	718	12		
6	L	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		

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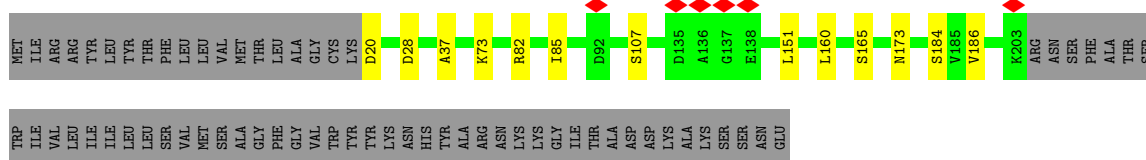
Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	489	Total	C	N	O	S	0	0
			3802	2410	662	718	12		
6	N	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		
6	O	489	Total	C	N	O	S	1	0
			3810	2415	665	718	12		
6	P	484	Total	C	N	O	S	0	0
			3764	2384	656	712	12		

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.

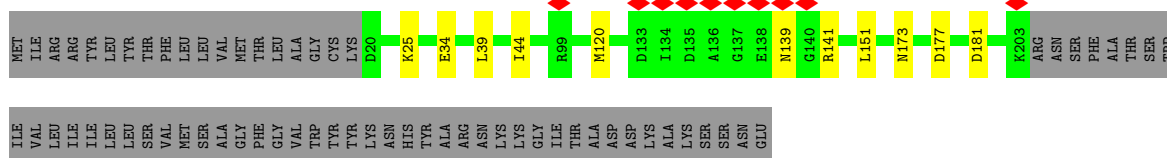
• Molecule 1: Lipoprotein PrgK

Chain AA: 



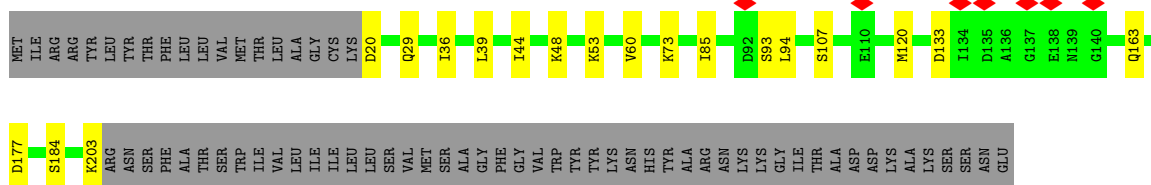
• Molecule 1: Lipoprotein PrgK

Chain AB: 



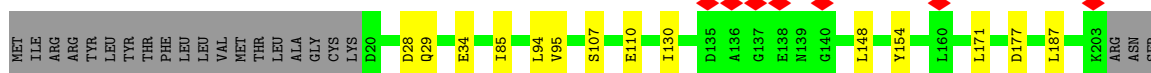
• Molecule 1: Lipoprotein PrgK

Chain AC: 



• Molecule 1: Lipoprotein PrgK

Chain AD: 



PHE
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LEU
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• Molecule 1: Lipoprotein PrgK



MET
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LEU
D20
D92
S93
L94
S107
E110
Q111
I130
D135
A136
G137
E138
L160
K168
N173
Y180
S184
K203
ARG
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• Molecule 1: Lipoprotein PrgK



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E112
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• Molecule 1: Lipoprotein PrgK



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• Molecule 1: Lipoprotein PrgK



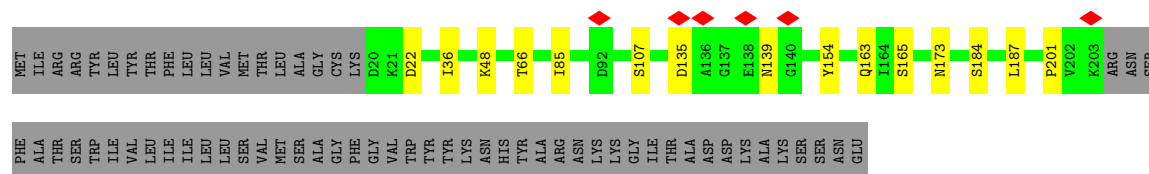
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G137
E138
N139
G140
Y154
N173
D177
S184
P201

• Molecule 1: Lipoprotein PrgK

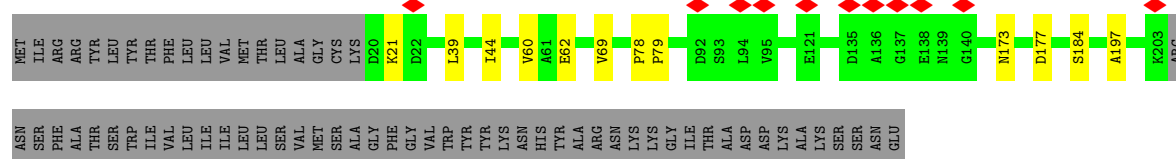


MET
ILE
ARG
TYR
LEU
TYR
PHE
MET
LEU
SER
VAL
PHE
GLY
THR
MET
GLY
PHE
VAL
SER
LEU
SER
LEU
D20
E34
L39
I44
V60
V69
K73
P78
P79
I85
D92
R99
S107
D133
I134
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A136
G137
E138
N139
G140
H147
R169
D177
Y180

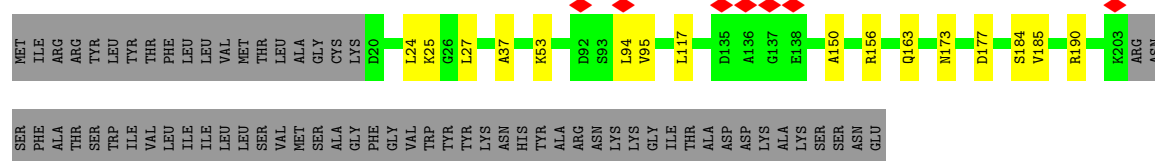




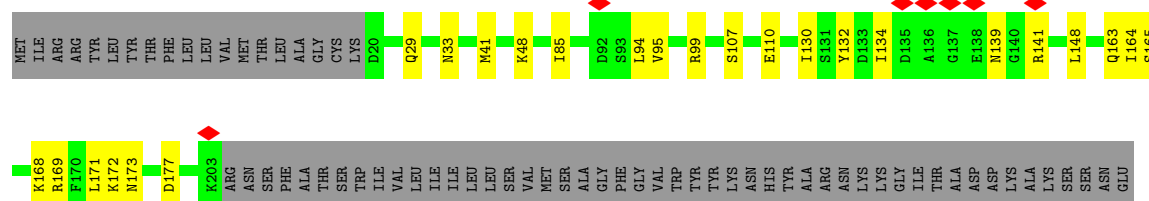
- Molecule 1: Lipoprotein PrgK



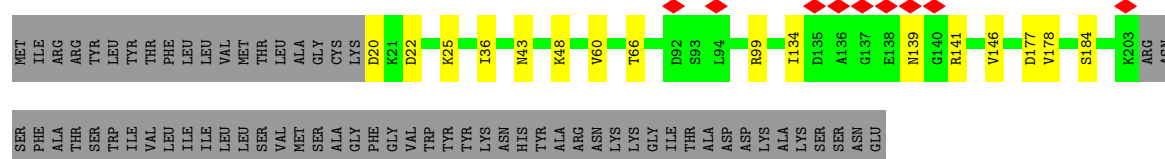
- Molecule 1: Lipoprotein PrgK



- Molecule 1: Lipoprotein PrgK

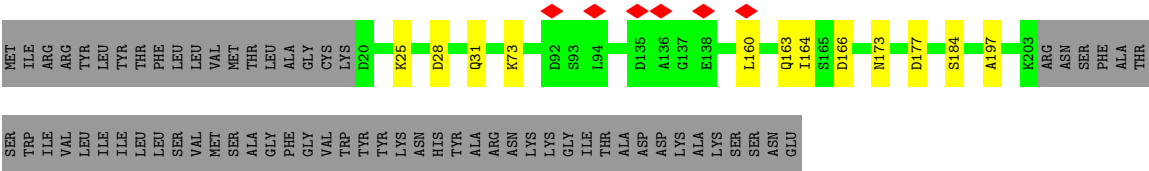


- Molecule 1: Lipoprotein PrgK

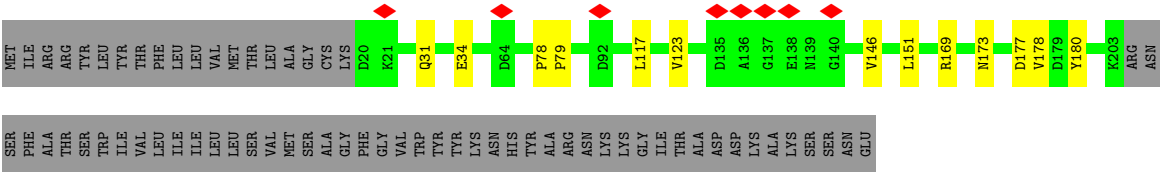


- Molecule 1: Lipoprotein PrgK

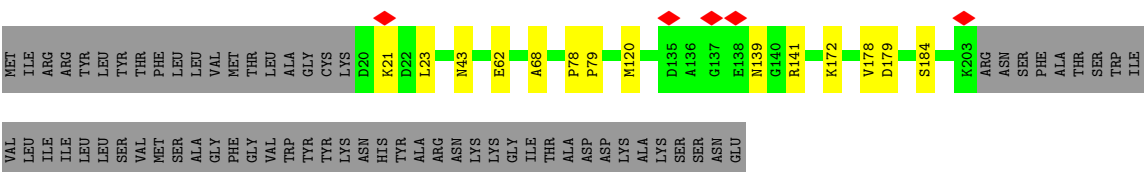




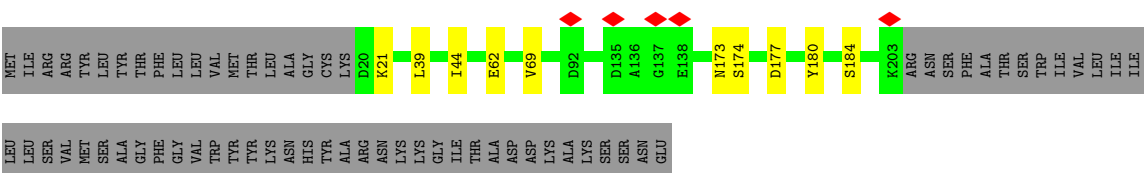
• Molecule 1: Lipoprotein PrgK



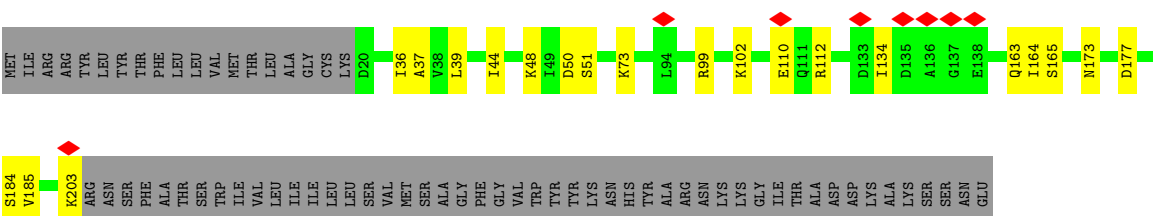
• Molecule 1: Lipoprotein PrgK



• Molecule 1: Lipoprotein PrgK

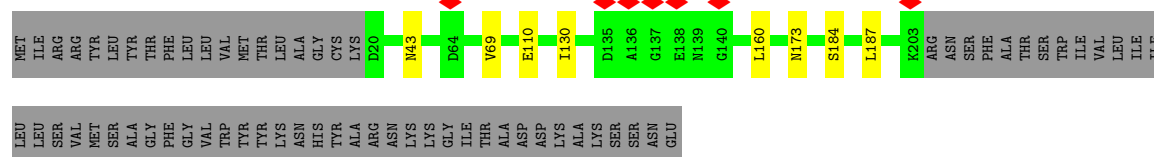


• Molecule 1: Lipoprotein PrgK



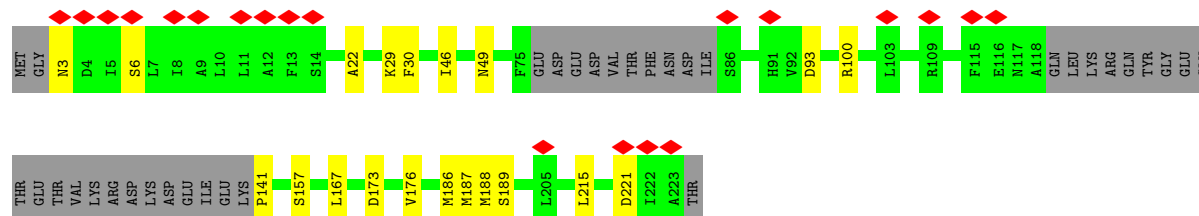
• Molecule 1: Lipoprotein PrgK

Chain AK: 



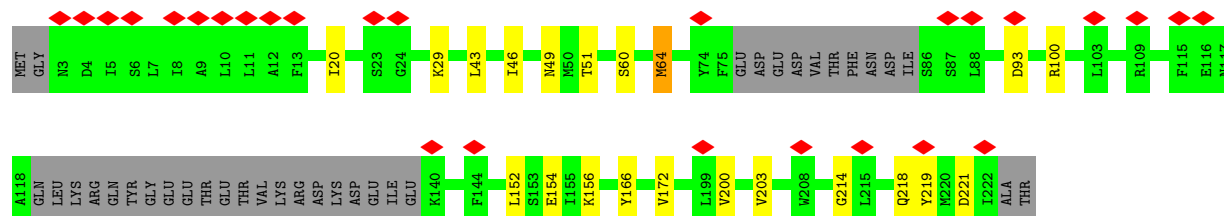
- Molecule 2: Surface presentation of antigens protein SpaP

Chain 0: 



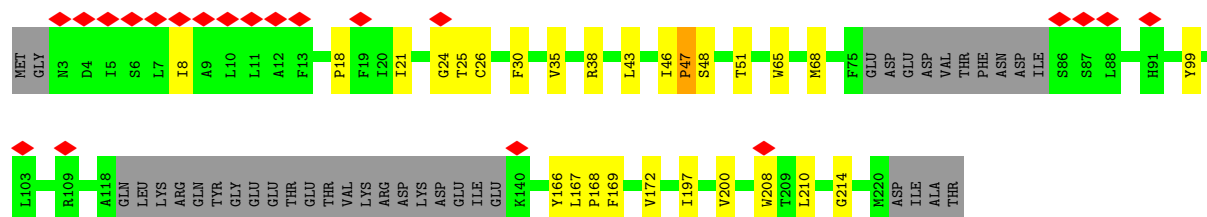
- Molecule 2: Surface presentation of antigens protein SpaP

Chain 1: 



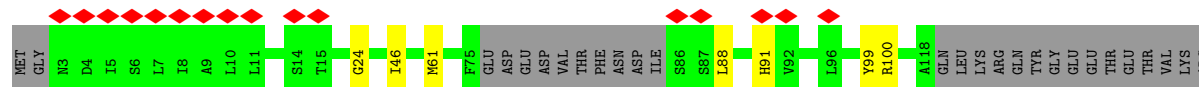
- Molecule 2: Surface presentation of antigens protein SpaP

Chain 2: 



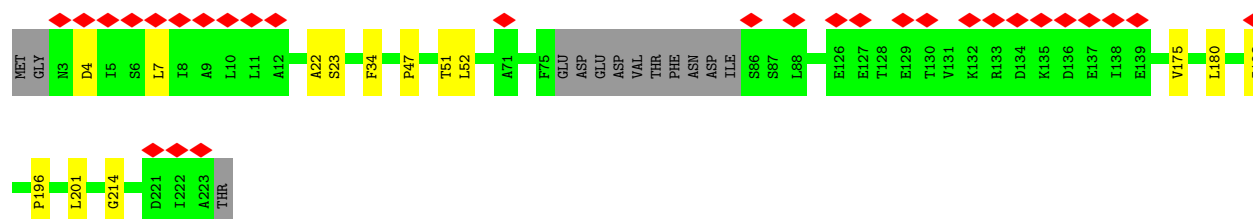
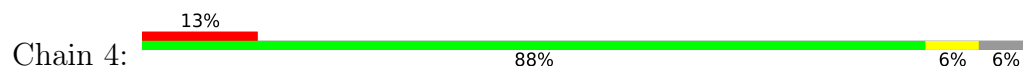
- Molecule 2: Surface presentation of antigens protein SpaP

Chain 3: 

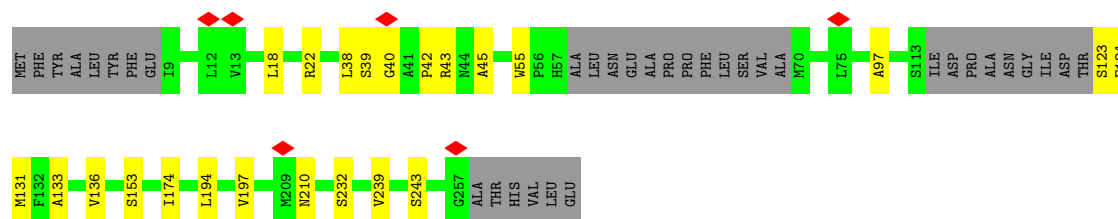
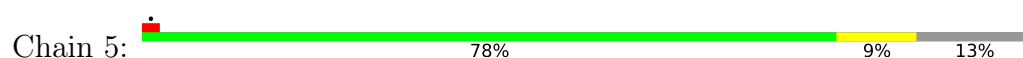




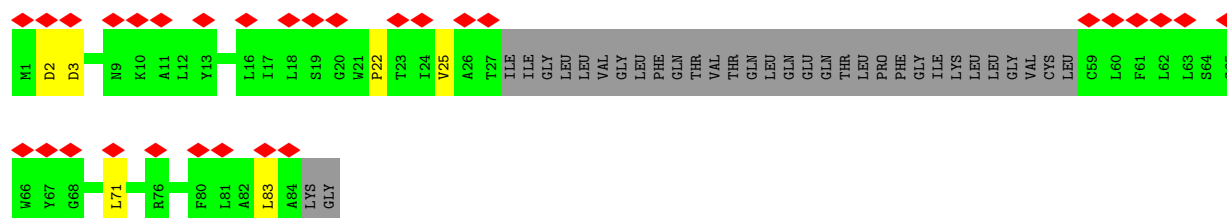
- Molecule 2: Surface presentation of antigens protein SpaP



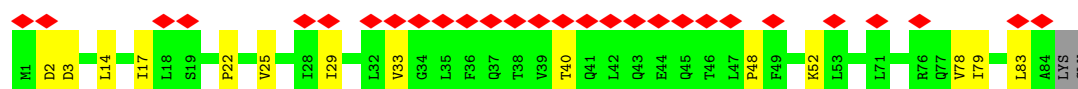
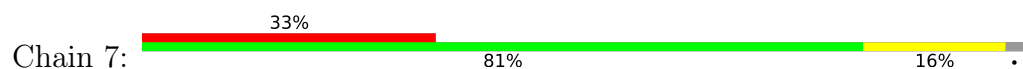
- Molecule 3: Surface presentation of antigens protein SpaR



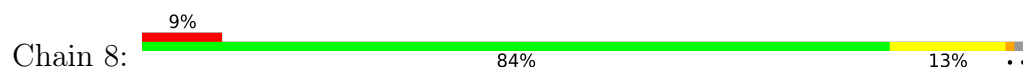
- Molecule 4: Surface presentation of antigens protein SpaQ

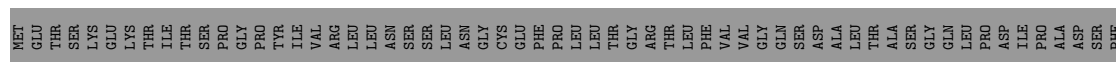


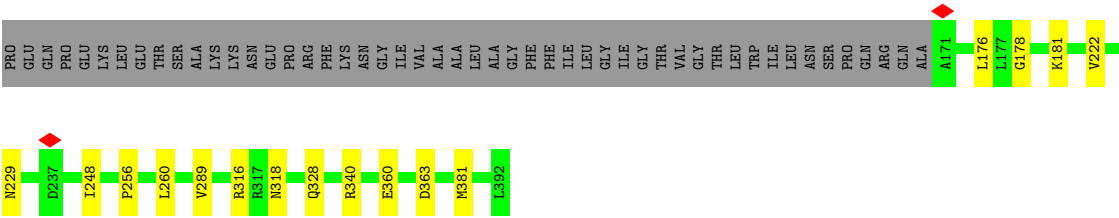
- Molecule 4: Surface presentation of antigens protein SpaQ



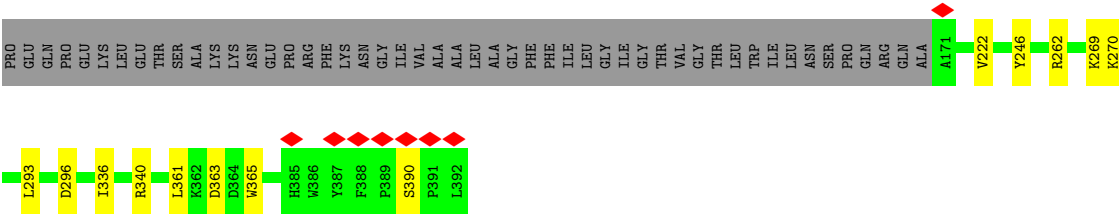
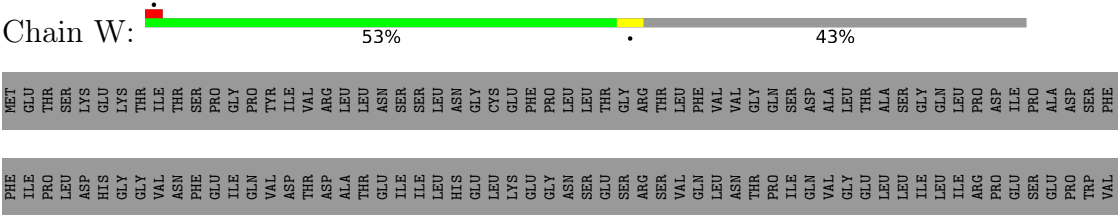
- Molecule 4: Surface presentation of antigens protein SpaQ



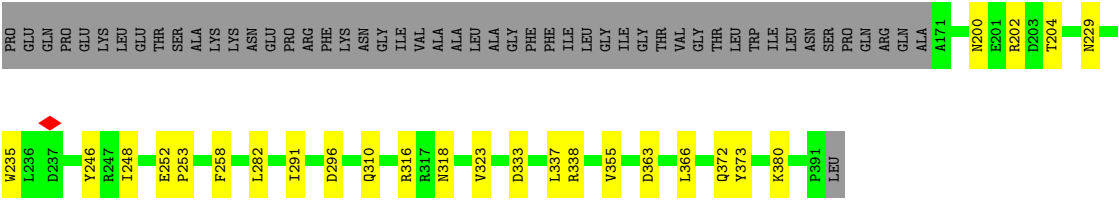
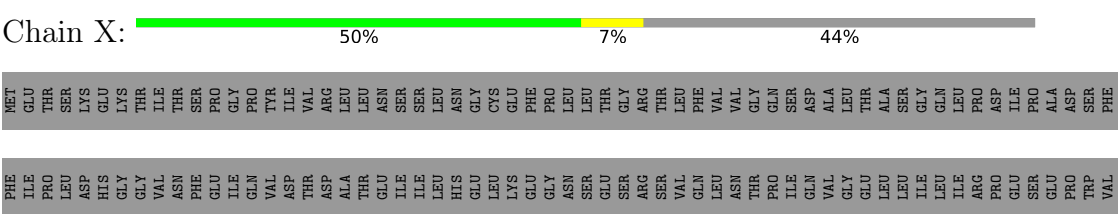




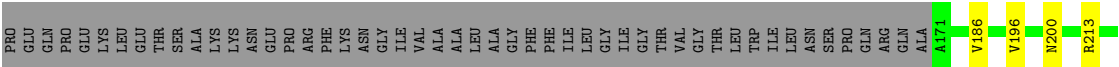
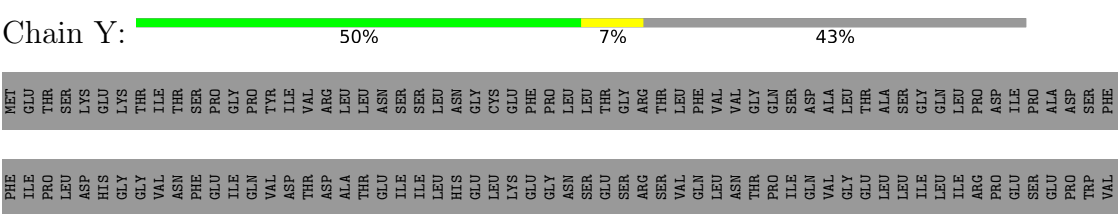
• Molecule 5: Protein PrgH



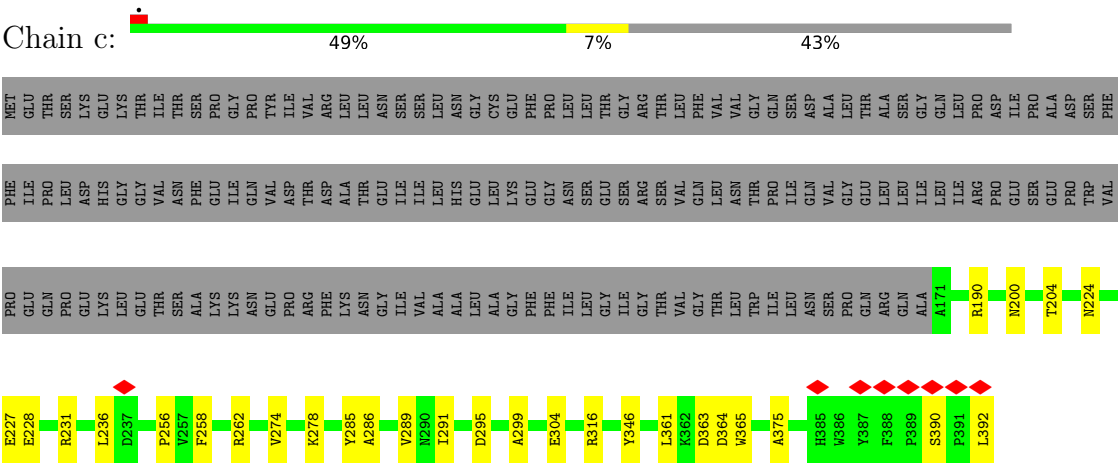
• Molecule 5: Protein PrgH



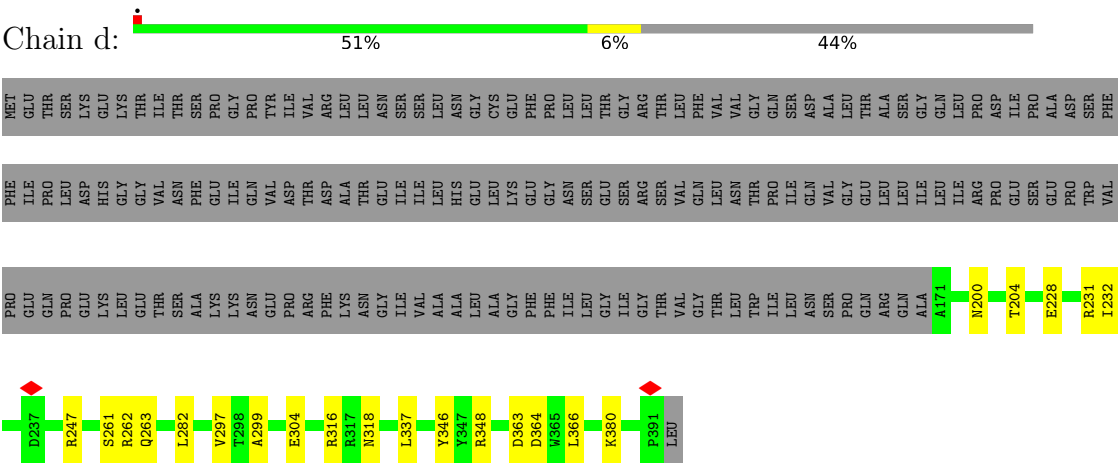
• Molecule 5: Protein PrgH



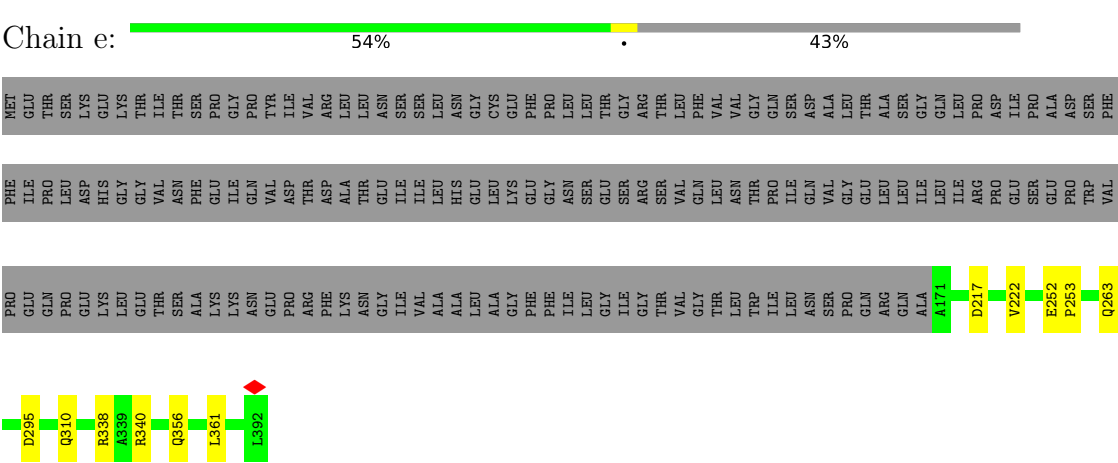
• Molecule 5: Protein PrgH



• Molecule 5: Protein PrgH

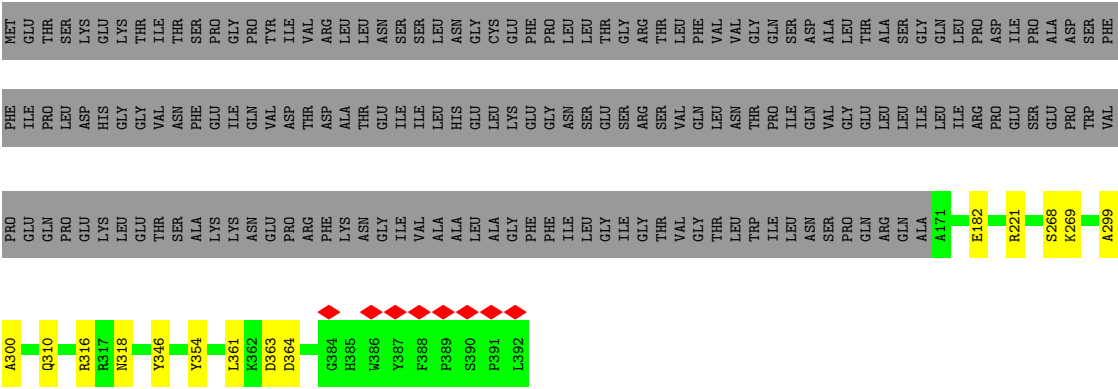


• Molecule 5: Protein PrgH

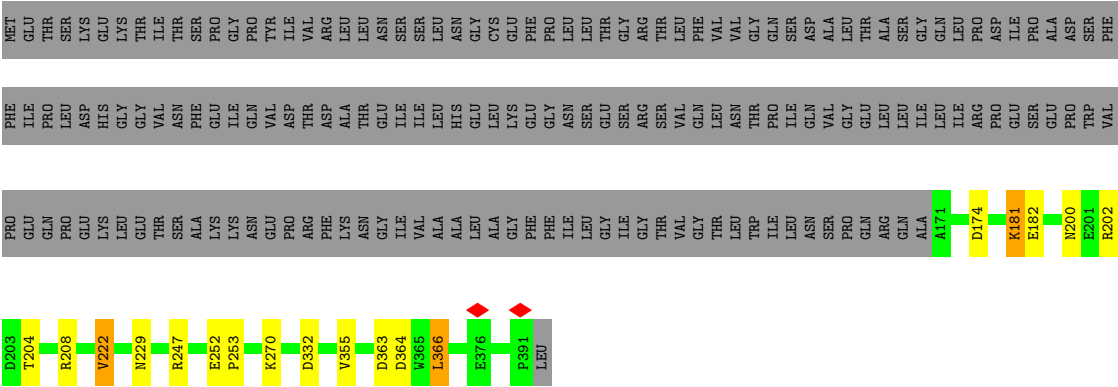


• Molecule 5: Protein PrgH

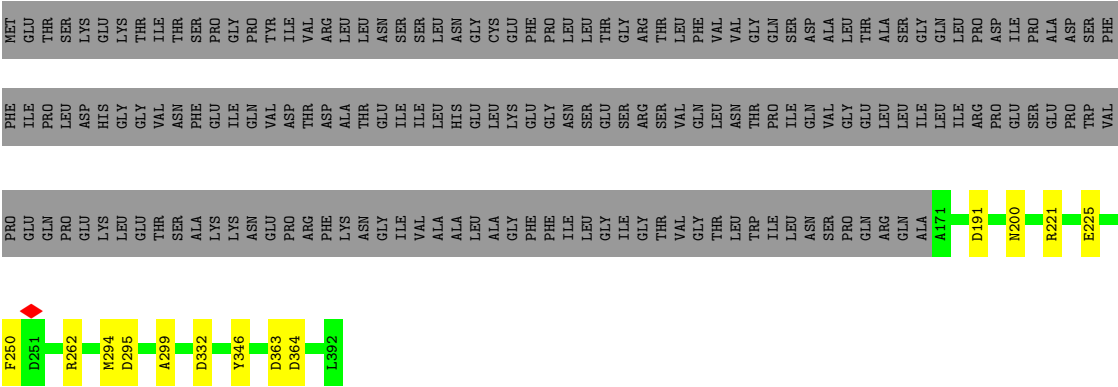




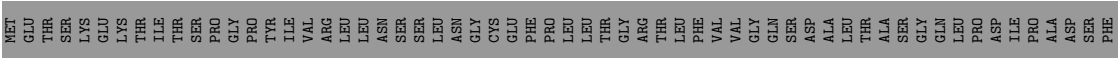
● Molecule 5: Protein PrgH



● Molecule 5: Protein PrgH



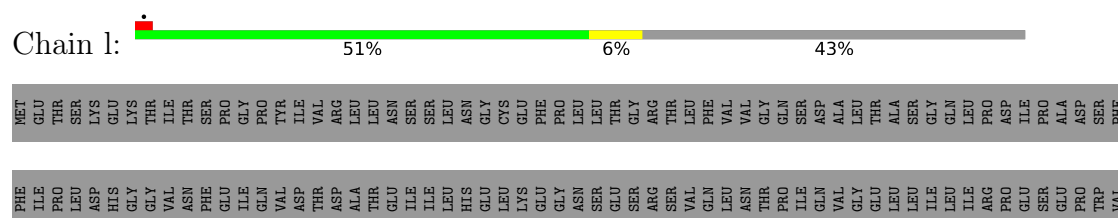
● Molecule 5: Protein PrgH



- Molecule 5: Protein PrgH

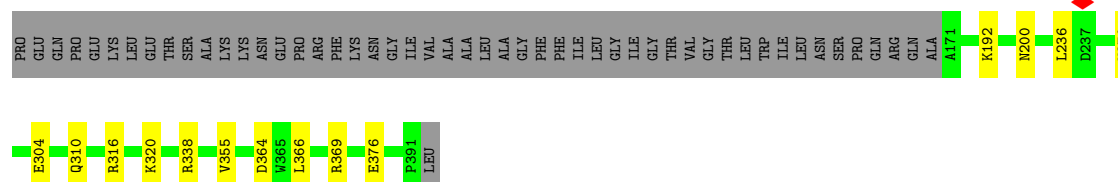
- Molecule 5: Protein PrgH

- Molecule 5: Protein PrgH



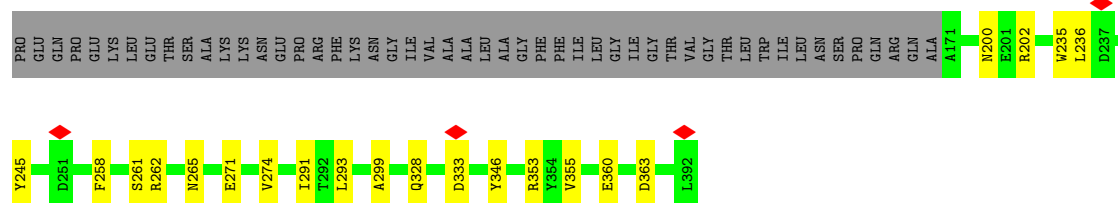
- Molecule 5: Protein PrgH

Chain m: 53% . 44%

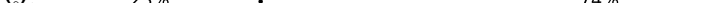


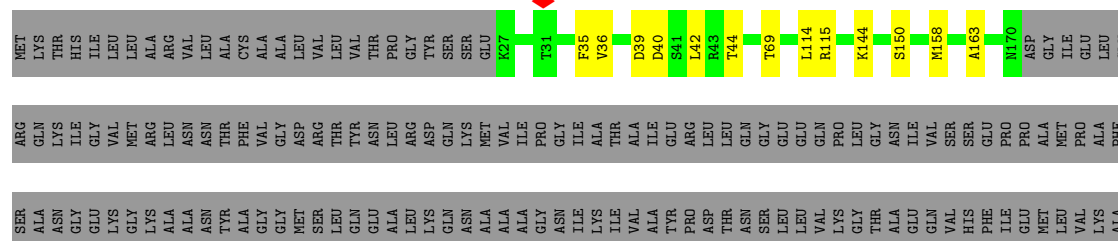
- Molecule 5: Protein PrgH

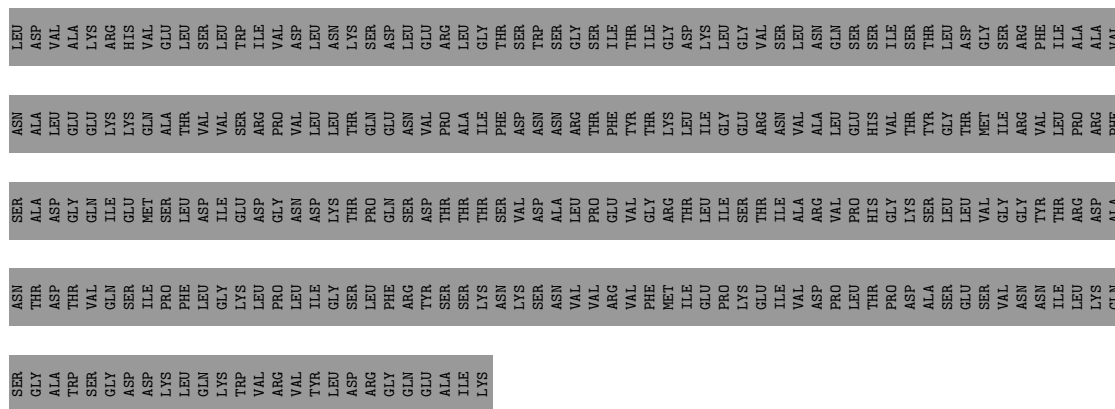
Chain n: 51% 5% 43%



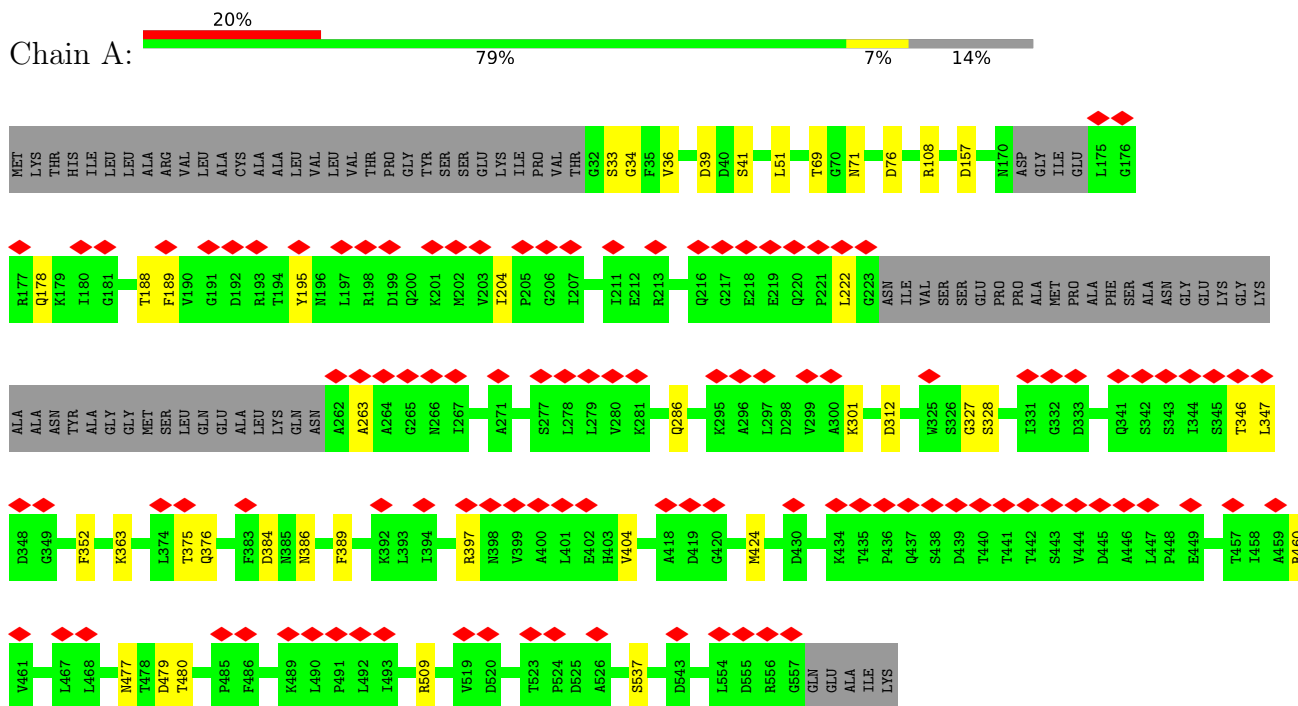
- Molecule 6: Protein InvG

Chain Q:  23% . 74%

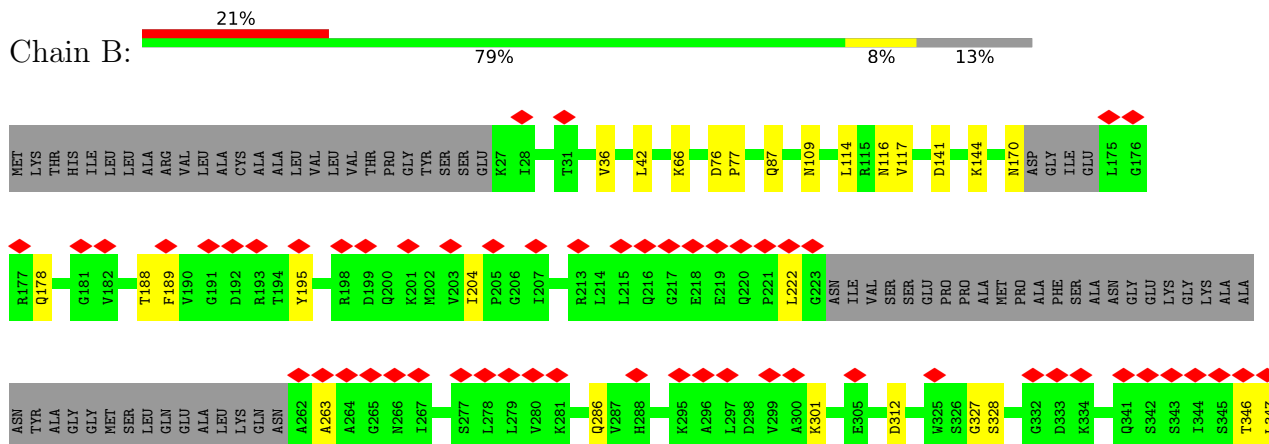




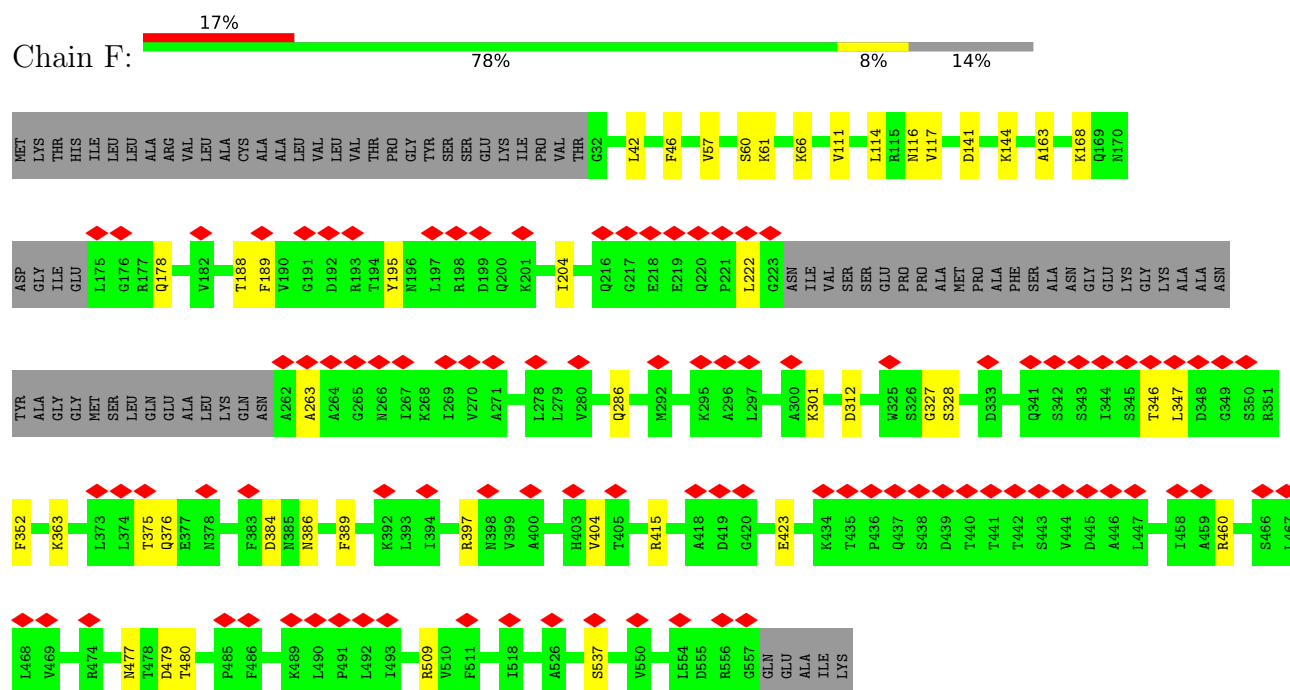
- Molecule 6: Protein InvG



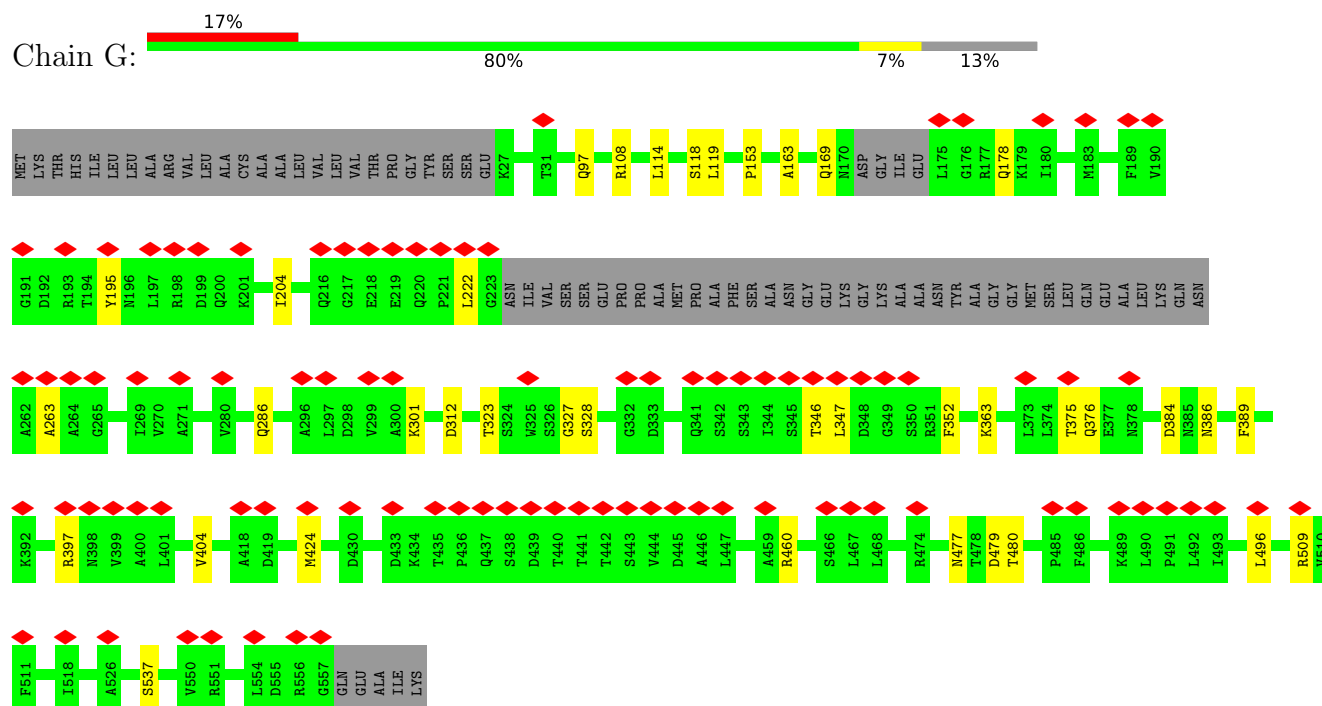
- Molecule 6: Protein InvG



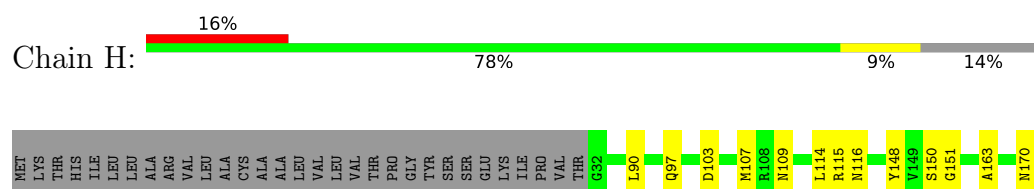
- Molecule 6: Protein InvG

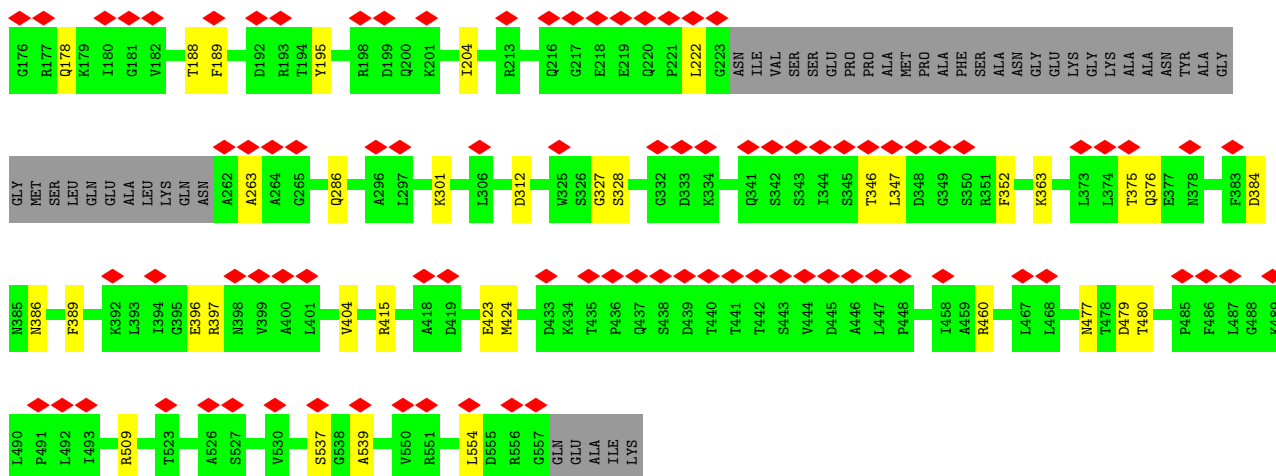


- Molecule 6: Protein InvG

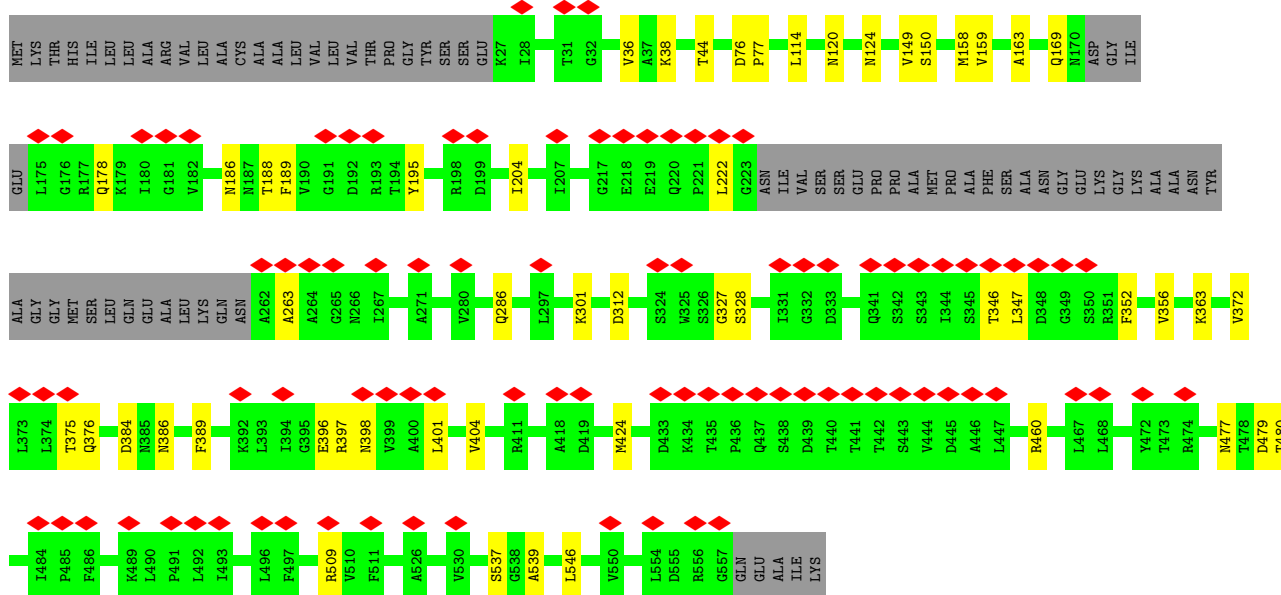
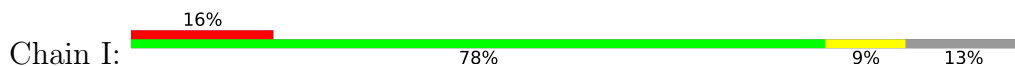


- Molecule 6: Protein InvG

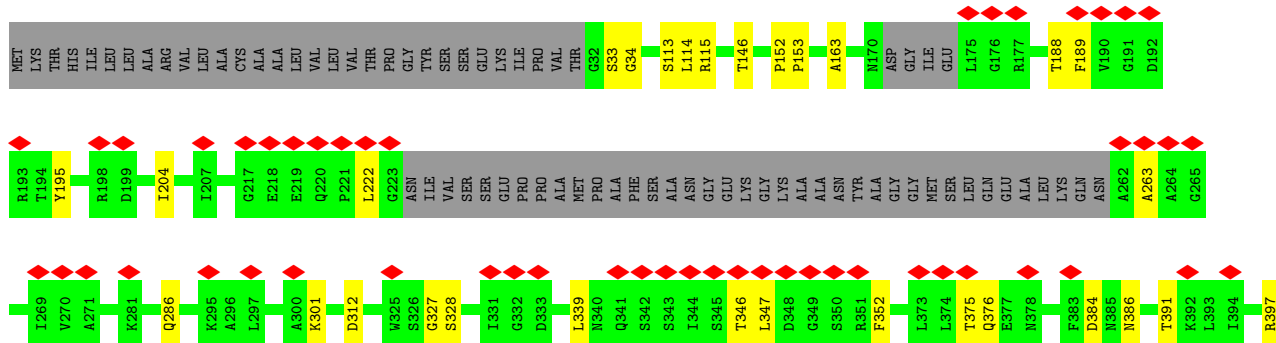
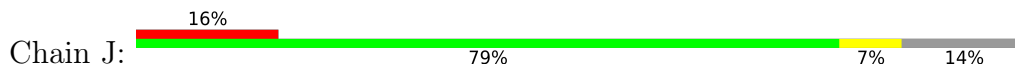


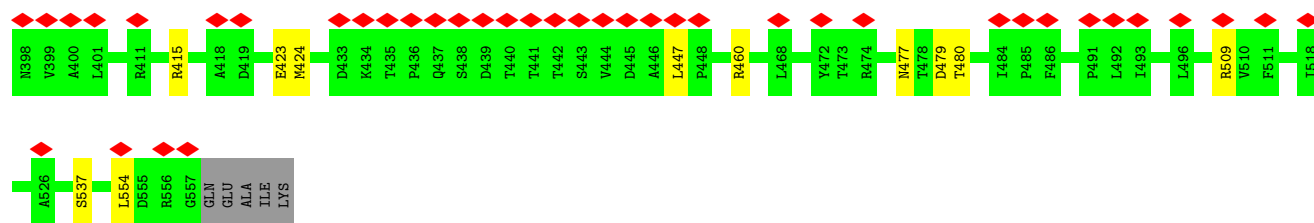


• Molecule 6: Protein InvG

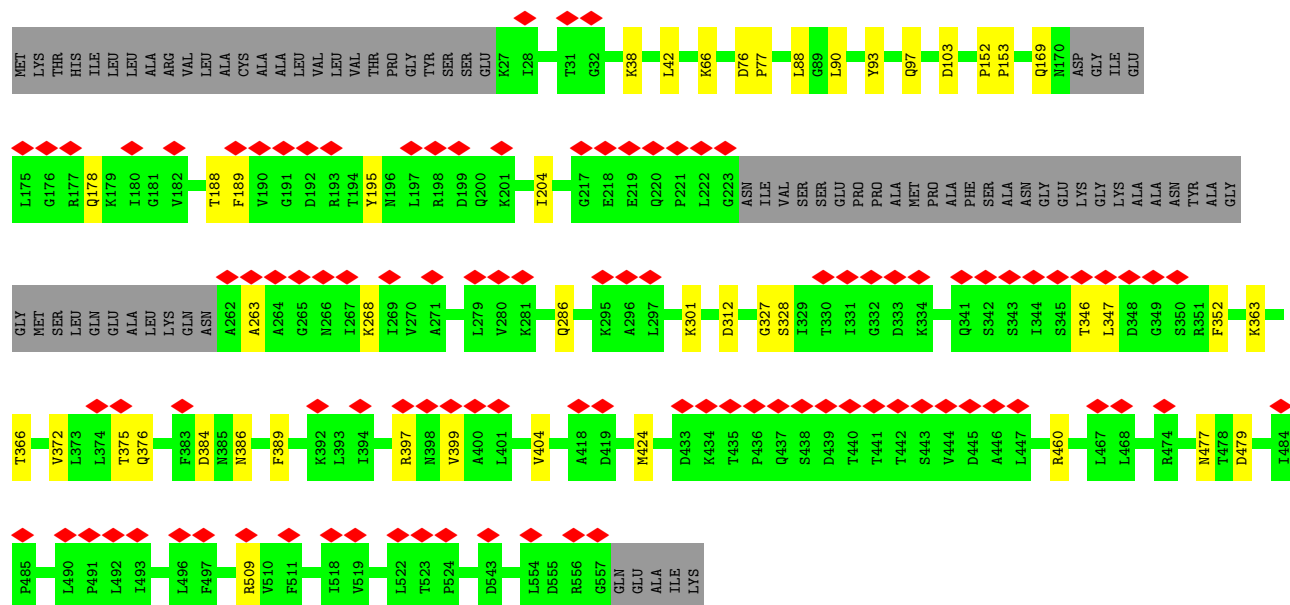
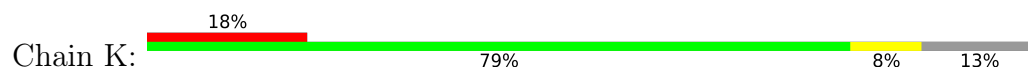


• Molecule 6: Protein InvG

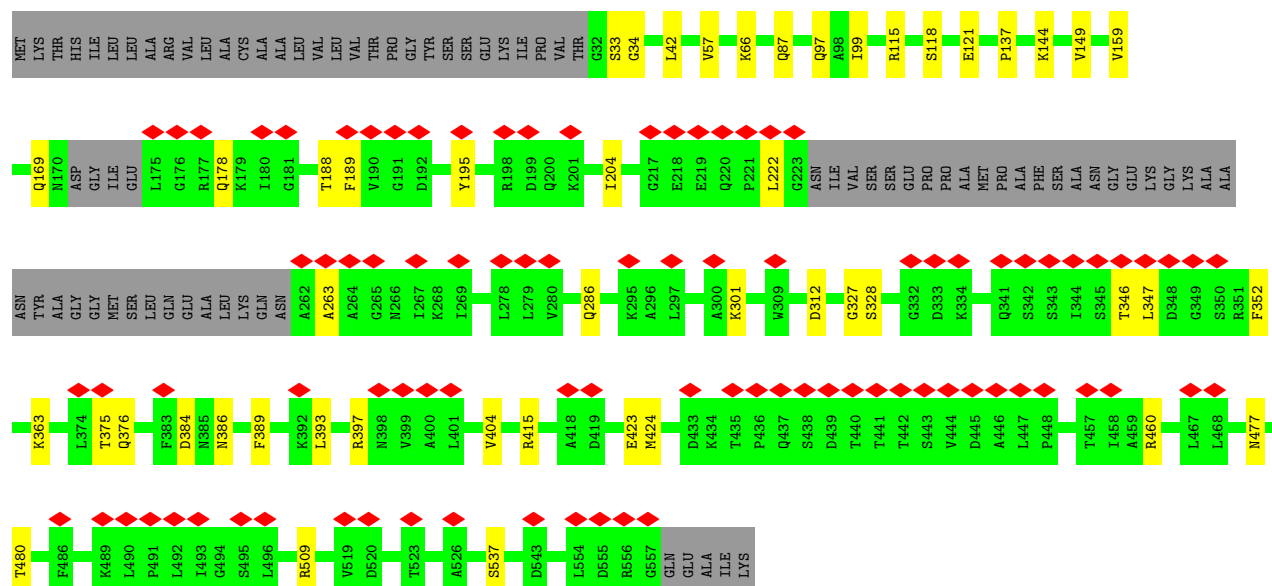
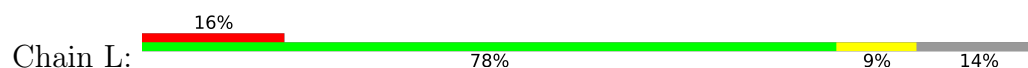


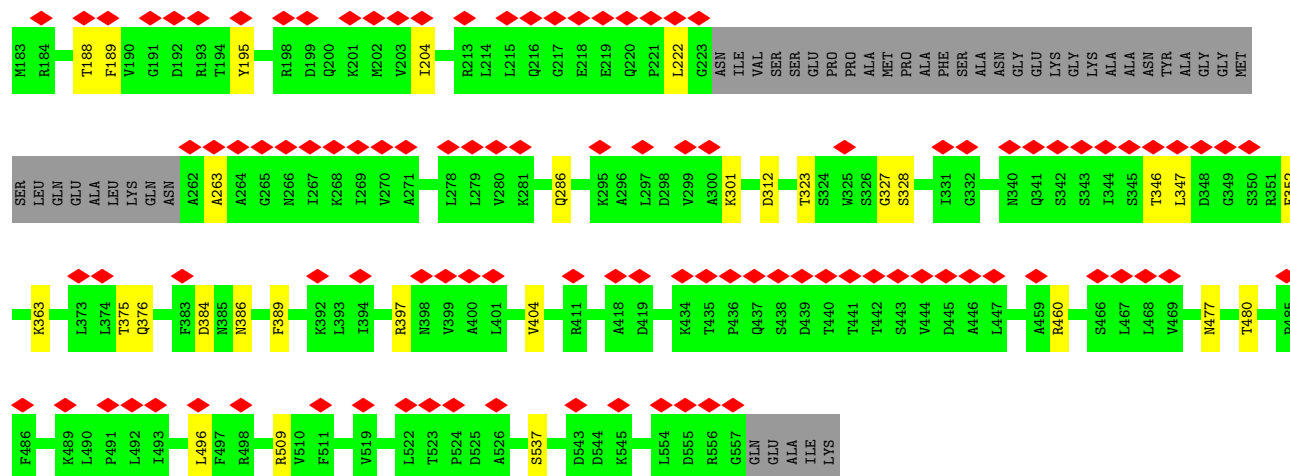


• Molecule 6: Protein InvG

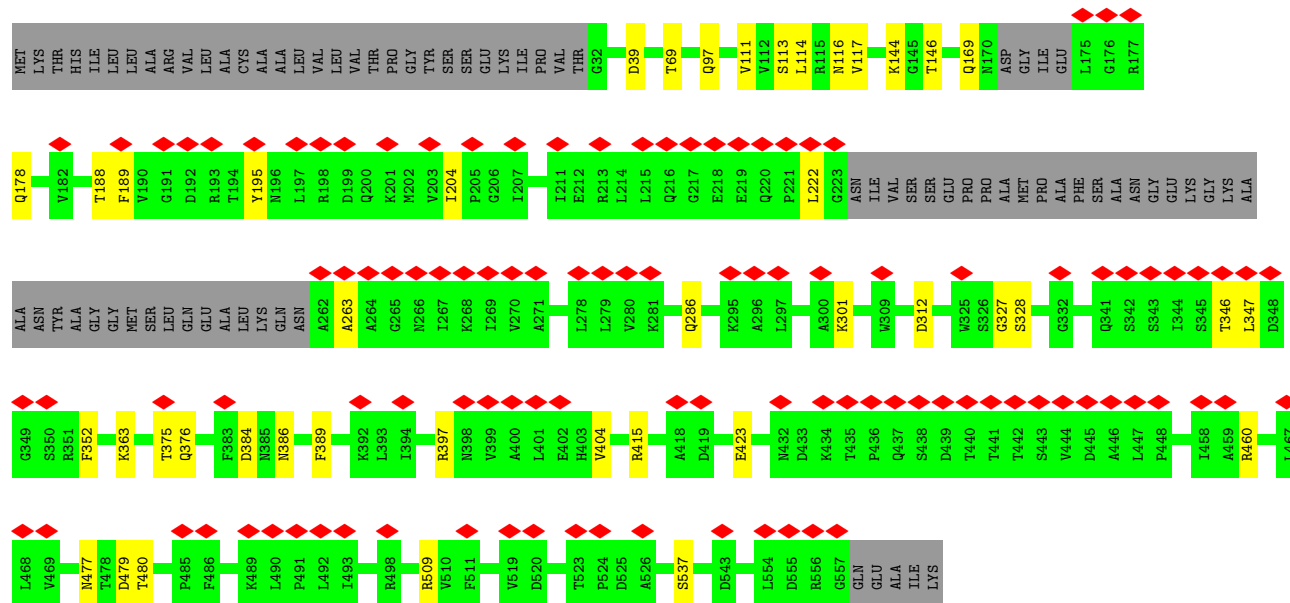
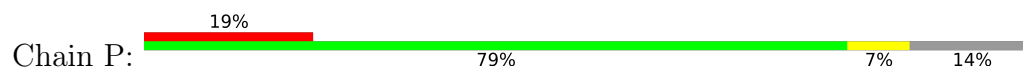


• Molecule 6: Protein InvG





• Molecule 6: Protein InvG



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51816	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	427.5, 427.5, 427.5	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.71, 1.71, 1.71	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.33	0/1458	0.52	0/1979
1	AB	0.34	0/1458	0.53	0/1979
1	AC	0.32	0/1458	0.52	0/1979
1	AD	0.33	0/1458	0.56	0/1979
1	AE	0.33	0/1458	0.54	0/1979
1	AF	0.34	0/1458	0.52	0/1979
1	AG	0.33	0/1458	0.51	0/1979
1	AH	0.32	0/1458	0.52	0/1979
1	AI	0.33	0/1458	0.54	0/1979
1	AJ	0.33	0/1458	0.53	0/1979
1	AK	0.33	0/1458	0.54	0/1979
1	AL	0.33	0/1458	0.54	0/1979
1	o	0.32	0/1458	0.53	0/1979
1	p	0.31	0/1458	0.50	0/1979
1	q	0.32	0/1458	0.50	0/1979
1	r	0.32	0/1458	0.54	0/1979
1	s	0.33	0/1458	0.53	0/1979
1	t	0.32	0/1458	0.56	0/1979
1	u	0.32	0/1458	0.55	0/1979
1	v	0.34	0/1458	0.55	0/1979
1	w	0.32	0/1458	0.52	0/1979
1	x	0.33	0/1458	0.52	0/1979
1	y	0.33	0/1458	0.52	0/1979
1	z	0.33	0/1458	0.55	0/1979
2	0	0.30	0/1501	0.70	0/2040
2	1	0.32	0/1508	0.69	0/2049
2	2	0.29	0/1497	0.69	1/2032 (0.0%)
2	3	0.27	0/1553	0.62	0/2107
2	4	0.30	0/1710	0.65	0/2318
3	5	0.31	0/1758	0.65	0/2402
4	6	0.22	0/414	0.60	0/565
4	7	0.29	0/657	0.75	1/897 (0.1%)
4	8	0.28	0/657	0.73	0/897
4	9	0.28	0/660	0.62	0/900

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
5	E	0.30	0/1881	0.53	0/2541
5	R	0.30	0/1872	0.54	0/2530
5	S	0.31	0/1876	0.56	0/2536
5	T	0.31	0/1881	0.54	0/2541
5	U	0.30	0/1872	0.54	0/2530
5	V	0.30	0/1876	0.52	0/2536
5	W	0.29	0/1881	0.52	0/2541
5	X	0.29	0/1872	0.51	0/2530
5	Y	0.31	0/1876	0.56	0/2536
5	Z	0.30	0/1881	0.52	0/2541
5	a	0.30	0/1872	0.51	0/2530
5	b	0.32	0/1876	0.56	0/2536
5	c	0.31	0/1881	0.54	0/2541
5	d	0.30	0/1872	0.50	0/2530
5	e	0.31	0/1876	0.55	0/2536
5	f	0.31	0/1881	0.52	0/2541
5	g	0.30	0/1872	0.54	0/2530
5	h	0.31	0/1876	0.56	0/2536
5	i	0.30	0/1881	0.52	0/2541
5	j	0.30	0/1872	0.55	0/2530
5	k	0.31	0/1876	0.54	0/2536
5	l	0.31	0/1881	0.52	0/2541
5	m	0.30	0/1872	0.50	0/2530
5	n	0.31	0/1876	0.54	0/2536
6	A	0.26	0/3827	0.50	0/5180
6	B	0.26	0/3877	0.50	0/5248
6	C	0.26	0/3827	0.50	0/5180
6	D	0.26	0/3866	0.50	0/5234
6	F	0.26	0/3827	0.50	0/5180
6	G	0.26	0/3877	0.51	0/5248
6	H	0.26	0/3827	0.50	0/5180
6	I	0.26	0/3877	0.50	0/5248
6	J	0.26	0/3827	0.51	0/5180
6	K	0.26	0/3877	0.51	0/5248
6	L	0.26	0/3827	0.52	0/5180
6	M	0.26	0/3866	0.50	0/5234
6	N	0.26	0/3827	0.50	0/5180
6	O	0.26	0/3877	0.51	0/5248
6	P	0.26	0/3827	0.50	0/5180
6	Q	0.31	0/1181	0.57	0/1593
All	All	0.29	0/150853	0.53	2/204300 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	8	0	2
5	b	0	1
5	k	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	167	LEU	N-CA-C	5.23	121.38	109.81
4	7	40	THR	CA-CB-CG2	5.04	119.06	110.50

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	8	16	LEU	Mainchain
4	8	40	THR	Peptide
5	b	366	LEU	Peptide
5	k	366	LEU	Peptide

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	AA	1431	0	1424	12	0
1	AB	1431	0	1424	9	0
1	AC	1431	0	1424	14	0
1	AD	1431	0	1424	9	0
1	AE	1431	0	1424	8	0
1	AF	1431	0	1424	9	0
1	AG	1431	0	1424	10	0
1	AH	1431	0	1424	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AI	1431	0	1424	12	0
1	AJ	1431	0	1424	17	0
1	AK	1431	0	1424	7	0
1	AL	1431	0	1424	12	0
1	o	1431	0	1424	11	0
1	p	1431	0	1424	10	0
1	q	1431	0	1424	5	0
1	r	1431	0	1424	11	0
1	s	1431	0	1424	9	0
1	t	1431	0	1424	12	0
1	u	1431	0	1424	16	0
1	v	1431	0	1424	11	0
1	w	1431	0	1424	10	0
1	x	1431	0	1424	10	0
1	y	1431	0	1424	9	0
1	z	1431	0	1424	9	0
2	0	1468	0	1509	12	0
2	1	1475	0	1525	13	0
2	2	1464	0	1524	18	0
2	3	1520	0	1577	11	0
2	4	1672	0	1734	10	0
3	5	1718	0	1767	14	0
4	6	405	0	418	5	0
4	7	644	0	685	9	0
4	8	644	0	685	6	0
4	9	647	0	692	8	0
5	E	1836	0	1800	16	0
5	R	1827	0	1789	10	0
5	S	1831	0	1788	13	0
5	T	1836	0	1800	19	0
5	U	1827	0	1789	13	0
5	V	1831	0	1788	10	0
5	W	1836	0	1800	9	0
5	X	1827	0	1789	17	0
5	Y	1831	0	1788	16	0
5	Z	1836	0	1800	10	0
5	a	1827	0	1789	8	0
5	b	1831	0	1788	12	0
5	c	1836	0	1800	18	0
5	d	1827	0	1789	14	0
5	e	1831	0	1788	6	0
5	f	1836	0	1800	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	g	1827	0	1789	13	0
5	h	1831	0	1788	10	0
5	i	1836	0	1800	6	0
5	j	1827	0	1789	13	0
5	k	1831	0	1788	8	0
5	l	1836	0	1800	17	0
5	m	1827	0	1789	11	0
5	n	1831	0	1788	11	0
6	A	3764	0	3815	28	0
6	B	3810	0	3875	31	0
6	C	3764	0	3815	30	0
6	D	3802	0	3862	29	0
6	F	3764	0	3815	30	0
6	G	3810	0	3875	27	0
6	H	3764	0	3815	37	0
6	I	3810	0	3875	42	0
6	J	3764	0	3815	30	0
6	K	3810	0	3875	33	0
6	L	3764	0	3815	33	0
6	M	3802	0	3862	25	0
6	N	3764	0	3815	30	0
6	O	3810	0	3875	29	0
6	P	3764	0	3815	30	0
6	Q	1154	0	1163	10	0
All	All	147873	0	148090	907	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 3.

The worst 5 of 907 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:397:ARG:HD3	6:I:397:ARG:HG3	1.33	1.07
6:K:397:ARG:HD3	6:L:397:ARG:HG3	1.57	0.84
6:A:397:ARG:HG3	6:P:397:ARG:HD3	1.59	0.84
6:L:397:ARG:HD3	6:M:397:ARG:HG3	1.62	0.82
6:G:397:ARG:HD3	6:H:397:ARG:HG3	1.62	0.82

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	AA	182/252 (72%)	174 (96%)	8 (4%)	0	100	100
1	AB	182/252 (72%)	178 (98%)	4 (2%)	0	100	100
1	AC	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	AD	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	AE	182/252 (72%)	177 (97%)	5 (3%)	0	100	100
1	AF	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	AG	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	AH	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	AI	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	AJ	182/252 (72%)	178 (98%)	4 (2%)	0	100	100
1	AK	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	AL	182/252 (72%)	177 (97%)	5 (3%)	0	100	100
1	o	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	p	182/252 (72%)	172 (94%)	10 (6%)	0	100	100
1	q	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	r	182/252 (72%)	174 (96%)	8 (4%)	0	100	100
1	s	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	t	182/252 (72%)	179 (98%)	3 (2%)	0	100	100
1	u	182/252 (72%)	178 (98%)	4 (2%)	0	100	100
1	v	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	w	182/252 (72%)	177 (97%)	5 (3%)	0	100	100
1	x	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	y	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	z	182/252 (72%)	174 (96%)	8 (4%)	0	100	100
2	0	183/224 (82%)	178 (97%)	4 (2%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	183/224 (82%)	176 (96%)	6 (3%)	1 (0%)	24	57
2	2	181/224 (81%)	174 (96%)	6 (3%)	1 (1%)	21	54
2	3	188/224 (84%)	185 (98%)	3 (2%)	0	100	100
2	4	208/224 (93%)	199 (96%)	9 (4%)	0	100	100
3	5	222/263 (84%)	216 (97%)	6 (3%)	0	100	100
4	6	49/86 (57%)	48 (98%)	1 (2%)	0	100	100
4	7	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
4	8	82/86 (95%)	79 (96%)	3 (4%)	0	100	100
4	9	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
5	E	220/392 (56%)	213 (97%)	7 (3%)	0	100	100
5	R	219/392 (56%)	213 (97%)	6 (3%)	0	100	100
5	S	220/392 (56%)	208 (94%)	12 (6%)	0	100	100
5	T	220/392 (56%)	210 (96%)	10 (4%)	0	100	100
5	U	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
5	V	220/392 (56%)	207 (94%)	13 (6%)	0	100	100
5	W	220/392 (56%)	212 (96%)	8 (4%)	0	100	100
5	X	219/392 (56%)	213 (97%)	6 (3%)	0	100	100
5	Y	220/392 (56%)	205 (93%)	15 (7%)	0	100	100
5	Z	220/392 (56%)	210 (96%)	10 (4%)	0	100	100
5	a	219/392 (56%)	213 (97%)	6 (3%)	0	100	100
5	b	220/392 (56%)	206 (94%)	14 (6%)	0	100	100
5	c	220/392 (56%)	211 (96%)	9 (4%)	0	100	100
5	d	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
5	e	220/392 (56%)	208 (94%)	12 (6%)	0	100	100
5	f	220/392 (56%)	209 (95%)	11 (5%)	0	100	100
5	g	219/392 (56%)	210 (96%)	9 (4%)	0	100	100
5	h	220/392 (56%)	207 (94%)	13 (6%)	0	100	100
5	i	220/392 (56%)	212 (96%)	8 (4%)	0	100	100
5	j	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
5	k	220/392 (56%)	205 (93%)	15 (7%)	0	100	100
5	l	220/392 (56%)	210 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	m	219/392 (56%)	214 (98%)	5 (2%)	0	100	100
5	n	220/392 (56%)	207 (94%)	13 (6%)	0	100	100
6	A	478/562 (85%)	458 (96%)	20 (4%)	0	100	100
6	B	484/562 (86%)	461 (95%)	23 (5%)	0	100	100
6	C	478/562 (85%)	455 (95%)	23 (5%)	0	100	100
6	D	483/562 (86%)	459 (95%)	24 (5%)	0	100	100
6	F	478/562 (85%)	457 (96%)	21 (4%)	0	100	100
6	G	484/562 (86%)	458 (95%)	26 (5%)	0	100	100
6	H	478/562 (85%)	456 (95%)	22 (5%)	0	100	100
6	I	484/562 (86%)	462 (96%)	22 (4%)	0	100	100
6	J	478/562 (85%)	456 (95%)	22 (5%)	0	100	100
6	K	484/562 (86%)	460 (95%)	24 (5%)	0	100	100
6	L	478/562 (85%)	456 (95%)	22 (5%)	0	100	100
6	M	483/562 (86%)	458 (95%)	25 (5%)	0	100	100
6	N	478/562 (85%)	455 (95%)	23 (5%)	0	100	100
6	O	484/562 (86%)	461 (95%)	23 (5%)	0	100	100
6	P	478/562 (85%)	457 (96%)	21 (4%)	0	100	100
6	Q	143/562 (25%)	139 (97%)	4 (3%)	0	100	100
All	All	18453/26175 (70%)	17682 (96%)	768 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	0	49	ASN
2	2	47	PRO
2	1	49	ASN

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	AA	155/215 (72%)	155 (100%)	0	100	100
1	AB	155/215 (72%)	155 (100%)	0	100	100
1	AC	155/215 (72%)	155 (100%)	0	100	100
1	AD	155/215 (72%)	155 (100%)	0	100	100
1	AE	155/215 (72%)	155 (100%)	0	100	100
1	AF	155/215 (72%)	155 (100%)	0	100	100
1	AG	155/215 (72%)	155 (100%)	0	100	100
1	AH	155/215 (72%)	155 (100%)	0	100	100
1	AI	155/215 (72%)	153 (99%)	2 (1%)	61	71
1	AJ	155/215 (72%)	155 (100%)	0	100	100
1	AK	155/215 (72%)	155 (100%)	0	100	100
1	AL	155/215 (72%)	155 (100%)	0	100	100
1	o	155/215 (72%)	154 (99%)	1 (1%)	78	79
1	p	155/215 (72%)	155 (100%)	0	100	100
1	q	155/215 (72%)	155 (100%)	0	100	100
1	r	155/215 (72%)	155 (100%)	0	100	100
1	s	155/215 (72%)	154 (99%)	1 (1%)	78	79
1	t	155/215 (72%)	155 (100%)	0	100	100
1	u	155/215 (72%)	154 (99%)	1 (1%)	78	79
1	v	155/215 (72%)	155 (100%)	0	100	100
1	w	155/215 (72%)	155 (100%)	0	100	100
1	x	155/215 (72%)	155 (100%)	0	100	100
1	y	155/215 (72%)	155 (100%)	0	100	100
1	z	155/215 (72%)	155 (100%)	0	100	100
2	0	162/199 (81%)	161 (99%)	1 (1%)	78	79
2	1	164/199 (82%)	161 (98%)	3 (2%)	51	67
2	2	164/199 (82%)	164 (100%)	0	100	100
2	3	170/199 (85%)	167 (98%)	3 (2%)	51	67
2	4	187/199 (94%)	187 (100%)	0	100	100
3	5	187/219 (85%)	186 (100%)	1 (0%)	81	81
4	6	41/71 (58%)	41 (100%)	0	100	100
4	7	69/71 (97%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	8	69/71 (97%)	68 (99%)	1 (1%)	59	70
4	9	70/71 (99%)	70 (100%)	0	100	100
5	E	190/337 (56%)	190 (100%)	0	100	100
5	R	189/337 (56%)	187 (99%)	2 (1%)	65	73
5	S	188/337 (56%)	187 (100%)	1 (0%)	81	81
5	T	190/337 (56%)	188 (99%)	2 (1%)	65	73
5	U	189/337 (56%)	188 (100%)	1 (0%)	81	81
5	V	188/337 (56%)	186 (99%)	2 (1%)	65	73
5	W	190/337 (56%)	189 (100%)	1 (0%)	81	81
5	X	189/337 (56%)	188 (100%)	1 (0%)	81	81
5	Y	188/337 (56%)	187 (100%)	1 (0%)	81	81
5	Z	190/337 (56%)	190 (100%)	0	100	100
5	a	189/337 (56%)	187 (99%)	2 (1%)	65	73
5	b	188/337 (56%)	187 (100%)	1 (0%)	81	81
5	c	190/337 (56%)	190 (100%)	0	100	100
5	d	189/337 (56%)	188 (100%)	1 (0%)	81	81
5	e	188/337 (56%)	186 (99%)	2 (1%)	65	73
5	f	190/337 (56%)	189 (100%)	1 (0%)	81	81
5	g	189/337 (56%)	185 (98%)	4 (2%)	47	64
5	h	188/337 (56%)	188 (100%)	0	100	100
5	i	190/337 (56%)	189 (100%)	1 (0%)	81	81
5	j	189/337 (56%)	188 (100%)	1 (0%)	81	81
5	k	188/337 (56%)	187 (100%)	1 (0%)	81	81
5	l	190/337 (56%)	190 (100%)	0	100	100
5	m	189/337 (56%)	187 (99%)	2 (1%)	65	73
5	n	188/337 (56%)	186 (99%)	2 (1%)	65	73
6	A	414/477 (87%)	413 (100%)	1 (0%)	87	87
6	B	420/477 (88%)	419 (100%)	1 (0%)	87	87
6	C	414/477 (87%)	413 (100%)	1 (0%)	87	87
6	D	419/477 (88%)	418 (100%)	1 (0%)	87	87
6	F	414/477 (87%)	412 (100%)	2 (0%)	81	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	G	420/477 (88%)	419 (100%)	1 (0%)	87	87
6	H	414/477 (87%)	413 (100%)	1 (0%)	87	87
6	I	420/477 (88%)	419 (100%)	1 (0%)	87	87
6	J	414/477 (87%)	413 (100%)	1 (0%)	87	87
6	K	420/477 (88%)	419 (100%)	1 (0%)	87	87
6	L	414/477 (87%)	413 (100%)	1 (0%)	87	87
6	M	419/477 (88%)	418 (100%)	1 (0%)	87	87
6	N	414/477 (87%)	412 (100%)	2 (0%)	81	81
6	O	420/477 (88%)	419 (100%)	1 (0%)	87	87
6	P	414/477 (87%)	412 (100%)	2 (0%)	81	81
6	Q	125/477 (26%)	125 (100%)	0	100	100
All	All	15914/22378 (71%)	15853 (100%)	61 (0%)	81	83

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	f	182	GLU
6	M	328	SER
5	k	355	VAL
6	L	328	SER
6	P	111	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 210 such sidechains are listed below:

Mol	Chain	Res	Type
6	A	398	ASN
6	G	170	ASN
6	O	378	ASN
6	B	135	ASN
6	C	432	ASN

5.3.3 RNA ⓘ

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.

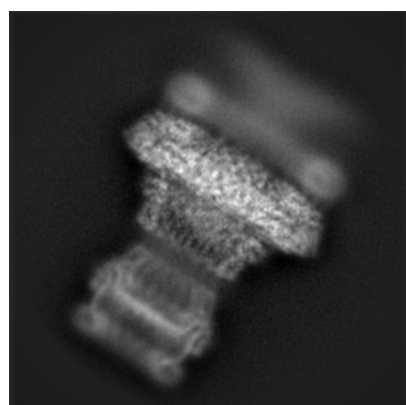
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20310. These allow visual inspection of the internal detail of the map and identification of artifacts.

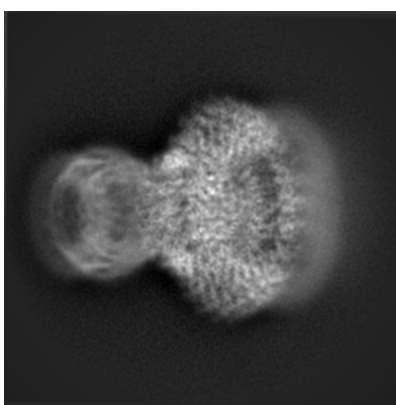
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

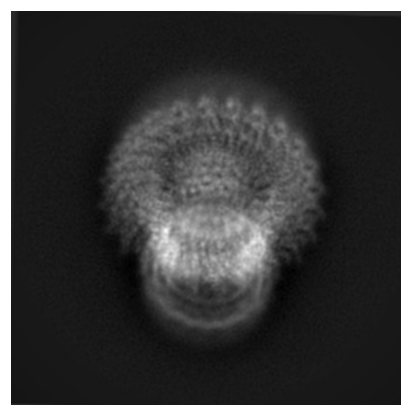
6.1.1 Primary map



X



Y

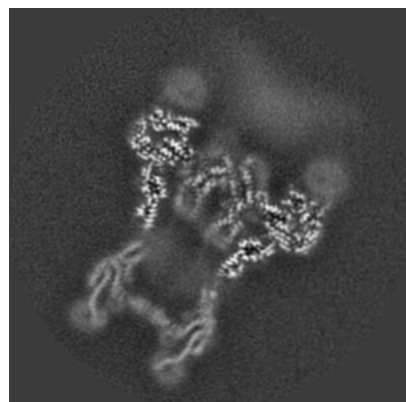


Z

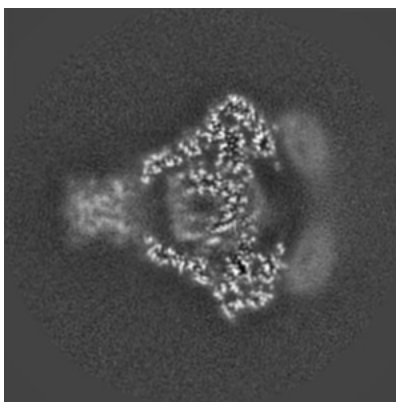
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

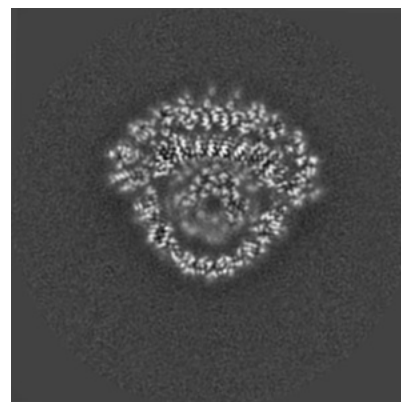
6.2.1 Primary map



X Index: 125



Y Index: 125

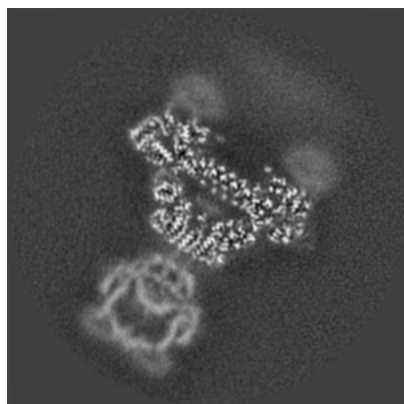


Z Index: 125

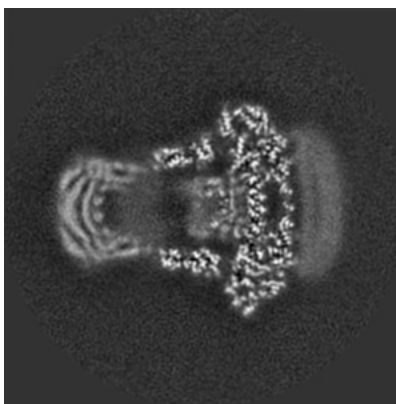
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

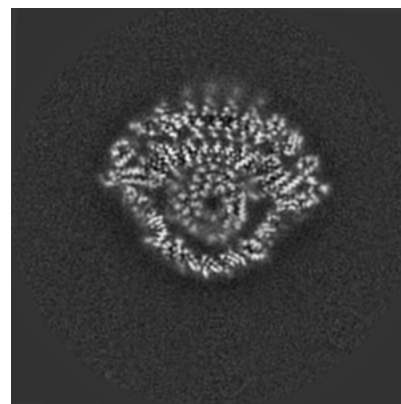
6.3.1 Primary map



X Index: 97



Y Index: 113

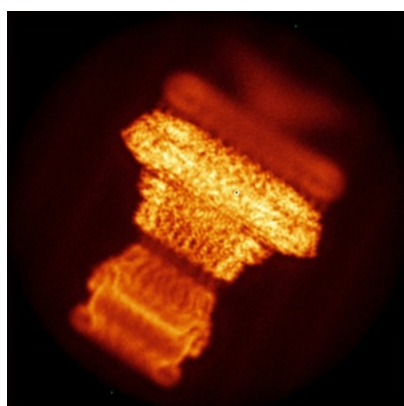


Z Index: 129

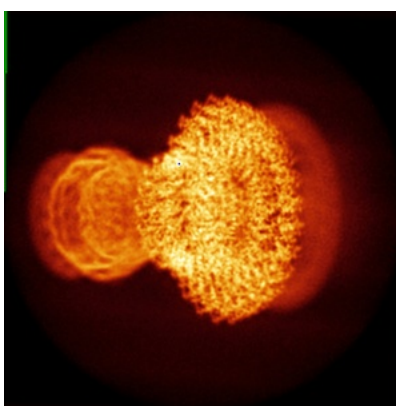
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

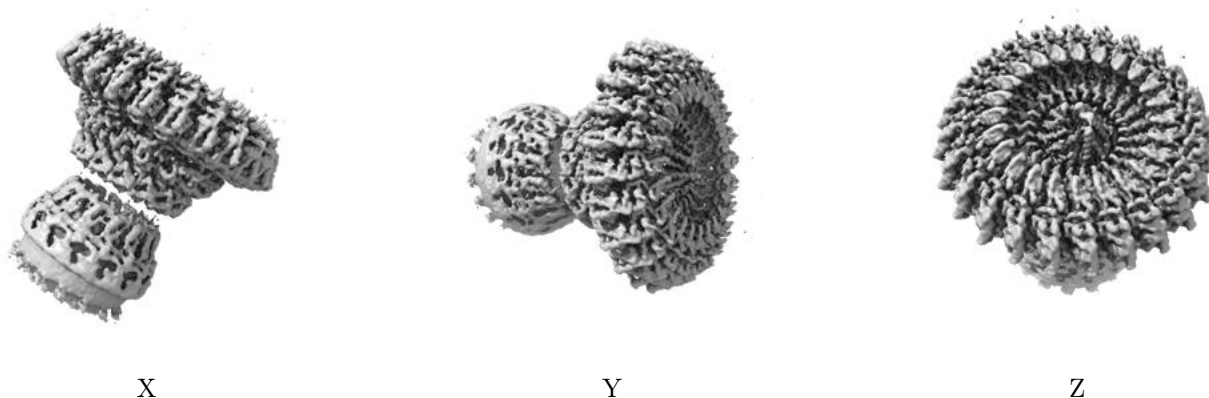


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

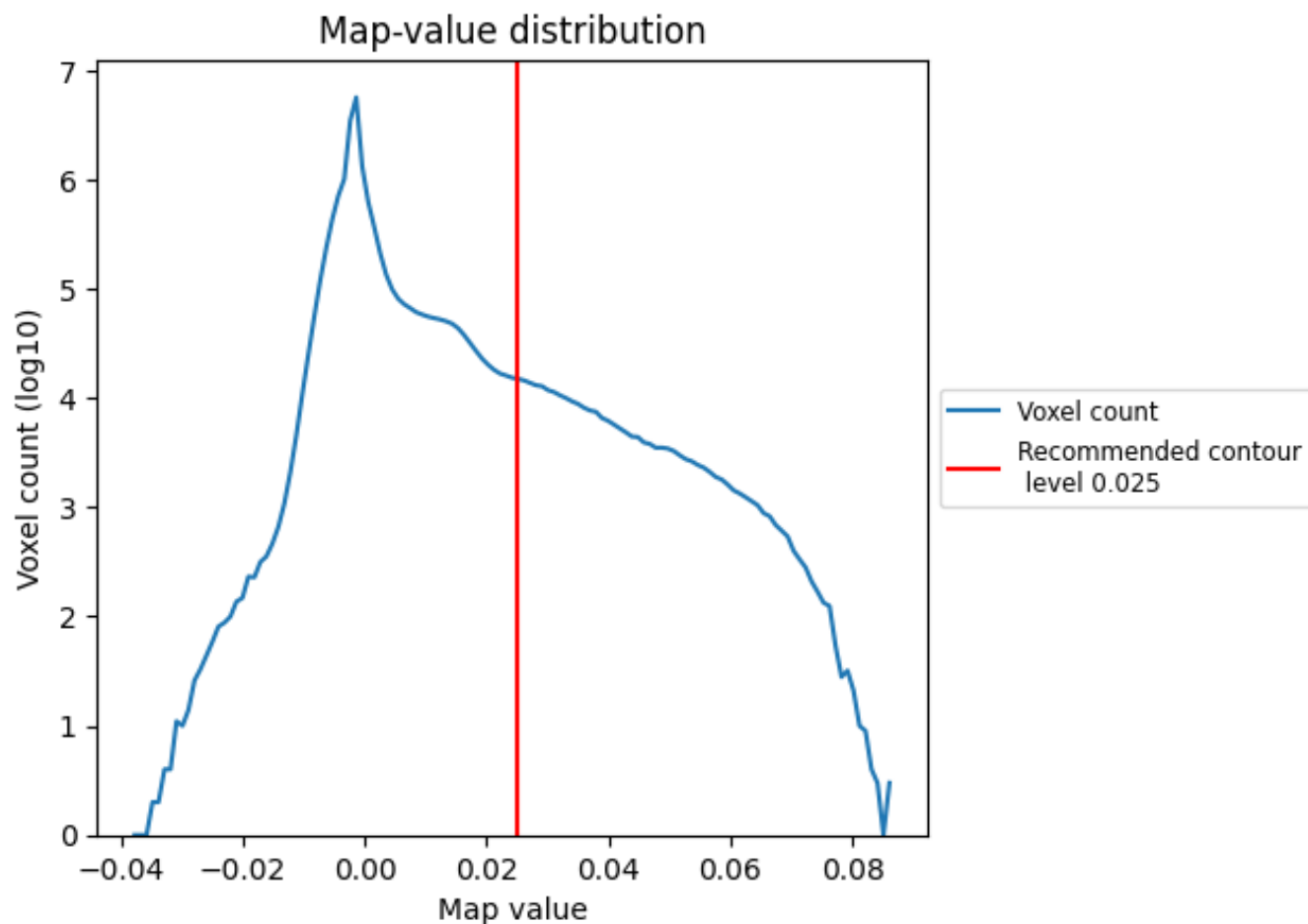
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

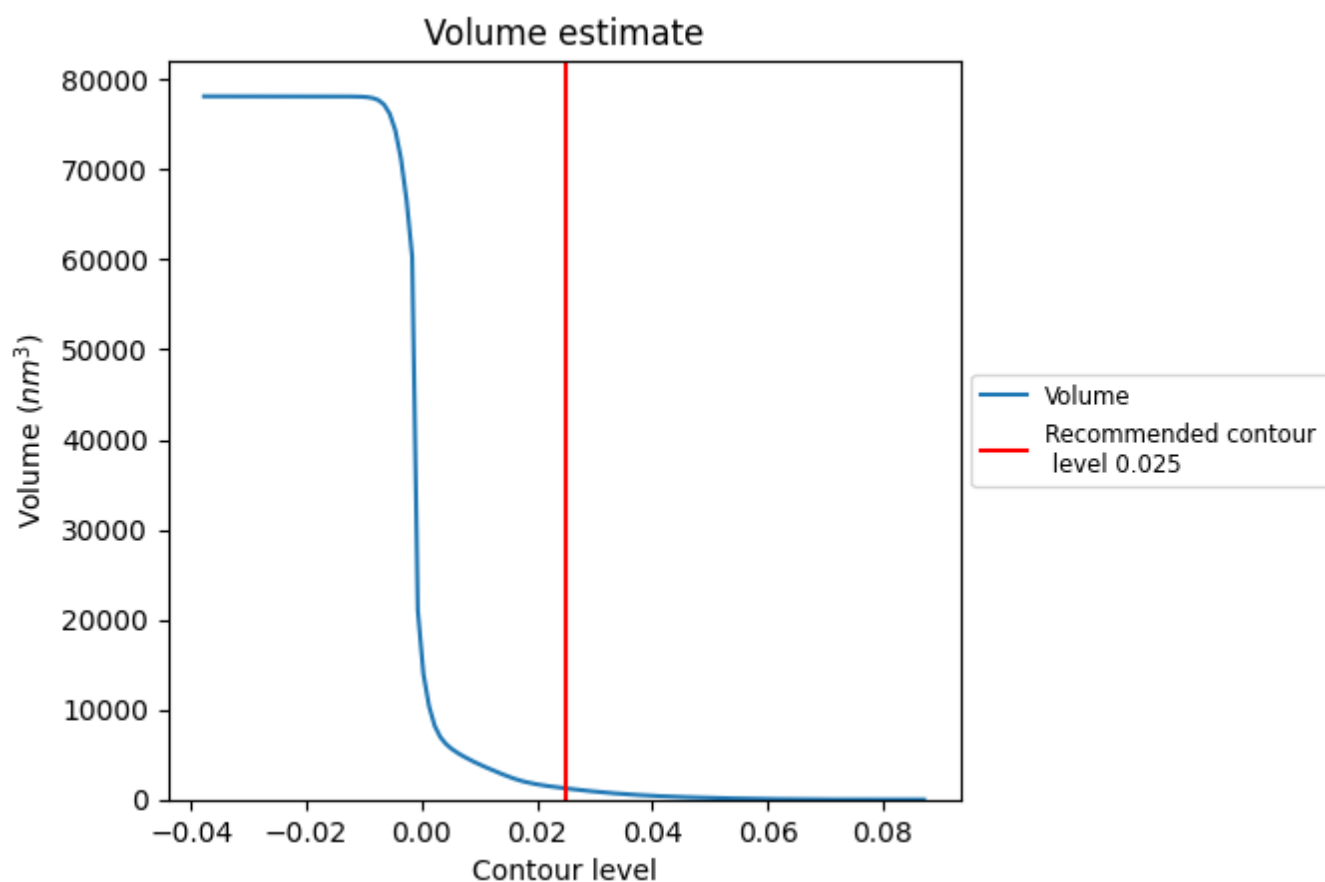
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

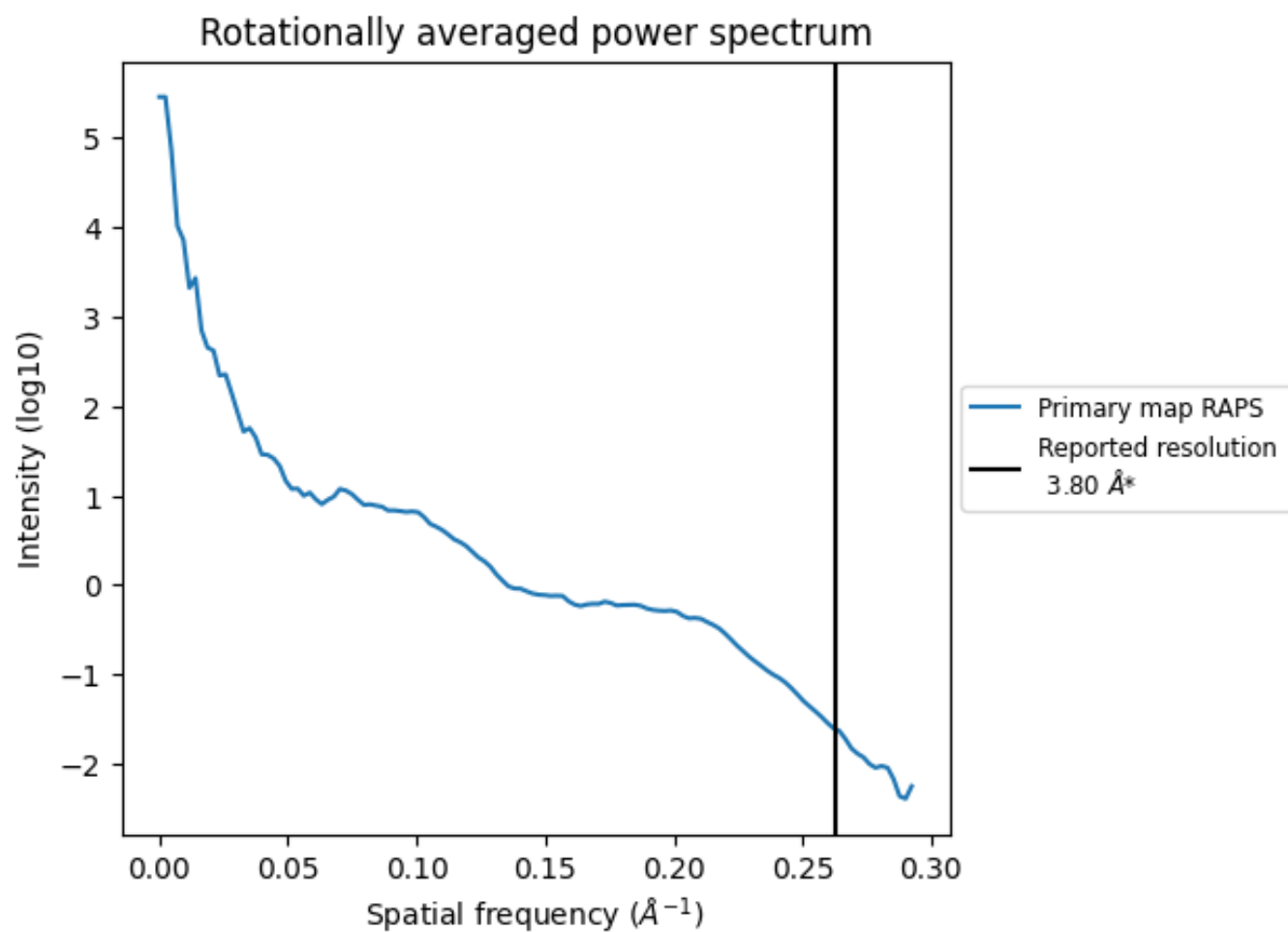
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1245 nm³; this corresponds to an approximate mass of 1124 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 0.263 Å⁻¹

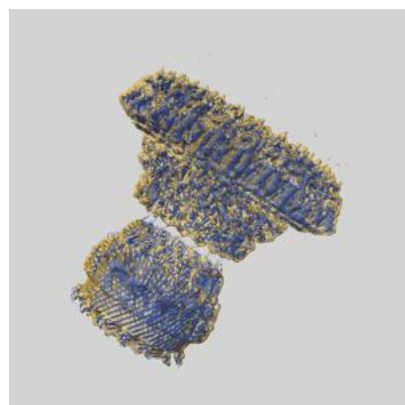
8 Fourier-Shell correlation

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

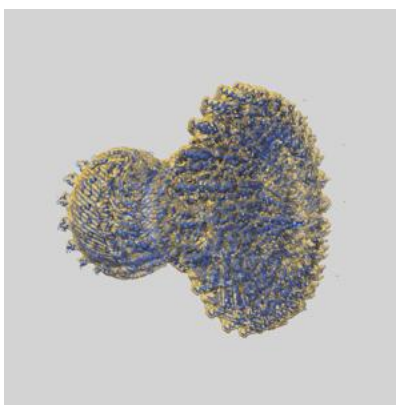
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20310 and PDB model 6Q14. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

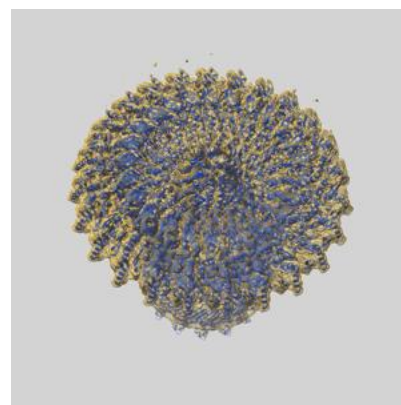
9.1 Map-model overlay [i](#)



X



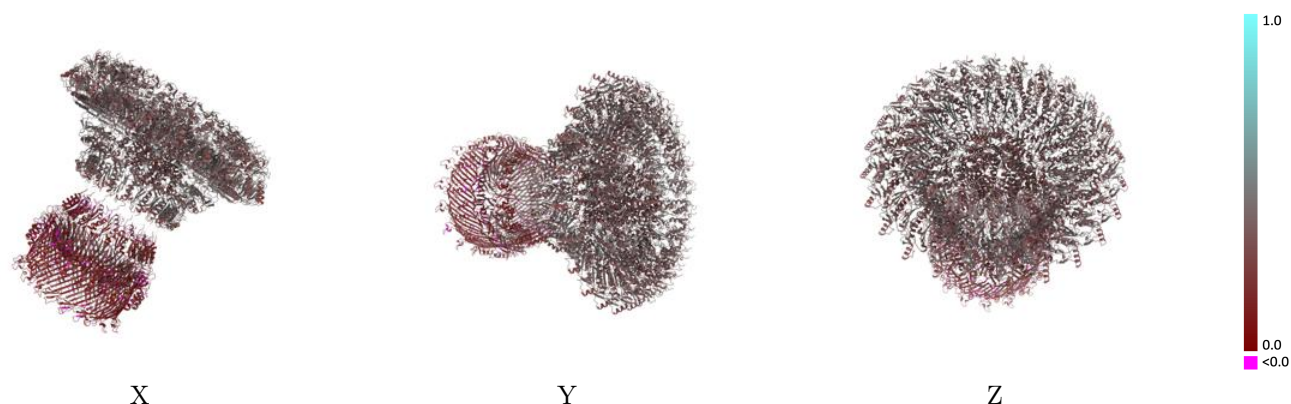
Y



Z

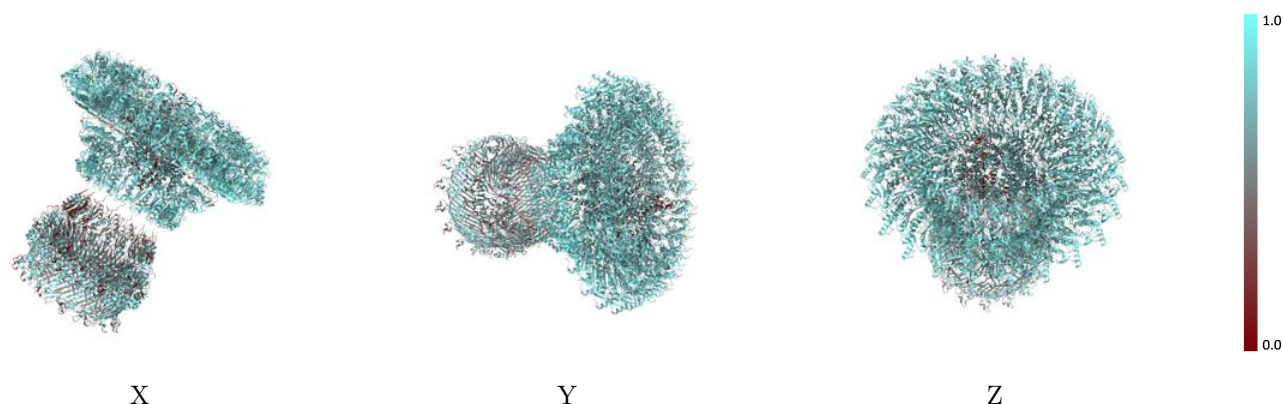
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



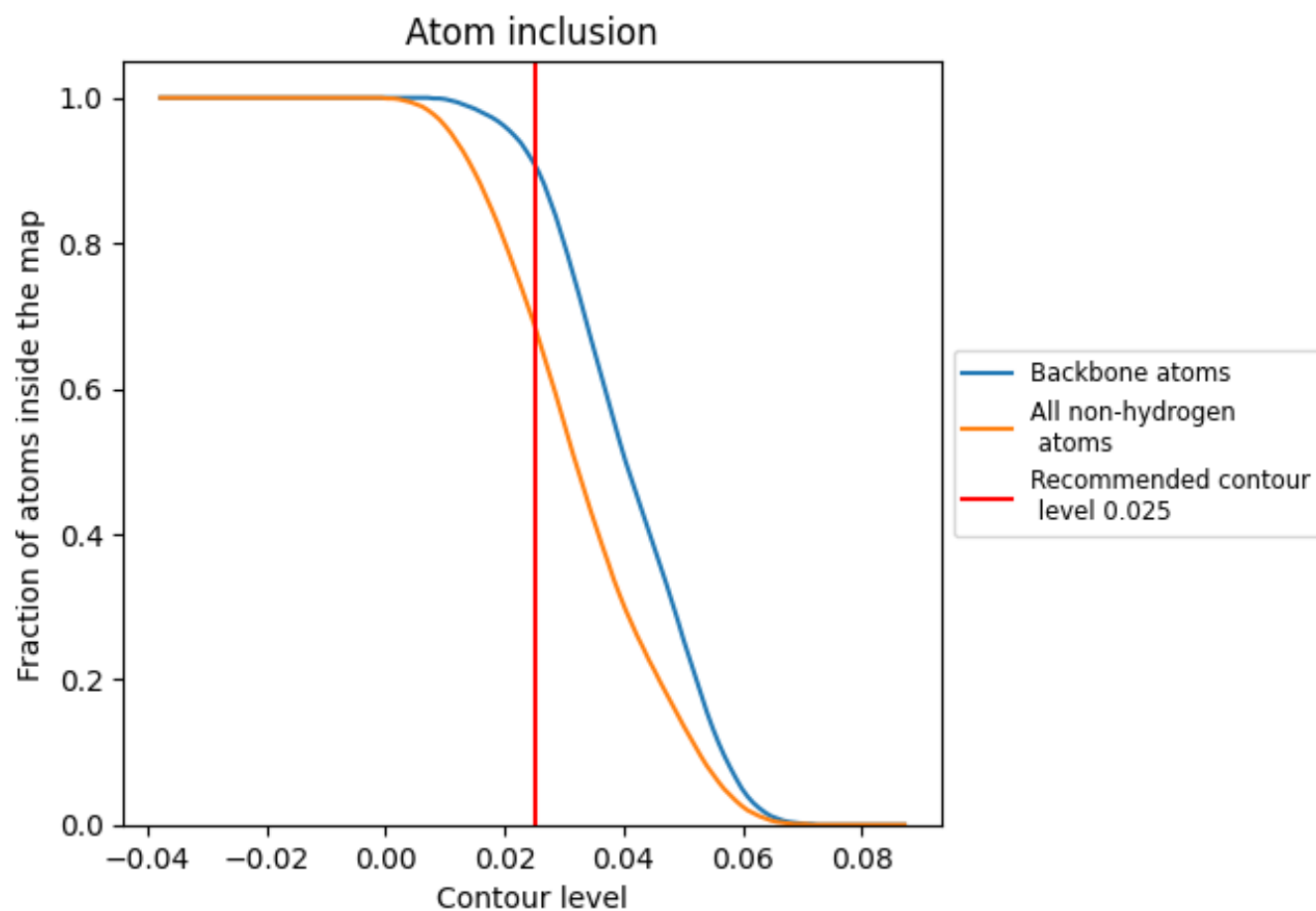
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 69% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6880	 0.3220
0	 0.6200	 0.3330
1	 0.5840	 0.3070
2	 0.5890	 0.3140
3	 0.5980	 0.3190
4	 0.5880	 0.3200
5	 0.6910	 0.3510
6	 0.3690	 0.3360
7	 0.4290	 0.3130
8	 0.5870	 0.3110
9	 0.6410	 0.3330
A	 0.5900	 0.2300
AA	 0.7410	 0.3980
AB	 0.7230	 0.3880
AC	 0.7380	 0.3910
AD	 0.7330	 0.3860
AE	 0.7270	 0.3780
AF	 0.7360	 0.3910
AG	 0.7490	 0.3910
AH	 0.7410	 0.3950
AI	 0.7470	 0.3990
AJ	 0.7440	 0.3960
AK	 0.7540	 0.3980
AL	 0.7330	 0.3870
B	 0.5890	 0.2220
C	 0.5920	 0.2230
D	 0.6050	 0.2310
E	 0.7480	 0.3760
F	 0.6060	 0.2290
G	 0.6100	 0.2370
H	 0.6180	 0.2470
I	 0.6230	 0.2440
J	 0.6180	 0.2370
K	 0.6100	 0.2370
L	 0.6080	 0.2380



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Chain	Atom inclusion	Q-score
M	0.5990	0.2300
N	0.5920	0.2320
O	0.5900	0.2320
P	0.5920	0.2290
Q	0.8080	0.3950
R	0.7820	0.3740
S	0.7820	0.3700
T	0.7560	0.3730
U	0.7860	0.3760
V	0.7840	0.3770
W	0.7780	0.3920
X	0.7860	0.3790
Y	0.7900	0.3730
Z	0.7650	0.3820
a	0.7890	0.3790
b	0.8080	0.3910
c	0.7820	0.3920
d	0.7980	0.3900
e	0.7950	0.3910
f	0.7680	0.3820
g	0.7860	0.3730
h	0.7900	0.3870
i	0.7610	0.3850
j	0.7990	0.3940
k	0.7970	0.3890
l	0.7580	0.3770
m	0.7890	0.3840
n	0.7770	0.3660
o	0.7430	0.3990
p	0.7250	0.3840
q	0.7220	0.3790
r	0.7320	0.3840
s	0.7280	0.3830
t	0.7380	0.3980
u	0.7490	0.3980
v	0.7310	0.3880
w	0.7250	0.3800
x	0.7240	0.3770
y	0.7410	0.3880
z	0.7500	0.4020