wwPDB EM Validation Summary Report

Oct 26, 2024 – 07:35 PM EDT

PDB ID	:	6Q16
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:

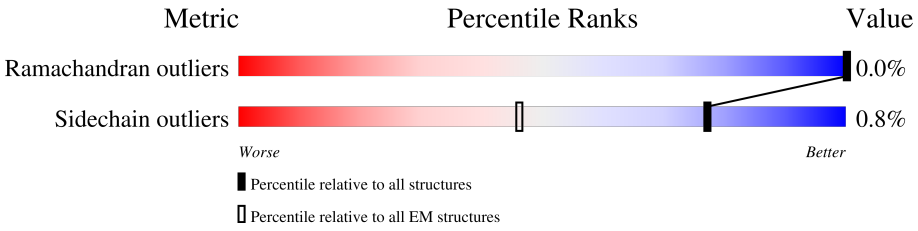
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	7% 72% • 27%
1	AB	252	7% 73% 27%
1	AC	252	5% 73% 27%
1	AD	252	6% 73% 27%
1	AE	252	6% 72% • 27%
1	AF	252	8% 73% 27%
1	AG	252	6% 73% 27%
1	AH	252	6% 73% 27%
1	AI	252	6% 72% • 27%

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Mol	Chain	Length	Quality of chain
1	AJ	252	8% 72% 27%
1	AK	252	6% 73% 27%
1	AL	252	7% 73% 27%
1	o	252	8% 72% 27%
1	p	252	8% 73% 27%
1	q	252	8% 72% 27%
1	r	252	9% 73% 27%
1	s	252	7% 73% 27%
1	t	252	8% 72% 27%
1	u	252	6% 73% 27%
1	v	252	8% 71% 27%
1	w	252	6% 72% 27%
1	x	252	5% 73% 27%
1	y	252	5% 72% 27%
1	z	252	6% 72% 27%
2	A	562	24% 75%
2	B	562	25% 74%
2	C	562	25% 75%
2	D	562	25% 74%
2	F	562	25% 75%
2	G	562	25% 74%
2	H	562	24% 75%
2	I	562	25% 74%
2	J	562	25% 75%
2	K	562	25% 74%

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Mol	Chain	Length	Quality of chain
2	L	562	25% 75%
2	M	562	25% 74%
2	N	562	25% 75%
2	O	562	25% 74%
2	P	562	25% 75%
2	Q	562	25% 74%
3	E	392	6% 56% 43%
3	R	392	56% 44%
3	S	392	56% 43%
3	T	392	5% 57% 43%
3	U	392	56% 44%
3	V	392	56% 43%
3	W	392	6% 56% 43%
3	X	392	55% 44%
3	Y	392	56% 43%
3	Z	392	7% 57% 43%
3	a	392	56% 44%
3	b	392	56% 43%
3	c	392	56% 43%
3	d	392	56% 44%
3	e	392	5% 56% 43%
3	f	392	5% 57% 43%
3	g	392	56% 44%
3	h	392	56% 43%
3	i	392	5% 56% 43%

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Mol	Chain	Length	Quality of chain
3	j	392	56% 44%
3	k	392	56% 43%
3	l	392	5% 56% 43%
3	m	392	56% 44%
3	n	392	56% 43%
4	0	224	17% 88% 11%
4	1	224	15% 88% 11%
4	2	224	17% 87% 12%
4	3	224	17% 91% 9%
4	4	224	18% 98%
5	5	263	8% 93% 6%
6	6	86	47% 62% 38%
6	7	86	64% 98%
6	8	86	26% 94%
6	9	86	20% 98%
7	AM	101	15% 38% 61%
7	AN	101	22% 77% 23%
7	AO	101	24% 86% 13%
7	AP	101	21% 86% 12%
7	AQ	101	25% 86% 12%
7	AR	101	33% 87% 13%
8	AS	80	35% 70% 26%
8	AT	80	25% 66% 8% 26%
8	AU	80	28% 66% 8% 26%
8	AV	80	28% 69% 5% 26%

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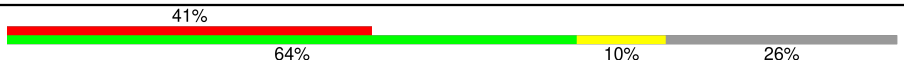
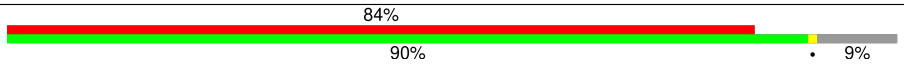
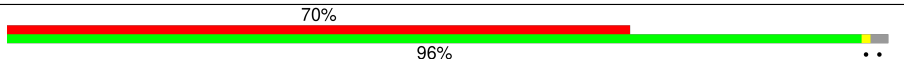
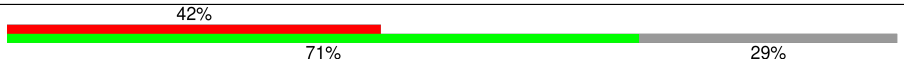
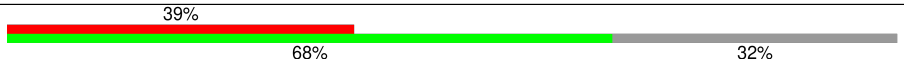
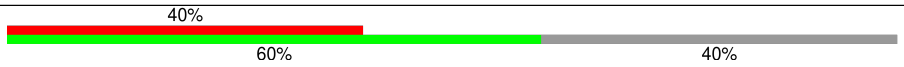
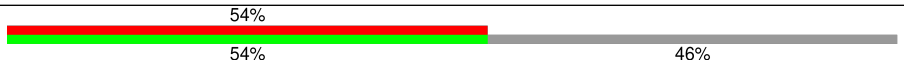
Mol	Chain	Length	Quality of chain
8	AW	80	
8	AX	80	
8	AY	80	
8	AZ	80	
8	BA	80	
8	BB	80	
8	BC	80	
8	BD	80	
8	BE	80	

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

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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 Protein InvG.

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

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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 405	C 276	N 61	O 67	S 1	0	0
6	7	84	Total 644	C 436	N 97	O 109	S 2	0	0
6	8	84	Total 644	C 436	N 97	O 109	S 2	0	0
6	9	84	Total 647	C 438	N 97	O 109	S 3	0	0

- Molecule 7 is a protein called Protein PrgJ.

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

- Molecule 8 is a protein called Protein PrgI.

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

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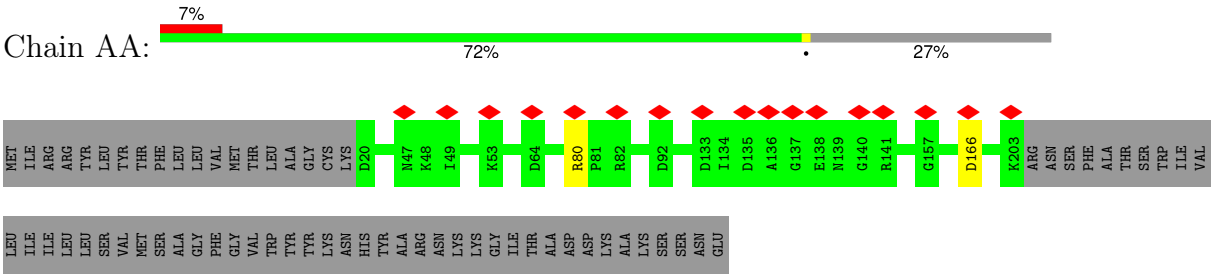
Mol	Chain	Residues	Atoms				AltConf	Trace
8	BA	54	Total 437	C 275	N 73	O 89	0	0
8	BB	48	Total 388	C 247	N 64	O 77	0	0
8	BC	48	Total 388	C 247	N 64	O 77	0	0
8	BD	48	Total 388	C 247	N 64	O 77	0	0
8	BE	43	Total 346	C 219	N 59	O 68	0	0

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.

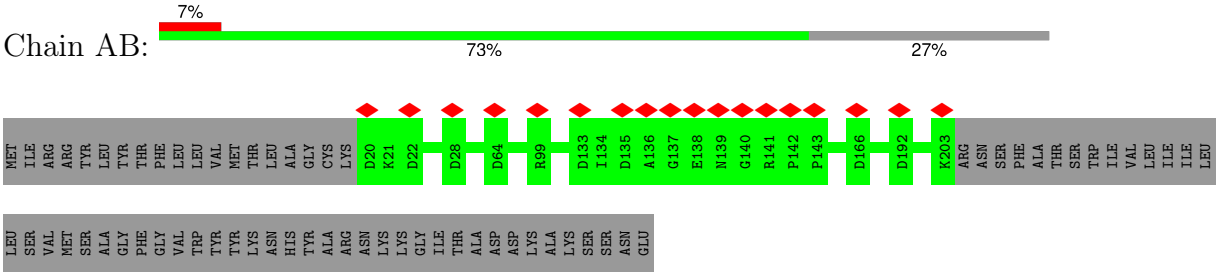
• Molecule 1: Lipoprotein PrgK

Chain AA:



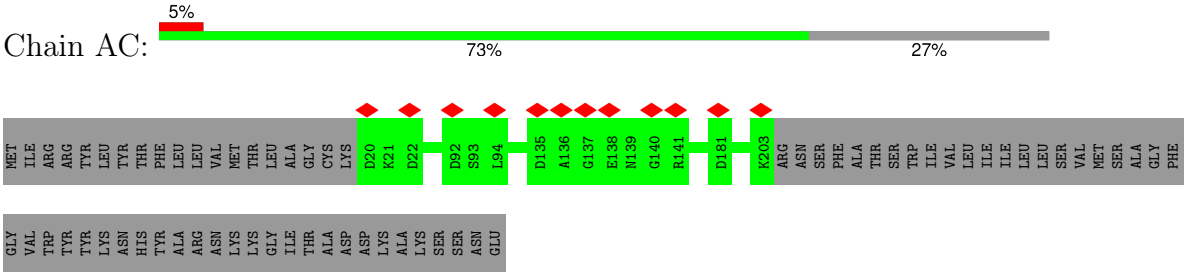
• Molecule 1: Lipoprotein PrgK

Chain AB:



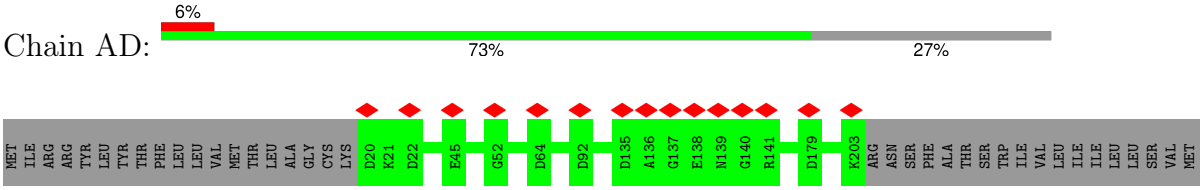
• Molecule 1: Lipoprotein PrgK

Chain AC:



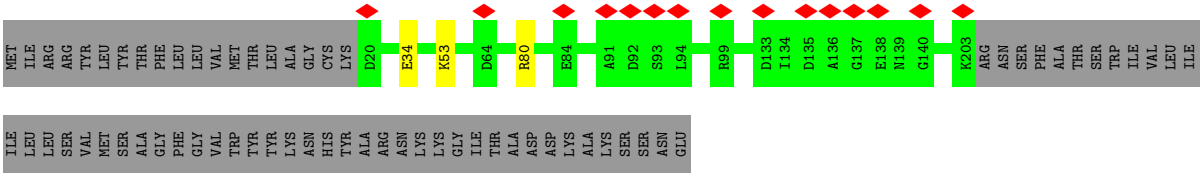
• Molecule 1: Lipoprotein PrgK

Chain AD:



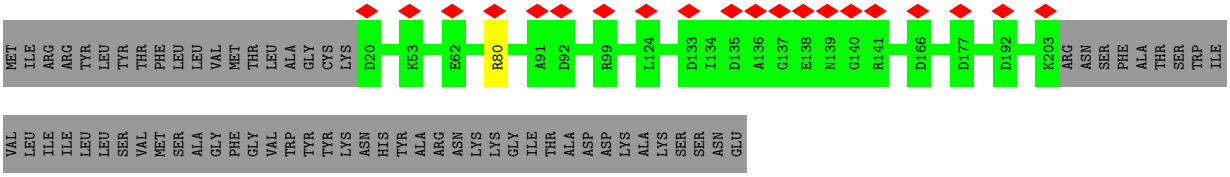
• Molecule 1: Lipoprotein PrgK

Chain AE:



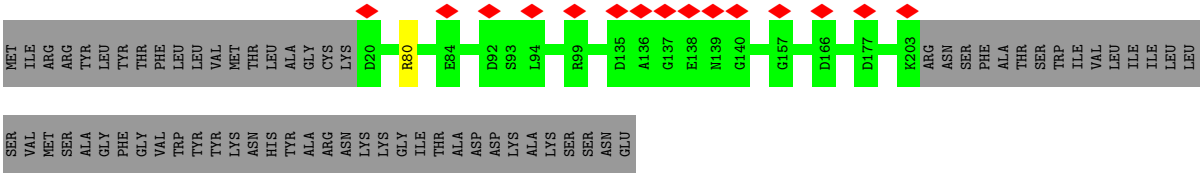
• Molecule 1: Lipoprotein PrgK

Chain AF:



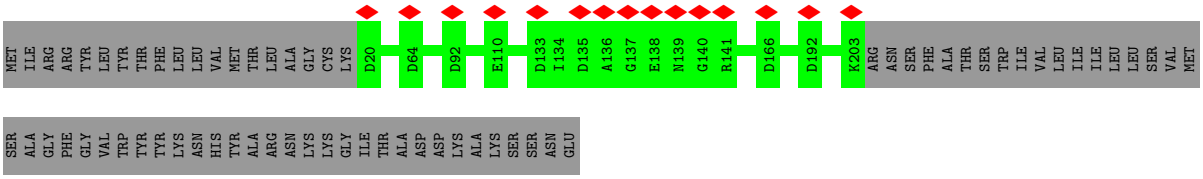
• Molecule 1: Lipoprotein PrgK

Chain AG:



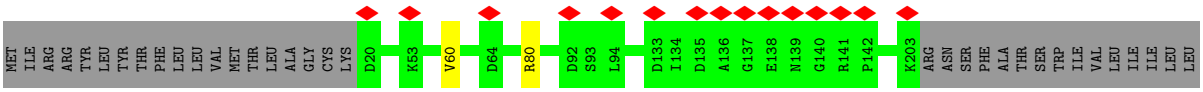
• Molecule 1: Lipoprotein PrgK

Chain AH:

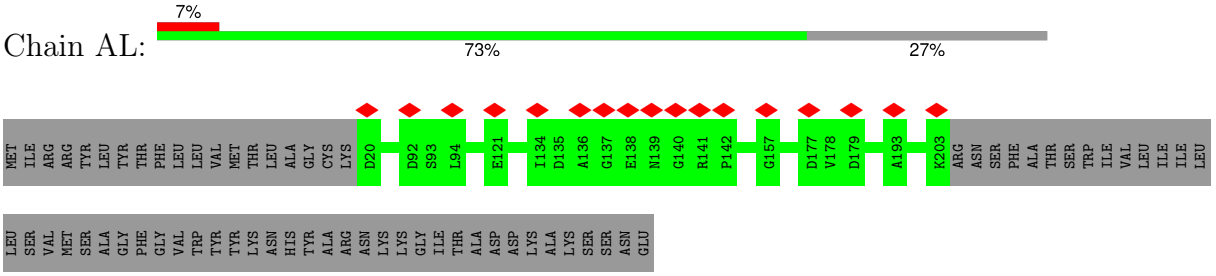


• Molecule 1: Lipoprotein PrgK

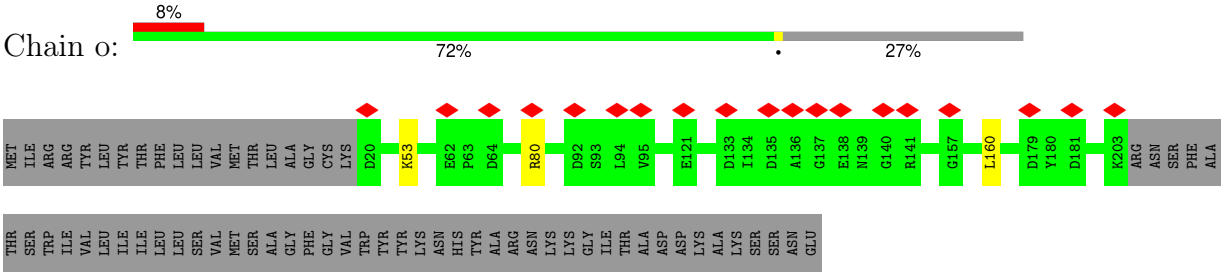
Chain AI:



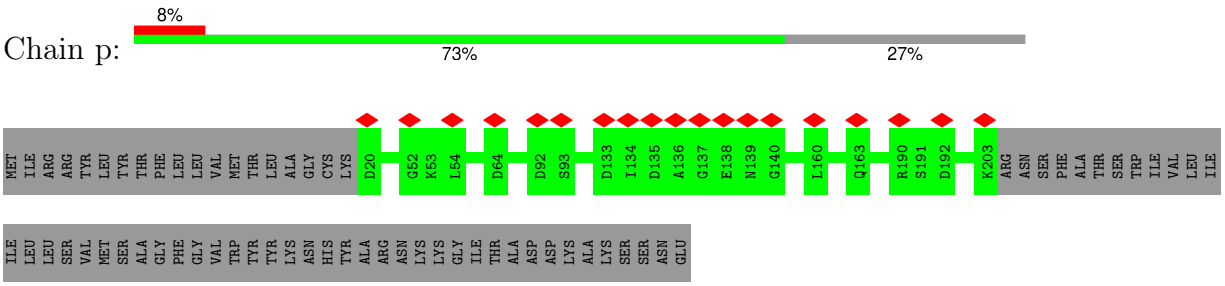
• Molecule 1: Lipoprotein PrgK



• Molecule 1: Lipoprotein PrgK



• Molecule 1: Lipoprotein PrgK



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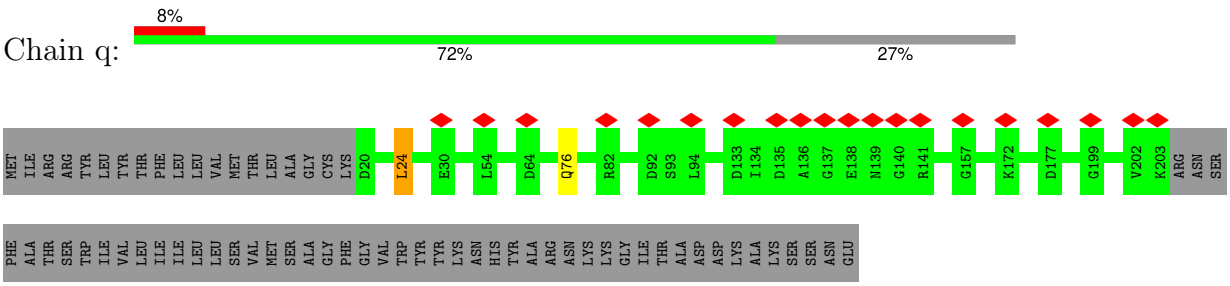
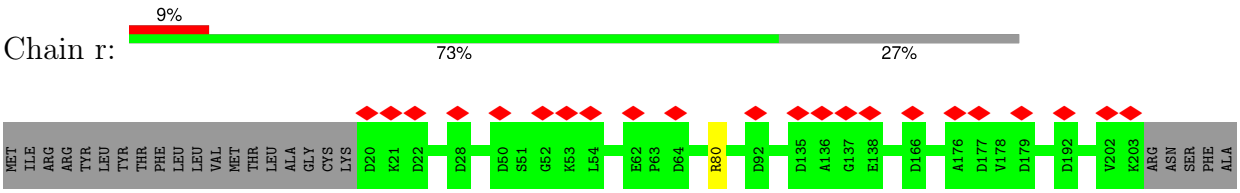


• Molecule 1: Lipoprotein PrgK



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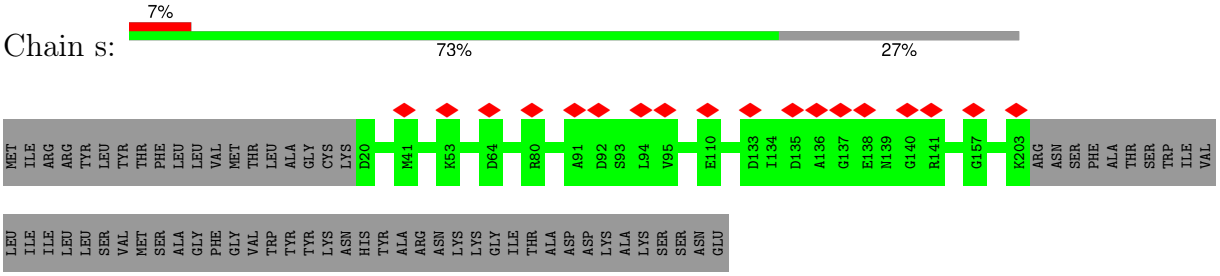
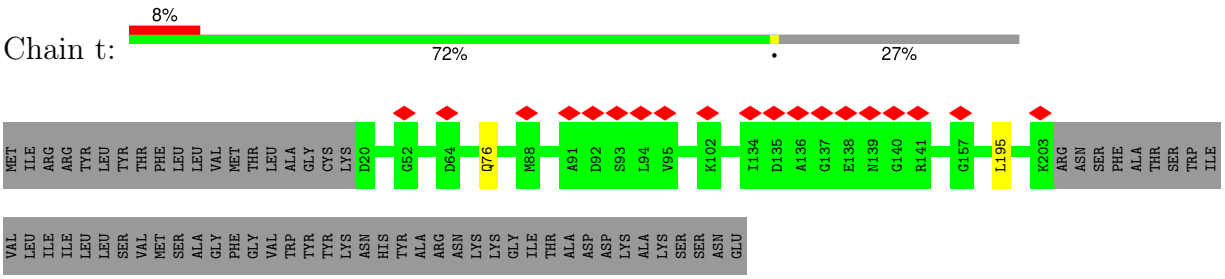
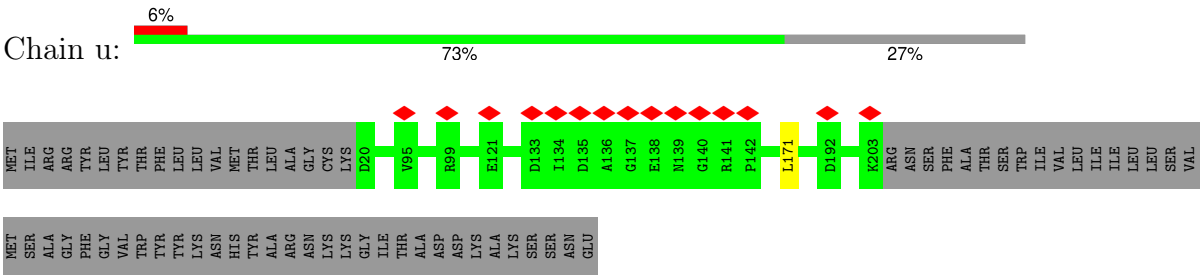


• Molecule 1: Lipoprotein PrgK



• Molecule 1: Lipoprotein PrgK



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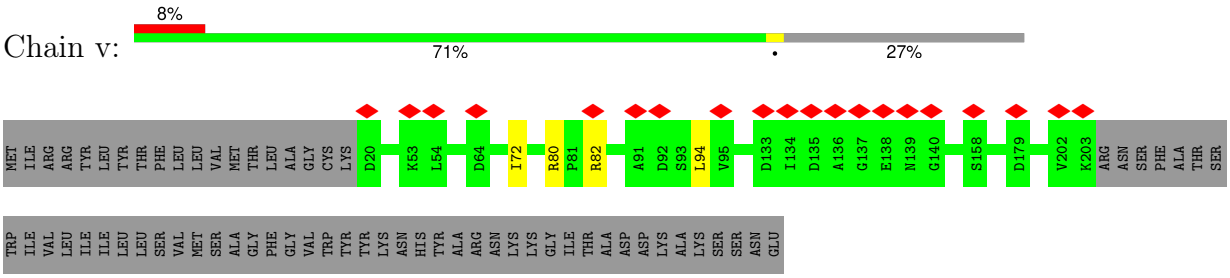
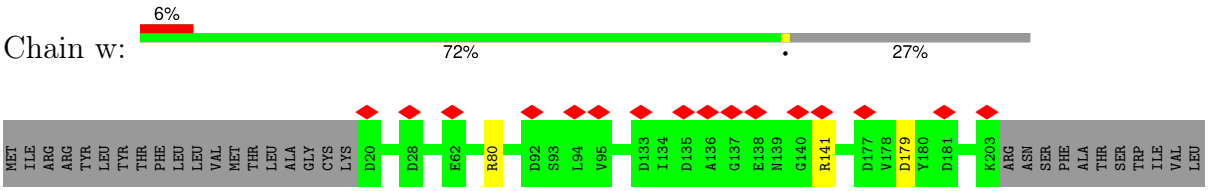
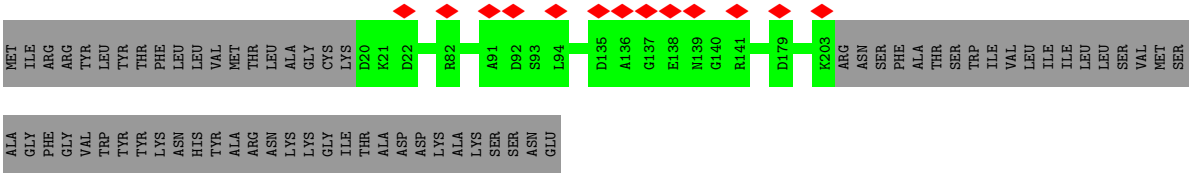


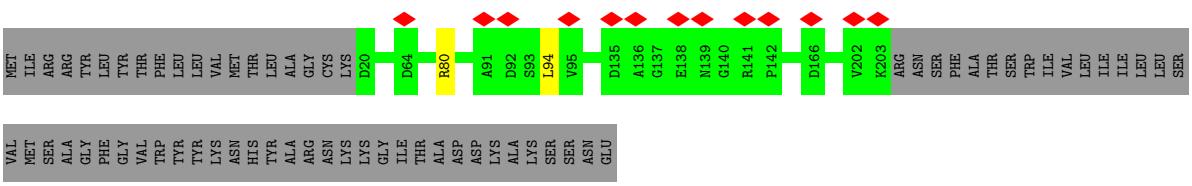
• Molecule 1: Lipoprotein PrgK



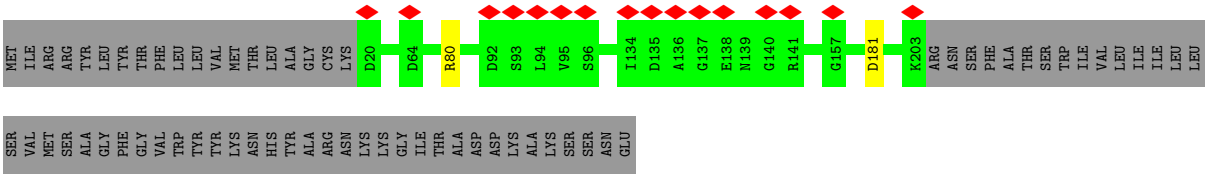
• Molecule 1: Lipoprotein PrgK



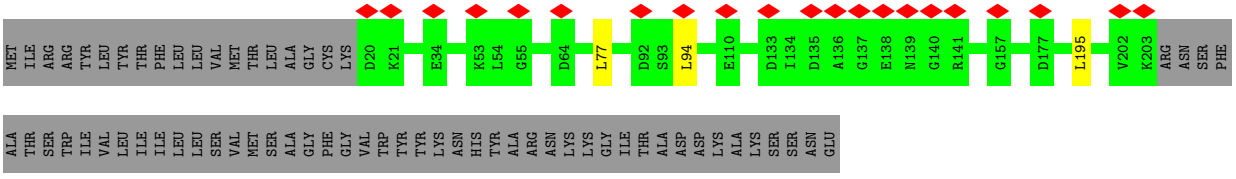
• Molecule 1: Lipoprotein PrgK



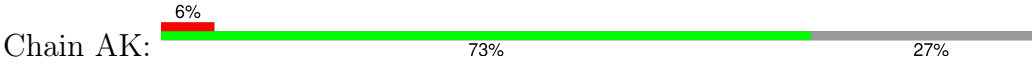
• Molecule 1: Lipoprotein PrgK

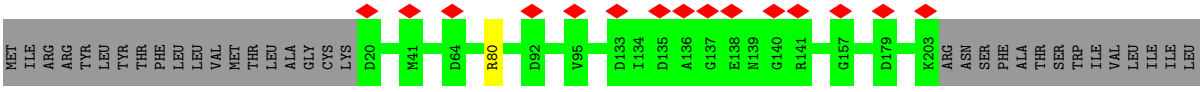


• Molecule 1: Lipoprotein PrgK



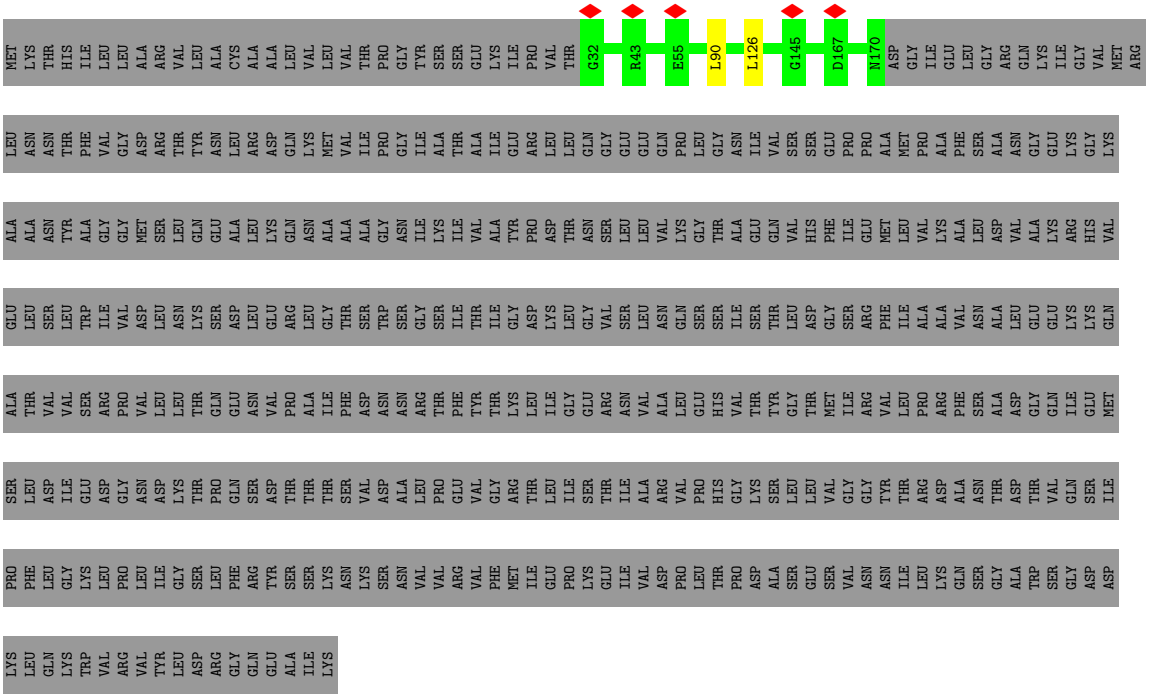
• Molecule 1: Lipoprotein PrgK





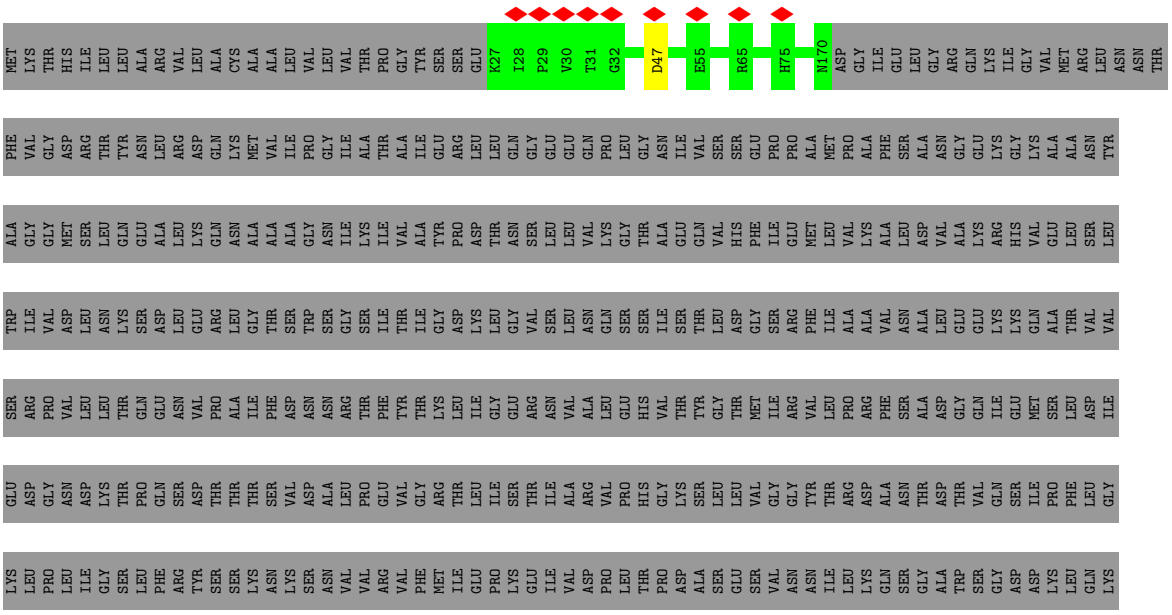
• Molecule 2: Protein InvG

Chain A:



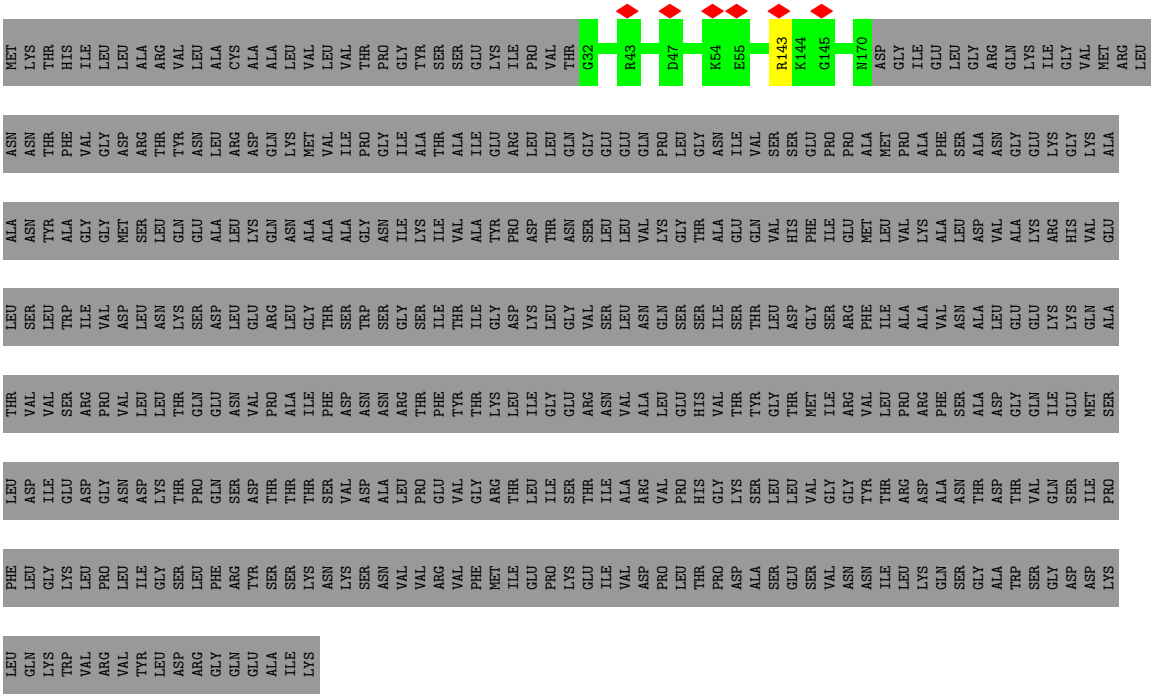
• Molecule 2: Protein InvG

Chain B:



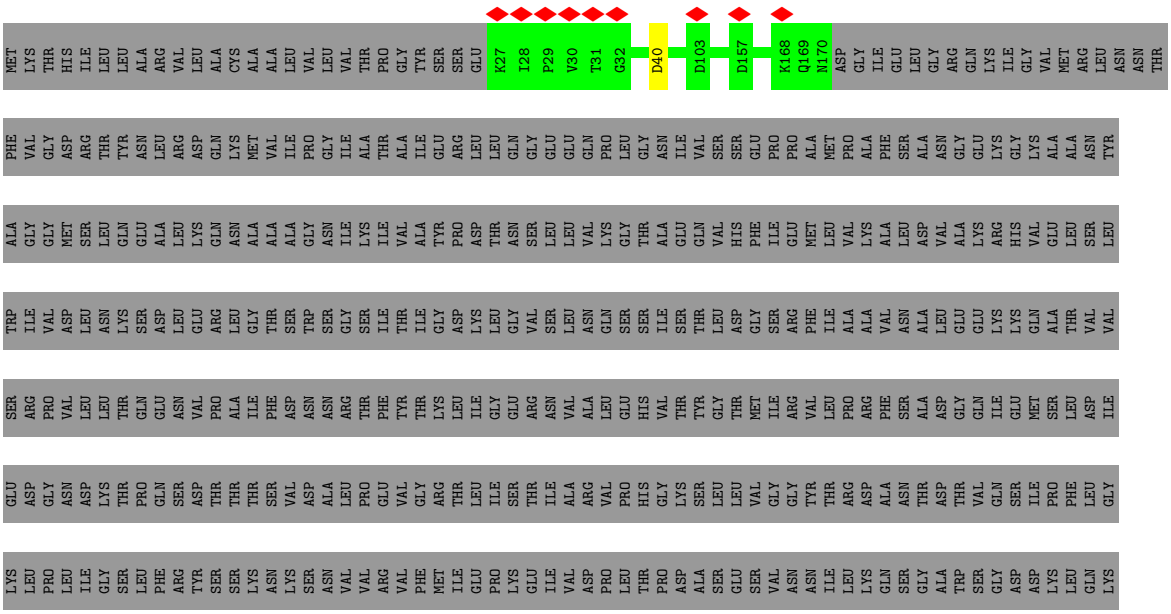
• Molecule 2: Protein InvG

Chain C:



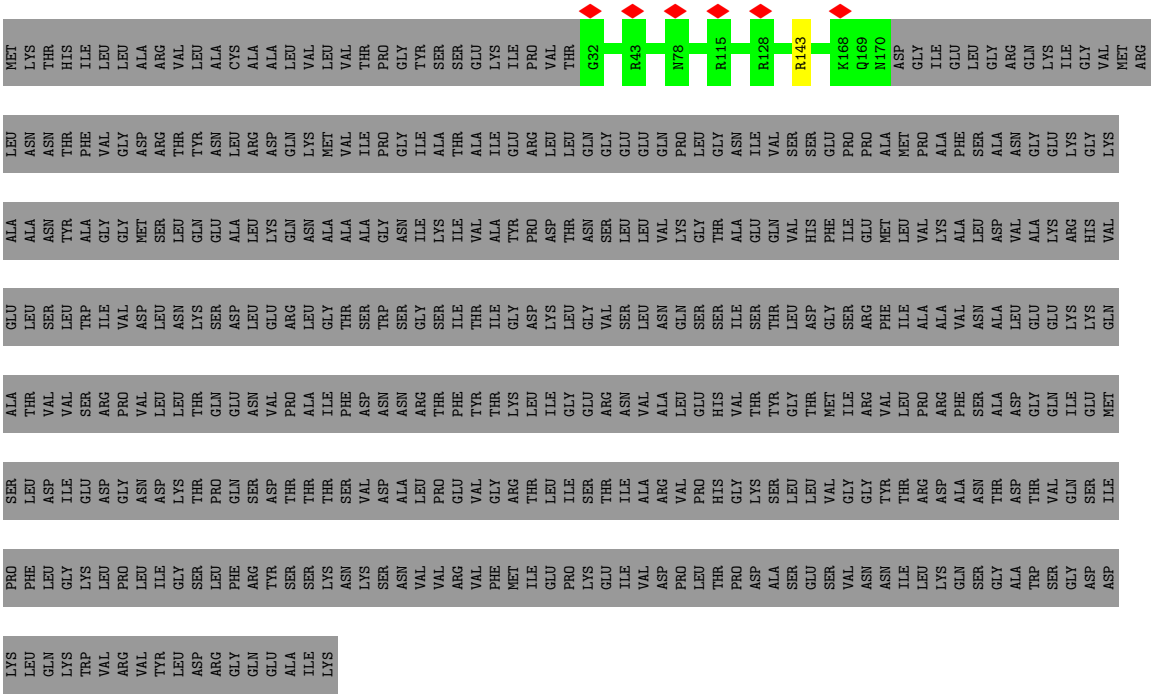
• Molecule 2: Protein InvG

Chain D:



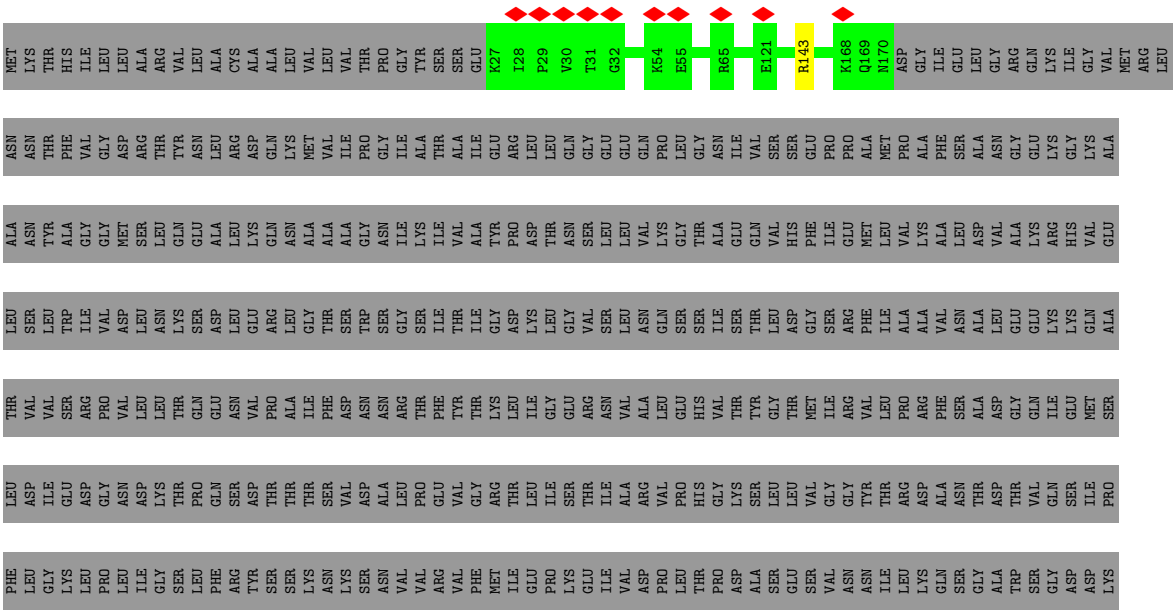
• Molecule 2: Protein InvG

Chain F:



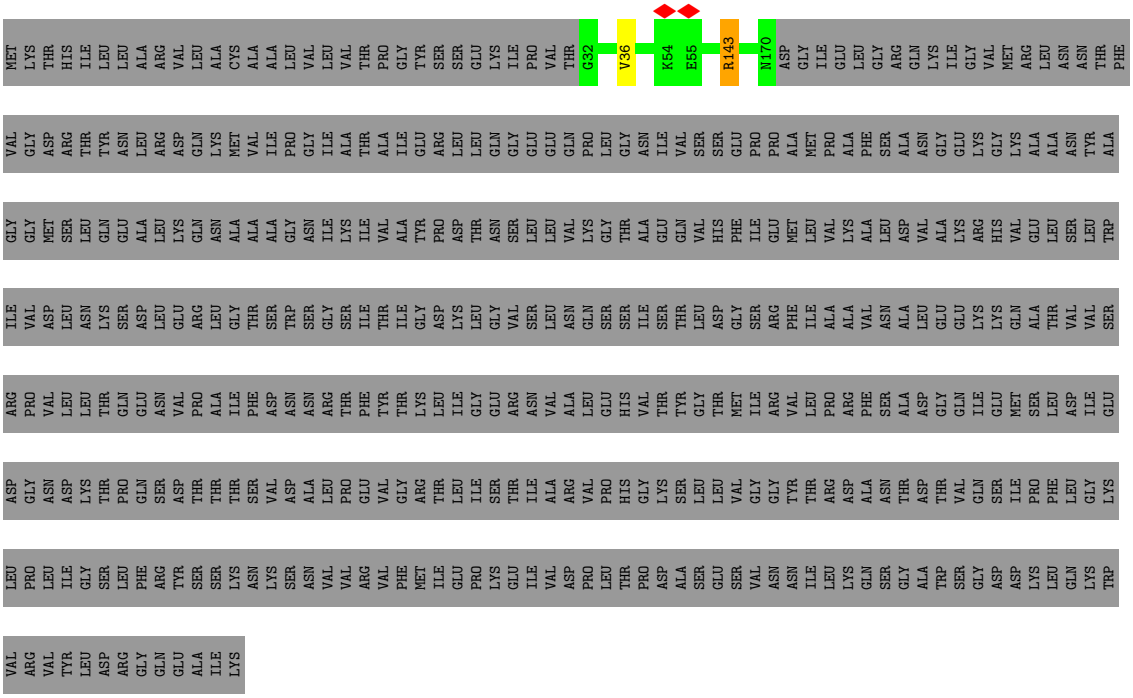
• Molecule 2: Protein InvG

Chain G:



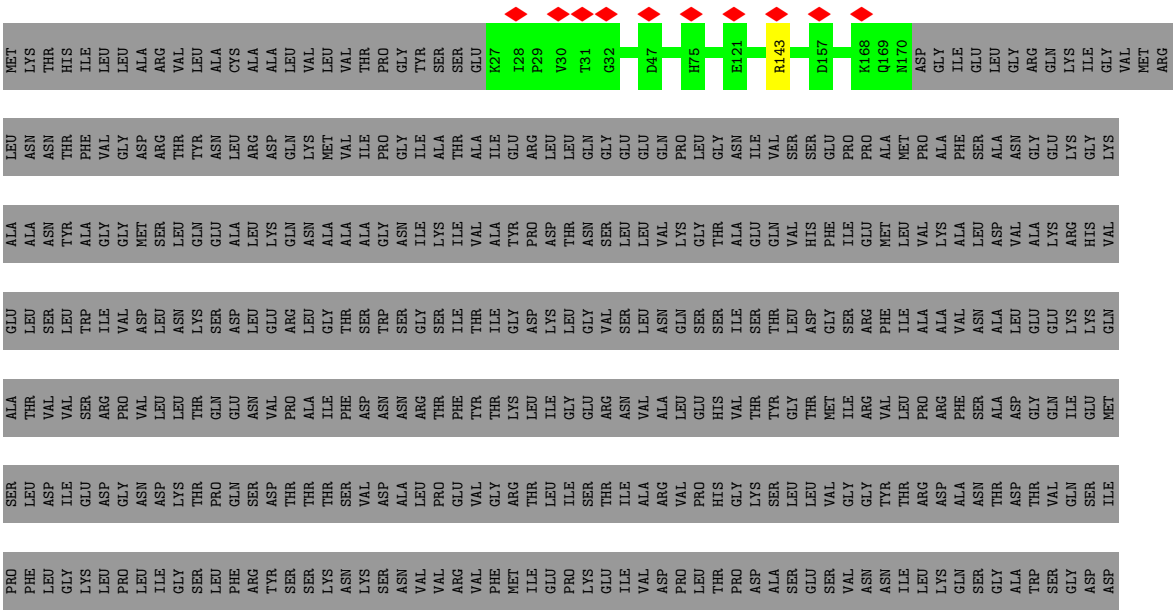
• Molecule 2: Protein InvG

Chain H:



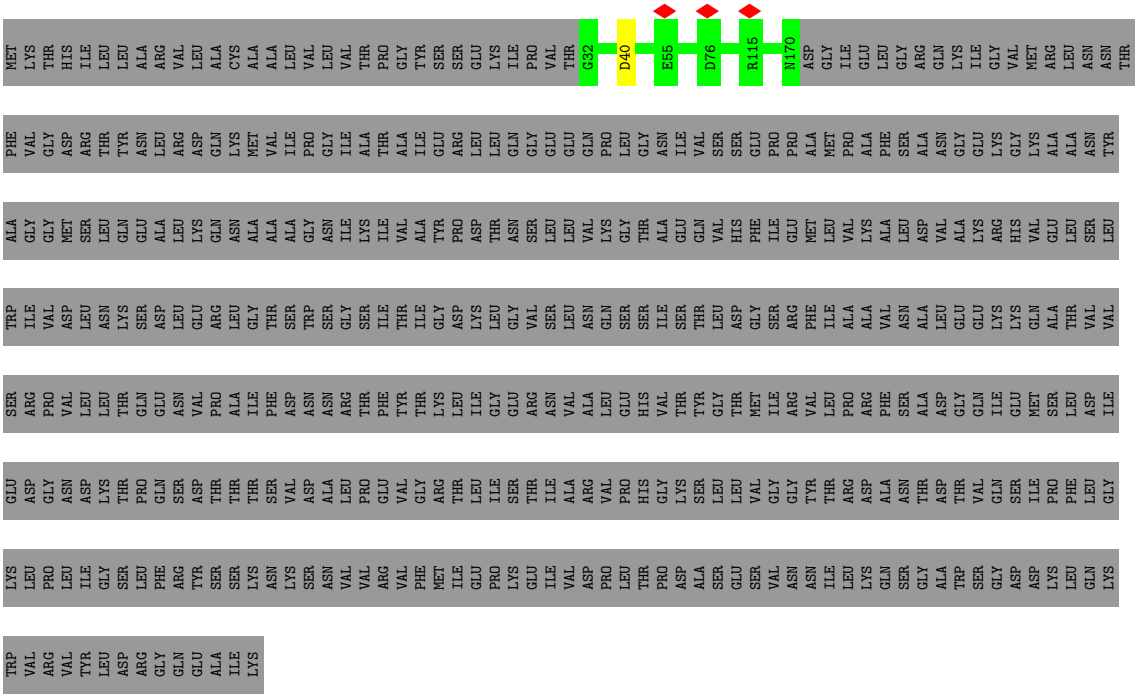
• Molecule 2: Protein InvG

Chain I:



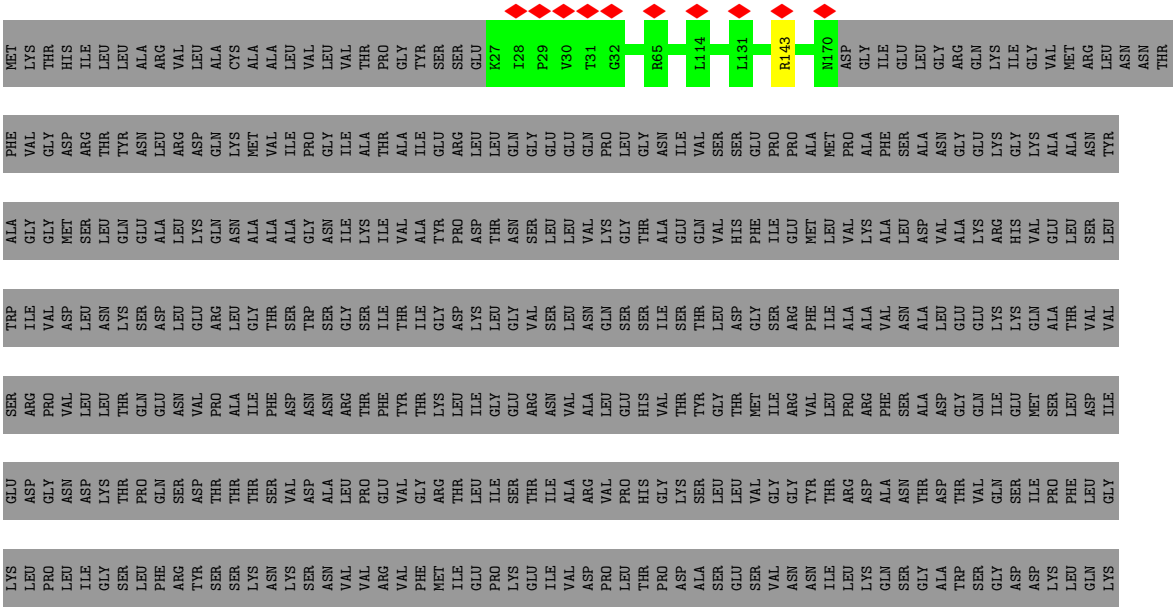
• Molecule 2: Protein InvG

Chain J:



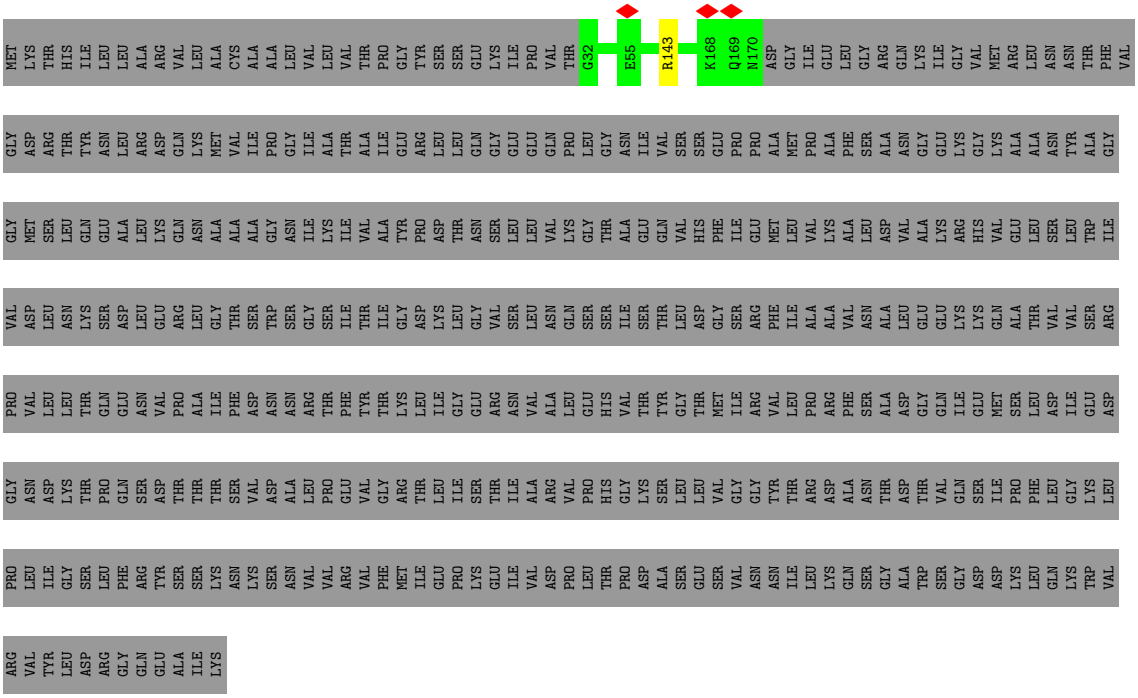
• Molecule 2: Protein InvG

Chain K:



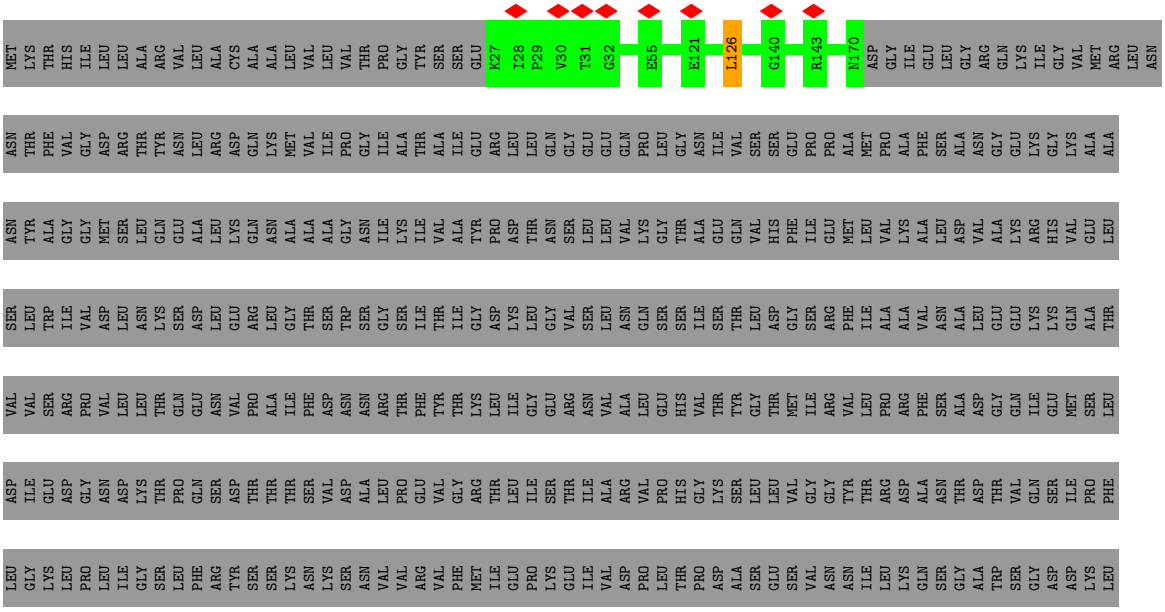
• Molecule 2: Protein InvG

Chain L:



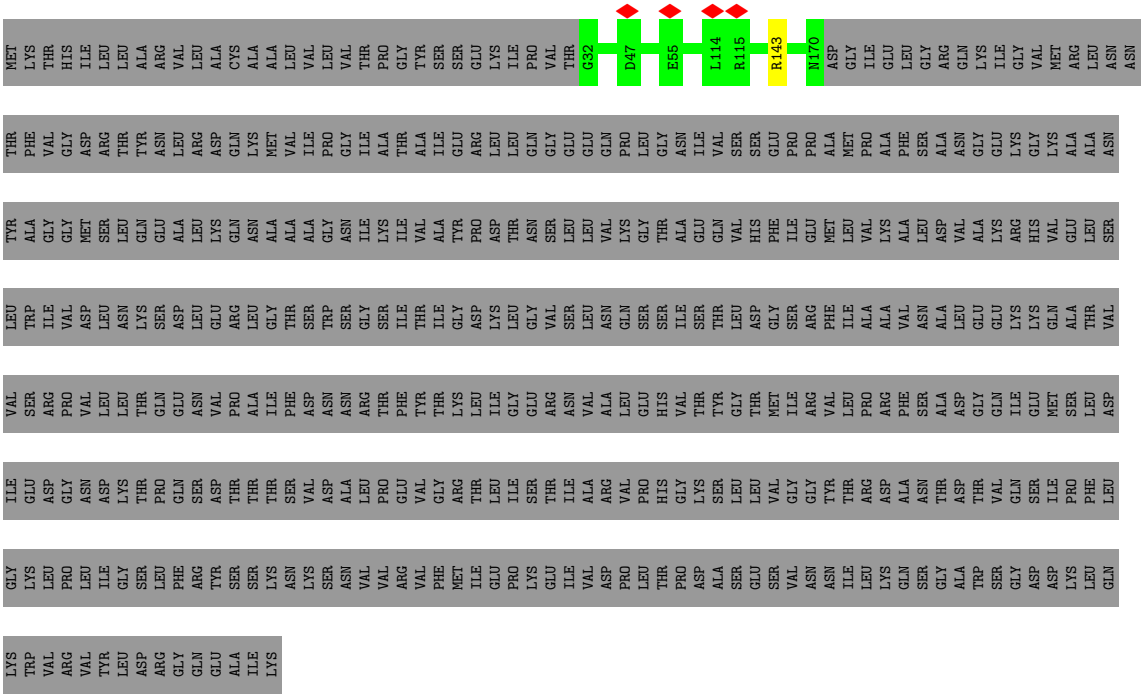
• Molecule 2: Protein InvG

Chain M:



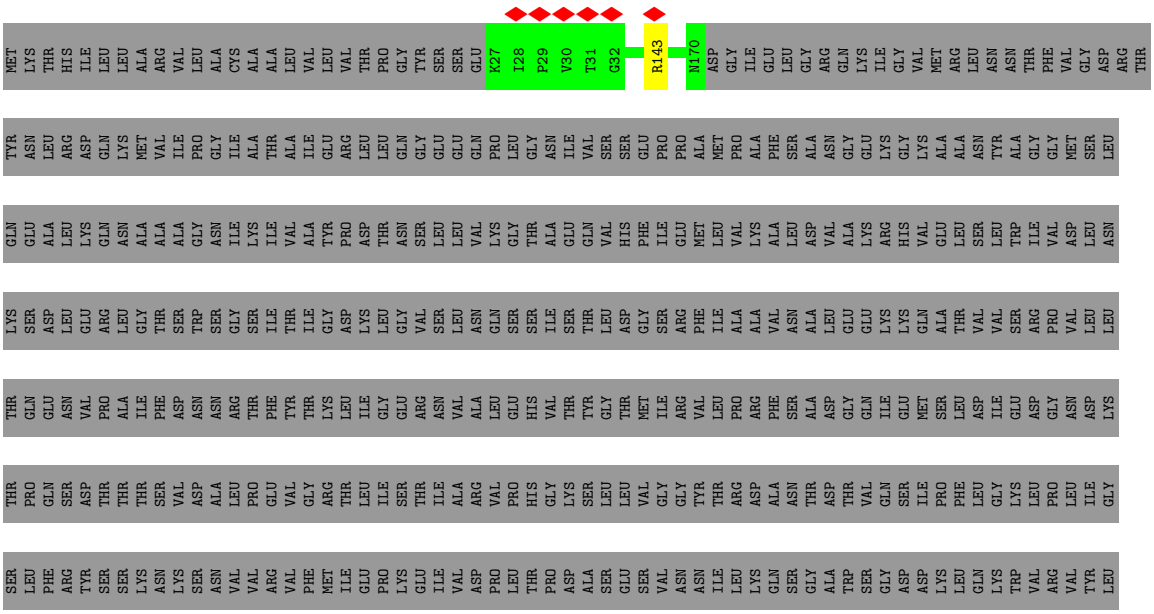
• Molecule 2: Protein InvG

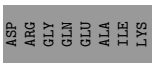
Chain N:



• Molecule 2: Protein InvG

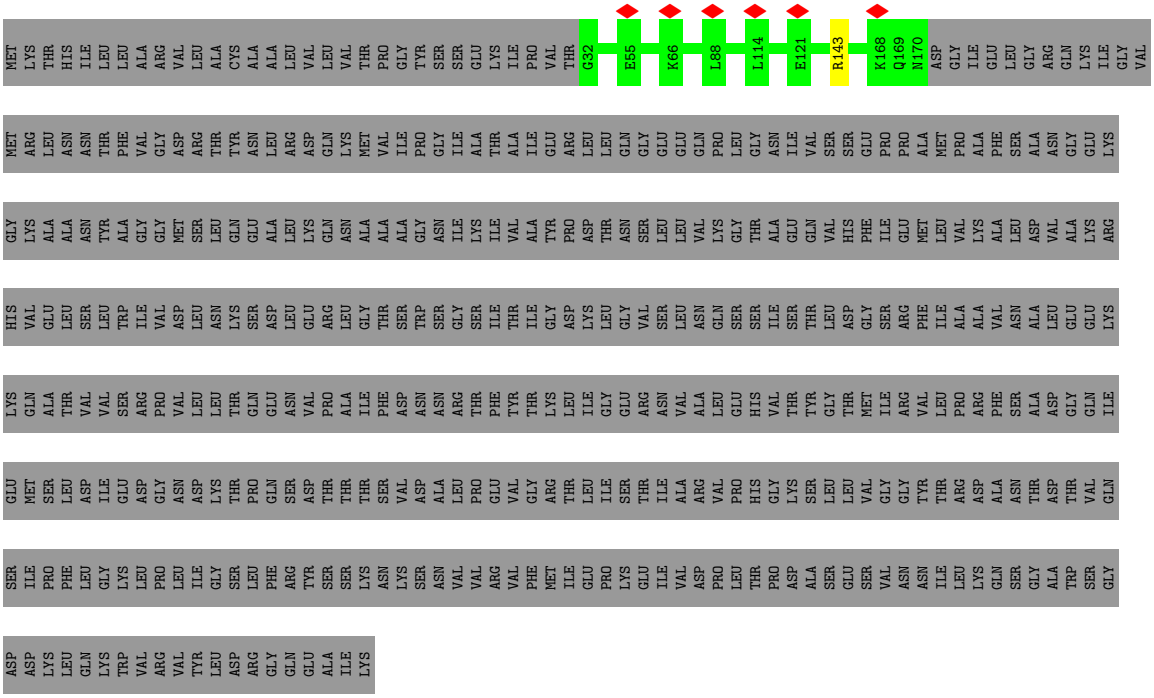
Chain O:





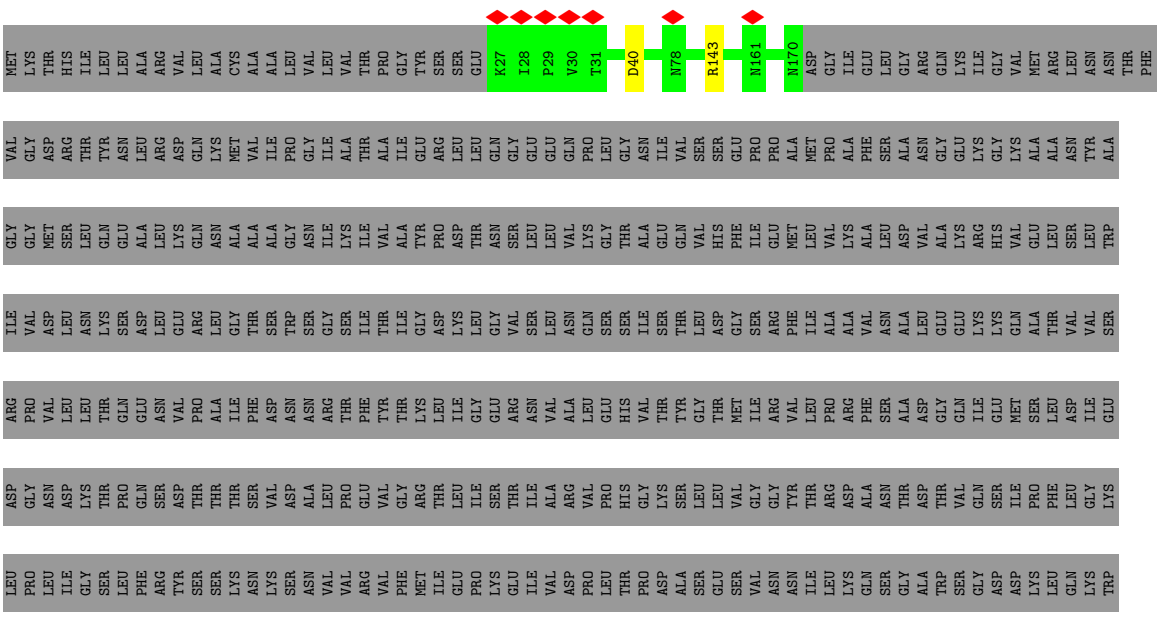
• Molecule 2: Protein InvG

Chain P:



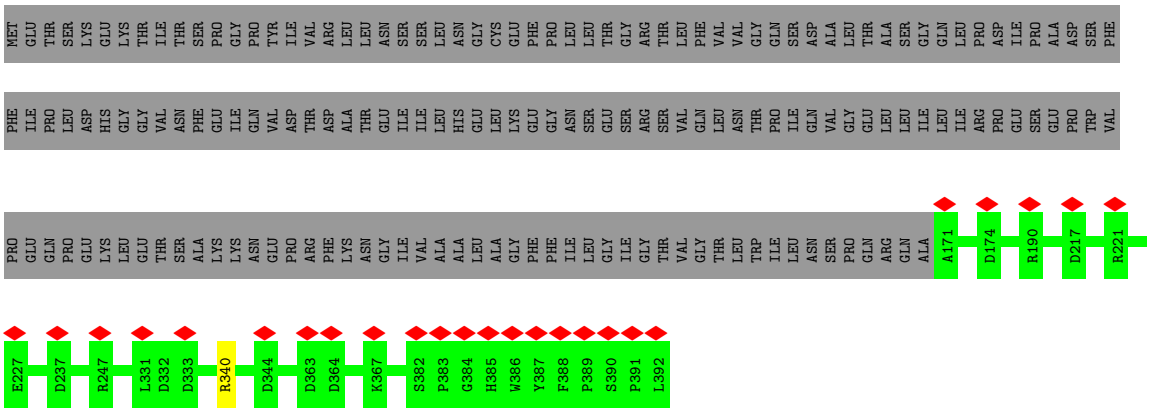
• Molecule 2: Protein InvG

Chain Q:



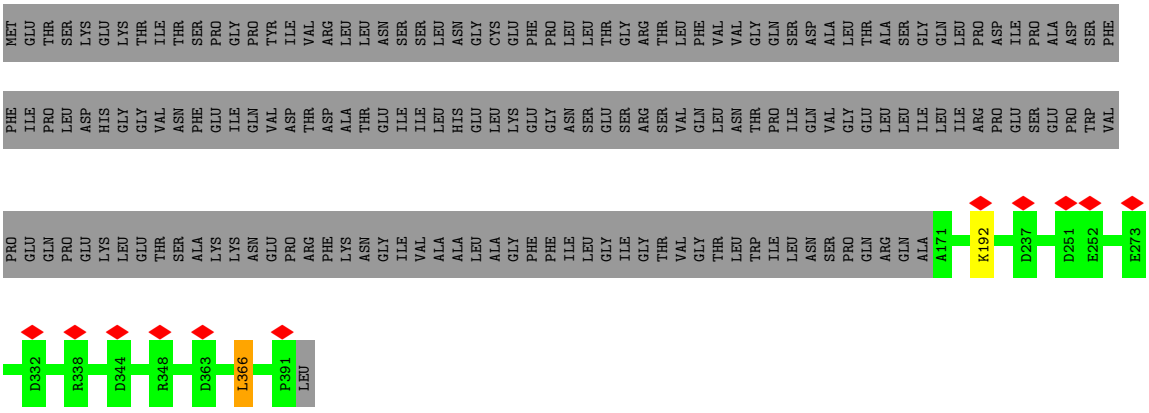
• Molecule 3: Protein PrgH

Chain E:



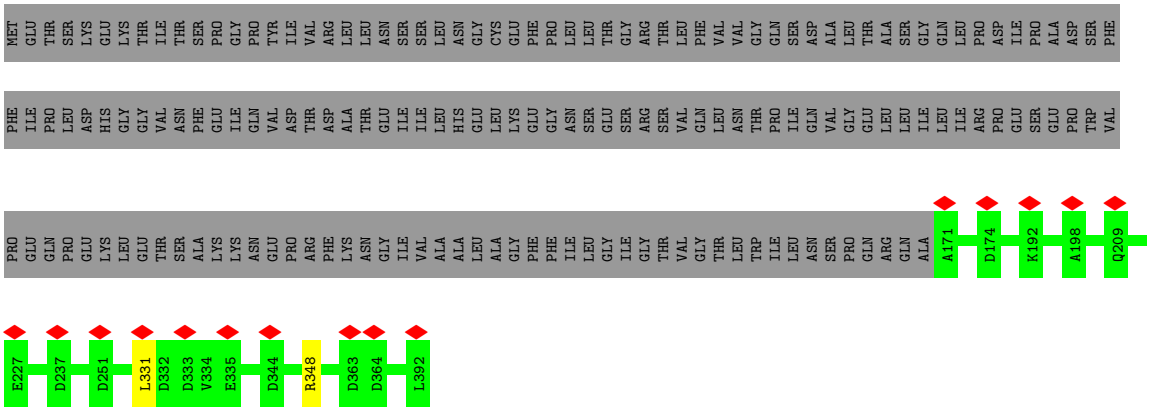
• Molecule 3: Protein PrgH

Chain R:



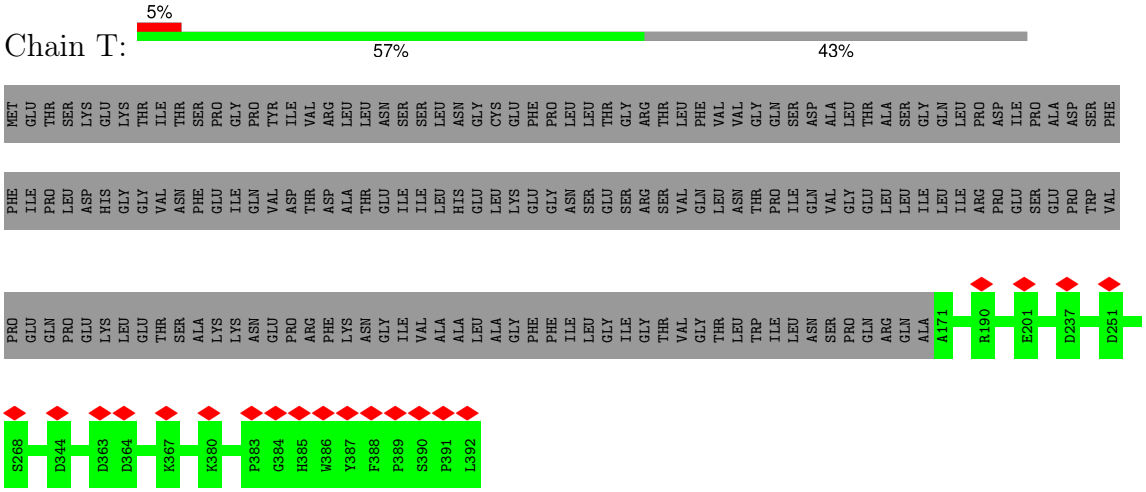
• Molecule 3: Protein PrgH

Chain S:



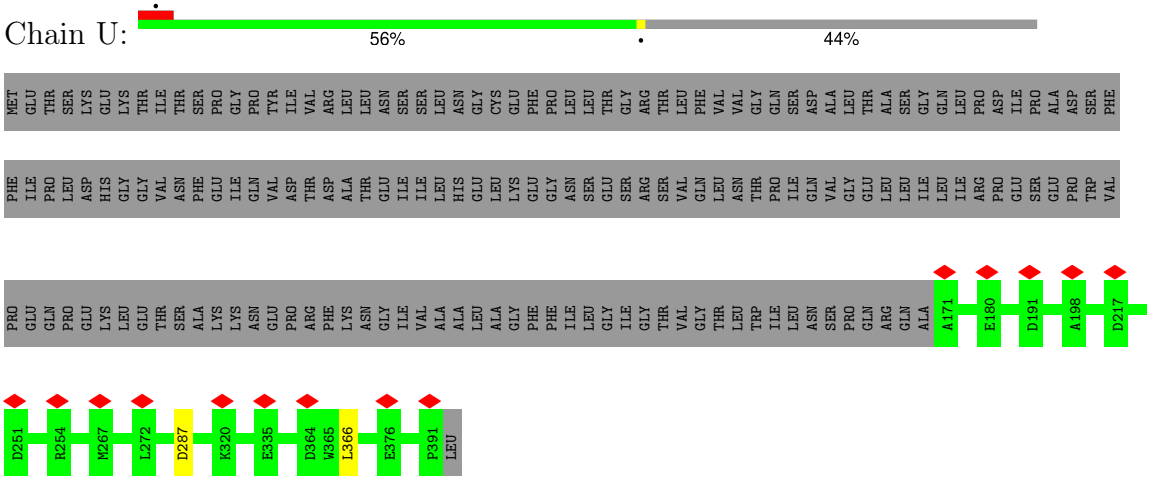
• Molecule 3: Protein PrgH

Chain T:



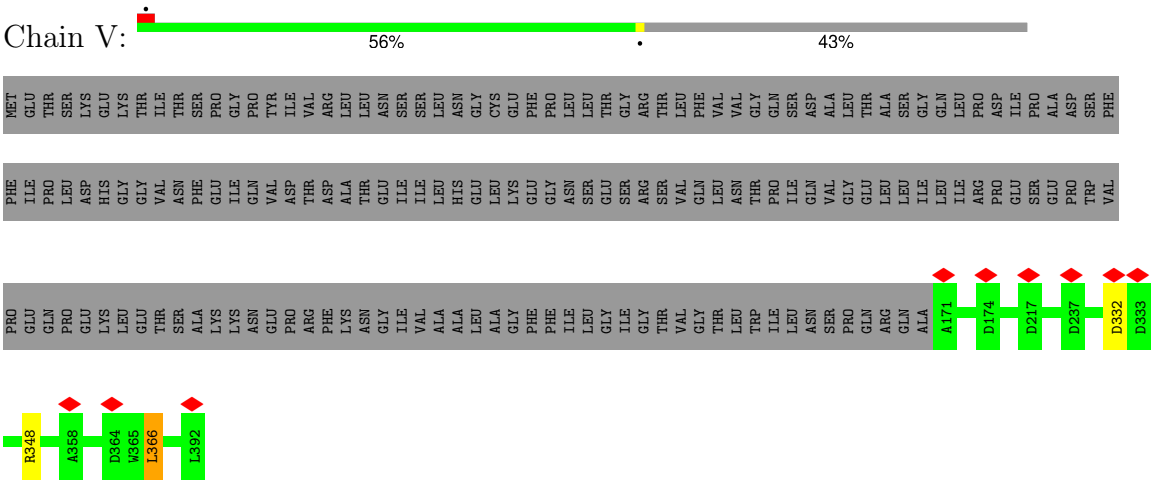
• Molecule 3: Protein PrgH

Chain U:



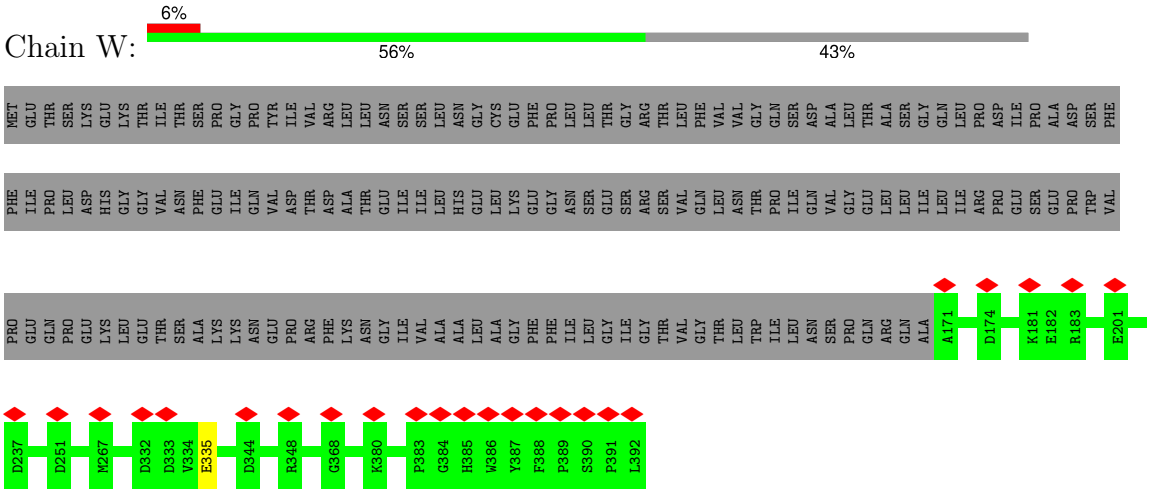
• Molecule 3: Protein PrgH

Chain V:



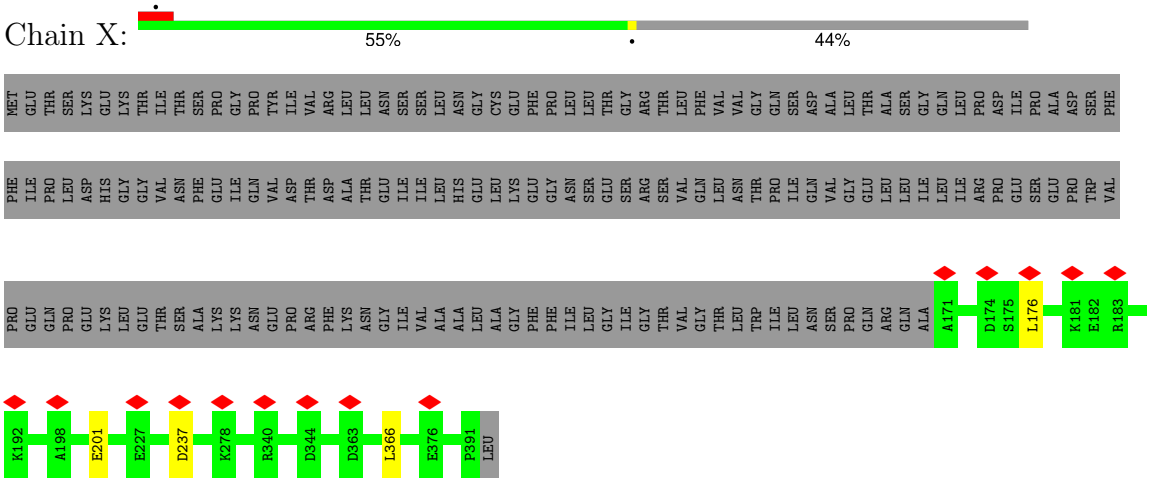
• Molecule 3: Protein PrgH

Chain W:



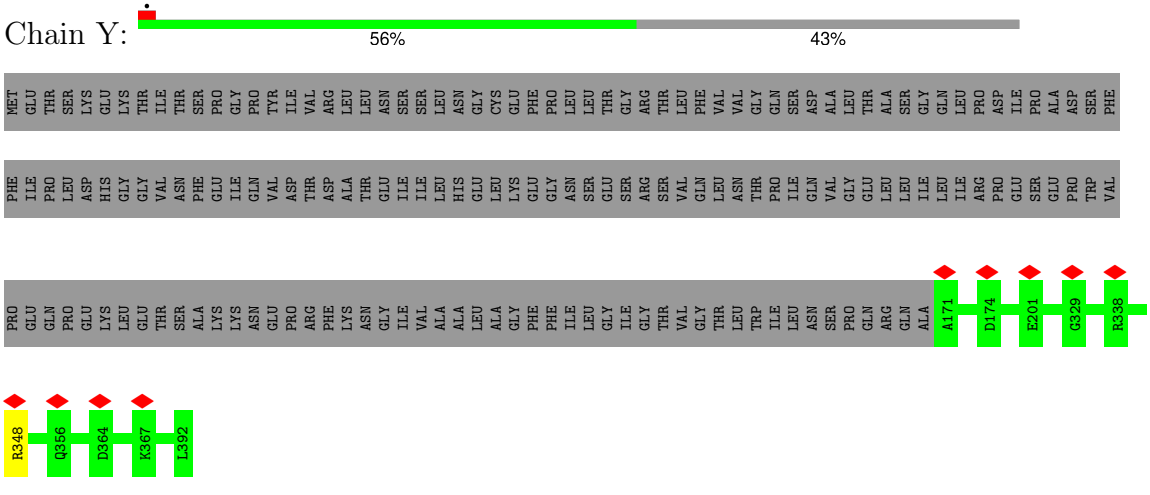
• Molecule 3: Protein PrgH

Chain X:



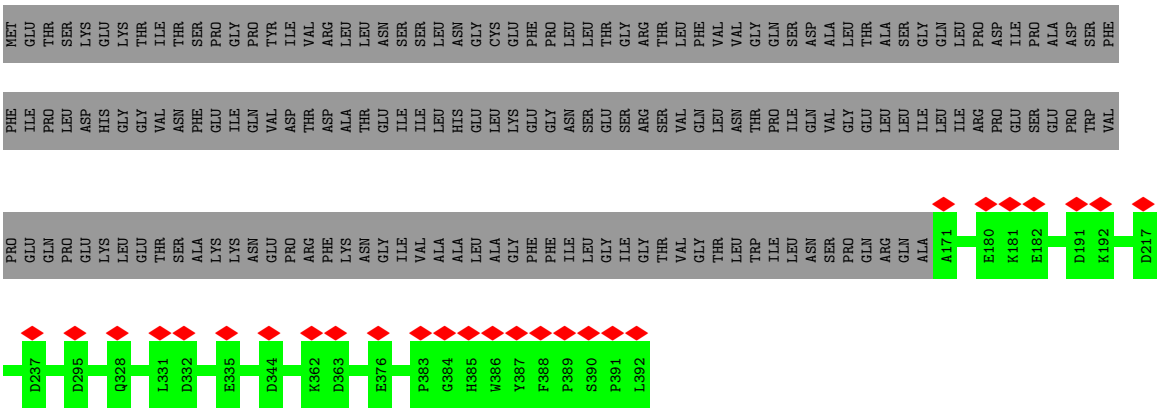
• Molecule 3: Protein PrgH

Chain Y:



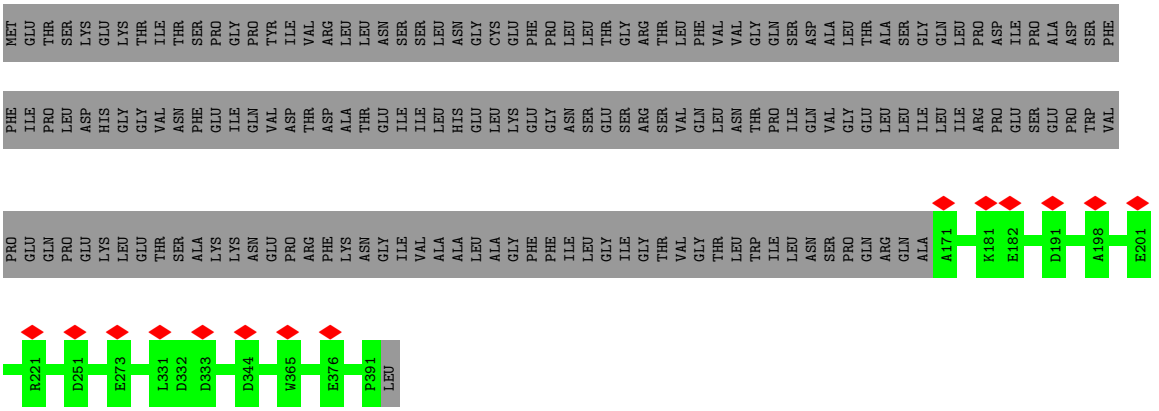
• Molecule 3: Protein PrgH

Chain Z:



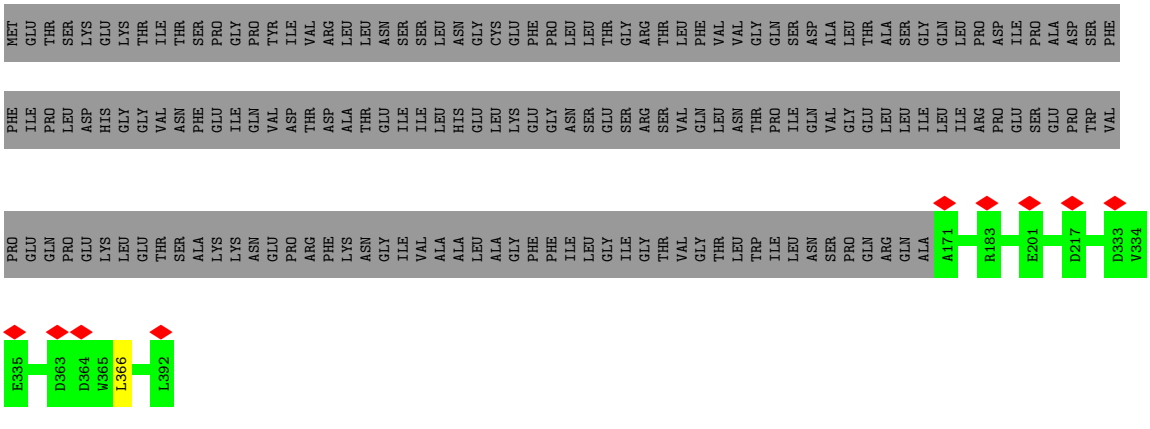
• Molecule 3: Protein PrgH

Chain a:



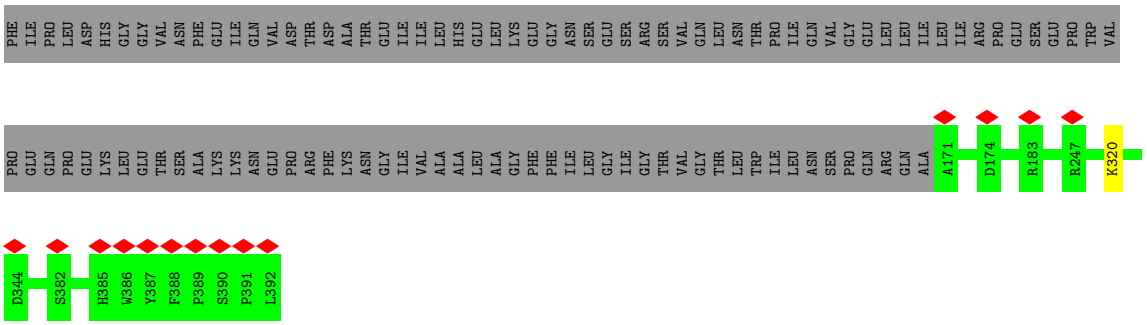
• Molecule 3: Protein PrgH

Chain b:



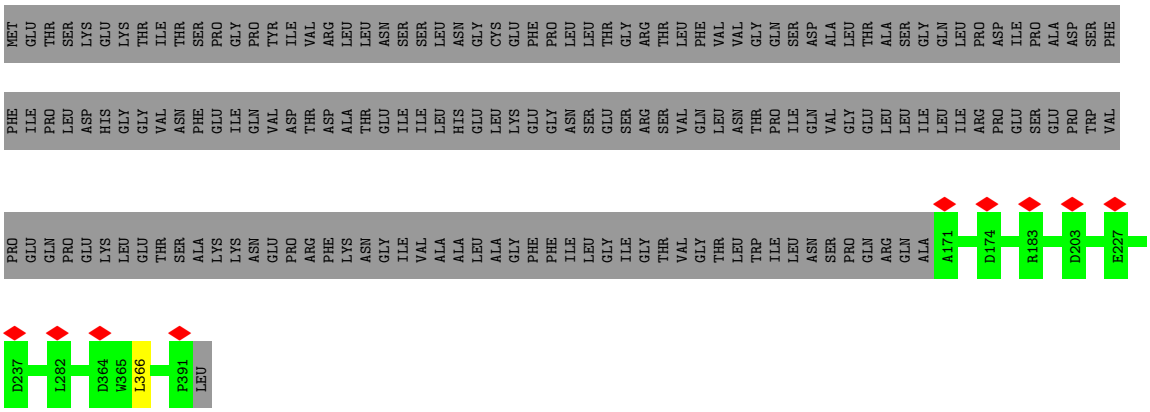
• Molecule 3: Protein PrgH

Chain c:



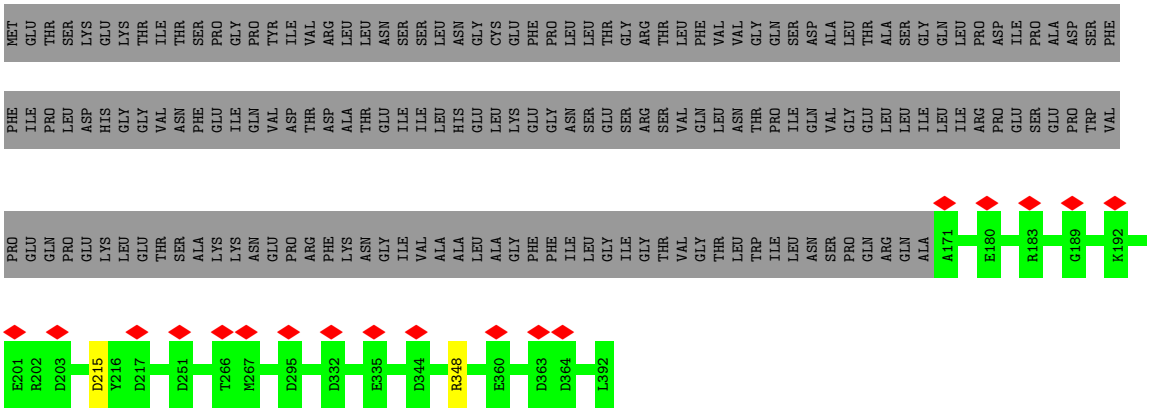
• Molecule 3: Protein PrgH

Chain d:



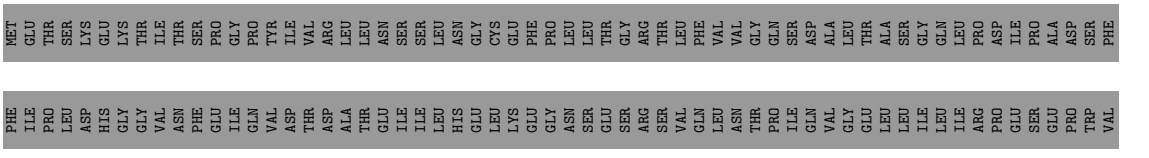
• Molecule 3: Protein PrgH

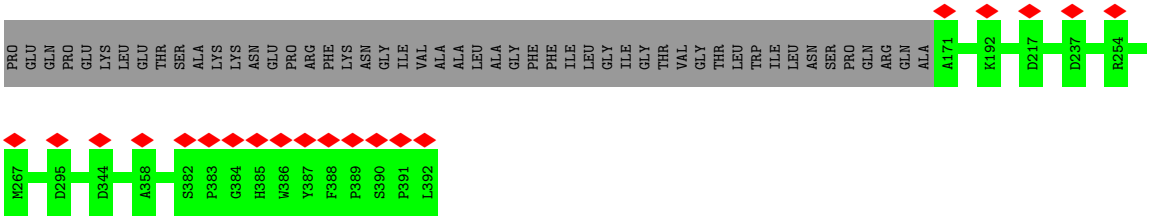
Chain e:



• Molecule 3: Protein PrgH

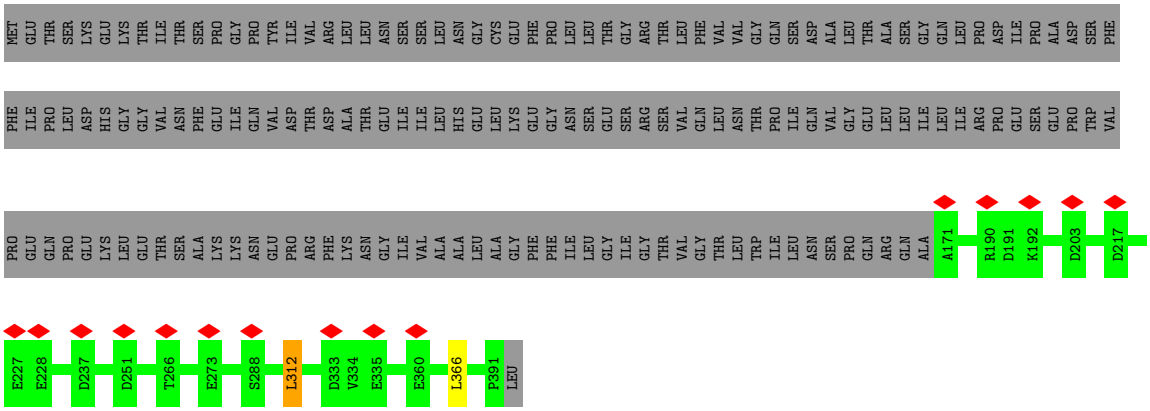
Chain f:





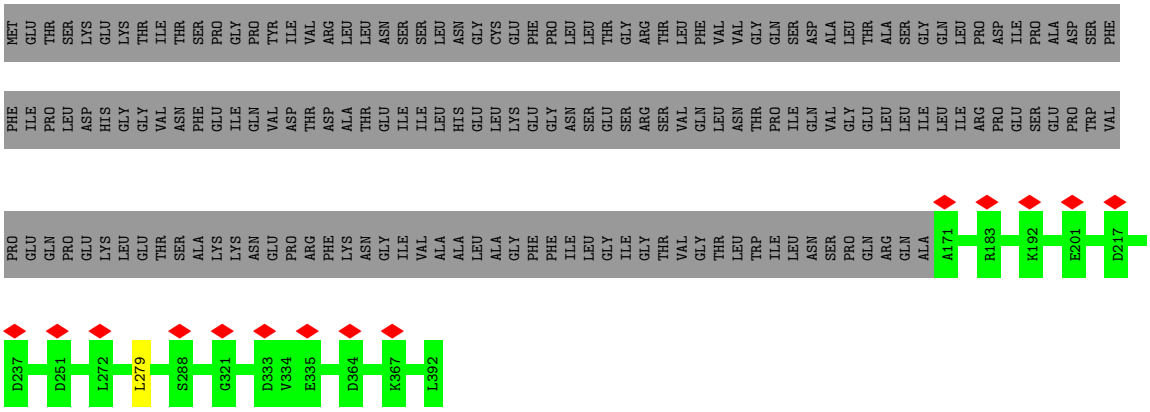
• Molecule 3: Protein PrgH

Chain g:



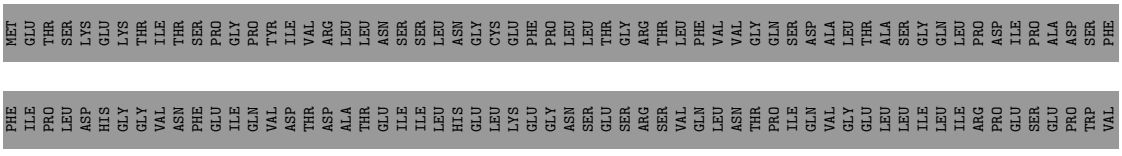
• Molecule 3: Protein PrgH

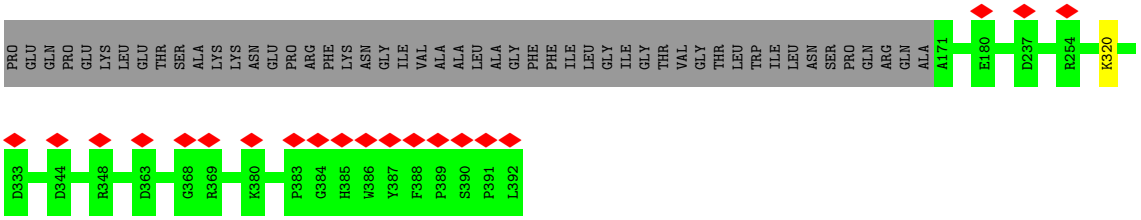
Chain h:



• Molecule 3: Protein PrgH

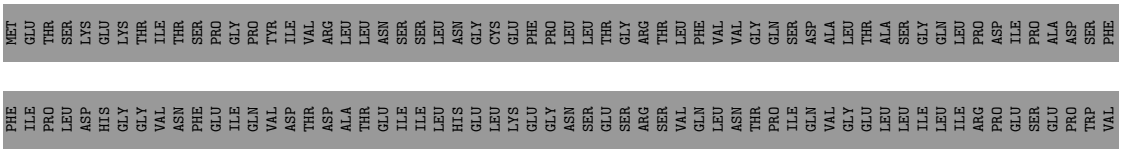
Chain i:





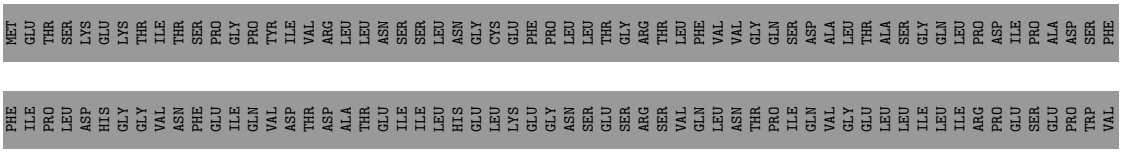
• Molecule 3: Protein PrgH

Chain j:



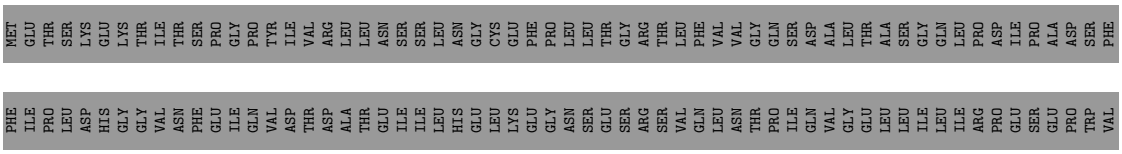
• Molecule 3: Protein PrgH

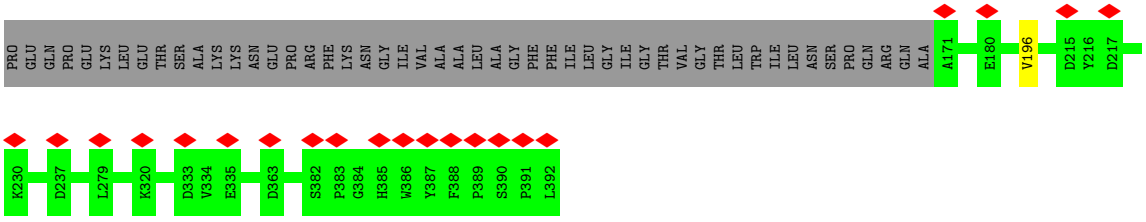
Chain k:



• Molecule 3: Protein PrgH

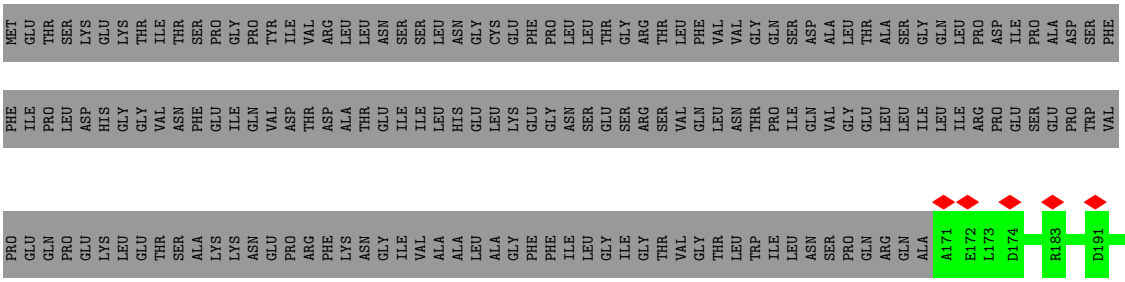
Chain l:





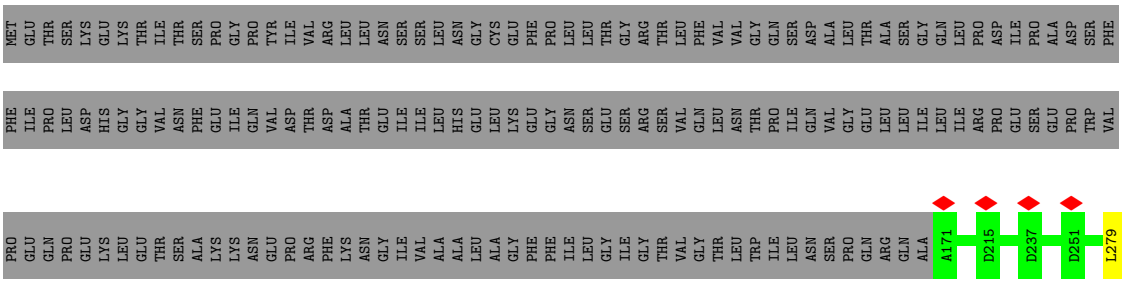
• Molecule 3: Protein PrgH

Chain m:



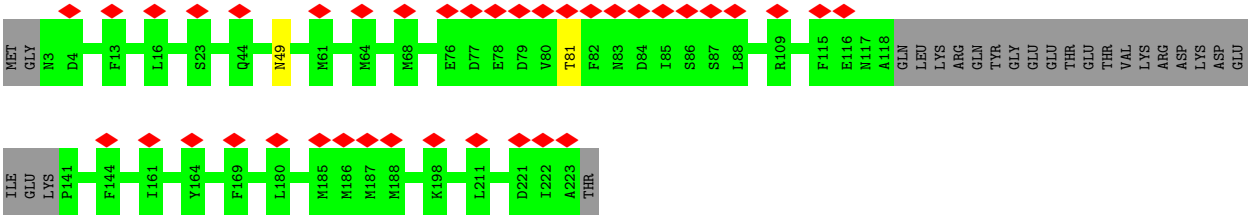
• Molecule 3: Protein PrgH

Chain n:



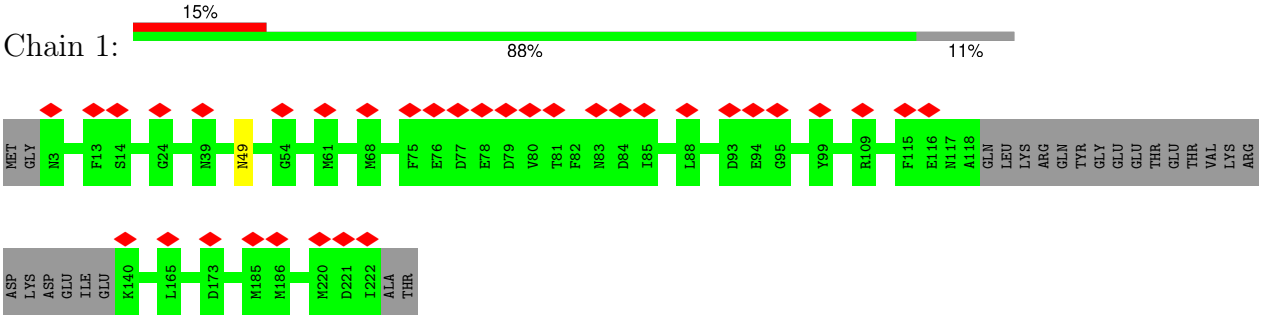
• Molecule 4: Surface presentation of antigens protein SpaP

Chain 0:



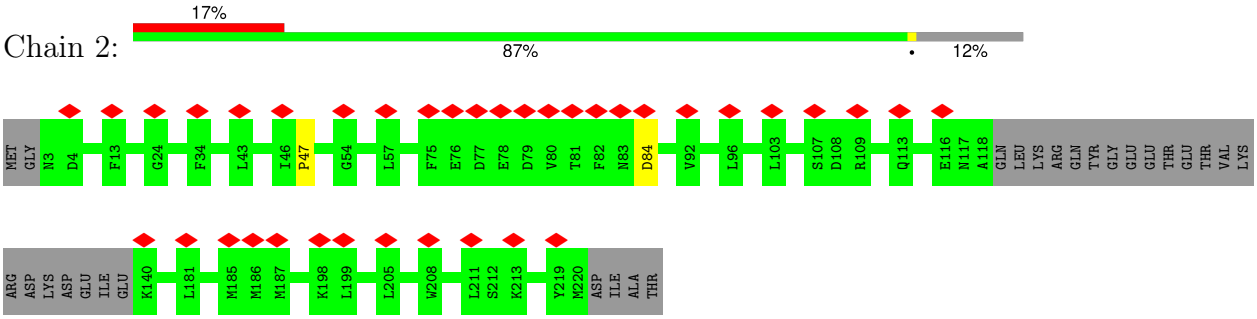
• Molecule 4: Surface presentation of antigens protein SpaP

Chain 1:



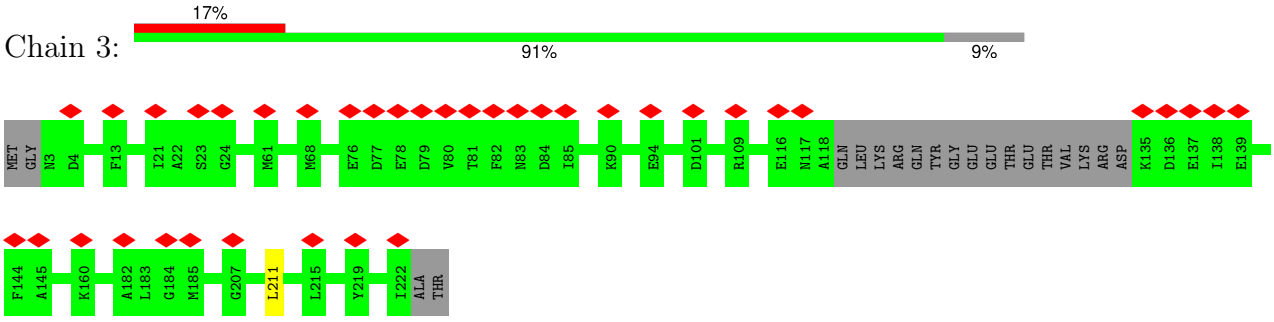
• Molecule 4: Surface presentation of antigens protein SpaP

Chain 2:



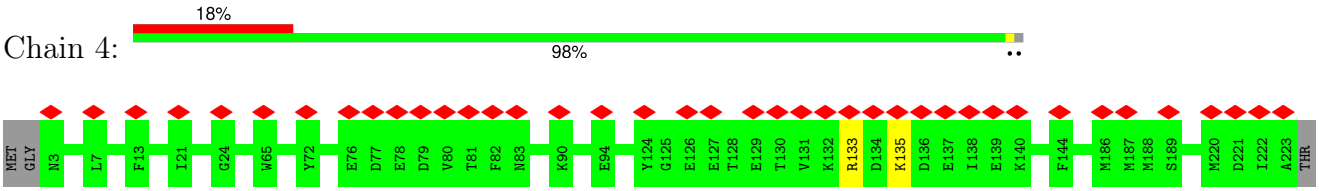
• Molecule 4: Surface presentation of antigens protein SpaP

Chain 3:



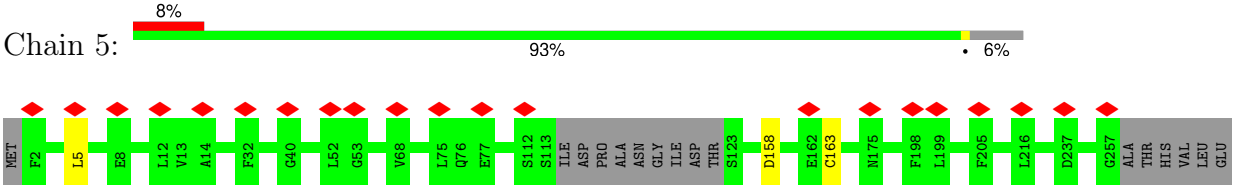
• Molecule 4: Surface presentation of antigens protein SpaP

Chain 4:



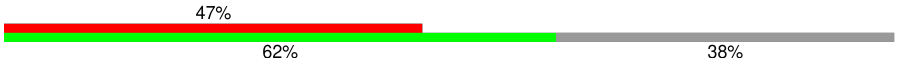
• Molecule 5: Surface presentation of antigens protein SpaR

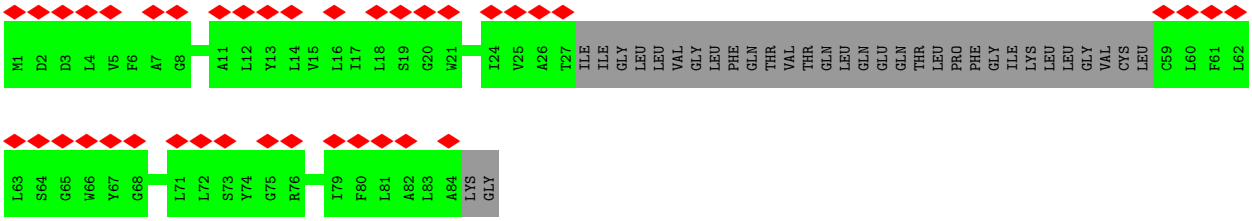
Chain 5:



• Molecule 6: Surface presentation of antigens protein SpaQ

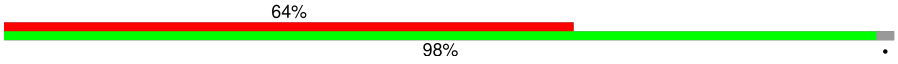
Chain 6:





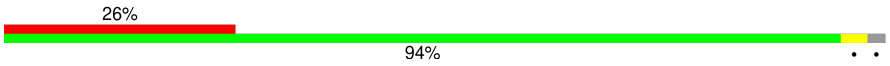
• Molecule 6: Surface presentation of antigens protein SpaQ

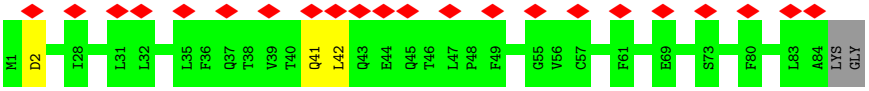
Chain 7:



• Molecule 6: Surface presentation of antigens protein SpaQ

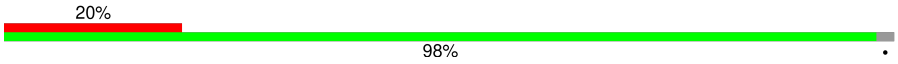
Chain 8:

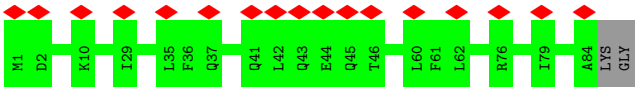




• Molecule 6: Surface presentation of antigens protein SpaQ

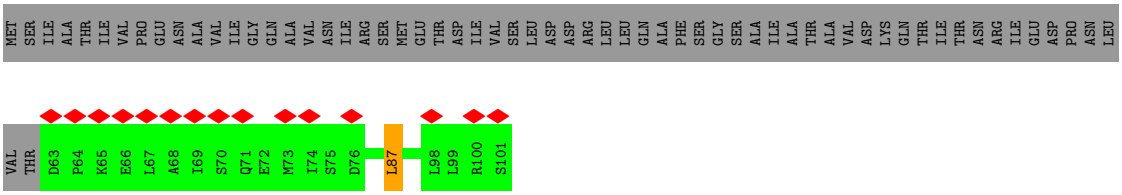
Chain 9:





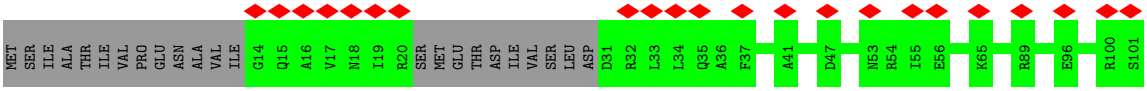
• Molecule 7: Protein PrgJ

Chain AM:



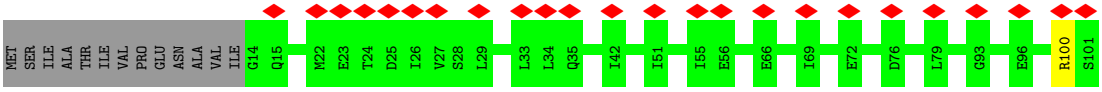
• Molecule 7: Protein PrgJ

Chain AN:



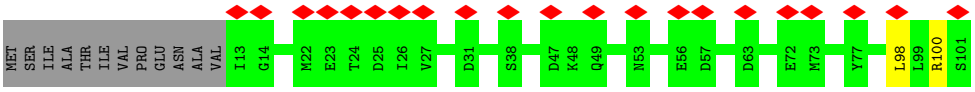
• Molecule 7: Protein PrgJ

Chain AO:



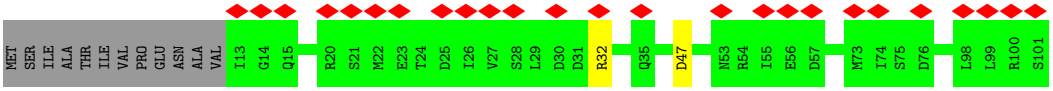
• Molecule 7: Protein PrgJ

Chain AP:



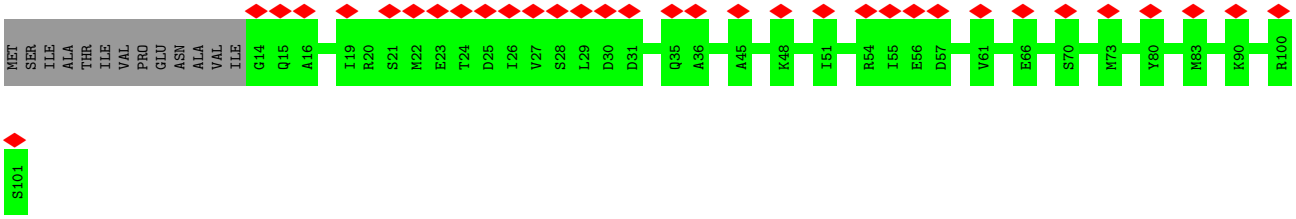
• Molecule 7: Protein PrgJ

Chain AQ:



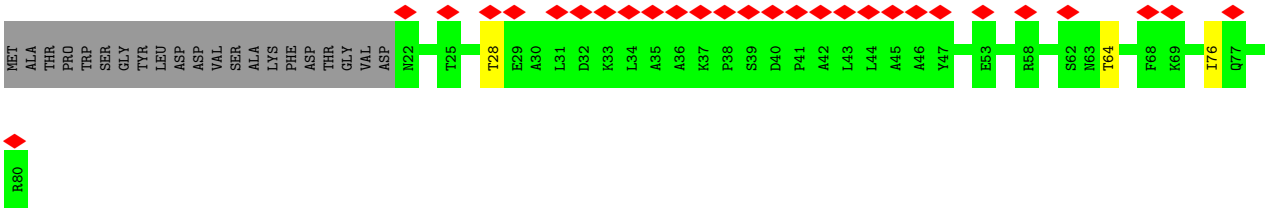
• Molecule 7: Protein PrgJ

Chain AR:



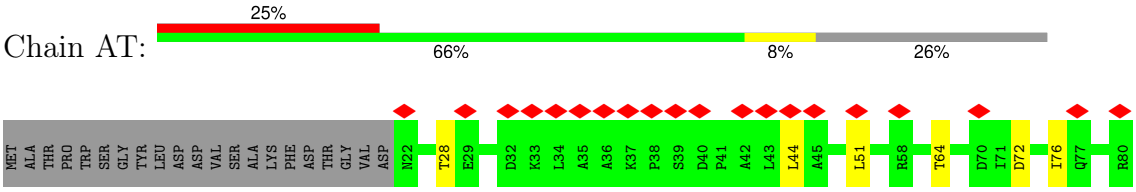
• Molecule 8: Protein PrgI

Chain AS:



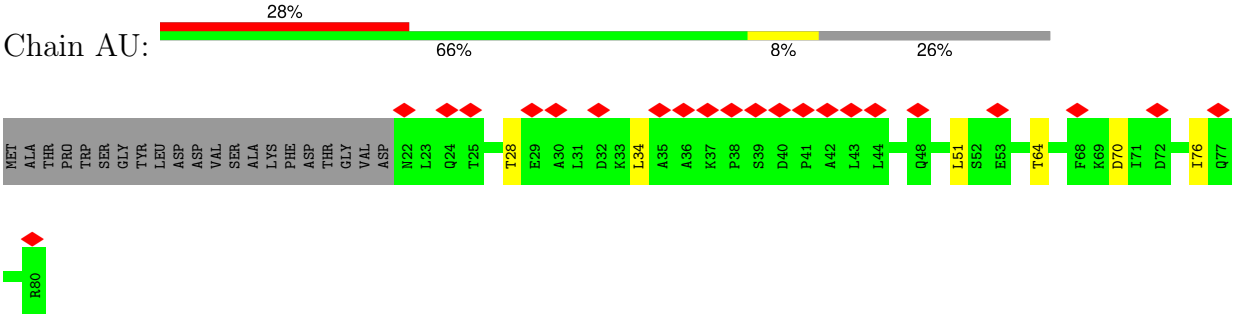
• Molecule 8: Protein PrgI

Chain AT:



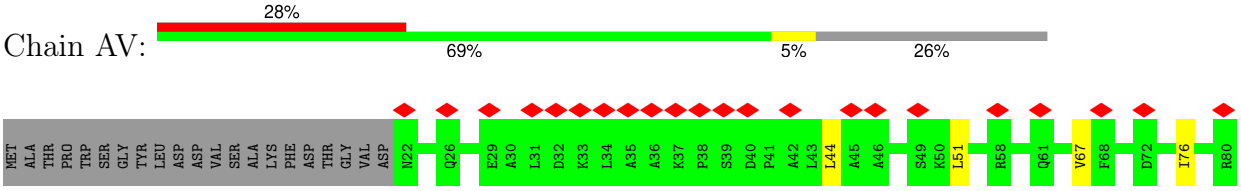
• Molecule 8: Protein PrgI

Chain AU:



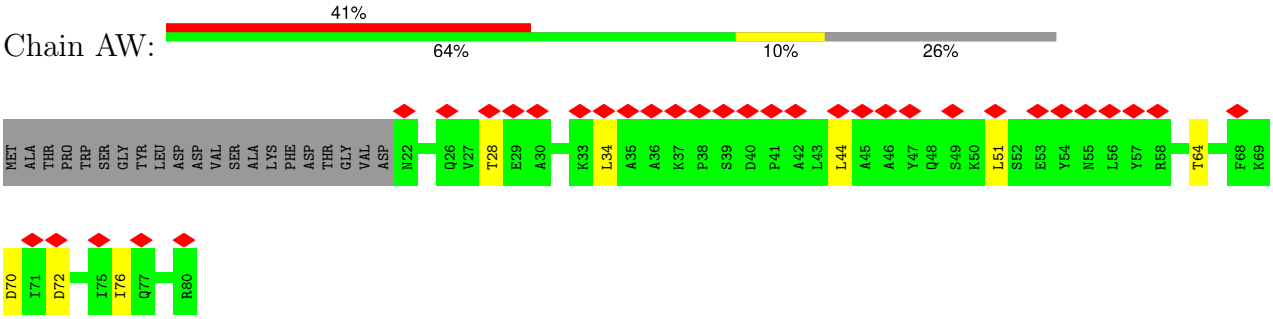
• Molecule 8: Protein PrgI

Chain AV:



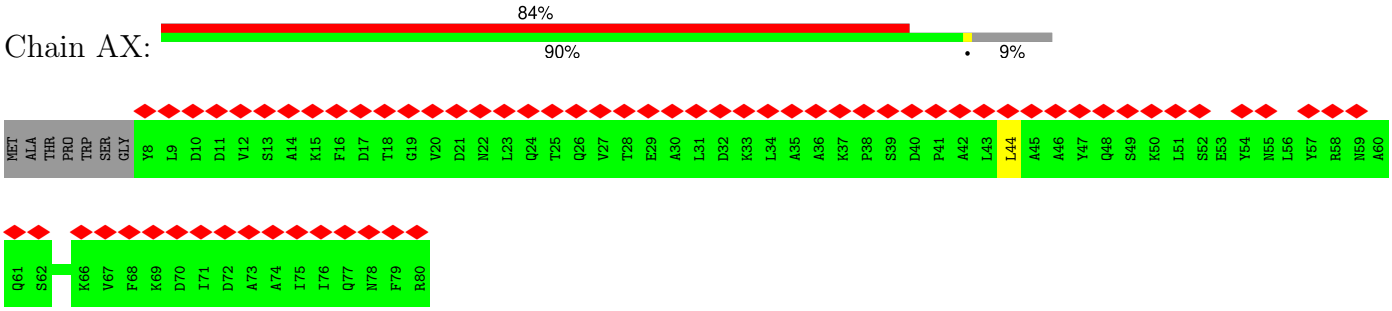
• Molecule 8: Protein PrgI

Chain AW:



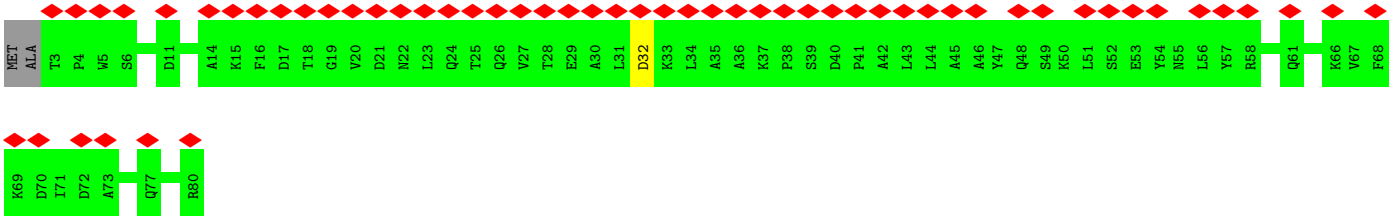
• Molecule 8: Protein PrgI

Chain AX:



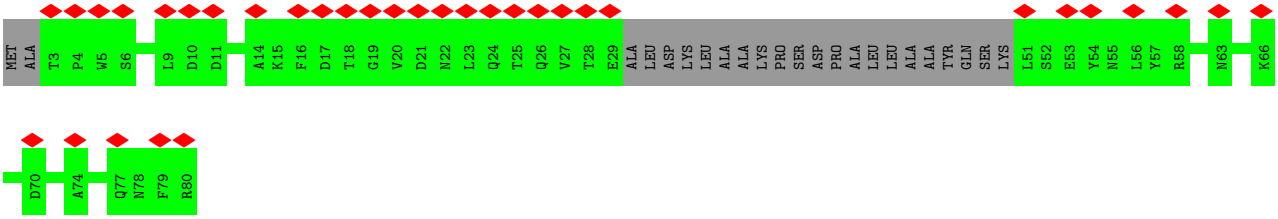
• Molecule 8: Protein PrgI

Chain AY:



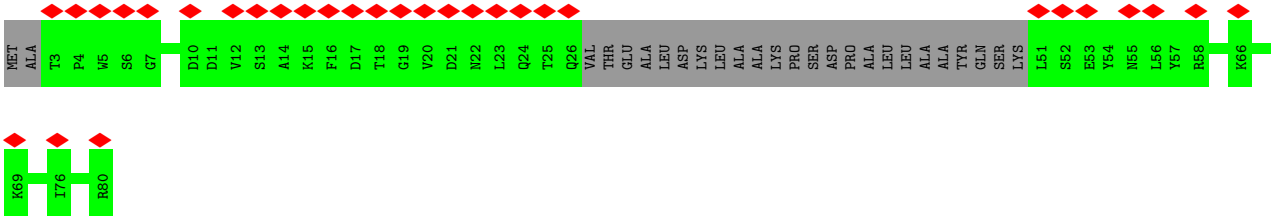
• Molecule 8: Protein PrgI

Chain AZ:



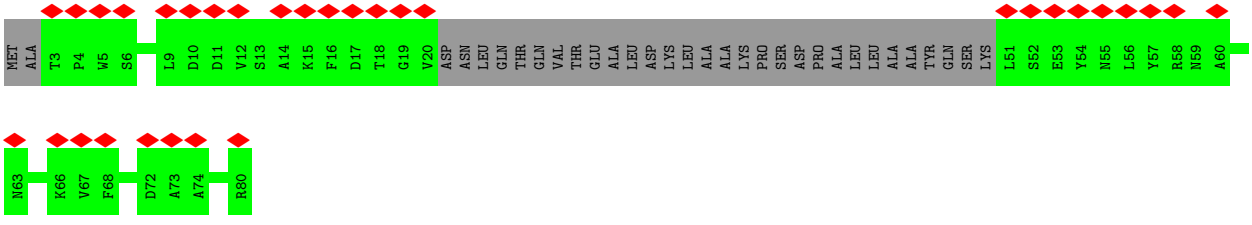
• Molecule 8: Protein PrgI

Chain BA:



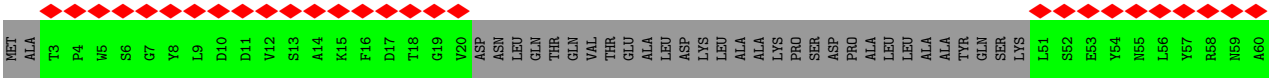
• Molecule 8: Protein PrgI

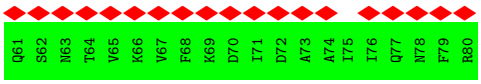
Chain BB:



• Molecule 8: Protein PrgI

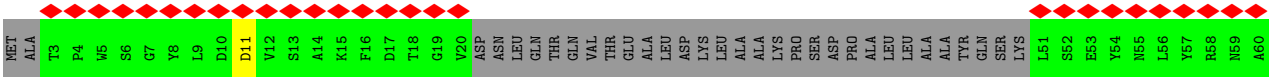
Chain BC:





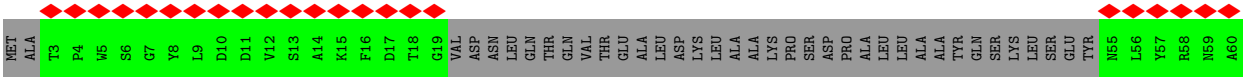
• Molecule 8: Protein PrgI

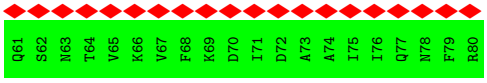
Chain BD:



• Molecule 8: Protein PrgI

Chain BE:





4 Experimental information (i)

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 ($e^-/Å^2$)	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 (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	0.43	0/1458	0.61	0/1979
1	AB	0.40	0/1458	0.59	0/1979
1	AC	0.43	0/1458	0.60	0/1979
1	AD	0.40	0/1458	0.61	0/1979
1	AE	0.42	0/1458	0.60	0/1979
1	AF	0.42	0/1458	0.59	0/1979
1	AG	0.42	0/1458	0.59	0/1979
1	AH	0.41	0/1458	0.58	0/1979
1	AI	0.41	0/1458	0.61	0/1979
1	AJ	0.41	0/1458	0.64	2/1979 (0.1%)
1	AK	0.40	0/1458	0.59	0/1979
1	AL	0.41	0/1458	0.60	0/1979
1	o	0.41	0/1458	0.59	1/1979 (0.1%)
1	p	0.40	0/1458	0.57	0/1979
1	q	0.42	1/1458 (0.1%)	0.58	1/1979 (0.1%)
1	r	0.39	0/1458	0.60	0/1979
1	s	0.40	0/1458	0.59	0/1979
1	t	0.42	1/1458 (0.1%)	0.63	1/1979 (0.1%)
1	u	0.40	0/1458	0.62	1/1979 (0.1%)
1	v	0.42	0/1458	0.60	1/1979 (0.1%)
1	w	0.40	0/1458	0.61	1/1979 (0.1%)
1	x	0.41	0/1458	0.61	0/1979
1	y	0.42	0/1458	0.62	1/1979 (0.1%)
1	z	0.41	0/1458	0.63	1/1979 (0.1%)
2	A	0.39	0/1131	0.65	3/1525 (0.2%)
2	B	0.41	0/1181	0.65	1/1593 (0.1%)
2	C	0.40	0/1131	0.60	0/1525
2	D	0.41	0/1170	0.59	0/1579
2	F	0.41	0/1131	0.59	0/1525
2	G	0.40	0/1181	0.60	0/1593
2	H	0.45	0/1131	0.63	1/1525 (0.1%)
2	I	0.39	0/1181	0.59	0/1593
2	J	0.42	0/1131	0.58	0/1525
2	K	0.41	0/1181	0.61	0/1593

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
2	L	0.41	0/1131	0.59	0/1525
2	M	0.39	0/1170	0.61	1/1579 (0.1%)
2	N	0.42	0/1131	0.59	0/1525
2	O	0.40	0/1181	0.63	0/1593
2	P	0.41	0/1131	0.58	0/1525
2	Q	0.41	0/1181	0.62	0/1593
3	E	0.39	0/1881	0.58	0/2541
3	R	0.39	0/1872	0.62	2/2530 (0.1%)
3	S	0.40	0/1876	0.58	1/2536 (0.0%)
3	T	0.38	0/1881	0.56	0/2541
3	U	0.38	0/1872	0.60	1/2530 (0.0%)
3	V	0.38	0/1876	0.63	2/2536 (0.1%)
3	W	0.38	0/1881	0.58	0/2541
3	X	0.38	0/1872	0.63	2/2530 (0.1%)
3	Y	0.40	0/1876	0.59	0/2536
3	Z	0.39	0/1881	0.57	0/2541
3	a	0.40	0/1872	0.58	0/2530
3	b	0.39	0/1876	0.57	0/2536
3	c	0.40	0/1881	0.58	0/2541
3	d	0.39	0/1872	0.56	0/2530
3	e	0.39	0/1876	0.59	0/2536
3	f	0.39	0/1881	0.58	0/2541
3	g	0.37	0/1872	0.59	1/2530 (0.0%)
3	h	0.41	0/1876	0.62	1/2536 (0.0%)
3	i	0.38	0/1881	0.56	0/2541
3	j	0.39	0/1872	0.59	0/2530
3	k	0.41	0/1876	0.59	0/2536
3	l	0.41	0/1881	0.60	0/2541
3	m	0.40	0/1872	0.62	0/2530
3	n	0.38	0/1876	0.59	1/2536 (0.0%)
4	0	0.40	0/1598	0.64	0/2172
4	1	0.37	0/1605	0.64	0/2181
4	2	0.36	0/1589	0.63	0/2159
4	3	0.38	0/1642	0.60	0/2230
4	4	0.39	0/1799	0.63	0/2441
5	5	0.39	0/1935	0.68	2/2647 (0.1%)
6	6	0.32	0/414	0.72	0/565
6	7	0.35	0/657	0.69	0/897
6	8	0.37	0/657	0.69	1/897 (0.1%)
6	9	0.38	0/660	0.64	0/900
7	AM	0.40	0/300	0.78	1/403 (0.2%)
7	AN	0.35	0/646	0.59	0/870
7	AO	0.33	0/671	0.59	0/908

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
7	AP	0.36	0/679	0.64	0/919
7	AQ	0.32	0/679	0.63	1/919 (0.1%)
7	AR	0.33	0/671	0.62	0/908
8	AS	0.35	0/472	0.65	0/638
8	AT	0.35	0/472	0.59	0/638
8	AU	0.37	0/472	0.62	0/638
8	AV	0.39	0/472	0.70	1/638 (0.2%)
8	AW	0.35	0/472	0.56	0/638
8	AX	0.33	0/582	0.56	1/788 (0.1%)
8	AY	0.39	0/623	0.62	1/846 (0.1%)
8	AZ	0.31	0/467	0.50	0/632
8	BA	0.31	0/444	0.49	0/600
8	BB	0.33	0/395	0.66	0/533
8	BC	0.30	0/395	0.54	0/533
8	BD	0.32	0/395	0.61	1/533 (0.2%)
8	BE	0.32	0/352	0.59	0/474
All	All	0.40	2/120713 (0.0%)	0.60	36/163413 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	q	76	GLN	C-N	-5.89	1.20	1.34
1	t	76	GLN	C-N	-5.27	1.22	1.34

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	90	LEU	CA-CB-CG	8.54	134.93	115.30
2	B	47	ASP	CB-CG-OD1	8.49	125.94	118.30
7	AQ	47	ASP	CB-CG-OD2	7.27	124.84	118.30
5	5	158	ASP	CB-CG-OD2	7.17	124.75	118.30
3	h	279	LEU	CA-CB-CG	7.15	131.74	115.30

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)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	182/252 (72%)	173 (95%)	9 (5%)	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%)	174 (96%)	8 (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%)	177 (97%)	5 (3%)	0	100	100
1	AJ	182/252 (72%)	177 (97%)	5 (3%)	0	100	100
1	AK	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	AL	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	o	182/252 (72%)	177 (97%)	5 (3%)	0	100	100
1	p	182/252 (72%)	175 (96%)	7 (4%)	0	100	100
1	q	182/252 (72%)	176 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	r	182/252 (72%)	174 (96%)	8 (4%)	0	100	100
1	s	182/252 (72%)	176 (97%)	6 (3%)	0	100	100
1	t	182/252 (72%)	179 (98%)	3 (2%)	0	100	100
1	u	182/252 (72%)	177 (97%)	5 (3%)	0	100	100
1	v	182/252 (72%)	176 (97%)	6 (3%)	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%)	175 (96%)	7 (4%)	0	100	100
2	A	137/562 (24%)	136 (99%)	1 (1%)	0	100	100
2	B	143/562 (25%)	139 (97%)	4 (3%)	0	100	100
2	C	137/562 (24%)	134 (98%)	3 (2%)	0	100	100
2	D	142/562 (25%)	138 (97%)	4 (3%)	0	100	100
2	F	137/562 (24%)	135 (98%)	2 (2%)	0	100	100
2	G	143/562 (25%)	137 (96%)	6 (4%)	0	100	100
2	H	137/562 (24%)	134 (98%)	3 (2%)	0	100	100
2	I	143/562 (25%)	141 (99%)	2 (1%)	0	100	100
2	J	137/562 (24%)	134 (98%)	3 (2%)	0	100	100
2	K	143/562 (25%)	139 (97%)	4 (3%)	0	100	100
2	L	137/562 (24%)	135 (98%)	2 (2%)	0	100	100
2	M	142/562 (25%)	137 (96%)	5 (4%)	0	100	100
2	N	137/562 (24%)	134 (98%)	3 (2%)	0	100	100
2	O	143/562 (25%)	140 (98%)	3 (2%)	0	100	100
2	P	137/562 (24%)	136 (99%)	1 (1%)	0	100	100
2	Q	143/562 (25%)	139 (97%)	4 (3%)	0	100	100
3	E	220/392 (56%)	212 (96%)	8 (4%)	0	100	100
3	R	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
3	S	220/392 (56%)	209 (95%)	11 (5%)	0	100	100
3	T	220/392 (56%)	210 (96%)	10 (4%)	0	100	100
3	U	219/392 (56%)	213 (97%)	6 (3%)	0	100	100
3	V	220/392 (56%)	207 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	W	220/392 (56%)	211 (96%)	9 (4%)	0	100	100
3	X	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
3	Y	220/392 (56%)	204 (93%)	16 (7%)	0	100	100
3	Z	220/392 (56%)	210 (96%)	10 (4%)	0	100	100
3	a	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
3	b	220/392 (56%)	207 (94%)	13 (6%)	0	100	100
3	c	220/392 (56%)	210 (96%)	10 (4%)	0	100	100
3	d	219/392 (56%)	213 (97%)	6 (3%)	0	100	100
3	e	220/392 (56%)	208 (94%)	12 (6%)	0	100	100
3	f	220/392 (56%)	209 (95%)	11 (5%)	0	100	100
3	g	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
3	h	220/392 (56%)	207 (94%)	13 (6%)	0	100	100
3	i	220/392 (56%)	211 (96%)	9 (4%)	0	100	100
3	j	219/392 (56%)	213 (97%)	6 (3%)	0	100	100
3	k	220/392 (56%)	206 (94%)	14 (6%)	0	100	100
3	l	220/392 (56%)	210 (96%)	10 (4%)	0	100	100
3	m	219/392 (56%)	212 (97%)	7 (3%)	0	100	100
3	n	220/392 (56%)	207 (94%)	13 (6%)	0	100	100
4	0	195/224 (87%)	189 (97%)	5 (3%)	1 (0%)	25	62
4	1	195/224 (87%)	186 (95%)	8 (4%)	1 (0%)	25	62
4	2	193/224 (86%)	187 (97%)	5 (3%)	1 (0%)	25	62
4	3	200/224 (89%)	195 (98%)	5 (2%)	0	100	100
4	4	220/224 (98%)	209 (95%)	11 (5%)	0	100	100
5	5	243/263 (92%)	224 (92%)	19 (8%)	0	100	100
6	6	49/86 (57%)	46 (94%)	3 (6%)	0	100	100
6	7	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
6	8	82/86 (95%)	80 (98%)	1 (1%)	1 (1%)	11	44
6	9	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
7	AM	37/101 (37%)	37 (100%)	0	0	100	100
7	AN	79/101 (78%)	79 (100%)	0	0	100	100
7	AO	86/101 (85%)	84 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AP	87/101 (86%)	87 (100%)	0	0	100	100
7	AQ	87/101 (86%)	87 (100%)	0	0	100	100
7	AR	86/101 (85%)	83 (96%)	3 (4%)	0	100	100
8	AS	57/80 (71%)	55 (96%)	2 (4%)	0	100	100
8	AT	57/80 (71%)	55 (96%)	2 (4%)	0	100	100
8	AU	57/80 (71%)	55 (96%)	2 (4%)	0	100	100
8	AV	57/80 (71%)	55 (96%)	2 (4%)	0	100	100
8	AW	57/80 (71%)	55 (96%)	2 (4%)	0	100	100
8	AX	71/80 (89%)	68 (96%)	3 (4%)	0	100	100
8	AY	76/80 (95%)	73 (96%)	3 (4%)	0	100	100
8	AZ	53/80 (66%)	52 (98%)	1 (2%)	0	100	100
8	BA	50/80 (62%)	47 (94%)	3 (6%)	0	100	100
8	BB	44/80 (55%)	43 (98%)	1 (2%)	0	100	100
8	BC	44/80 (55%)	44 (100%)	0	0	100	100
8	BD	44/80 (55%)	43 (98%)	1 (2%)	0	100	100
8	BE	39/80 (49%)	37 (95%)	2 (5%)	0	100	100
All	All	14587/27821 (52%)	14062 (96%)	521 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	8	42	LEU
4	0	49	ASN
4	1	49	ASN
4	2	47	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	AA	155/215 (72%)	153 (99%)	2 (1%)	65 77
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%)	152 (98%)	3 (2%)	52 69
1	AF	155/215 (72%)	154 (99%)	1 (1%)	84 88
1	AG	155/215 (72%)	154 (99%)	1 (1%)	84 88
1	AH	155/215 (72%)	155 (100%)	0	100 100
1	AI	155/215 (72%)	153 (99%)	2 (1%)	65 77
1	AJ	155/215 (72%)	154 (99%)	1 (1%)	84 88
1	AK	155/215 (72%)	154 (99%)	1 (1%)	84 88
1	AL	155/215 (72%)	155 (100%)	0	100 100
1	o	155/215 (72%)	153 (99%)	2 (1%)	65 77
1	p	155/215 (72%)	155 (100%)	0	100 100
1	q	155/215 (72%)	154 (99%)	1 (1%)	84 88
1	r	155/215 (72%)	154 (99%)	1 (1%)	84 88
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%)	152 (98%)	3 (2%)	52 69
1	w	155/215 (72%)	153 (99%)	2 (1%)	65 77
1	x	155/215 (72%)	155 (100%)	0	100 100
1	y	155/215 (72%)	154 (99%)	1 (1%)	84 88
1	z	155/215 (72%)	154 (99%)	1 (1%)	84 88
2	A	119/477 (25%)	119 (100%)	0	100 100
2	B	125/477 (26%)	125 (100%)	0	100 100
2	C	119/477 (25%)	118 (99%)	1 (1%)	79 84
2	D	124/477 (26%)	123 (99%)	1 (1%)	79 84
2	F	119/477 (25%)	118 (99%)	1 (1%)	79 84
2	G	125/477 (26%)	124 (99%)	1 (1%)	79 84
2	H	119/477 (25%)	117 (98%)	2 (2%)	56 72
2	I	125/477 (26%)	124 (99%)	1 (1%)	79 84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	119/477 (25%)	118 (99%)	1 (1%)	79	84
2	K	125/477 (26%)	124 (99%)	1 (1%)	79	84
2	L	119/477 (25%)	118 (99%)	1 (1%)	79	84
2	M	124/477 (26%)	123 (99%)	1 (1%)	79	84
2	N	119/477 (25%)	118 (99%)	1 (1%)	79	84
2	O	125/477 (26%)	124 (99%)	1 (1%)	79	84
2	P	119/477 (25%)	118 (99%)	1 (1%)	79	84
2	Q	125/477 (26%)	123 (98%)	2 (2%)	58	74
3	E	190/337 (56%)	189 (100%)	1 (0%)	86	90
3	R	189/337 (56%)	187 (99%)	2 (1%)	70	80
3	S	188/337 (56%)	187 (100%)	1 (0%)	86	90
3	T	190/337 (56%)	190 (100%)	0	100	100
3	U	189/337 (56%)	188 (100%)	1 (0%)	86	90
3	V	188/337 (56%)	186 (99%)	2 (1%)	70	80
3	W	190/337 (56%)	189 (100%)	1 (0%)	86	90
3	X	189/337 (56%)	187 (99%)	2 (1%)	70	80
3	Y	188/337 (56%)	187 (100%)	1 (0%)	86	90
3	Z	190/337 (56%)	190 (100%)	0	100	100
3	a	189/337 (56%)	189 (100%)	0	100	100
3	b	188/337 (56%)	188 (100%)	0	100	100
3	c	190/337 (56%)	189 (100%)	1 (0%)	86	90
3	d	189/337 (56%)	188 (100%)	1 (0%)	86	90
3	e	188/337 (56%)	186 (99%)	2 (1%)	70	80
3	f	190/337 (56%)	190 (100%)	0	100	100
3	g	189/337 (56%)	187 (99%)	2 (1%)	70	80
3	h	188/337 (56%)	188 (100%)	0	100	100
3	i	190/337 (56%)	189 (100%)	1 (0%)	86	90
3	j	189/337 (56%)	189 (100%)	0	100	100
3	k	188/337 (56%)	187 (100%)	1 (0%)	86	90
3	l	190/337 (56%)	189 (100%)	1 (0%)	86	90
3	m	189/337 (56%)	188 (100%)	1 (0%)	86	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	n	188/337 (56%)	188 (100%)	0	100 100
4	0	175/199 (88%)	174 (99%)	1 (1%)	84 88
4	1	177/199 (89%)	177 (100%)	0	100 100
4	2	175/199 (88%)	174 (99%)	1 (1%)	84 88
4	3	180/199 (90%)	179 (99%)	1 (1%)	84 88
4	4	197/199 (99%)	195 (99%)	2 (1%)	73 81
5	5	205/219 (94%)	204 (100%)	1 (0%)	86 90
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%)	75 (99%)	1 (1%)	65 77
7	AP	77/88 (88%)	75 (97%)	2 (3%)	41 61
7	AQ	77/88 (88%)	76 (99%)	1 (1%)	65 77
7	AR	76/88 (86%)	76 (100%)	0	100 100
8	AS	50/67 (75%)	47 (94%)	3 (6%)	16 39
8	AT	50/67 (75%)	44 (88%)	6 (12%)	4 18
8	AU	50/67 (75%)	44 (88%)	6 (12%)	4 18
8	AV	50/67 (75%)	47 (94%)	3 (6%)	16 39
8	AW	50/67 (75%)	42 (84%)	8 (16%)	2 13
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%)	48 (100%)	0	100 100
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	12615/23777 (53%)	12519 (99%)	96 (1%)	77 84

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AJ	77	LEU
8	AS	64	THR
4	0	81	THR
7	AM	87	LEU
8	AT	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 136 such sidechains are listed below:

Mol	Chain	Res	Type
7	AO	53	ASN
8	AS	48	GLN
8	AZ	78	ASN
3	W	318	ASN
3	V	318	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

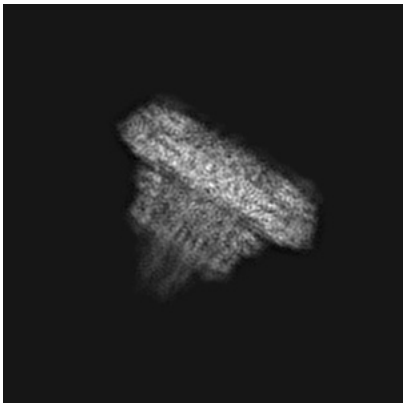
6 Map visualisation

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.

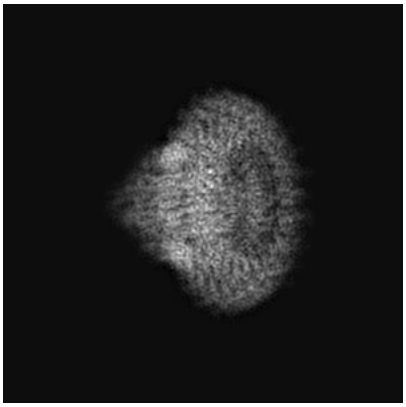
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

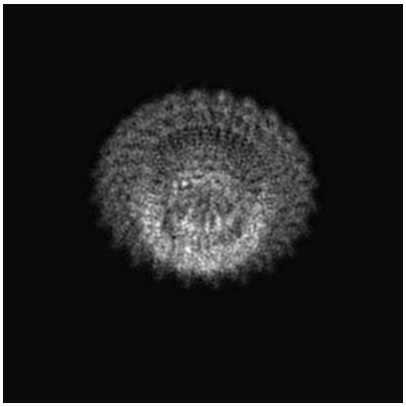
6.1.1 Primary map



X



Y

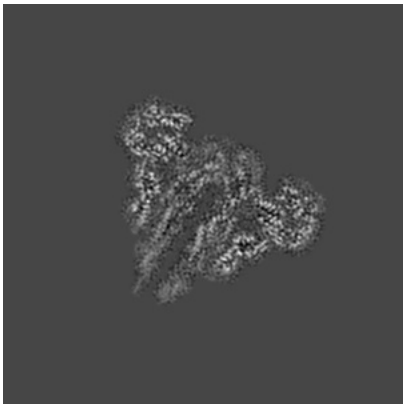


Z

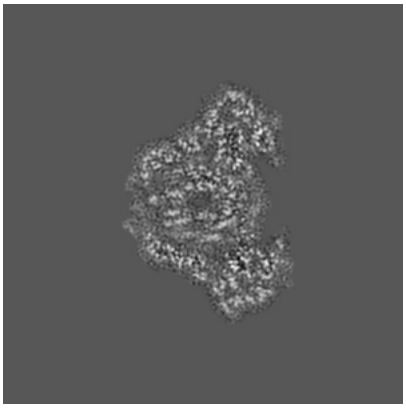
The images above show the map projected in three orthogonal directions.

6.2 Central slices

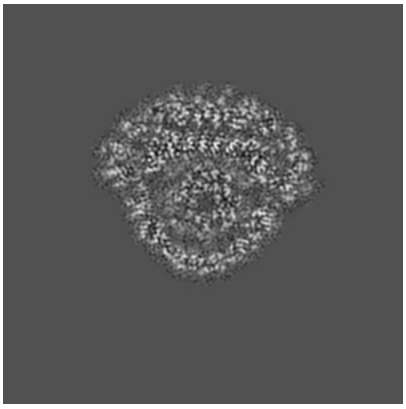
6.2.1 Primary map



X Index: 125



Y Index: 125



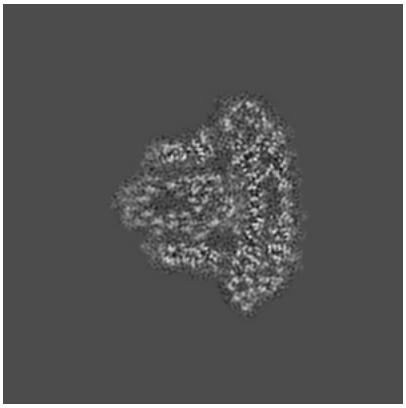
Z Index: 125

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

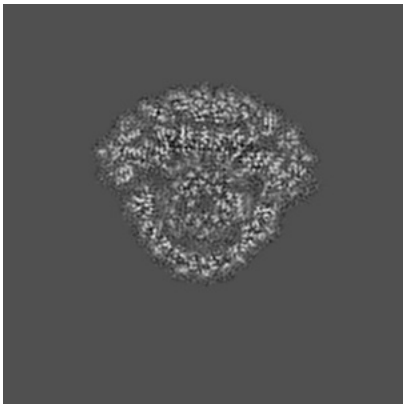
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 114



Y Index: 112

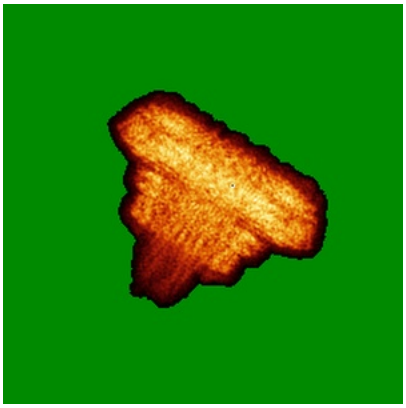


Z Index: 123

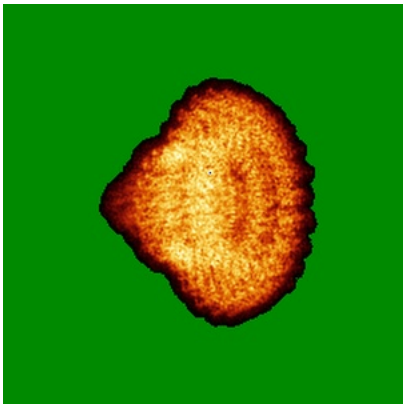
The images above show the largest variance slices of the map in three orthogonal directions.

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

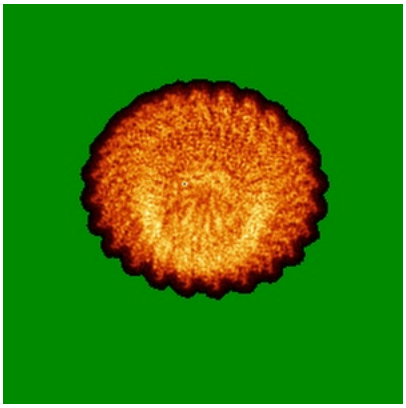
6.4.1 Primary map



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

X Y Z

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.

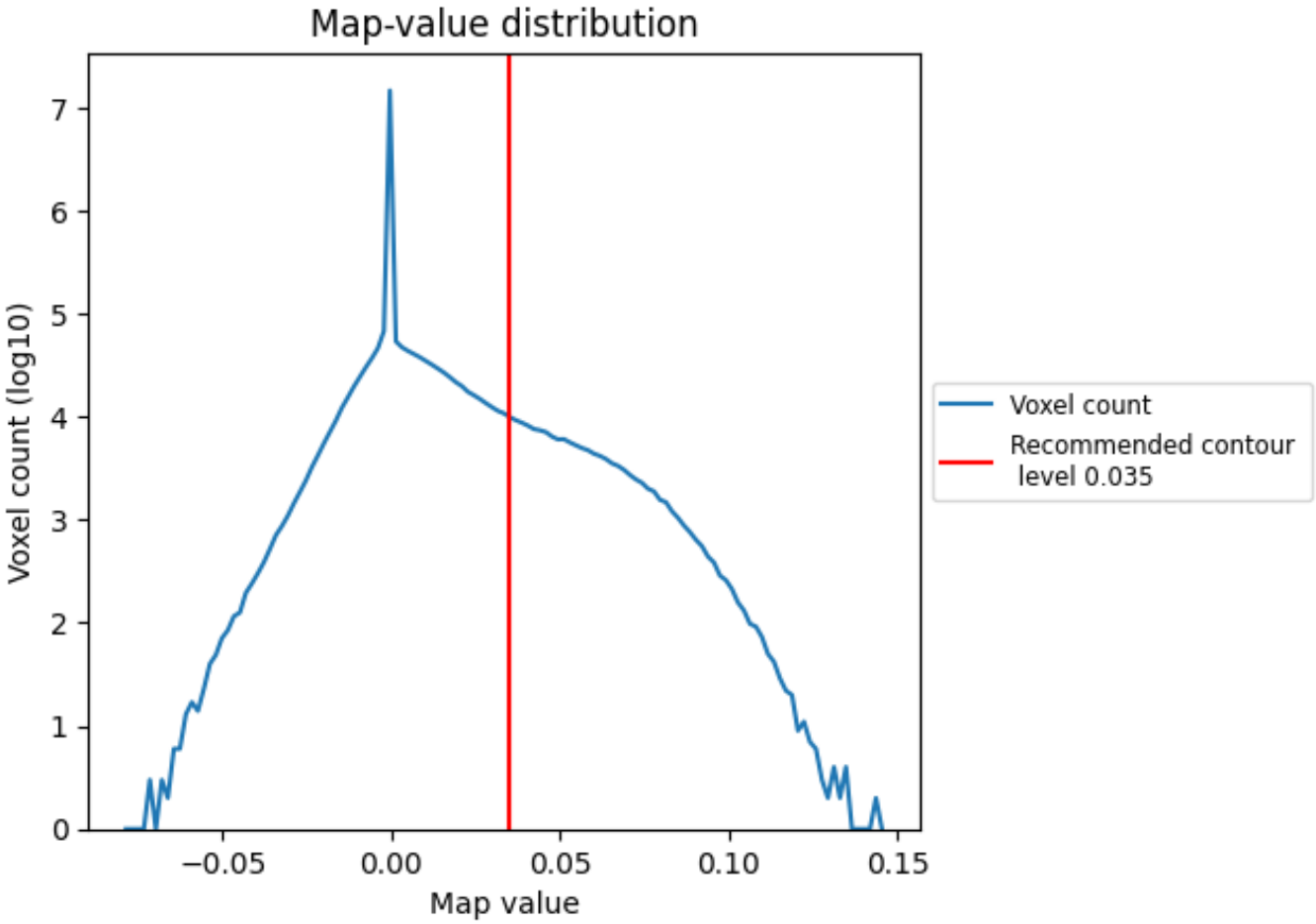
6.6 Mask visualisation (i)

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

7 Map analysis

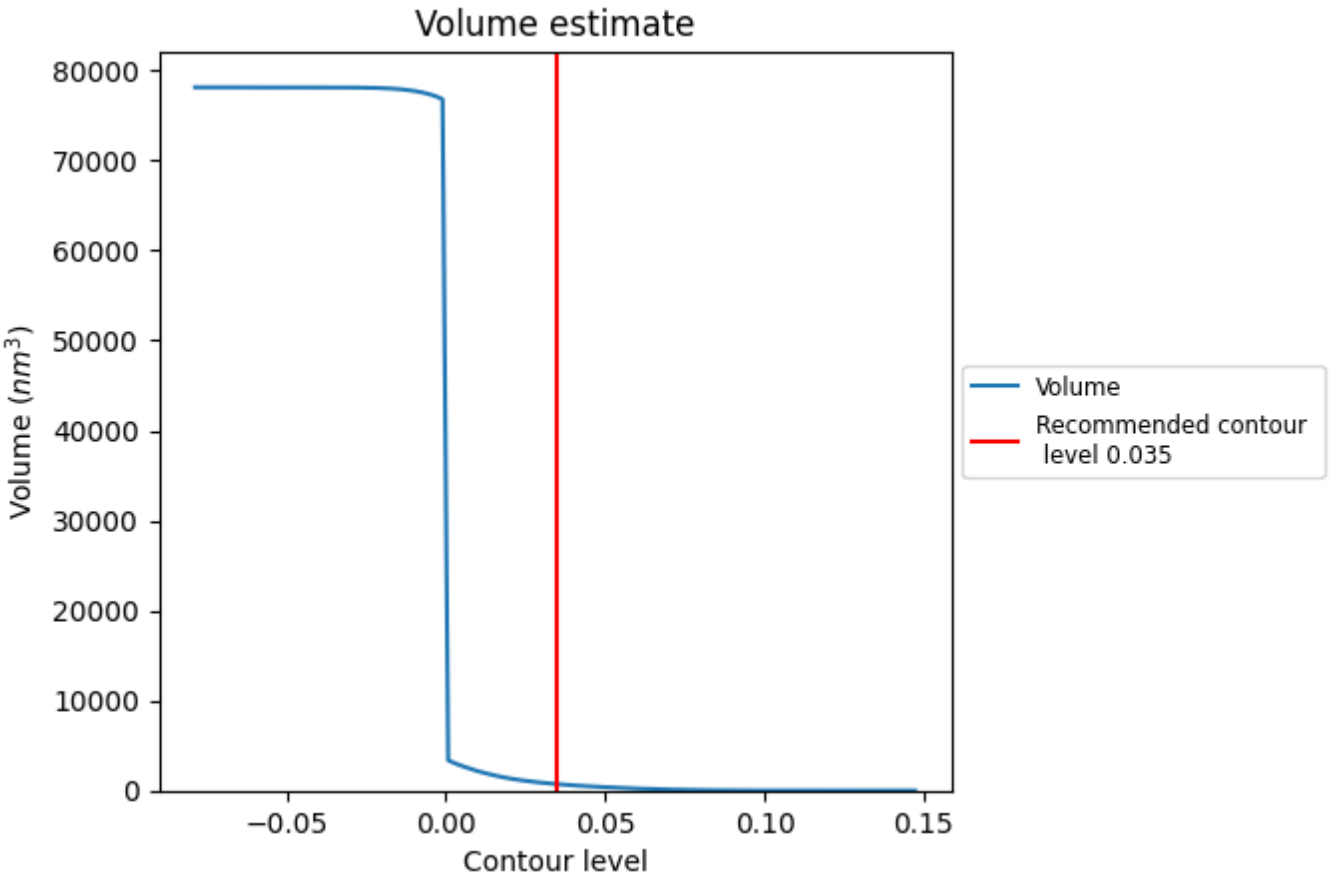
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

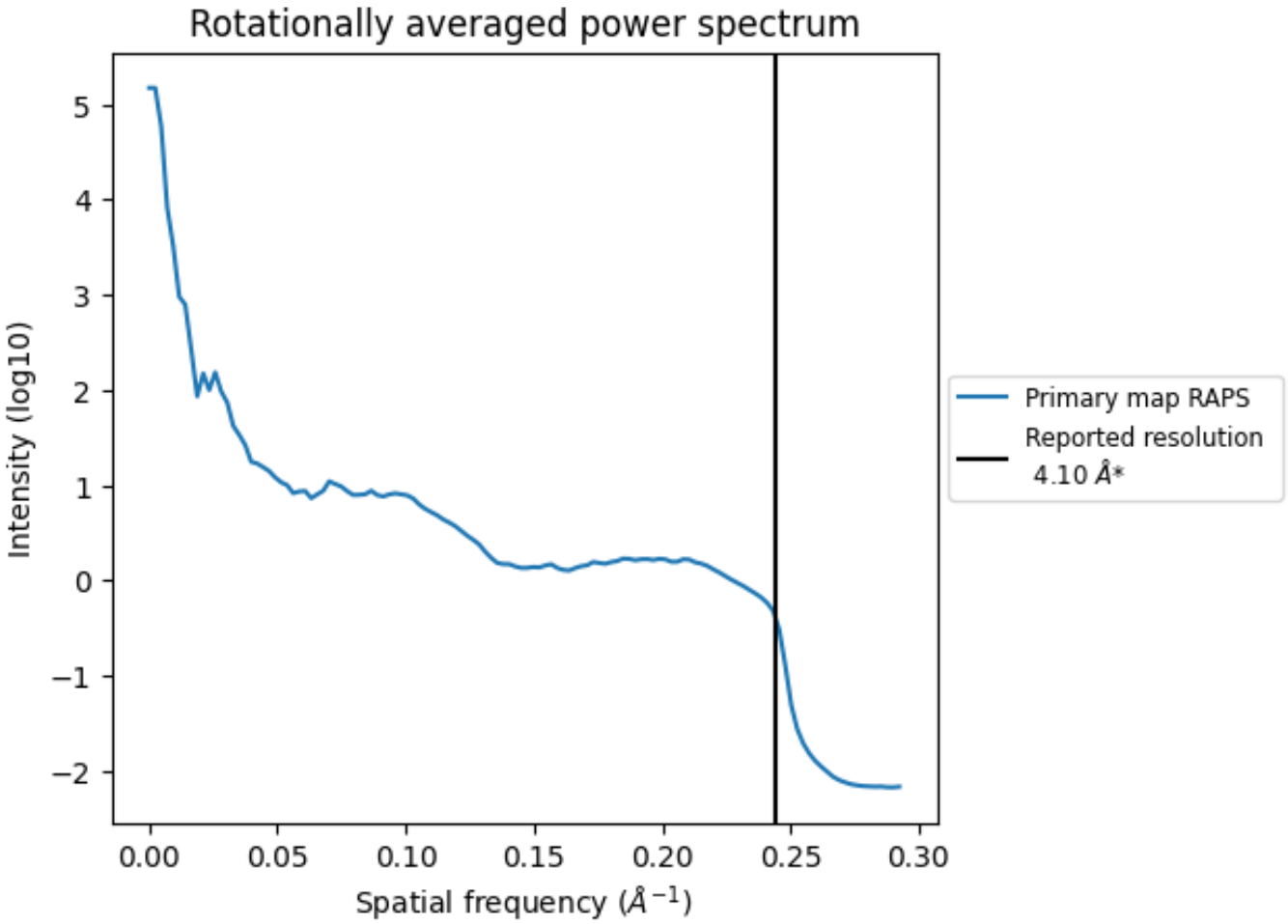
7.2 Volume estimate (i)



The volume at the recommended contour level is 715 nm^3; 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 (i)



*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

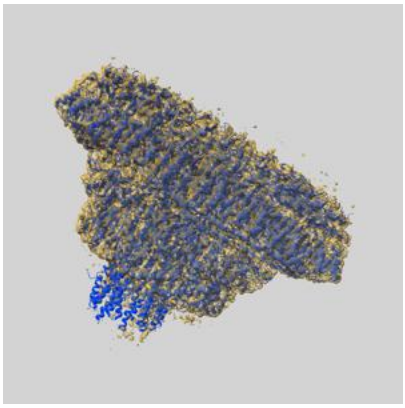
8 Fourier-Shell correlation (i)

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

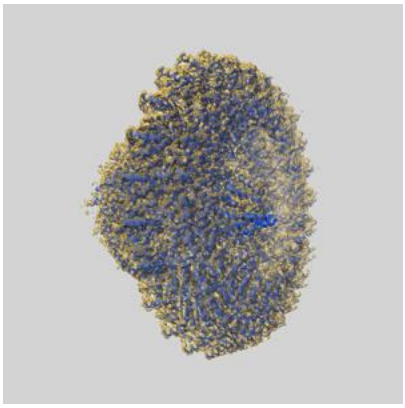
9 Map-model fit

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.

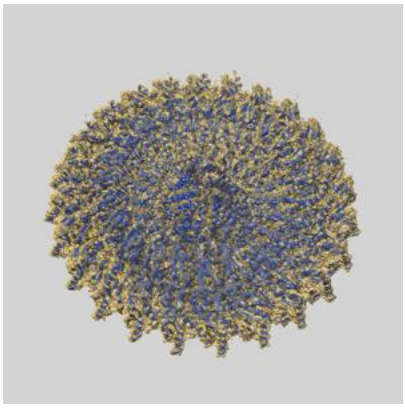
9.1 Map-model overlay



X



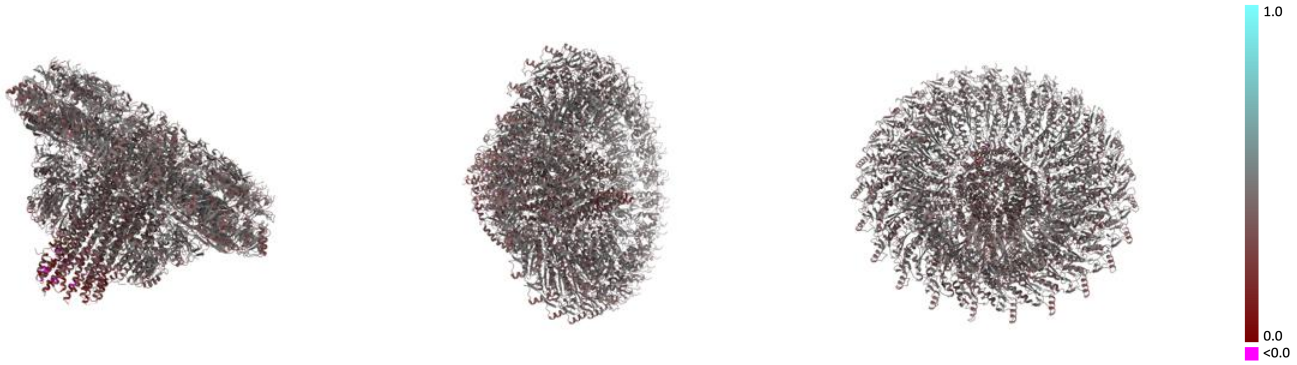
Y



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.

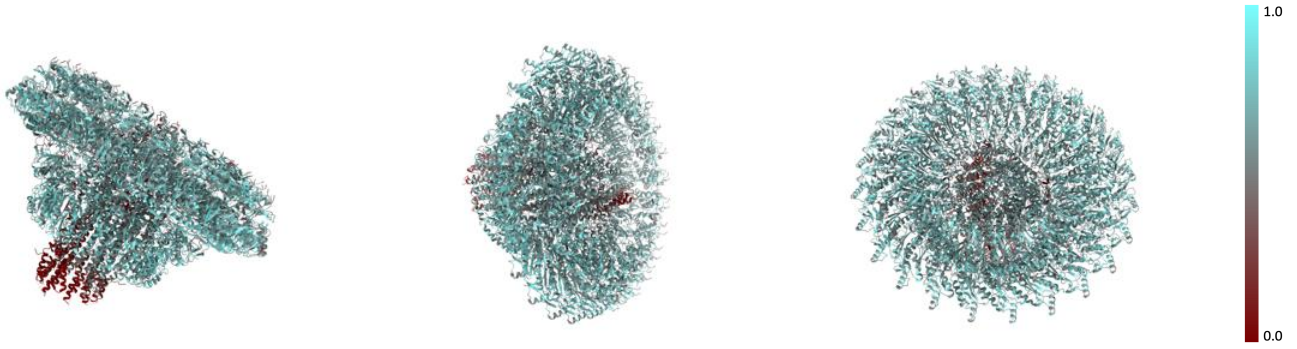
9.2 Q-score mapped to coordinate model



X Y Z

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

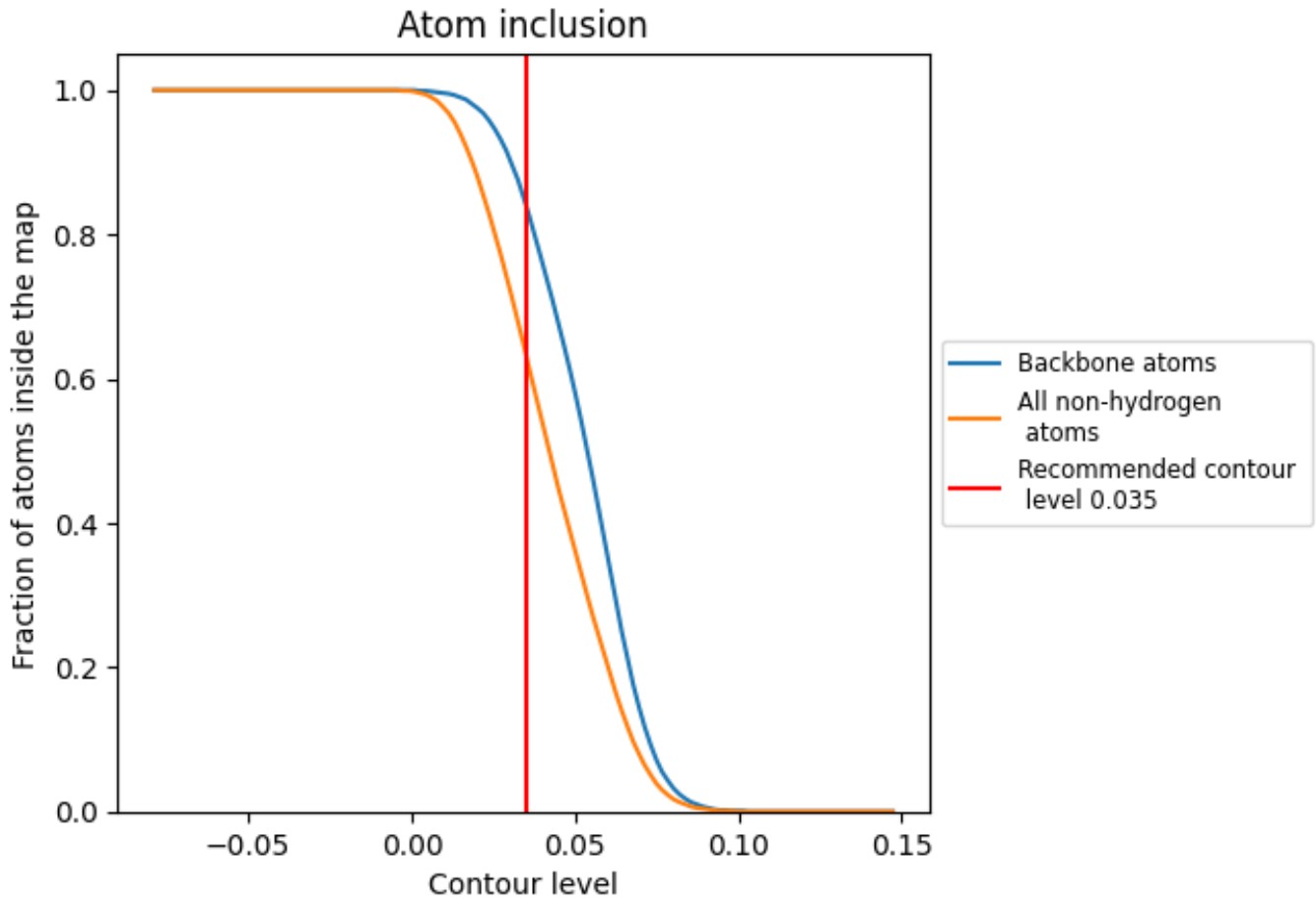
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).

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