



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:40 PM UTC

PDB ID : 6Q16 / pdb_00006q16
EMDB ID : EMD-20556
Title : Focussed refinement of InvGN0N1:PrgHK:SpaPQR:PrgIJ from Salmonella SPI-1 injectisome NC-base
Authors : Hu, J.; Worrall, L.J.; Strynadka, N.C.J.
Deposited on : 2019-08-02
Resolution : 4.10 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:

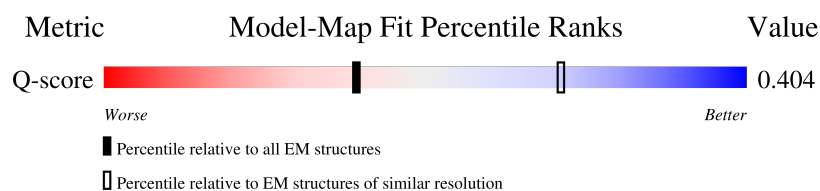
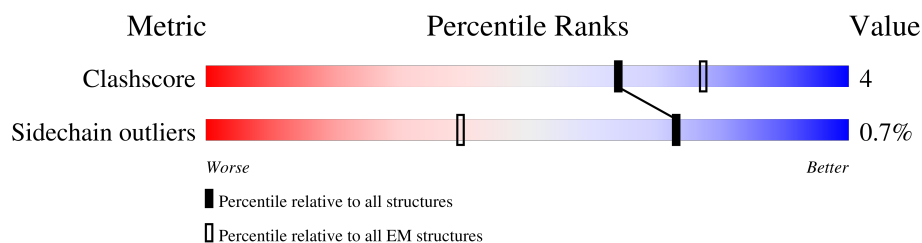
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

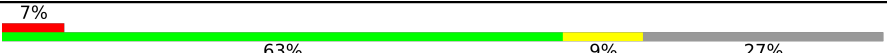
The reported resolution of this entry is 4.10 Å.

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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	
1	AE	252	

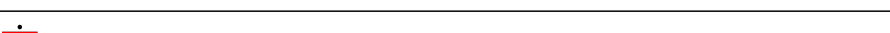
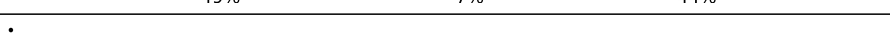
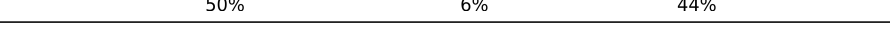
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Mol	Chain	Length	Quality of chain
1	AF	252	
1	AG	252	
1	AH	252	
1	AI	252	
1	AJ	252	
1	AK	252	
1	AL	252	
1	o	252	
1	p	252	
1	q	252	
1	r	252	
1	s	252	
1	t	252	
1	u	252	
1	v	252	
1	w	252	
1	x	252	
1	y	252	
1	z	252	
2	A	562	
2	B	562	
2	C	562	
2	D	562	
2	F	562	
2	G	562	

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Mol	Chain	Length	Quality of chain
2	H	562	
2	I	562	
2	J	562	
2	K	562	
2	L	562	
2	M	562	
2	N	562	
2	O	562	
2	P	562	
2	Q	562	
3	E	392	
3	R	392	
3	S	392	
3	T	392	
3	U	392	
3	V	392	
3	W	392	
3	X	392	
3	Y	392	
3	Z	392	
3	a	392	
3	b	392	
3	c	392	
3	d	392	
3	e	392	

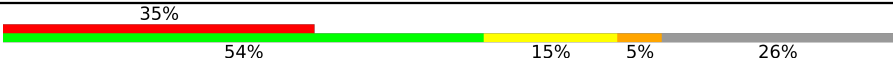
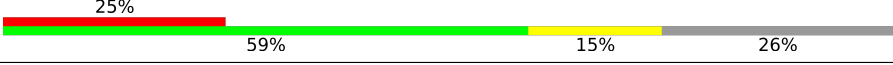
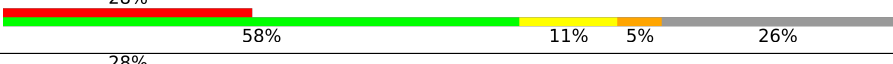
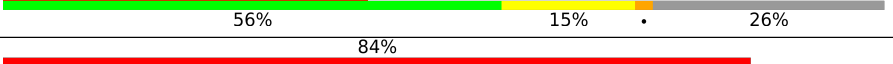
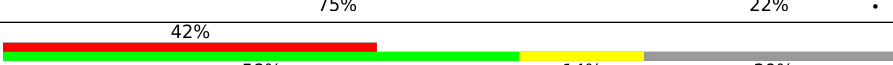
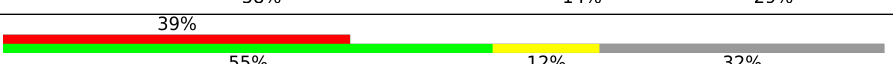
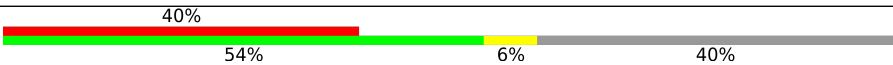
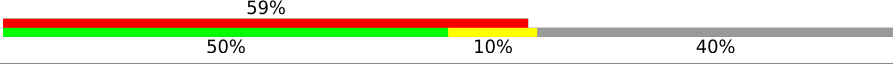
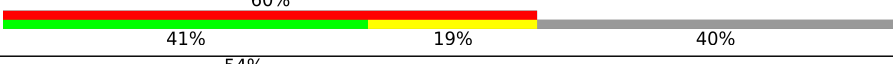
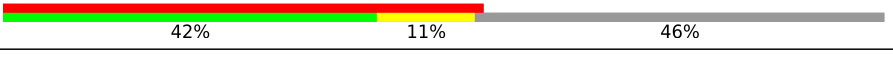
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Mol	Chain	Length	Quality of chain
3	f	392	
3	g	392	
3	h	392	
3	i	392	
3	j	392	
3	k	392	
3	l	392	
3	m	392	
3	n	392	
4	0	224	
4	1	224	
4	2	224	
4	3	224	
4	4	224	
5	5	263	
6	6	86	
6	7	86	
6	8	86	
6	9	86	
7	AM	101	
7	AN	101	
7	AO	101	
7	AP	101	
7	AQ	101	
7	AR	101	

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Mol	Chain	Length	Quality of chain
8	AS	80	
8	AT	80	
8	AU	80	
8	AV	80	
8	AW	80	
8	AX	80	
8	AY	80	
8	AZ	80	
8	BA	80	
8	BB	80	
8	BC	80	
8	BD	80	
8	BE	80	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 118198 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 1431	C 901	N 250	O 277	S 3	0	0
1	w	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	x	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	y	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	z	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AJ	184	Total 1431	C 901	N 250	O 277	S 3	0	0
1	AK	184	Total 1431	C 901	N 250	O 277	S 3	0	0

- Molecule 2 is a protein called Protein InvG.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	139	Total 1108	C 710	N 189	O 203	S 6	0	0
2	B	144	Total 1154	C 741	N 198	O 209	S 6	1	0
2	C	139	Total 1108	C 710	N 189	O 203	S 6	0	0
2	D	144	Total 1146	C 736	N 195	O 209	S 6	0	0
2	F	139	Total 1108	C 710	N 189	O 203	S 6	0	0
2	G	144	Total 1154	C 741	N 198	O 209	S 6	1	0
2	H	139	Total 1108	C 710	N 189	O 203	S 6	0	0
2	I	144	Total 1154	C 741	N 198	O 209	S 6	1	0
2	J	139	Total 1108	C 710	N 189	O 203	S 6	0	0
2	K	144	Total 1154	C 741	N 198	O 209	S 6	1	0
2	L	139	Total 1108	C 710	N 189	O 203	S 6	0	0
2	M	144	Total 1146	C 736	N 195	O 209	S 6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	139	Total	C	N	O	S	0	0
			1108	710	189	203	6		
2	O	144	Total	C	N	O	S	1	0
			1154	741	198	209	6		
2	P	139	Total	C	N	O	S	0	0
			1108	710	189	203	6		
2	Q	144	Total	C	N	O	S	1	0
			1154	741	198	209	6		

- Molecule 3 is a protein called Protein PrgH.

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	0	199	Total	C	N	O	S	0	0
			1562	1041	231	279	11		
4	1	199	Total	C	N	O	S	0	0
			1569	1047	232	279	11		
4	2	197	Total	C	N	O	S	0	0
			1553	1037	230	275	11		
4	3	204	Total	C	N	O	S	0	0
			1606	1071	238	286	11		
4	4	221	Total	C	N	O	S	1	0
			1758	1163	266	318	11		

- Molecule 5 is a protein called Surface presentation of antigens protein SpaR.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	247	Total	C	N	O	S	0	0
			1885	1252	300	320	13		

- Molecule 6 is a protein called Surface presentation of antigens protein SpaQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	53	Total	C	N	O	S	0	0
			405	276	61	67	1		
6	7	84	Total	C	N	O	S	0	0
			644	436	97	109	2		
6	8	84	Total	C	N	O	S	0	0
			644	436	97	109	2		
6	9	84	Total	C	N	O	S	0	0
			647	438	97	109	3		

- Molecule 7 is a protein called Protein PrgJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AM	39	Total	C	N	O	S	0	0
			298	187	49	60	2		
7	AN	78	Total	C	N	O	S	7	0
			644	396	116	130	2		
7	AO	88	Total	C	N	O	S	0	0
			667	410	114	140	3		
7	AP	89	Total	C	N	O	S	0	0
			675	416	115	141	3		
7	AQ	89	Total	C	N	O	S	0	0
			675	416	115	141	3		
7	AR	88	Total	C	N	O	S	0	0
			667	410	114	140	3		

- Molecule 8 is a protein called Protein PrgI.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AS	59	Total	C	N	O	0	0
			466	294	80	92		
8	AT	59	Total	C	N	O	0	0
			466	294	80	92		
8	AU	59	Total	C	N	O	0	0
			466	294	80	92		
8	AV	59	Total	C	N	O	0	0
			466	294	80	92		
8	AW	59	Total	C	N	O	0	0
			466	294	80	92		
8	AX	73	Total	C	N	O	0	0
			574	362	95	117		
8	AY	78	Total	C	N	O	0	0
			612	387	101	124		
8	AZ	57	Total	C	N	O	0	0
			460	289	76	95		

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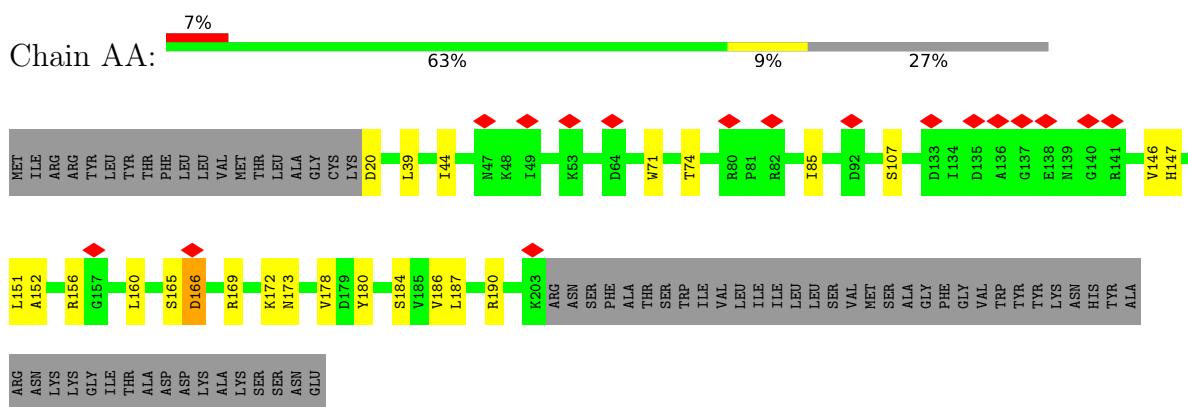
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Mol	Chain	Residues	Atoms				AltConf	Trace
8	BA	54	Total	C	N	O	0	0
			437	275	73	89		
8	BB	48	Total	C	N	O	0	0
			388	247	64	77		
8	BC	48	Total	C	N	O	0	0
			388	247	64	77		
8	BD	48	Total	C	N	O	0	0
			388	247	64	77		
8	BE	43	Total	C	N	O	0	0
			346	219	59	68		

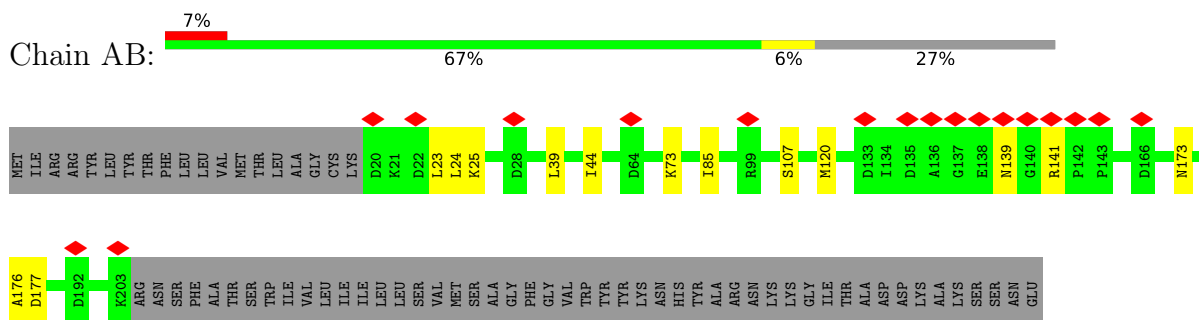
3 Residue-property plots

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

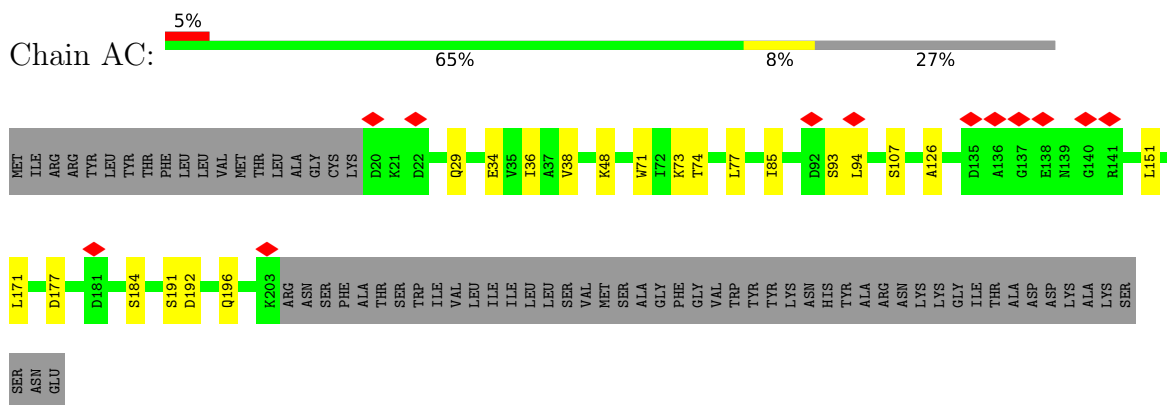
- Molecule 1: Lipoprotein PrgK



- Molecule 1: Lipoprotein PrgK

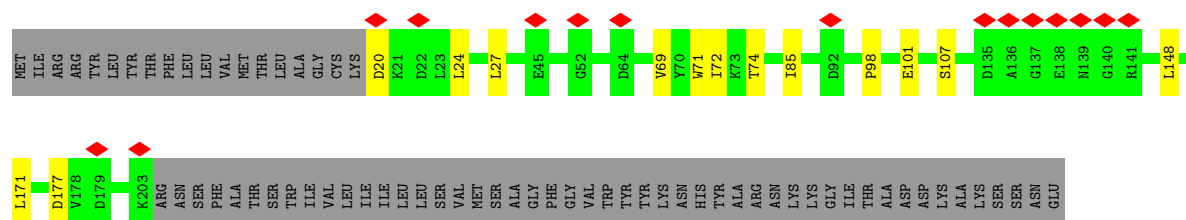


- Molecule 1: Lipoprotein PrgK



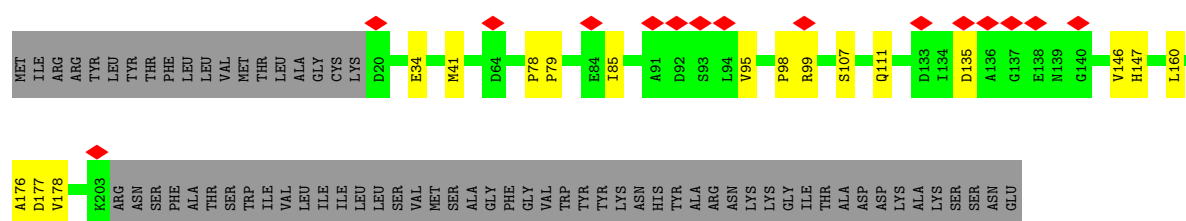
- Molecule 1: Lipoprotein PrgK

Chain AD: 



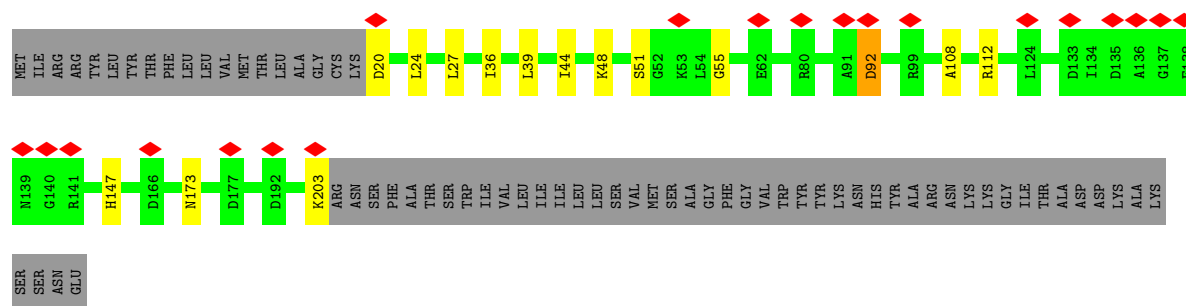
- Molecule 1: Lipoprotein PrgK

Chain AE: 



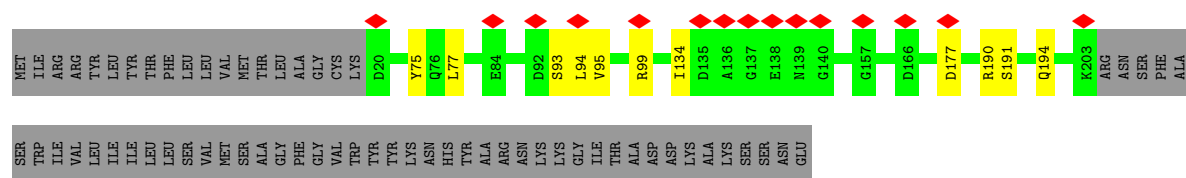
- Molecule 1: Lipoprotein PrgK

Chain AF: 



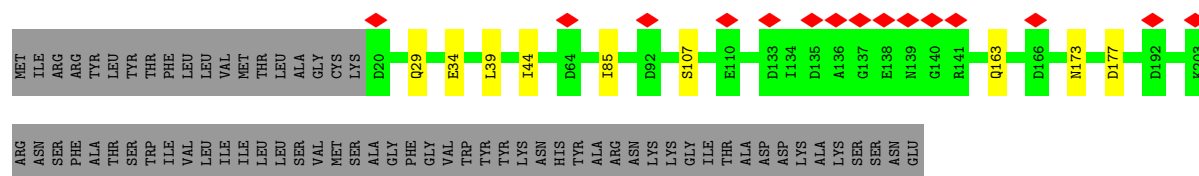
- Molecule 1: Lipoprotein PrgK

Chain AG: 

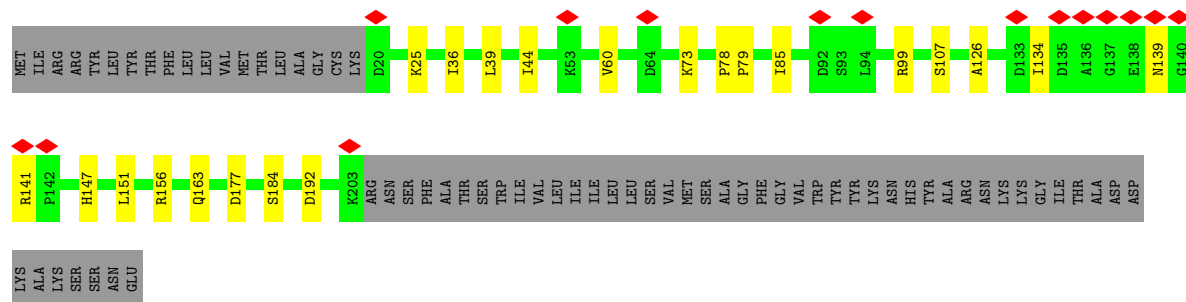


- Molecule 1: Lipoprotein PrgK

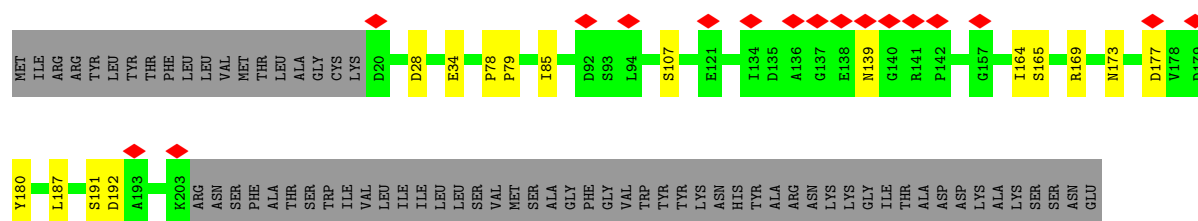
Chain AH: 



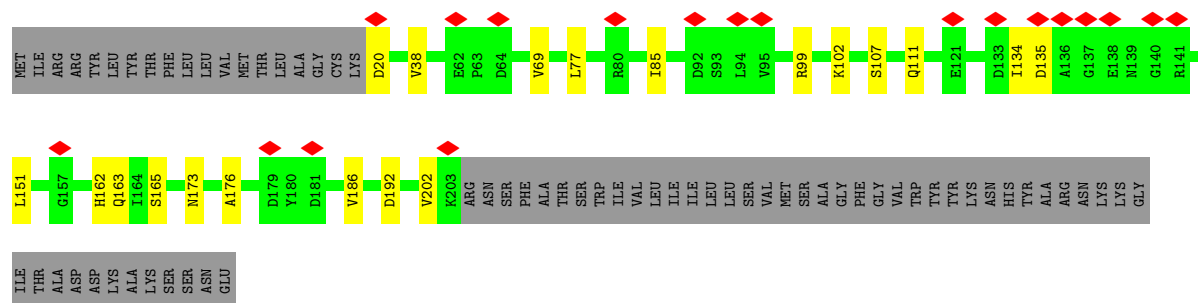
- Molecule 1: Lipoprotein PrgK



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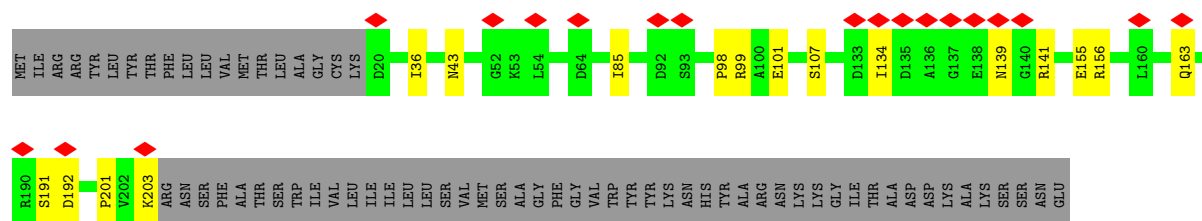


- Molecule 1: Lipoprotein PrgK

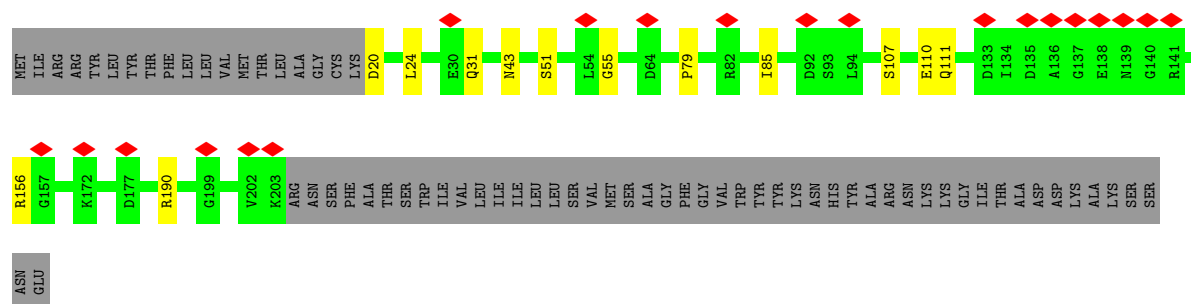


- Molecule 1: Lipoprotein PrgK

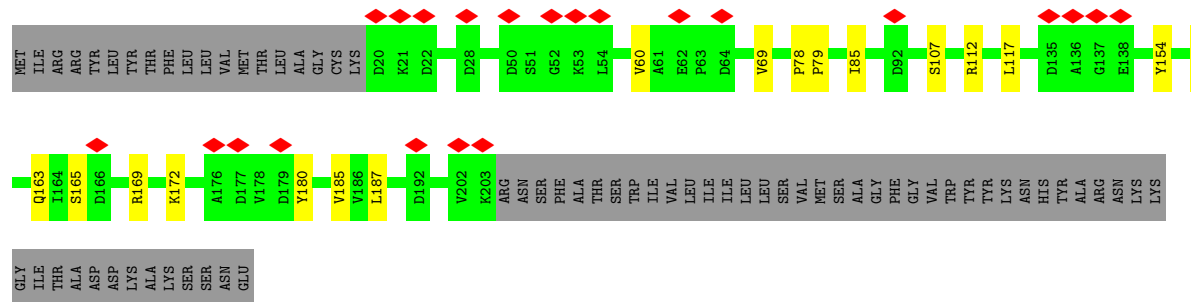




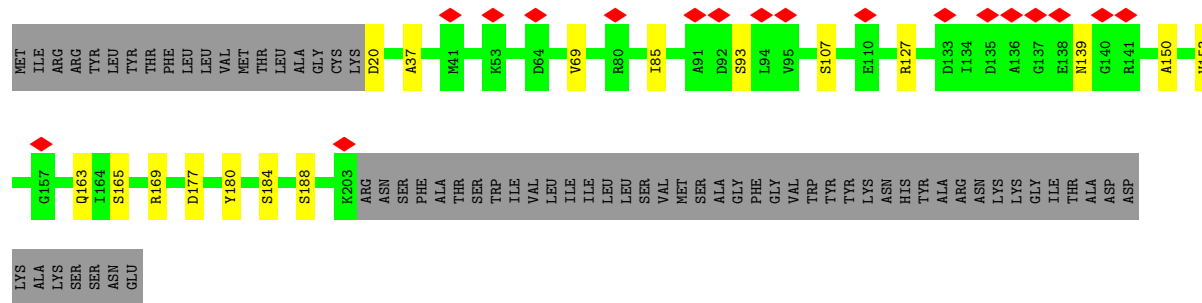
• Molecule 1: Lipoprotein PrgK



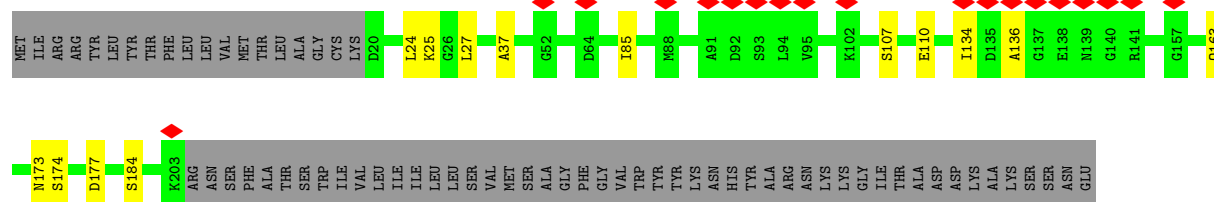
• Molecule 1: Lipoprotein PrgK



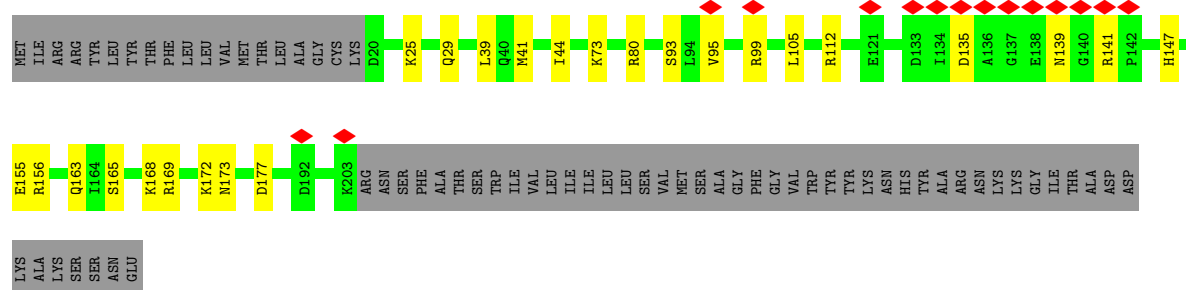
• Molecule 1: Lipoprotein PrgK



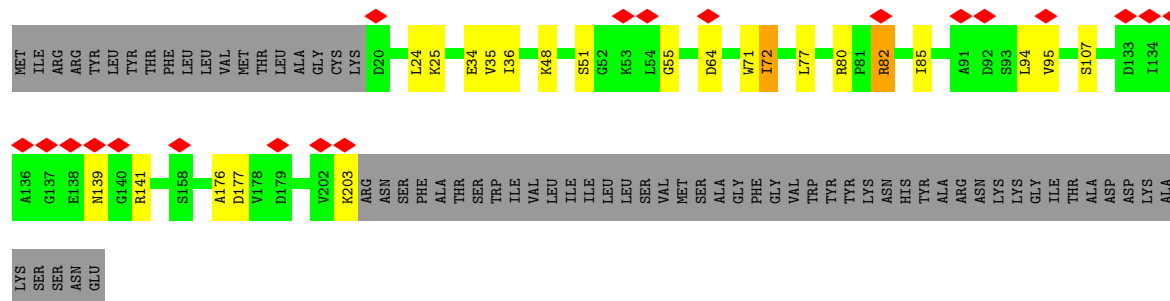
• Molecule 1: Lipoprotein PrgK



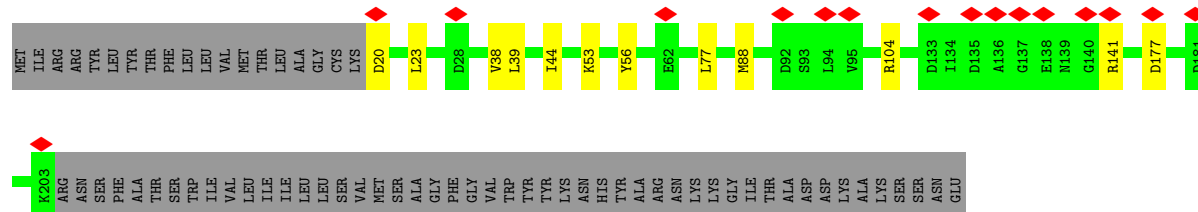
- Molecule 1: Lipoprotein PrgK



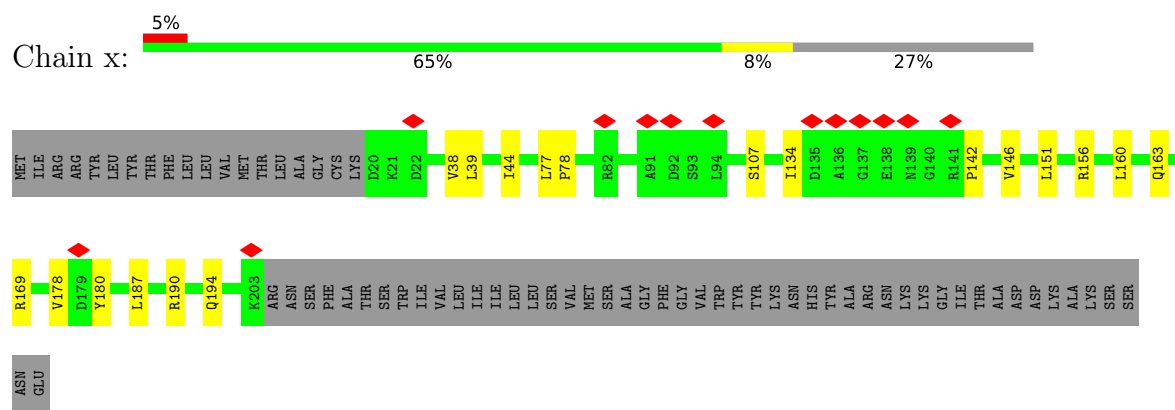
- Molecule 1: Lipoprotein PrgK



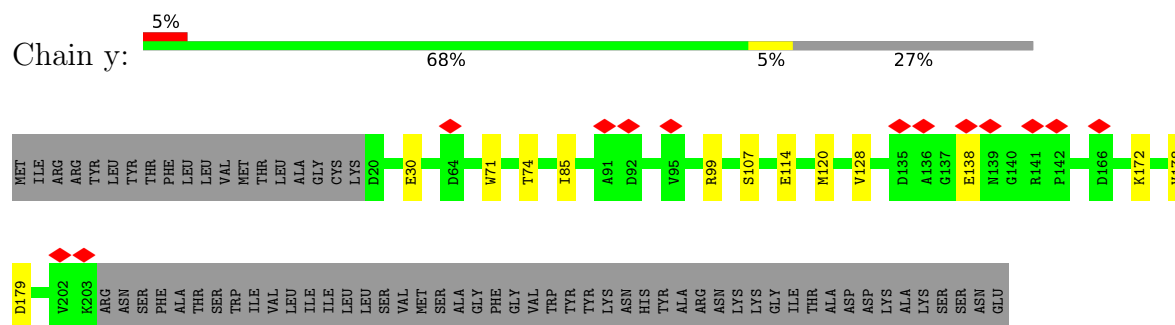
- Molecule 1: Lipoprotein PrgK



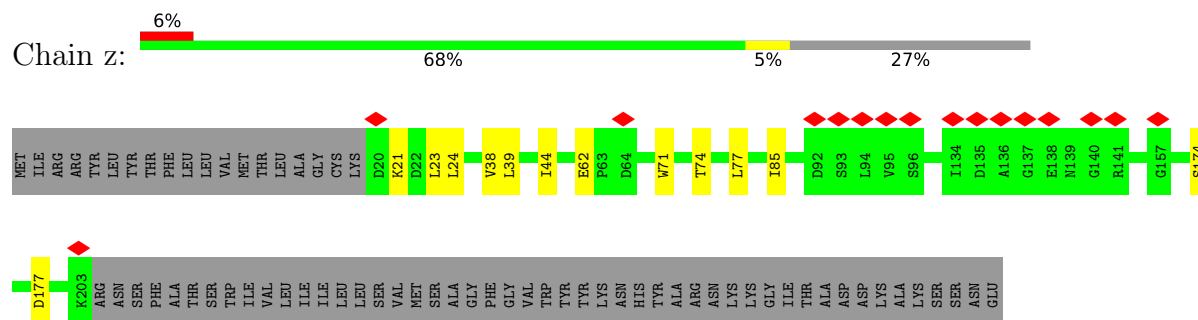
- Molecule 1: Lipoprotein PrgK



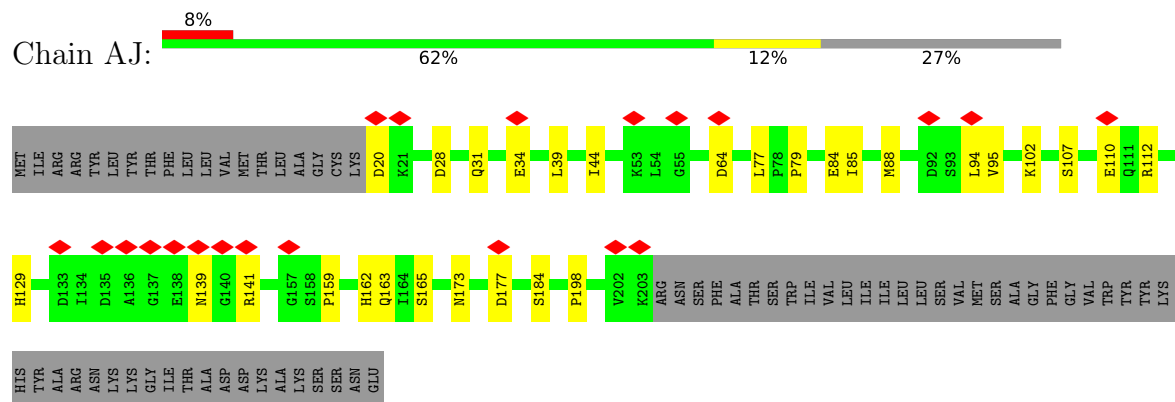
- Molecule 1: Lipoprotein PrgK



- Molecule 1: Lipoprotein PrgK

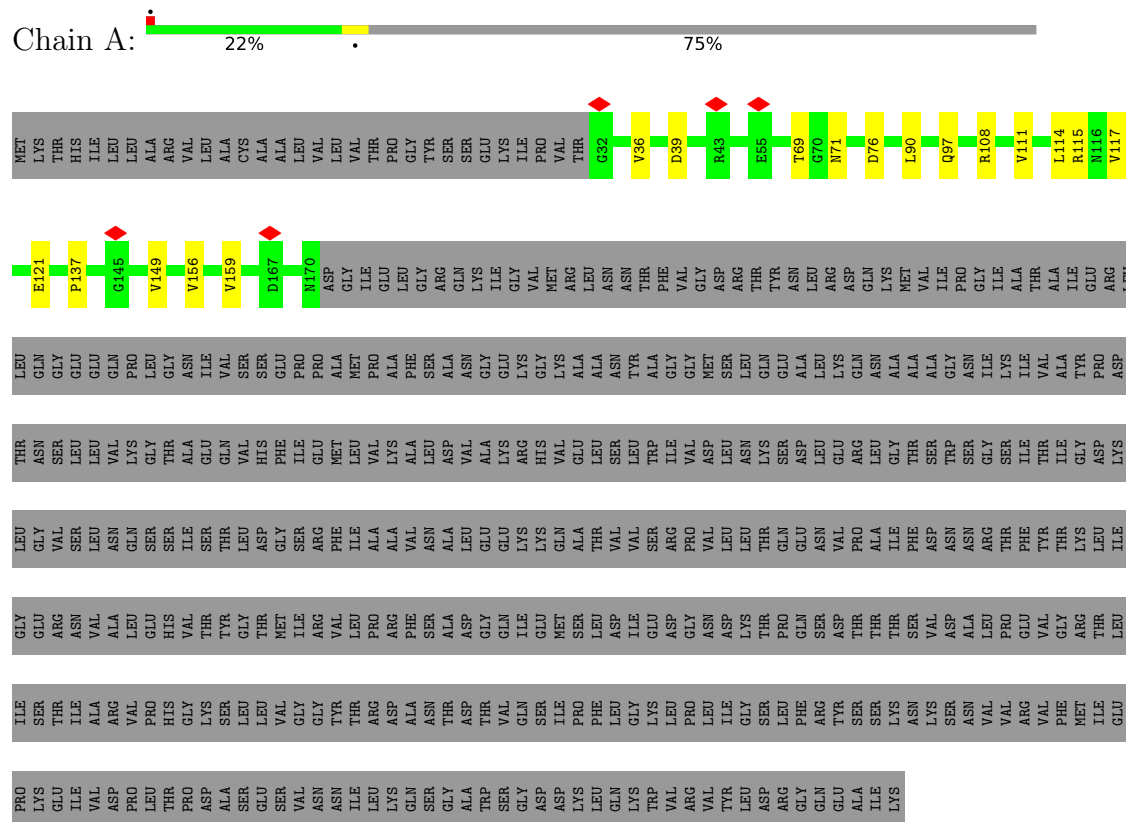


- Molecule 1: Lipoprotein PrgK

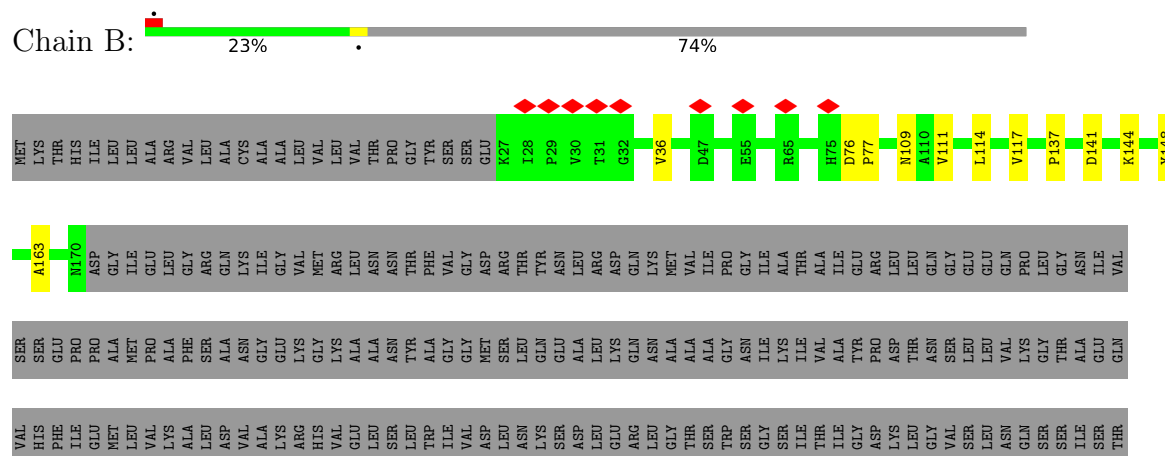


- Molecule 1: Lipoprotein PrgK

- Molecule 2: Protein InvG



- Molecule 2: Protein InvG



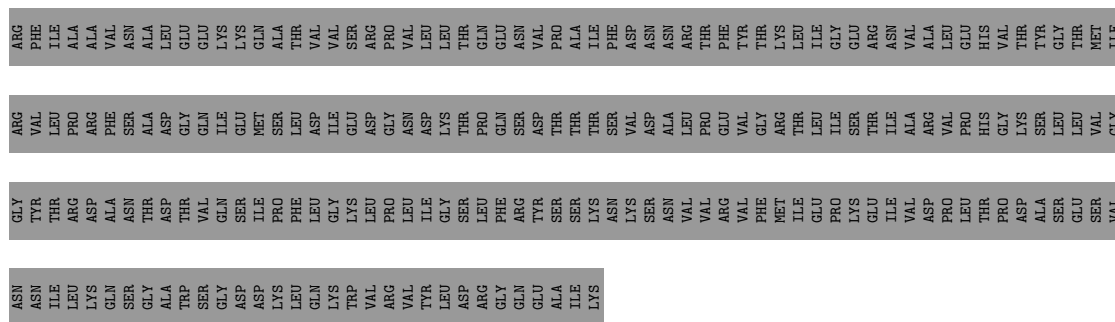
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- Molecule 2: Protein InvG

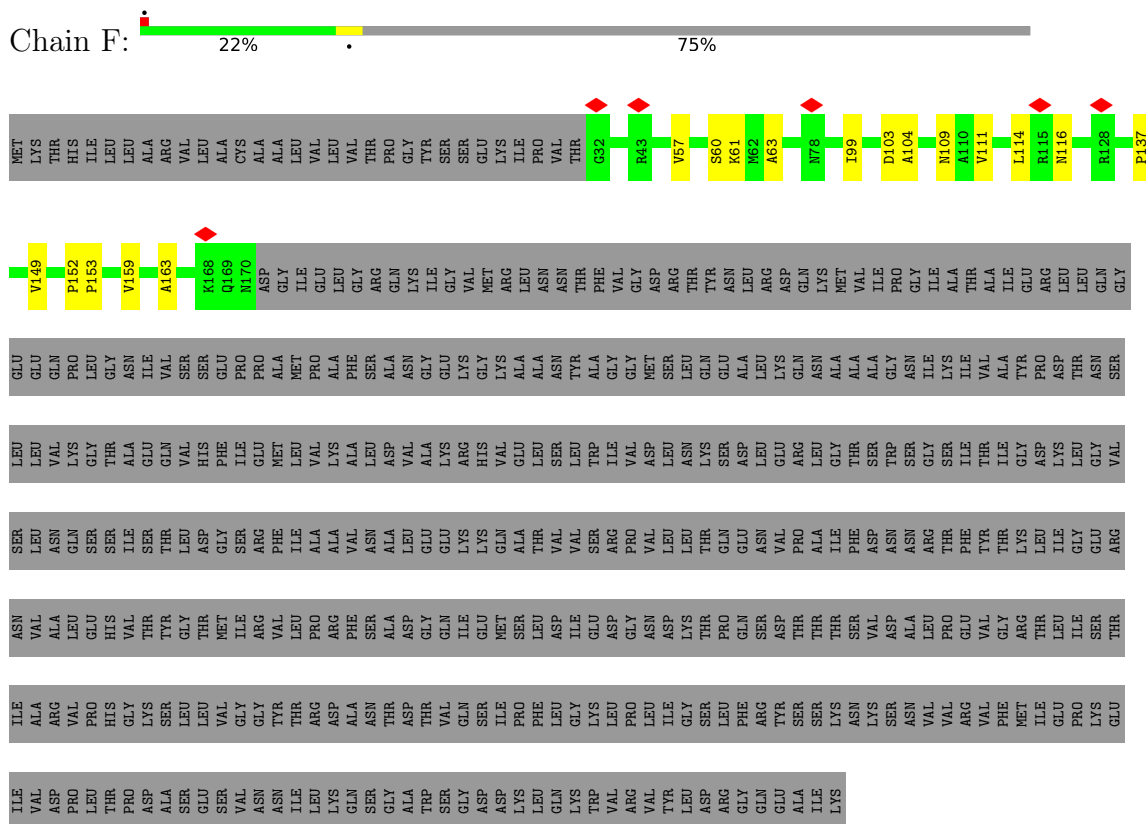
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- Molecule 2: Protein InvG

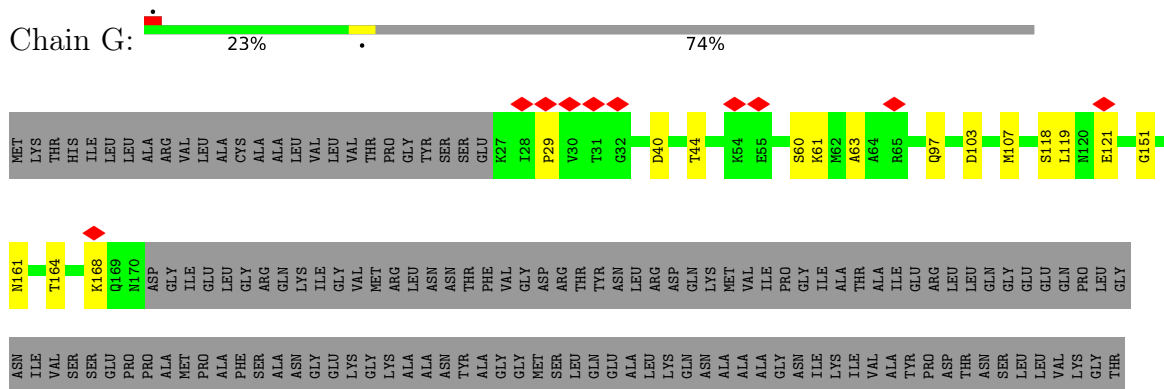
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- Molecule 2: Protein InvG

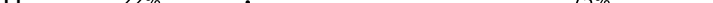


- Molecule 2: Protein InvG



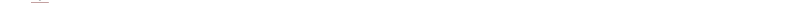
[illegible]

- Molecule 2: Protein InvG

Chain H:  22% . 75%

[illegible]

- Molecule 2: Protein InvG

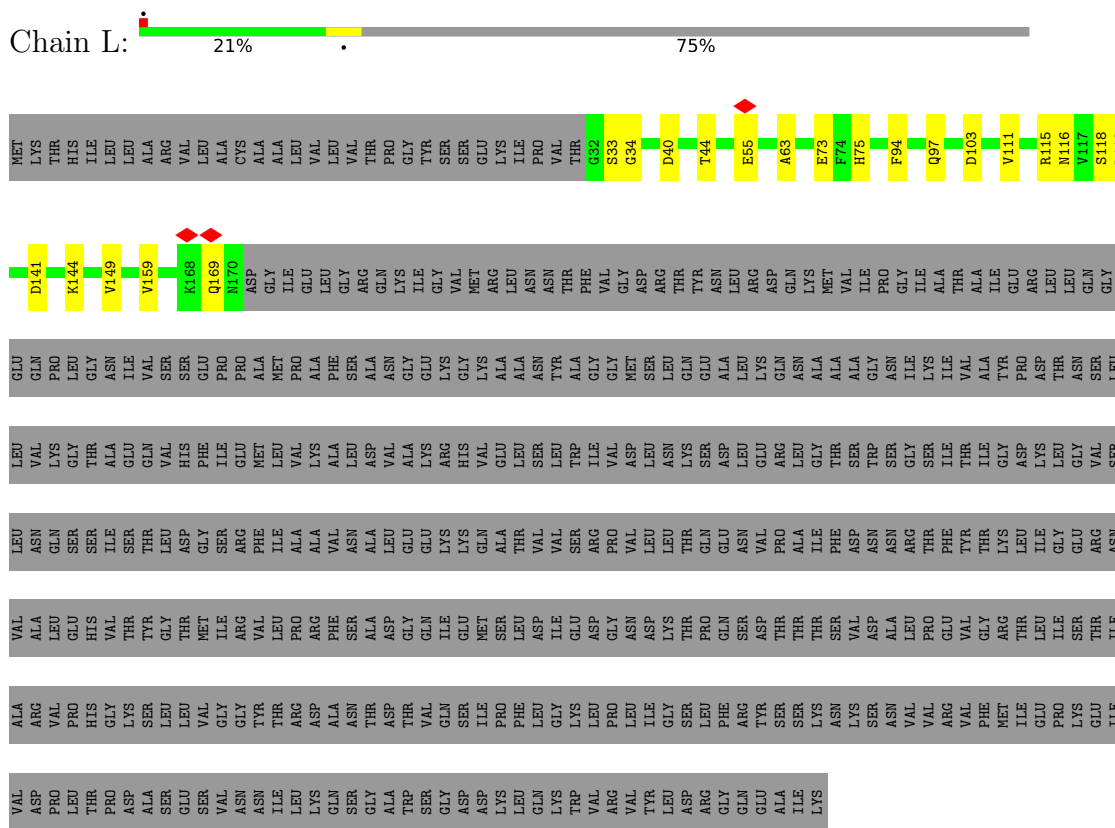
Chain I:  23% 74%

ASN	ILE	VAL	SER	SER	GLU	PRO	PRO	MET	ALA	MET	PRO	ALA	PHE	SER	ALA	ASN	GLY	GLU	LYS	GLY	LYS	ALA	ALA	TYR	ALA	GLY	GLY	MET	SER	LEU	GLN	GLU	ALA	ALA	ASP	THR	ASN	LYS	VAL	VAL	ALA	ALA	TYR	PRO	ASP	THR	ASN	SER	LEU	GLU	E121	R143	K144	G151
P163	D157	K168	Q169	N170	ASP	GLY	ILE	GLU	LEU	GLY	ARG	GLN	LYS	ILE	VAL	GLY	VAL	PRO	ARG	LEU	ASN	THR	THR	PHE	VAL	GLY	ASP	ARG	THR	THR	Tyr	ASN	LEU	ARG	LEU	GLN	GLY	GLU	ILE	THR	ALA	ILE	GLU	ARG	LEU	LEU	GLN	GLY	GLU	GLN	PRO	LEU	GLY	
MET	LYS	THR	HIS	ILE	LEU	LEU	ALA	ARG	VAL	LEU	ALA	CYS	ALA	ALA	LEU	VAL	VAL	THR	PRO	GLY	TVR	SER	SER	GLU	K27	I28	P29	V30	T31	G32	V36	A37	X38	S41	T44	D47	H75	D76	P77	M107	R108	S118	L119	M120	E121	R143	K144	G151						

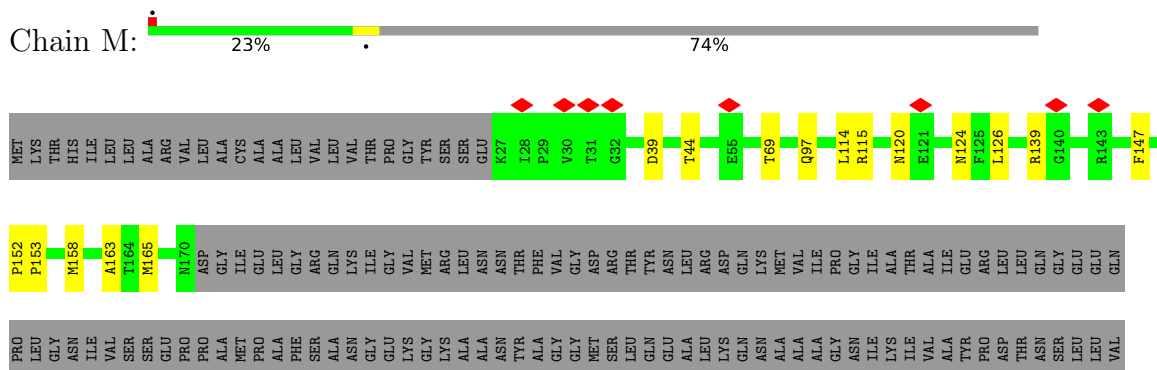


[illegible]

- Molecule 2: Protein InvG

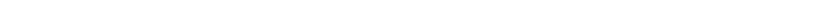


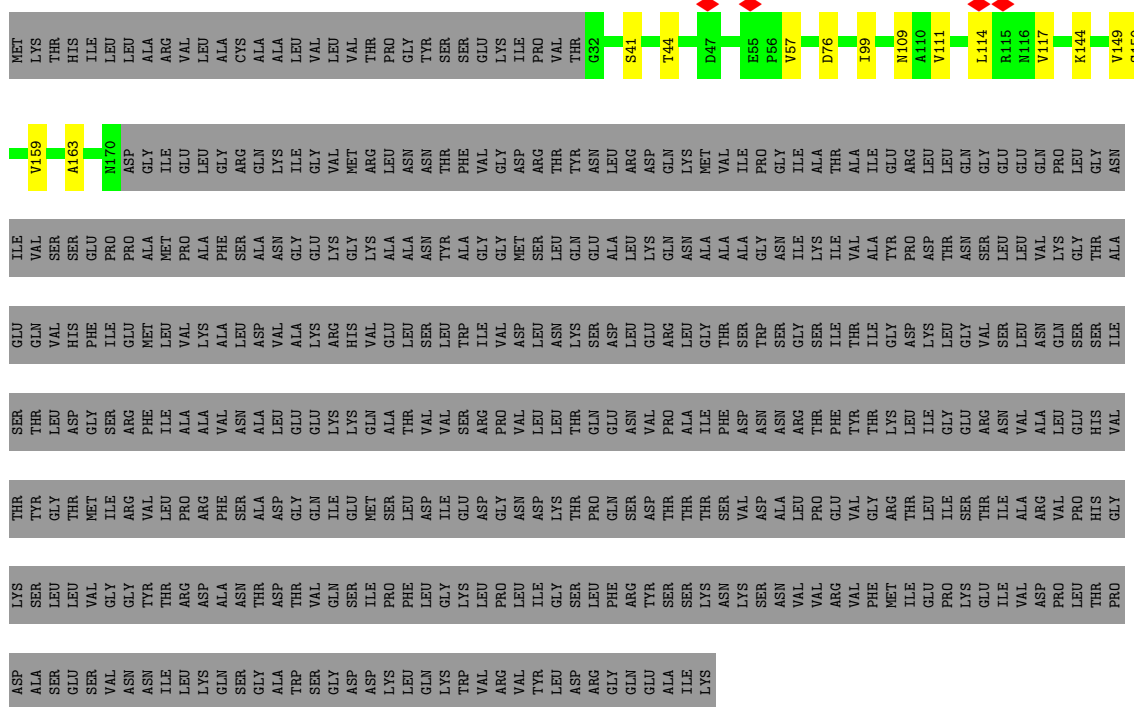
- Molecule 2: Protein InvG



[illegible]

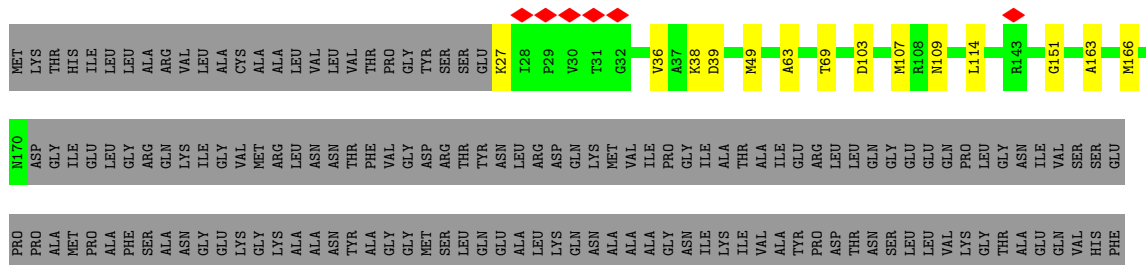
- Molecule 2: Protein InvG

Chain N:  22% 75%



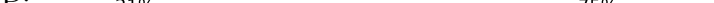
- Molecule 2: Protein InvG

Chain 0: 23% 74%



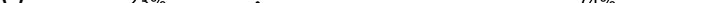
[illegible]

- Molecule 2: Protein InvG

Chain P:  21% 75%

[illegible]

- Molecule 2: Protein InvG

Chain Q:  23% 74%

Sequence logos for the 1000 Genomes Project. The top logo displays nucleotide conservation across 1000 samples, with a peak at position 1000 (G) and a dip at position 1001 (A). The bottom logo displays amino acid conservation across 1000 samples, with a peak at position 1000 (G) and a dip at position 1001 (A).

[illegible]

- Molecule 3: Protein PrgH



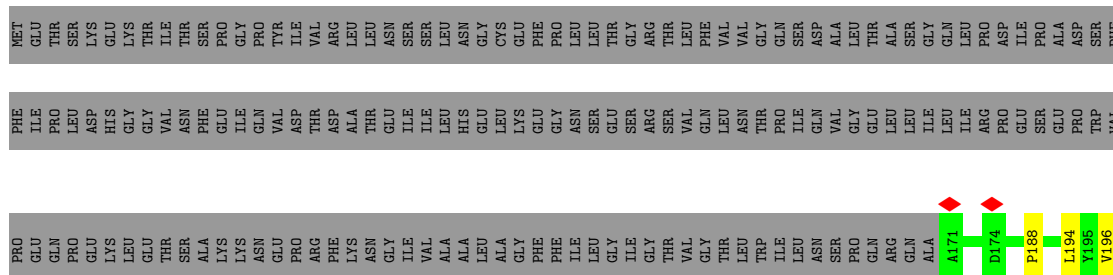
S390	P391	L392	D217	R221	E227	E228	R231	D237	Y246	R247	P256	V257	F258	V274	K278	V289	N290	I291	D296	E304	R316	R317	N318	L331	D332	D333	R340	Q341	F342	V343	D344	L361	R362	D363	D364	V365	L366	R367	S382	P383	G384		
◆	◆	◆	◆	◆	◆			◆		◆														◆	◆	◆							◆	◆	◆	◆	◆	◆	◆	◆	◆	◆	◆
NET	GLU	THR	LYS	GLU	LYS	THR	THR	THR	PRO	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PHE	ILE	PRO	LEU	ASP	HIS	GLY	VAL	ILE	ASN	PHE	GLU	ILE	GLY	VAL	ASP	THR	ASP	ALA	LEU	LEU	GLY	ILE	ILE	ASN	GLY	ASN	LEU	THR	GLN	PRO	ILE	ILE	GLN	LEU	ILE	ILE	ARG	PRO	ASP	ILE	PRO	THR	THR

- Molecule 3: Protein PrgH

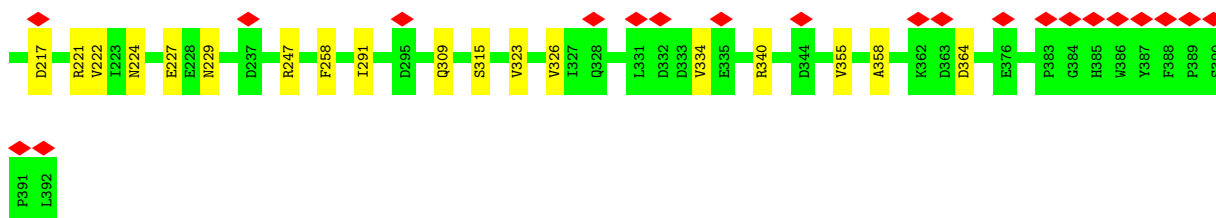
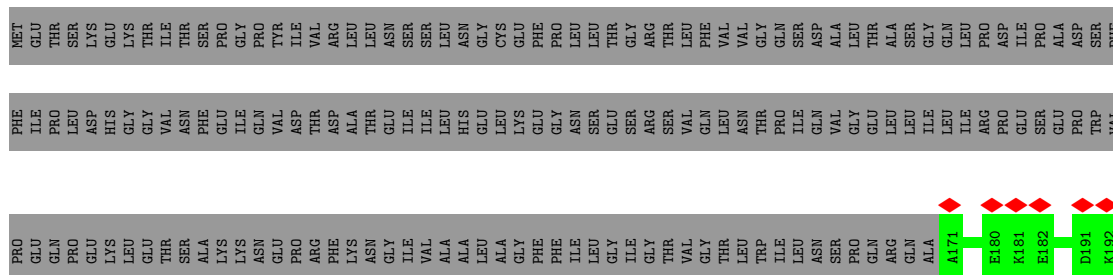


R221	R229	D237	A244	R247	I248	H249	F250	D251	E252	V257	N265	E271	L272	E273	V274	N290	E304	R316	R317	N318	D322	R338	A339	R340	D344	R348	Q356	D363	K360	P391	LEU											
PRO	GLU	GLN	PRO	GLU	THR	THR	LYS	GLU	GLU	ARG	PHE	ASN	GLY	ILE	VAL	ALA	LEU	ALA	GLY	PHE	ILE	ILE	GLY	THR	VAL	THR	ILE	LEU	ASN	ARG	K192	R202	D217	K218	N219							
PHE	ILE	PRO	LEU	ASP	HIS	GLY	GLY	VAL	VAL	THR	ASP	ALA	THR	ILE	ILE	HIS	GLU	LEU	GLY	ASN	GLY	THR	LEU	VAL	ASN	THR	LEU	PHE	GLN	VAL	GLY	LEU	ILE	ARG	PRO	GLY	SER	PRO	GLU	ASP	THR	VAL
MET	GLU	LYS	LYS	GLY	THR	THR	GLY	THR	THR	PRO	ARG	ASN	GLY	ILE	VAL	ALA	LEU	ALA	GLY	PHE	ILE	ILE	GLY	THR	VAL	ASN	THR	LEU	PHE	GLN	VAL	GLY	LEU	ILE	ARG	PRO	ASP	ILE	ALA	ASP	SER	PHE

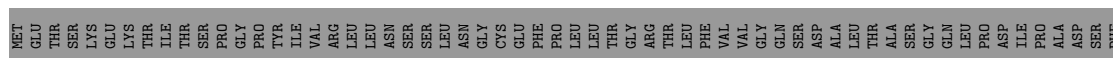
- Molecule 3: Protein PrgH



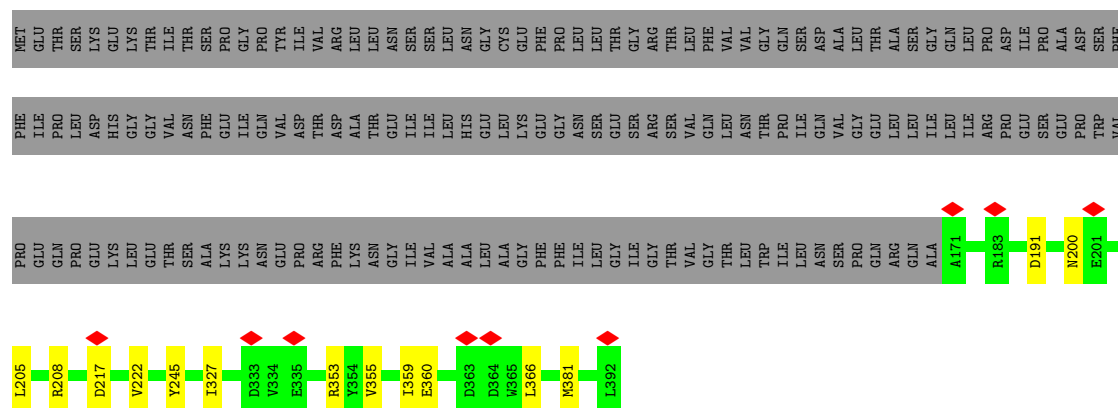
- Molecule 3: Protein PrgH



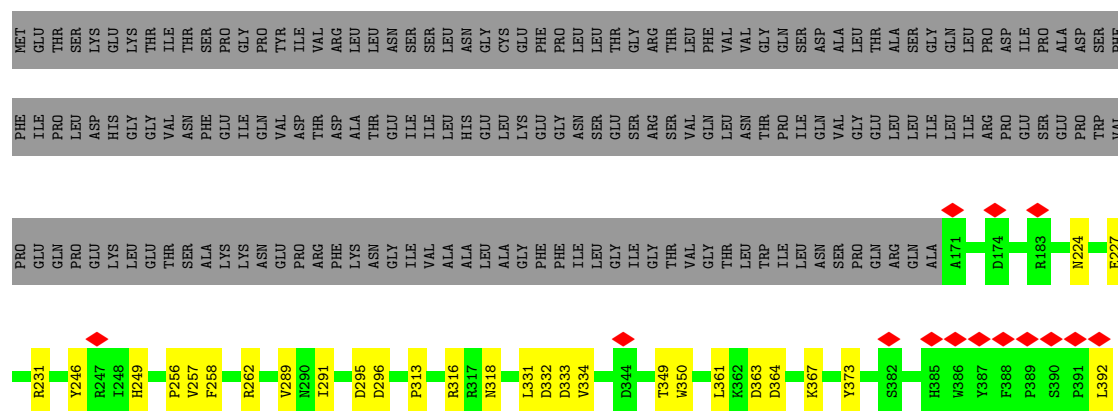
- Molecule 3: Protein PrgH



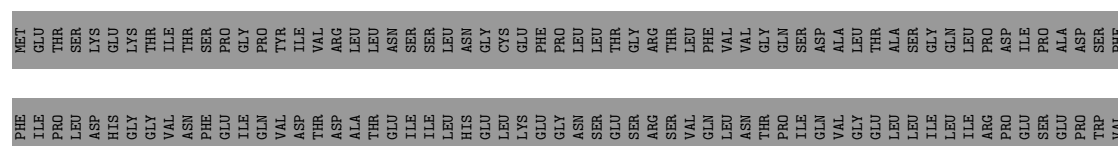
- Molecule 3: Protein PrgH



- Molecule 3: Protein PrgH

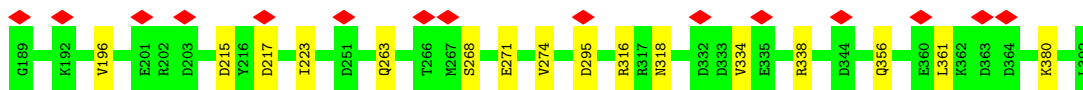
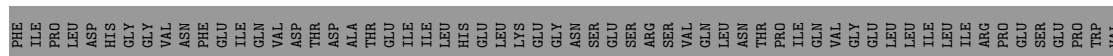


- Molecule 3: Protein PrgH

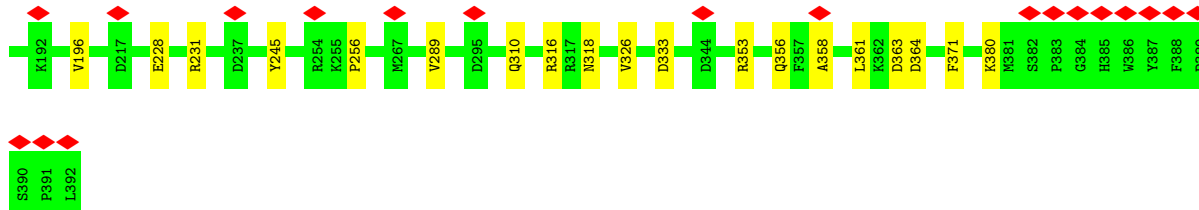
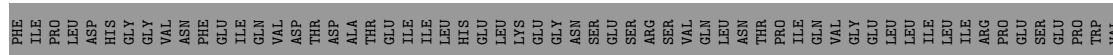




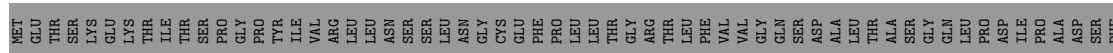
Chain e:

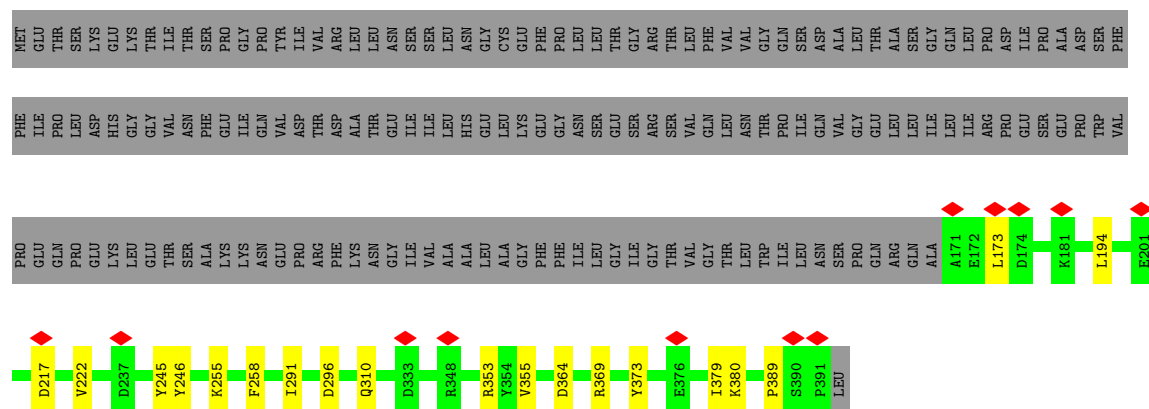


Chain f:

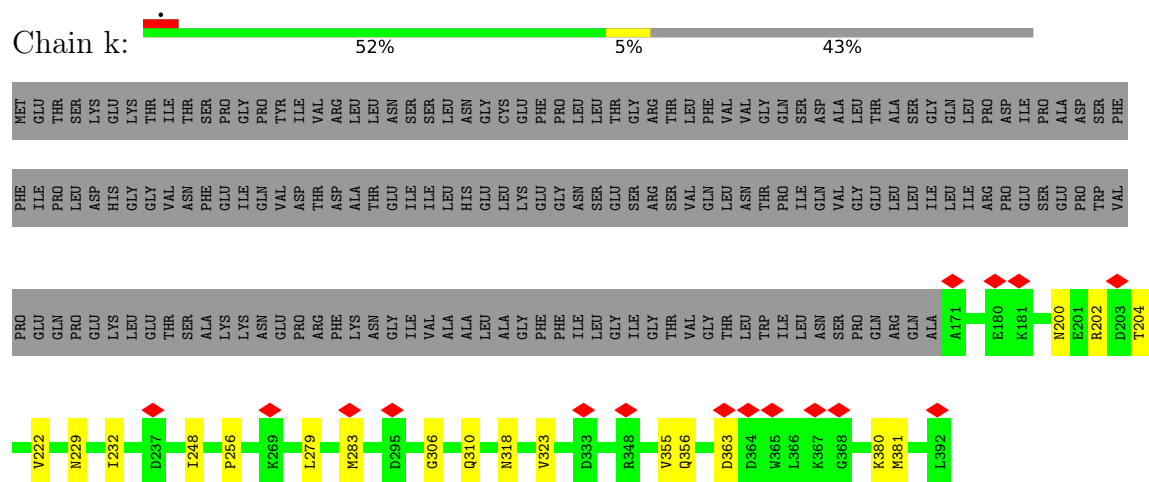


Chain g: 50% 6% 44%

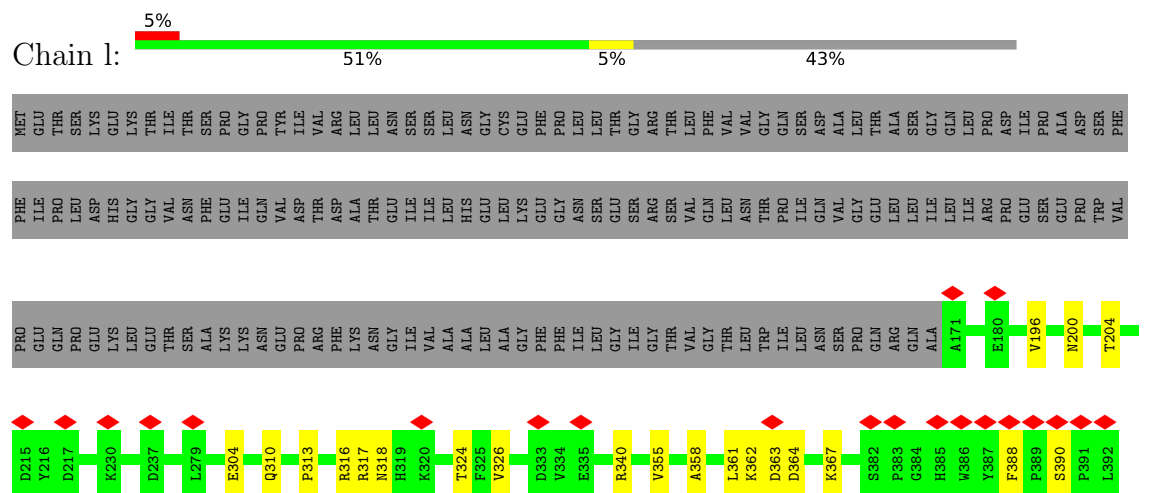




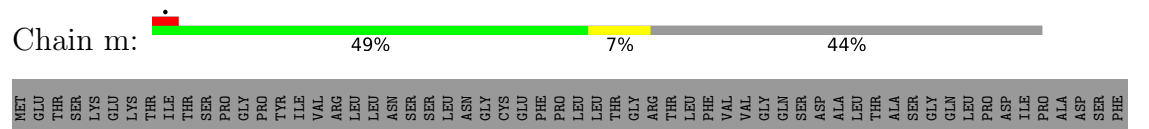
- Molecule 3: Protein PrgH



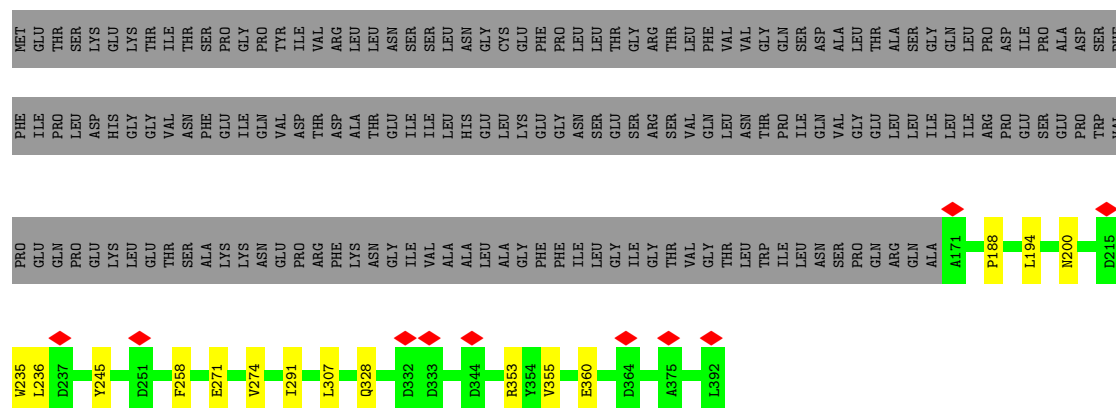
- Molecule 3: Protein PrgH



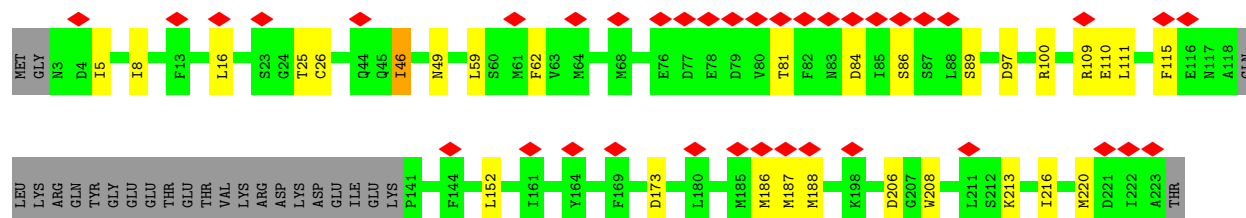
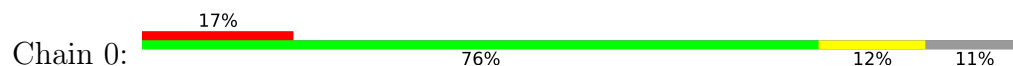
- Molecule 3: Protein PrgH



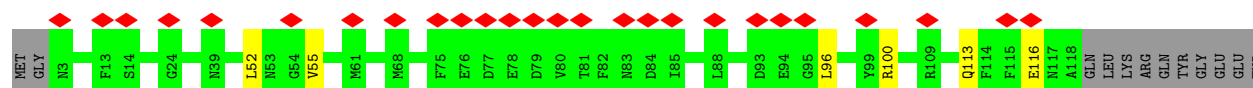
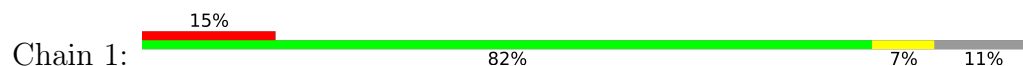
- Molecule 3: Protein PrgH

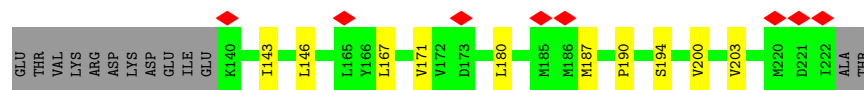


- Molecule 4: Surface presentation of antigens protein SpaP

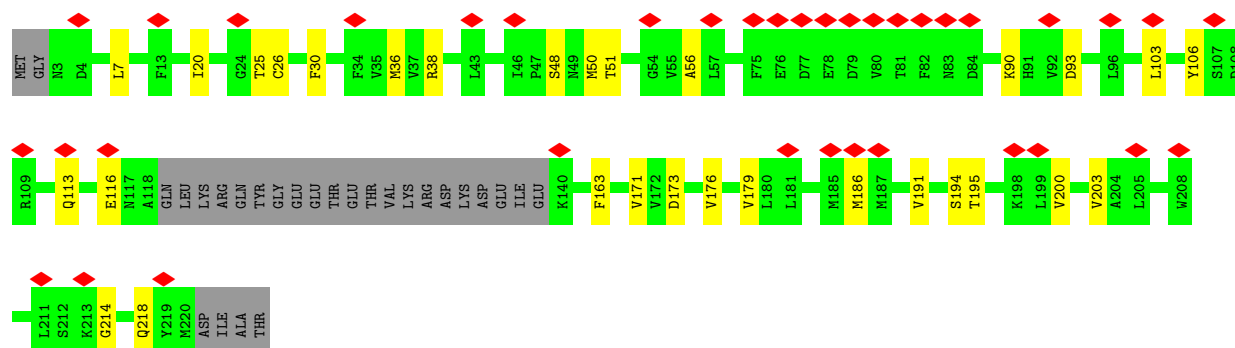
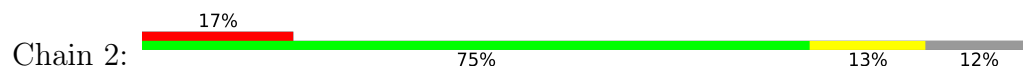


- Molecule 4: Surface presentation of antigens protein SpaP

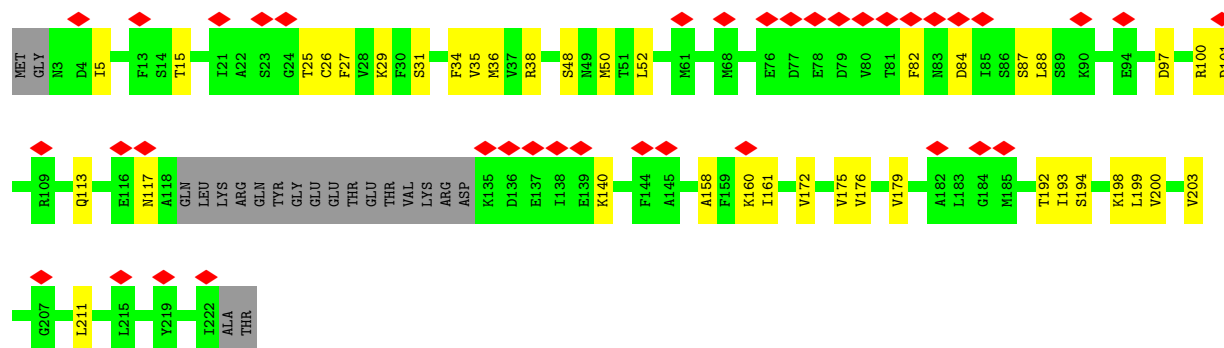
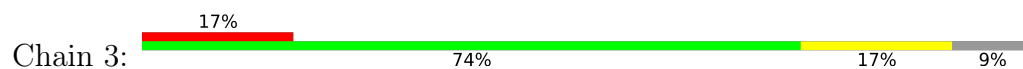




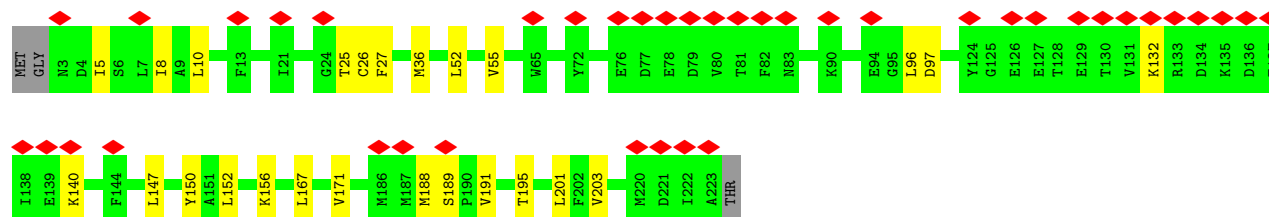
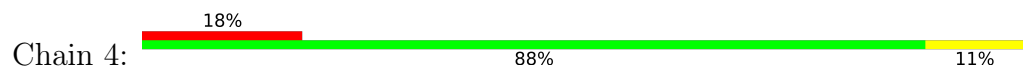
• Molecule 4: Surface presentation of antigens protein SpaP



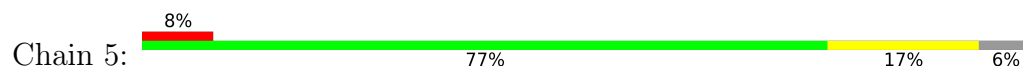
• Molecule 4: Surface presentation of antigens protein SpaP

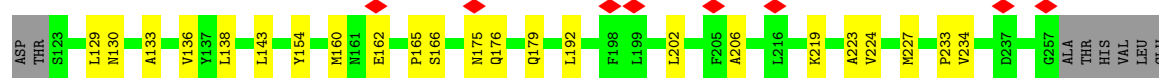


• Molecule 4: Surface presentation of antigens protein SpaP

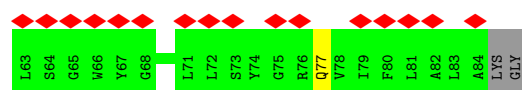
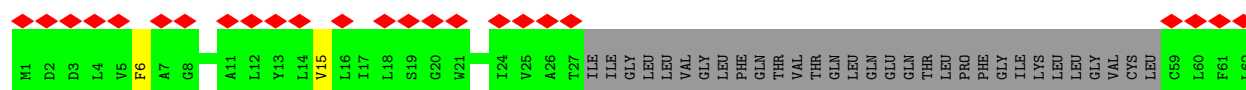


• Molecule 5: Surface presentation of antigens protein SpaR

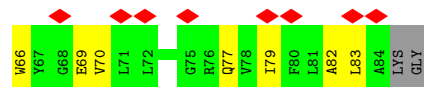
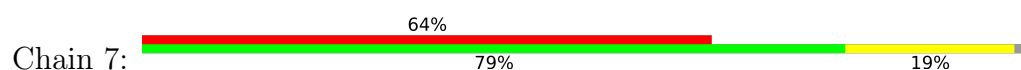




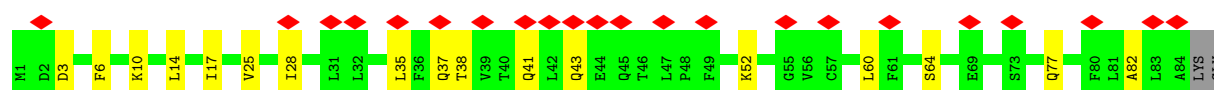
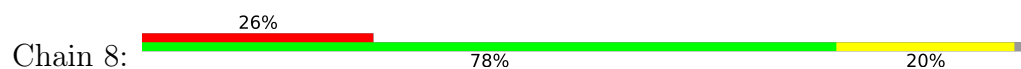
• Molecule 6: Surface presentation of antigens protein SpaQ



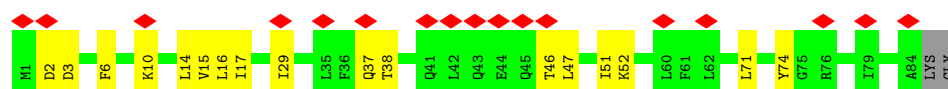
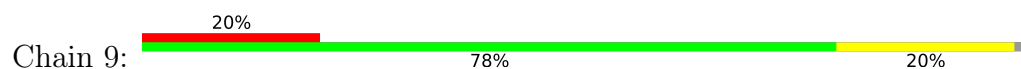
• Molecule 6: Surface presentation of antigens protein SpaQ



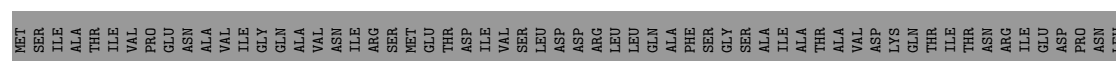
• Molecule 6: Surface presentation of antigens protein SpaQ

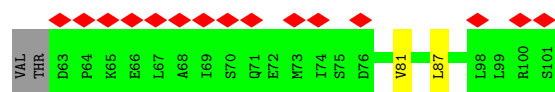


• Molecule 6: Surface presentation of antigens protein SpaQ

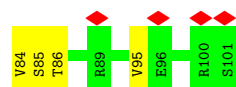
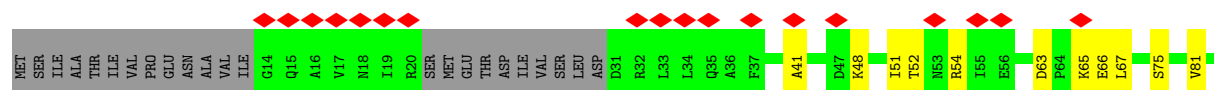


• Molecule 7: Protein PrgJ

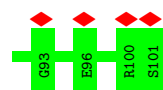
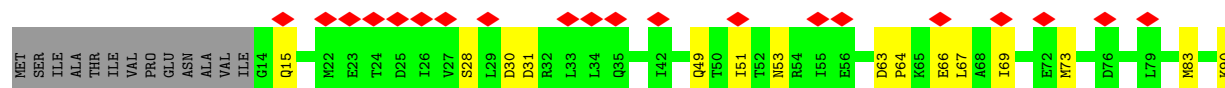
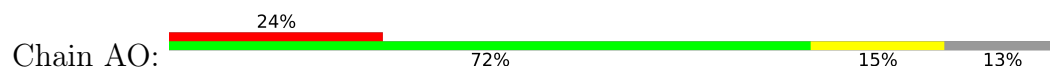




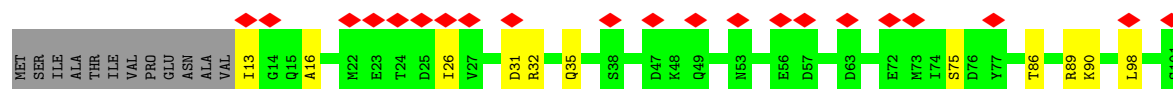
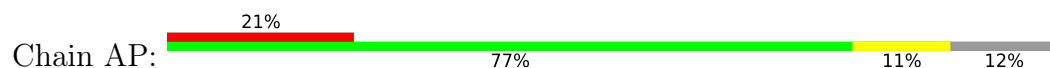
• Molecule 7: Protein PrgJ



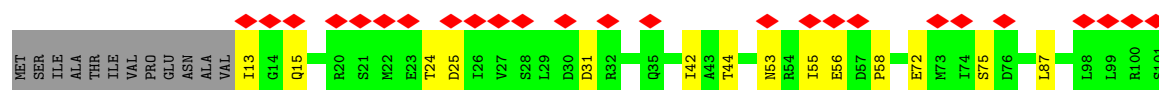
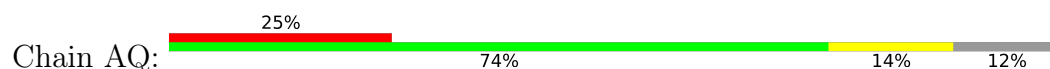
• Molecule 7: Protein PrgJ



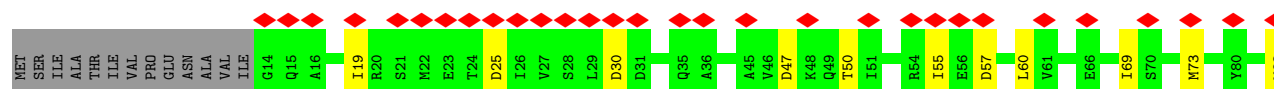
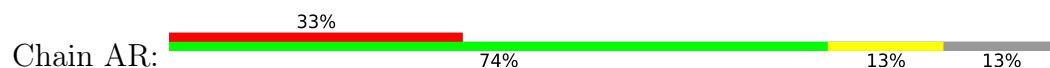
• Molecule 7: Protein PrgJ

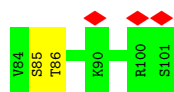


• Molecule 7: Protein PrgJ

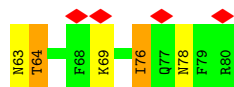
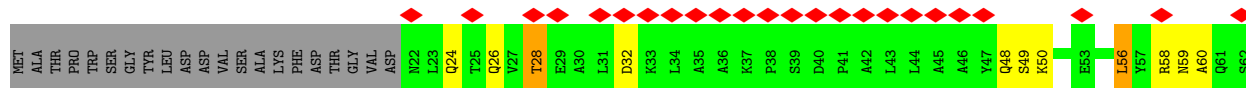


• Molecule 7: Protein PrgJ

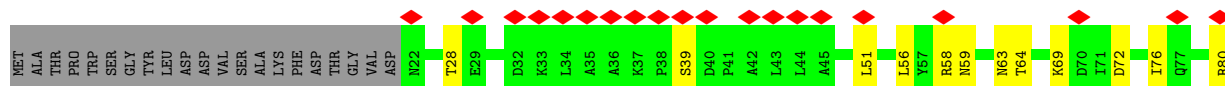




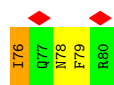
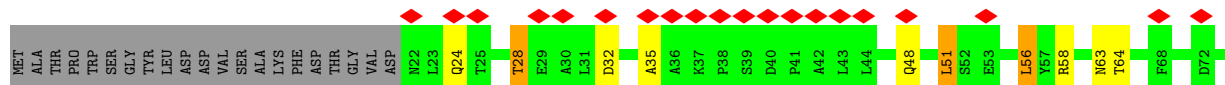
• Molecule 8: Protein PrgI



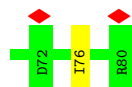
• Molecule 8: Protein PrgI



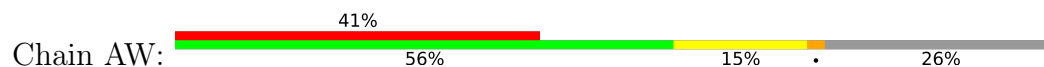
• Molecule 8: Protein PrgI

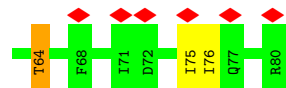
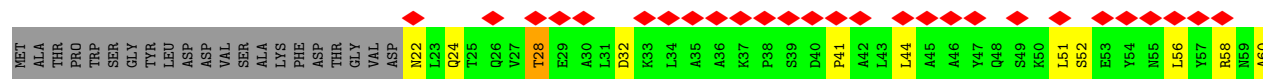


• Molecule 8: Protein PrgI

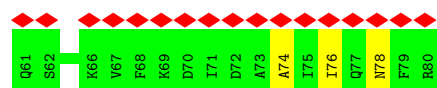
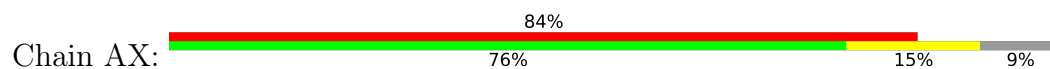


• Molecule 8: Protein PrgI

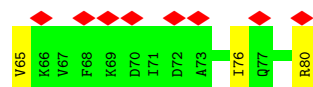
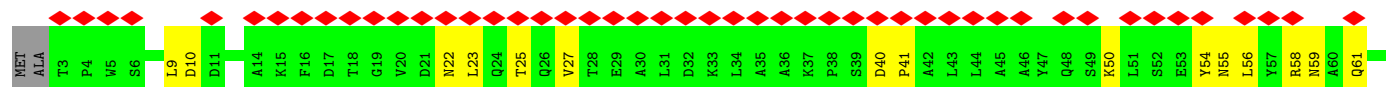
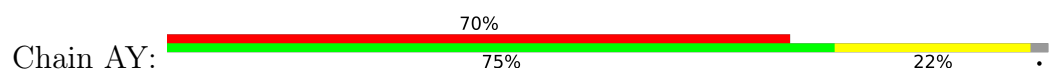




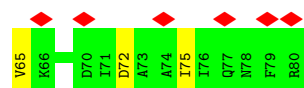
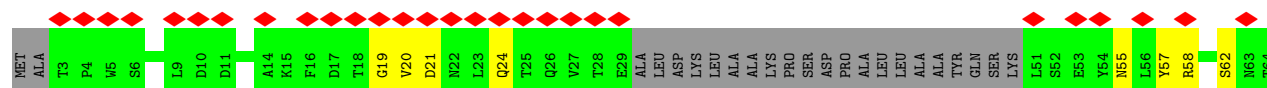
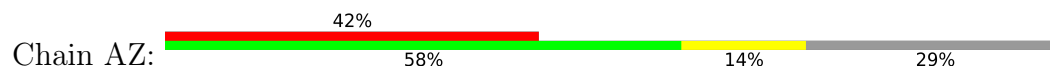
• Molecule 8: Protein PrgI



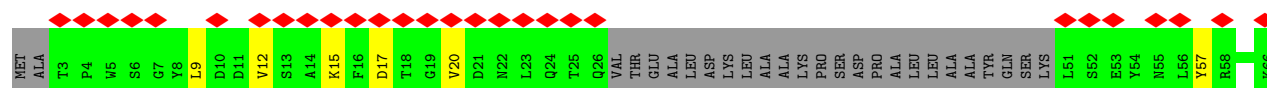
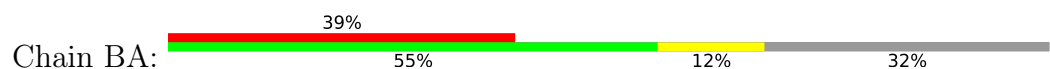
• Molecule 8: Protein PrgI



• Molecule 8: Protein PrgI

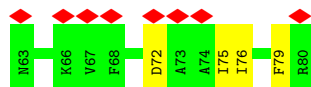
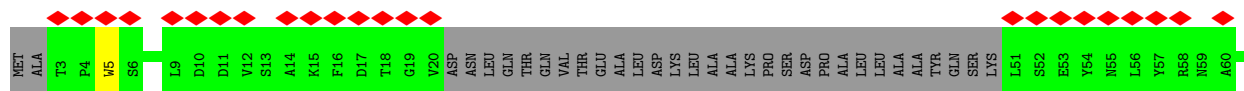
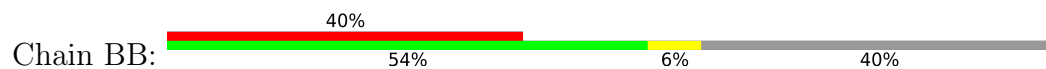


• Molecule 8: Protein PrgI

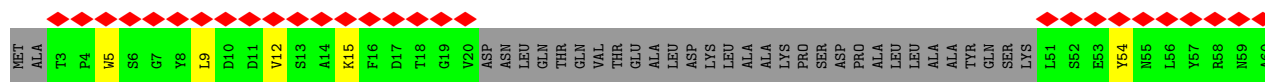




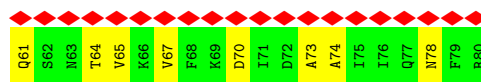
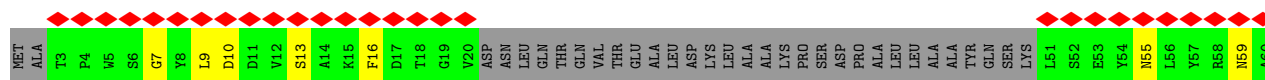
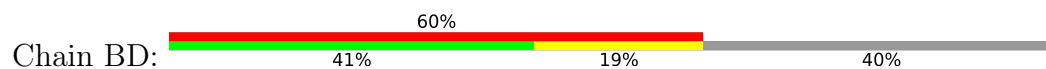
• Molecule 8: Protein PrgI



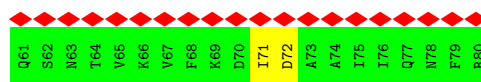
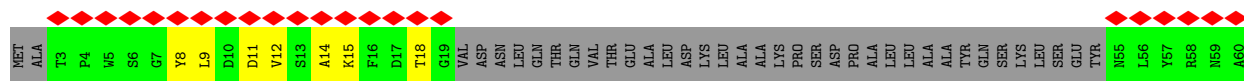
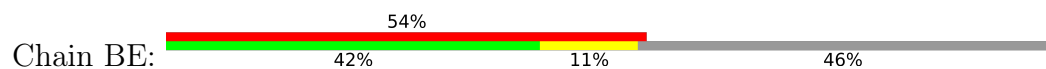
• Molecule 8: Protein PrgI



• Molecule 8: Protein PrgI



• Molecule 8: Protein PrgI



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19141	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	0.147	Depositor
Minimum map value	-0.079	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	427.5, 427.5, 427.5	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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	0.36	0/1458	0.61	0/1979
1	AB	0.34	0/1458	0.59	0/1979
1	AC	0.37	0/1458	0.61	0/1979
1	AD	0.34	0/1458	0.60	0/1979
1	AE	0.36	0/1458	0.60	0/1979
1	AF	0.34	0/1458	0.59	0/1979
1	AG	0.35	0/1458	0.59	0/1979
1	AH	0.34	0/1458	0.61	0/1979
1	AI	0.36	0/1458	0.62	0/1979
1	AJ	0.37	0/1458	0.66	0/1979
1	AK	0.34	0/1458	0.61	0/1979
1	AL	0.35	0/1458	0.60	0/1979
1	o	0.34	0/1458	0.58	0/1979
1	p	0.33	0/1458	0.59	0/1979
1	q	0.34	0/1458	0.57	0/1979
1	r	0.33	0/1458	0.61	0/1979
1	s	0.33	0/1458	0.61	0/1979
1	t	0.35	0/1458	0.65	0/1979
1	u	0.35	0/1458	0.65	0/1979
1	v	0.42	0/1458	0.65	0/1979
1	w	0.34	0/1458	0.60	0/1979
1	x	0.36	0/1458	0.65	1/1979 (0.1%)
1	y	0.36	0/1458	0.62	0/1979
1	z	0.36	0/1458	0.63	0/1979
2	A	0.33	0/1131	0.64	1/1525 (0.1%)
2	B	0.33	0/1181	0.63	0/1593
2	C	0.33	0/1131	0.62	0/1525
2	D	0.34	0/1170	0.61	0/1579
2	F	0.34	0/1131	0.64	0/1525
2	G	0.34	0/1181	0.66	2/1593 (0.1%)
2	H	0.37	0/1131	0.65	1/1525 (0.1%)
2	I	0.33	0/1181	0.60	0/1593
2	J	0.35	0/1131	0.62	0/1525
2	K	0.35	0/1181	0.65	0/1593

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	L	0.34	0/1131	0.64	0/1525
2	M	0.32	0/1170	0.62	0/1579
2	N	0.35	0/1131	0.63	0/1525
2	O	0.34	0/1181	0.62	0/1593
2	P	0.33	0/1131	0.61	0/1525
2	Q	0.34	0/1181	0.65	0/1593
3	E	0.31	0/1881	0.60	0/2541
3	R	0.32	0/1872	0.64	0/2530
3	S	0.32	0/1876	0.63	0/2536
3	T	0.31	0/1881	0.58	0/2541
3	U	0.31	0/1872	0.62	0/2530
3	V	0.31	0/1876	0.61	0/2536
3	W	0.31	0/1881	0.62	0/2541
3	X	0.31	0/1872	0.62	0/2530
3	Y	0.32	0/1876	0.63	0/2536
3	Z	0.31	0/1881	0.59	0/2541
3	a	0.31	0/1872	0.60	0/2530
3	b	0.31	0/1876	0.62	0/2536
3	c	0.32	0/1881	0.61	0/2541
3	d	0.32	0/1872	0.56	0/2530
3	e	0.32	0/1876	0.62	0/2536
3	f	0.31	0/1881	0.61	0/2541
3	g	0.30	0/1872	0.59	0/2530
3	h	0.33	0/1876	0.66	0/2536
3	i	0.30	0/1881	0.58	0/2541
3	j	0.32	0/1872	0.62	0/2530
3	k	0.33	0/1876	0.64	0/2536
3	l	0.33	0/1881	0.63	0/2541
3	m	0.31	0/1872	0.62	0/2530
3	n	0.32	0/1876	0.62	0/2536
4	0	0.34	0/1598	0.67	0/2172
4	1	0.32	0/1605	0.68	1/2181 (0.0%)
4	2	0.30	0/1589	0.67	0/2159
4	3	0.33	0/1642	0.62	0/2230
4	4	0.34	0/1799	0.65	0/2441
5	5	0.34	0/1935	0.72	0/2647
6	6	0.27	0/414	0.71	0/565
6	7	0.30	0/657	0.70	0/897
6	8	0.32	0/657	0.74	0/897
6	9	0.32	0/660	0.66	0/900
7	AM	0.37	0/300	0.87	0/403
7	AN	0.28	0/646	0.63	0/870
7	AO	0.31	0/671	0.65	0/908

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	AP	0.31	0/679	0.71	0/919
7	AQ	0.28	0/679	0.64	0/919
7	AR	0.29	0/671	0.71	0/908
8	AS	0.31	0/472	0.65	0/638
8	AT	0.29	0/472	0.61	0/638
8	AU	0.32	0/472	0.61	0/638
8	AV	0.33	0/472	0.73	0/638
8	AW	0.30	0/472	0.59	0/638
8	AX	0.27	0/582	0.61	0/788
8	AY	0.32	0/623	0.67	0/846
8	AZ	0.24	0/467	0.51	0/632
8	BA	0.24	0/444	0.50	0/600
8	BB	0.28	0/395	0.67	0/533
8	BC	0.25	0/395	0.56	0/533
8	BD	0.26	0/395	0.58	0/533
8	BE	0.27	0/352	0.69	0/474
All	All	0.33	0/120713	0.63	6/163413 (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
3	b	0	1
6	8	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	x	134	ILE	N-CA-C	-7.48	106.60	113.71
2	A	90	LEU	CA-CB-CG	5.32	134.93	116.30
4	1	167	LEU	N-CA-C	5.20	121.31	109.81
2	H	143	ARG	CA-CB-CG	5.19	124.47	114.10
2	G	29	PRO	CA-C-N	5.11	131.18	121.97

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	8	41	GLN	Peptide
3	b	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	17	0
1	AB	1431	0	1424	10	0
1	AC	1431	0	1424	14	0
1	AD	1431	0	1424	9	0
1	AE	1431	0	1424	14	0
1	AF	1431	0	1424	13	0
1	AG	1431	0	1424	7	0
1	AH	1431	0	1424	9	0
1	AI	1431	0	1424	14	0
1	AJ	1431	0	1424	22	0
1	AK	1431	0	1424	9	0
1	AL	1431	0	1424	12	0
1	o	1431	0	1424	18	0
1	p	1431	0	1424	12	0
1	q	1431	0	1424	8	0
1	r	1431	0	1424	12	0
1	s	1431	0	1424	13	0
1	t	1431	0	1424	13	0
1	u	1431	0	1424	20	0
1	v	1431	0	1424	17	0
1	w	1431	0	1424	10	0
1	x	1431	0	1424	12	0
1	y	1431	0	1424	9	0
1	z	1431	0	1424	8	0
2	A	1108	0	1103	11	0
2	B	1154	0	1163	8	0
2	C	1108	0	1103	11	0
2	D	1146	0	1150	9	0
2	F	1108	0	1103	10	0
2	G	1154	0	1163	8	0
2	H	1108	0	1103	6	0
2	I	1154	0	1163	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	1108	0	1103	8	0
2	K	1154	0	1163	10	0
2	L	1108	0	1103	13	0
2	M	1146	0	1150	11	0
2	N	1108	0	1103	10	0
2	O	1154	0	1163	10	0
2	P	1108	0	1103	13	0
2	Q	1154	0	1163	11	0
3	E	1836	0	1800	16	0
3	R	1827	0	1789	17	0
3	S	1831	0	1788	17	0
3	T	1836	0	1800	17	0
3	U	1827	0	1789	21	0
3	V	1831	0	1788	12	0
3	W	1836	0	1800	16	0
3	X	1827	0	1789	17	0
3	Y	1831	0	1788	14	0
3	Z	1836	0	1800	11	0
3	a	1827	0	1789	11	0
3	b	1831	0	1788	10	0
3	c	1836	0	1800	19	0
3	d	1827	0	1789	10	0
3	e	1831	0	1788	12	0
3	f	1836	0	1800	17	0
3	g	1827	0	1789	17	0
3	h	1831	0	1788	19	0
3	i	1836	0	1800	17	0
3	j	1827	0	1789	13	0
3	k	1831	0	1788	12	0
3	l	1836	0	1800	15	0
3	m	1827	0	1789	18	0
3	n	1831	0	1788	8	0
4	0	1562	0	1597	22	0
4	1	1569	0	1613	9	0
4	2	1553	0	1598	24	0
4	3	1606	0	1649	22	0
4	4	1758	0	1806	19	0
5	5	1885	0	1931	31	0
6	6	405	0	418	2	0
6	7	644	0	685	11	0
6	8	644	0	685	10	0
6	9	647	0	692	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	AM	298	0	307	1	0
7	AN	644	0	654	11	0
7	AO	667	0	672	10	0
7	AP	675	0	683	8	0
7	AQ	675	0	683	10	0
7	AR	667	0	672	9	0
8	AS	466	0	470	14	0
8	AT	466	0	470	5	0
8	AU	466	0	470	10	0
8	AV	466	0	470	7	0
8	AW	466	0	470	9	0
8	AX	574	0	566	8	0
8	AY	612	0	598	11	0
8	AZ	460	0	435	9	0
8	BA	437	0	413	6	0
8	BB	388	0	369	4	0
8	BC	388	0	369	7	0
8	BD	388	0	369	9	0
8	BE	346	0	329	7	0
All	All	118198	0	117437	955	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 4.

The worst 5 of 955 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:v:139:ASN:HD21	1:v:141:ARG:HE	1.32	0.77
2:Q:39:ASP:H	2:Q:69:THR:HG22	1.55	0.72
3:V:267:MET:HG3	3:V:271:GLU:HG3	1.74	0.69
2:I:169:GLN:HE22	2:J:115:ARG:HA	1.57	0.69
2:A:39:ASP:H	2:A:69:THR:HG22	1.59	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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%)	154 (99%)	1 (1%)	78	80
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%)	154 (99%)	1 (1%)	78	80
1	AF	155/215 (72%)	154 (99%)	1 (1%)	78	80
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%)	154 (99%)	1 (1%)	78	80
1	AJ	155/215 (72%)	154 (99%)	1 (1%)	78	80
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	80
1	p	155/215 (72%)	155 (100%)	0	100	100
1	q	155/215 (72%)	154 (99%)	1 (1%)	78	80
1	r	155/215 (72%)	154 (99%)	1 (1%)	78	80
1	s	155/215 (72%)	155 (100%)	0	100	100
1	t	155/215 (72%)	155 (100%)	0	100	100
1	u	155/215 (72%)	155 (100%)	0	100	100
1	v	155/215 (72%)	153 (99%)	2 (1%)	61	72
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	A	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	B	125/477 (26%)	125 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	119/477 (25%)	119 (100%)	0	100	100
2	D	124/477 (26%)	123 (99%)	1 (1%)	73	77
2	F	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	G	125/477 (26%)	124 (99%)	1 (1%)	73	77
2	H	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	I	125/477 (26%)	125 (100%)	0	100	100
2	J	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	K	125/477 (26%)	125 (100%)	0	100	100
2	L	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	M	75/477 (16%)	74 (99%)	1 (1%)	61	72
2	N	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	O	125/477 (26%)	125 (100%)	0	100	100
2	P	119/477 (25%)	118 (99%)	1 (1%)	73	77
2	Q	125/477 (26%)	124 (99%)	1 (1%)	73	77
3	E	190/337 (56%)	190 (100%)	0	100	100
3	R	97/337 (29%)	97 (100%)	0	100	100
3	Z	156/337 (46%)	154 (99%)	2 (1%)	61	72
3	a	189/337 (56%)	188 (100%)	1 (0%)	81	82
3	b	188/337 (56%)	187 (100%)	1 (0%)	81	82
3	c	190/337 (56%)	190 (100%)	0	100	100
3	d	189/337 (56%)	188 (100%)	1 (0%)	81	82
3	e	188/337 (56%)	187 (100%)	1 (0%)	81	82
3	f	190/337 (56%)	190 (100%)	0	100	100
3	g	189/337 (56%)	185 (98%)	4 (2%)	47	65
3	h	188/337 (56%)	188 (100%)	0	100	100
3	i	190/337 (56%)	190 (100%)	0	100	100
3	j	189/337 (56%)	187 (99%)	2 (1%)	65	74
3	k	188/337 (56%)	187 (100%)	1 (0%)	81	82
3	l	163/337 (48%)	161 (99%)	2 (1%)	63	73
3	m	189/337 (56%)	185 (98%)	4 (2%)	47	65
3	n	188/337 (56%)	187 (100%)	1 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	0	175/199 (88%)	172 (98%)	3 (2%)	53	68
4	1	177/199 (89%)	177 (100%)	0	100	100
4	2	175/199 (88%)	175 (100%)	0	100	100
4	3	180/199 (90%)	179 (99%)	1 (1%)	78	80
4	4	197/199 (99%)	197 (100%)	0	100	100
5	5	205/219 (94%)	204 (100%)	1 (0%)	81	82
6	6	41/71 (58%)	41 (100%)	0	100	100
6	7	69/71 (97%)	69 (100%)	0	100	100
6	8	69/71 (97%)	69 (100%)	0	100	100
6	9	70/71 (99%)	70 (100%)	0	100	100
7	AM	34/88 (39%)	33 (97%)	1 (3%)	37	58
7	AN	71/88 (81%)	71 (100%)	0	100	100
7	AO	76/88 (86%)	76 (100%)	0	100	100
7	AP	77/88 (88%)	76 (99%)	1 (1%)	61	72
7	AQ	77/88 (88%)	77 (100%)	0	100	100
7	AR	76/88 (86%)	76 (100%)	0	100	100
8	AS	50/67 (75%)	46 (92%)	4 (8%)	11	33
8	AT	50/67 (75%)	44 (88%)	6 (12%)	5	20
8	AU	50/67 (75%)	45 (90%)	5 (10%)	7	26
8	AV	50/67 (75%)	45 (90%)	5 (10%)	7	26
8	AW	50/67 (75%)	44 (88%)	6 (12%)	5	20
8	AX	62/67 (92%)	62 (100%)	0	100	100
8	AY	66/67 (98%)	66 (100%)	0	100	100
8	AZ	51/67 (76%)	51 (100%)	0	100	100
8	BA	48/67 (72%)	47 (98%)	1 (2%)	47	65
8	BB	42/67 (63%)	42 (100%)	0	100	100
8	BC	42/67 (63%)	42 (100%)	0	100	100
8	BD	42/67 (63%)	42 (100%)	0	100	100
8	BE	37/67 (55%)	37 (100%)	0	100	100
All	All	11091/21418 (52%)	11016 (99%)	75 (1%)	73	79

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	AT	76	ILE
8	AW	56	LEU
8	AU	51	LEU
8	AV	56	LEU
3	g	366	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 184 such sidechains are listed below:

Mol	Chain	Res	Type
1	u	139	ASN
5	5	210	ASN
1	v	139	ASN
1	AK	139	ASN
6	8	41	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

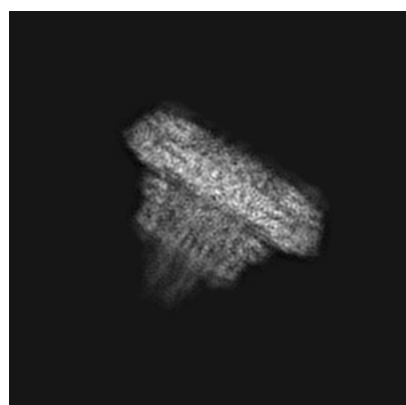
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20556. These allow visual inspection of the internal detail of the map and identification of artifacts.

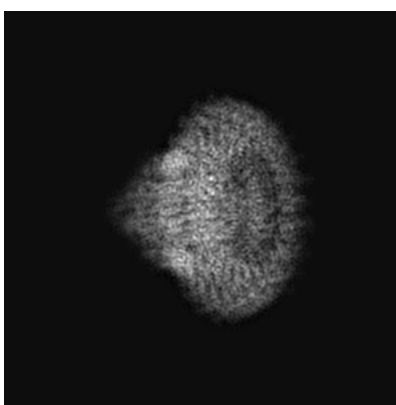
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

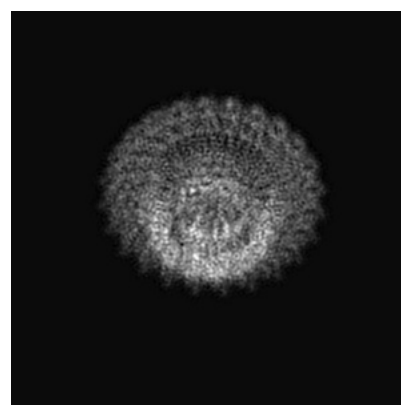
6.1.1 Primary map



X



Y

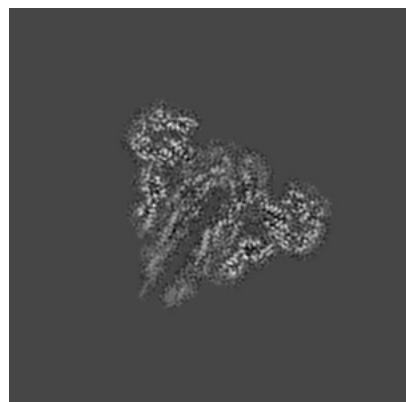


Z

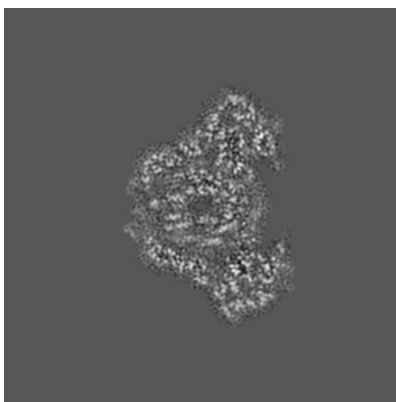
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

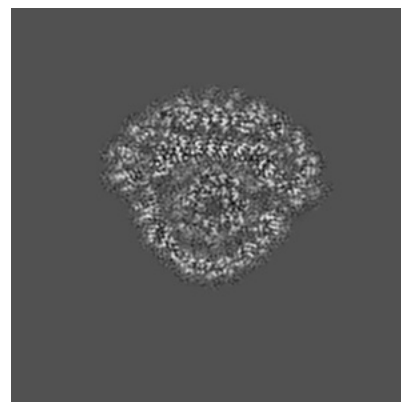
6.2.1 Primary map



X Index: 125



Y Index: 125



Z Index: 125

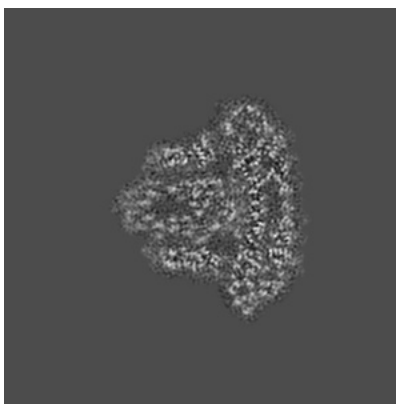
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

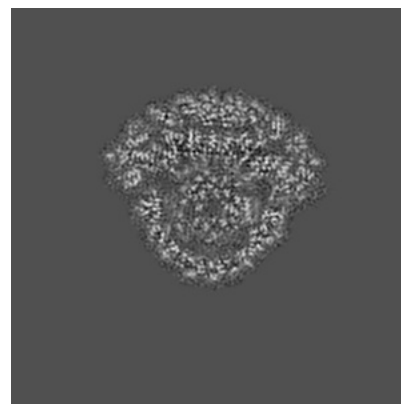
6.3.1 Primary map



X Index: 114



Y Index: 112

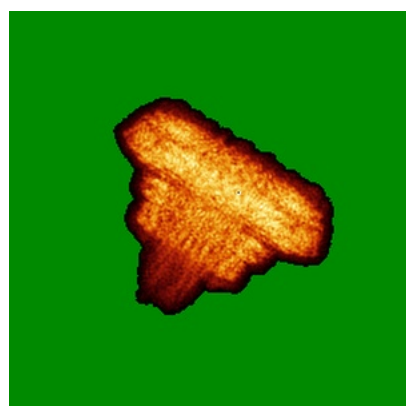


Z Index: 123

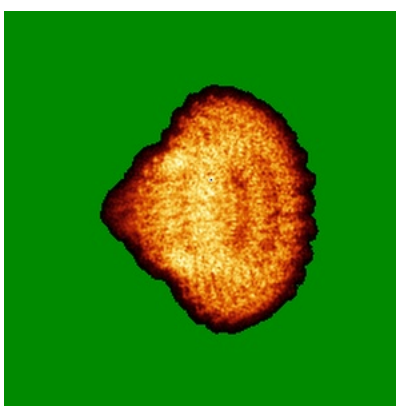
The images above show the largest variance slices of the map in three orthogonal directions.

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

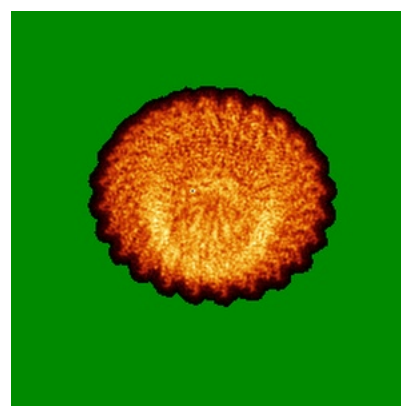
6.4.1 Primary map



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 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

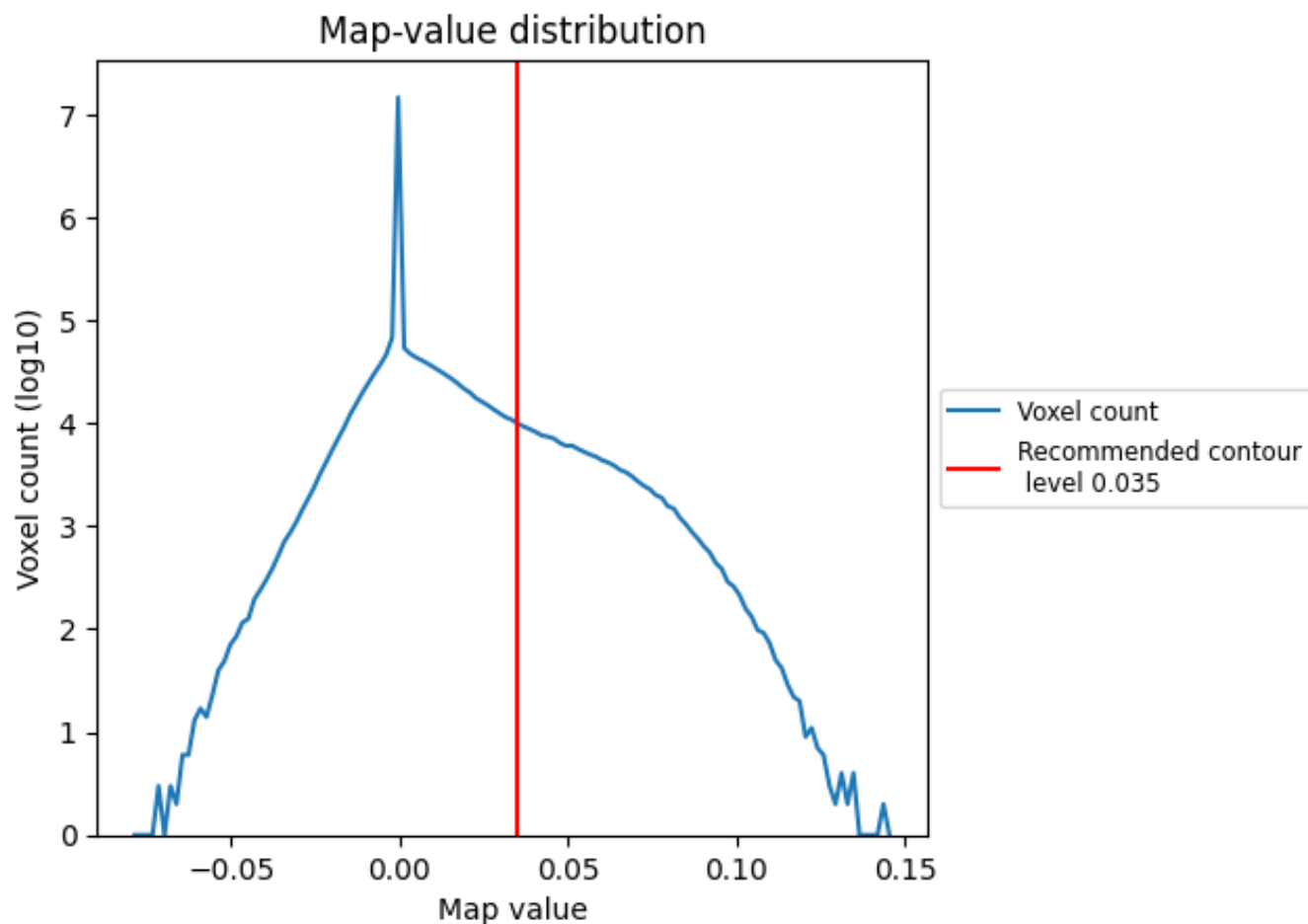
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

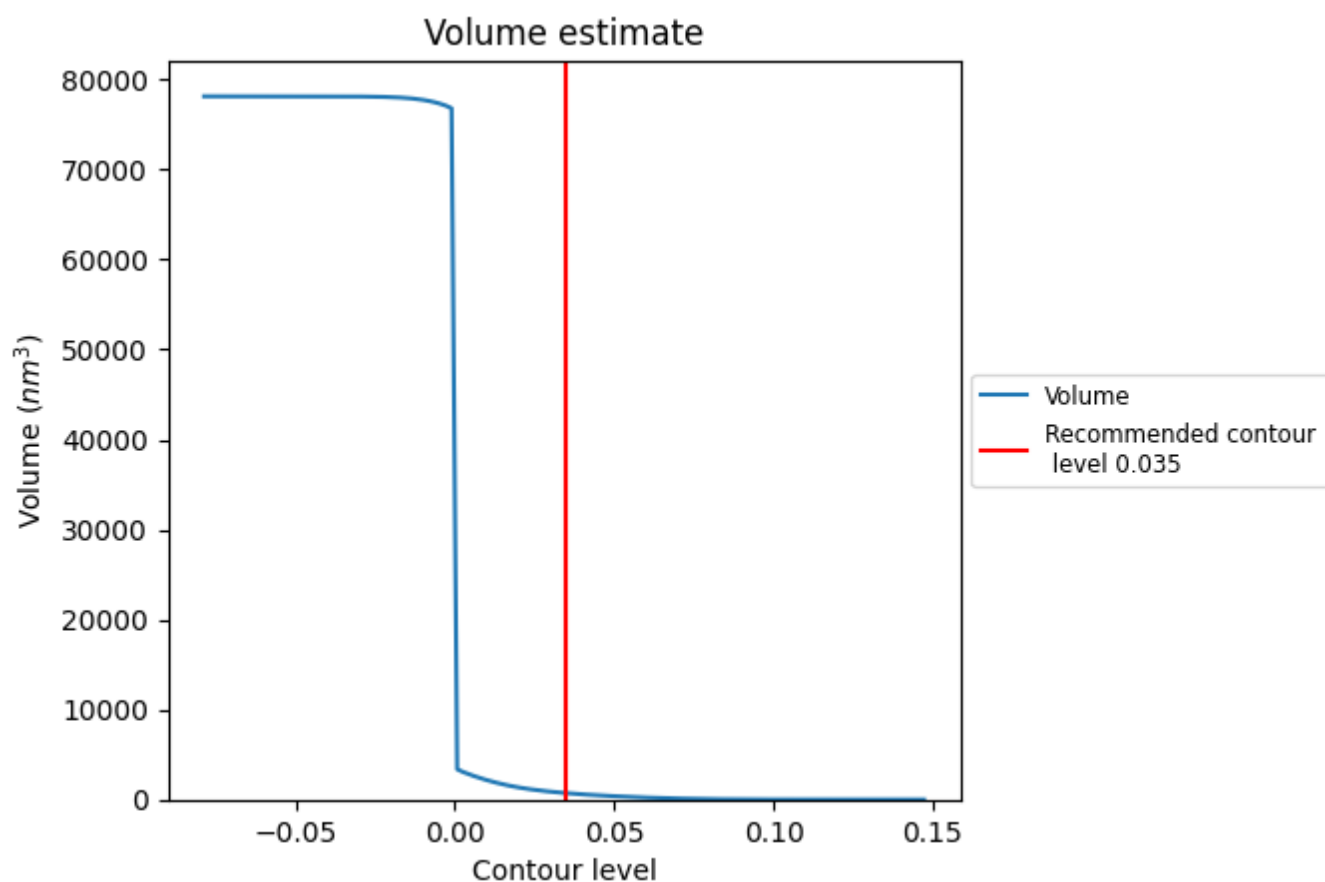
This section contains the results of statistical analysis of the map.

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.

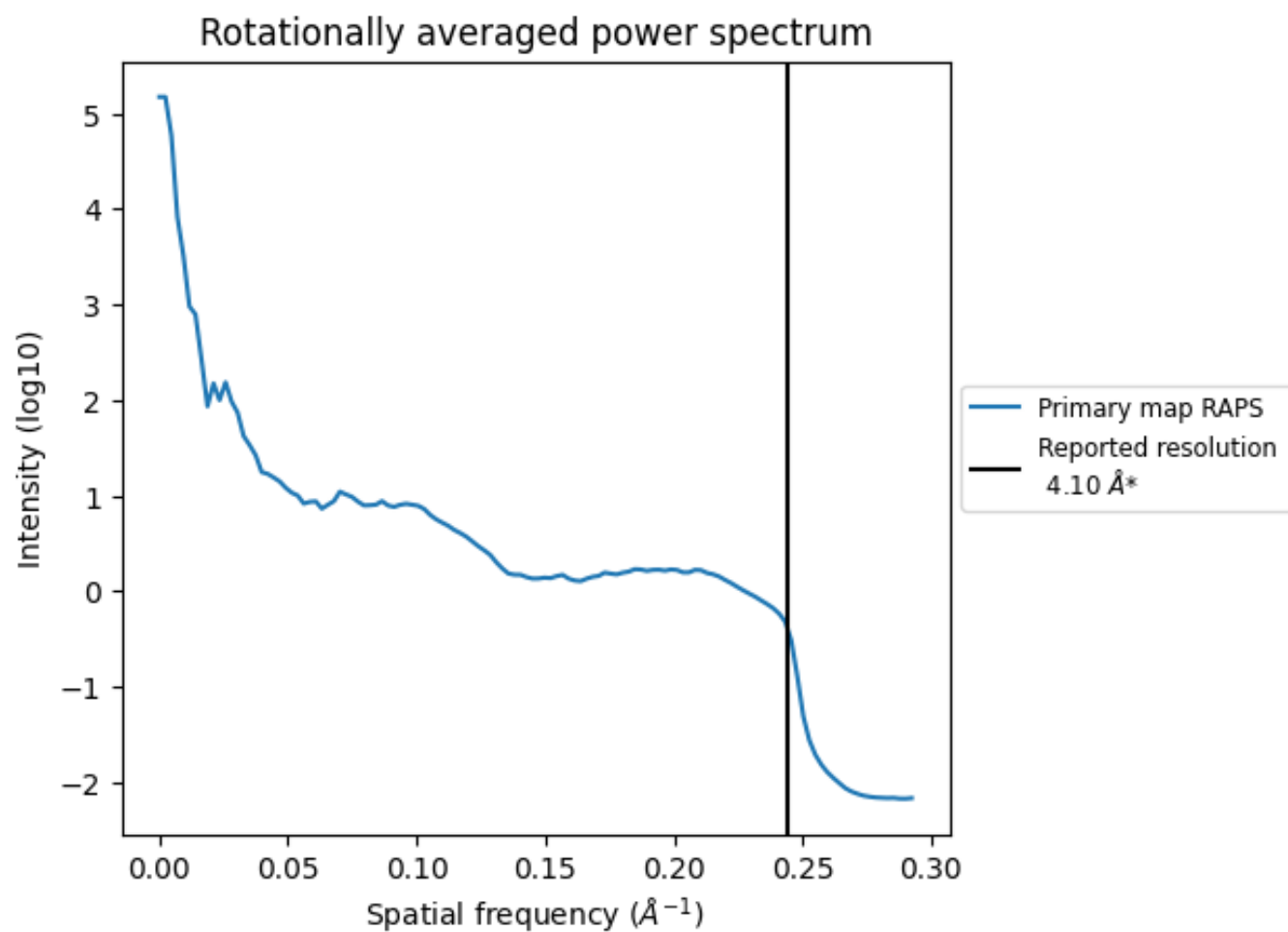
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 715 nm³; this corresponds to an approximate mass of 646 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 0.244 Å⁻¹

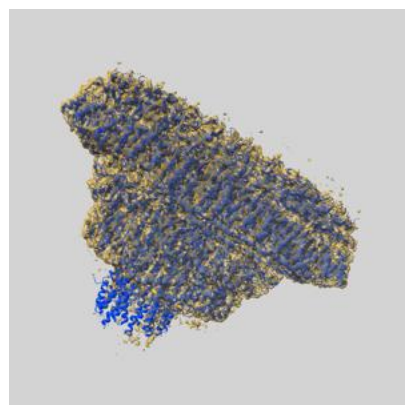
8 Fourier-Shell correlation

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

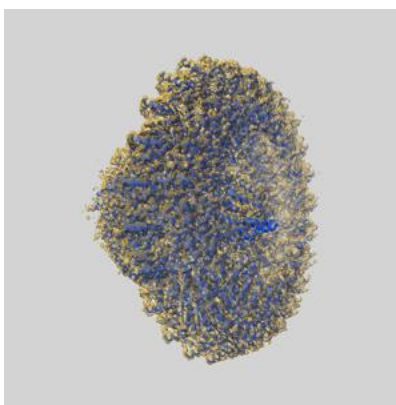
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20556 and PDB model 6Q16. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

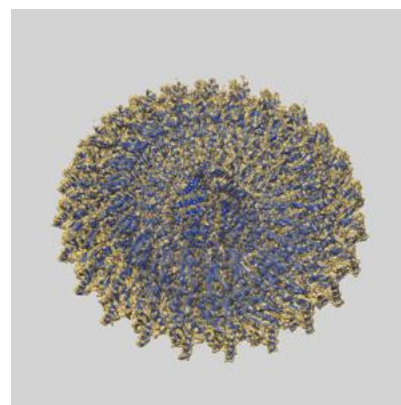
9.1 Map-model overlay [i](#)



X



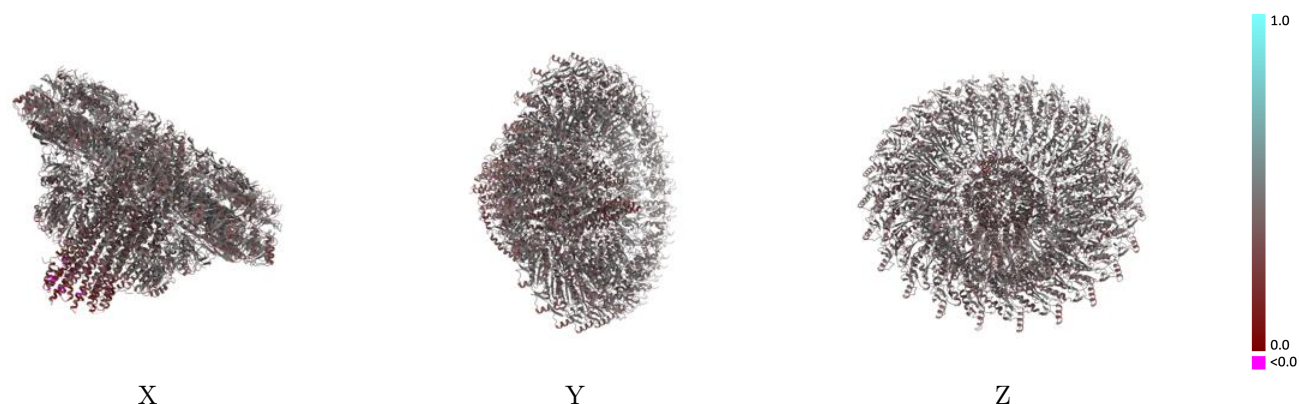
Y



Z

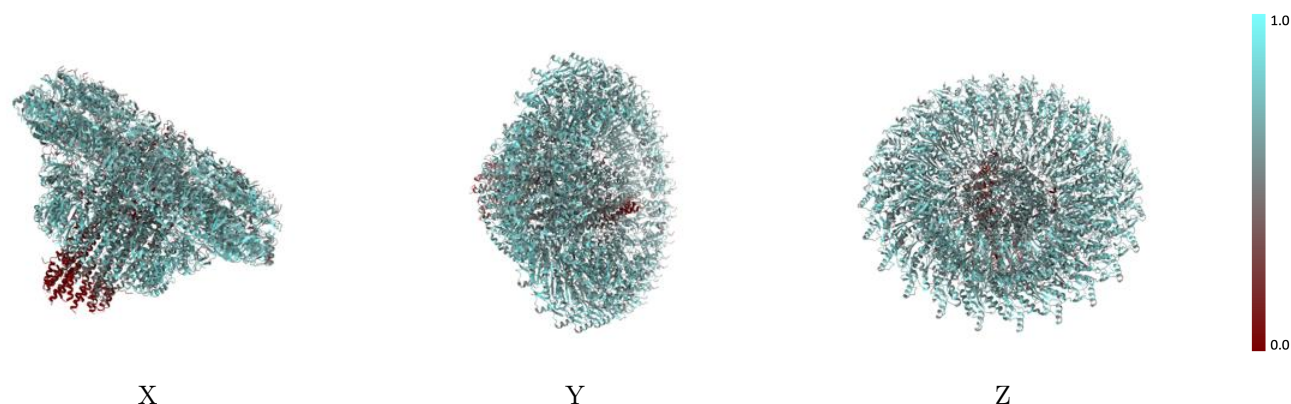
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



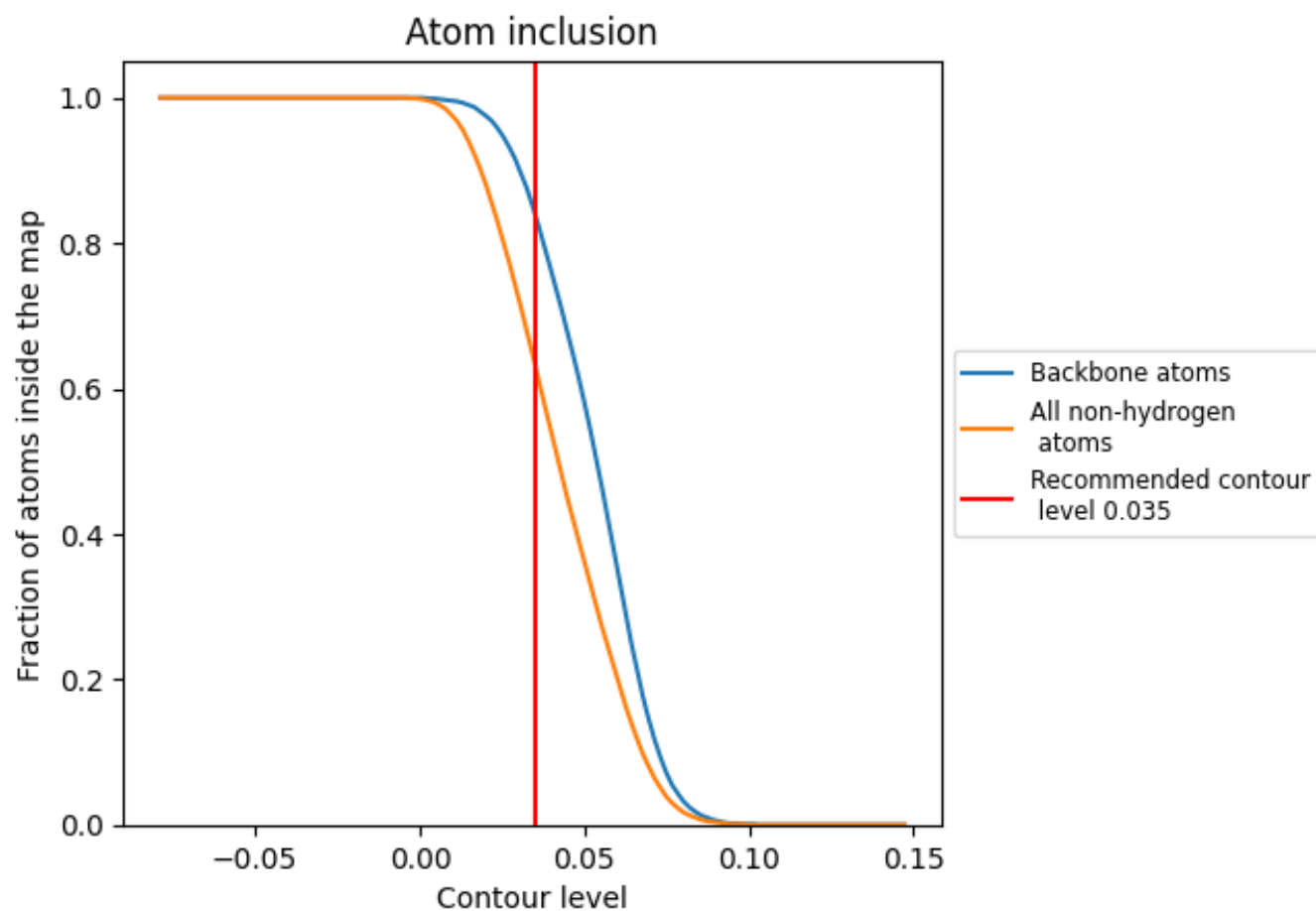
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 63% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6340	 0.4040
0	 0.5530	 0.3700
1	 0.5440	 0.3610
2	 0.5420	 0.3690
3	 0.5660	 0.3750
4	 0.5500	 0.3790
5	 0.6250	 0.4070
6	 0.2590	 0.3530
7	 0.3120	 0.3520
8	 0.4930	 0.3670
9	 0.5500	 0.3760
A	 0.7020	 0.4050
AA	 0.6490	 0.4220
AB	 0.6600	 0.4270
AC	 0.6740	 0.4340
AD	 0.6530	 0.4250
AE	 0.6660	 0.4250
AF	 0.6490	 0.4340
AG	 0.6650	 0.4230
AH	 0.6550	 0.4280
AI	 0.6610	 0.4230
AJ	 0.6460	 0.4260
AK	 0.6520	 0.4200
AL	 0.6710	 0.4290
AM	 0.5000	 0.3590
AN	 0.4840	 0.3490
AO	 0.4990	 0.3630
AP	 0.5130	 0.3510
AQ	 0.5020	 0.3480
AR	 0.4460	 0.3380
AS	 0.4200	 0.3130
AT	 0.4790	 0.2900
AU	 0.4640	 0.3050
AV	 0.4490	 0.2850
AW	 0.3640	 0.2910



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Chain	Atom inclusion	Q-score
AX	 0.0990	 0.2850
AY	 0.2520	 0.2530
AZ	 0.3190	 0.2720
B	 0.6950	 0.4010
BA	 0.3150	 0.2660
BB	 0.2760	 0.2440
BC	 0.0660	 0.2520
BD	 0.0260	 0.2330
BE	 0.0500	 0.1660
C	 0.7160	 0.4140
D	 0.6910	 0.4050
E	 0.6390	 0.3980
F	 0.7000	 0.4120
G	 0.6950	 0.4180
H	 0.7220	 0.4150
I	 0.6920	 0.4060
J	 0.7120	 0.4160
K	 0.6890	 0.4050
L	 0.7250	 0.4150
M	 0.6940	 0.4100
N	 0.7120	 0.4160
O	 0.6950	 0.4080
P	 0.7000	 0.4010
Q	 0.6930	 0.4000
R	 0.6950	 0.4100
S	 0.6930	 0.4120
T	 0.6500	 0.4110
U	 0.6840	 0.4200
V	 0.6810	 0.4160
W	 0.6290	 0.4120
X	 0.6900	 0.4150
Y	 0.6880	 0.4200
Z	 0.6350	 0.4150
a	 0.6790	 0.4200
b	 0.6940	 0.4240
c	 0.6660	 0.4180
d	 0.7110	 0.4240
e	 0.6930	 0.4110
f	 0.6700	 0.4150
g	 0.6890	 0.4160
h	 0.6940	 0.4150
i	 0.6620	 0.4160

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Chain	Atom inclusion	Q-score
j	 0.6930	 0.4180
k	 0.6980	 0.4150
l	 0.6540	 0.4130
m	 0.6910	 0.4140
n	 0.7010	 0.4220
o	 0.6520	 0.4300
p	 0.6420	 0.4230
q	 0.6450	 0.4220
r	 0.6410	 0.4270
s	 0.6340	 0.4220
t	 0.6320	 0.4230
u	 0.6380	 0.4220
v	 0.6290	 0.4140
w	 0.6410	 0.4230
x	 0.6620	 0.4300
y	 0.6620	 0.4170
z	 0.6540	 0.4280