



## wwPDB EM Validation Summary Report ⓘ

Jun 3, 2026 – 05:40 PM EDT

PDB ID : 9YFG / pdb\_00009yfg  
EMDB ID : EMD-72891  
Title : Flagellar outer membrane complex in *Vibrio cholerae* at disassembled, closed state  
Authors : Guo, W.; Yue, J.; Liu, J.  
Deposited on : 2025-09-25  
Resolution : 3.55 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](mailto: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>.

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

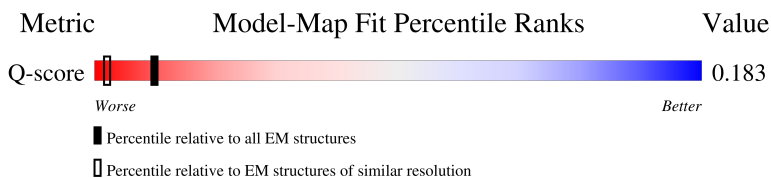
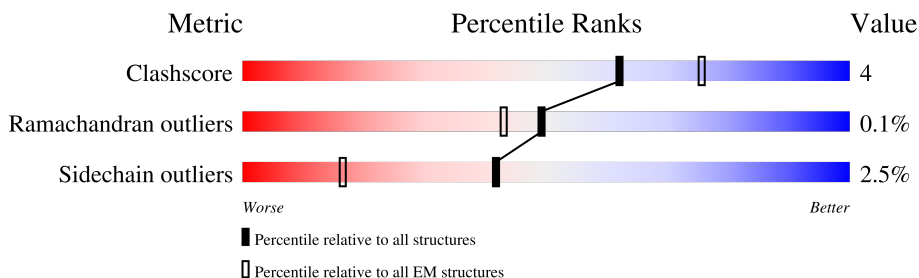
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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





The reported resolution of this entry is 3.55 Å.

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
















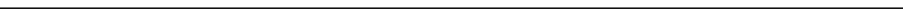











Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12819 ( 3.05 - 4.05 )

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  $\geq 3$ , 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	227	
1	Ab	227	
1	Ac	227	
1	Ad	227	


























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Mol	Chain	Length	Quality of chain
1	Ae	227	 80% 18% .
1	Af	227	 79% 19% ..
1	Ag	227	 78% 19% ..
1	Ah	227	 77% 21% ..
1	Ai	227	 83% 14% ..
1	Aj	227	 82% 15% .
1	Ak	227	 81% 17% .
1	Al	227	 83% 15% .
1	Am	227	 79% 19% .
1	An	227	 81% 17% .
1	Ao	227	 85% 12% .
1	Ap	227	 83% 15% .
1	Aq	227	 83% 15% .
1	Ar	227	 79% 19% .
1	As	227	 81% 17% .
1	At	227	 78% 20% .
1	Au	227	 78% 20% .
1	Av	227	 81% 17% .
1	Aw	227	 85% 13% .
1	Ax	227	 80% 19% .
1	Ay	227	 81% 17% .
1	Az	227	 78% 20% .
2	Ba	343	 85% 15%
2	Bb	343	 85% 15% .
2	Bc	343	 83% 17%



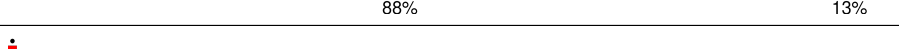
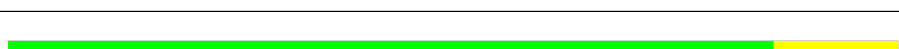



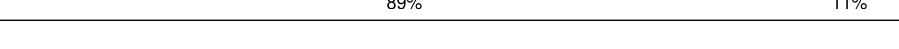



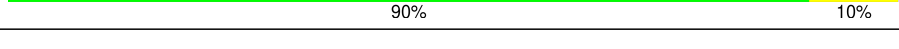

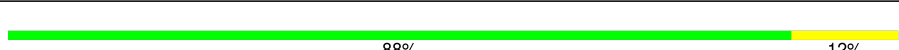


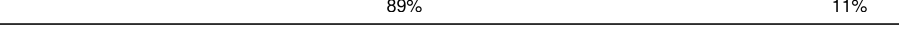







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Mol	Chain	Length	Quality of chain
2	Bd	343	
2	Be	343	
2	Bf	343	
2	Bg	343	
2	Bh	343	
2	Bi	343	
2	Bj	343	
2	Bk	343	
2	Bl	343	
2	Bm	343	
2	Bn	343	
2	Bo	343	
2	Bp	343	
2	Bq	343	
2	Br	343	
2	Bs	343	
2	Bt	343	
2	Bu	343	
2	Bv	343	
2	Bw	343	
2	Bx	343	
2	By	343	
2	Bz	343	
3	Ca	352	
3	Cb	352	







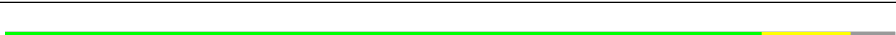
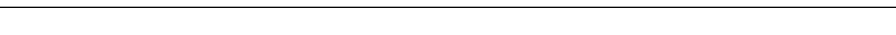
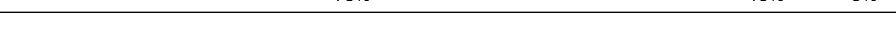
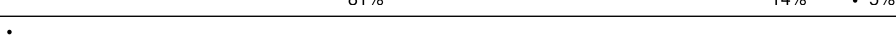
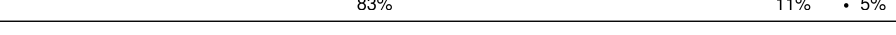
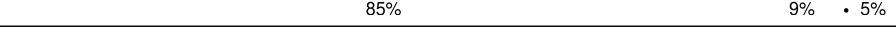













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Mol	Chain	Length	Quality of chain
3	Cc	352	 91% 9%
3	Cd	352	 89% 11%
3	Ce	352	 88% 13%
3	Cf	352	 88% 11%
3	Cg	352	 86% 14%
3	Ch	352	 86% 14%
3	Ci	352	 90% 9%
3	Cj	352	 88% 13%
3	Ck	352	 89% 11%
3	Cl	352	 91% 9%
3	Cm	352	 86% 14%
3	Cn	352	 89% 11%
3	Co	352	 88% 13%
3	Cp	352	 90% 10%
3	Cq	352	 88% 12%
3	Cr	352	 88% 12%
3	Cs	352	 88% 12%
3	Ct	352	 86% 13%
3	Cu	352	 89% 11%
3	Cv	352	 89% 11%
3	Cw	352	 89% 11%
3	Cx	352	 91% 9%
3	Cy	352	 89% 11%
3	Cz	352	 89% 10%
4	Da	271	85% 9% 5%

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Mol	Chain	Length	Quality of chain
4	Db	271	 86% 8% • 5%
4	Dc	271	 82% 13% • 5%
4	Dd	271	 84% 11% 5%
4	De	271	 82% 12% • 5%
4	Df	271	 81% 13% • 5%
4	Dg	271	 80% 14% • 5%
4	Dh	271	 85% 10% 5%
4	Di	271	 78% 15% • 5%
4	Dj	271	 81% 14% • 5%
4	Dk	271	 83% 11% • 5%
4	Dl	271	 85% 9% • 5%
4	Dm	271	 82% 13% 5%
4	Dn	271	 84% 11% 5%
4	Do	271	 83% 11% • 5%
4	Dp	271	 86% 9% 5%
4	Dq	271	 83% 11% • 5%
4	Dr	271	 83% 11% • 5%
4	Ds	271	 82% 11% • 5%
4	Dt	271	 83% 11% • 5%
4	Du	271	 79% 14% • 5%
4	Dv	271	 83% 11% • 5%
4	Dw	271	 82% 11% • 5%
4	Dx	271	 83% 11% 5%
4	Dy	271	 82% 12% • 5%
4	Dz	271	 86% 9% • 5%

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Mol	Chain	Length	Quality of chain
5	Ea	183	
5	Eb	183	
5	Ec	183	
5	Ed	183	
5	Ee	183	
5	Ef	183	
5	Eg	183	
5	Eh	183	
5	Ei	183	
5	Ej	183	
5	Ek	183	
5	El	183	
5	Em	183	
5	En	183	
5	Eo	183	
5	Ep	183	
5	Eq	183	
5	Er	183	
5	Es	183	
5	Et	183	
5	Eu	183	
5	Ev	183	
5	Ew	183	
5	Ex	183	
5	Ey	183	

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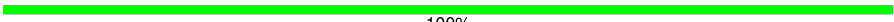














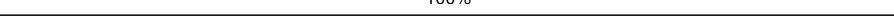









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Mol	Chain	Length	Quality of chain
5	Ez	183	
6	Fa	12	
6	Fb	12	
6	Fc	12	
6	Fd	12	
6	Fe	12	
6	Ff	12	
6	Fg	12	
6	Fh	12	
6	Fi	12	
6	Fj	12	
6	Fk	12	
6	Fl	12	
6	Fm	12	
6	Fn	12	
6	Fo	12	
6	Fp	12	
6	Fq	12	
6	Fr	12	
6	Fs	12	
6	Ft	12	
6	Fu	12	
6	Fv	12	
6	Fw	12	
6	Fx	12	

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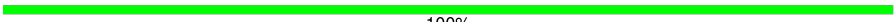


























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Mol	Chain	Length	Quality of chain
6	Fy	12	 100%
6	Fz	12	 92% 8%
6	Ga	12	 92% 8%
6	Gb	12	 83% 17%
6	Gc	12	 83% 17%
6	Gd	12	 75% 25%
6	Ge	12	 100%
6	Gf	12	 17% 100%
6	Gg	12	 100%
6	Gh	12	 92% 8%
6	Gi	12	 100%
6	Gj	12	 92% 8%
6	Gk	12	 92% 8%
6	Gl	12	 83% 17%
6	Gm	12	 100%
6	Gn	12	 92% 8%
6	Go	12	 83% 17%
6	Gp	12	 92% 8%
6	Gq	12	 75% 25%
6	Gr	12	 92% 8%
6	Gs	12	 8% 100%
6	Gt	12	 8% 92% 8%
6	Gu	12	 92% 8%
6	Gv	12	 92% 8%
6	Gw	12	 83% 17%














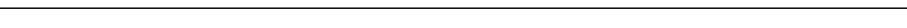











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Mol	Chain	Length	Quality of chain
6	Gx	12	 100%
6	Gy	12	 92% 8%
6	Gz	12	 92% 8%
7	Ha	105	 84% 13% ..
7	Hc	105	 87% 11% ..
7	He	105	 90% 8% ..
7	Hg	105	 86% 13% .
7	Hi	105	 91% 8% .
7	Hk	105	 90% 10% .
7	Hm	105	 90% 8% ..
7	Ho	105	 90% 10% .
7	Hq	105	 86% 12% ..
7	Hs	105	 87% 11% ..
7	Hu	105	 87% 11% ..
7	Hw	105	 87% 11% ..
7	Hy	105	 90% 10% .
7	Ia	105	 86% 12% ..
7	Ic	105	 90% 9% ..
7	Ie	105	 90% 8% ..
7	Ig	105	 85% 14% .
7	Ii	105	 88% 11% .
7	Ik	105	 89% 10% .
7	Im	105	 84% 14% ..
7	Io	105	 86% 12% ..
7	Iq	105	 89% 9% ..



























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Mol	Chain	Length	Quality of chain
7	Is	105	 88% 10% ..
7	Iu	105	 88% 10% ..
7	Iw	105	 88% 10% ..
7	Iy	105	 90% 9% .
7	Ja	105	 86% 12% ..
7	Jc	105	 84% 14% ..
7	Je	105	 83% 15% ..
7	Jg	105	 86% 11% ..
7	Ji	105	 83% 14% ..
7	Js	105	 85% 12% ..
7	Jm	105	 87% 10% ..
7	Jo	105	 85% 14% .
7	Jq	105	 84% 14% ..
7	Js	105	 85% 13% ..
7	Ju	105	 84% 14% ..
7	Jw	105	 87% 10% ..
7	Jy	105	 88% 11% .
7	Ka	105	 87% 11% ..
7	Kc	105	 89% 10% ..
7	Ke	105	 86% 12% ..
7	Kg	105	 90% 9% ..
7	Ki	105	 89% 10% .
7	Kk	105	 90% 9% ..
7	Km	105	 89% 10% ..
7	Ko	105	 89% 10% ..







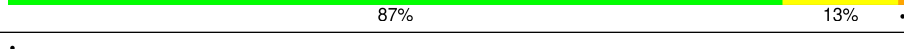
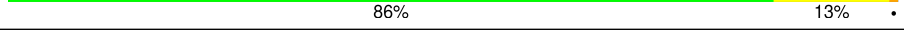
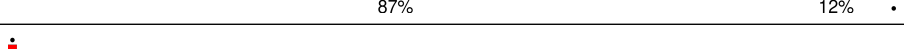
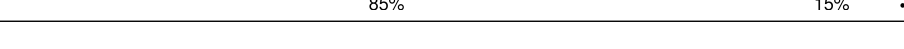
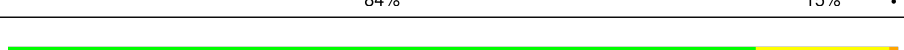

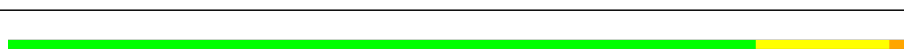

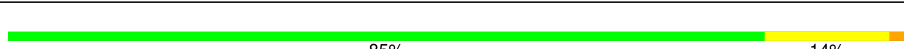





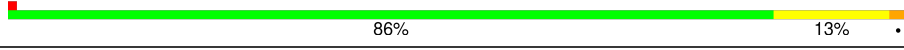
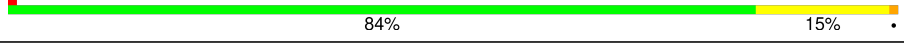



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Mol	Chain	Length	Quality of chain
7	Kq	105	
7	Ks	105	
7	Ku	105	
7	Kw	105	
7	Ky	105	
7	La	105	
7	Lc	105	
7	Le	105	
7	Lg	105	
7	Li	105	
7	Lk	105	
8	Hb	190	
8	Hd	190	
8	Hf	190	
8	Hh	190	
8	Hj	190	
8	Hl	190	
8	Hn	190	
8	Hp	190	
8	Hr	190	
8	Ht	190	
8	Hv	190	
8	Hx	190	
8	Hx	190	
8	Hx	190	
8	Hx	190	














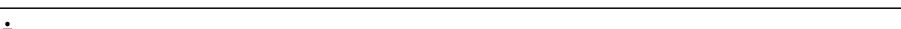





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Mol	Chain	Length	Quality of chain
8	Id	190	
8	If	190	
8	Ih	190	
8	Ij	190	
8	Il	190	
8	In	190	
8	Ip	190	
8	Ir	190	
8	It	190	
8	Iv	190	
8	Ix	190	
8	Iz	190	
8	Jb	190	
8	Jd	190	
8	Jf	190	
8	Jh	190	
8	Jj	190	
8	Jl	190	
8	Jn	190	
8	Jp	190	
8	Jr	190	
8	Jt	190	
8	Jv	190	
8	Jx	190	
8	Jz	190	

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Mol	Chain	Length	Quality of chain
8	Kb	190	 86% 13% .
8	Kd	190	 86% 13% .
8	Kf	190	 88% 12% .
8	Kh	190	 86% 13% .
8	Kj	190	 87% 12% .
8	Kl	190	 87% 12% .
8	Kn	190	 89% 10% .
8	Kp	190	 84% 15% .
8	Kr	190	 84% 15% .
8	Kt	190	 85% 13% .
8	Kv	190	 86% 13% .
8	Kx	190	 87% 12% .
8	Kz	190	 86% 13% .
8	Lb	190	 86% 12% .
8	Ld	190	 83% 16% .
8	Lf	190	 84% 15% .
8	Lh	190	 83% 16% .
8	Lj	190	 84% 15% .
8	Ll	190	 82% 17% .

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 412635 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 Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ab	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ac	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ad	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ae	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Af	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ag	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ah	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ai	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Aj	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ak	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Al	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Am	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	An	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ao	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ap	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Aq	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ar	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	As	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	At	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Au	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Av	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Aw	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ax	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Ay	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		
1	Az	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		

- Molecule 2 is a protein called Flagellar P-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ba	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bb	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bc	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bd	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Be	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bf	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bg	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bh	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bi	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bj	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Bk	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bl	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bm	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bn	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bo	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bp	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bq	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Br	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bs	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bt	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bu	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bv	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bw	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bx	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	By	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		
2	Bz	343	Total	C	N	O	S	0	0
			2501	1570	436	488	7		

- Molecule 3 is a protein called Flagellar protein FlgT.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ca	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cb	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cc	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Cd	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Ce	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cf	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cg	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Ch	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Ci	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cj	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Ck	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cl	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cm	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cn	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Co	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cp	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cq	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cr	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cs	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Ct	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cu	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cv	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cw	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cx	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Cy	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
3	Cz	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

- Molecule 4 is a protein called Sodium-type flagellar protein MotY.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Da	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Db	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dc	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dd	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	De	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Df	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dg	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dh	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Di	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dj	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dk	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dl	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dm	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dn	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Do	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dp	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dq	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Dr	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Ds	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dt	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Du	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dv	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dw	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dx	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
4	Dy	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
4	Dz	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		

- Molecule 5 is a protein called Sodium-type flagellar protein MotX.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ea	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Eb	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Ec	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ed	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Ee	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ef	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Eg	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Eh	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Ei	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ej	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ek	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	El	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Em	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	En	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Eo	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ep	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Eq	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Er	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Es	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Et	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Eu	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ev	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Ew	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ex	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
5	Ey	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
5	Ez	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		

- Molecule 6 is a protein called FlgP.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Fa	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Fb	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Fc	12	Total	C	N	O	S	0	0
			105	66	19	19	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	Fd	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fe	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Ff	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fg	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fh	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fi	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fj	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fk	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fl	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fm	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fn	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fo	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fp	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fq	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fr	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fs	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Ft	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fu	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fv	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fw	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fx	12	Total 105	C 66	N 19	O 19	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	Fy	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Fz	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Ga	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gb	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gc	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gd	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Ge	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gf	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gg	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gh	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gi	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gj	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gk	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gl	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gm	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gn	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Go	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gp	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gq	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gr	12	Total 105	C 66	N 19	O 19	S 1	0	0
6	Gs	12	Total 105	C 66	N 19	O 19	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	Gt	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Gu	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Gv	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Gw	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Gx	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Gy	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
6	Gz	12	Total	C	N	O	S	0	0
			105	66	19	19	1		

- Molecule 7 is a protein called Lipoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ha	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hc	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	He	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hg	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hi	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hk	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hm	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Ho	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hq	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hs	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hu	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Hw	104	Total	C	N	O	S	0	0
			828	506	155	163	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Hy	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ia	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ic	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ie	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ig	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ii	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ik	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Im	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Io	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Iq	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Is	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Iu	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Iw	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Iy	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ja	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Jc	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Je	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Jg	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ji	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Js	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Jm	104	Total 828	C 506	N 155	O 163	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Jo	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Jq	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Js	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ju	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Jw	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Jy	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ka	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Kc	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ke	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Kg	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ki	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Kk	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Km	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ko	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Kq	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ks	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ku	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Kw	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Ky	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	La	104	Total 828	C 506	N 155	O 163	S 4	0	0
7	Lc	104	Total 828	C 506	N 155	O 163	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Le	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Lg	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Li	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
7	Lk	104	Total	C	N	O	S	0	0
			828	506	155	163	4		

- Molecule 8 is a protein called FlgO domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Hb	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hd	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hf	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hh	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hj	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hl	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hn	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hp	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hr	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Ht	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hv	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hx	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Hz	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Ib	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Id	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	If	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Ih	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Ij	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Il	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	In	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Ip	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Ir	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	It	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Iv	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Ix	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Iz	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jb	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jd	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jf	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jh	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jj	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jl	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jn	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jp	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jr	190	Total 1482	C 928	N 260	O 287	S 7	0	0
8	Jt	190	Total 1482	C 928	N 260	O 287	S 7	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Jv	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Jx	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Jz	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kb	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kd	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kf	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kh	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kj	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kl	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kn	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kp	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kr	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kt	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kv	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kx	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Kz	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Lb	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Ld	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Lf	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Lh	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
8	Lj	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		

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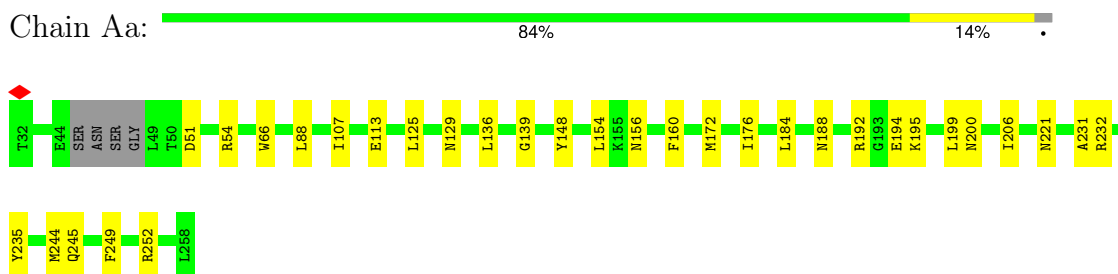
*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L1	190	1482	928	260	287	7	0	0

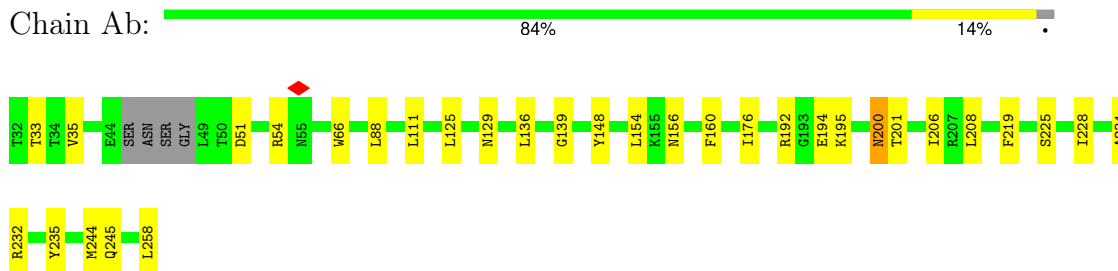
### 3 Residue-property plots

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.

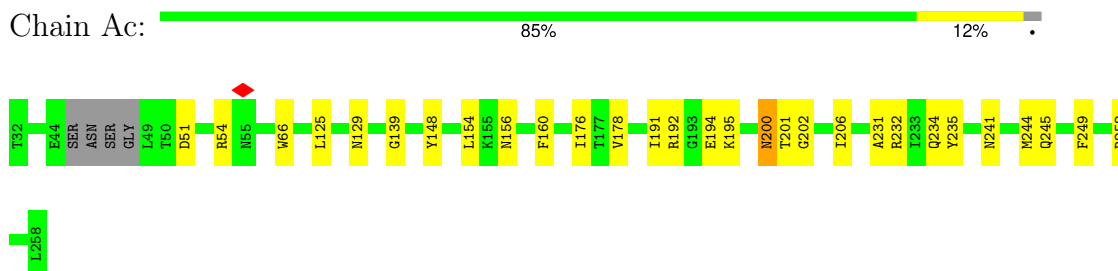
- Molecule 1: Flagellar L-ring protein



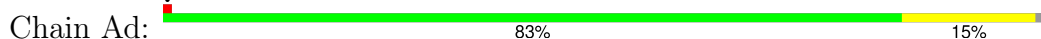
- Molecule 1: Flagellar L-ring protein

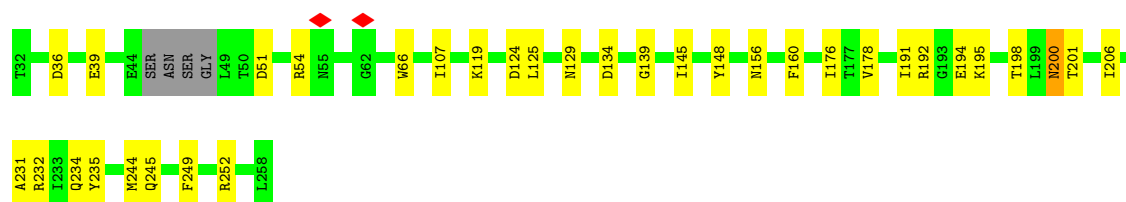


- Molecule 1: Flagellar L-ring protein



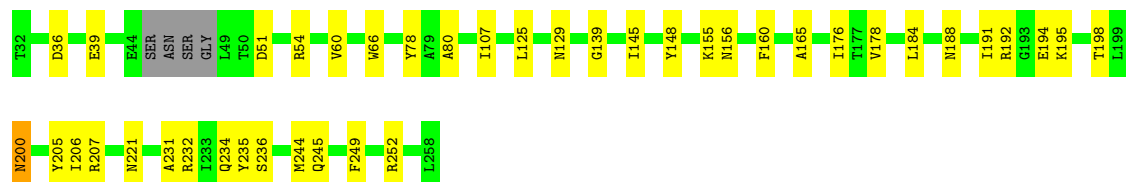
- Molecule 1: Flagellar L-ring protein





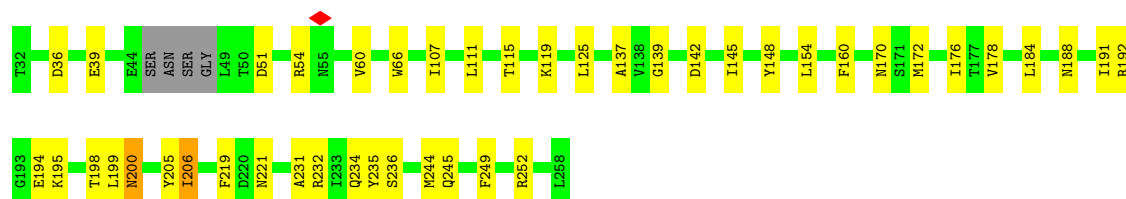
- Molecule 1: Flagellar L-ring protein

Chain Ae:  80%  18%



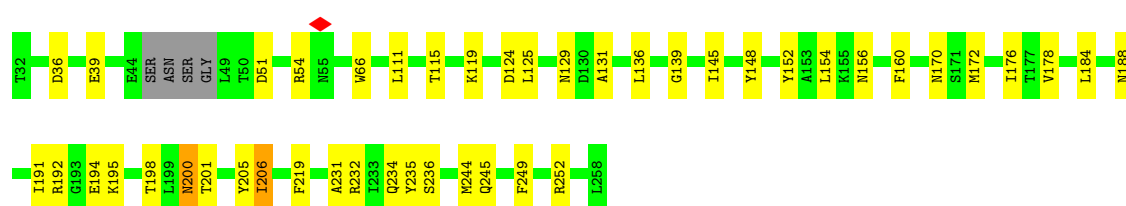
- Molecule 1: Flagellar L-ring protein

Chain Af:  79%  19%



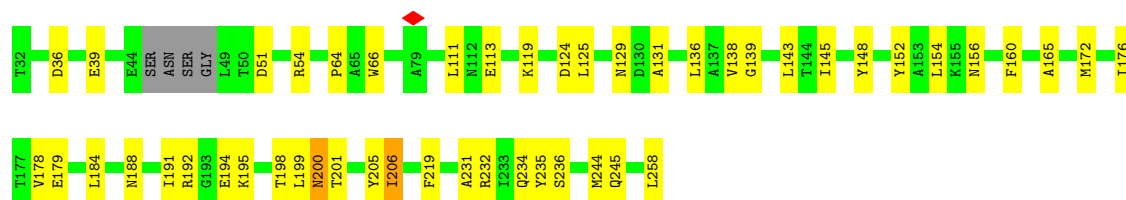
- Molecule 1: Flagellar L-ring protein

Chain Ag:  78%  19%




- Molecule 1: Flagellar L-ring protein

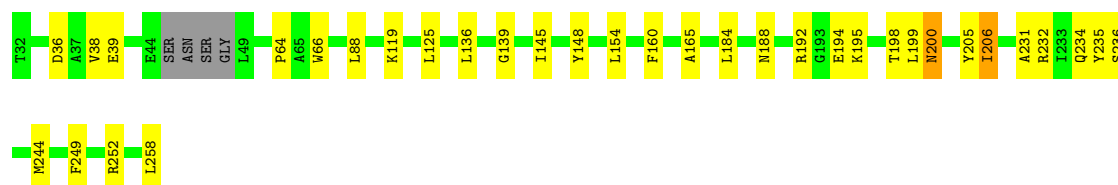
Chain Ah:  77%  21%




- Molecule 1: Flagellar L-ring protein

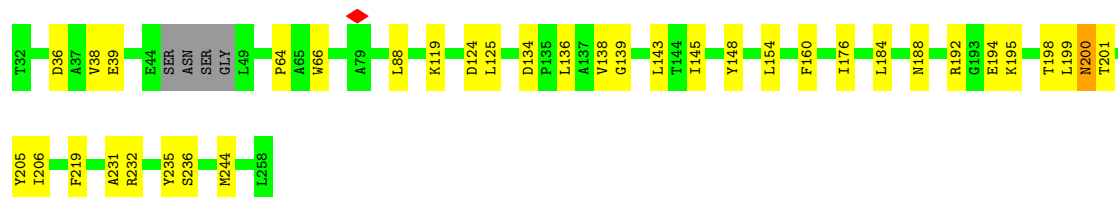


Chain Ai:  83% 14% ..




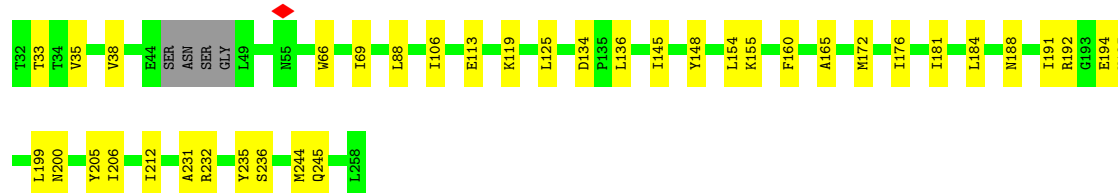
- Molecule 1: Flagellar L-ring protein

Chain Aj:  82% 15% .




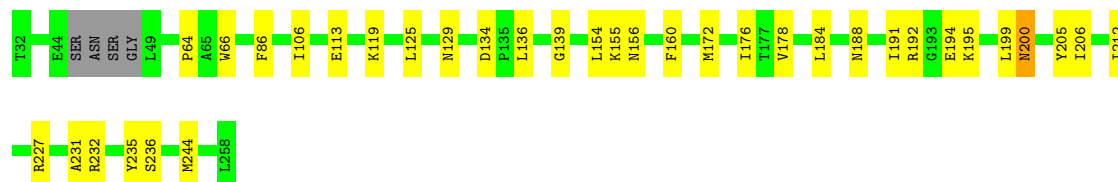
- Molecule 1: Flagellar L-ring protein

Chain Ak:  81% 17% .




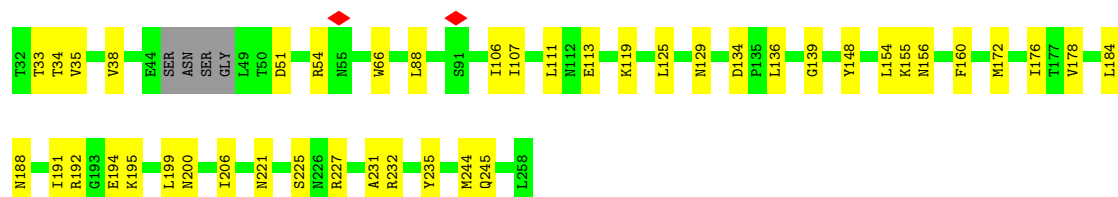
- Molecule 1: Flagellar L-ring protein

Chain Al:  83% 15% .

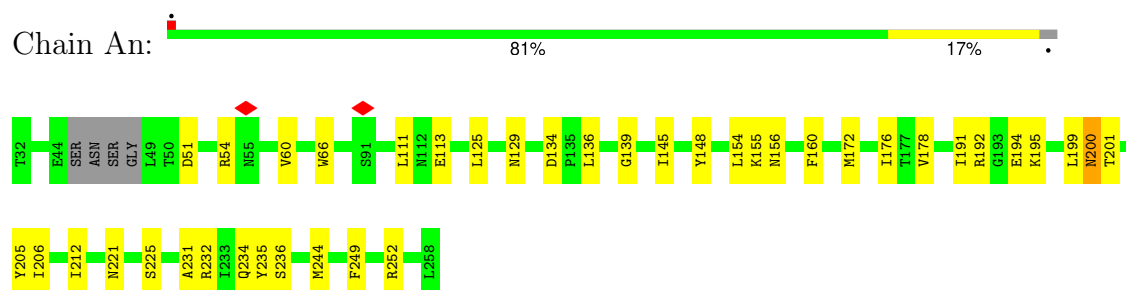


- Molecule 1: Flagellar L-ring protein

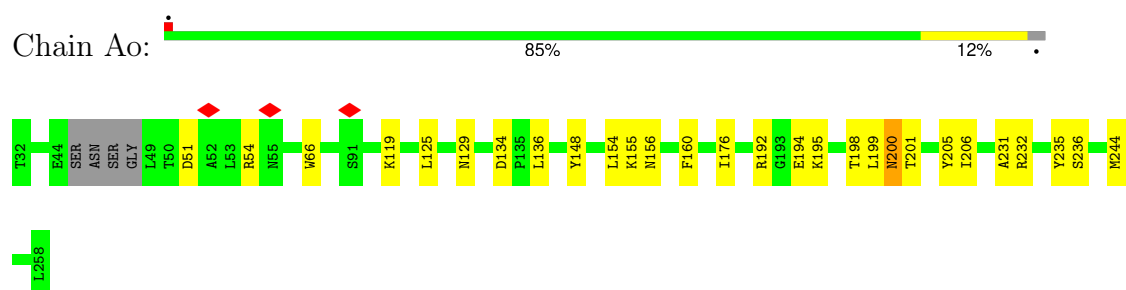
Chain Am:  79% 19% .



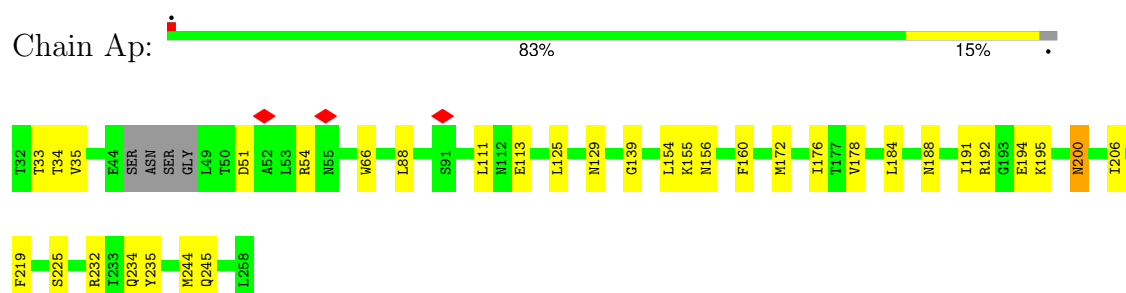
- Molecule 1: Flagellar L-ring protein



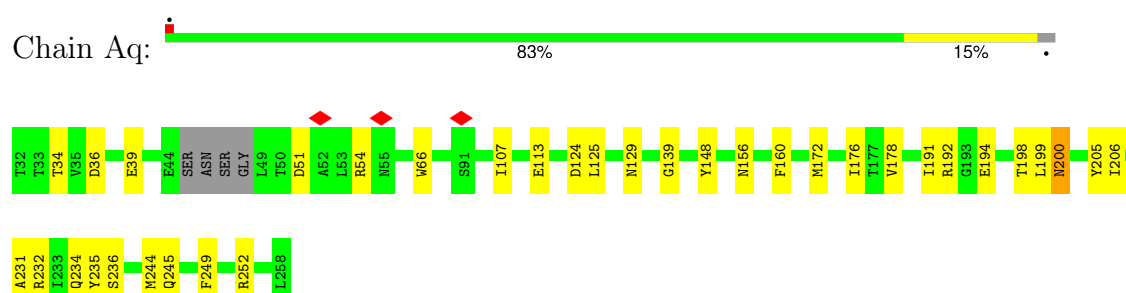
- Molecule 1: Flagellar L-ring protein



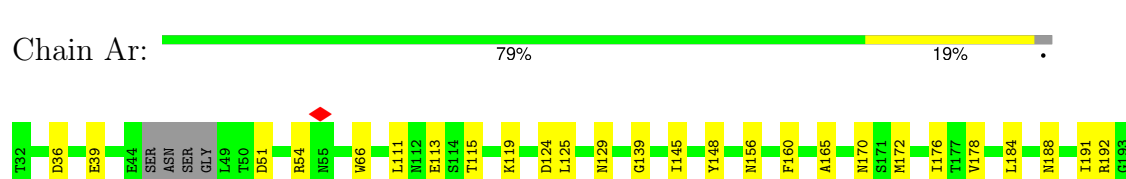
- Molecule 1: Flagellar L-ring protein

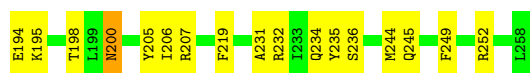


- Molecule 1: Flagellar L-ring protein



- Molecule 1: Flagellar L-ring protein





- Molecule 1: Flagellar L-ring protein

Chain As: 81% 17%



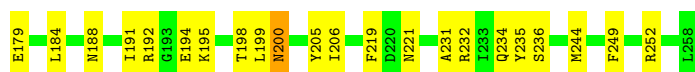
- Molecule 1: Flagellar L-ring protein

Chain At: 78% 20%



- Molecule 1: Flagellar L-ring protein

Chain Au: 78% 20%



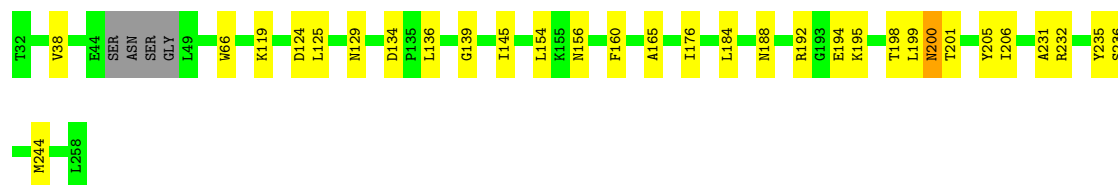
- Molecule 1: Flagellar L-ring protein

Chain Av: 81% 17%

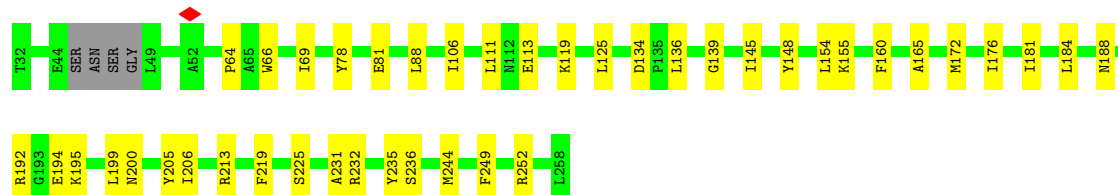
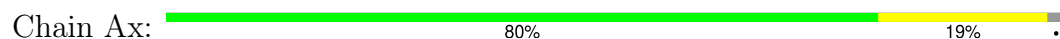


- Molecule 1: Flagellar L-ring protein

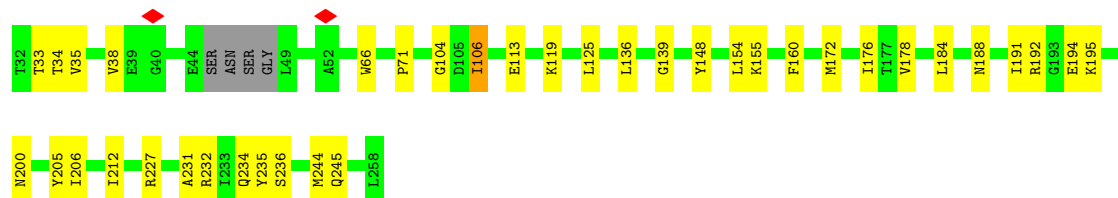
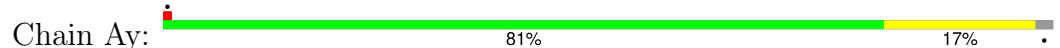
Chain Aw: 85% 13%



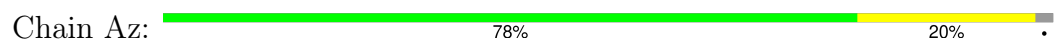
- Molecule 1: Flagellar L-ring protein



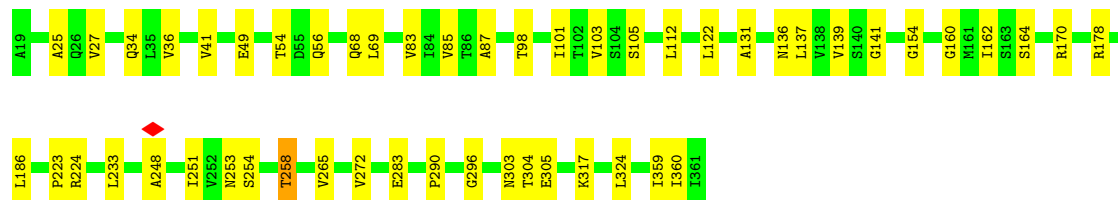
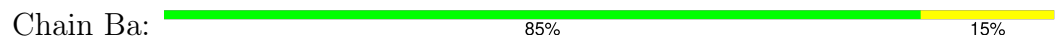
- Molecule 1: Flagellar L-ring protein




- Molecule 1: Flagellar L-ring protein

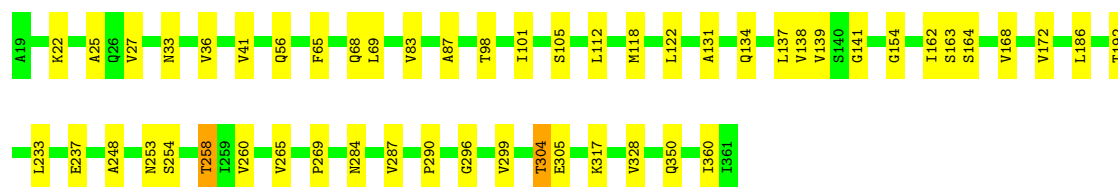


- Molecule 2: Flagellar P-ring protein




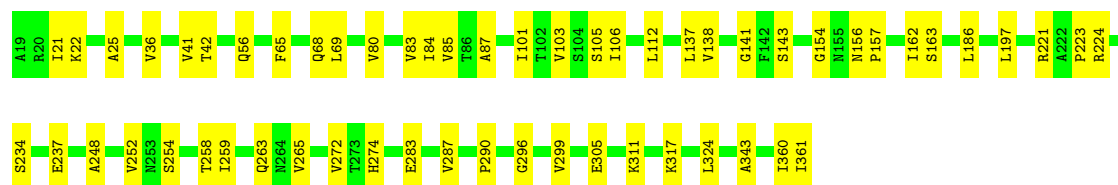
- Molecule 2: Flagellar P-ring protein

Chain Bb:  85% 15%




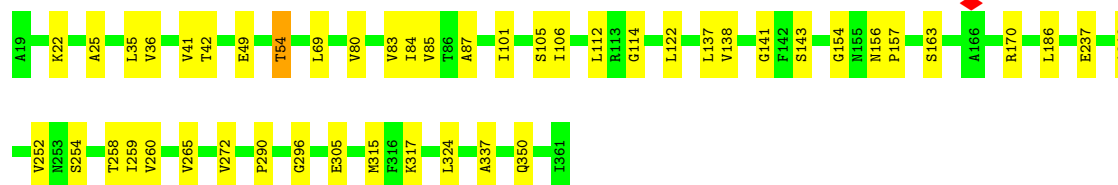
• Molecule 2: Flagellar P-ring protein

Chain Bc:  83% 17%




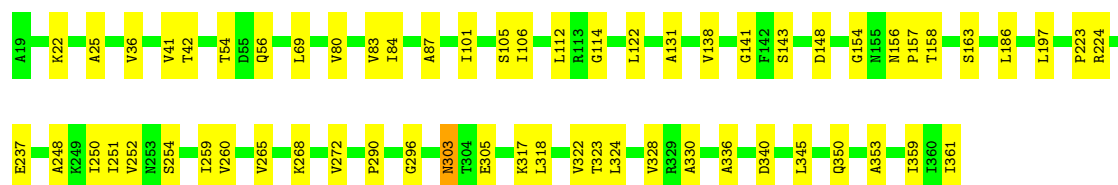
• Molecule 2: Flagellar P-ring protein

Chain Bd:  86% 13%




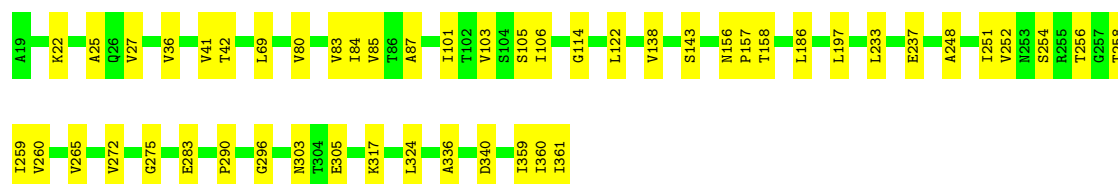
• Molecule 2: Flagellar P-ring protein

Chain Be:  82% 17%




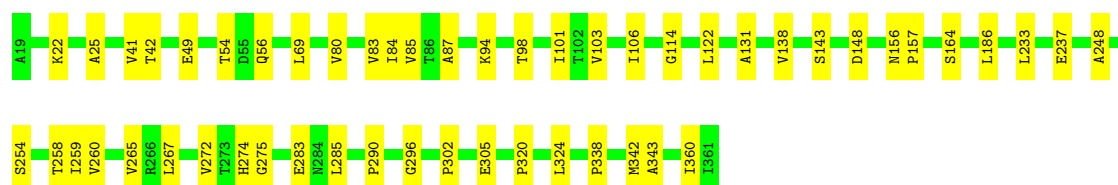
• Molecule 2: Flagellar P-ring protein

Chain Bf:  85% 15%




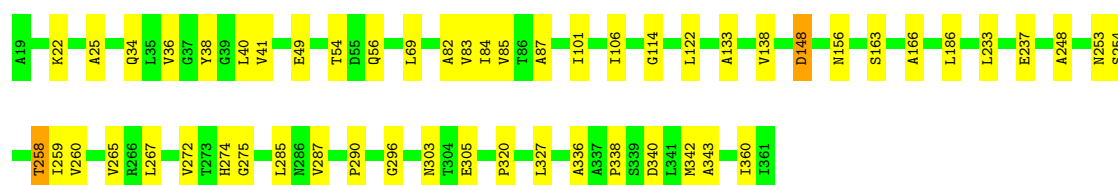
- Molecule 2: Flagellar P-ring protein

Chain Bg:  85% 15%




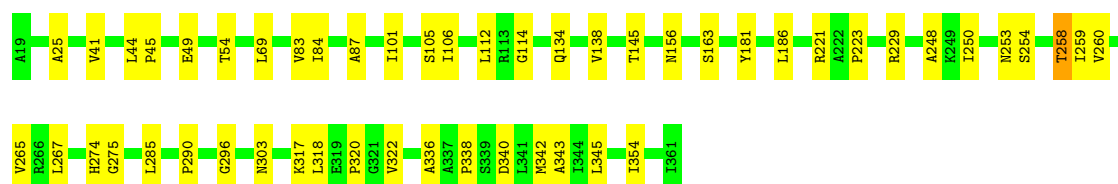
- Molecule 2: Flagellar P-ring protein

Chain Bh:  84% 15%




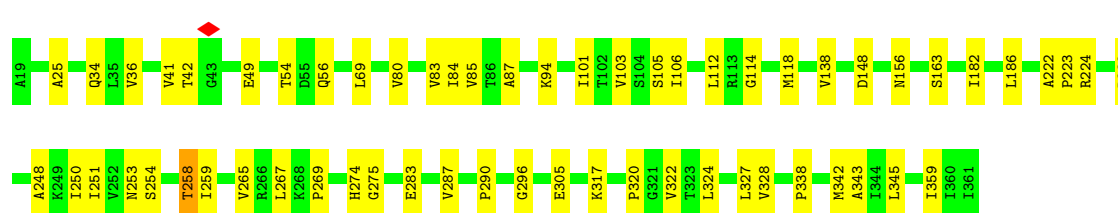
- Molecule 2: Flagellar P-ring protein

Chain Bi:  85% 15%




- Molecule 2: Flagellar P-ring protein

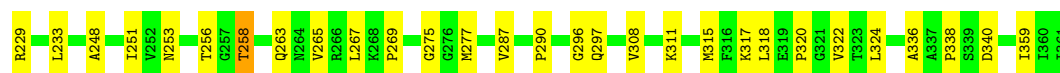
Chain Bj:  83% 17%



- Molecule 2: Flagellar P-ring protein

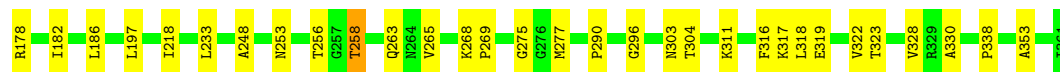
Chain Bk:  83% 17%





• Molecule 2: Flagellar P-ring protein

Chain B1:   82% 18%



• Molecule 2: Flagellar P-ring protein

Chain Bm:   81% 19%



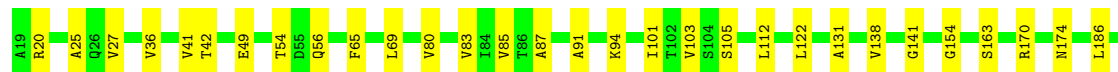
• Molecule 2: Flagellar P-ring protein

Chain Bn:   83% 17%



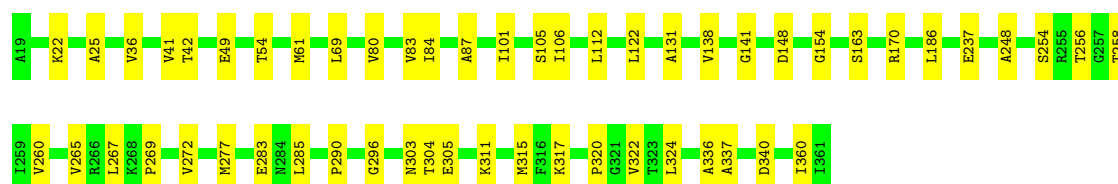
• Molecule 2: Flagellar P-ring protein

Chain Bo:   84% 16%



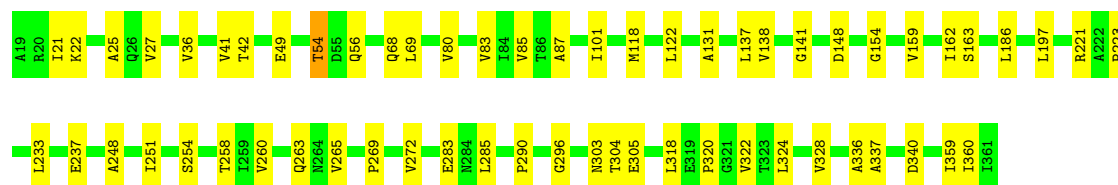
• Molecule 2: Flagellar P-ring protein

Chain Bp:   84% 16%



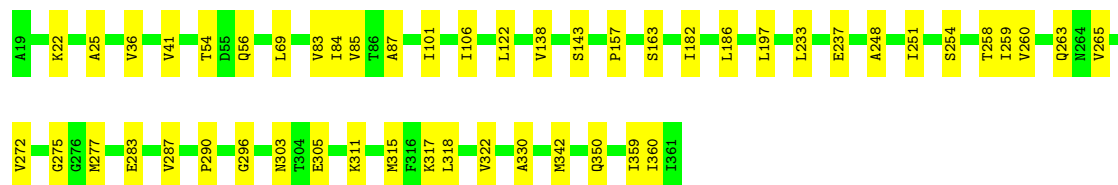
- Molecule 2: Flagellar P-ring protein

Chain Bq:   83% 17%



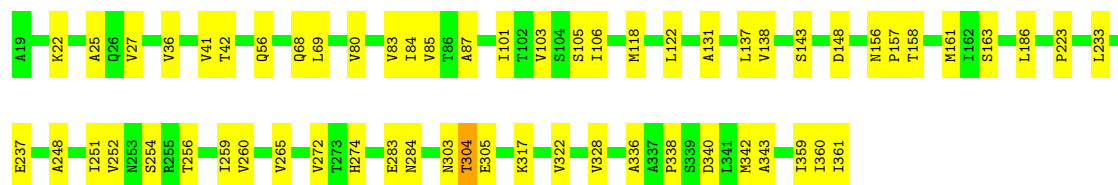
- Molecule 2: Flagellar P-ring protein

Chain Br:   85% 15%



- Molecule 2: Flagellar P-ring protein

Chain Bs:   83% 17%



- Molecule 2: Flagellar P-ring protein

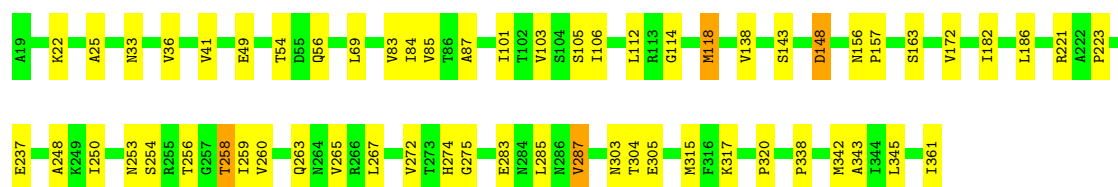
Chain Bt:   88% 12%



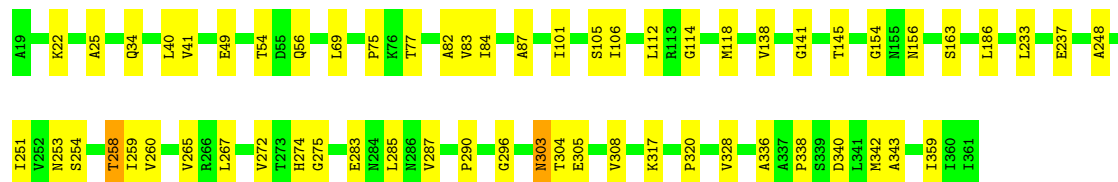
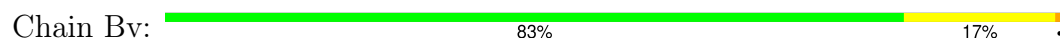
- Molecule 2: Flagellar P-ring protein

Chain Bu:   83% 16%

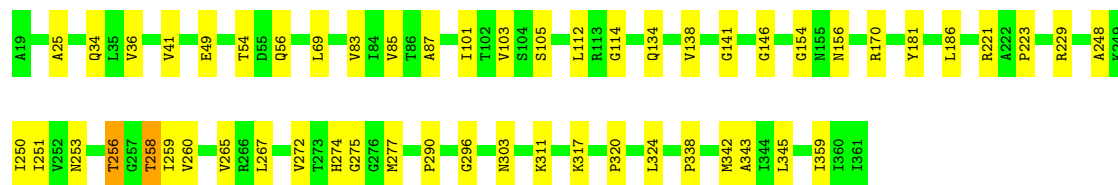
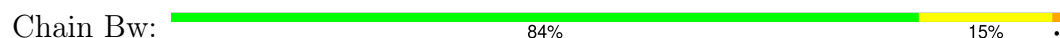




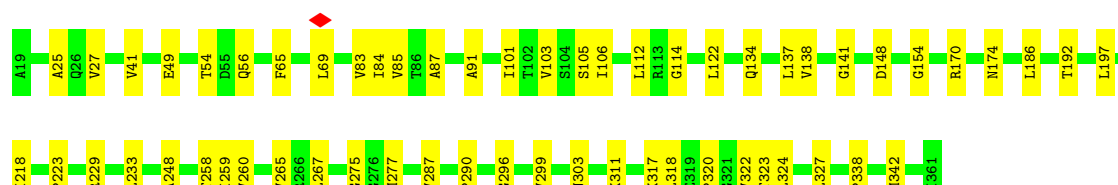
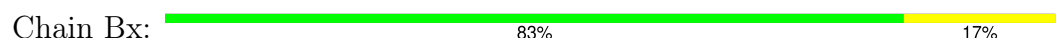
- Molecule 2: Flagellar P-ring protein



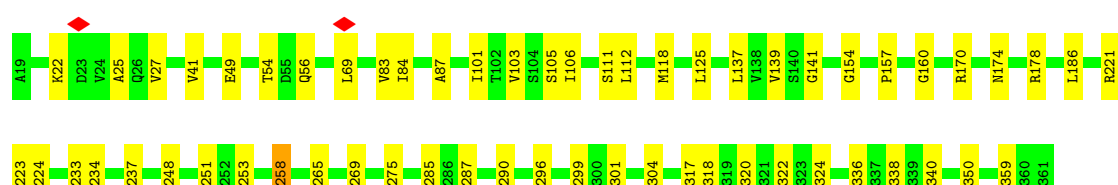
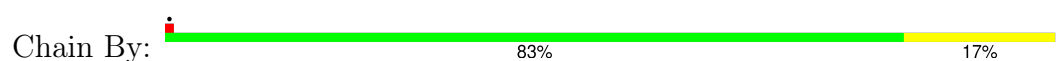
- Molecule 2: Flagellar P-ring protein




- Molecule 2: Flagellar P-ring protein

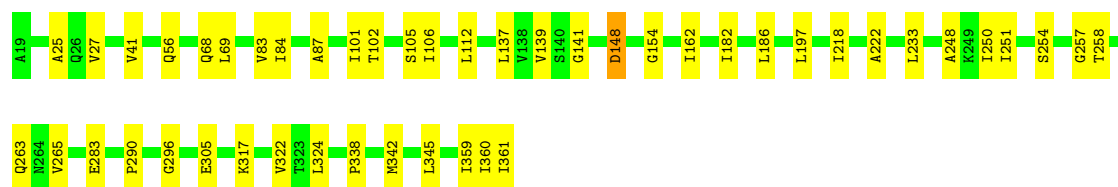


- Molecule 2: Flagellar P-ring protein



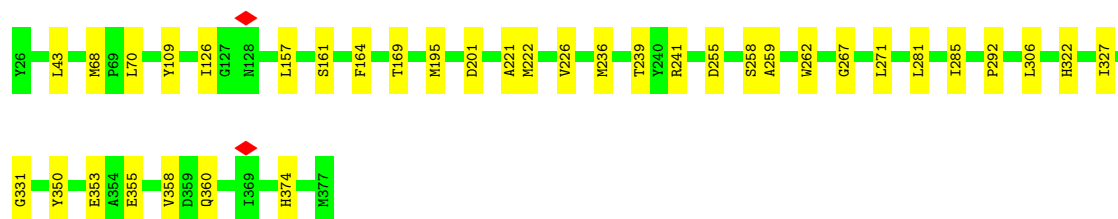
- Molecule 2: Flagellar P-ring protein

Chain Bz:  86% 13%




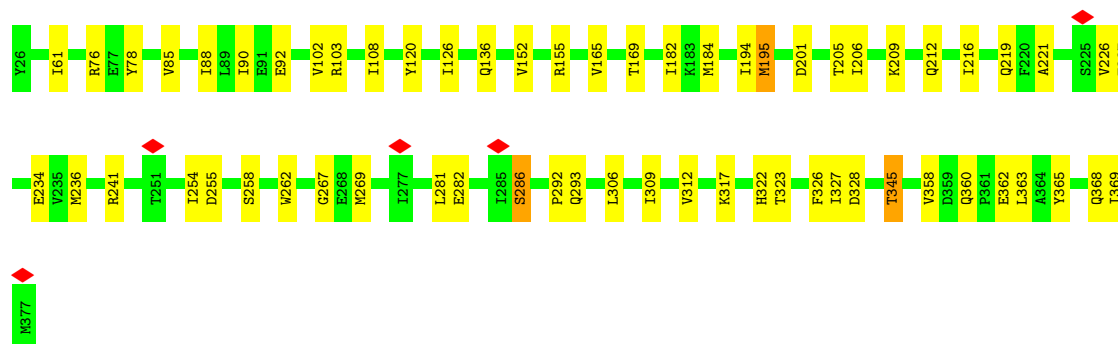
• Molecule 3: Flagellar protein FlgT

Chain Ca:  90% 10%



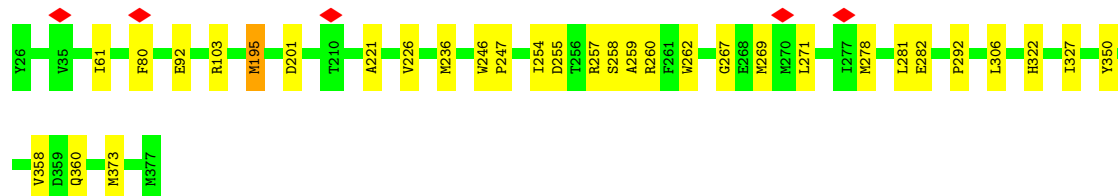
• Molecule 3: Flagellar protein FlgT

Chain Cb:  82% 17%




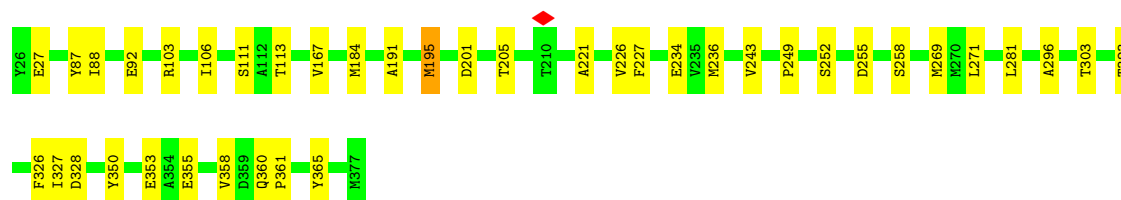
• Molecule 3: Flagellar protein FlgT

Chain Cc:  91% 9%

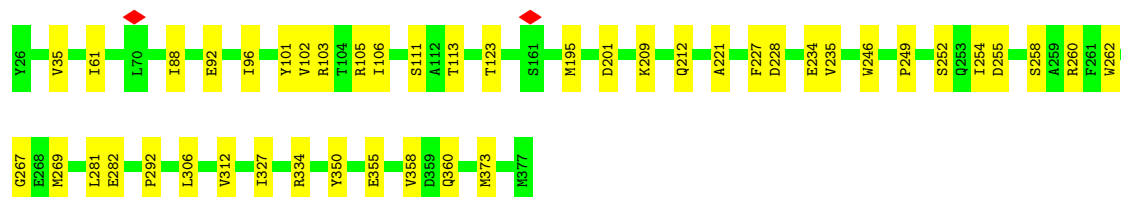
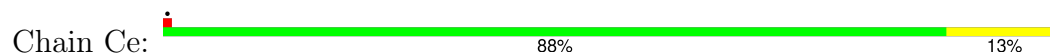


• Molecule 3: Flagellar protein FlgT

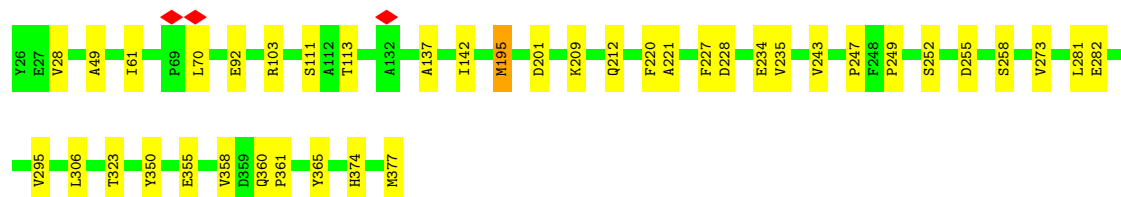
Chain Cd:  89% 11%



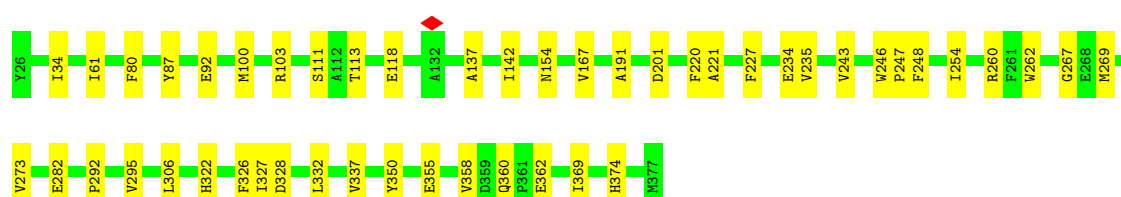
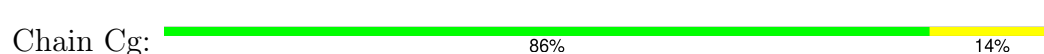
• Molecule 3: Flagellar protein FlgT



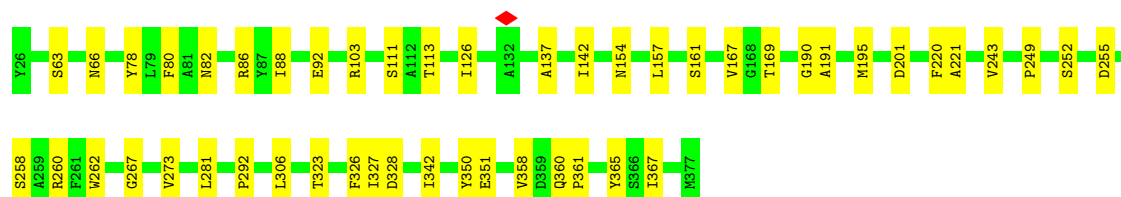
• Molecule 3: Flagellar protein FlgT



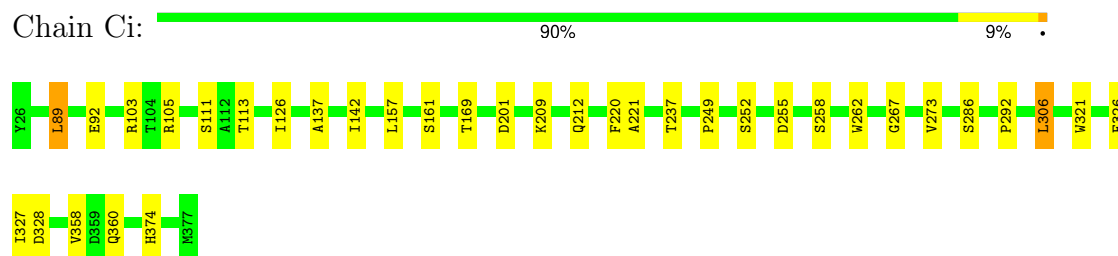
• Molecule 3: Flagellar protein FlgT



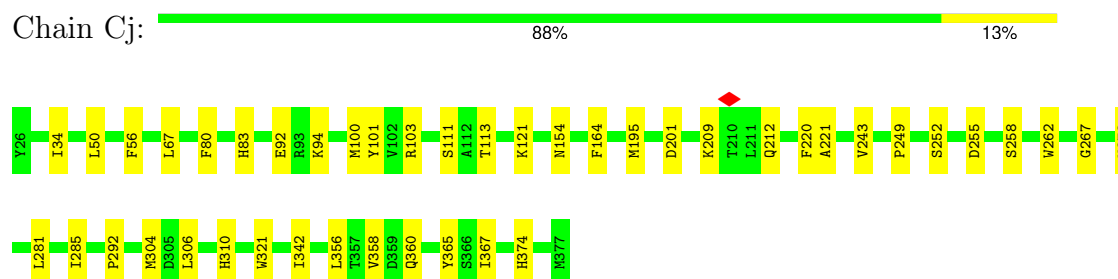
• Molecule 3: Flagellar protein FlgT



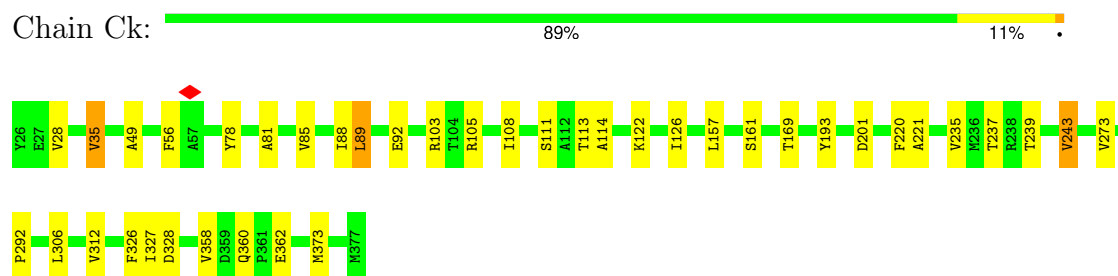
- Molecule 3: Flagellar protein FlgT



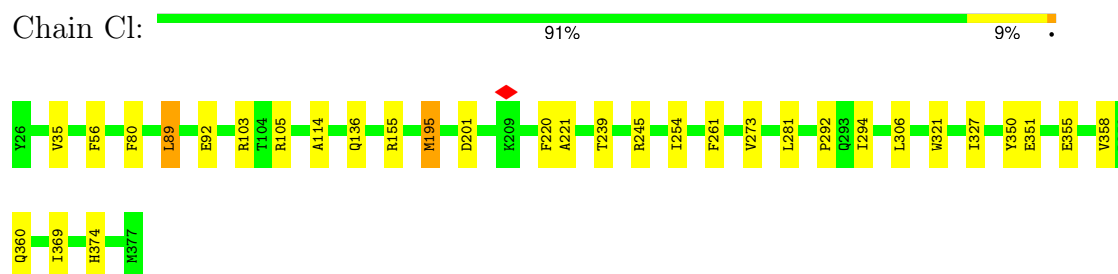
- Molecule 3: Flagellar protein FlgT



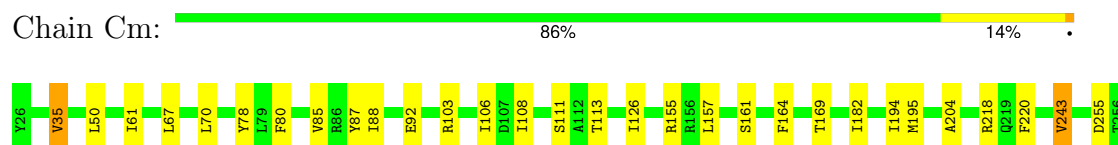
- Molecule 3: Flagellar protein FlgT



- Molecule 3: Flagellar protein FlgT



- Molecule 3: Flagellar protein FlgT





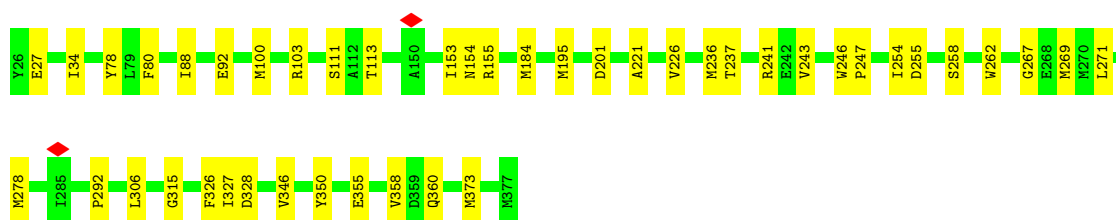
• Molecule 3: Flagellar protein FlgT

Chain Cn: 89% 11%



• Molecule 3: Flagellar protein FlgT

Chain Co: 88% 13%



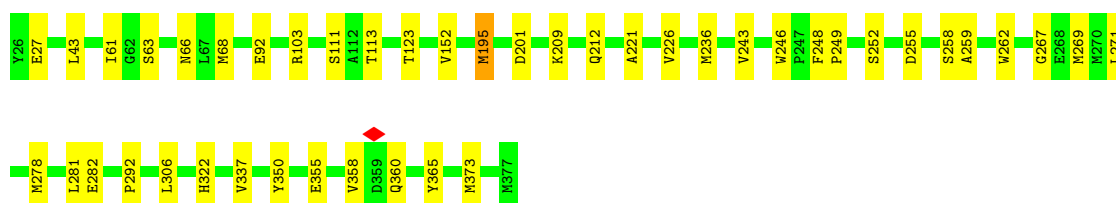
• Molecule 3: Flagellar protein FlgT

Chain Cp: 90% 10%



• Molecule 3: Flagellar protein FlgT

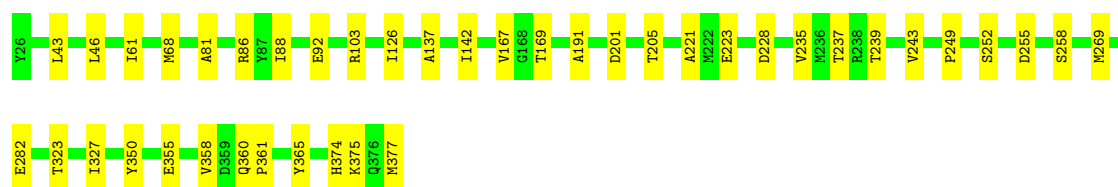
Chain Cq: 88% 12%



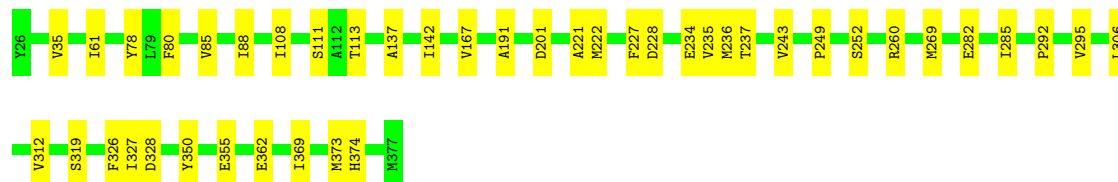
• Molecule 3: Flagellar protein FlgT

Chain Cr: 88% 12%

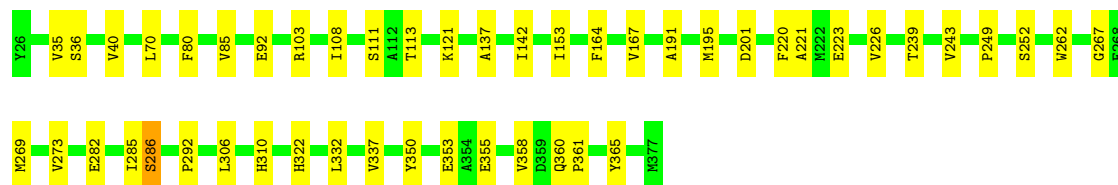
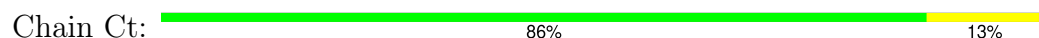




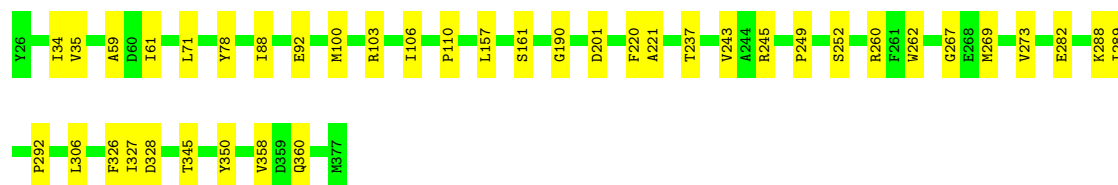
• Molecule 3: Flagellar protein FlgT



• Molecule 3: Flagellar protein FlgT



• Molecule 3: Flagellar protein FlgT

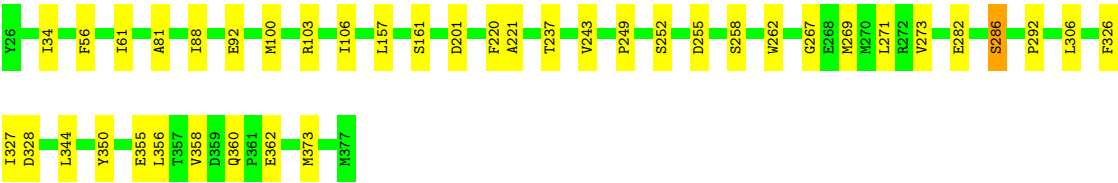


• Molecule 3: Flagellar protein FlgT



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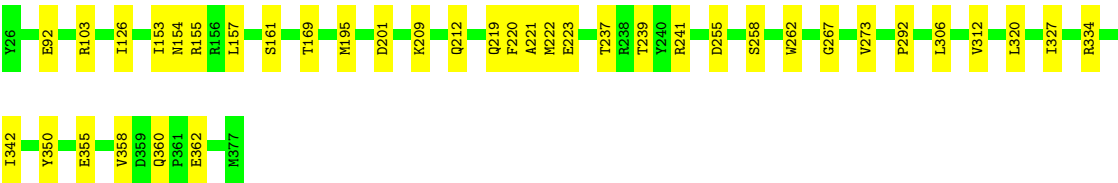
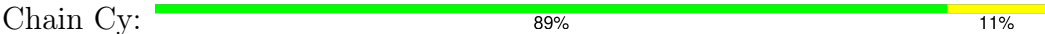




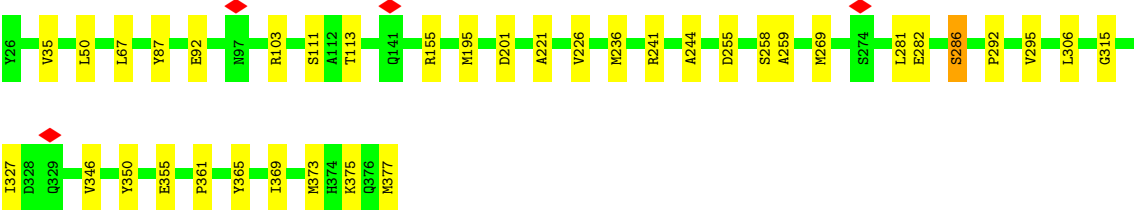
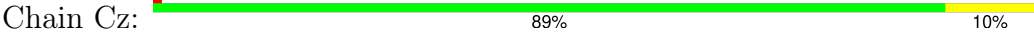
• Molecule 3: Flagellar protein FlgT



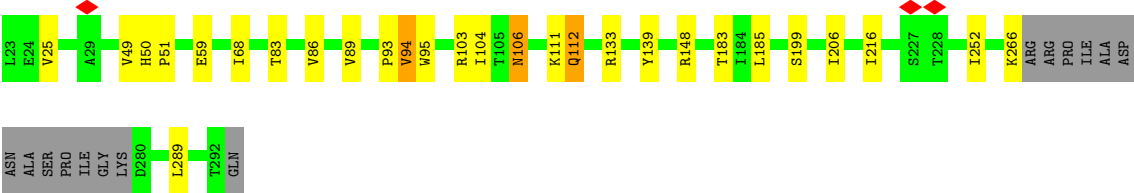
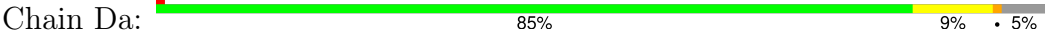
• Molecule 3: Flagellar protein FlgT



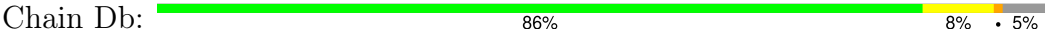
• Molecule 3: Flagellar protein FlgT

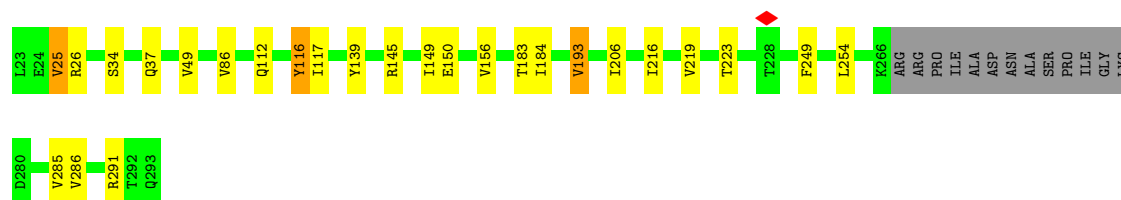


• Molecule 4: Sodium-type flagellar protein MotY

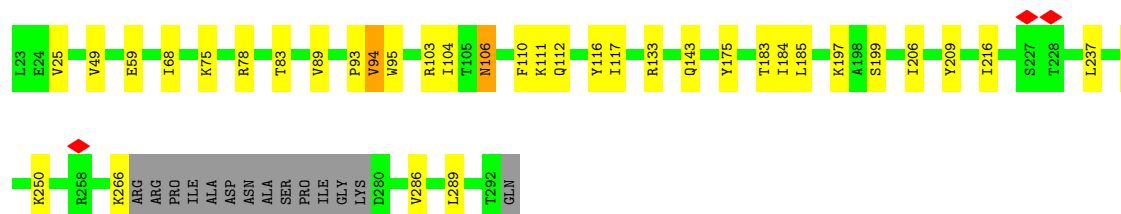
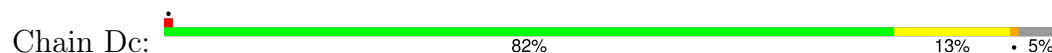


• Molecule 4: Sodium-type flagellar protein MotY

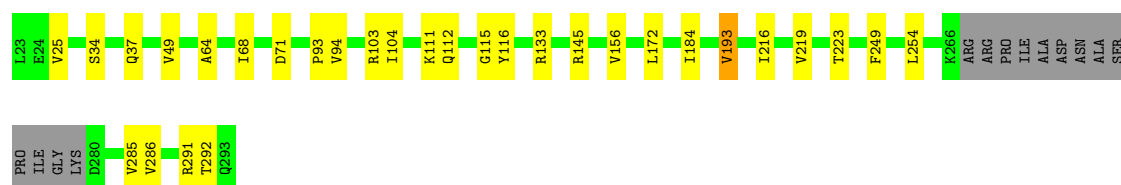
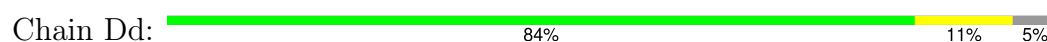




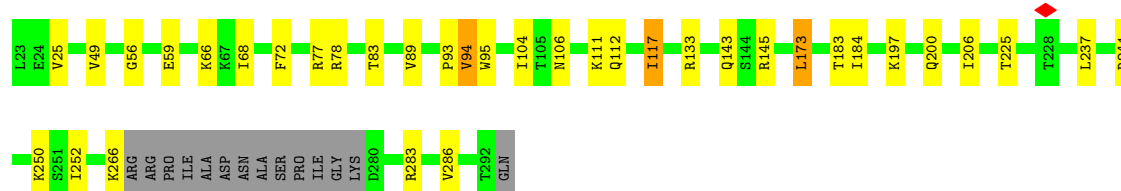
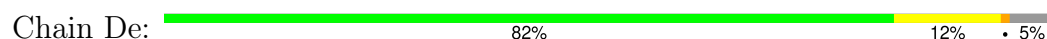
• Molecule 4: Sodium-type flagellar protein MotY



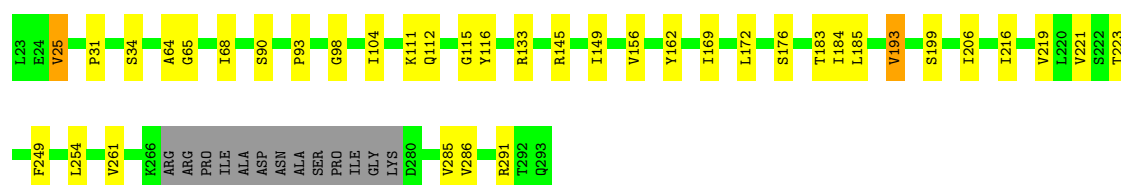
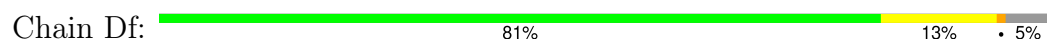
• Molecule 4: Sodium-type flagellar protein MotY



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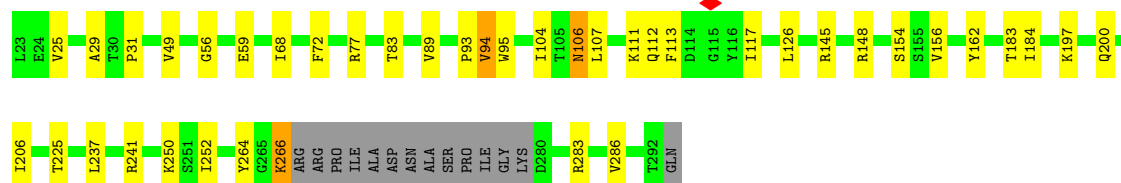
• Molecule 4: Sodium-type flagellar protein MotY




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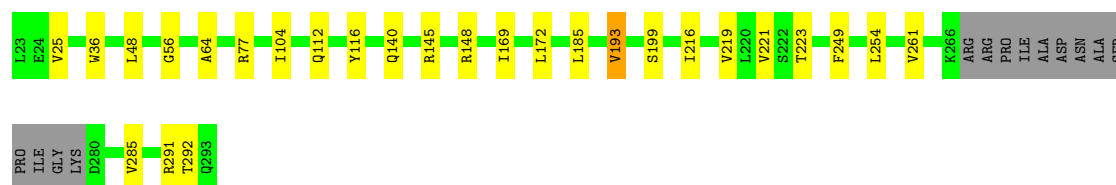


Chain Dg:  80% 14% • 5%




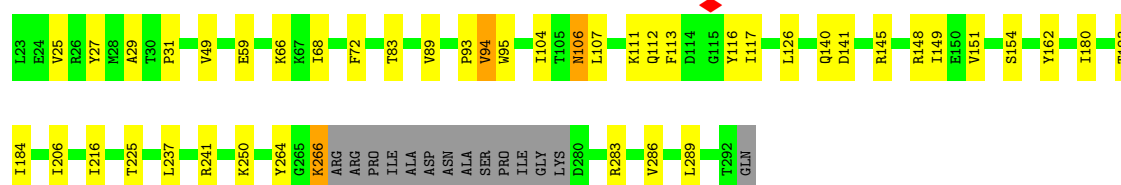
- Molecule 4: Sodium-type flagellar protein MotY

Chain Dh:  85% 10% 5%




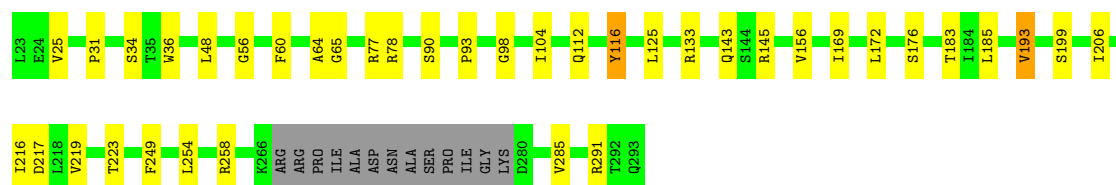
- Molecule 4: Sodium-type flagellar protein MotY

Chain Di:  78% 15% • 5%




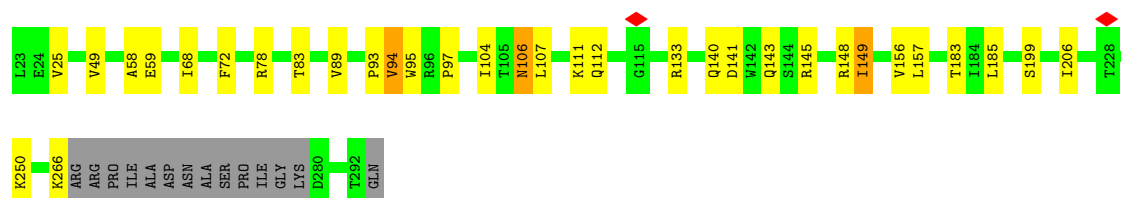
- Molecule 4: Sodium-type flagellar protein MotY

Chain Dj:  81% 14% • 5%

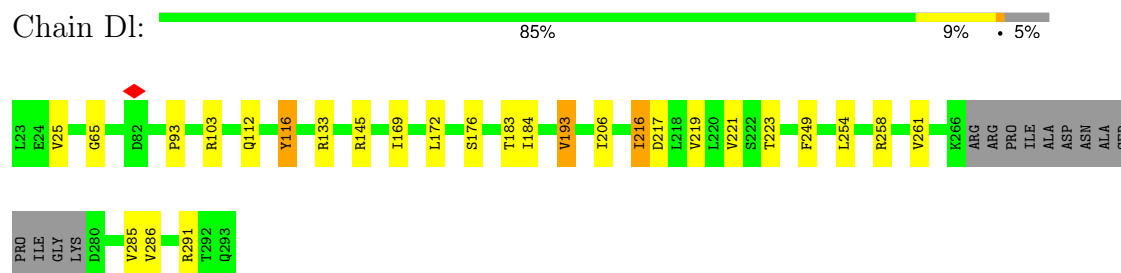


- Molecule 4: Sodium-type flagellar protein MotY

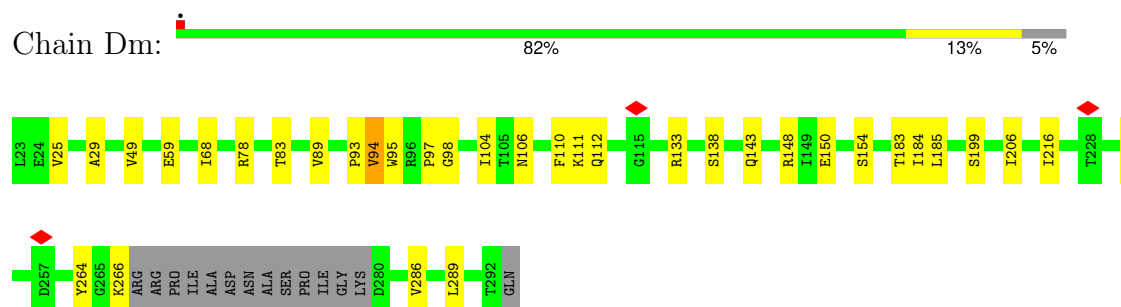
Chain Dk:  83% 11% • 5%



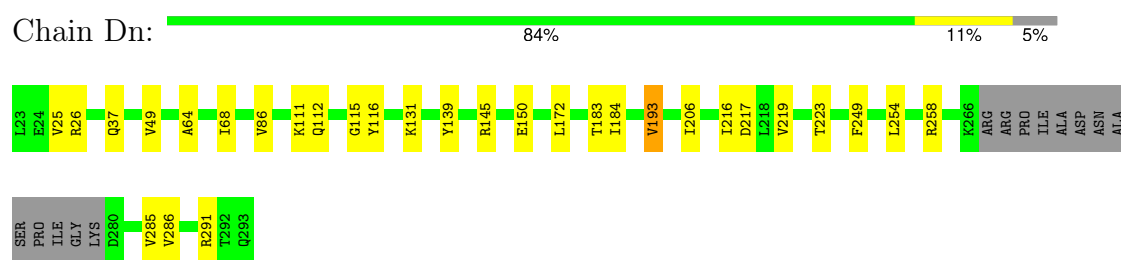
- Molecule 4: Sodium-type flagellar protein MotY



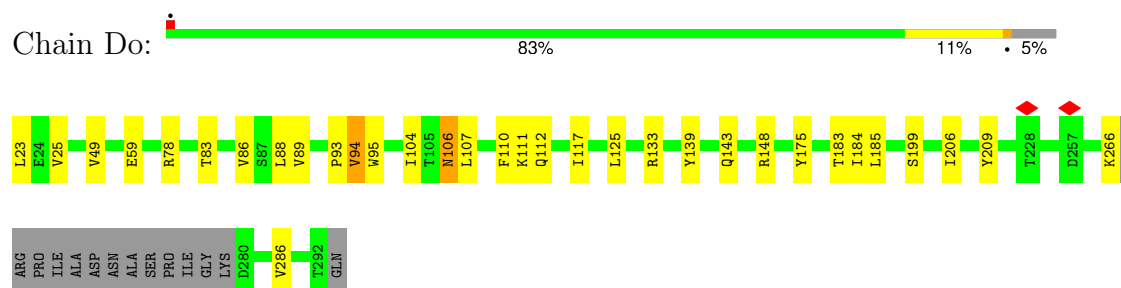
- Molecule 4: Sodium-type flagellar protein MotY



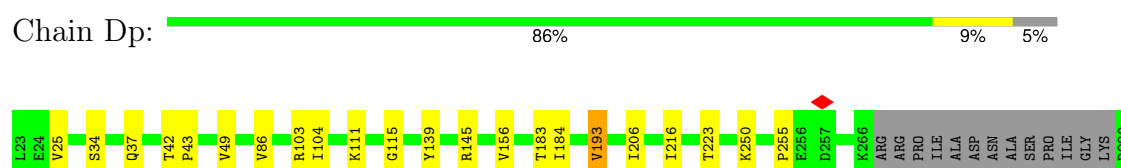
- Molecule 4: Sodium-type flagellar protein MotY



- Molecule 4: Sodium-type flagellar protein MotY



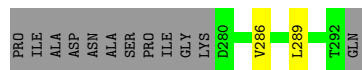
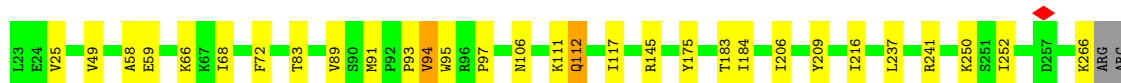
- Molecule 4: Sodium-type flagellar protein MotY





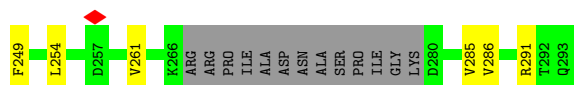
- Molecule 4: Sodium-type flagellar protein MotY

Chain Dq: 83% 11% • 5%



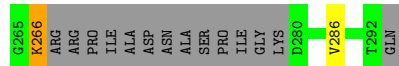
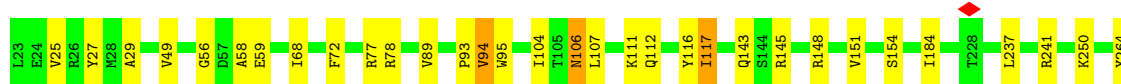
- Molecule 4: Sodium-type flagellar protein MotY

Chain Dr: 83% 11% • 5%



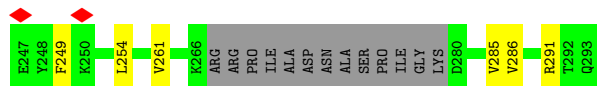
- Molecule 4: Sodium-type flagellar protein MotY

Chain Ds: 82% 11% • 5%



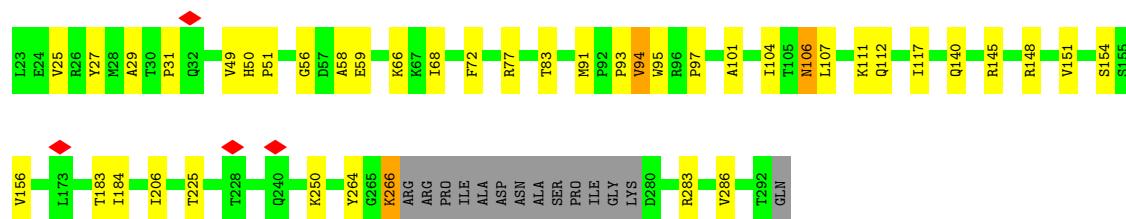
- Molecule 4: Sodium-type flagellar protein MotY

Chain Dt: 83% 11% • 5%

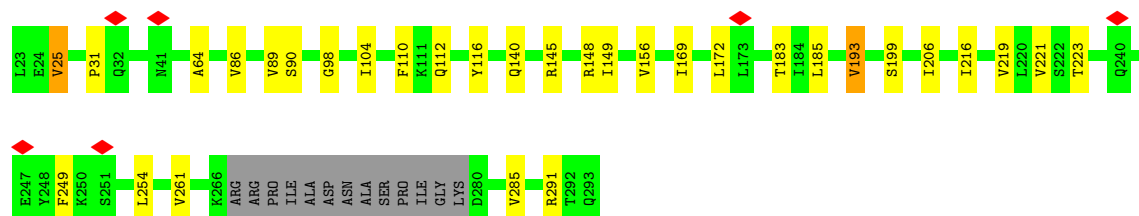
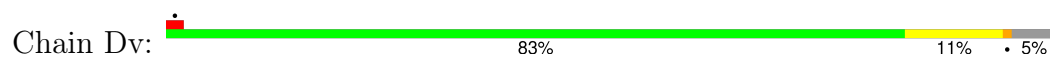


- Molecule 4: Sodium-type flagellar protein MotY

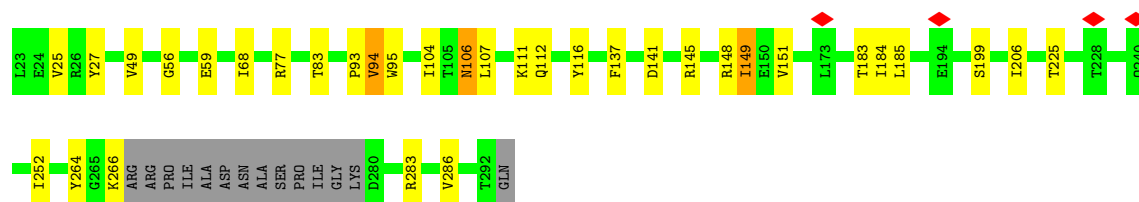
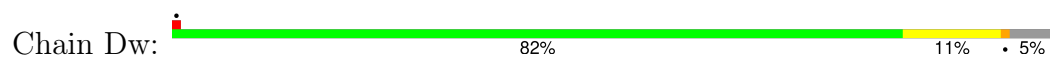
Chain Du: 79% 14% • 5%



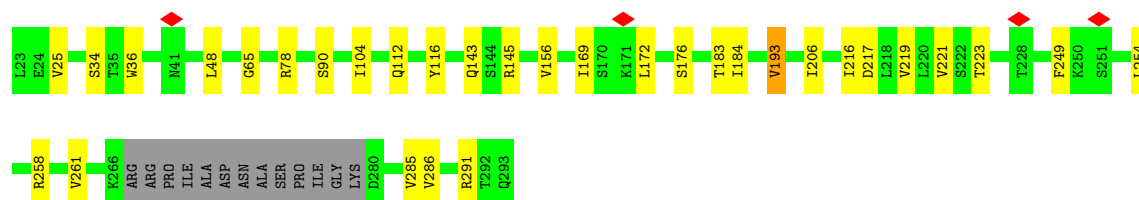
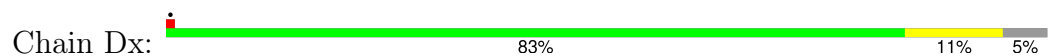
• Molecule 4: Sodium-type flagellar protein MotY



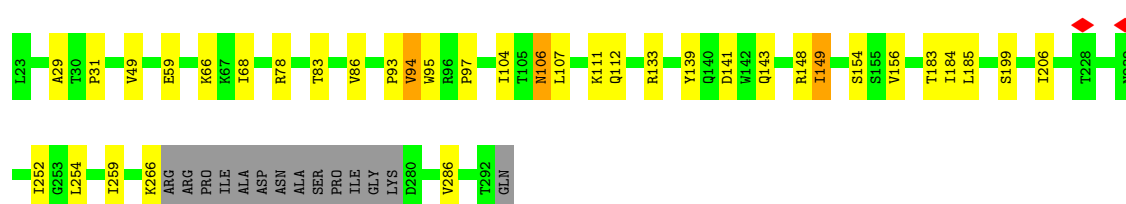
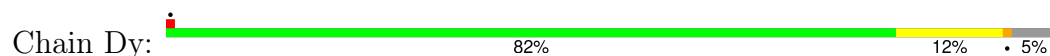
• Molecule 4: Sodium-type flagellar protein MotY



• Molecule 4: Sodium-type flagellar protein MotY

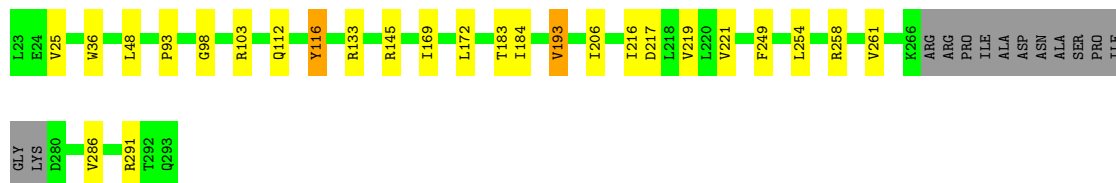


• Molecule 4: Sodium-type flagellar protein MotY




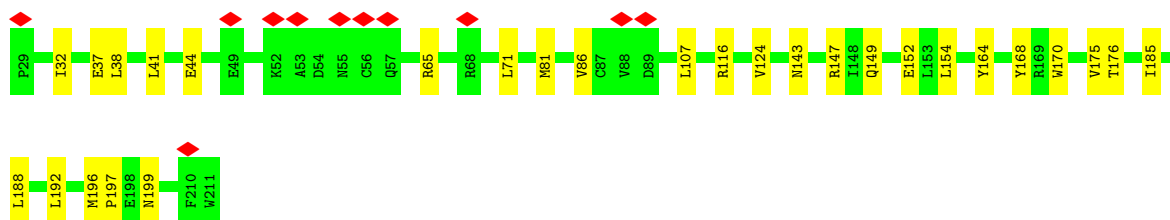
- Molecule 4: Sodium-type flagellar protein MotY

Chain Dz:  86% 9% 5%




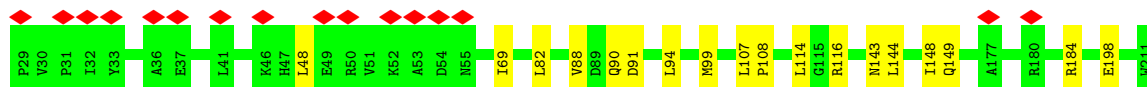
- Molecule 5: Sodium-type flagellar protein MotX

Chain Ea:  6% 85% 15%




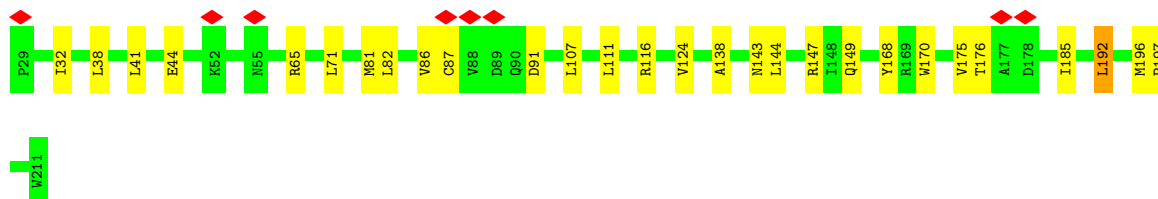
- Molecule 5: Sodium-type flagellar protein MotX

Chain Eb:  9% 90% 10%



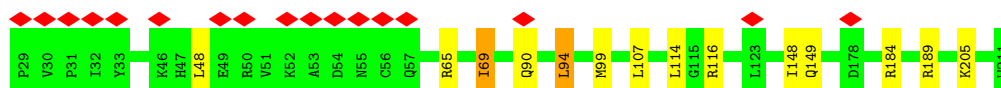
- Molecule 5: Sodium-type flagellar protein MotX

Chain Ec:  85% 15%




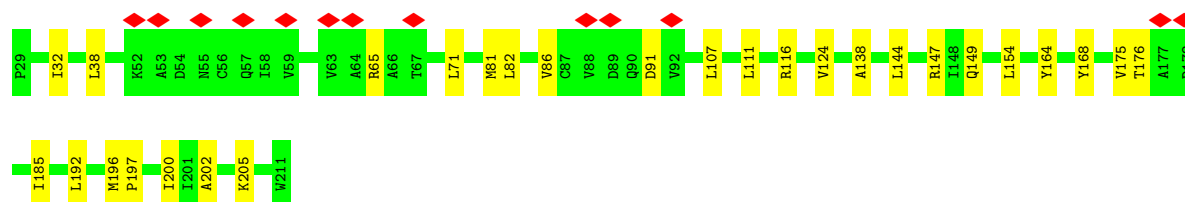
- Molecule 5: Sodium-type flagellar protein MotX

Chain Ed:  9% 92% 7%

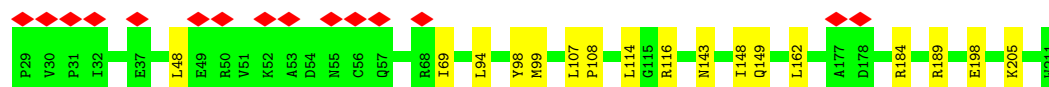


- Molecule 5: Sodium-type flagellar protein MotX

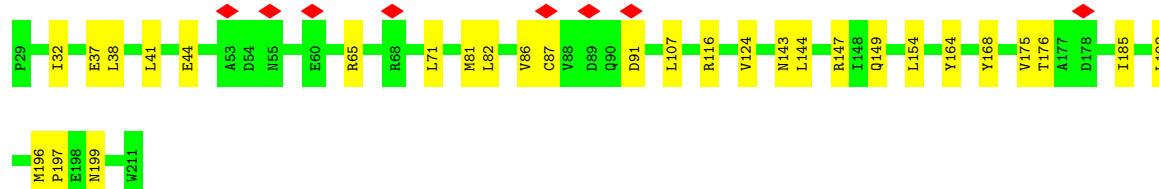
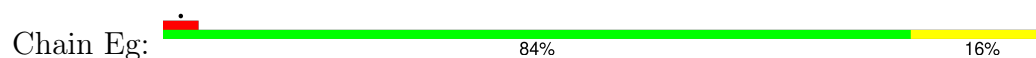
Chain Ee:  7% 85% 15%



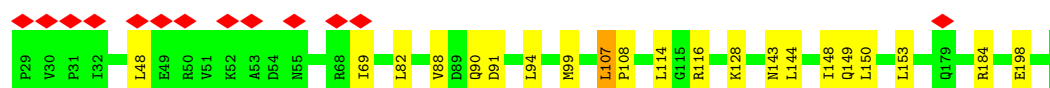
- Molecule 5: Sodium-type flagellar protein MotX



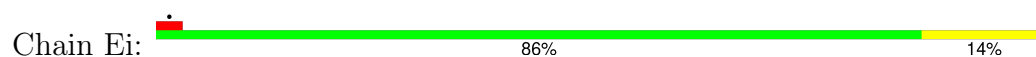
- Molecule 5: Sodium-type flagellar protein MotX



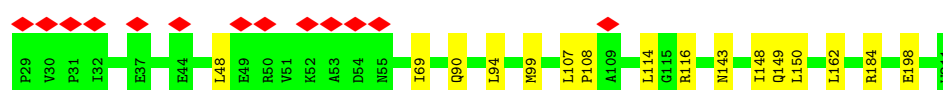
- Molecule 5: Sodium-type flagellar protein MotX



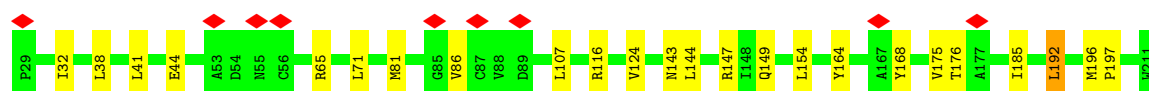
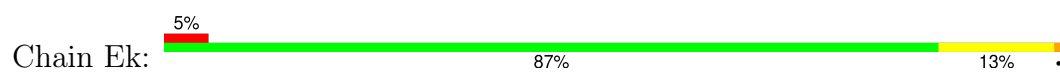
- Molecule 5: Sodium-type flagellar protein MotX



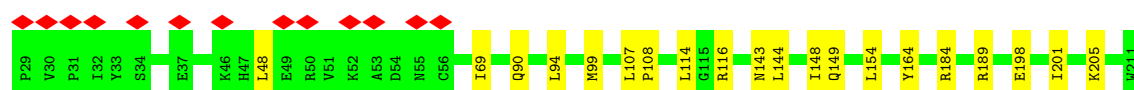
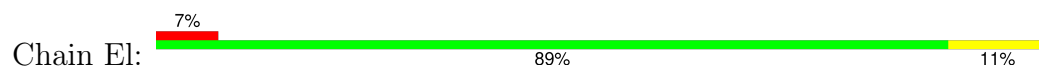
- Molecule 5: Sodium-type flagellar protein MotX



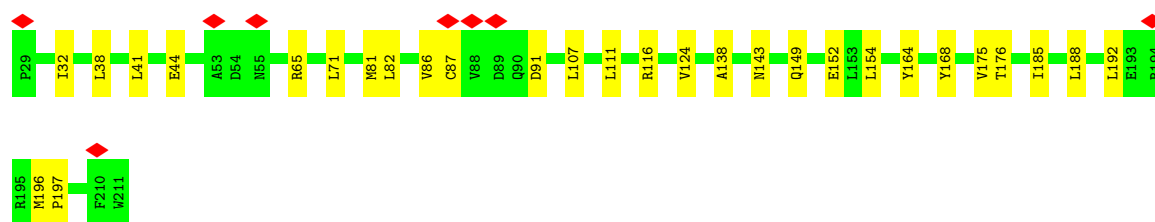
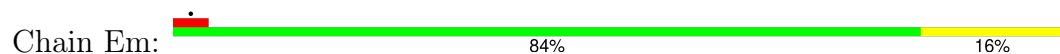
- Molecule 5: Sodium-type flagellar protein MotX



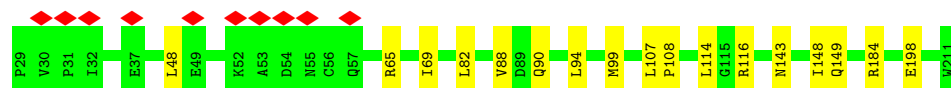
- Molecule 5: Sodium-type flagellar protein MotX



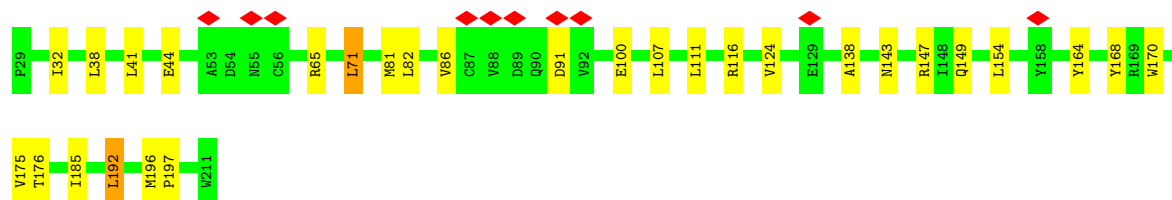
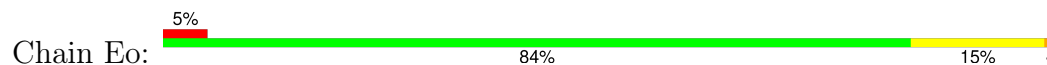
- Molecule 5: Sodium-type flagellar protein MotX



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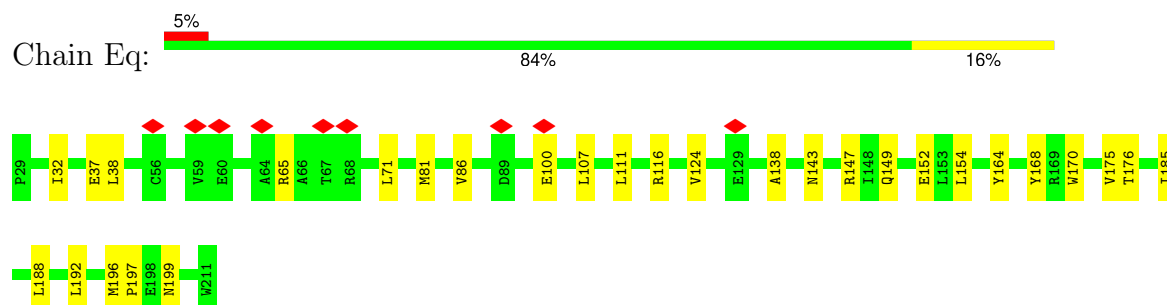
- Molecule 5: Sodium-type flagellar protein MotX



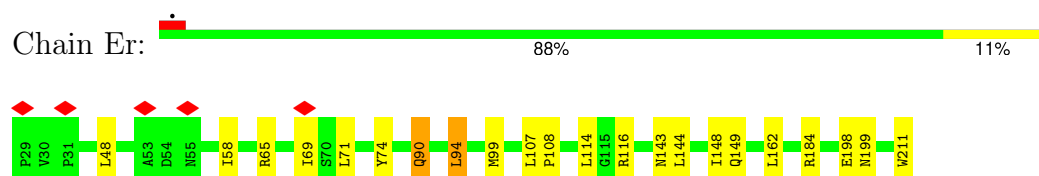
- Molecule 5: Sodium-type flagellar protein MotX



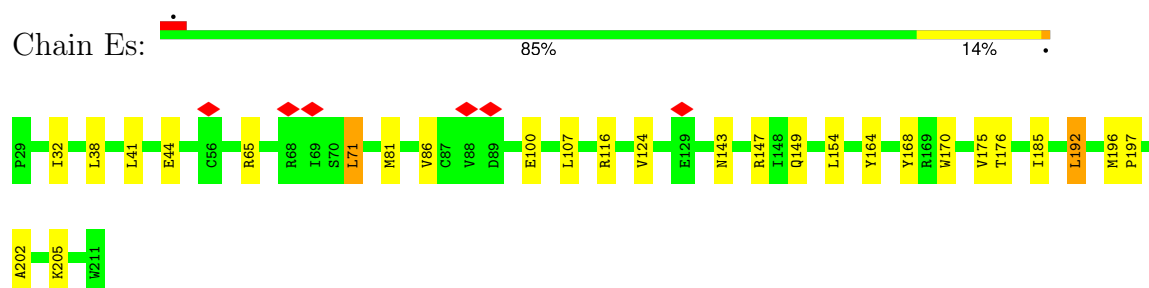
- Molecule 5: Sodium-type flagellar protein MotX



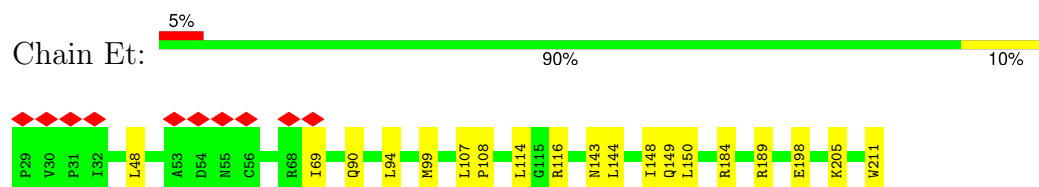
- Molecule 5: Sodium-type flagellar protein MotX



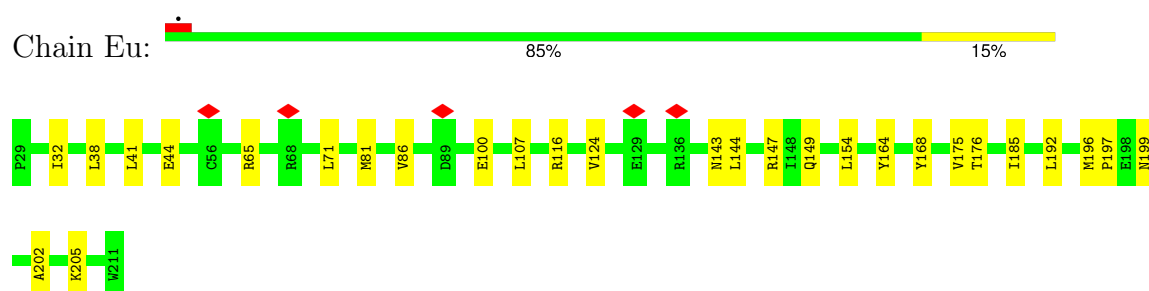
- Molecule 5: Sodium-type flagellar protein MotX



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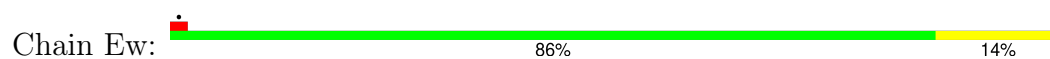
- Molecule 5: Sodium-type flagellar protein MotX



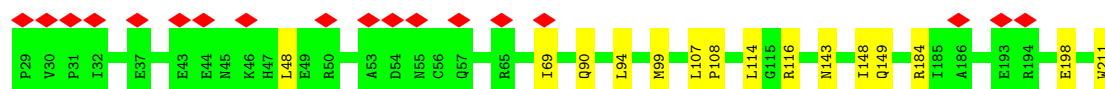




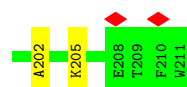
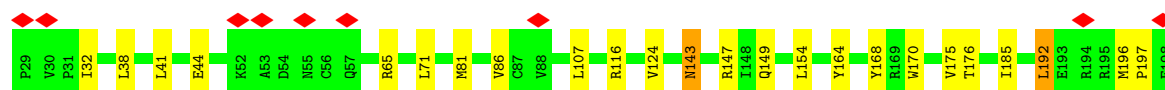
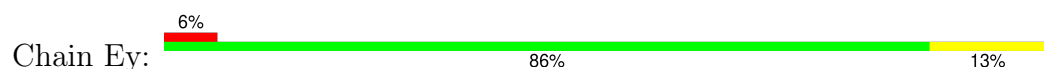
- Molecule 5: Sodium-type flagellar protein MotX



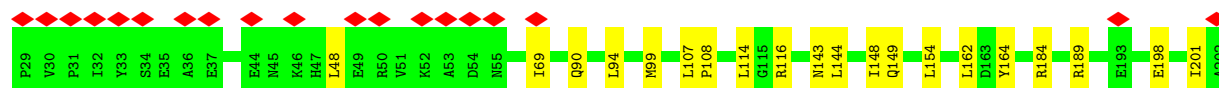
- Molecule 5: Sodium-type flagellar protein MotX



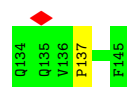
- Molecule 5: Sodium-type flagellar protein MotX



- Molecule 5: Sodium-type flagellar protein MotX



- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP



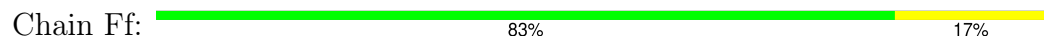
There are no outlier residues recorded for this chain.

- Molecule 6: FlgP



There are no outlier residues recorded for this chain.

- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP



There are no outlier residues recorded for this chain.

- Molecule 6: FlgP

Chain Fj:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: FlgP

Chain Fk:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: FlgP

Chain Fl:  92% 8%



- Molecule 6: FlgP

Chain Fm:  100%

There are no outlier residues recorded for this chain.

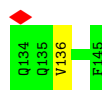
- Molecule 6: FlgP

Chain Fn:  92% 8%



- Molecule 6: FlgP

Chain Fo:  8% 92% 8%



- Molecule 6: FlgP

Chain Fp:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: FlgP

Chain Fq:  100%

There are no outlier residues recorded for this chain.

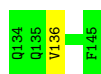
- Molecule 6: FlgP

Chain Fr:  92% 8%



• Molecule 6: FlgP

Chain Fs:  92% 8%




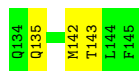
• Molecule 6: FlgP

Chain Ft:  92% 8%



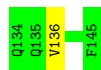
• Molecule 6: FlgP

Chain Fu:  75% 25%



• Molecule 6: FlgP

Chain Fv:  92% 8%



• Molecule 6: FlgP

Chain Fw:  92% 8%



• Molecule 6: FlgP

Chain Fx:  100%

There are no outlier residues recorded for this chain.

• Molecule 6: FlgP

Chain Fy:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: FlgP

Chain Fz:  92% 8%




- Molecule 6: FlgP

Chain Ga:  92% 8%




- Molecule 6: FlgP

Chain Gb:  83% 17%




- Molecule 6: FlgP

Chain Gc:  83% 17%



- Molecule 6: FlgP

Chain Gd:  75% 25%



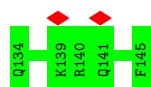
- Molecule 6: FlgP

Chain Ge:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: FlgP

Chain Gf:  17% 100%



## • Molecule 6: FlgP

Chain Gg:  100%

There are no outlier residues recorded for this chain.

## • Molecule 6: FlgP

Chain Gh:  92% 8%

## • Molecule 6: FlgP

Chain Gi:  100%

There are no outlier residues recorded for this chain.


## • Molecule 6: FlgP

Chain Gj:  92% 8%

## • Molecule 6: FlgP

Chain Gk:  92% 8%

## • Molecule 6: FlgP

Chain Gl:  83% 17%

## • Molecule 6: FlgP

Chain Gm:  100%

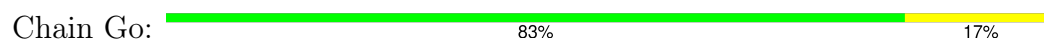
There are no outlier residues recorded for this chain.

## • Molecule 6: FlgP

Chain Gn:  92% 8%



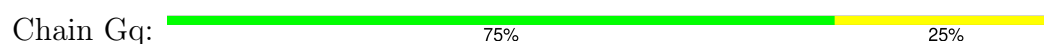
- Molecule 6: FlgP



- Molecule 6: FlgP



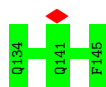
- Molecule 6: FlgP



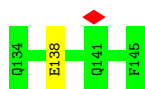
- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP

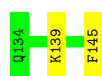
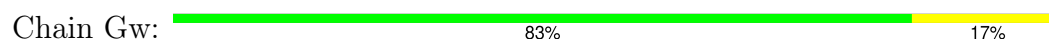




- Molecule 6: FlgP



- Molecule 6: FlgP



- Molecule 6: FlgP

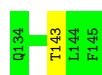


There are no outlier residues recorded for this chain.

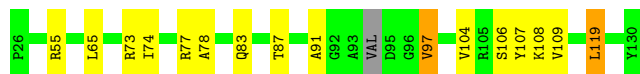
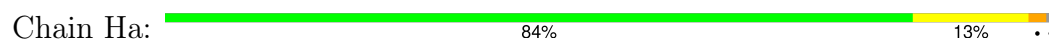
- Molecule 6: FlgP



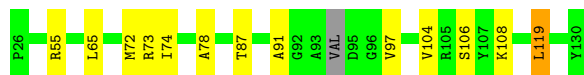
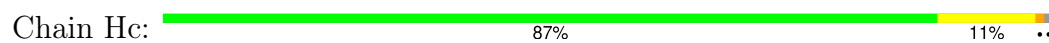
- Molecule 6: FlgP



- Molecule 7: Lipoprotein



- Molecule 7: Lipoprotein






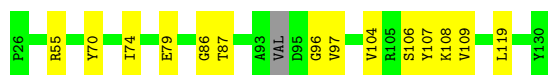
## ● Molecule 7: Lipoprotein

Chain He:  90% 8% ..




## ● Molecule 7: Lipoprotein

Chain Hg:  86% 13% .



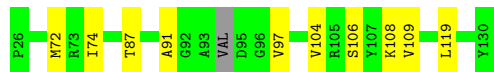
## ● Molecule 7: Lipoprotein

Chain Hi:  91% 8% .



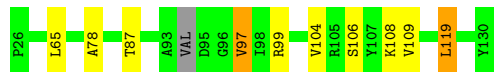
## ● Molecule 7: Lipoprotein

Chain Hk:  90% 10% .



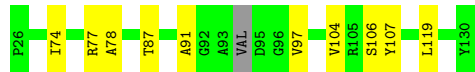
## ● Molecule 7: Lipoprotein

Chain Hm:  90% 8% ..




## ● Molecule 7: Lipoprotein

Chain Ho:  90% 10% .


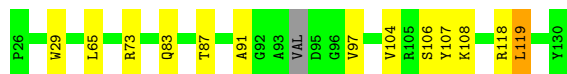


## ● Molecule 7: Lipoprotein


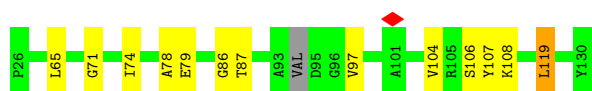
Chain Hq:  86% 12% ..




## • Molecule 7: Lipoprotein

Chain Hs:  87% 11% ..

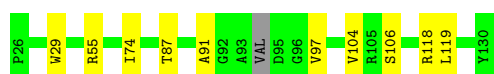
## • Molecule 7: Lipoprotein

Chain Hu:  87% 11% ..


## • Molecule 7: Lipoprotein

Chain Hw:  87% 11% ..


## • Molecule 7: Lipoprotein

Chain Hy:  90% 10% ..


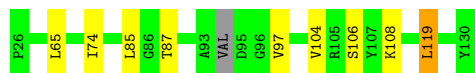
## • Molecule 7: Lipoprotein

Chain Ia:  86% 12% ..


## • Molecule 7: Lipoprotein

Chain Ic:  90% 9% ..


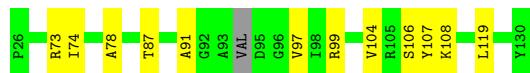
## • Molecule 7: Lipoprotein

Chain Ie:  90% 8% ..


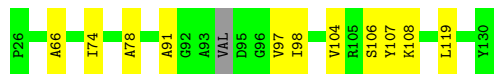
## • Molecule 7: Lipoprotein

Chain Ig:  85% 14%


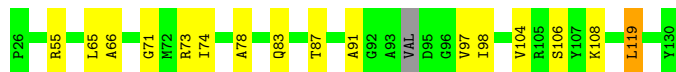
## • Molecule 7: Lipoprotein

Chain Ii:  88% 11%


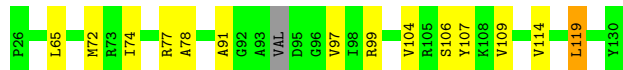
## • Molecule 7: Lipoprotein

Chain Ik:  89% 10%


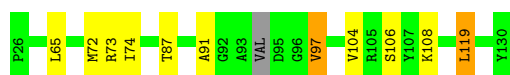
## • Molecule 7: Lipoprotein

Chain Im:  84% 14%


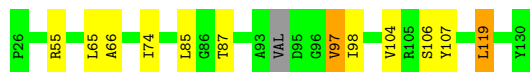
## • Molecule 7: Lipoprotein

Chain Io:  86% 12%


## • Molecule 7: Lipoprotein

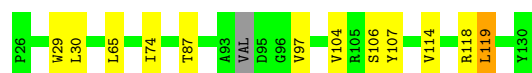
Chain Iq:  89% 9%

## • Molecule 7: Lipoprotein


Chain Is:  88% 10%

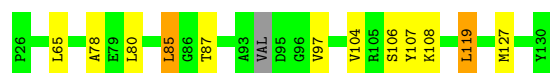
## • Molecule 7: Lipoprotein

Chain Iu:  88% 10% ..




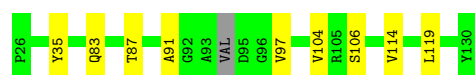
• Molecule 7: Lipoprotein

Chain Iw:  88% 10% ..




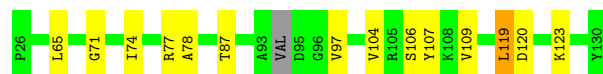
• Molecule 7: Lipoprotein

Chain Iy:  90% 9% ..




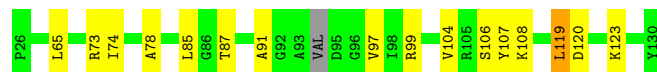
• Molecule 7: Lipoprotein

Chain Ja:  86% 12% ..




• Molecule 7: Lipoprotein

Chain Jc:  84% 14% ..




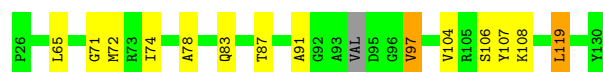
• Molecule 7: Lipoprotein

Chain Je:  83% 15% ..




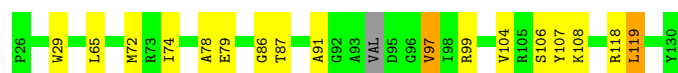
• Molecule 7: Lipoprotein

Chain Jg:  86% 11% ..




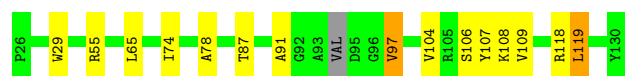
• Molecule 7: Lipoprotein

Chain Ji:  83% 14% ..



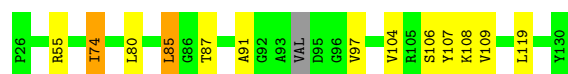
• Molecule 7: Lipoprotein

Chain Jk:  85% 12% ..




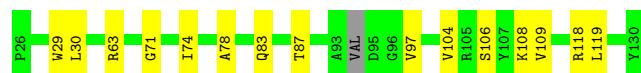
• Molecule 7: Lipoprotein

Chain Jm:  87% 10% ..




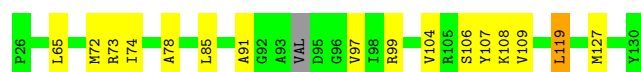
• Molecule 7: Lipoprotein

Chain Jo:  85% 14% ..




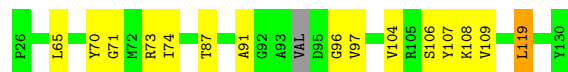
• Molecule 7: Lipoprotein

Chain Jq:  84% 14% ..




• Molecule 7: Lipoprotein

Chain Js:  85% 13% ..




• Molecule 7: Lipoprotein

Chain Ju:  84% 14% ..




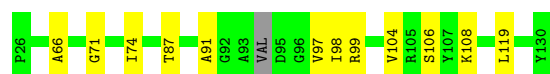
• Molecule 7: Lipoprotein

Chain Jw:  87% 10% ..




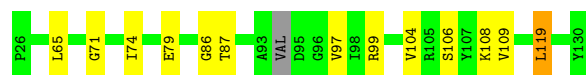
• Molecule 7: Lipoprotein

Chain Jy:  88% 11% .




• Molecule 7: Lipoprotein

Chain Ka:  87% 11% ..




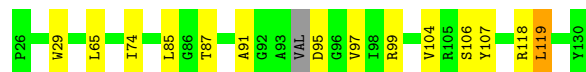
• Molecule 7: Lipoprotein

Chain Kc:  89% 10% ..



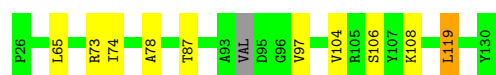
• Molecule 7: Lipoprotein

Chain Ke:  86% 12% ..




• Molecule 7: Lipoprotein

Chain Kg:  90% 9% ..



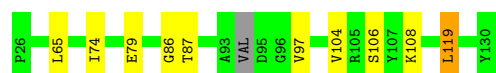
• Molecule 7: Lipoprotein

Chain Ki:  89% 10% .



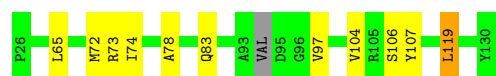
• Molecule 7: Lipoprotein

Chain Kk:  90% 9% ..




• Molecule 7: Lipoprotein

Chain Km:  89% 10% ..




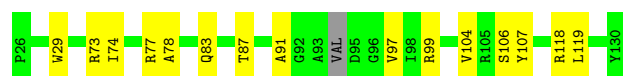
• Molecule 7: Lipoprotein

Chain Ko:  89% 10% ..




• Molecule 7: Lipoprotein

Chain Kq:  85% 14% .



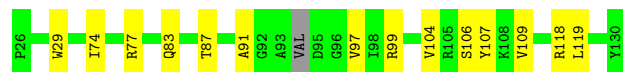
• Molecule 7: Lipoprotein

Chain Ks:  85% 13% ..



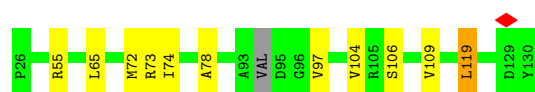
• Molecule 7: Lipoprotein

Chain Ku:  86% 13% .




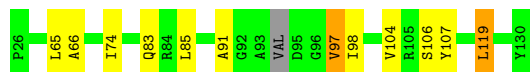
• Molecule 7: Lipoprotein

Chain Kw:  89% 10% ..




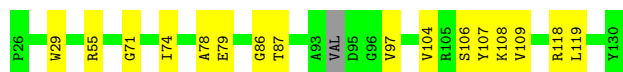
• Molecule 7: Lipoprotein

Chain Ky:  88% 10% ..



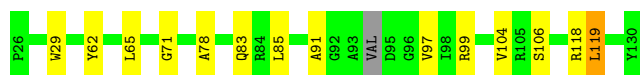
• Molecule 7: Lipoprotein

Chain La:  84% 15% .




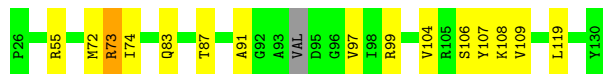
• Molecule 7: Lipoprotein

Chain Lc:  86% 12% ..




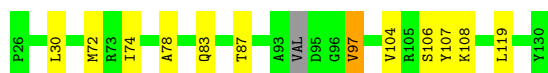
• Molecule 7: Lipoprotein

Chain Le:  85% 13% ..




• Molecule 7: Lipoprotein

Chain Lg:  88% 10% ..



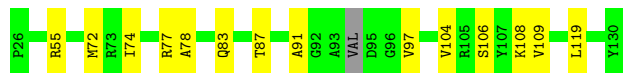
• Molecule 7: Lipoprotein

Chain Li:  84% 13% ..



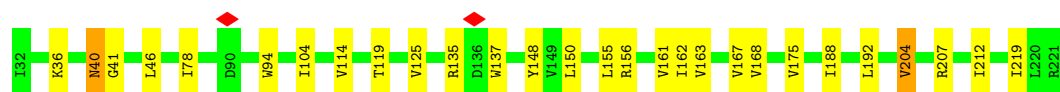
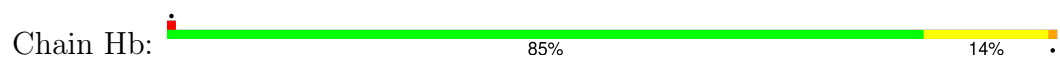
• Molecule 7: Lipoprotein

Chain Lk:  86% 13% .

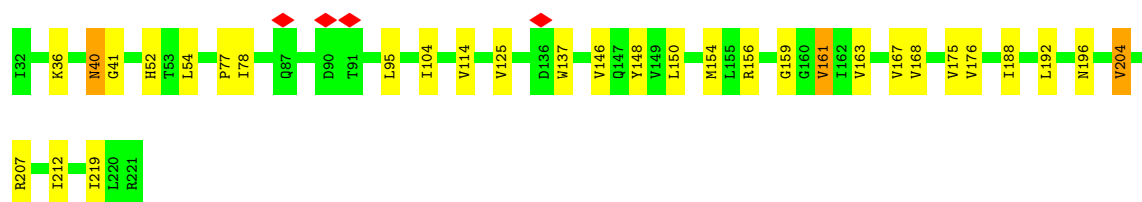
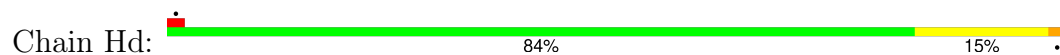


• Molecule 8: FlgO domain-containing protein

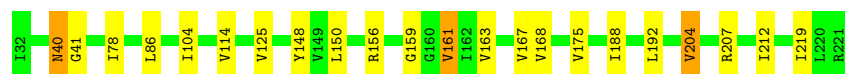
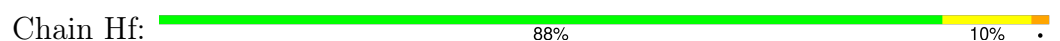




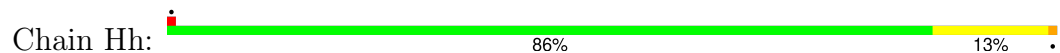
- Molecule 8: FlgO domain-containing protein



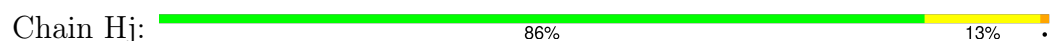
- Molecule 8: FlgO domain-containing protein



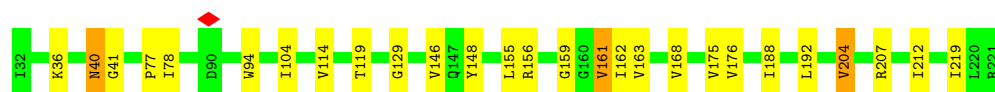
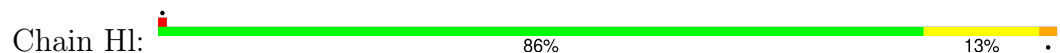
- Molecule 8: FlgO domain-containing protein



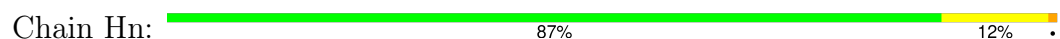
- Molecule 8: FlgO domain-containing protein

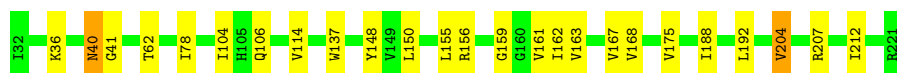


- Molecule 8: FlgO domain-containing protein

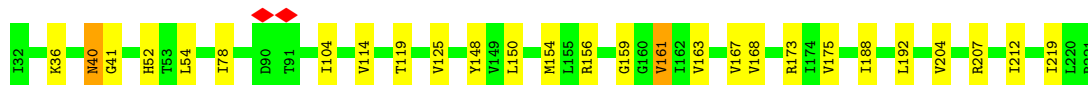
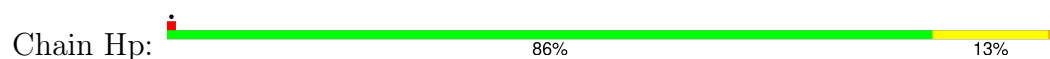


- Molecule 8: FlgO domain-containing protein

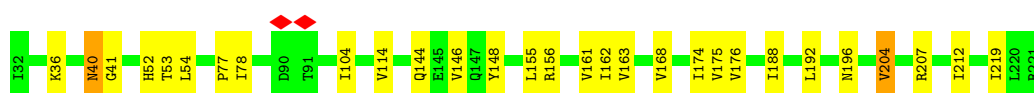
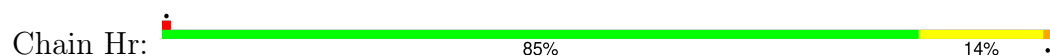




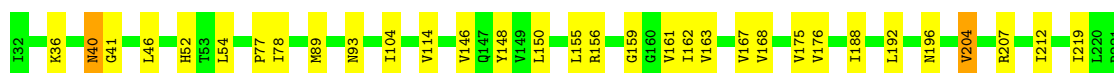
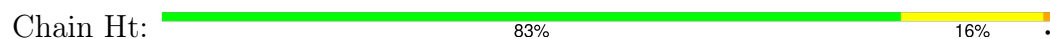
- Molecule 8: FlgO domain-containing protein



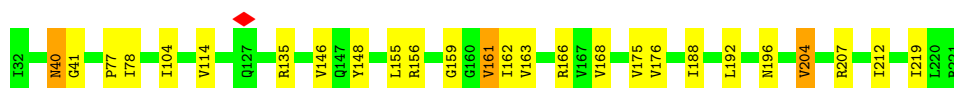
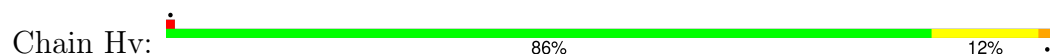
- Molecule 8: FlgO domain-containing protein



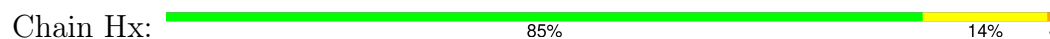
- Molecule 8: FlgO domain-containing protein



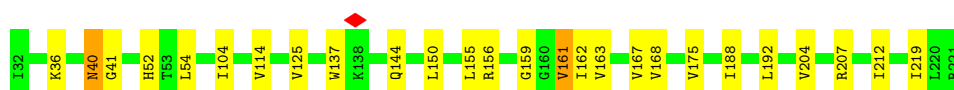
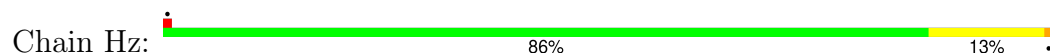
- Molecule 8: FlgO domain-containing protein




- Molecule 8: FlgO domain-containing protein



- Molecule 8: FlgO domain-containing protein



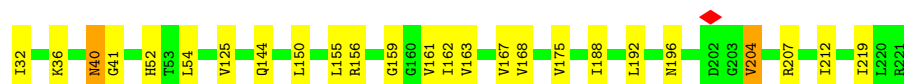
- Molecule 8: FlgO domain-containing protein

Chain Ib:  85% 14%




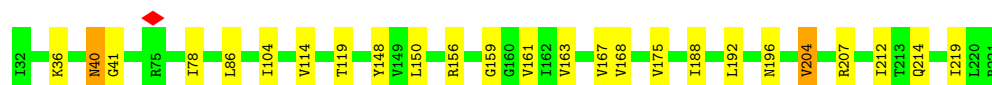
• Molecule 8: FlgO domain-containing protein

Chain Id:  87% 12%




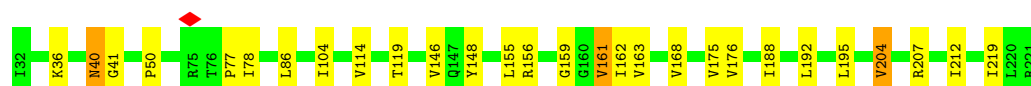
• Molecule 8: FlgO domain-containing protein

Chain If:  87% 12%




• Molecule 8: FlgO domain-containing protein

Chain Ih:  85% 13%




• Molecule 8: FlgO domain-containing protein

Chain Ij:  85% 14%




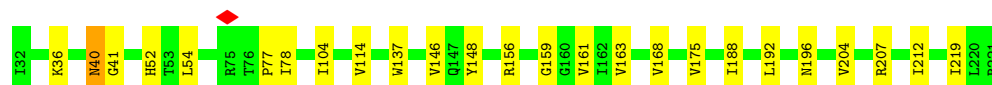
• Molecule 8: FlgO domain-containing protein

Chain Il:  87% 12%




• Molecule 8: FlgO domain-containing protein

Chain In:  87% 13%




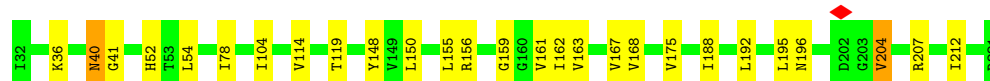
- Molecule 8: FlgO domain-containing protein

Chain Ip:  87% 13%




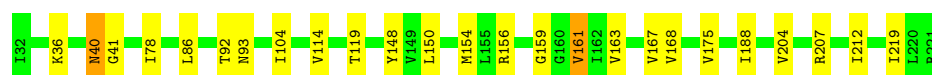
- Molecule 8: FlgO domain-containing protein

Chain Ir:  86% 13%




- Molecule 8: FlgO domain-containing protein

Chain It:  87% 12%




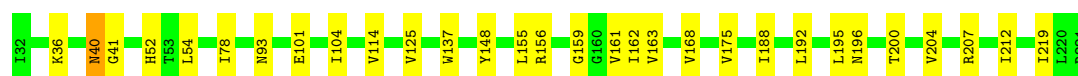
- Molecule 8: FlgO domain-containing protein

Chain Iv:  85% 15%




- Molecule 8: FlgO domain-containing protein

Chain Ix:  84% 15%




- Molecule 8: FlgO domain-containing protein

Chain Iz:  84% 15%




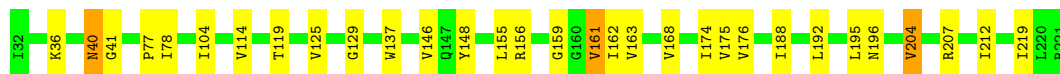
- Molecule 8: FlgO domain-containing protein

Chain Jb:  86% 13%




- Molecule 8: FlgO domain-containing protein

Chain Jd:  84% 15% .




- Molecule 8: FlgO domain-containing protein

Chain Jf:  86% 13% .




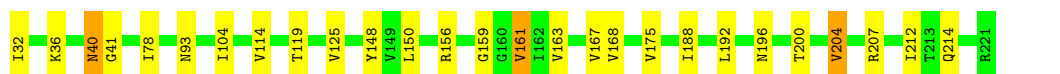
- Molecule 8: FlgO domain-containing protein

Chain Jh:  85% 14% .




- Molecule 8: FlgO domain-containing protein

Chain Jj:  86% 13% .




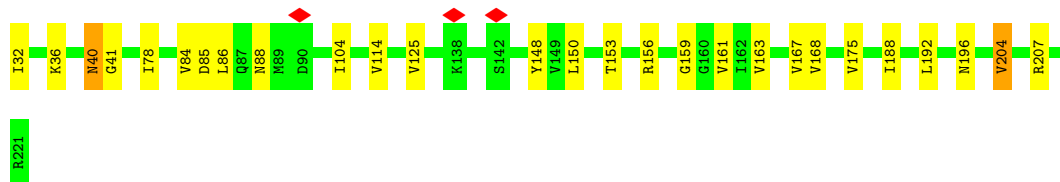
- Molecule 8: FlgO domain-containing protein

Chain Jl:  88% 11% .




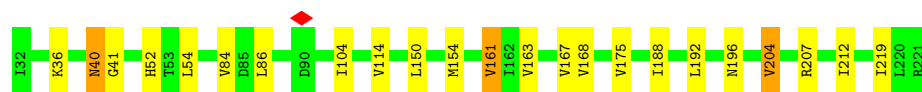
- Molecule 8: FlgO domain-containing protein

Chain Jn:  85% 14% .

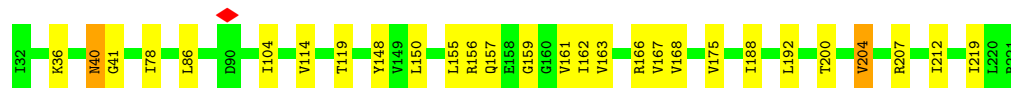
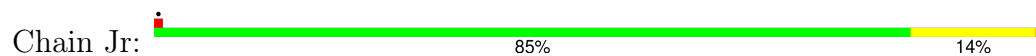


- Molecule 8: FlgO domain-containing protein

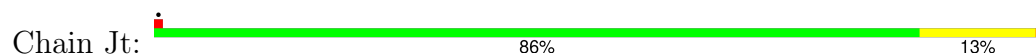
Chain Jp:  88% 11% .



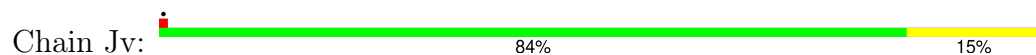
- Molecule 8: FlgO domain-containing protein



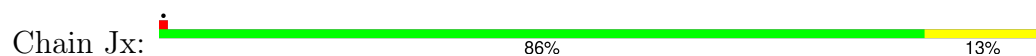
- Molecule 8: FlgO domain-containing protein



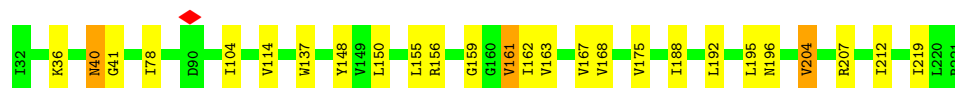
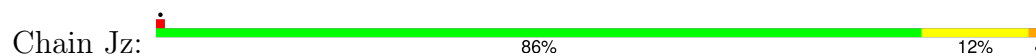
- Molecule 8: FlgO domain-containing protein



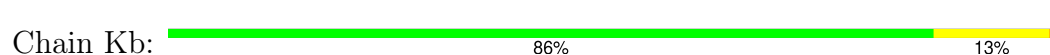
- Molecule 8: FlgO domain-containing protein




- Molecule 8: FlgO domain-containing protein



- Molecule 8: FlgO domain-containing protein



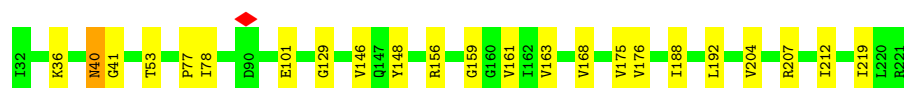
- Molecule 8: FlgO domain-containing protein

Chain Kd:  86% 13%



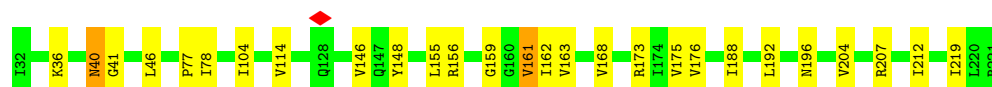
• Molecule 8: FlgO domain-containing protein

Chain Kf:  88% 12%




• Molecule 8: FlgO domain-containing protein

Chain Kh:  86% 13%




• Molecule 8: FlgO domain-containing protein

Chain Kj:  87% 12%



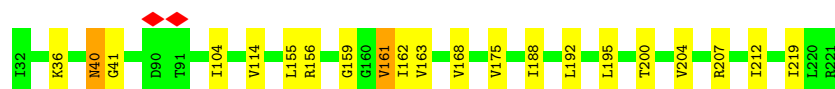
• Molecule 8: FlgO domain-containing protein

Chain Kl:  87% 12%




• Molecule 8: FlgO domain-containing protein

Chain Kn:  89% 10%




• Molecule 8: FlgO domain-containing protein

Chain Kp:  84% 15%




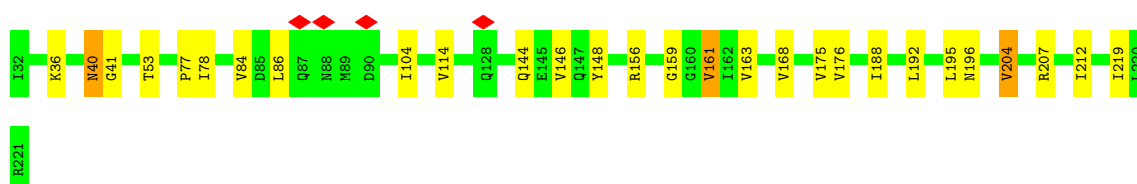
- Molecule 8: FlgO domain-containing protein

Chain Kr:  84% 15%




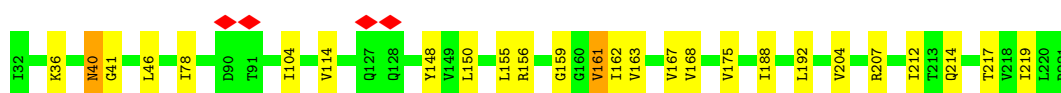
- Molecule 8: FlgO domain-containing protein

Chain Kt:  85% 13%



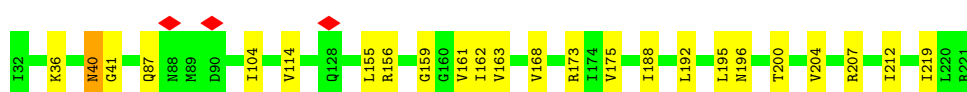
- Molecule 8: FlgO domain-containing protein

Chain Kv:  86% 13%




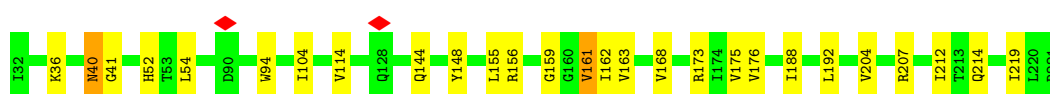
- Molecule 8: FlgO domain-containing protein

Chain Kx:  87% 12%




- Molecule 8: FlgO domain-containing protein

Chain Kz:  86% 13%




- Molecule 8: FlgO domain-containing protein

Chain Lb:  86% 12%




- Molecule 8: FlgO domain-containing protein

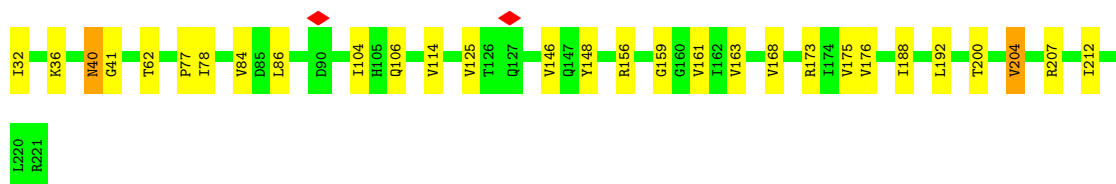


Chain Ld:  83% 16%




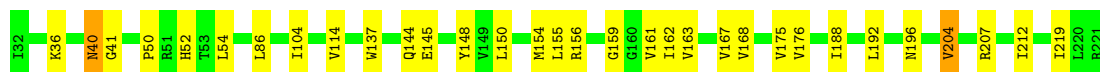
- Molecule 8: FlgO domain-containing protein

Chain Lf:  84% 15%




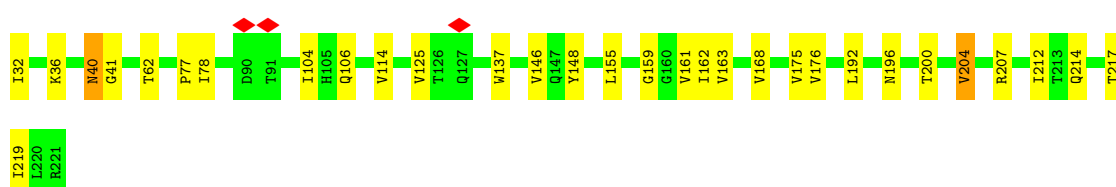
- Molecule 8: FlgO domain-containing protein

Chain Lh:  83% 16%




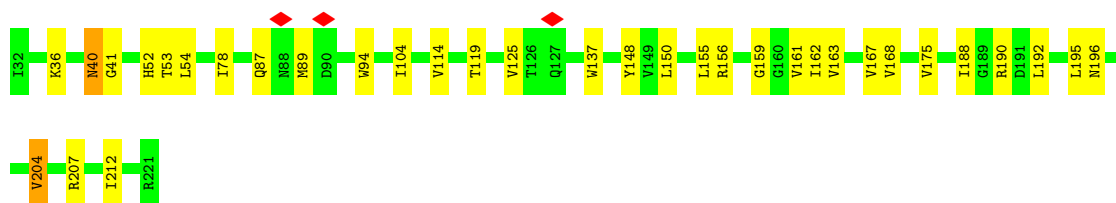
- Molecule 8: FlgO domain-containing protein

Chain Lj:  84% 15%



- Molecule 8: FlgO domain-containing protein

Chain Ll:  82% 17%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	177296	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	70	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.772	Depositor
Minimum map value	-0.417	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	640.63995, 640.63995, 640.63995	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	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	0.11	0/1699	0.26	0/2303
1	Ab	0.11	0/1699	0.27	0/2303
1	Ac	0.11	0/1699	0.28	0/2303
1	Ad	0.11	0/1699	0.29	0/2303
1	Ae	0.11	0/1699	0.28	0/2303
1	Af	0.11	0/1699	0.28	0/2303
1	Ag	0.11	0/1699	0.29	0/2303
1	Ah	0.11	0/1699	0.28	0/2303
1	Ai	0.12	0/1699	0.28	0/2303
1	Aj	0.11	0/1699	0.27	0/2303
1	Ak	0.11	0/1699	0.27	0/2303
1	Al	0.11	0/1699	0.28	0/2303
1	Am	0.11	0/1699	0.27	0/2303
1	An	0.11	0/1699	0.27	0/2303
1	Ao	0.11	0/1699	0.27	0/2303
1	Ap	0.11	0/1699	0.28	0/2303
1	Aq	0.11	0/1699	0.28	0/2303
1	Ar	0.11	0/1699	0.27	0/2303
1	As	0.11	0/1699	0.28	0/2303
1	At	0.12	0/1699	0.28	0/2303
1	Au	0.12	0/1699	0.29	0/2303
1	Av	0.12	0/1699	0.27	0/2303
1	Aw	0.11	0/1699	0.27	0/2303
1	Ax	0.11	0/1699	0.26	0/2303
1	Ay	0.11	0/1699	0.28	0/2303
1	Az	0.11	0/1699	0.28	0/2303
2	Ba	0.12	0/2535	0.28	0/3442
2	Bb	0.12	0/2535	0.28	0/3442
2	Bc	0.13	0/2535	0.28	0/3442
2	Bd	0.13	0/2535	0.28	0/3442
2	Be	0.12	0/2535	0.28	0/3442
2	Bf	0.13	0/2535	0.29	0/3442
2	Bg	0.12	0/2535	0.28	0/3442
2	Bh	0.13	0/2535	0.28	0/3442

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	Bi	0.12	0/2535	0.29	0/3442
2	Bj	0.12	0/2535	0.28	0/3442
2	Bk	0.13	0/2535	0.30	1/3442 (0.0%)
2	Bl	0.13	0/2535	0.30	0/3442
2	Bm	0.13	0/2535	0.29	0/3442
2	Bn	0.13	0/2535	0.28	0/3442
2	Bo	0.12	0/2535	0.28	0/3442
2	Bp	0.13	0/2535	0.28	0/3442
2	Bq	0.13	0/2535	0.29	0/3442
2	Br	0.13	0/2535	0.29	0/3442
2	Bs	0.13	0/2535	0.29	0/3442
2	Bt	0.13	0/2535	0.28	0/3442
2	Bu	0.13	0/2535	0.28	0/3442
2	Bv	0.12	0/2535	0.30	0/3442
2	Bw	0.12	0/2535	0.27	0/3442
2	Bx	0.12	0/2535	0.28	0/3442
2	By	0.13	0/2535	0.29	0/3442
2	Bz	0.12	0/2535	0.29	0/3442
3	Ca	0.13	0/2816	0.28	0/3809
3	Cb	0.12	0/2816	0.27	0/3809
3	Cc	0.10	0/2816	0.27	0/3809
3	Cd	0.11	0/2816	0.28	0/3809
3	Ce	0.11	0/2816	0.27	0/3809
3	Cf	0.11	0/2816	0.27	0/3809
3	Cg	0.11	0/2816	0.29	0/3809
3	Ch	0.11	0/2816	0.28	0/3809
3	Ci	0.11	0/2816	0.27	0/3809
3	Cj	0.12	0/2816	0.27	0/3809
3	Ck	0.11	0/2816	0.28	1/3809 (0.0%)
3	Cl	0.12	0/2816	0.30	1/3809 (0.0%)
3	Cm	0.11	0/2816	0.26	0/3809
3	Cn	0.11	0/2816	0.29	1/3809 (0.0%)
3	Co	0.11	0/2816	0.27	0/3809
3	Cp	0.11	0/2816	0.27	0/3809
3	Cq	0.11	0/2816	0.28	0/3809
3	Cr	0.11	0/2816	0.27	0/3809
3	Cs	0.11	0/2816	0.27	0/3809
3	Ct	0.11	0/2816	0.27	0/3809
3	Cu	0.11	0/2816	0.28	0/3809
3	Cv	0.11	0/2816	0.28	0/3809
3	Cw	0.11	0/2816	0.27	0/3809
3	Cx	0.10	0/2816	0.26	0/3809
3	Cy	0.11	0/2816	0.26	0/3809

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
3	Cz	0.11	0/2816	0.26	0/3809
4	Da	0.12	0/2129	0.30	0/2882
4	Db	0.12	0/2124	0.30	0/2877
4	Dc	0.12	0/2129	0.29	0/2882
4	Dd	0.12	0/2124	0.31	0/2877
4	De	0.12	0/2129	0.29	0/2882
4	Df	0.13	0/2124	0.34	0/2877
4	Dg	0.12	0/2129	0.30	0/2882
4	Dh	0.12	0/2124	0.31	0/2877
4	Di	0.12	0/2129	0.31	0/2882
4	Dj	0.12	0/2124	0.32	0/2877
4	Dk	0.12	0/2129	0.30	0/2882
4	Dl	0.12	0/2124	0.31	0/2877
4	Dm	0.12	0/2129	0.30	0/2882
4	Dn	0.12	0/2124	0.32	0/2877
4	Do	0.12	0/2129	0.29	0/2882
4	Dp	0.12	0/2124	0.31	0/2877
4	Dq	0.12	0/2129	0.29	0/2882
4	Dr	0.12	0/2124	0.32	0/2877
4	Ds	0.12	0/2129	0.29	0/2882
4	Dt	0.12	0/2124	0.32	0/2877
4	Du	0.12	0/2129	0.30	0/2882
4	Dv	0.12	0/2124	0.32	0/2877
4	Dw	0.12	0/2129	0.30	0/2882
4	Dx	0.12	0/2124	0.32	0/2877
4	Dy	0.12	0/2129	0.30	0/2882
4	Dz	0.12	0/2124	0.30	0/2877
5	Ea	0.11	0/1494	0.27	0/2027
5	Eb	0.11	0/1523	0.28	0/2062
5	Ec	0.11	0/1494	0.27	0/2027
5	Ed	0.11	0/1523	0.29	0/2062
5	Ee	0.10	0/1494	0.27	0/2027
5	Ef	0.11	0/1523	0.29	0/2062
5	Eg	0.11	0/1494	0.27	0/2027
5	Uh	0.11	0/1523	0.28	0/2062
5	Ei	0.11	0/1494	0.27	0/2027
5	Ej	0.11	0/1523	0.26	0/2062
5	Ek	0.11	0/1494	0.28	0/2027
5	El	0.11	0/1523	0.26	0/2062
5	Em	0.11	0/1494	0.28	0/2027
5	En	0.17	0/1523	0.29	0/2062
5	Eo	0.11	0/1494	0.27	0/2027
5	Ep	0.12	0/1523	0.26	0/2062

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
5	Eq	0.10	0/1494	0.27	0/2027
5	Er	0.11	0/1523	0.28	0/2062
5	Es	0.11	0/1494	0.27	0/2027
5	Et	0.11	0/1523	0.26	0/2062
5	Eu	0.11	0/1494	0.28	0/2027
5	Ev	0.11	0/1523	0.28	0/2062
5	Ew	0.11	0/1494	0.28	0/2027
5	Ex	0.11	0/1523	0.28	0/2062
5	Ey	0.11	0/1494	0.28	0/2027
5	Ez	0.11	0/1523	0.28	0/2062
6	Fa	0.15	0/106	0.35	0/139
6	Fb	0.13	0/106	0.33	0/139
6	Fc	0.13	0/106	0.32	0/139
6	Fd	0.16	0/106	0.33	0/139
6	Fe	0.14	0/106	0.37	0/139
6	Ff	0.14	0/106	0.36	0/139
6	Fg	0.13	0/106	0.33	0/139
6	Fh	0.14	0/106	0.34	0/139
6	Fi	0.13	0/106	0.39	0/139
6	Fj	0.13	0/106	0.35	0/139
6	Fk	0.15	0/106	0.35	0/139
6	Fl	0.14	0/106	0.36	0/139
6	Fm	0.15	0/106	0.34	0/139
6	Fn	0.16	0/106	0.33	0/139
6	Fo	0.14	0/106	0.36	0/139
6	Fp	0.14	0/106	0.36	0/139
6	Fq	0.16	0/106	0.33	0/139
6	Fr	0.17	0/106	0.36	0/139
6	Fs	0.13	0/106	0.37	0/139
6	Ft	0.14	0/106	0.36	0/139
6	Fu	0.15	0/106	0.35	0/139
6	Fv	0.18	0/106	0.35	0/139
6	Fw	0.14	0/106	0.35	0/139
6	Fx	0.15	0/106	0.38	0/139
6	Fy	0.13	0/106	0.32	0/139
6	Fz	0.18	0/106	0.47	0/139
6	Ga	0.14	0/106	0.37	0/139
6	Gb	0.14	0/106	0.40	0/139
6	Gc	0.15	0/106	0.38	0/139
6	Gd	0.12	0/106	0.36	0/139
6	Ge	0.19	0/106	0.45	0/139
6	Gf	0.14	0/106	0.37	0/139
6	Gg	0.14	0/106	0.38	0/139

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
6	Gh	0.14	0/106	0.42	0/139
6	Gi	0.14	0/106	0.40	0/139
6	Gj	0.12	0/106	0.37	0/139
6	Gk	0.14	0/106	0.39	0/139
6	Gl	0.14	0/106	0.36	0/139
6	Gm	0.14	0/106	0.35	0/139
6	Gn	0.14	0/106	0.47	0/139
6	Go	0.12	0/106	0.36	0/139
6	Gp	0.15	0/106	0.36	0/139
6	Gq	0.11	0/106	0.38	0/139
6	Gr	0.15	0/106	0.40	0/139
6	Gs	0.12	0/106	0.42	0/139
6	Gt	0.15	0/106	0.41	0/139
6	Gu	0.13	0/106	0.39	0/139
6	Gv	0.13	0/106	0.40	0/139
6	Gw	0.18	0/106	0.53	0/139
6	Gx	0.16	0/106	0.39	0/139
6	Gy	0.17	0/106	0.47	0/139
6	Gz	0.15	0/106	0.36	0/139
7	Ha	0.10	0/836	0.25	0/1119
7	Hc	0.10	0/836	0.25	0/1119
7	He	0.10	0/836	0.27	0/1119
7	Hg	0.10	0/836	0.28	0/1119
7	Hi	0.10	0/836	0.25	0/1119
7	Hk	0.09	0/836	0.28	0/1119
7	Hm	0.10	0/836	0.25	0/1119
7	Ho	0.09	0/836	0.26	0/1119
7	Hq	0.10	0/836	0.25	0/1119
7	Hs	0.10	0/836	0.26	0/1119
7	Hu	0.10	0/836	0.26	0/1119
7	Hw	0.09	0/836	0.24	0/1119
7	Hy	0.11	0/836	0.25	0/1119
7	Ia	0.11	0/836	0.27	0/1119
7	Ic	0.10	0/836	0.26	0/1119
7	Ie	0.10	0/836	0.27	0/1119
7	Ig	0.10	0/836	0.25	0/1119
7	Ii	0.11	0/836	0.27	0/1119
7	Ik	0.10	0/836	0.27	0/1119
7	Im	0.10	0/836	0.25	0/1119
7	Io	0.11	0/836	0.26	0/1119
7	Iq	0.10	0/836	0.26	0/1119
7	Is	0.11	0/836	0.25	0/1119
7	Iu	0.10	0/836	0.25	0/1119

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
7	Iw	0.10	0/836	0.27	0/1119
7	Iy	0.10	0/836	0.27	0/1119
7	Ja	0.10	0/836	0.26	0/1119
7	Jc	0.10	0/836	0.27	0/1119
7	Je	0.10	0/836	0.27	0/1119
7	Jg	0.09	0/836	0.25	0/1119
7	Ji	0.10	0/836	0.25	0/1119
7	Jk	0.10	0/836	0.26	0/1119
7	Jm	0.11	0/836	0.27	0/1119
7	Jo	0.09	0/836	0.26	0/1119
7	Jq	0.10	0/836	0.28	0/1119
7	Js	0.10	0/836	0.25	0/1119
7	Ju	0.09	0/836	0.26	0/1119
7	Jw	0.10	0/836	0.26	0/1119
7	Jy	0.10	0/836	0.27	0/1119
7	Ka	0.09	0/836	0.25	0/1119
7	Kc	0.11	0/836	0.26	0/1119
7	Ke	0.10	0/836	0.27	0/1119
7	Kg	0.09	0/836	0.25	0/1119
7	Ki	0.11	0/836	0.26	0/1119
7	Kk	0.10	0/836	0.26	0/1119
7	Km	0.11	0/836	0.28	0/1119
7	Ko	0.10	0/836	0.26	0/1119
7	Kq	0.09	0/836	0.24	0/1119
7	Ks	0.10	0/836	0.25	0/1119
7	Ku	0.11	0/836	0.27	0/1119
7	Kw	0.10	0/836	0.27	0/1119
7	Ky	0.10	0/836	0.25	0/1119
7	La	0.10	0/836	0.27	0/1119
7	Lc	0.09	0/836	0.25	0/1119
7	Le	0.10	0/836	0.25	0/1119
7	Lg	0.10	0/836	0.26	0/1119
7	Li	0.10	0/836	0.26	0/1119
7	Lk	0.10	0/836	0.26	0/1119
8	Hb	0.11	0/1508	0.28	0/2045
8	Hd	0.10	0/1508	0.28	0/2045
8	Hf	0.10	0/1508	0.27	0/2045
8	Hh	0.10	0/1508	0.27	0/2045
8	Hj	0.10	0/1508	0.26	0/2045
8	Hl	0.10	0/1508	0.27	0/2045
8	Hn	0.10	0/1508	0.27	0/2045
8	Hp	0.10	0/1508	0.27	0/2045
8	Hr	0.10	0/1508	0.28	0/2045



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
8	Ht	0.10	0/1508	0.27	0/2045
8	Hv	0.10	0/1508	0.27	0/2045
8	Hx	0.10	0/1508	0.26	0/2045
8	Hz	0.11	0/1508	0.29	0/2045
8	Ib	0.10	0/1508	0.27	0/2045
8	Id	0.10	0/1508	0.27	0/2045
8	If	0.10	0/1508	0.27	0/2045
8	Ih	0.11	0/1508	0.27	0/2045
8	Ij	0.10	0/1508	0.27	0/2045
8	Il	0.10	0/1508	0.28	0/2045
8	In	0.10	0/1508	0.27	0/2045
8	Ip	0.11	0/1508	0.27	0/2045
8	Ir	0.10	0/1508	0.27	0/2045
8	It	0.10	0/1508	0.28	0/2045
8	Iv	0.10	0/1508	0.28	0/2045
8	Ix	0.10	0/1508	0.28	0/2045
8	Iz	0.10	0/1508	0.28	0/2045
8	Jb	0.10	0/1508	0.26	0/2045
8	Jd	0.10	0/1508	0.28	0/2045
8	Jf	0.10	0/1508	0.27	0/2045
8	Jh	0.10	0/1508	0.27	0/2045
8	Jj	0.10	0/1508	0.27	0/2045
8	Jl	0.10	0/1508	0.27	0/2045
8	Jn	0.10	0/1508	0.27	0/2045
8	Jp	0.10	0/1508	0.27	0/2045
8	Jr	0.10	0/1508	0.27	0/2045
8	Jt	0.10	0/1508	0.27	0/2045
8	Jv	0.10	0/1508	0.27	0/2045
8	Jx	0.10	0/1508	0.27	0/2045
8	Jz	0.10	0/1508	0.29	0/2045
8	Kb	0.10	0/1508	0.26	0/2045
8	Kd	0.10	0/1508	0.26	0/2045
8	Kf	0.10	0/1508	0.28	0/2045
8	Kh	0.10	0/1508	0.28	0/2045
8	Kj	0.10	0/1508	0.27	0/2045
8	Kl	0.10	0/1508	0.27	0/2045
8	Kn	0.10	0/1508	0.27	0/2045
8	Kp	0.11	0/1508	0.28	0/2045
8	Kr	0.10	0/1508	0.27	0/2045
8	Kt	0.10	0/1508	0.28	0/2045
8	Kv	0.10	0/1508	0.27	0/2045
8	Kx	0.10	0/1508	0.28	0/2045
8	Kz	0.11	0/1508	0.27	0/2045

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
8	Lb	0.10	0/1508	0.28	0/2045
8	Ld	0.10	0/1508	0.27	0/2045
8	Lf	0.10	0/1508	0.28	0/2045
8	Lh	0.10	0/1508	0.27	0/2045
8	Lj	0.10	0/1508	0.28	0/2045
8	Ll	0.10	0/1508	0.27	0/2045
All	All	0.11	0/419274	0.28	4/567168 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Cn	114	ALA	CB-CA-C	-5.13	110.25	117.23
2	Bk	297	GLN	CB-CA-C	-5.07	110.34	117.23
3	Cl	114	ALA	CB-CA-C	-5.05	110.36	117.23
3	Ck	114	ALA	CB-CA-C	-5.03	110.39	117.23

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Aa	1674	0	1609	22	0
1	Ab	1674	0	1609	24	0
1	Ac	1674	0	1609	21	0
1	Ad	1674	0	1609	24	0
1	Ae	1674	0	1609	29	0
1	Af	1674	0	1609	30	0
1	Ag	1674	0	1609	34	0
1	Ah	1674	0	1609	37	0
1	Ai	1674	0	1609	30	0
1	Aj	1674	0	1609	29	0
1	Ak	1674	0	1609	27	0
1	Al	1674	0	1609	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Am	1674	0	1609	30	0
1	An	1674	0	1609	28	0
1	Ao	1674	0	1609	22	0
1	Ap	1674	0	1609	24	0
1	Aq	1674	0	1609	24	0
1	Ar	1674	0	1609	31	0
1	As	1674	0	1609	29	0
1	At	1674	0	1609	33	0
1	Au	1674	0	1609	34	0
1	Av	1674	0	1609	31	0
1	Aw	1674	0	1609	26	0
1	Ax	1674	0	1609	31	0
1	Ay	1674	0	1609	30	0
1	Az	1674	0	1609	33	0
2	Ba	2501	0	2549	35	0
2	Bb	2501	0	2549	35	0
2	Bc	2501	0	2549	38	0
2	Bd	2501	0	2549	32	0
2	Be	2501	0	2549	39	0
2	Bf	2501	0	2549	31	0
2	Bg	2501	0	2549	33	0
2	Bh	2501	0	2549	39	0
2	Bi	2501	0	2549	34	0
2	Bj	2501	0	2549	37	0
2	Bk	2501	0	2549	37	0
2	Bl	2501	0	2549	42	0
2	Bm	2501	0	2549	45	0
2	Bn	2501	0	2549	38	0
2	Bo	2501	0	2549	36	0
2	Bp	2501	0	2549	34	0
2	Bq	2501	0	2549	37	0
2	Br	2501	0	2549	32	0
2	Bs	2501	0	2549	39	0
2	Bt	2501	0	2549	30	0
2	Bu	2501	0	2549	42	0
2	Bv	2501	0	2549	40	0
2	Bw	2501	0	2549	38	0
2	Bx	2501	0	2549	37	0
2	By	2501	0	2549	40	0
2	Bz	2501	0	2549	29	0
3	Ca	2770	0	2749	21	0
3	Cb	2770	0	2749	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Cc	2770	0	2749	22	0
3	Cd	2770	0	2749	22	0
3	Ce	2770	0	2749	24	0
3	Cf	2770	0	2749	24	0
3	Cg	2770	0	2749	26	0
3	Ch	2770	0	2749	27	0
3	Ci	2770	0	2749	16	0
3	Cj	2770	0	2749	22	0
3	Ck	2770	0	2749	22	0
3	Cl	2770	0	2749	18	0
3	Cm	2770	0	2749	28	0
3	Cn	2770	0	2749	21	0
3	Co	2770	0	2749	25	0
3	Cp	2770	0	2749	21	0
3	Cq	2770	0	2749	27	0
3	Cr	2770	0	2749	23	0
3	Cs	2770	0	2749	23	0
3	Ct	2770	0	2749	27	0
3	Cu	2770	0	2749	22	0
3	Cv	2770	0	2749	23	0
3	Cw	2770	0	2749	22	0
3	Cx	2770	0	2749	14	0
3	Cy	2770	0	2749	25	0
3	Cz	2770	0	2749	23	0
4	Da	2085	0	2022	18	0
4	Db	2080	0	2003	15	0
4	Dc	2085	0	2022	19	0
4	Dd	2080	0	2003	16	0
4	De	2085	0	2022	19	0
4	Df	2080	0	2003	22	0
4	Dg	2085	0	2022	26	0
4	Dh	2080	0	2003	16	0
4	Di	2085	0	2022	27	0
4	Dj	2080	0	2003	24	0
4	Dk	2085	0	2022	21	0
4	Dl	2080	0	2003	15	0
4	Dm	2085	0	2022	19	0
4	Dn	2080	0	2003	16	0
4	Do	2085	0	2022	18	0
4	Dp	2080	0	2003	13	0
4	Dq	2085	0	2022	17	0
4	Dr	2080	0	2003	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Ds	2085	0	2022	20	0
4	Dt	2080	0	2003	19	0
4	Du	2085	0	2022	26	0
4	Dv	2080	0	2003	19	0
4	Dw	2085	0	2022	19	0
4	Dx	2080	0	2003	17	0
4	Dy	2085	0	2022	22	0
4	Dz	2080	0	2003	15	0
5	Ea	1466	0	1434	12	0
5	Eb	1494	0	1478	6	0
5	Ec	1466	0	1434	12	0
5	Ed	1494	0	1478	6	0
5	Ee	1466	0	1434	13	0
5	Ef	1494	0	1478	7	0
5	Eg	1466	0	1434	13	0
5	Uh	1494	0	1478	8	0
5	Ei	1466	0	1434	10	0
5	Ej	1494	0	1478	6	0
5	Ek	1466	0	1434	10	0
5	El	1494	0	1478	8	0
5	Em	1466	0	1434	12	0
5	En	1494	0	1478	7	0
5	Eo	1466	0	1434	14	0
5	Ep	1494	0	1478	7	0
5	Eq	1466	0	1434	13	0
5	Er	1494	0	1478	13	0
5	Es	1466	0	1434	13	0
5	Et	1494	0	1478	7	0
5	Eu	1466	0	1434	12	0
5	Ev	1494	0	1478	8	0
5	Ew	1466	0	1434	11	0
5	Ex	1494	0	1478	6	0
5	Ey	1466	0	1434	12	0
5	Ez	1494	0	1478	9	0
6	Fa	105	0	107	1	0
6	Fb	105	0	107	0	0
6	Fc	105	0	107	1	0
6	Fd	105	0	107	0	0
6	Fe	105	0	107	0	0
6	Ff	105	0	107	2	0
6	Fg	105	0	107	1	0
6	Fh	105	0	107	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Fi	105	0	107	0	0
6	Fj	105	0	107	0	0
6	Fk	105	0	107	0	0
6	Fl	105	0	107	1	0
6	Fm	105	0	107	0	0
6	Fn	105	0	107	1	0
6	Fo	105	0	107	1	0
6	Fp	105	0	107	0	0
6	Fq	105	0	107	0	0
6	Fr	105	0	107	1	0
6	Fs	105	0	107	1	0
6	Ft	105	0	107	2	0
6	Fu	105	0	107	4	0
6	Fv	105	0	107	1	0
6	Fw	105	0	107	1	0
6	Fx	105	0	107	0	0
6	Fy	105	0	107	0	0
6	Fz	105	0	107	1	0
6	Ga	105	0	107	1	0
6	Gb	105	0	107	2	0
6	Gc	105	0	107	2	0
6	Gd	105	0	107	2	0
6	Ge	105	0	107	0	0
6	Gf	105	0	107	0	0
6	Gg	105	0	107	0	0
6	Gh	105	0	107	0	0
6	Gi	105	0	107	0	0
6	Gj	105	0	107	1	0
6	Gk	105	0	107	1	0
6	Gl	105	0	107	1	0
6	Gm	105	0	107	0	0
6	Gn	105	0	107	0	0
6	Go	105	0	107	2	0
6	Gp	105	0	107	1	0
6	Gq	105	0	107	4	0
6	Gr	105	0	107	0	0
6	Gs	105	0	107	0	0
6	Gt	105	0	107	0	0
6	Gu	105	0	107	0	0
6	Gv	105	0	107	0	0
6	Gw	105	0	107	2	0
6	Gx	105	0	107	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Gy	105	0	107	0	0
6	Gz	105	0	107	1	0
7	Ha	828	0	820	12	0
7	Hc	828	0	820	9	0
7	He	828	0	820	7	0
7	Hg	828	0	820	7	0
7	Hi	828	0	820	4	0
7	Hk	828	0	820	5	0
7	Hm	828	0	820	7	0
7	Ho	828	0	820	6	0
7	Hq	828	0	820	10	0
7	Hs	828	0	820	9	0
7	Hu	828	0	820	8	0
7	Hw	828	0	820	8	0
7	Hy	828	0	820	5	0
7	Ia	828	0	820	9	0
7	Ic	828	0	820	7	0
7	Ie	828	0	820	4	0
7	Ig	828	0	820	10	0
7	Ii	828	0	820	8	0
7	Ik	828	0	820	7	0
7	Im	828	0	820	11	0
7	Io	828	0	820	10	0
7	Iq	828	0	820	8	0
7	Is	828	0	820	7	0
7	Iu	828	0	820	7	0
7	Iw	828	0	820	8	0
7	Iy	828	0	820	5	0
7	Ja	828	0	820	9	0
7	Jc	828	0	820	11	0
7	Je	828	0	820	11	0
7	Jg	828	0	820	11	0
7	Ji	828	0	820	12	0
7	Jk	828	0	820	10	0
7	Jm	828	0	820	8	0
7	Jo	828	0	820	9	0
7	Jq	828	0	820	10	0
7	Js	828	0	820	10	0
7	Ju	828	0	820	10	0
7	Jw	828	0	820	10	0
7	Jy	828	0	820	7	0
7	Ka	828	0	820	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Kc	828	0	820	7	0
7	Ke	828	0	820	7	0
7	Kg	828	0	820	7	0
7	Ki	828	0	820	5	0
7	Kk	828	0	820	5	0
7	Km	828	0	820	7	0
7	Ko	828	0	820	8	0
7	Kq	828	0	820	10	0
7	Ks	828	0	820	10	0
7	Ku	828	0	820	8	0
7	Kw	828	0	820	7	0
7	Ky	828	0	820	8	0
7	La	828	0	820	9	0
7	Lc	828	0	820	9	0
7	Le	828	0	820	10	0
7	Lg	828	0	820	9	0
7	Li	828	0	820	12	0
7	Lk	828	0	820	9	0
8	Hb	1482	0	1448	18	0
8	Hd	1482	0	1448	21	0
8	Hf	1482	0	1448	14	0
8	Hh	1482	0	1448	17	0
8	Hj	1482	0	1448	17	0
8	Hl	1482	0	1448	18	0
8	Hn	1482	0	1448	16	0
8	Hp	1482	0	1448	16	0
8	Hr	1482	0	1448	19	0
8	Ht	1482	0	1448	21	0
8	Hv	1482	0	1448	18	0
8	Hx	1482	0	1448	19	0
8	Hz	1482	0	1448	17	0
8	Ib	1482	0	1448	19	0
8	Id	1482	0	1448	18	0
8	If	1482	0	1448	16	0
8	Ih	1482	0	1448	18	0
8	Ij	1482	0	1448	18	0
8	Il	1482	0	1448	17	0
8	In	1482	0	1448	17	0
8	Ip	1482	0	1448	16	0
8	Ir	1482	0	1448	17	0
8	It	1482	0	1448	14	0
8	Iv	1482	0	1448	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	Ix	1482	0	1448	21	0
8	Iz	1482	0	1448	19	0
8	Jb	1482	0	1448	17	0
8	Jd	1482	0	1448	20	0
8	Jf	1482	0	1448	17	0
8	Jh	1482	0	1448	19	0
8	Jj	1482	0	1448	17	0
8	Jl	1482	0	1448	15	0
8	Jn	1482	0	1448	20	0
8	Jp	1482	0	1448	15	0
8	Jr	1482	0	1448	17	0
8	Jt	1482	0	1448	18	0
8	Jv	1482	0	1448	17	0
8	Jx	1482	0	1448	16	0
8	Jz	1482	0	1448	17	0
8	Kb	1482	0	1448	18	0
8	Kd	1482	0	1448	17	0
8	Kf	1482	0	1448	16	0
8	Kh	1482	0	1448	19	0
8	Kj	1482	0	1448	18	0
8	Kl	1482	0	1448	17	0
8	Kn	1482	0	1448	13	0
8	Kp	1482	0	1448	18	0
8	Kr	1482	0	1448	21	0
8	Kt	1482	0	1448	20	0
8	Kv	1482	0	1448	16	0
8	Kx	1482	0	1448	17	0
8	Kz	1482	0	1448	18	0
8	Lb	1482	0	1448	19	0
8	Ld	1482	0	1448	22	0
8	Lf	1482	0	1448	20	0
8	Lh	1482	0	1448	21	0
8	Lj	1482	0	1448	20	0
8	Ll	1482	0	1448	23	0
All	All	412635	0	406871	3490	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 3490 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Bk:56:GLN:HE22	2:Bl:69:LEU:H	1.32	0.78
1:Ao:125:LEU:HB3	1:Ar:244:MET:HE3	1.70	0.73
1:Ad:125:LEU:HB3	1:Ag:244:MET:HE3	1.70	0.72
1:Aq:125:LEU:HB3	1:At:244:MET:HE3	1.72	0.72
2:Bx:56:GLN:HE22	2:By:69:LEU:H	1.37	0.71

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	Ab	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	Ac	219/227 (96%)	212 (97%)	7 (3%)	0	100	100
1	Ad	219/227 (96%)	211 (96%)	8 (4%)	0	100	100
1	Ae	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	Af	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	Ag	219/227 (96%)	212 (97%)	7 (3%)	0	100	100
1	Ah	219/227 (96%)	211 (96%)	8 (4%)	0	100	100
1	Ai	219/227 (96%)	212 (97%)	7 (3%)	0	100	100
1	Aj	219/227 (96%)	212 (97%)	7 (3%)	0	100	100
1	Ak	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
1	Al	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
1	Am	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
1	An	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	Ao	219/227 (96%)	211 (96%)	8 (4%)	0	100	100
1	Ap	219/227 (96%)	212 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aq	219/227 (96%)	212 (97%)	7 (3%)	0	100	100
1	Ar	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
1	As	219/227 (96%)	211 (96%)	8 (4%)	0	100	100
1	At	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
1	Au	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	Av	219/227 (96%)	210 (96%)	9 (4%)	0	100	100
1	Aw	219/227 (96%)	210 (96%)	9 (4%)	0	100	100
1	Ax	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
1	Ay	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
1	Az	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
2	Ba	341/343 (99%)	334 (98%)	7 (2%)	0	100	100
2	Bb	341/343 (99%)	331 (97%)	10 (3%)	0	100	100
2	Bc	341/343 (99%)	333 (98%)	8 (2%)	0	100	100
2	Bd	341/343 (99%)	332 (97%)	9 (3%)	0	100	100
2	Be	341/343 (99%)	331 (97%)	10 (3%)	0	100	100
2	Bf	341/343 (99%)	333 (98%)	8 (2%)	0	100	100
2	Bg	341/343 (99%)	331 (97%)	10 (3%)	0	100	100
2	Bh	341/343 (99%)	328 (96%)	13 (4%)	0	100	100
2	Bi	341/343 (99%)	332 (97%)	9 (3%)	0	100	100
2	Bj	341/343 (99%)	334 (98%)	7 (2%)	0	100	100
2	Bk	341/343 (99%)	330 (97%)	11 (3%)	0	100	100
2	Bl	341/343 (99%)	332 (97%)	9 (3%)	0	100	100
2	Bm	341/343 (99%)	330 (97%)	11 (3%)	0	100	100
2	Bn	341/343 (99%)	328 (96%)	13 (4%)	0	100	100
2	Bo	341/343 (99%)	329 (96%)	12 (4%)	0	100	100
2	Bp	341/343 (99%)	331 (97%)	10 (3%)	0	100	100
2	Bq	341/343 (99%)	332 (97%)	9 (3%)	0	100	100
2	Br	341/343 (99%)	332 (97%)	9 (3%)	0	100	100
2	Bs	341/343 (99%)	328 (96%)	13 (4%)	0	100	100
2	Bt	341/343 (99%)	328 (96%)	13 (4%)	0	100	100
2	Bu	341/343 (99%)	330 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Bv	341/343 (99%)	327 (96%)	14 (4%)	0	100	100
2	Bw	341/343 (99%)	330 (97%)	11 (3%)	0	100	100
2	Bx	341/343 (99%)	329 (96%)	12 (4%)	0	100	100
2	By	341/343 (99%)	332 (97%)	9 (3%)	0	100	100
2	Bz	341/343 (99%)	330 (97%)	11 (3%)	0	100	100
3	Ca	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cb	350/352 (99%)	333 (95%)	17 (5%)	0	100	100
3	Cc	350/352 (99%)	339 (97%)	11 (3%)	0	100	100
3	Cd	350/352 (99%)	337 (96%)	13 (4%)	0	100	100
3	Ce	350/352 (99%)	339 (97%)	11 (3%)	0	100	100
3	Cf	350/352 (99%)	340 (97%)	10 (3%)	0	100	100
3	Cg	350/352 (99%)	333 (95%)	17 (5%)	0	100	100
3	Ch	350/352 (99%)	339 (97%)	11 (3%)	0	100	100
3	Ci	350/352 (99%)	340 (97%)	10 (3%)	0	100	100
3	Cj	350/352 (99%)	340 (97%)	10 (3%)	0	100	100
3	Ck	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cl	350/352 (99%)	333 (95%)	17 (5%)	0	100	100
3	Cm	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
3	Cn	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Co	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cp	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cq	350/352 (99%)	337 (96%)	13 (4%)	0	100	100
3	Cr	350/352 (99%)	340 (97%)	10 (3%)	0	100	100
3	Cs	350/352 (99%)	339 (97%)	11 (3%)	0	100	100
3	Ct	350/352 (99%)	338 (97%)	12 (3%)	0	100	100
3	Cu	350/352 (99%)	337 (96%)	13 (4%)	0	100	100
3	Cv	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cw	350/352 (99%)	340 (97%)	10 (3%)	0	100	100
3	Cx	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cy	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
3	Cz	350/352 (99%)	341 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Da	253/271 (93%)	233 (92%)	20 (8%)	0	100	100
4	Db	254/271 (94%)	231 (91%)	21 (8%)	2 (1%)	16	49
4	Dc	253/271 (93%)	231 (91%)	22 (9%)	0	100	100
4	Dd	254/271 (94%)	233 (92%)	20 (8%)	1 (0%)	30	61
4	De	253/271 (93%)	235 (93%)	18 (7%)	0	100	100
4	Df	254/271 (94%)	229 (90%)	24 (9%)	1 (0%)	30	61
4	Dg	253/271 (93%)	233 (92%)	20 (8%)	0	100	100
4	Dh	254/271 (94%)	231 (91%)	22 (9%)	1 (0%)	30	61
4	Di	253/271 (93%)	232 (92%)	21 (8%)	0	100	100
4	Dj	254/271 (94%)	231 (91%)	21 (8%)	2 (1%)	16	49
4	Dk	253/271 (93%)	232 (92%)	21 (8%)	0	100	100
4	Dl	254/271 (94%)	231 (91%)	21 (8%)	2 (1%)	16	49
4	Dm	253/271 (93%)	234 (92%)	19 (8%)	0	100	100
4	Dn	254/271 (94%)	234 (92%)	19 (8%)	1 (0%)	30	61
4	Do	253/271 (93%)	233 (92%)	20 (8%)	0	100	100
4	Dp	254/271 (94%)	229 (90%)	24 (9%)	1 (0%)	30	61
4	Dq	253/271 (93%)	233 (92%)	20 (8%)	0	100	100
4	Dr	254/271 (94%)	229 (90%)	24 (9%)	1 (0%)	30	61
4	Ds	253/271 (93%)	236 (93%)	17 (7%)	0	100	100
4	Dt	254/271 (94%)	229 (90%)	24 (9%)	1 (0%)	30	61
4	Du	253/271 (93%)	233 (92%)	20 (8%)	0	100	100
4	Dv	254/271 (94%)	231 (91%)	22 (9%)	1 (0%)	30	61
4	Dw	253/271 (93%)	236 (93%)	17 (7%)	0	100	100
4	Dx	254/271 (94%)	232 (91%)	21 (8%)	1 (0%)	30	61
4	Dy	253/271 (93%)	230 (91%)	23 (9%)	0	100	100
4	Dz	254/271 (94%)	232 (91%)	20 (8%)	2 (1%)	16	49
5	Ea	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
5	Eb	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Ec	181/183 (99%)	172 (95%)	8 (4%)	1 (1%)	21	54
5	Ed	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Ee	181/183 (99%)	171 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Ef	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
5	Eg	181/183 (99%)	170 (94%)	10 (6%)	1 (1%)	21	54
5	Eh	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Ei	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
5	Ej	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Ek	181/183 (99%)	170 (94%)	11 (6%)	0	100	100
5	El	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Em	181/183 (99%)	172 (95%)	8 (4%)	1 (1%)	21	54
5	En	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Eo	181/183 (99%)	171 (94%)	10 (6%)	0	100	100
5	Ep	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Eq	181/183 (99%)	171 (94%)	10 (6%)	0	100	100
5	Er	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Es	181/183 (99%)	170 (94%)	11 (6%)	0	100	100
5	Et	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Eu	181/183 (99%)	171 (94%)	10 (6%)	0	100	100
5	Ev	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Ew	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
5	Ex	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
5	Ey	181/183 (99%)	171 (94%)	10 (6%)	0	100	100
5	Ez	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
6	Fa	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fb	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fc	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fd	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fe	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Ff	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fg	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fh	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fi	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fj	10/12 (83%)	8 (80%)	2 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Fk	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fl	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fm	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fn	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Fo	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fp	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fq	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fr	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Fs	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Ft	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fu	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fv	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fw	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fx	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fy	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Fz	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
6	Ga	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Gb	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gc	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gd	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Ge	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gf	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Gg	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Gh	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Gi	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gj	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gk	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gl	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gm	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gn	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Go	10/12 (83%)	8 (80%)	2 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Gp	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gq	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Gr	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gs	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gt	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gu	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
6	Gv	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gw	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gx	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gy	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
6	Gz	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
7	Ha	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hc	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	He	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hg	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Hi	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Hk	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hm	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ho	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hq	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hs	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hu	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hw	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Hy	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ia	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ic	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ie	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ig	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ii	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ik	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Im	102/105 (97%)	97 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	Io	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Iq	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Is	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Iu	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Iw	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Iy	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ja	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Jc	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Je	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Jg	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ji	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Jk	102/105 (97%)	95 (93%)	7 (7%)	0	100	100
7	Jm	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Jo	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Jq	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Js	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ju	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Jw	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Jy	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ka	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Kc	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ke	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Kg	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ki	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Kk	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Km	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Ko	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Kq	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ks	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Ku	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Kw	102/105 (97%)	96 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	Ky	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	La	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Lc	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
7	Le	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Lg	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Li	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
7	Lk	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
8	Hb	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Hd	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Hf	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
8	Hh	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
8	Hj	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
8	Hl	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
8	Hn	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Hp	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	Hr	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	Ht	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
8	Hv	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Hx	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Hx	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Hx	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Ib	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Id	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	If	188/190 (99%)	178 (95%)	9 (5%)	1 (0%)	24	57
8	Ih	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
8	Ij	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Il	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	In	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	Ip	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Ir	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
8	It	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
8	Iv	188/190 (99%)	179 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	Ix	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Iz	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
8	Jb	188/190 (99%)	178 (95%)	9 (5%)	1 (0%)	24	57
8	Jd	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Jf	188/190 (99%)	178 (95%)	9 (5%)	1 (0%)	24	57
8	Jh	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Jj	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Jl	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
8	Jn	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
8	Jp	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
8	Jr	188/190 (99%)	177 (94%)	10 (5%)	1 (0%)	24	57
8	Jt	188/190 (99%)	177 (94%)	10 (5%)	1 (0%)	24	57
8	Jv	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Jx	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Jz	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	Kb	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Kd	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Kf	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
8	Kh	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Kj	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
8	Kl	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
8	Kn	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	Kp	188/190 (99%)	177 (94%)	10 (5%)	1 (0%)	24	57
8	Kr	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
8	Kt	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Kv	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Kx	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Kz	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
8	Lb	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Ld	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
8	Lf	188/190 (99%)	177 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	Lh	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
8	Lj	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
8	Ll	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
All	All	52297/53510 (98%)	49923 (96%)	2339 (4%)	35 (0%)	49	79

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	Db	193	VAL
4	Dh	193	VAL
4	Dl	193	VAL
4	Df	193	VAL
4	Dn	193	VAL

### 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	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Ab	182/186 (98%)	180 (99%)	2 (1%)	65	74
1	Ac	182/186 (98%)	180 (99%)	2 (1%)	65	74
1	Ad	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Ae	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Af	182/186 (98%)	177 (97%)	5 (3%)	39	61
1	Ag	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Ah	182/186 (98%)	177 (97%)	5 (3%)	39	61
1	Ai	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Aj	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Ak	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Al	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Am	182/186 (98%)	178 (98%)	4 (2%)	45	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	An	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Ao	182/186 (98%)	180 (99%)	2 (1%)	65	74
1	Ap	182/186 (98%)	180 (99%)	2 (1%)	65	74
1	Aq	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Ar	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	As	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	At	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Au	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Av	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Aw	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Ax	182/186 (98%)	178 (98%)	4 (2%)	45	65
1	Ay	182/186 (98%)	179 (98%)	3 (2%)	55	69
1	Az	182/186 (98%)	178 (98%)	4 (2%)	45	65
2	Ba	267/269 (99%)	263 (98%)	4 (2%)	57	70
2	Bb	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bc	267/269 (99%)	263 (98%)	4 (2%)	57	70
2	Bd	267/269 (99%)	264 (99%)	3 (1%)	65	74
2	Be	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bf	267/269 (99%)	264 (99%)	3 (1%)	65	74
2	Bg	267/269 (99%)	265 (99%)	2 (1%)	76	78
2	Bh	267/269 (99%)	264 (99%)	3 (1%)	65	74
2	Bi	267/269 (99%)	264 (99%)	3 (1%)	65	74
2	Bj	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bk	267/269 (99%)	259 (97%)	8 (3%)	36	59
2	Bl	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bm	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bn	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bo	267/269 (99%)	261 (98%)	6 (2%)	45	65
2	Bp	267/269 (99%)	262 (98%)	5 (2%)	50	67
2	Bq	267/269 (99%)	260 (97%)	7 (3%)	40	62
2	Br	267/269 (99%)	262 (98%)	5 (2%)	50	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Bs	267/269 (99%)	261 (98%)	6 (2%)	45	65
2	Bt	267/269 (99%)	264 (99%)	3 (1%)	65	74
2	Bu	267/269 (99%)	259 (97%)	8 (3%)	36	59
2	Bv	267/269 (99%)	261 (98%)	6 (2%)	45	65
2	Bw	267/269 (99%)	265 (99%)	2 (1%)	76	78
2	Bx	267/269 (99%)	263 (98%)	4 (2%)	57	70
2	By	267/269 (99%)	263 (98%)	4 (2%)	57	70
2	Bz	267/269 (99%)	263 (98%)	4 (2%)	57	70
3	Ca	299/303 (99%)	297 (99%)	2 (1%)	76	78
3	Cb	299/303 (99%)	293 (98%)	6 (2%)	48	66
3	Cc	299/303 (99%)	297 (99%)	2 (1%)	76	78
3	Cd	299/303 (99%)	294 (98%)	5 (2%)	53	69
3	Ce	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Cf	299/303 (99%)	296 (99%)	3 (1%)	68	75
3	Cg	299/303 (99%)	294 (98%)	5 (2%)	53	69
3	Ch	299/303 (99%)	296 (99%)	3 (1%)	68	75
3	Ci	299/303 (99%)	294 (98%)	5 (2%)	53	69
3	Cj	299/303 (99%)	297 (99%)	2 (1%)	76	78
3	Ck	299/303 (99%)	294 (98%)	5 (2%)	53	69
3	Cl	299/303 (99%)	296 (99%)	3 (1%)	68	75
3	Cm	299/303 (99%)	294 (98%)	5 (2%)	53	69
3	Cn	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Co	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Cp	299/303 (99%)	298 (100%)	1 (0%)	86	82
3	Cq	299/303 (99%)	296 (99%)	3 (1%)	68	75
3	Cr	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Cs	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Ct	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Cu	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Cv	299/303 (99%)	297 (99%)	2 (1%)	76	78
3	Cw	299/303 (99%)	295 (99%)	4 (1%)	61	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Cx	299/303 (99%)	295 (99%)	4 (1%)	61	72
3	Cy	299/303 (99%)	297 (99%)	2 (1%)	76	78
3	Cz	299/303 (99%)	296 (99%)	3 (1%)	68	75
4	Da	231/243 (95%)	224 (97%)	7 (3%)	36	59
4	Db	229/243 (94%)	227 (99%)	2 (1%)	70	76
4	Dc	231/243 (95%)	222 (96%)	9 (4%)	28	54
4	Dd	229/243 (94%)	225 (98%)	4 (2%)	53	69
4	De	231/243 (95%)	221 (96%)	10 (4%)	26	51
4	Df	229/243 (94%)	225 (98%)	4 (2%)	53	69
4	Dg	231/243 (95%)	223 (96%)	8 (4%)	32	56
4	Dh	229/243 (94%)	227 (99%)	2 (1%)	70	76
4	Di	231/243 (95%)	223 (96%)	8 (4%)	32	56
4	Dj	229/243 (94%)	227 (99%)	2 (1%)	70	76
4	Dk	231/243 (95%)	223 (96%)	8 (4%)	32	56
4	Dl	229/243 (94%)	226 (99%)	3 (1%)	61	72
4	Dm	231/243 (95%)	222 (96%)	9 (4%)	28	54
4	Dn	229/243 (94%)	226 (99%)	3 (1%)	61	72
4	Do	231/243 (95%)	223 (96%)	8 (4%)	32	56
4	Dp	229/243 (94%)	227 (99%)	2 (1%)	70	76
4	Dq	231/243 (95%)	222 (96%)	9 (4%)	28	54
4	Dr	229/243 (94%)	226 (99%)	3 (1%)	61	72
4	Ds	231/243 (95%)	223 (96%)	8 (4%)	32	56
4	Dt	229/243 (94%)	227 (99%)	2 (1%)	70	76
4	Du	231/243 (95%)	225 (97%)	6 (3%)	40	62
4	Dv	229/243 (94%)	226 (99%)	3 (1%)	61	72
4	Dw	231/243 (95%)	222 (96%)	9 (4%)	28	54
4	Dx	229/243 (94%)	227 (99%)	2 (1%)	70	76
4	Dy	231/243 (95%)	225 (97%)	6 (3%)	40	62
4	Dz	229/243 (94%)	227 (99%)	2 (1%)	70	76
5	Ea	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Eb	154/154 (100%)	147 (96%)	7 (4%)	24	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	Ec	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Ed	154/154 (100%)	149 (97%)	5 (3%)	34	58
5	Ee	149/154 (97%)	144 (97%)	5 (3%)	32	57
5	Ef	154/154 (100%)	149 (97%)	5 (3%)	34	58
5	Eg	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Eh	154/154 (100%)	146 (95%)	8 (5%)	21	48
5	Ei	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Ej	154/154 (100%)	148 (96%)	6 (4%)	28	54
5	Ek	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	El	154/154 (100%)	148 (96%)	6 (4%)	28	54
5	Em	149/154 (97%)	143 (96%)	6 (4%)	28	53
5	En	154/154 (100%)	150 (97%)	4 (3%)	40	62
5	Eo	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Ep	154/154 (100%)	149 (97%)	5 (3%)	34	58
5	Eq	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Er	154/154 (100%)	149 (97%)	5 (3%)	34	58
5	Es	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Et	154/154 (100%)	147 (96%)	7 (4%)	24	51
5	Eu	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Ev	154/154 (100%)	148 (96%)	6 (4%)	28	54
5	Ew	149/154 (97%)	143 (96%)	6 (4%)	28	53
5	Ex	154/154 (100%)	149 (97%)	5 (3%)	34	58
5	Ey	149/154 (97%)	142 (95%)	7 (5%)	23	50
5	Ez	154/154 (100%)	148 (96%)	6 (4%)	28	54
6	Fa	12/12 (100%)	12 (100%)	0	100	100
6	Fb	12/12 (100%)	12 (100%)	0	100	100
6	Fc	12/12 (100%)	12 (100%)	0	100	100
6	Fd	12/12 (100%)	12 (100%)	0	100	100
6	Fe	12/12 (100%)	12 (100%)	0	100	100
6	Ff	12/12 (100%)	12 (100%)	0	100	100
6	Fg	12/12 (100%)	12 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Fh	12/12 (100%)	12 (100%)	0	100	100
6	Fi	12/12 (100%)	12 (100%)	0	100	100
6	Fj	12/12 (100%)	12 (100%)	0	100	100
6	Fk	12/12 (100%)	12 (100%)	0	100	100
6	Fl	12/12 (100%)	12 (100%)	0	100	100
6	Fm	12/12 (100%)	12 (100%)	0	100	100
6	Fn	12/12 (100%)	12 (100%)	0	100	100
6	Fo	12/12 (100%)	12 (100%)	0	100	100
6	Fp	12/12 (100%)	12 (100%)	0	100	100
6	Fq	12/12 (100%)	12 (100%)	0	100	100
6	Fr	12/12 (100%)	12 (100%)	0	100	100
6	Fs	12/12 (100%)	12 (100%)	0	100	100
6	Ft	12/12 (100%)	12 (100%)	0	100	100
6	Fu	12/12 (100%)	12 (100%)	0	100	100
6	Fv	12/12 (100%)	12 (100%)	0	100	100
6	Fw	12/12 (100%)	12 (100%)	0	100	100
6	Fx	12/12 (100%)	12 (100%)	0	100	100
6	Fy	12/12 (100%)	12 (100%)	0	100	100
6	Fz	12/12 (100%)	12 (100%)	0	100	100
6	Ga	12/12 (100%)	12 (100%)	0	100	100
6	Gb	12/12 (100%)	12 (100%)	0	100	100
6	Gc	12/12 (100%)	12 (100%)	0	100	100
6	Gd	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Ge	12/12 (100%)	12 (100%)	0	100	100
6	Gf	12/12 (100%)	12 (100%)	0	100	100
6	Gg	12/12 (100%)	12 (100%)	0	100	100
6	Gh	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gi	12/12 (100%)	12 (100%)	0	100	100
6	Gj	12/12 (100%)	12 (100%)	0	100	100
6	Gk	12/12 (100%)	12 (100%)	0	100	100
6	Gl	12/12 (100%)	11 (92%)	1 (8%)	10	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Gm	12/12 (100%)	12 (100%)	0	100	100
6	Gn	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Go	12/12 (100%)	12 (100%)	0	100	100
6	Gp	12/12 (100%)	12 (100%)	0	100	100
6	Gq	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gr	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gs	12/12 (100%)	12 (100%)	0	100	100
6	Gt	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gu	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gv	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gw	12/12 (100%)	12 (100%)	0	100	100
6	Gx	12/12 (100%)	12 (100%)	0	100	100
6	Gy	12/12 (100%)	11 (92%)	1 (8%)	10	35
6	Gz	12/12 (100%)	12 (100%)	0	100	100
7	Ha	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Hc	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	He	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Hg	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Hi	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Hk	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Hm	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ho	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Hq	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Hs	84/85 (99%)	81 (96%)	3 (4%)	31	56
7	Hu	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Hw	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Hy	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ia	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ic	84/85 (99%)	81 (96%)	3 (4%)	31	56
7	Ie	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Ig	84/85 (99%)	80 (95%)	4 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Ii	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ik	84/85 (99%)	81 (96%)	3 (4%)	31	56
7	Im	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Io	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Iq	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Is	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Iu	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Iw	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Iy	84/85 (99%)	81 (96%)	3 (4%)	31	56
7	Ja	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Jc	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Je	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Jg	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ji	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Js	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Jm	84/85 (99%)	78 (93%)	6 (7%)	13	40
7	Jo	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Jq	84/85 (99%)	78 (93%)	6 (7%)	13	40
7	Js	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Ju	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Jw	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Jy	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ka	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Kc	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ke	84/85 (99%)	78 (93%)	6 (7%)	13	40
7	Kg	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ki	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Kk	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Km	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ko	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Kq	84/85 (99%)	80 (95%)	4 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Ks	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ku	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Kw	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Ky	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	La	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Lc	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Le	84/85 (99%)	78 (93%)	6 (7%)	13	40
7	Lg	84/85 (99%)	80 (95%)	4 (5%)	23	50
7	Li	84/85 (99%)	79 (94%)	5 (6%)	17	45
7	Lk	84/85 (99%)	79 (94%)	5 (6%)	17	45
8	Hb	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Hd	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Hf	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Hh	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Hj	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Hl	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Hn	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Hp	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Hr	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Ht	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Hv	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Hx	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Hz	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Ib	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Id	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	If	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Ih	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Ij	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Il	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	In	165/169 (98%)	163 (99%)	2 (1%)	63	73
8	Ip	165/169 (98%)	162 (98%)	3 (2%)	51	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	Ir	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	It	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Iv	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Ix	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Iz	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Jb	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Jd	165/169 (98%)	159 (96%)	6 (4%)	31	56
8	Jf	165/169 (98%)	159 (96%)	6 (4%)	31	56
8	Jh	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Jj	165/169 (98%)	159 (96%)	6 (4%)	31	56
8	Jl	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Jn	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Jp	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Jr	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Jt	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Jv	165/169 (98%)	159 (96%)	6 (4%)	31	56
8	Jx	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Jz	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Kb	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Kd	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Kf	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Kh	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Kj	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Kl	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Kn	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Kp	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Kr	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Kt	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Kv	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Kx	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Kz	165/169 (98%)	161 (98%)	4 (2%)	43	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	Lb	165/169 (98%)	160 (97%)	5 (3%)	36	59
8	Ld	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Lf	165/169 (98%)	161 (98%)	4 (2%)	43	63
8	Lh	165/169 (98%)	162 (98%)	3 (2%)	51	68
8	Lj	165/169 (98%)	159 (96%)	6 (4%)	31	56
8	Ll	165/169 (98%)	160 (97%)	5 (3%)	36	59
All	All	44433/45386 (98%)	43323 (98%)	1110 (2%)	42	63

5 of 1110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	Jv	200	THR
8	Kb	163	VAL
8	Jv	163	VAL
7	Kw	97	VAL
4	Dp	25	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1062 such sidechains are listed below:

Mol	Chain	Res	Type
8	Jv	52	HIS
8	Kd	40	ASN
8	Jv	40	ASN
7	Lg	68	GLN
4	Dc	106	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [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.

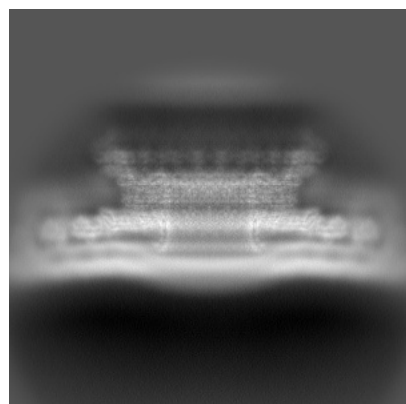
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72891. These allow visual inspection of the internal detail of the map and identification of artifacts.

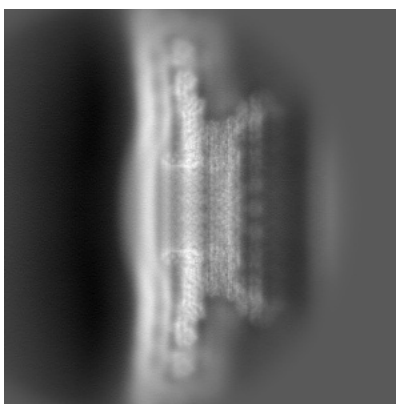
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

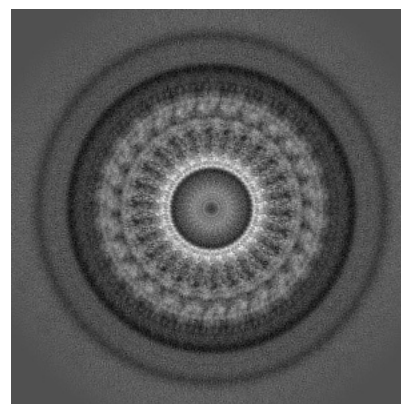
#### 6.1.1 Primary map



X

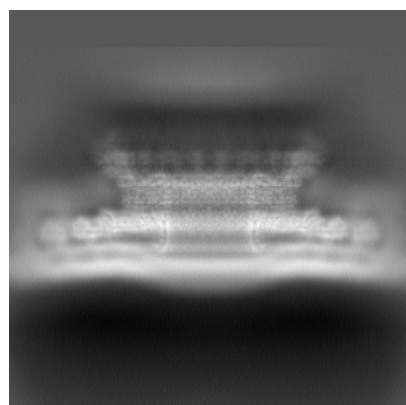


Y

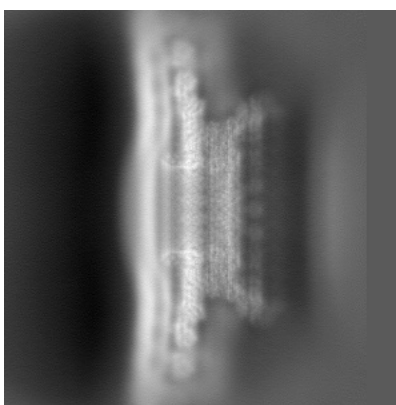


Z

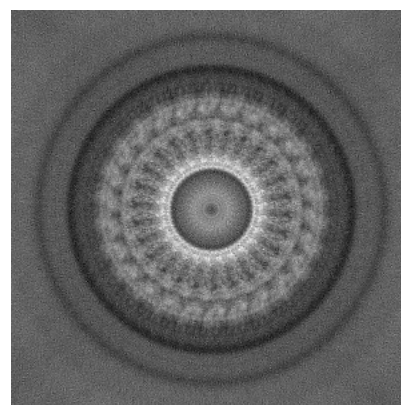
#### 6.1.2 Raw map



X



Y



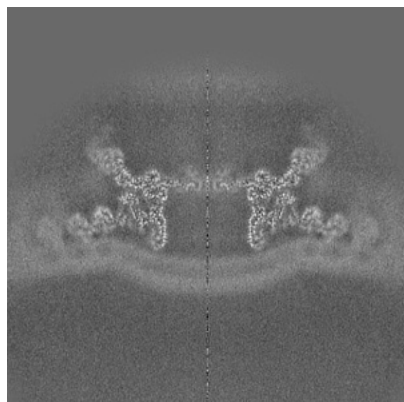
Z

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

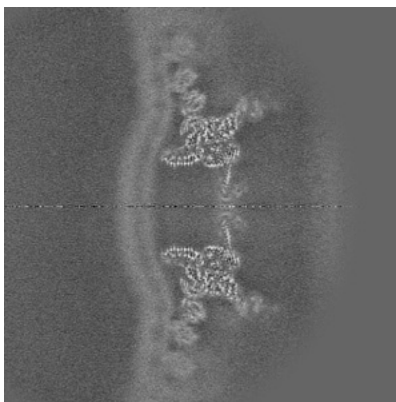


## 6.2 Central slices [i](#)

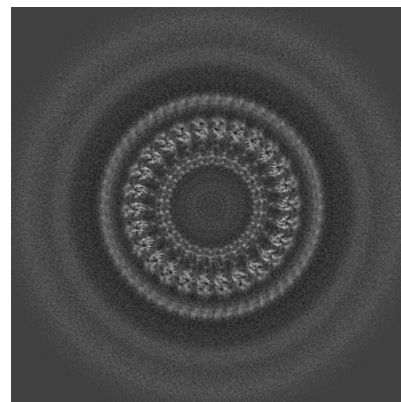
### 6.2.1 Primary map



X Index: 224

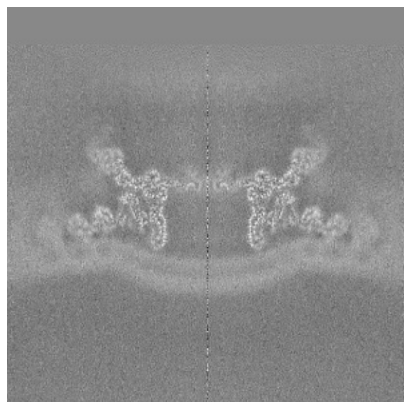


Y Index: 224

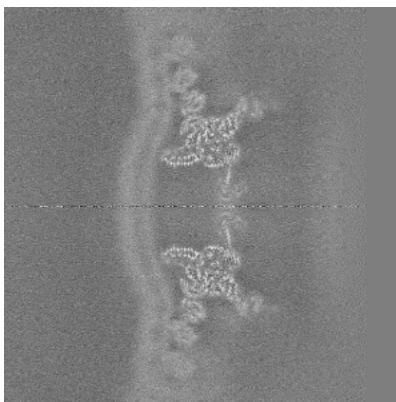


Z Index: 224

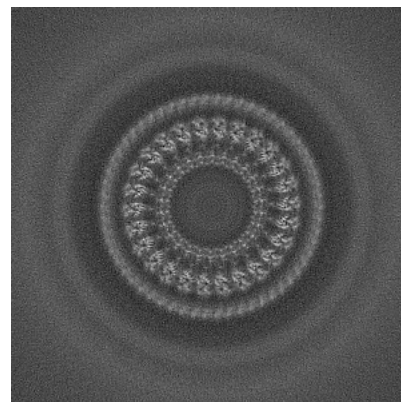
### 6.2.2 Raw map



X Index: 224



Y Index: 224

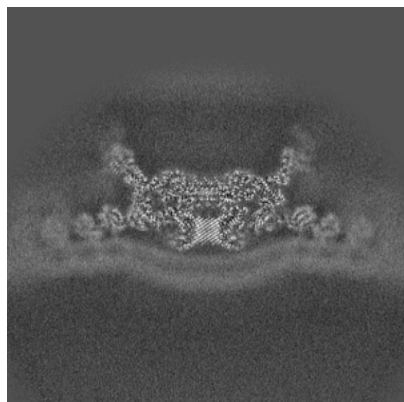


Z Index: 224

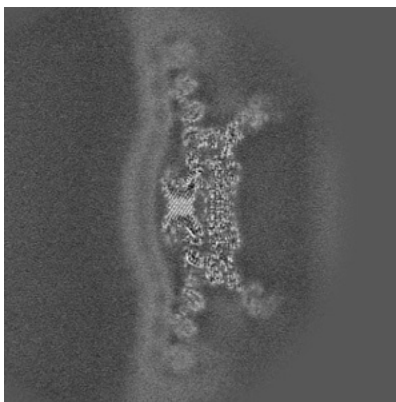
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

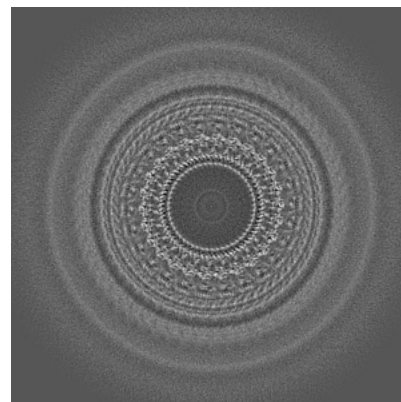
### 6.3.1 Primary map



X Index: 177

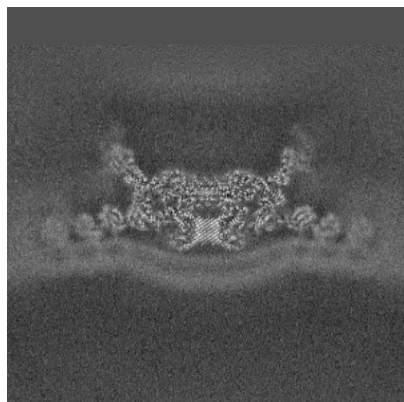


Y Index: 272

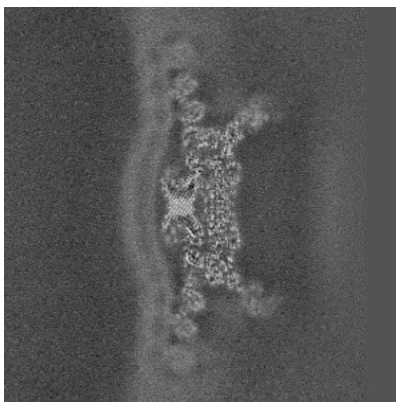


Z Index: 209

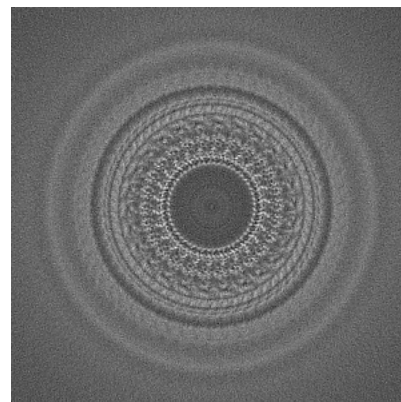
### 6.3.2 Raw map



X Index: 177



Y Index: 272

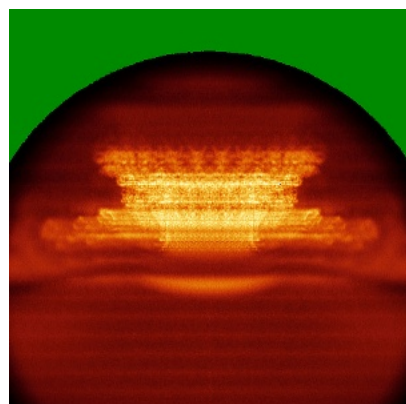


Z Index: 208

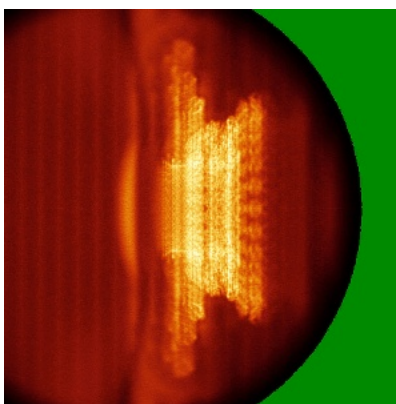
The images above show the largest variance slices of the map in three orthogonal directions.

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

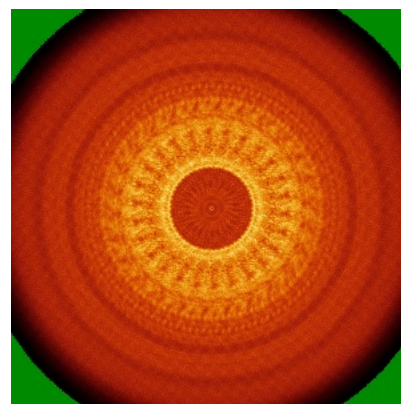
### 6.4.1 Primary map



X

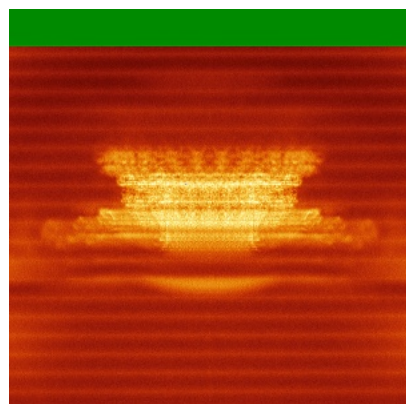


Y

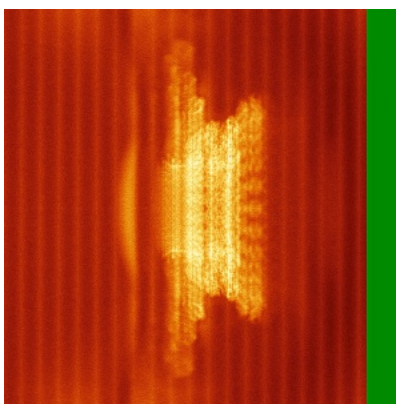


Z

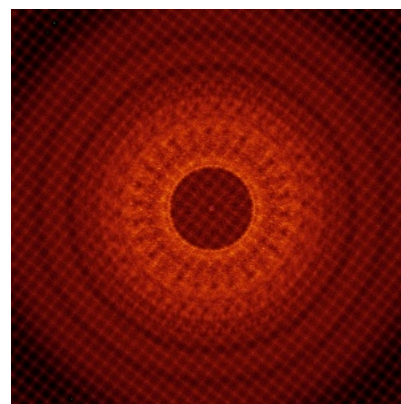
### 6.4.2 Raw map



X



Y



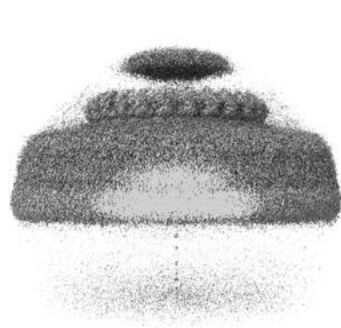
Z

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

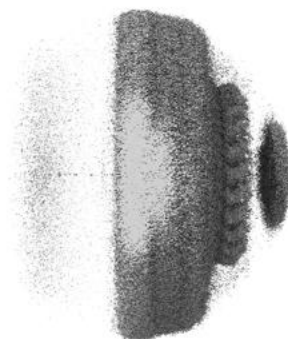


## 6.5 Orthogonal surface views [i](#)

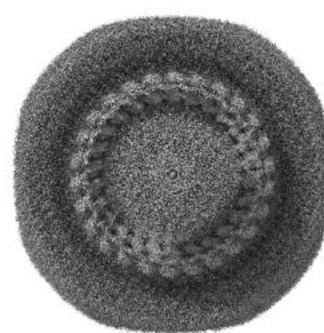
### 6.5.1 Primary map



X



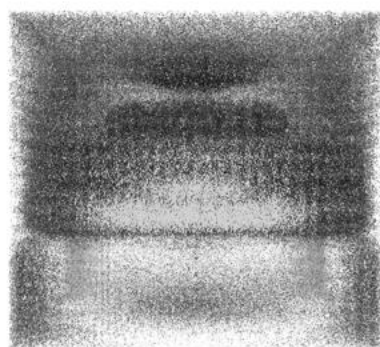
Y



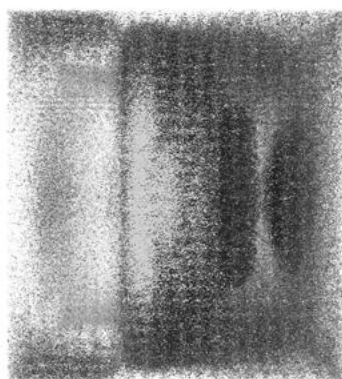
Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

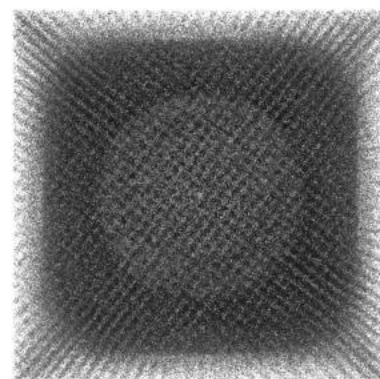
### 6.5.2 Raw map



X



Y



Z

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

## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

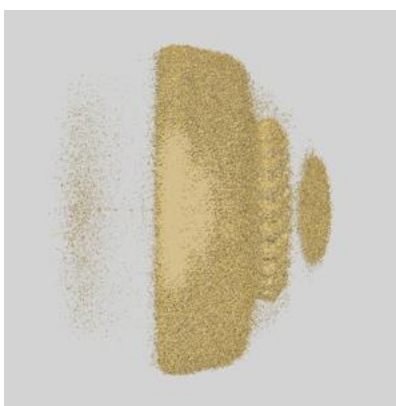
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

### 6.6.1 emd\_72891\_msk\_1.map [i](#)



X



Y

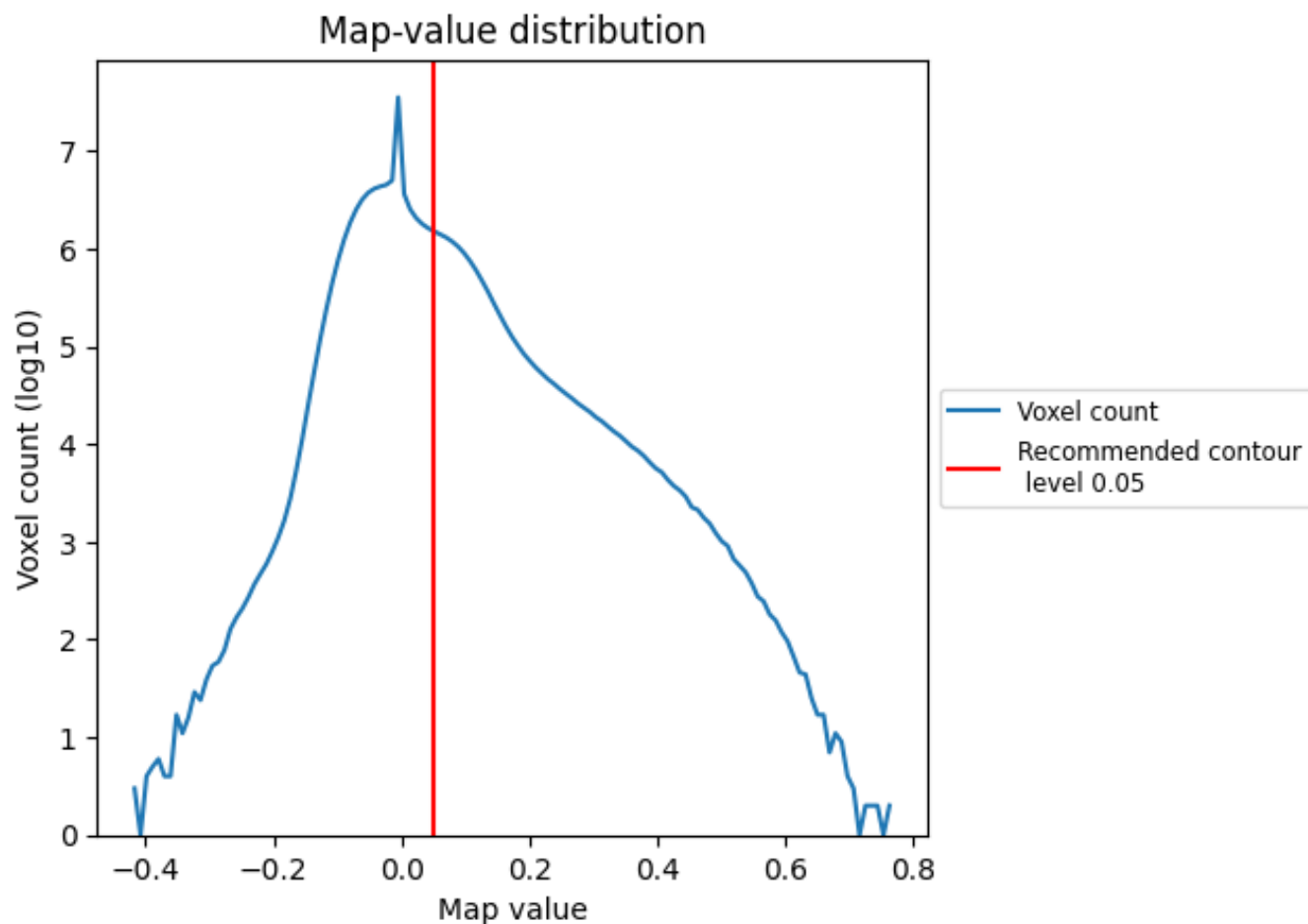


Z

## 7 Map analysis [i](#)

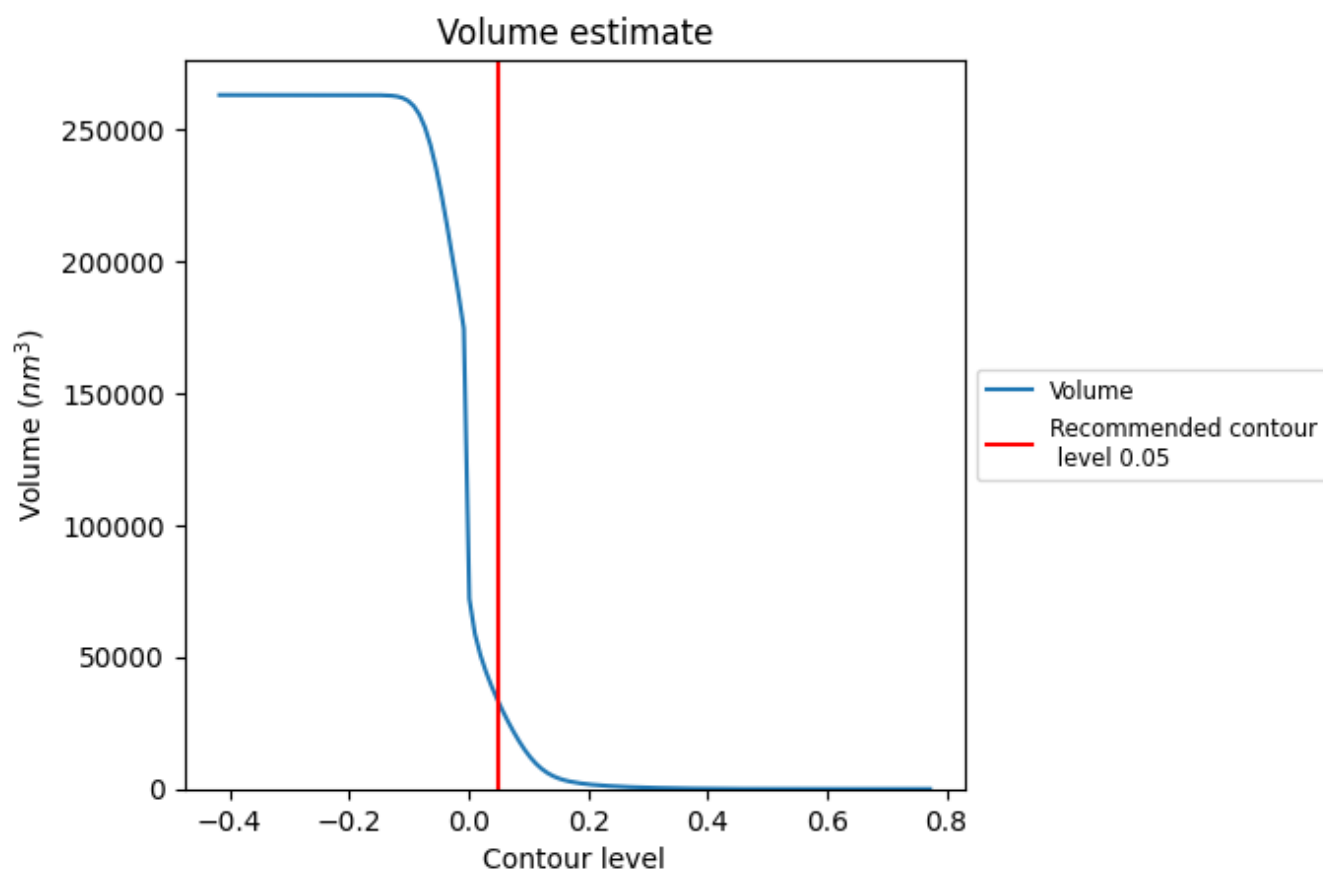
This section contains the results of statistical analysis of the map.

### 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.

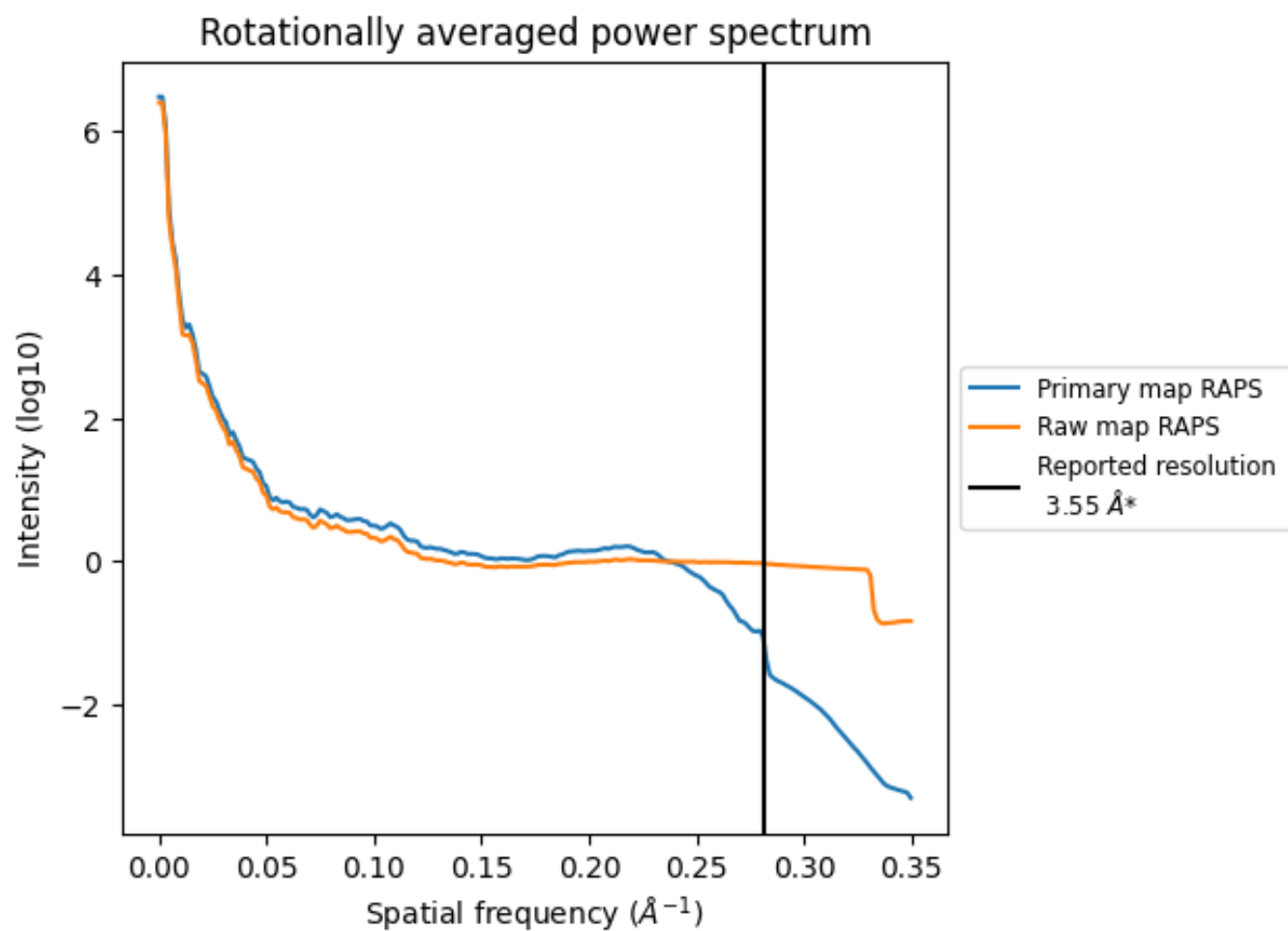
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 32880  $\text{nm}^3$ ; this corresponds to an approximate mass of 29702 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 ⓘ



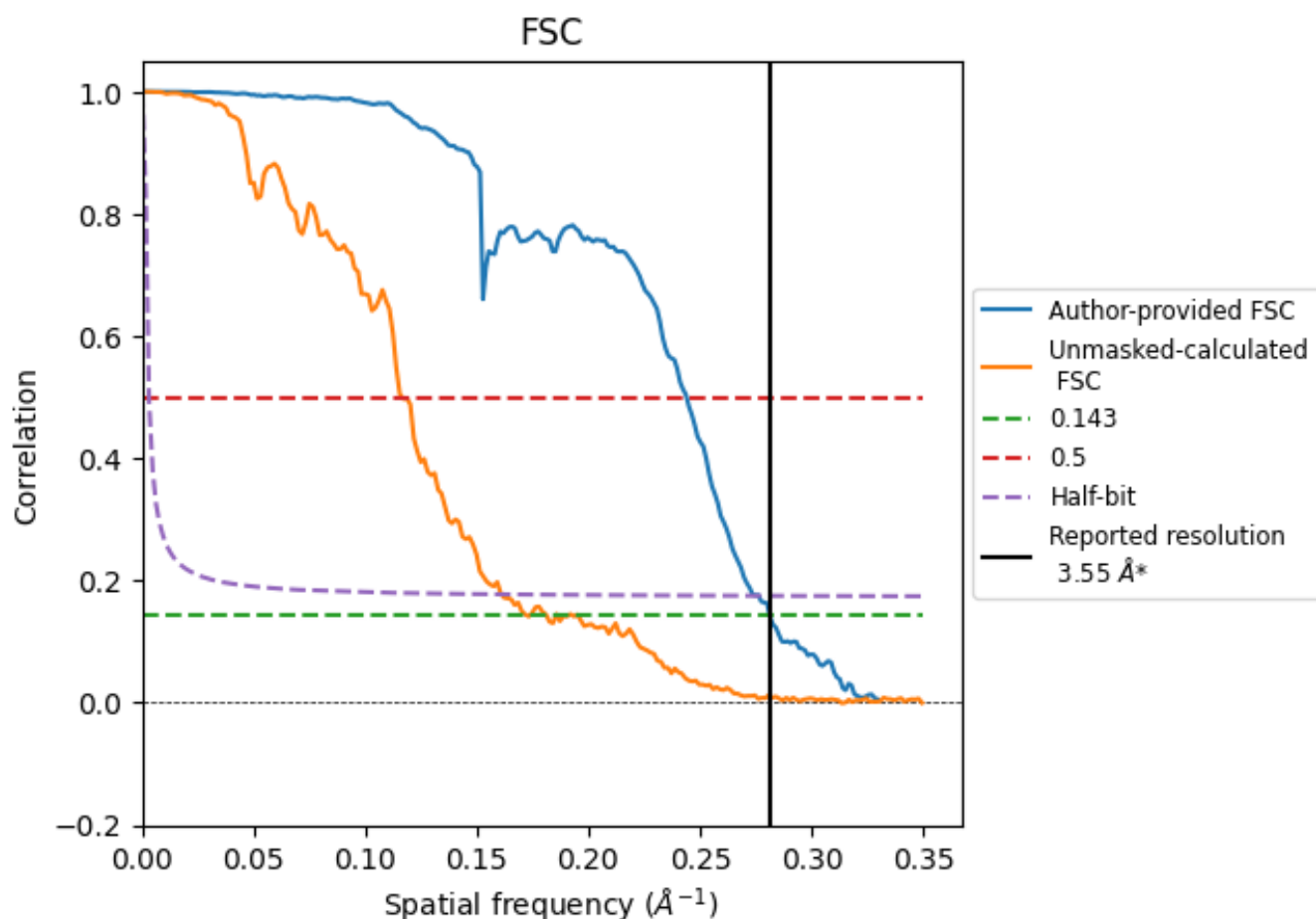
\*Reported resolution corresponds to spatial frequency of 0.282 Å<sup>-1</sup>



## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.282 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

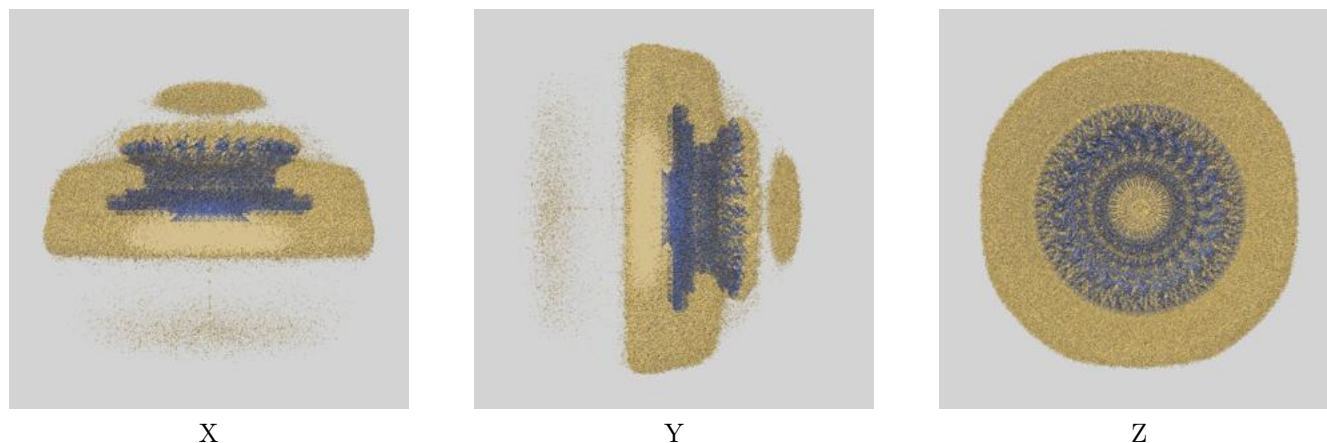
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.55	-	-
Author-provided FSC curve	3.55	4.10	3.62
Unmasked-calculated*	5.80	8.58	6.21

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.80 differs from the reported value 3.55 by more than 10 %

## 9 Map-model fit [i](#)

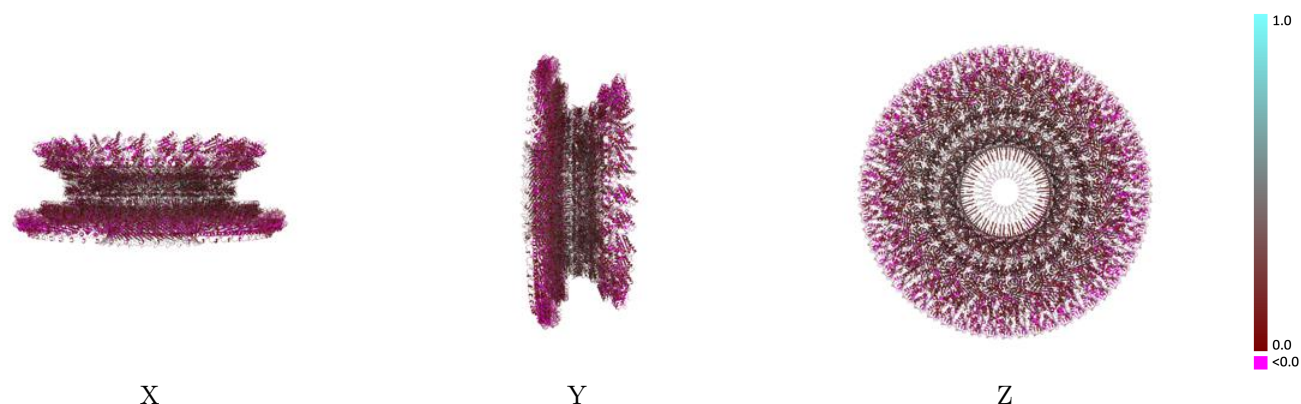
This section contains information regarding the fit between EMDB map EMD-72891 and PDB model 9YFG. Per-residue inclusion information can be found in section 3 on page 31.

### 9.1 Map-model overlay [i](#)



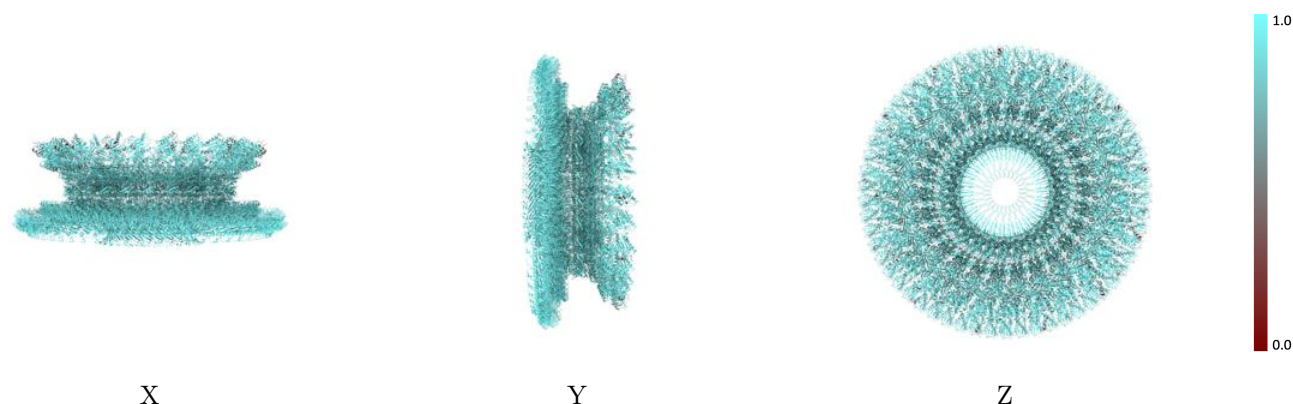
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



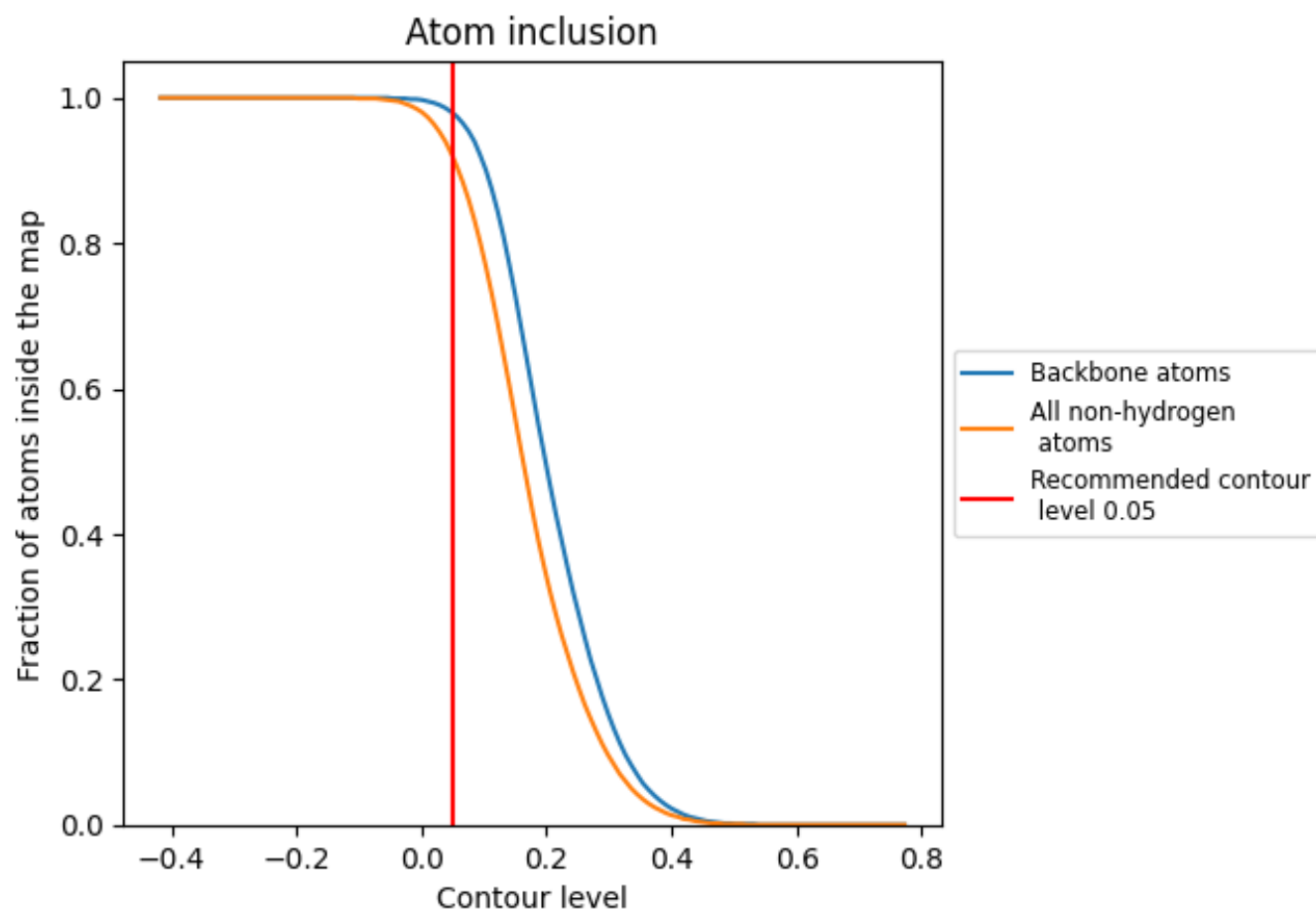
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 92% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.1830
Aa	 0.9120	 0.2900
Ab	 0.9190	 0.3010
Ac	 0.9250	 0.3020
Ad	 0.9280	 0.3020
Ae	 0.9280	 0.2970
Af	 0.9200	 0.2900
Ag	 0.9320	 0.2820
Ah	 0.9220	 0.2670
Ai	 0.9080	 0.2450
Aj	 0.9070	 0.2290
Ak	 0.9030	 0.2170
Al	 0.8980	 0.2040
Am	 0.8860	 0.1980
An	 0.8940	 0.2010
Ao	 0.8980	 0.2110
Ap	 0.9000	 0.2350
Aq	 0.8970	 0.2290
Ar	 0.9000	 0.2430
As	 0.9080	 0.2510
At	 0.9130	 0.2540
Au	 0.9130	 0.2600
Av	 0.9200	 0.2560
Aw	 0.9170	 0.2570
Ax	 0.9180	 0.2630
Ay	 0.9160	 0.2650
Az	 0.9080	 0.2790
Ba	 0.9080	 0.2080
Bb	 0.9190	 0.2230
Bc	 0.9200	 0.2310
Bd	 0.9090	 0.2410
Be	 0.9130	 0.2490
Bf	 0.9140	 0.2560
Bg	 0.9160	 0.2620
Bh	 0.9150	 0.2670























































































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Chain	Atom inclusion	Q-score
Bi	 0.9200	 0.2680
Bj	 0.9230	 0.2690
Bk	 0.9330	 0.2650
Bl	 0.9270	 0.2620
Bm	 0.9290	 0.2620
Bn	 0.9260	 0.2660
Bo	 0.9300	 0.2730
Bp	 0.9370	 0.2790
Bq	 0.9280	 0.2880
Br	 0.9270	 0.2930
Bs	 0.9240	 0.2910
Bt	 0.9260	 0.2790
Bu	 0.9180	 0.2650
Bv	 0.9130	 0.2520
Bw	 0.9100	 0.2320
Bx	 0.9050	 0.2240
By	 0.9070	 0.2120
Bz	 0.9060	 0.2130
Ca	 0.8760	 0.1750
Cb	 0.8720	 0.1510
Cc	 0.8830	 0.1630
Cd	 0.8840	 0.1820
Ce	 0.8980	 0.1920
Cf	 0.8930	 0.1940
Cg	 0.8980	 0.2080
Ch	 0.9140	 0.2340
Ci	 0.9120	 0.2250
Cj	 0.9130	 0.2140
Ck	 0.8980	 0.2080
Cl	 0.9000	 0.2010
Cm	 0.9060	 0.2260
Cn	 0.9110	 0.2410
Co	 0.9110	 0.2340
Cp	 0.9170	 0.2280
Cq	 0.9240	 0.2430
Cr	 0.9250	 0.2630
Cs	 0.9210	 0.2600
Ct	 0.9310	 0.2640
Cu	 0.9260	 0.2700
Cv	 0.9230	 0.2770
Cw	 0.9130	 0.2570
Cx	 0.9020	 0.2240

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


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Chain	Atom inclusion	Q-score
Cy	 0.8900	 0.1860
Cz	 0.8860	 0.1900
Da	 0.9060	 0.1370
Db	 0.9290	 0.1670
Dc	 0.9050	 0.1260
Dd	 0.9200	 0.1700
De	 0.9160	 0.1480
Df	 0.9180	 0.1900
Dg	 0.9190	 0.1600
Dh	 0.9310	 0.1980
Di	 0.9190	 0.1770
Dj	 0.9300	 0.1970
Dk	 0.9190	 0.1840
Dl	 0.9310	 0.2100
Dm	 0.9300	 0.1990
Dn	 0.9280	 0.2270
Do	 0.9190	 0.2100
Dp	 0.9160	 0.2050
Dq	 0.9150	 0.1950
Dr	 0.9090	 0.1860
Ds	 0.9130	 0.1900
Dt	 0.8910	 0.1590
Du	 0.9030	 0.1750
Dv	 0.8960	 0.1720
Dw	 0.8990	 0.1780
Dx	 0.9000	 0.1680
Dy	 0.9060	 0.1680
Dz	 0.9280	 0.1790
Ea	 0.8730	 0.0400
Eb	 0.8300	 0.0680
Ec	 0.8580	 0.0600
Ed	 0.8460	 0.0590
Ee	 0.8590	 0.0930
Ef	 0.8410	 0.0710
Eg	 0.8940	 0.1130
Eh	 0.8570	 0.0930
Ei	 0.8950	 0.0850
Ej	 0.8550	 0.0790
Ek	 0.8970	 0.1070
El	 0.8520	 0.0810
Em	 0.8840	 0.0920
En	 0.8850	 0.0990

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Chain	Atom inclusion	Q-score
Eo	 0.8810	 0.1150
Ep	 0.8930	 0.1100
Eq	 0.8730	 0.1260
Er	 0.9120	 0.1120
Es	 0.8890	 0.1290
Et	 0.8930	 0.0970
Eu	 0.9040	 0.1410
Ev	 0.8880	 0.0930
Ew	 0.9090	 0.1220
Ex	 0.8460	 0.0930
Ey	 0.8760	 0.0570
Ez	 0.8230	 0.0780
Fa	 0.8060	 0.1810
Fb	 0.8350	 0.1120
Fc	 0.8830	 0.1480
Fd	 0.9030	 0.1500
Fe	 0.8640	 0.1470
Ff	 0.8450	 0.1040
Fg	 0.9130	 0.1470
Fh	 0.8250	 0.0740
Fi	 0.8930	 0.1020
Fj	 0.8350	 0.0890
Fk	 0.8450	 0.1000
Fl	 0.8830	 0.1110
Fm	 0.8640	 0.1110
Fn	 0.8540	 0.0790
Fo	 0.7960	 0.0880
Fp	 0.8740	 0.0990
Fq	 0.8640	 0.1760
Fr	 0.8830	 0.1510
Fs	 0.9130	 0.1590
Ft	 0.9220	 0.2040
Fu	 0.9130	 0.2220
Fv	 0.9220	 0.2150
Fw	 0.8450	 0.1400
Fx	 0.8930	 0.1200
Fy	 0.9420	 0.2130
Fz	 0.8930	 0.1950
Ga	 0.8640	 0.1150
Gb	 0.9320	 0.1520
Gc	 0.8640	 0.1470
Gd	 0.8830	 0.1590





















































































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Chain	Atom inclusion	Q-score
Ge	 0.9130	 0.0930
Gf	 0.8160	 0.0970
Gg	 0.9030	 0.1670
Gh	 0.8640	 0.2230
Gi	 0.9030	 0.1640
Gj	 0.9320	 0.1390
Gk	 0.9130	 0.1290
Gl	 0.9320	 0.1480
Gm	 0.9130	 0.2080
Gn	 0.9030	 0.2240
Go	 0.9320	 0.1400
Gp	 0.9520	 0.0900
Gq	 0.9320	 0.1710
Gr	 0.8740	 0.1280
Gs	 0.8450	 0.1080
Gt	 0.8740	 0.1960
Gu	 0.9220	 0.1500
Gv	 0.9220	 0.2030
Gw	 0.9320	 0.1460
Gx	 0.8450	 0.0880
Gy	 0.8350	 0.0940
Gz	 0.8350	 0.1210
Ha	 0.9410	 0.1530
Hb	 0.9370	 0.0990
Hc	 0.9400	 0.1620
Hd	 0.9290	 0.1060
He	 0.9330	 0.1810
Hf	 0.9360	 0.0960
Hg	 0.9420	 0.1720
Hh	 0.9370	 0.0960
Hi	 0.9420	 0.1800
Hj	 0.9470	 0.1130
Hk	 0.9520	 0.1850
Hl	 0.9350	 0.0930
Hm	 0.9610	 0.1950
Hn	 0.9340	 0.1020
Ho	 0.9400	 0.1950
Hp	 0.9360	 0.0930
Hq	 0.9570	 0.1870
Hr	 0.9500	 0.0900
HS	 0.9480	 0.2020
Ht	 0.9470	 0.0880





















































































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Chain	Atom inclusion	Q-score
Hu	 0.9590	 0.1960
Hv	 0.9550	 0.0830
Hw	 0.9510	 0.1970
Hx	 0.9540	 0.0890
Hy	 0.9460	 0.1870
Hz	 0.9510	 0.0870
Ia	 0.9560	 0.1830
Ib	 0.9550	 0.0930
Ic	 0.9430	 0.1870
Id	 0.9560	 0.0870
Ie	 0.9480	 0.1830
If	 0.9500	 0.0770
Ig	 0.9540	 0.1910
Ih	 0.9570	 0.0780
Ii	 0.9460	 0.1960
Ij	 0.9510	 0.1060
Ik	 0.9460	 0.2070
Il	 0.9500	 0.0910
Im	 0.9510	 0.1870
In	 0.9560	 0.0830
Io	 0.9470	 0.2100
Ip	 0.9460	 0.0910
Iq	 0.9410	 0.2020
Ir	 0.9490	 0.0980
Is	 0.9350	 0.1810
It	 0.9570	 0.1030
Iu	 0.9270	 0.1730
Iv	 0.9570	 0.1110
Iw	 0.9380	 0.1870
Ix	 0.9600	 0.1090
Iy	 0.9300	 0.1730
Iz	 0.9610	 0.1170
Ja	 0.9410	 0.1860
Jb	 0.9570	 0.1230
Jc	 0.9380	 0.1980
Jd	 0.9660	 0.1200
Je	 0.9410	 0.1920
Jf	 0.9610	 0.1100
Jg	 0.9360	 0.1940
Jh	 0.9500	 0.1080
Ji	 0.9380	 0.1880
Jj	 0.9660	 0.1280

























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Chain	Atom inclusion	Q-score
Jk	 0.9350	 0.1950
Jl	 0.9590	 0.1320
Jm	 0.9430	 0.1870
Jn	 0.9580	 0.1230
Jo	 0.9470	 0.2150
Jp	 0.9590	 0.1290
Jq	 0.9360	 0.2030
Jr	 0.9600	 0.1190
Js	 0.9420	 0.2210
Jt	 0.9550	 0.1340
Ju	 0.9420	 0.2180
Jv	 0.9560	 0.1230
Jw	 0.9430	 0.2060
Jx	 0.9550	 0.1190
Jy	 0.9450	 0.2030
Jz	 0.9520	 0.0980
Ka	 0.9460	 0.1790
Kb	 0.9610	 0.1060
Kc	 0.9360	 0.1950
Kd	 0.9530	 0.0960
Ke	 0.9510	 0.1930
Kf	 0.9490	 0.1070
Kg	 0.9430	 0.1820
Kh	 0.9500	 0.0990
Ki	 0.9380	 0.1570
Kj	 0.9480	 0.0950
Kk	 0.9420	 0.1800
Kl	 0.9470	 0.0950
Km	 0.9460	 0.1720
Kn	 0.9480	 0.1150
Ko	 0.9500	 0.1800
Kp	 0.9420	 0.1110
Kq	 0.9460	 0.1760
Kr	 0.9420	 0.1100
Ks	 0.9280	 0.1440
Kt	 0.9350	 0.0940
Ku	 0.9270	 0.1600
Kv	 0.9300	 0.0890
Kw	 0.9330	 0.1600
Kx	 0.9280	 0.1100
Ky	 0.9310	 0.1650
Kz	 0.9410	 0.0920

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Chain	Atom inclusion	Q-score
La	 0.9310	 0.1840
Lb	 0.9330	 0.1020
Lc	 0.9420	 0.1980
Ld	 0.9390	 0.1170
Le	 0.9400	 0.1970
Lf	 0.9300	 0.1180
Lg	 0.9410	 0.1950
Lh	 0.9410	 0.1110
Li	 0.9450	 0.1780
Lj	 0.9330	 0.1240
Lk	 0.9470	 0.1670
Ll	 0.9300	 0.1040