



wwPDB EM Validation Summary Report ⓘ

Jun 3, 2026 – 08:03 PM EDT

PDB ID : 9YH6 / pdb_00009yh6
EMDB ID : EMD-72961
Title : Composite structure of the sheathed flagellar motor in *Vibrio cholerae* adopting a lower FOMC conformation
Authors : Guo, W.B.; Yue, J.; Liu, J.
Deposited on : 2025-09-30
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

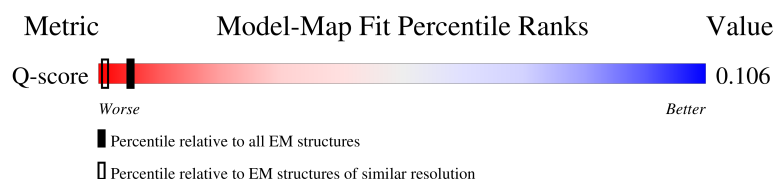
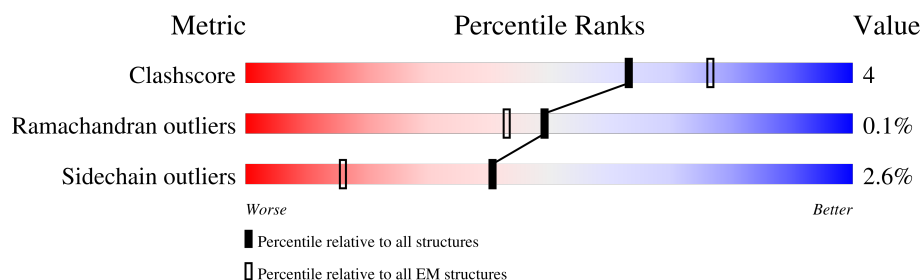
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	Aa	262	
1	Ab	262	
1	Ac	262	
1	Ad	262	

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Mol	Chain	Length	Quality of chain
1	Ae	262	
1	Af	262	
1	Ag	262	
1	Ah	262	
1	Ai	262	
1	Aj	262	
1	Ak	262	
1	Al	262	
1	Am	262	
1	An	262	
1	Ao	262	
1	Ap	262	
1	Aq	262	
1	Ar	262	
1	As	262	
1	At	262	
1	Au	262	
1	Av	262	
1	Aw	262	
1	Ax	262	
1	Ay	262	
1	Az	262	
1	Bb	262	
2	Ba	249	
2	Bc	249	



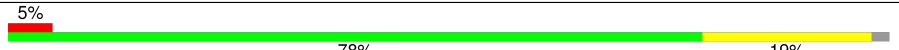
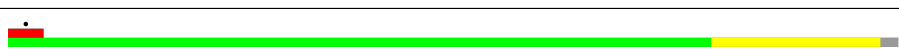

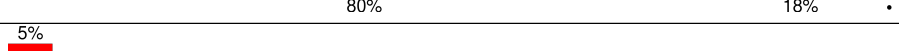
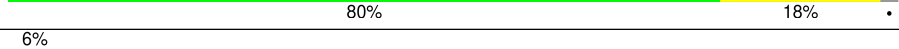





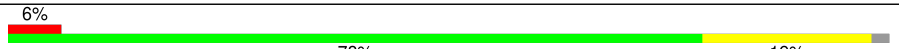


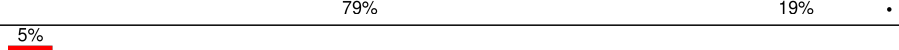








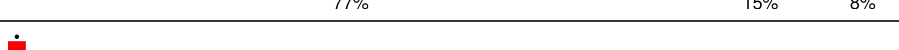
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Mol	Chain	Length	Quality of chain
2	Bd	249	
2	Bv	249	
2	Bw	249	
3	Be	434	
3	Bf	434	
3	Bg	434	
3	Bh	434	
3	Bi	434	
3	Bj	434	
3	Bk	434	
3	Bl	434	
3	Bm	434	
3	Bn	434	
3	Bo	434	
3	Bp	434	
3	Bq	434	
3	Br	434	
3	Bs	434	
3	Bt	434	
3	Bu	434	
4	Bx	227	
4	By	227	
4	Bz	227	
4	Ca	227	
4	Cb	227	







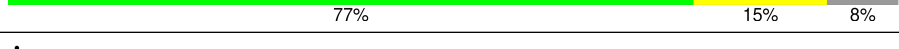
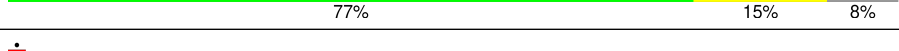
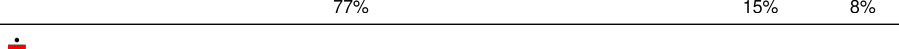
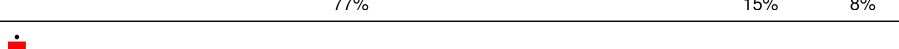
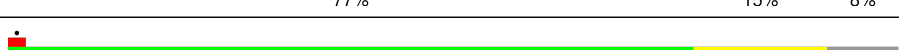

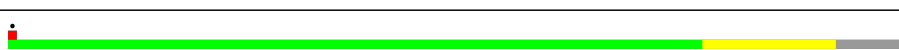

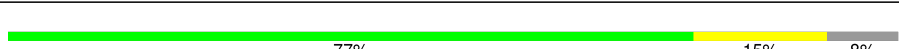





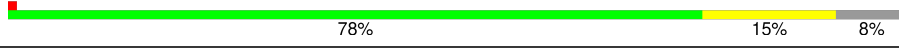
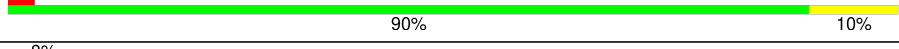
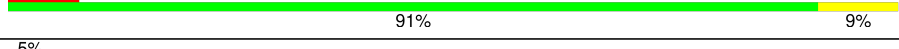


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Mol	Chain	Length	Quality of chain
4	Cc	227	
4	Cd	227	
4	Ce	227	
4	Cf	227	
4	Cg	227	
4	Ch	227	
4	Ci	227	
4	Cj	227	
4	Ck	227	
4	Cl	227	
4	Cm	227	
4	Cn	227	
4	Co	227	
4	Cp	227	
4	Cq	227	
4	Cr	227	
4	Cs	227	
4	Ct	227	
4	Cu	227	
4	Cv	227	
4	Cw	227	
5	Cx	343	
5	Cy	343	
5	Cz	343	
5	Da	343	

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Mol	Chain	Length	Quality of chain
5	Db	343	
5	Dc	343	
5	Dd	343	
5	De	343	
5	Df	343	
5	Dg	343	
5	Dh	343	
5	Di	343	
5	Dj	343	
5	Dk	343	
5	Dl	343	
5	Dm	343	
5	Dn	343	
5	Do	343	
5	Dp	343	
5	Dq	343	
5	Dr	343	
5	Ds	343	
5	Dt	343	
5	Du	343	
5	Dv	343	
5	Dw	343	
6	Dx	352	
6	Dy	352	
6	Dz	352	

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Mol	Chain	Length	Quality of chain
6	Ea	352	
6	Eb	352	
6	Ec	352	
6	Ed	352	
6	Ee	352	
6	Ef	352	
6	Eg	352	
6	Eh	352	
6	Ei	352	
6	Ej	352	
6	Ek	352	
6	El	352	
6	Em	352	
6	En	352	
6	Eo	352	
6	Ep	352	
6	Eq	352	
6	Er	352	
6	Es	352	
6	Et	352	
6	Eu	352	
6	Ev	352	
6	Ew	352	
7	Ex	271	
7	Ey	271	

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Mol	Chain	Length	Quality of chain
7	Ez	271	
7	Fa	271	
7	Fb	271	
7	Fc	271	
7	Fd	271	
7	Fe	271	
7	Ff	271	
7	Fg	271	
7	Fh	271	
7	Fi	271	
7	Fj	271	
7	Fk	271	
7	Fl	271	
7	Fm	271	
7	Fn	271	
7	Fo	271	
7	Fp	271	
7	Fq	271	
7	Fr	271	
7	Fs	271	
7	Ft	271	
7	Fu	271	
7	Fv	271	
7	Fw	271	
8	Fx	183	

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Mol	Chain	Length	Quality of chain
8	Fy	183	
8	Fz	183	
8	Ga	183	
8	Gb	183	
8	Gc	183	
8	Gd	183	
8	Ge	183	
8	Gf	183	
8	Gg	183	
8	Gh	183	
8	Gi	183	
8	Gj	183	
8	Gk	183	
8	Gl	183	
8	Gm	183	
8	Gn	183	
8	Go	183	
8	Gp	183	
8	Gq	183	
8	Gr	183	
8	Gs	183	
8	Gt	183	
8	Gu	183	
8	Gv	183	
8	Gw	183	

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Mol	Chain	Length	Quality of chain
9	Gx	12	
9	Gy	12	
9	Gz	12	
9	Ha	12	
9	Hb	12	
9	Hc	12	
9	Hd	12	
9	He	12	
9	Hf	12	
9	Hg	12	
9	Hh	12	
9	Hi	12	
9	Hj	12	
9	Hk	12	
9	Hl	12	
9	Hm	12	
9	Hn	12	
9	Ho	12	
9	Hp	12	
9	Hq	12	
9	Hr	12	
9	Hs	12	
9	Ht	12	
9	Hu	12	
9	Hv	12	

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Mol	Chain	Length	Quality of chain
9	Hw	12	
9	Hx	12	
9	Hy	12	
9	HZ	12	
9	Ia	12	
9	Ib	12	
9	Ic	12	
9	Id	12	
9	Ie	12	
9	If	12	
9	Ig	12	
9	Ih	12	
9	Ii	12	
9	Ij	12	
9	Ik	12	
9	Il	12	
9	Im	12	
9	In	12	
9	Io	12	
9	Ip	12	
9	Iq	12	
9	Ir	12	
9	Is	12	
9	It	12	
9	Iu	12	

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Mol	Chain	Length	Quality of chain
9	Iv	12	
9	Iw	12	
10	Ix	155	
10	Iy	155	
10	Iz	155	
10	Ja	155	
10	Jb	155	
10	Jc	155	
10	Jd	155	
10	Je	155	
10	Jf	155	
10	Jg	155	
10	Jh	155	
10	Ji	155	
10	Jj	155	
10	Jk	155	
10	Jl	155	
10	Jm	155	
10	Jn	155	
10	Jo	155	
10	Jp	155	
10	Jq	155	
10	Jr	155	
10	Js	155	
10	Jt	155	

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Mol	Chain	Length	Quality of chain
10	Ju	155	<div>99%</div> <div>81% 17%</div>
10	Jv	155	<div>99%</div> <div>84% 14%</div>
10	Jw	155	<div>98%</div> <div>82% 15%</div>
11	Jx	105	<div>21%</div> <div>81% 16%</div>
11	Jy	105	<div>15%</div> <div>83% 14%</div>
11	Jz	105	<div>26%</div> <div>83% 15%</div>
11	Ka	105	<div>19%</div> <div>84% 14%</div>
11	Kb	105	<div>17%</div> <div>83% 15%</div>
11	Kc	105	<div>20%</div> <div>84% 14%</div>
11	Kd	105	<div>22%</div> <div>84% 14%</div>
11	Ke	105	<div>24%</div> <div>84% 14%</div>
11	Kf	105	<div>21%</div> <div>86% 12%</div>
11	Kg	105	<div>21%</div> <div>83% 14%</div>
11	Kh	105	<div>15%</div> <div>83% 15%</div>
11	Ki	105	<div>16%</div> <div>83% 15%</div>
11	Kj	105	<div>15%</div> <div>82% 16%</div>
11	Kk	105	<div>16%</div> <div>83% 15%</div>
11	Kl	105	<div>22%</div> <div>83% 14%</div>
11	Km	105	<div>16%</div> <div>85% 13%</div>
11	Kn	105	<div>18%</div> <div>84% 14%</div>
11	Ko	105	<div>19%</div> <div>84% 14%</div>
11	Kp	105	<div>17%</div> <div>87% 10%</div>
11	Kq	105	<div>17%</div> <div>85% 13%</div>
11	Kr	105	<div>17%</div> <div>83% 15%</div>
11	Ks	105	<div>17%</div> <div>82% 16%</div>

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Mol	Chain	Length	Quality of chain
11	Kt	105	<div> <div>19%</div> <div>83%</div> <div>14%</div> <div>..</div> </div>
11	Ku	105	<div> <div>18%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
11	Kv	105	<div> <div>20%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
11	Kw	105	<div> <div>19%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
11	Kx	105	<div> <div>20%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
11	Ky	105	<div> <div>19%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
11	Kz	105	<div> <div>19%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
11	La	105	<div> <div>22%</div> <div>82%</div> <div>15%</div> <div>..</div> </div>
11	Lb	105	<div> <div>21%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
11	Lc	105	<div> <div>22%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
11	Ld	105	<div> <div>17%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
11	Le	105	<div> <div>19%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
11	Lf	105	<div> <div>23%</div> <div>84%</div> <div>13%</div> <div>..</div> </div>
11	Lg	105	<div> <div>18%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
11	Lh	105	<div> <div>16%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
11	Li	105	<div> <div>22%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>
11	Lj	105	<div> <div>28%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
11	Lk	105	<div> <div>15%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
11	Ll	105	<div> <div>27%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
11	Lm	105	<div> <div>21%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
11	Ln	105	<div> <div>20%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
11	Lo	105	<div> <div>20%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
11	Lp	105	<div> <div>17%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
11	Lq	105	<div> <div>23%</div> <div>84%</div> <div>13%</div> <div>..</div> </div>
11	Lr	105	<div> <div>19%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
11	Ls	105	21% 86% 12% ..
11	Lt	105	21% 85% 12% ..
11	Lu	105	32% 84% 15% .
11	Lv	105	27% 83% 15% ..
11	Lw	105	26% 84% 14% ..
11	Lx	105	23% 86% 12% ..
11	Ly	105	27% 87% 12% .
11	Lz	105	29% 85% 13% ..
11	Ma	105	18% 85% 13% ..
11	Mb	105	23% 86% 12% ..
11	Mc	105	22% 85% 13% ..
12	Md	190	38% 88% 11% .
12	Me	190	36% 87% 12% .
12	Mf	190	36% 87% 12% .
12	Mg	190	38% 88% 11% .
12	Mh	190	38% 88% 11% .
12	Mi	190	35% 88% 11% .
12	Mj	190	38% 88% 11% .
12	Mk	190	37% 88% 11% .
12	Ml	190	37% 87% 12% .
12	Mm	190	37% 88% 11% .
12	Mn	190	37% 87% 12% .
12	Mo	190	45% 88% 11% .
12	Mp	190	35% 87% 12% .
12	Mq	190	39% 88% 11% .

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Mol	Chain	Length	Quality of chain
12	Mr	190	<div> <div>36%</div> <div>88%</div> <div>11%</div> </div>
12	Ms	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Mt	190	<div> <div>37%</div> <div>88%</div> <div>11%</div> </div>
12	Mu	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Mv	190	<div> <div>37%</div> <div>88%</div> <div>11%</div> </div>
12	Mw	190	<div> <div>33%</div> <div>88%</div> <div>11%</div> </div>
12	Mx	190	<div> <div>43%</div> <div>88%</div> <div>11%</div> </div>
12	My	190	<div> <div>39%</div> <div>88%</div> <div>11%</div> </div>
12	Mz	190	<div> <div>39%</div> <div>87%</div> <div>12%</div> </div>
12	Na	190	<div> <div>35%</div> <div>88%</div> <div>11%</div> </div>
12	Nb	190	<div> <div>41%</div> <div>87%</div> <div>12%</div> </div>
12	Nc	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Nd	190	<div> <div>34%</div> <div>88%</div> <div>11%</div> </div>
12	Ne	190	<div> <div>34%</div> <div>88%</div> <div>11%</div> </div>
12	Nf	190	<div> <div>40%</div> <div>88%</div> <div>11%</div> </div>
12	Ng	190	<div> <div>34%</div> <div>88%</div> <div>12%</div> </div>
12	Nh	190	<div> <div>41%</div> <div>87%</div> <div>12%</div> </div>
12	Ni	190	<div> <div>37%</div> <div>87%</div> <div>12%</div> </div>
12	Nj	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Nk	190	<div> <div>37%</div> <div>88%</div> <div>11%</div> </div>
12	Nl	190	<div> <div>34%</div> <div>88%</div> <div>11%</div> </div>
12	Nm	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Nn	190	<div> <div>36%</div> <div>88%</div> <div>11%</div> </div>
12	No	190	<div> <div>34%</div> <div>87%</div> <div>12%</div> </div>
12	Np	190	<div> <div>35%</div> <div>88%</div> <div>11%</div> </div>

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Mol	Chain	Length	Quality of chain
12	Nq	190	<div> <div>36%</div> <div>87%</div> <div>12%</div> </div>
12	Nr	190	<div> <div>35%</div> <div>88%</div> <div>11%</div> </div>
12	Ns	190	<div> <div>37%</div> <div>88%</div> <div>11%</div> </div>
12	Nt	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Nu	190	<div> <div>36%</div> <div>88%</div> <div>11%</div> </div>
12	Nv	190	<div> <div>38%</div> <div>88%</div> <div>12%</div> </div>
12	Nw	190	<div> <div>39%</div> <div>88%</div> <div>11%</div> </div>
12	Nx	190	<div> <div>38%</div> <div>87%</div> <div>12%</div> </div>
12	Ny	190	<div> <div>33%</div> <div>88%</div> <div>11%</div> </div>
12	Nz	190	<div> <div>41%</div> <div>87%</div> <div>12%</div> </div>
12	Oa	190	<div> <div>41%</div> <div>88%</div> <div>11%</div> </div>
12	Ob	190	<div> <div>38%</div> <div>88%</div> <div>11%</div> </div>
12	Oc	190	<div> <div>37%</div> <div>88%</div> <div>11%</div> </div>
12	Od	190	<div> <div>39%</div> <div>88%</div> <div>11%</div> </div>
12	Oe	190	<div> <div>39%</div> <div>88%</div> <div>11%</div> </div>
12	Of	190	<div> <div>35%</div> <div>88%</div> <div>11%</div> </div>
12	Og	190	<div> <div>42%</div> <div>88%</div> <div>11%</div> </div>
12	Oh	190	<div> <div>36%</div> <div>87%</div> <div>12%</div> </div>
12	Oi	190	<div> <div>41%</div> <div>88%</div> <div>11%</div> </div>
13	Oj	144	<div> <div>95%</div> <div>85%</div> <div>15%</div> </div>
13	Ok	144	<div> <div>96%</div> <div>87%</div> <div>12%</div> </div>
13	Ol	144	<div> <div>97%</div> <div>86%</div> <div>14%</div> </div>
13	Om	144	<div> <div>94%</div> <div>90%</div> <div>10%</div> </div>
13	On	144	<div> <div>97%</div> <div>85%</div> <div>15%</div> </div>
13	Oo	144	<div> <div>96%</div> <div>85%</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
13	Op	144	<div> <div>97%</div> <div>88%</div> <div>12%</div> </div>
13	Oq	144	<div> <div>97%</div> <div>80%</div> <div>19%</div> </div>
13	Or	144	<div> <div>98%</div> <div>82%</div> <div>18%</div> </div>
13	Os	144	<div> <div>97%</div> <div>80%</div> <div>19%</div> </div>
13	Ot	144	<div> <div>99%</div> <div>78%</div> <div>20%</div> </div>
13	Ou	144	<div> <div>98%</div> <div>87%</div> <div>12%</div> </div>
13	Ov	144	<div> <div>98%</div> <div>91%</div> <div>8%</div> </div>
13	Ow	144	<div> <div>96%</div> <div>88%</div> <div>12%</div> </div>
13	Ox	144	<div> <div>97%</div> <div>88%</div> <div>12%</div> </div>
13	Oy	144	<div> <div>93%</div> <div>87%</div> <div>12%</div> </div>
13	Oz	144	<div> <div>95%</div> <div>77%</div> <div>21%</div> </div>
13	Pa	144	<div> <div>99%</div> <div>81%</div> <div>19%</div> </div>
13	Pb	144	<div> <div>99%</div> <div>84%</div> <div>15%</div> </div>
13	Pc	144	<div> <div>99%</div> <div>83%</div> <div>16%</div> </div>
13	Pd	144	<div> <div>96%</div> <div>88%</div> <div>12%</div> </div>
13	Pe	144	<div> <div>98%</div> <div>82%</div> <div>18%</div> </div>
13	Pf	144	<div> <div>98%</div> <div>81%</div> <div>17%</div> </div>
13	Pg	144	<div> <div>97%</div> <div>79%</div> <div>20%</div> </div>
13	Ph	144	<div> <div>93%</div> <div>81%</div> <div>19%</div> </div>
13	Pi	144	<div> <div>94%</div> <div>86%</div> <div>13%</div> </div>
13	Pj	144	<div> <div>95%</div> <div>81%</div> <div>19%</div> </div>
13	Pk	144	<div> <div>95%</div> <div>81%</div> <div>17%</div> </div>
13	Pl	144	<div> <div>97%</div> <div>88%</div> <div>12%</div> </div>
13	Pm	144	<div> <div>95%</div> <div>89%</div> <div>11%</div> </div>
13	Pn	144	<div> <div>95%</div> <div>83%</div> <div>16%</div> </div>

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Mol	Chain	Length	Quality of chain
13	Po	144	<div><div></div><div>97%</div><div>84%</div><div>14%</div><div></div></div>
13	Pp	144	<div><div></div><div>97%</div><div>76%</div><div>23%</div><div></div></div>
13	Pq	144	<div><div></div><div>95%</div><div>81%</div><div>19%</div><div></div></div>

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 574924 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 basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ab	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ac	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ad	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ae	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Af	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ag	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ah	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ai	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Aj	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ak	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Al	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Am	262	Total 1966	C 1215	N 339	O 403	S 9	0	0
1	An	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ao	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ap	252	Total 1893	C 1173	N 323	O 387	S 10	0	0
1	Aq	262	Total 1969	C 1217	N 339	O 403	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ar	247	Total	C	N	O	S	0	0
			1863	1156	317	380	10		
1	As	262	Total	C	N	O	S	0	0
			1969	1217	339	403	10		
1	At	251	Total	C	N	O	S	0	0
			1889	1171	322	386	10		
1	Au	262	Total	C	N	O	S	0	0
			1969	1217	339	403	10		
1	Av	247	Total	C	N	O	S	0	0
			1859	1154	316	379	10		
1	Aw	262	Total	C	N	O	S	0	0
			1969	1217	339	403	10		
1	Ax	249	Total	C	N	O	S	0	0
			1876	1163	320	383	10		
1	Ay	248	Total	C	N	O	S	0	0
			1864	1158	316	380	10		
1	Az	249	Total	C	N	O	S	0	0
			1873	1161	319	383	10		
1	Bb	253	Total	C	N	O	S	0	0
			1900	1178	324	388	10		

- Molecule 2 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ba	241	Total	C	N	O	S	0	0
			1811	1112	327	361	11		
2	Bc	249	Total	C	N	O	S	0	0
			1870	1149	336	373	12		
2	Bd	244	Total	C	N	O	S	0	0
			1833	1125	331	365	12		
2	Bv	232	Total	C	N	O	S	0	0
			1737	1066	312	347	12		
2	Bw	249	Total	C	N	O	S	0	0
			1868	1147	336	373	12		

- Molecule 3 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Be	268	Total	C	N	O	S	0	0
			2045	1273	354	414	4		
3	Bf	268	Total	C	N	O	S	0	0
			2045	1273	354	414	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Bg	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bh	268	Total 2045	C 1273	N 354	O 414	S 4	0	0
3	Bi	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bj	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bk	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bl	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bm	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bn	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bo	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bp	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bq	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Br	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bs	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bt	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bu	270	Total 2065	C 1285	N 359	O 417	S 4	0	0

- Molecule 4 is a protein called Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Bx	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	By	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Bz	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ca	223	Total 1674	C 1027	N 290	O 353	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Cb	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cc	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cd	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ce	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cf	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cg	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ch	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ci	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cj	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ck	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cl	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cm	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cn	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Co	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cp	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cq	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cr	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cs	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ct	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cu	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cv	223	Total 1674	C 1027	N 290	O 353	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Cw	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		

- Molecule 5 is a protein called Flagellar P-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Cx	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Cy	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Cz	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Da	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Db	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dc	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dd	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	De	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Df	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dg	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dh	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Di	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dj	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dk	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dl	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dm	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dn	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Do	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Dp	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dq	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dr	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Ds	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dt	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Du	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dv	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dw	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		

- Molecule 6 is a protein called Flagellar protein FlgT.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Dx	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Dy	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Dz	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ea	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eb	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ec	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ed	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ee	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ef	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eg	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eh	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ei	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ej	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ek	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	El	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Em	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	En	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eo	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ep	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eq	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Er	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Es	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Et	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eu	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ev	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ew	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

- Molecule 7 is a protein called Sodium-type flagellar protein MotY.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ex	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
7	Ey	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
7	Ez	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
7	Fa	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Fb	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fc	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fd	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fe	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Ff	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fg	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fh	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fi	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fj	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fk	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fl	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fm	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fn	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fo	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fp	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fq	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fr	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fs	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Ft	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fu	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fv	257	Total 2085	C 1312	N 362	O 404	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Fw	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		

- Molecule 8 is a protein called Sodium-type flagellar protein MotX.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Fx	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Fy	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Fz	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Ga	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gb	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gc	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gd	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Ge	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gf	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gg	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gh	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gi	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gj	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gk	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gl	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gm	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gn	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Go	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	Gp	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gq	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gr	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gs	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gt	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gu	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gv	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gw	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		

- Molecule 9 is a protein called FlgP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Gx	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Gy	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Gz	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Ha	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hb	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hc	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hd	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	He	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hf	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hg	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hh	12	Total	C	N	O	S	0	0
			105	66	19	19	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Hi	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hj	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hk	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hl	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hm	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hn	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ho	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hp	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hq	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hr	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hs	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ht	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hu	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hv	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hw	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hx	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hy	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hz	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ia	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ib	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ic	12	Total 105	C 66	N 19	O 19	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Id	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ie	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	If	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ig	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ih	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ii	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ij	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ik	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Il	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Im	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	In	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Io	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ip	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iq	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ir	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Is	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	It	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iu	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iv	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iw	12	Total 105	C 66	N 19	O 19	S 1	0	0

- Molecule 10 is a protein called Chemotaxis protein PomB.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ix	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Iy	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Iz	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Ja	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jb	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jc	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jd	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Je	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jf	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jg	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jh	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Ji	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jj	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jk	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jl	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jm	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jn	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jo	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jp	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jq	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jr	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Js	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	Jt	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Ju	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jv	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jw	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		

- Molecule 11 is a protein called Lipoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Jx	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Jy	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Jz	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Ka	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kb	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kc	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kd	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Ke	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kf	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kg	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kh	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Ki	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kj	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kk	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kl	104	Total	C	N	O	S	0	0
			828	506	155	163	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	Km	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kn	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ko	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kp	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kq	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kr	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ks	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kt	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ku	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kv	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kw	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kx	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ky	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kz	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	La	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lb	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lc	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ld	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Le	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lf	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lg	104	Total 828	C 506	N 155	O 163	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	Lh	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Li	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lj	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lk	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ll	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lm	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ln	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lo	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lp	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lq	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lr	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ls	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lt	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lu	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lv	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lw	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lx	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ly	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lz	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ma	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Mb	104	Total 828	C 506	N 155	O 163	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	Mc	104	Total	C	N	O	S	0	0
			828	506	155	163	4		

- Molecule 12 is a protein called FlgO domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Md	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Me	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mf	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mg	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mh	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mi	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mj	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mk	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Ml	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mm	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mn	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mo	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mp	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mq	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mr	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Ms	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mt	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mu	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Mv	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mw	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mx	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	My	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mz	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Na	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nb	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nc	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nd	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ne	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nf	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ng	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nh	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ni	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nj	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nk	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nl	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nm	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nn	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	No	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Np	190	Total 1482	C 928	N 260	O 287	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Nq	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nr	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ns	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nt	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nu	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nv	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nw	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nx	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ny	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nz	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Oa	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ob	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Oc	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Od	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Oe	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Of	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Og	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Oh	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Oi	190	Total 1482	C 928	N 260	O 287	S 7	0	0

- Molecule 13 is a protein called FliF.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Oj	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ok	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ol	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Om	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	On	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oo	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Op	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oq	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Or	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Os	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ot	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ou	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ov	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ow	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ox	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oy	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oz	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pa	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pb	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pc	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pd	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pe	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		

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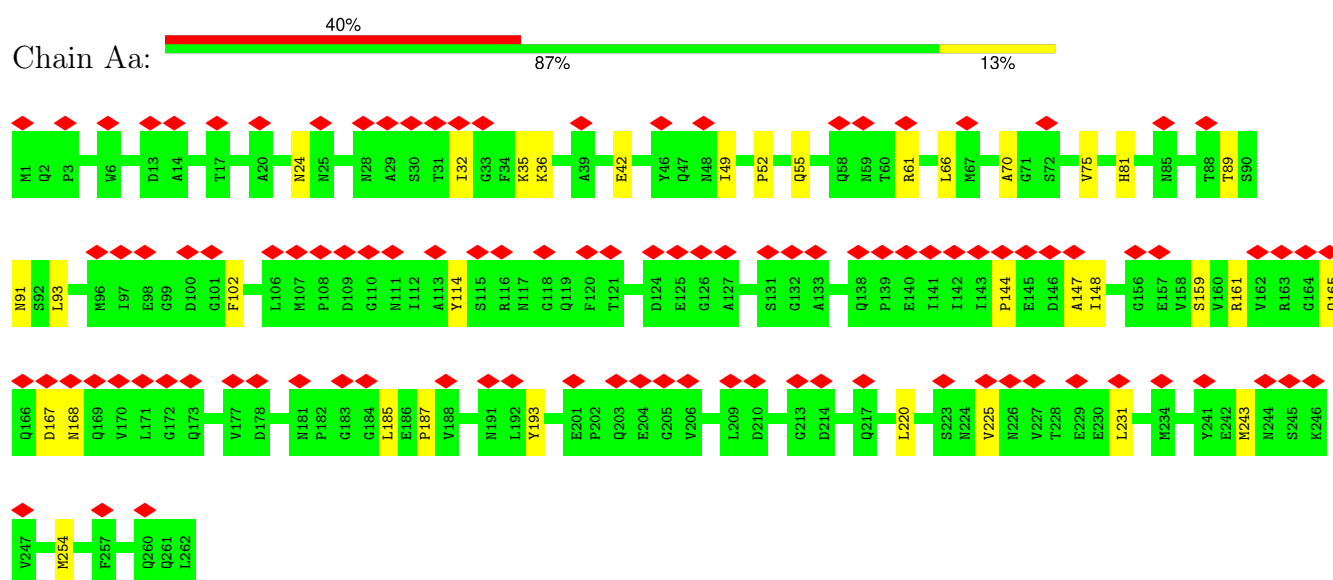
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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Pf	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pg	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Ph	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pi	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pj	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pk	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pl	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pm	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Pn	144	Total 1134	C 702	N 201	O 230	S 1	0	0
13	Po	144	Total 1134	C 702	N 201	O 230	S 1	0	0
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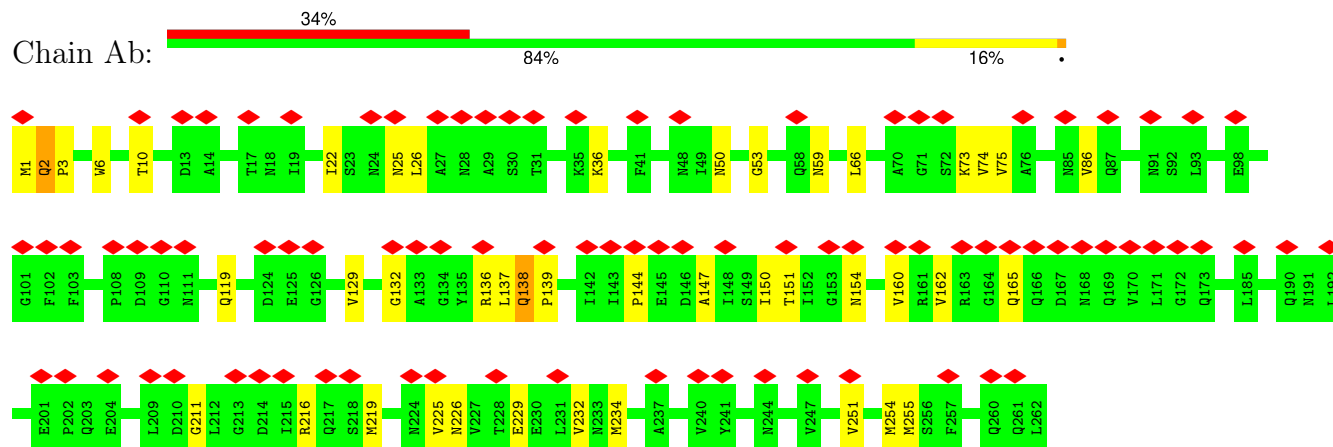
3 Residue-property plots

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.

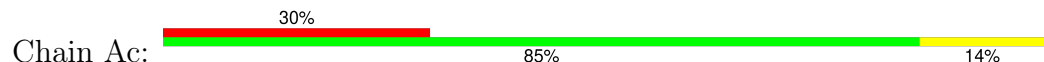
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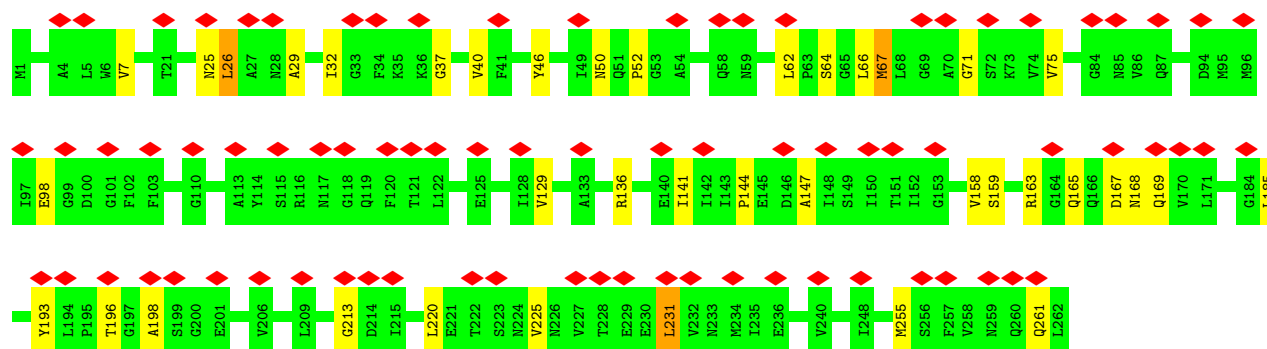


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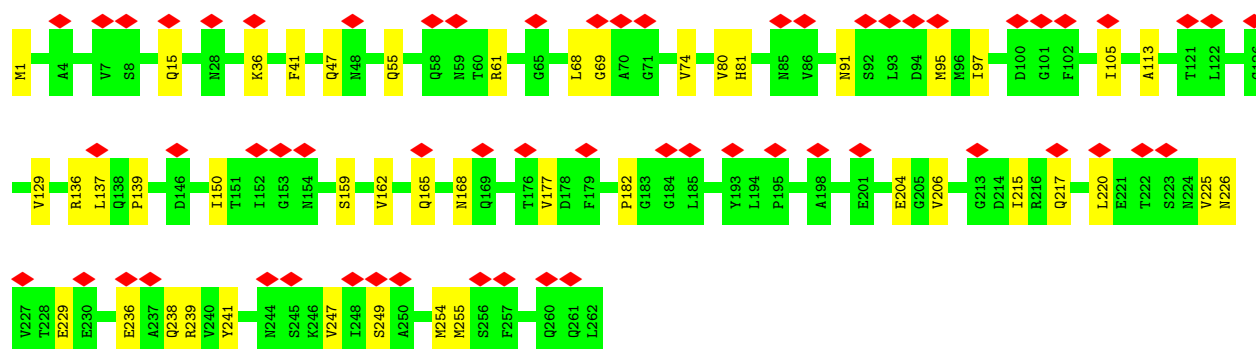
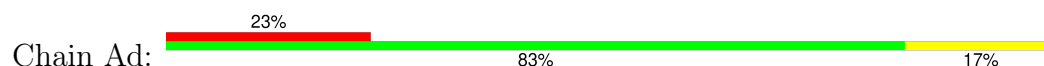


• Molecule 1: Flagellar basal-body rod protein FlgG

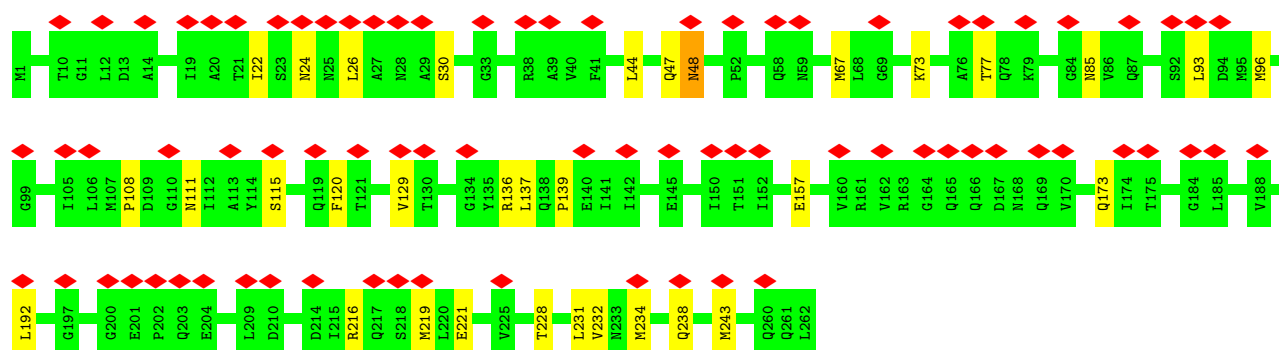




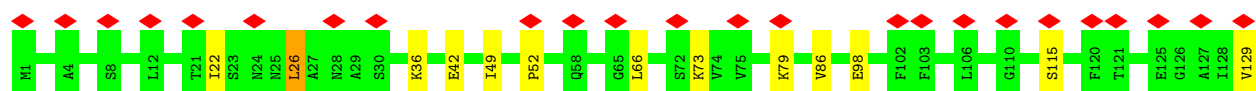
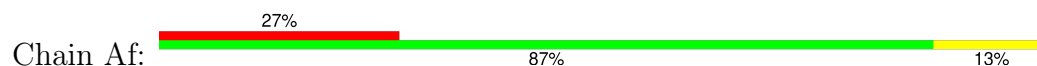
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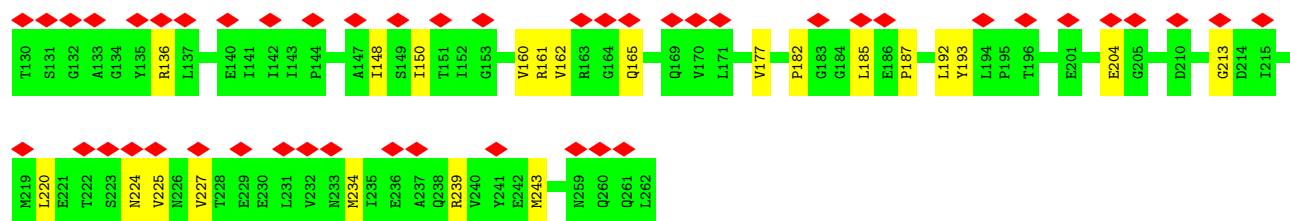


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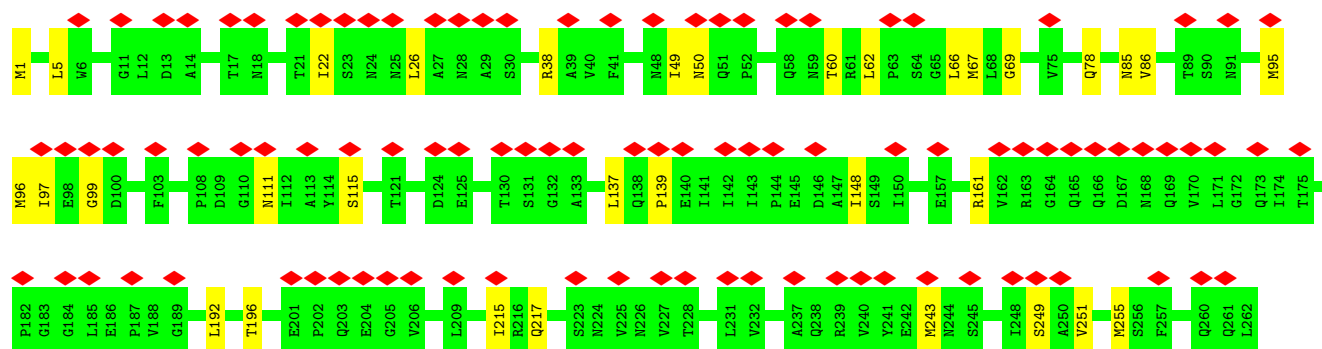
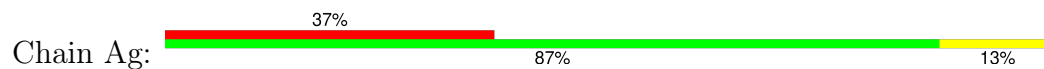


• Molecule 1: Flagellar basal-body rod protein FlgG

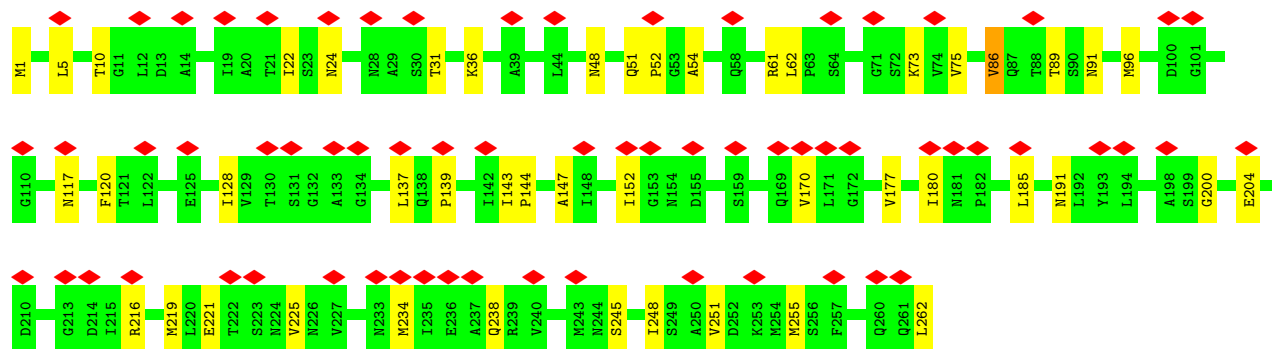
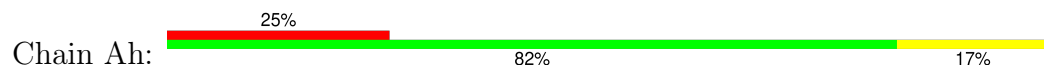




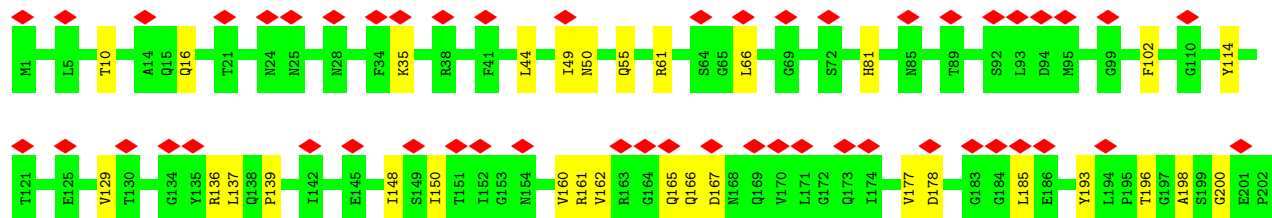
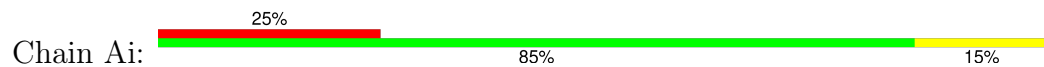
• Molecule 1: Flagellar basal-body rod protein FlgG



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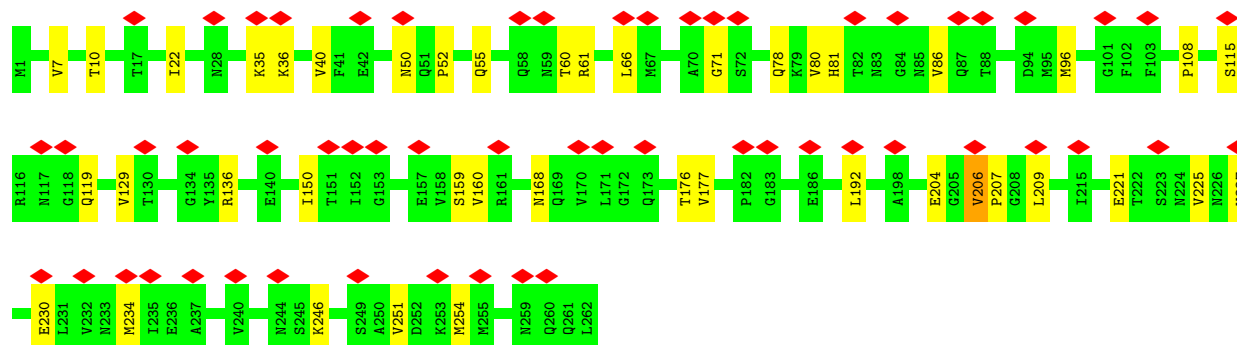
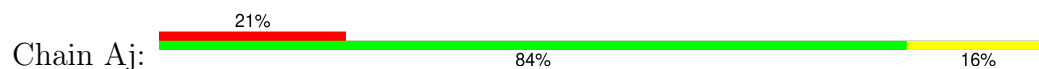


• Molecule 1: Flagellar basal-body rod protein FlgG

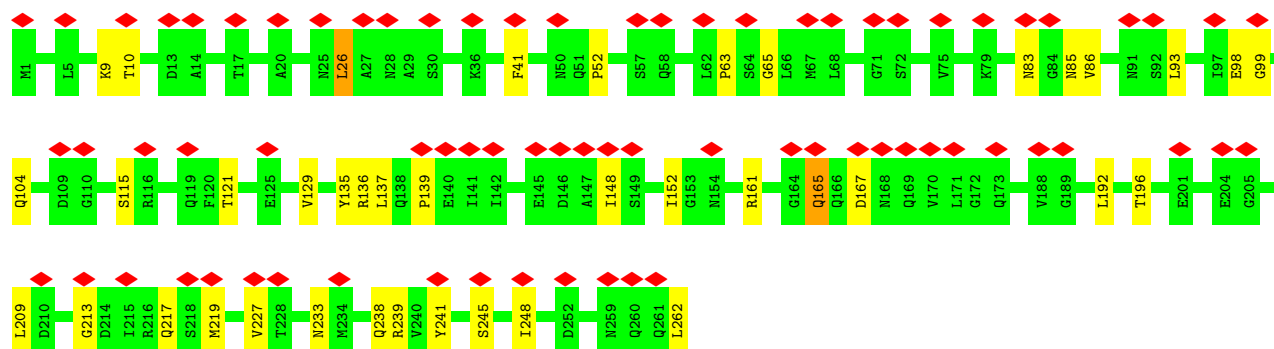
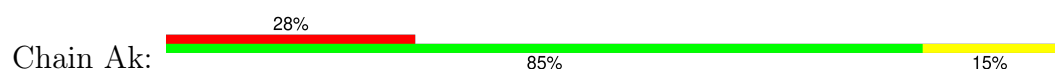




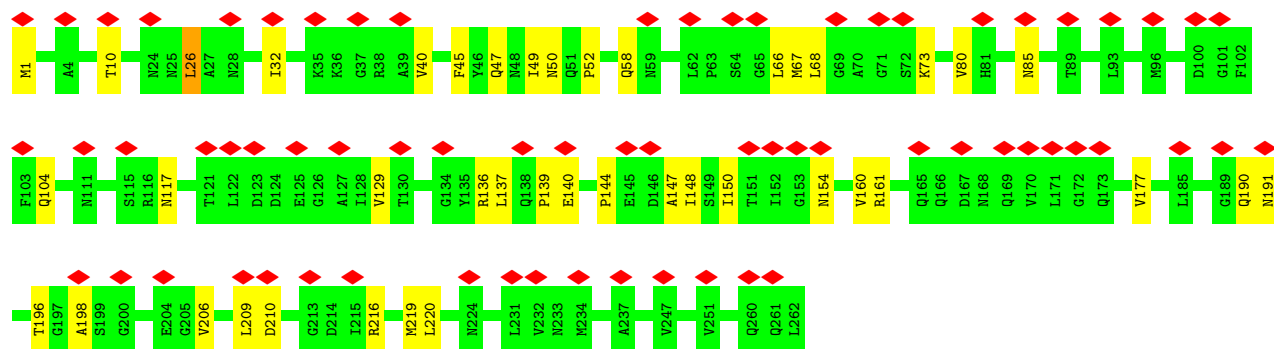
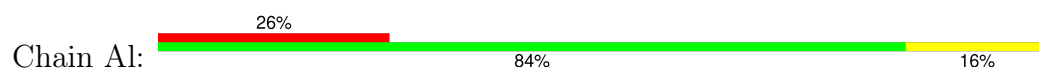
- Molecule 1: Flagellar basal-body rod protein FlgG



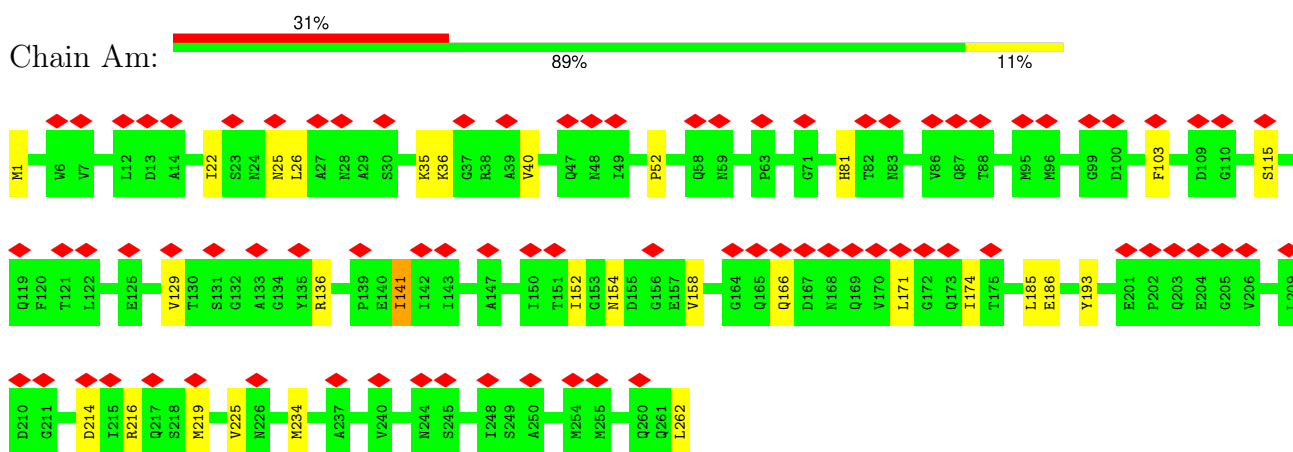
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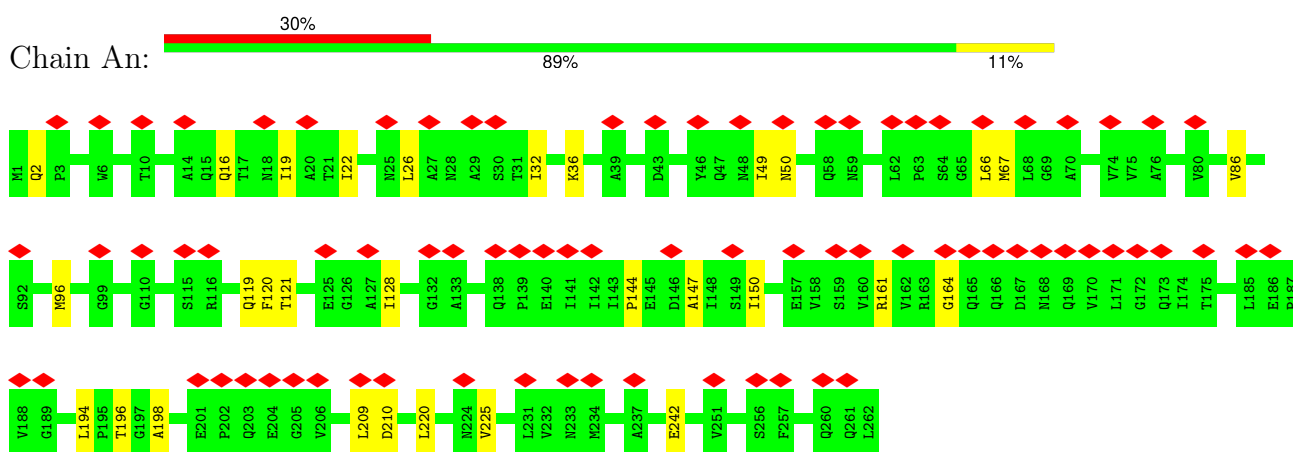
- Molecule 1: Flagellar basal-body rod protein FlgG



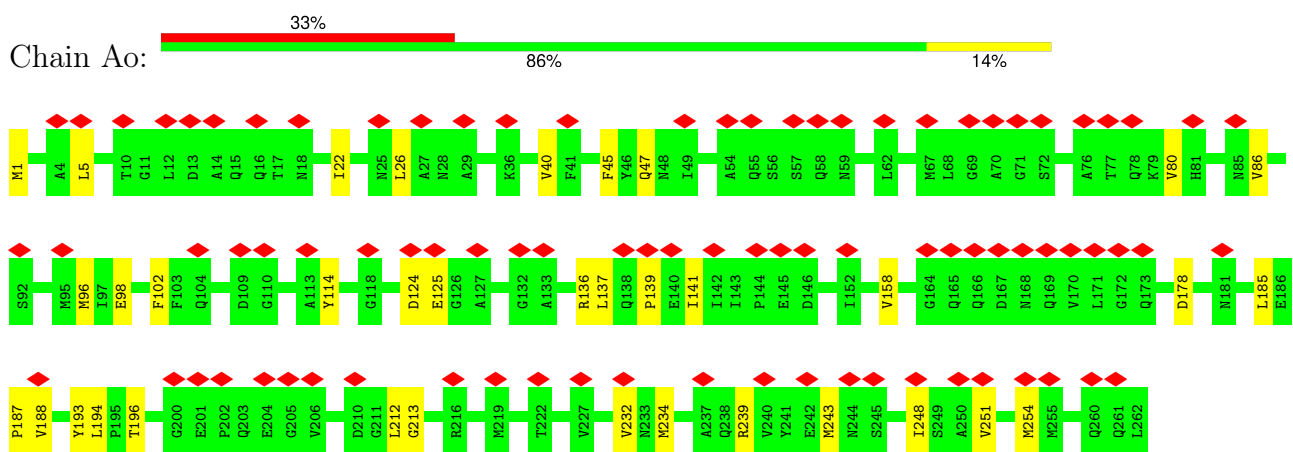
- Molecule 1: Flagellar basal-body rod protein FlgG



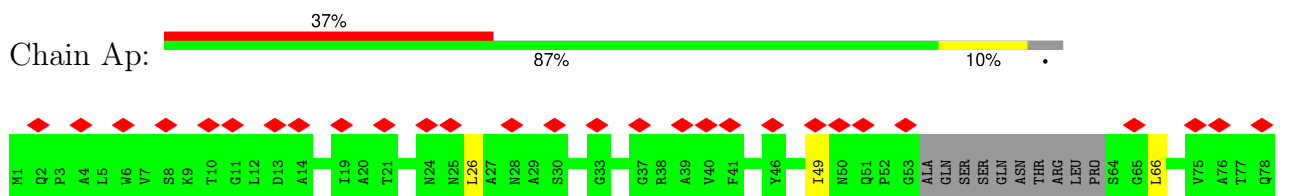
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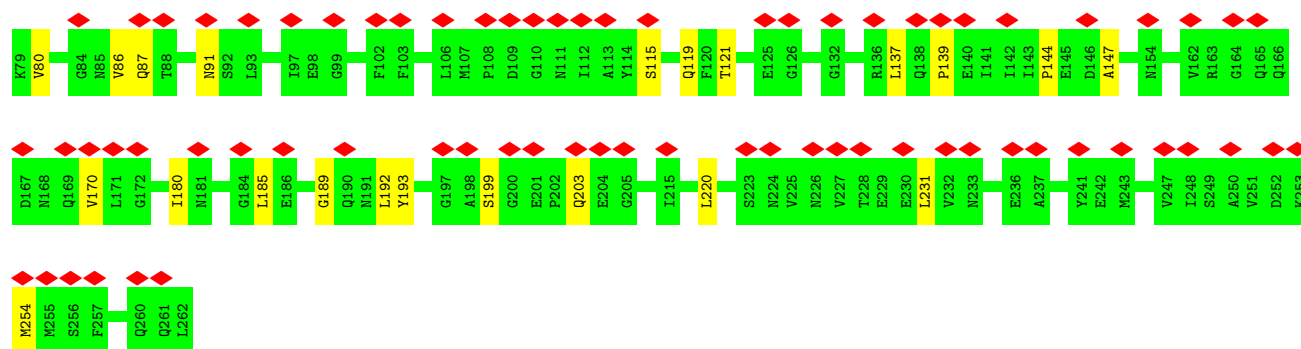


• Molecule 1: Flagellar basal-body rod protein FlgG

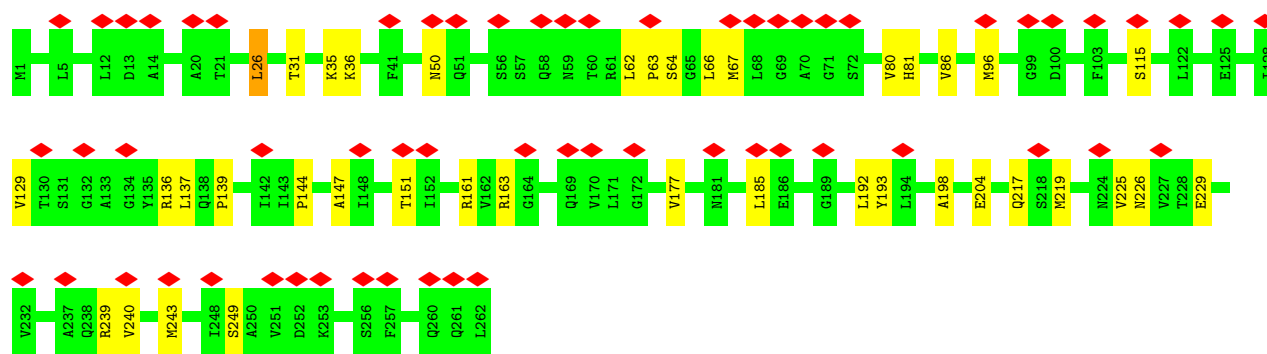
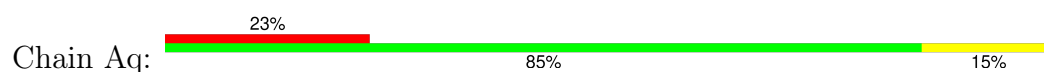


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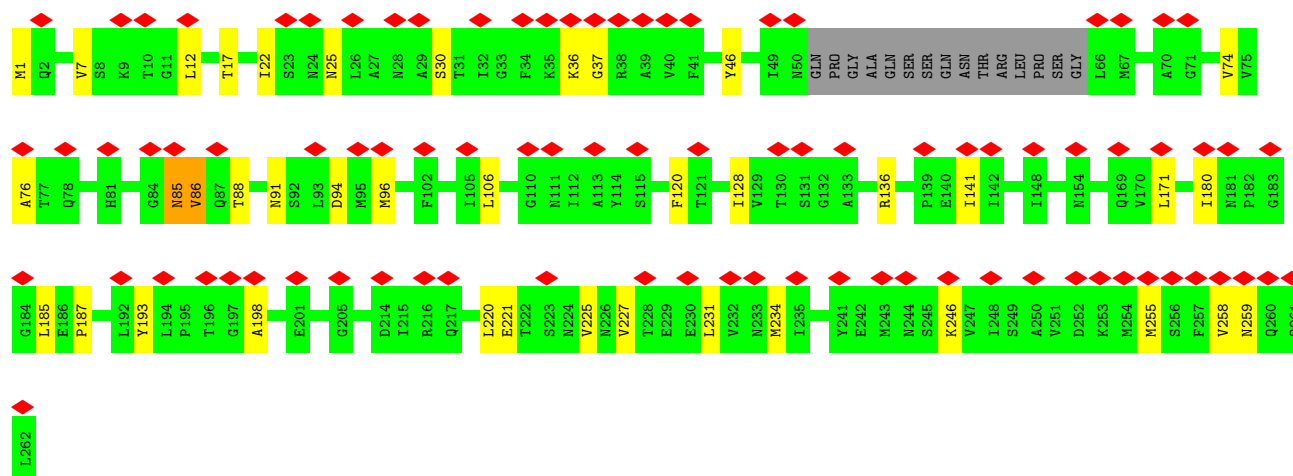
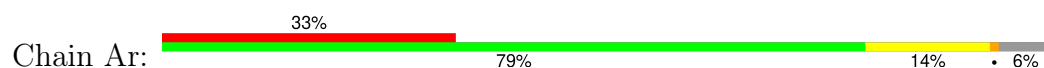




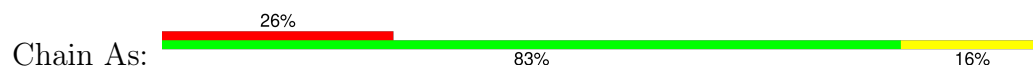
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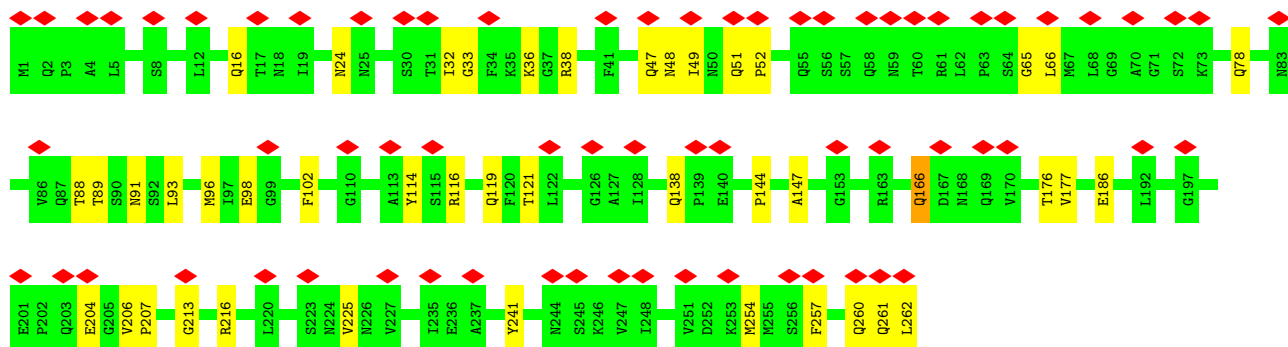


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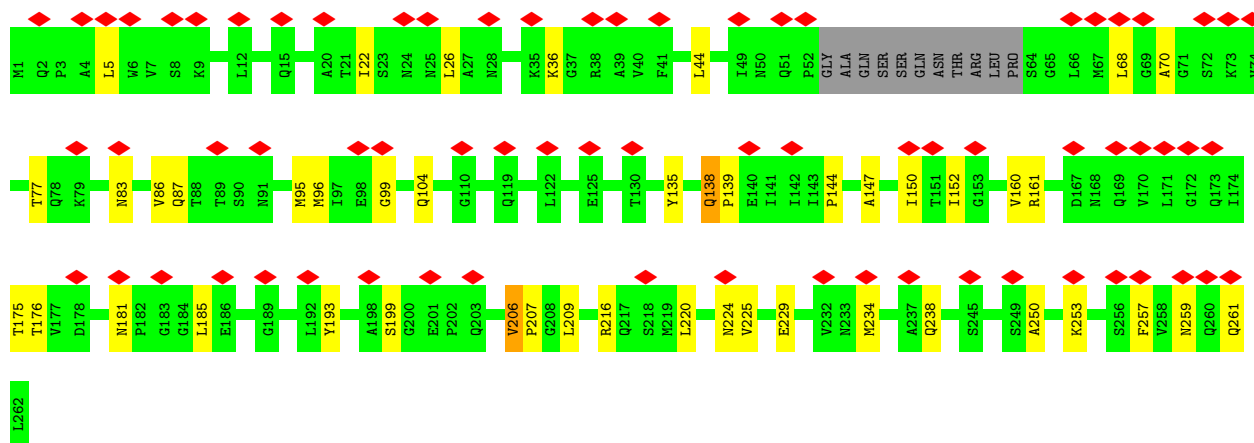
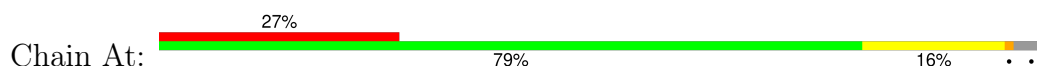


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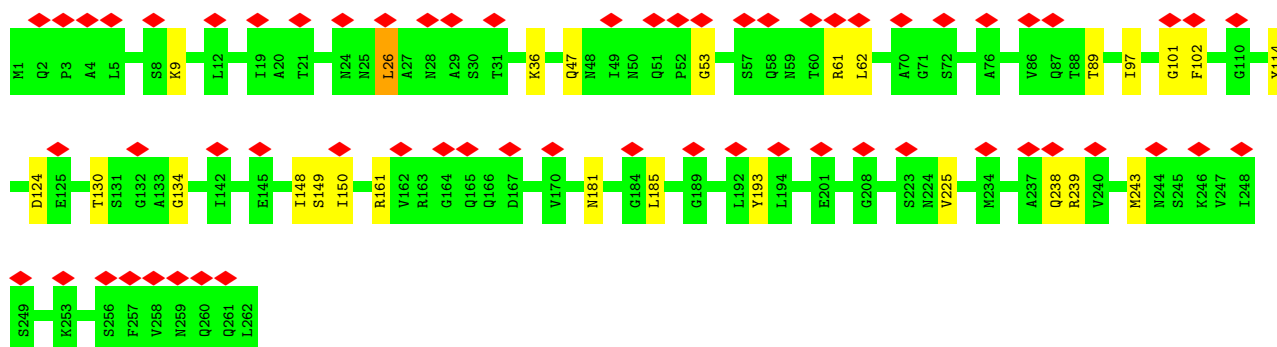




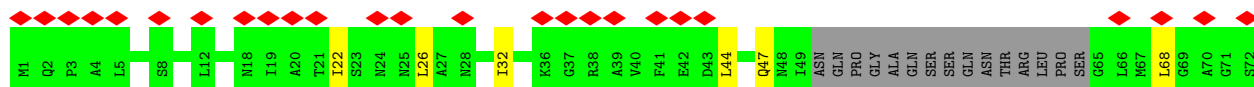
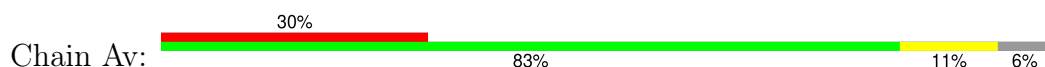
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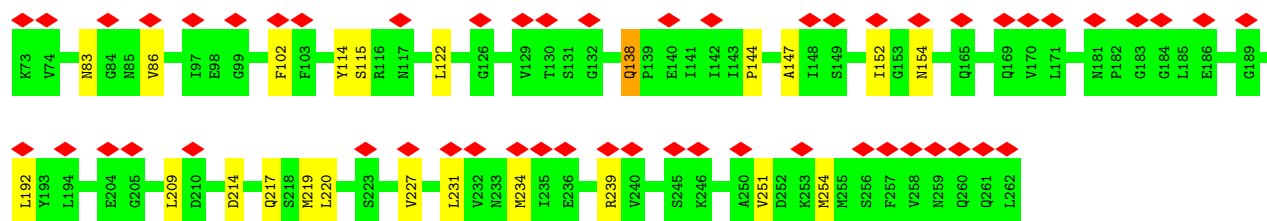


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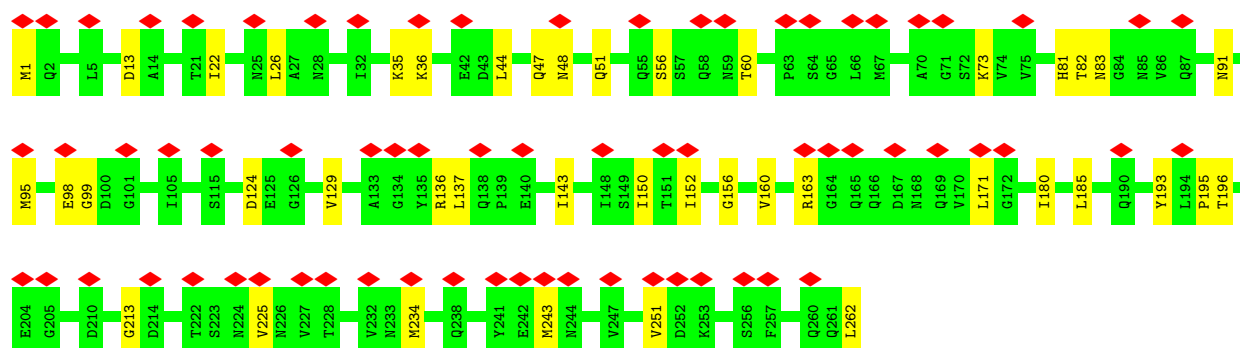
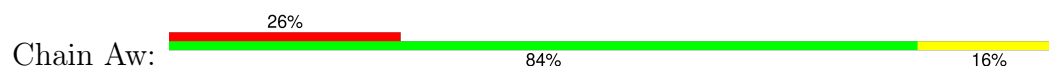


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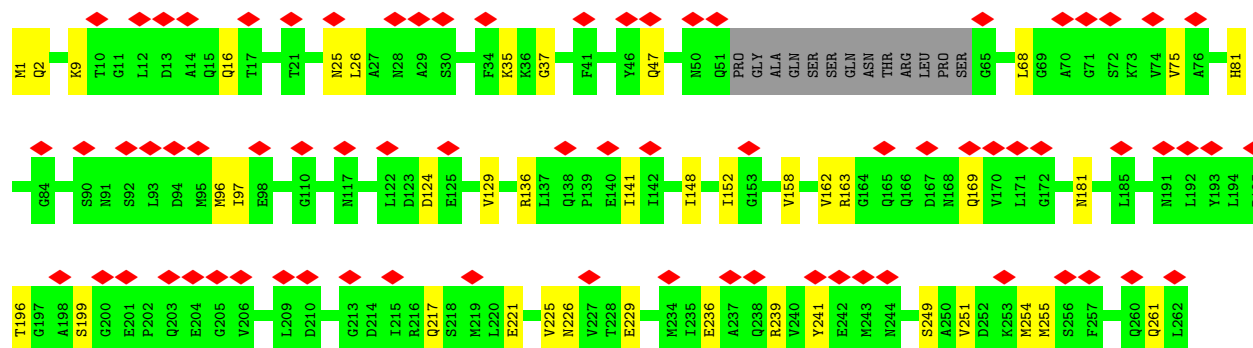
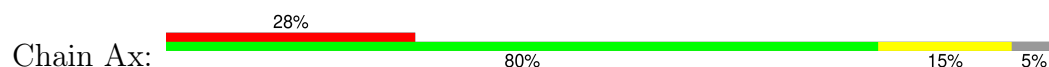




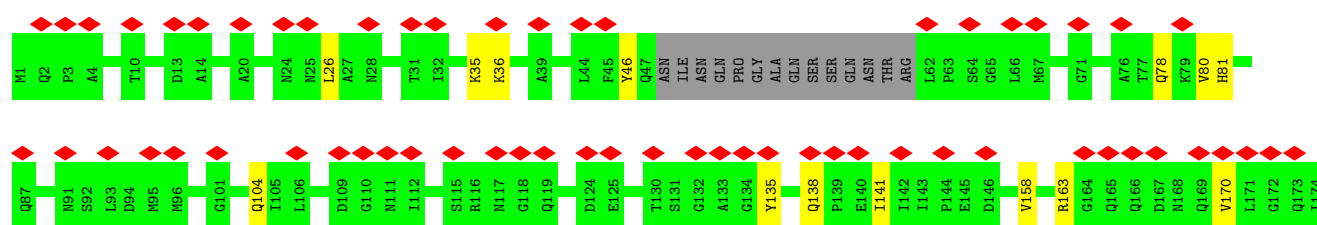
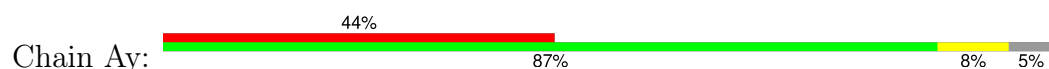
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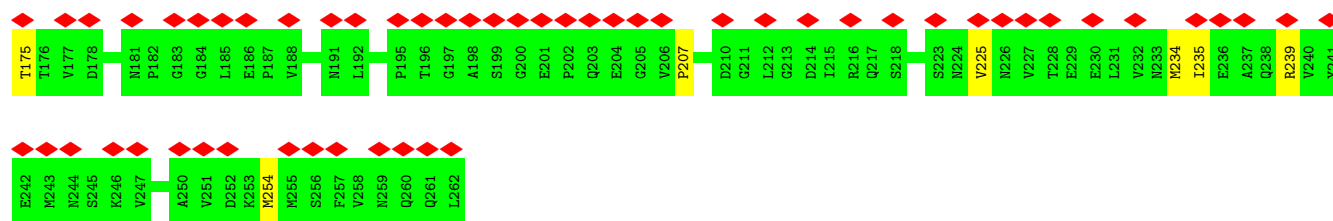


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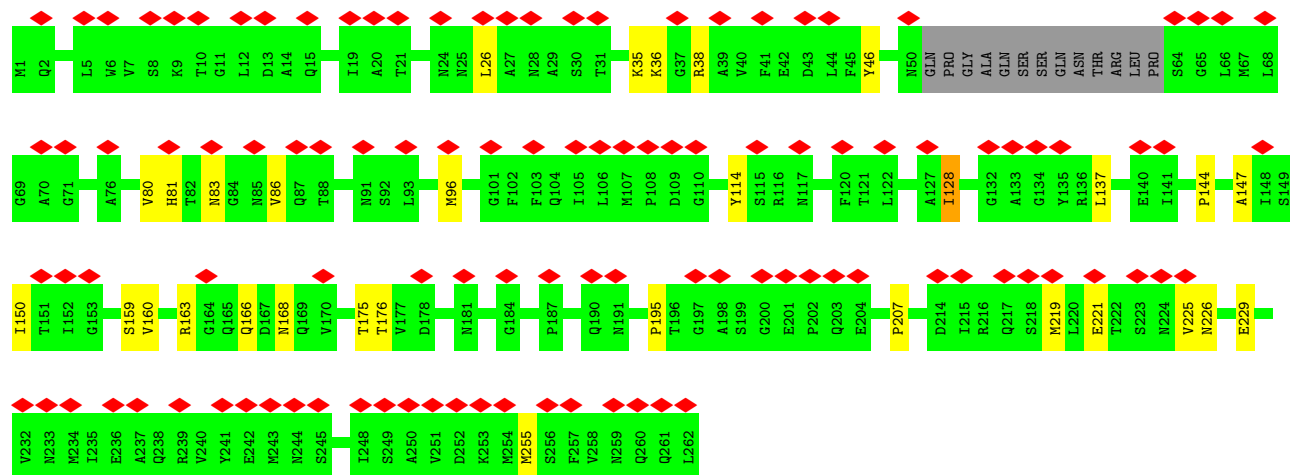
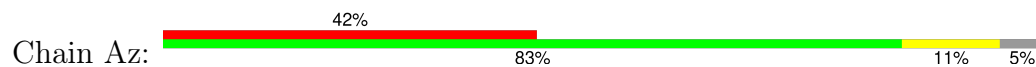


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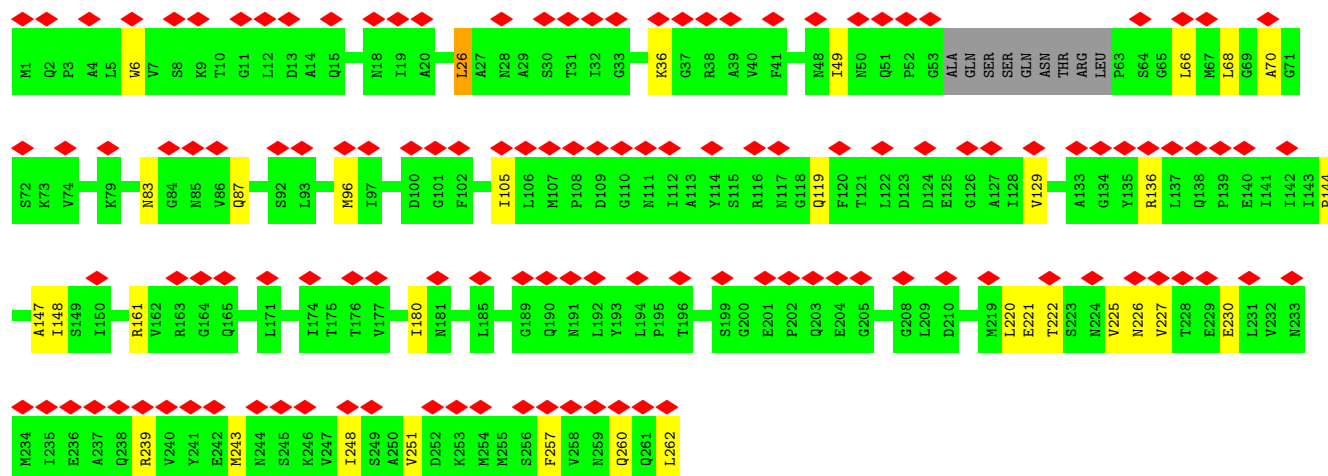
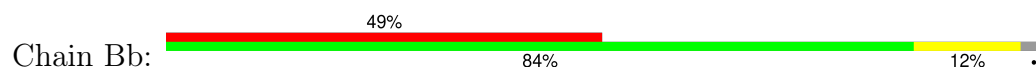




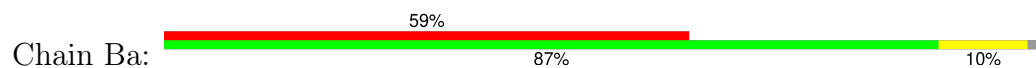
• Molecule 1: Flagellar basal-body rod protein FlgG

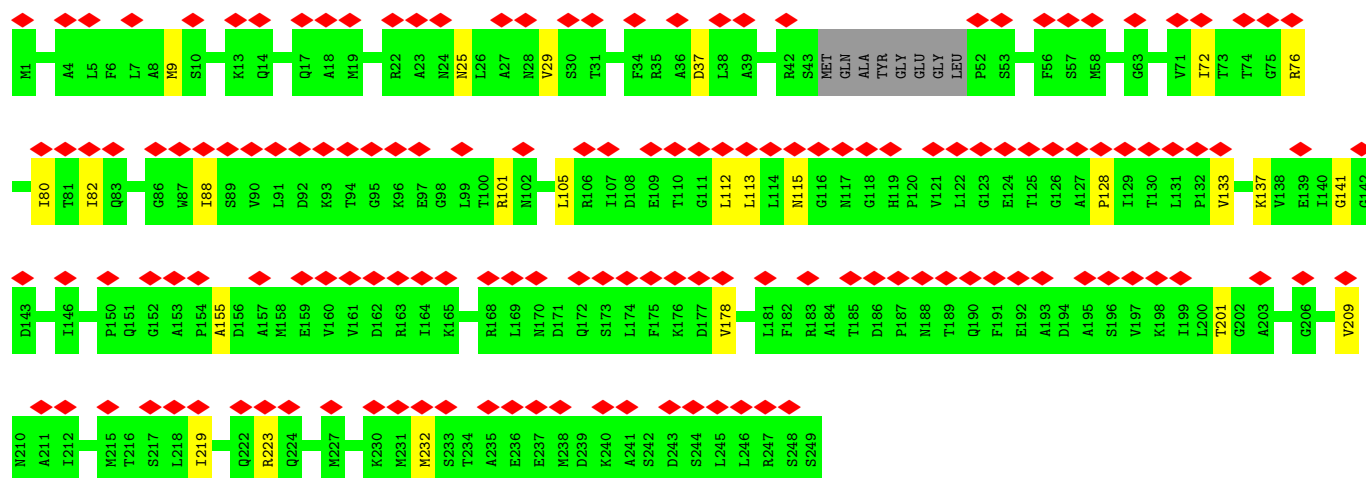


• Molecule 1: Flagellar basal-body rod protein FlgG



• Molecule 2: Flagellar basal-body rod protein FlgF

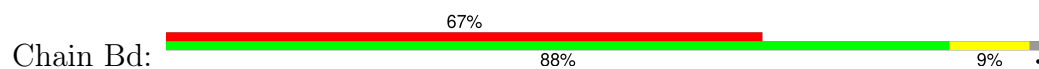


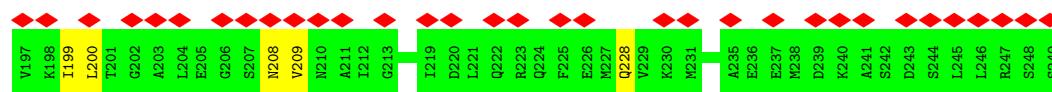


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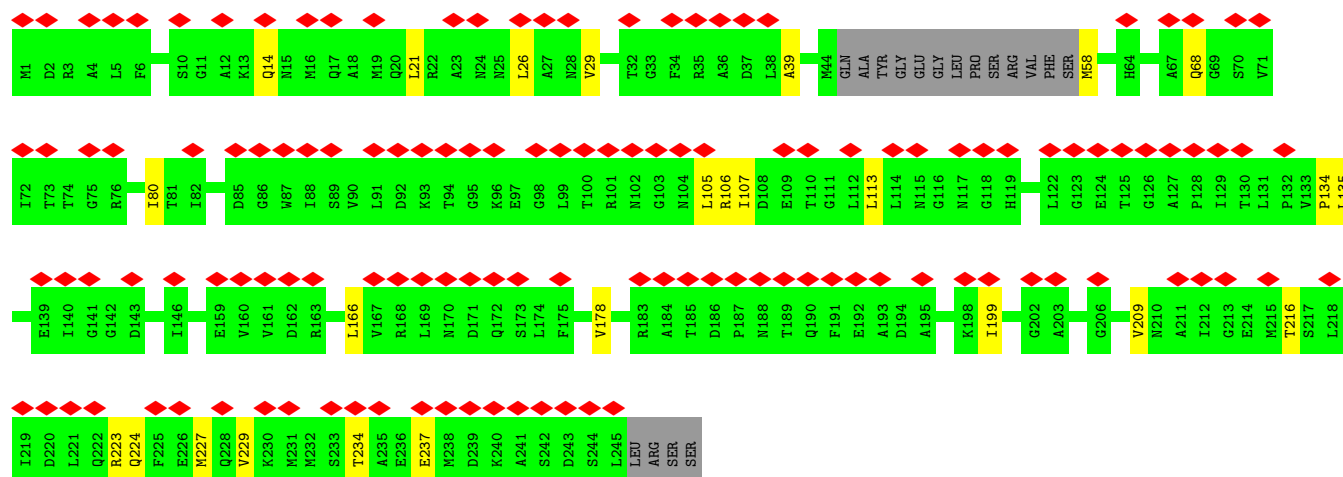
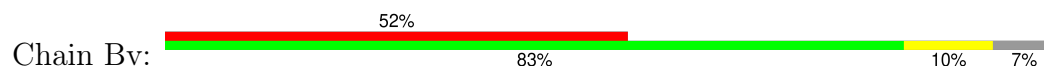


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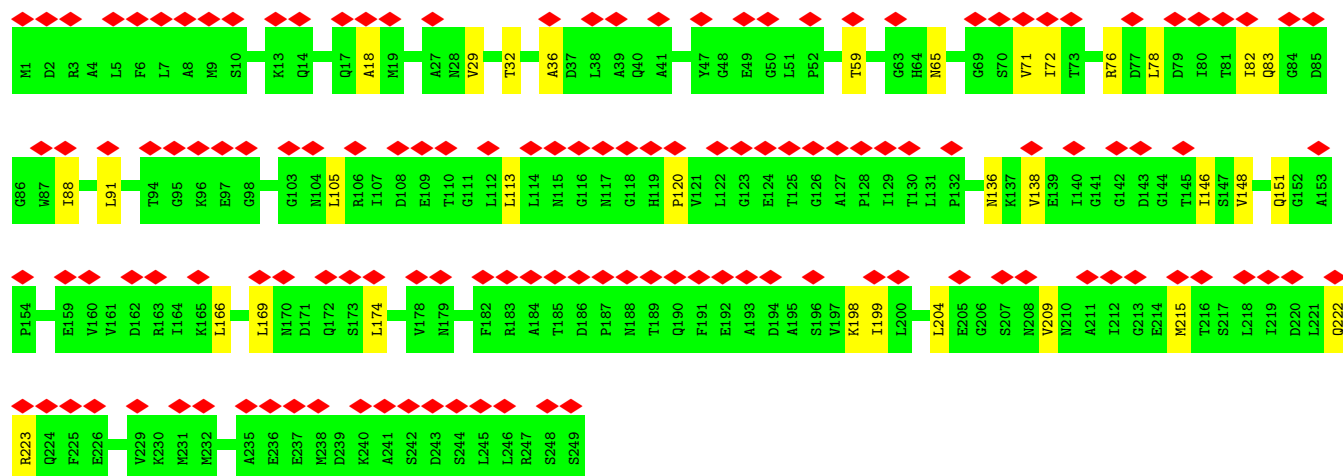




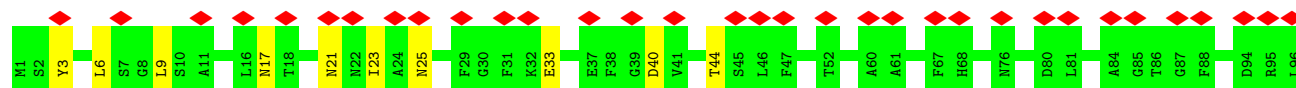
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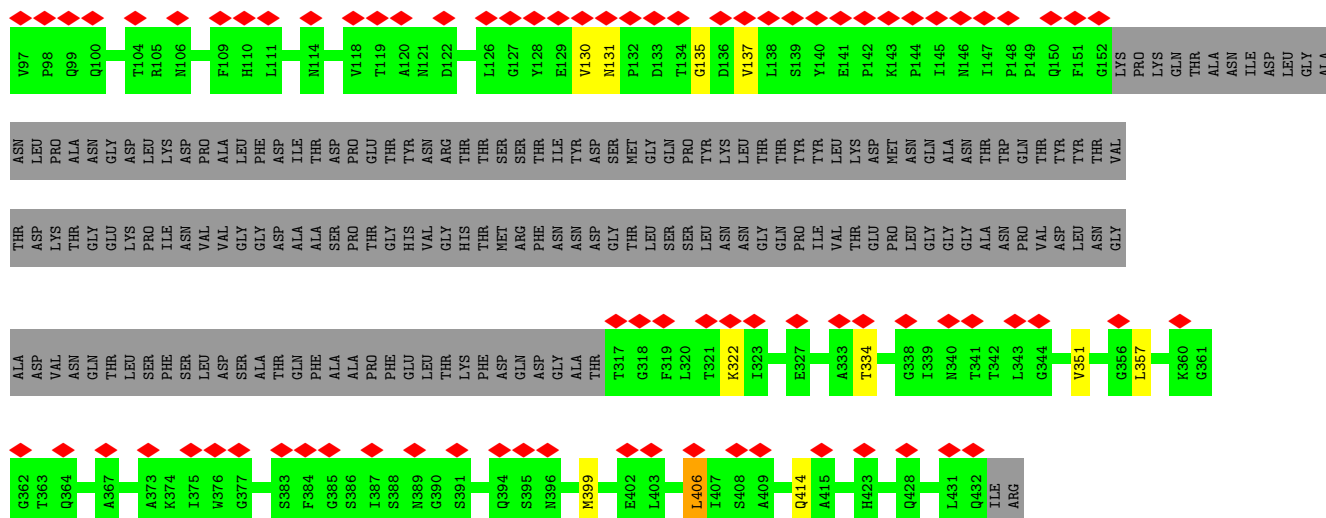


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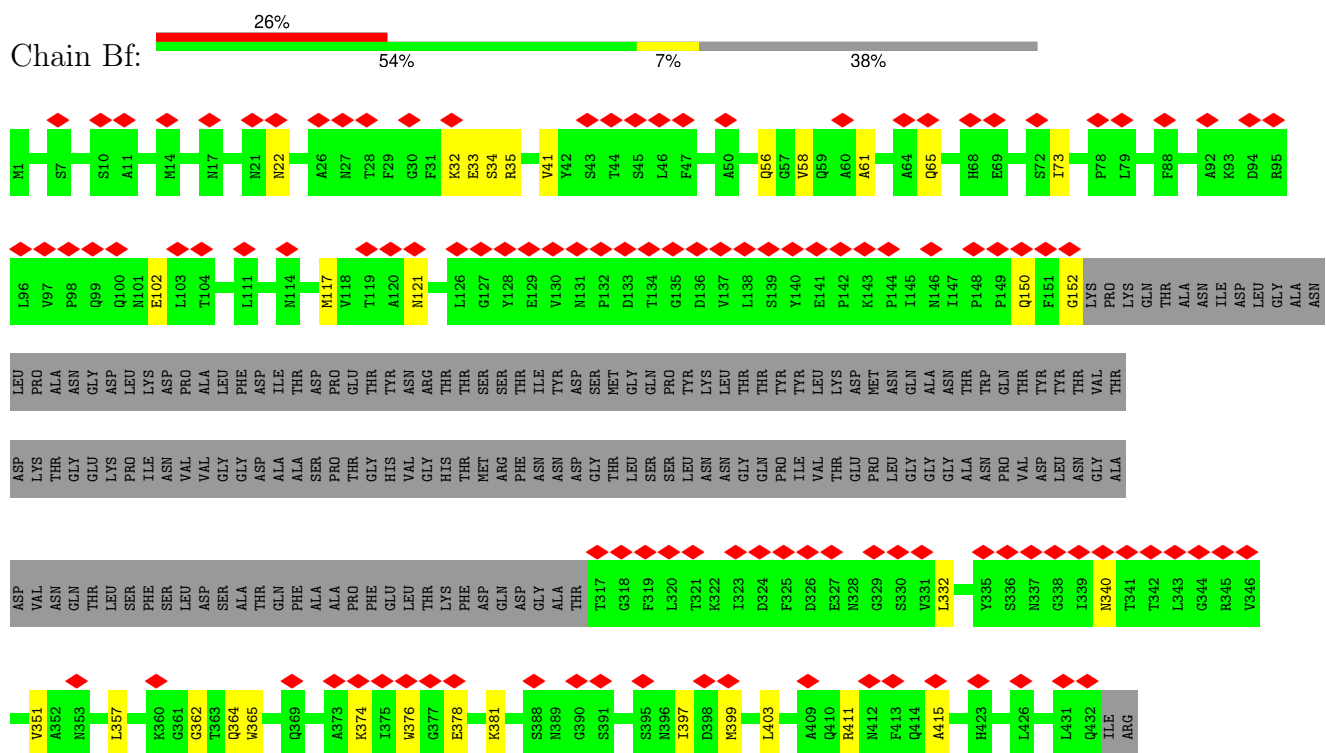


• Molecule 3: Flagellar hook protein FlgE

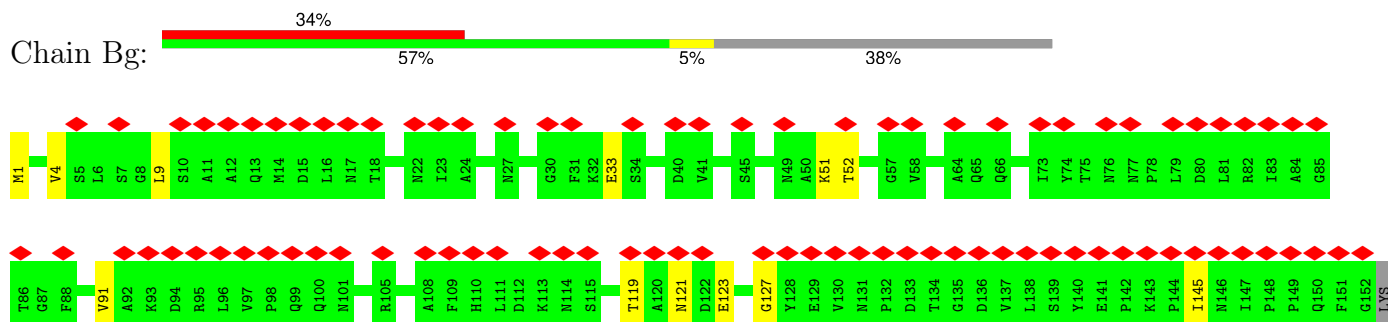


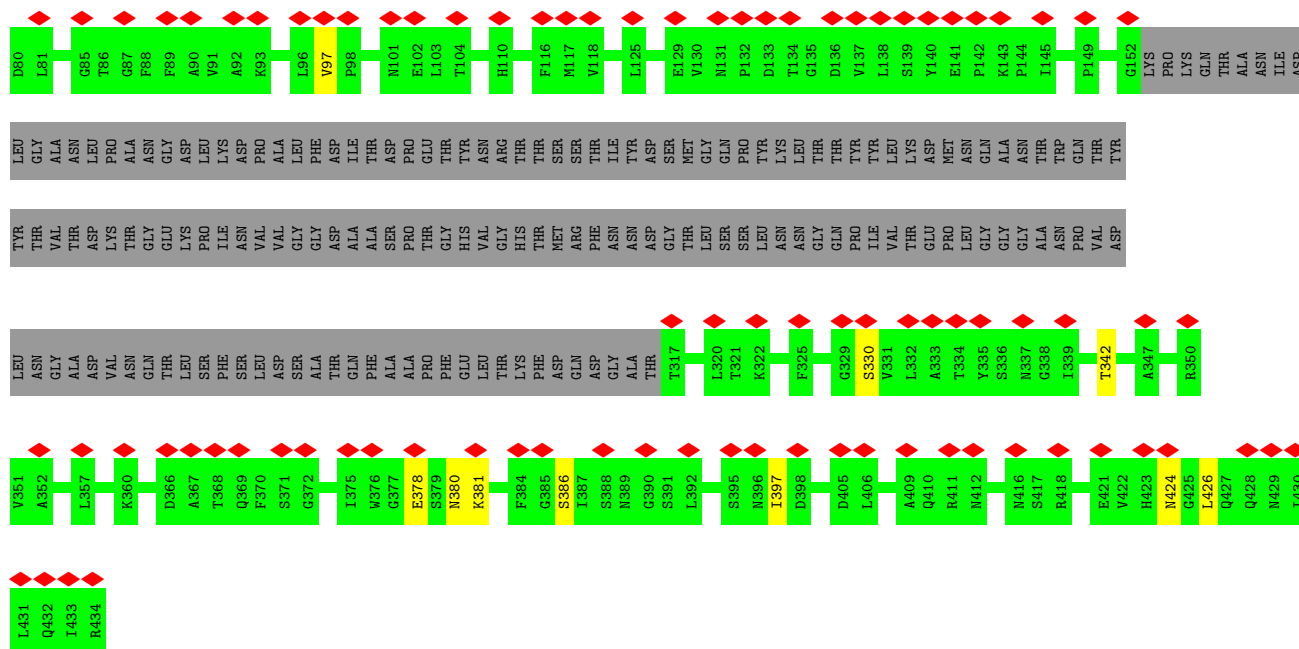


• Molecule 3: Flagellar hook protein FlgE

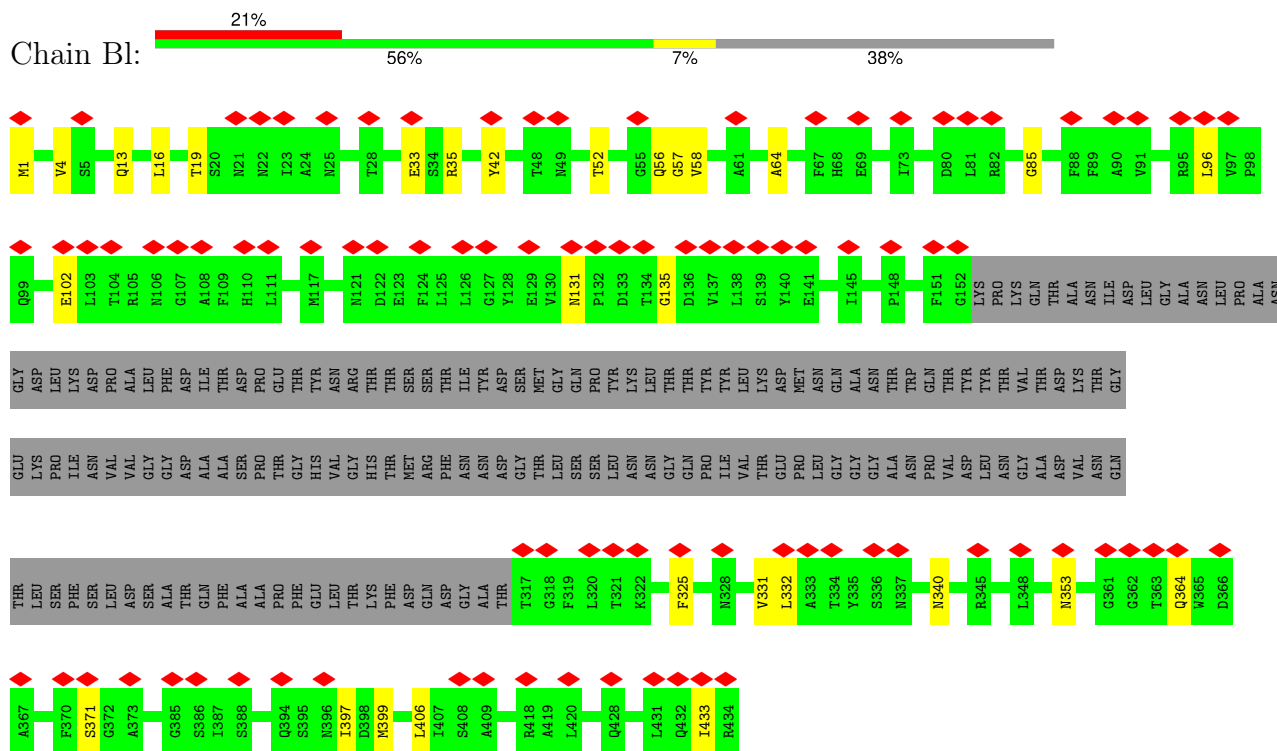


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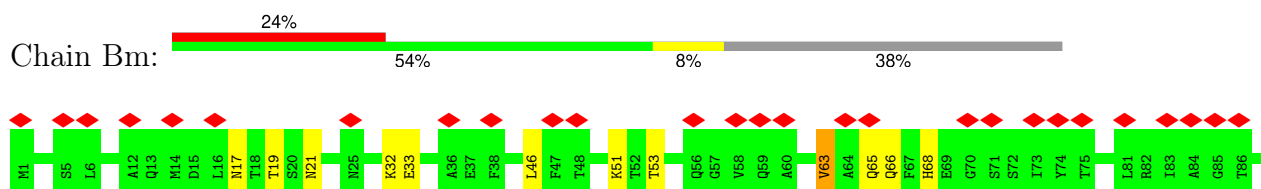


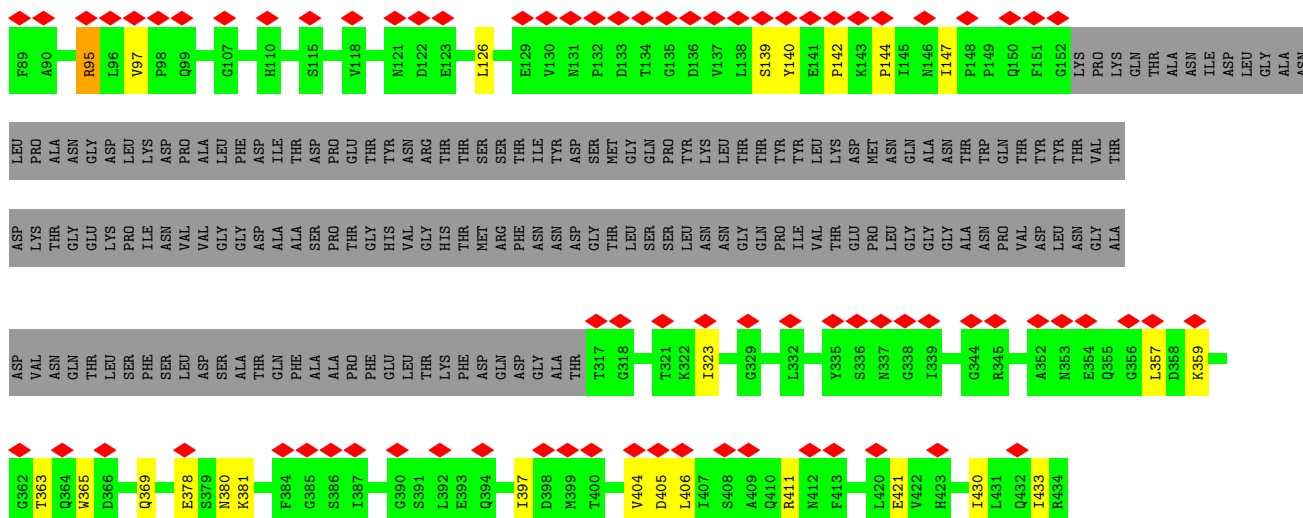


• Molecule 3: Flagellar hook protein FlgE

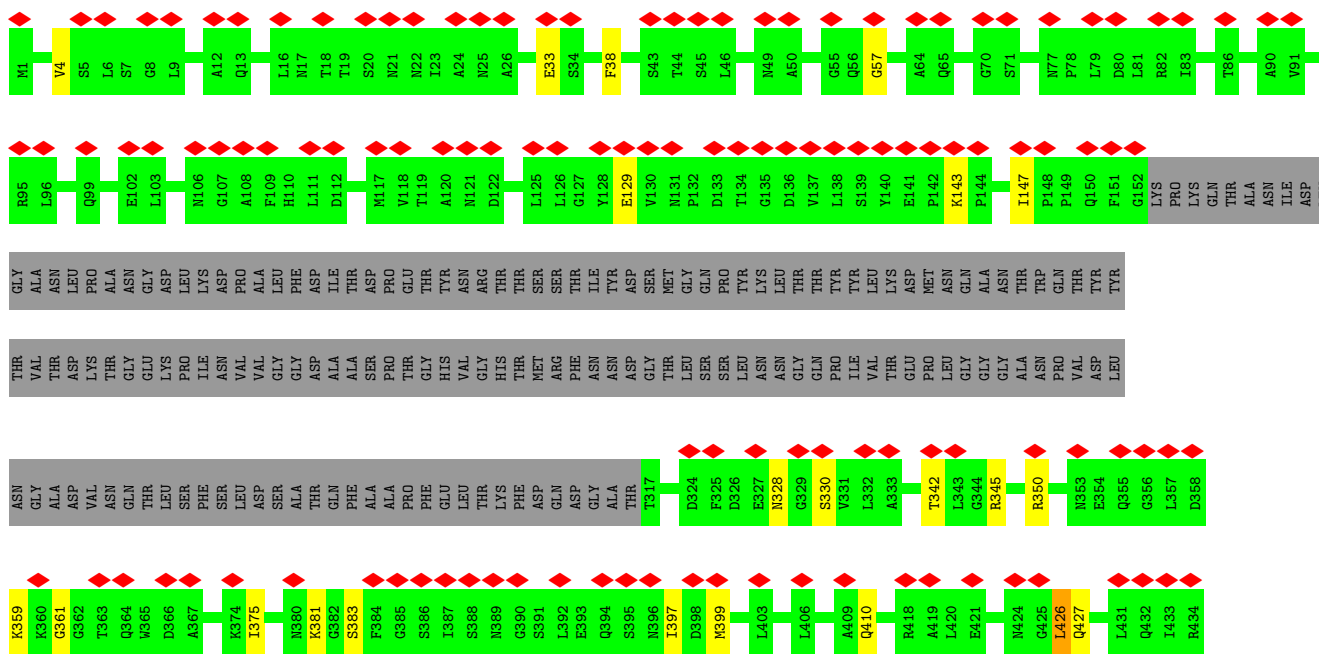


• Molecule 3: Flagellar hook protein FlgE

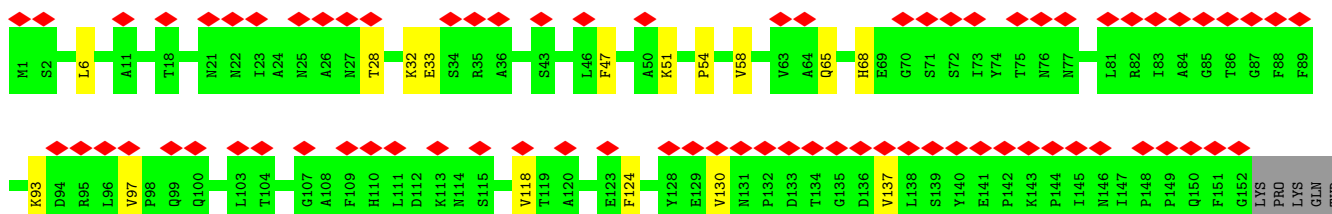




• Molecule 3: Flagellar hook protein FlgE

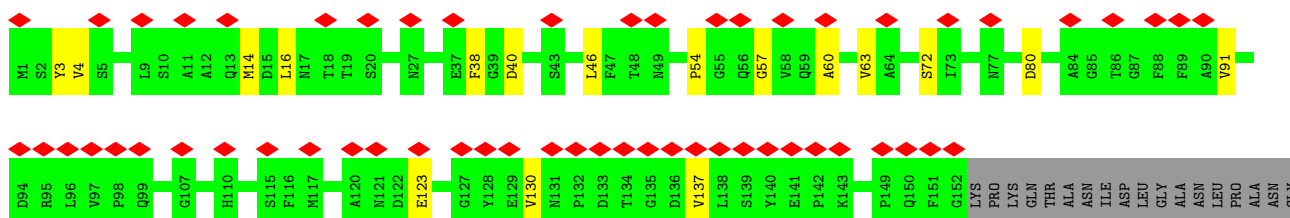


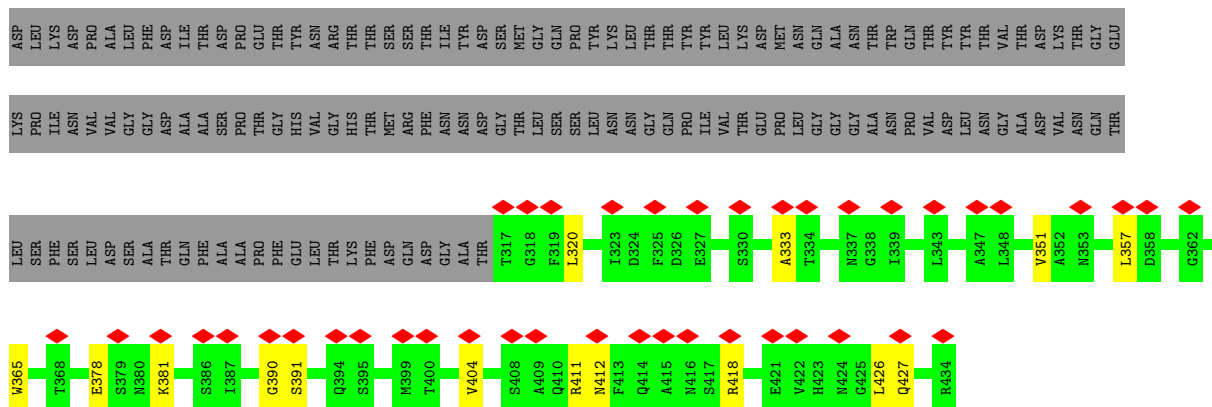
• Molecule 3: Flagellar hook protein FlgE



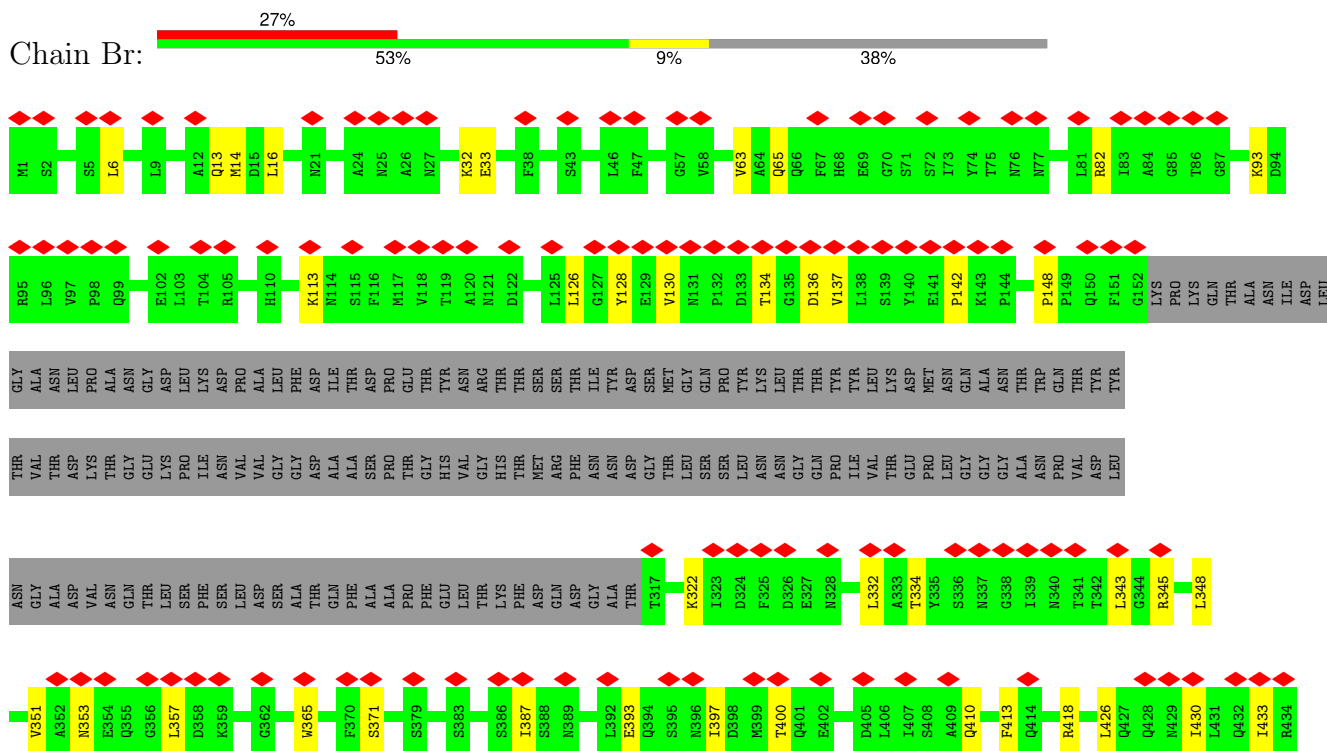


- Molecule 3: Flagellar hook protein FlgE

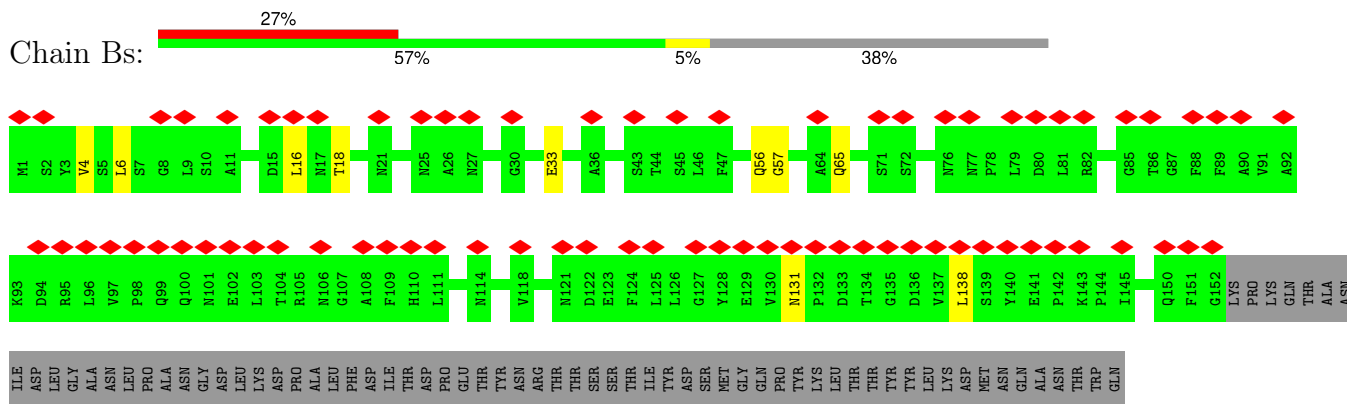




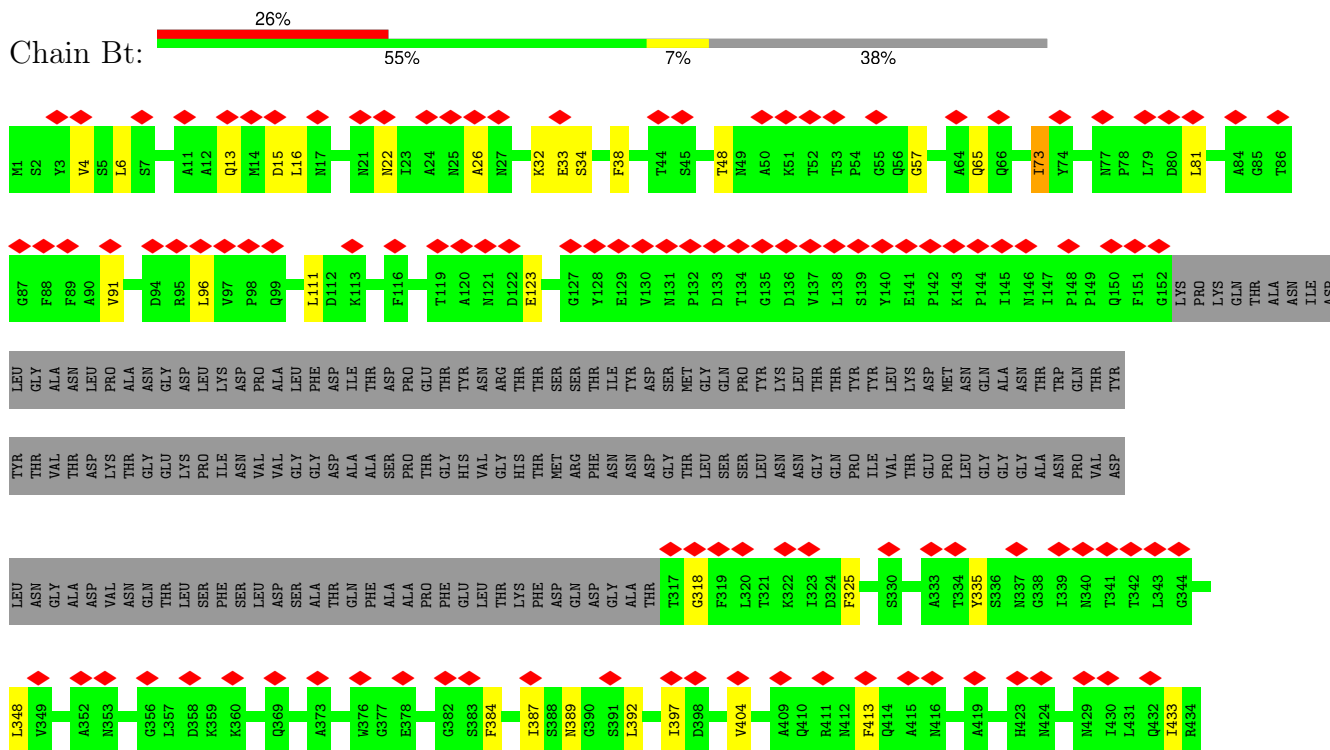
- Molecule 3: Flagellar hook protein FlgE



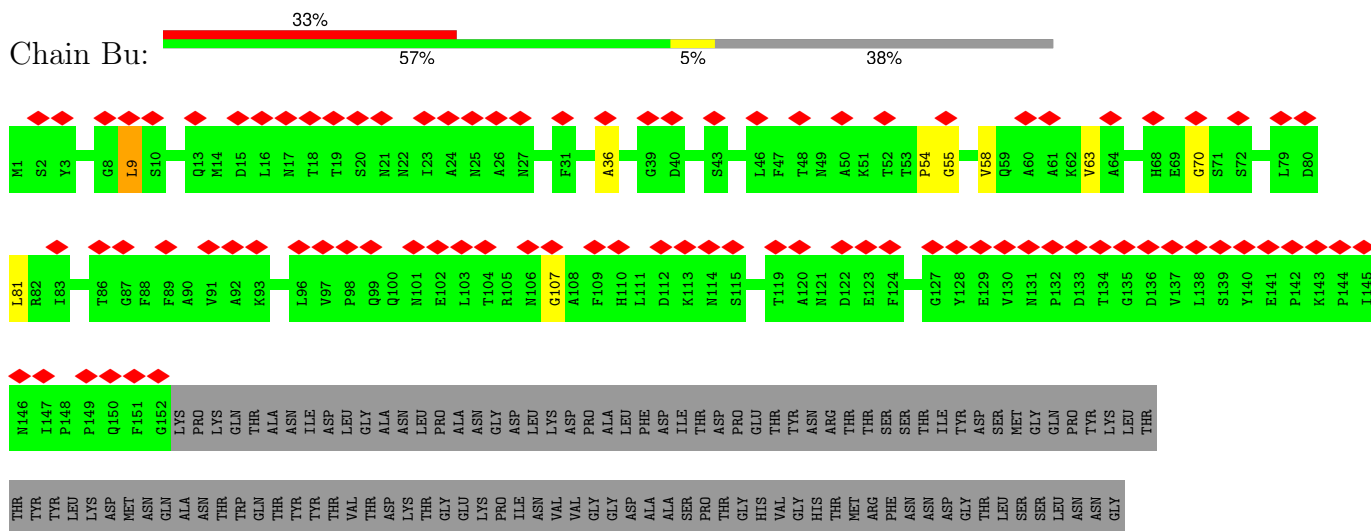
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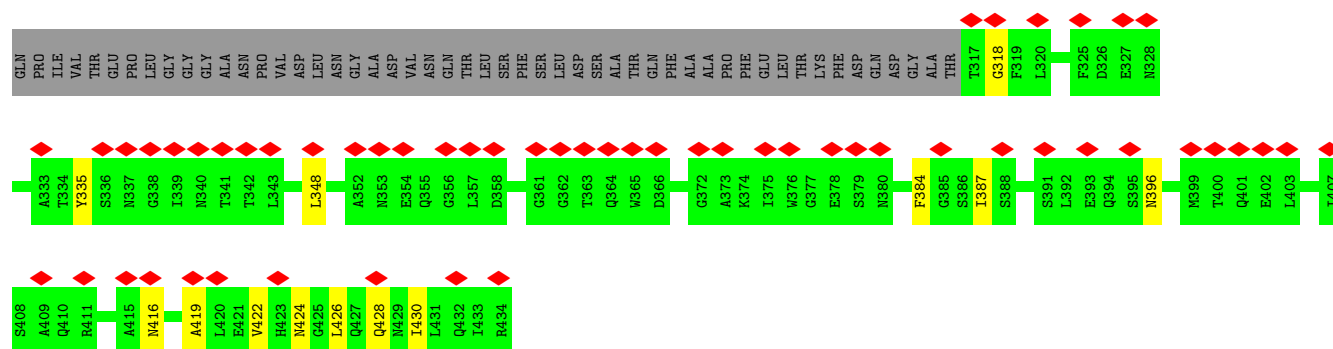


- Molecule 3: Flagellar hook protein FlgE



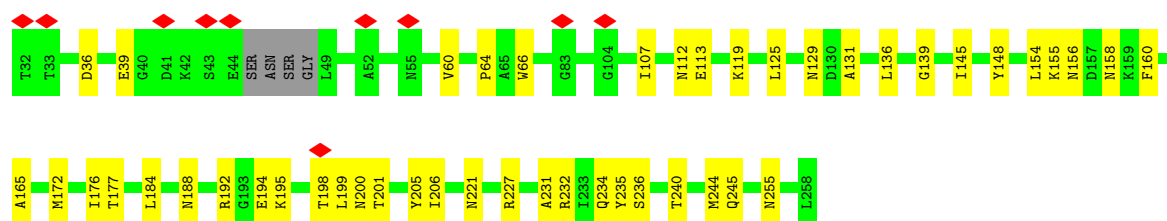
- Molecule 3: Flagellar hook protein FlgE





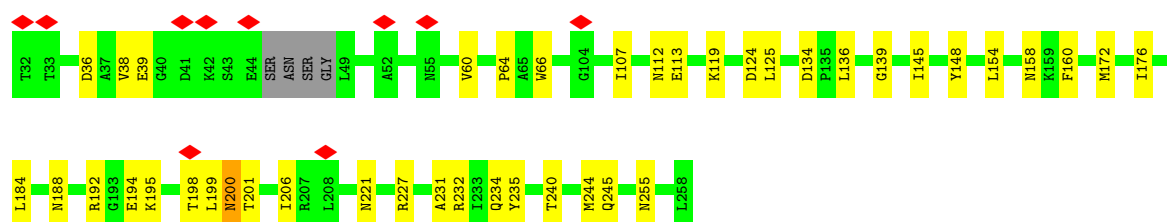
• Molecule 4: Flagellar L-ring protein

Chain Bx: 78% 21%



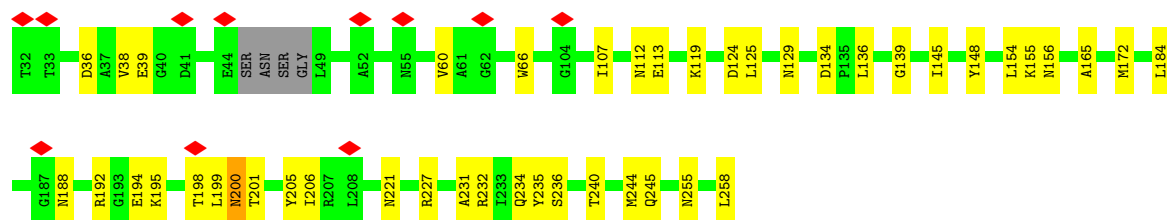
• Molecule 4: Flagellar L-ring protein

Chain By: 80% 18%



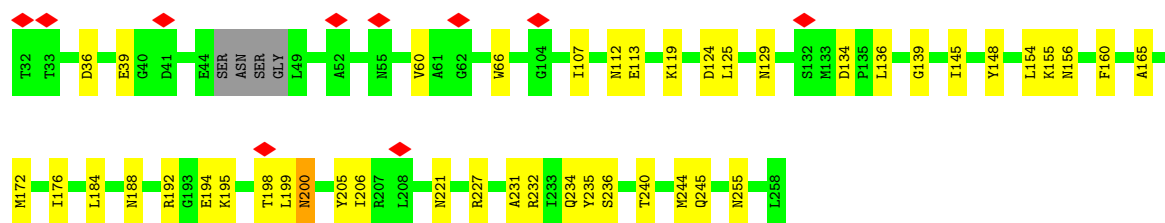
• Molecule 4: Flagellar L-ring protein

Chain Bz: 5% 78% 19%

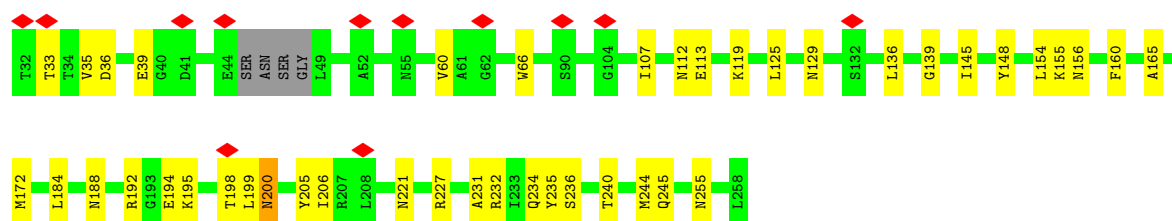
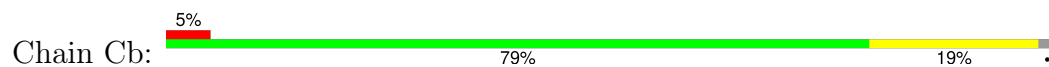


• Molecule 4: Flagellar L-ring protein

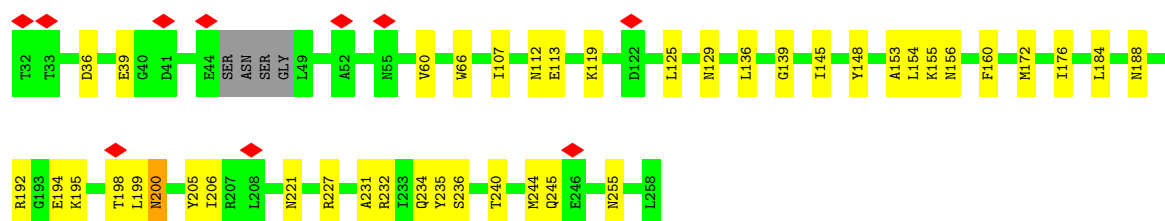
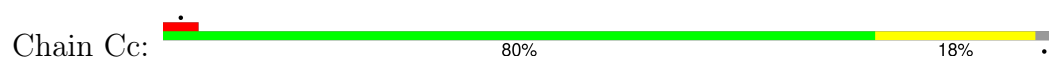
Chain Ca: 79% 19%



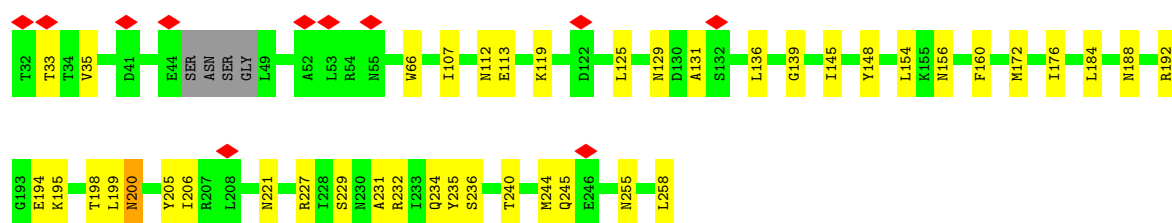
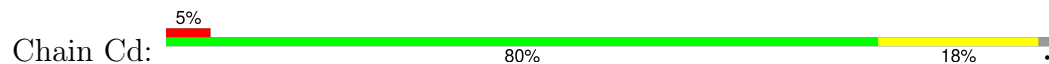
• Molecule 4: Flagellar L-ring protein



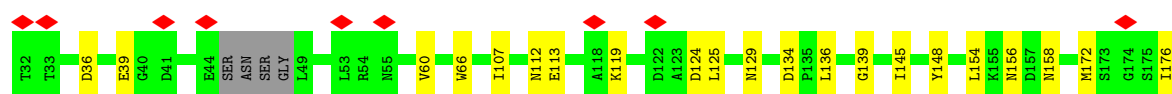
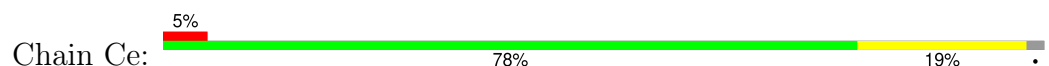
• Molecule 4: Flagellar L-ring protein

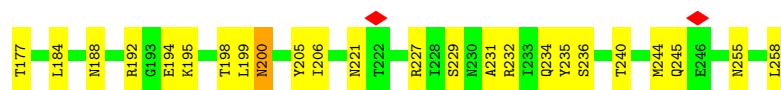


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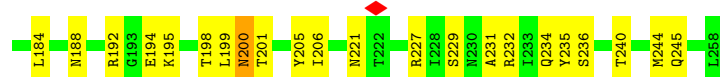
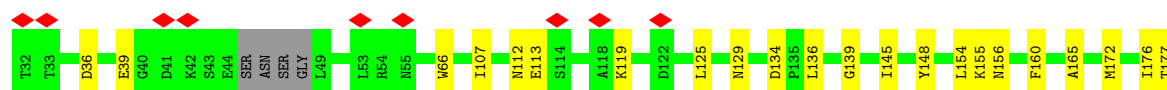
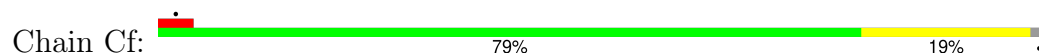


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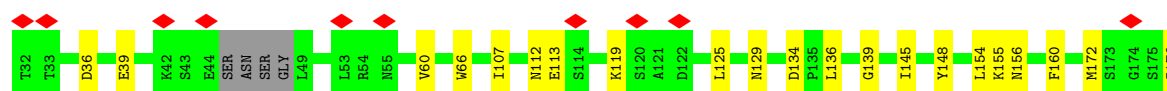
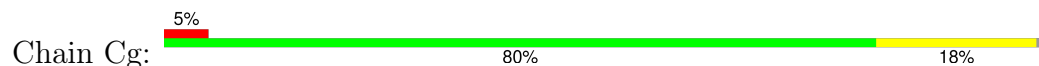




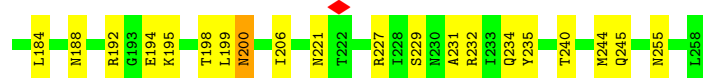
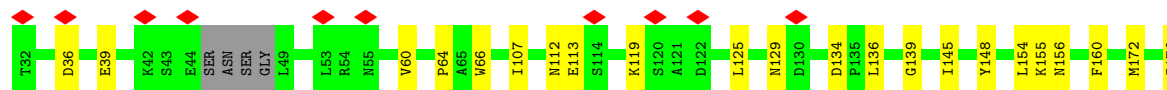
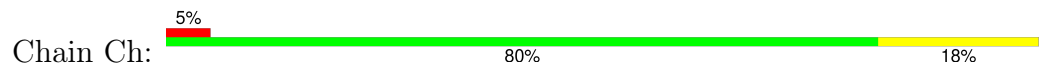
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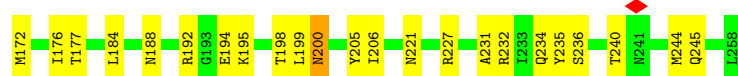
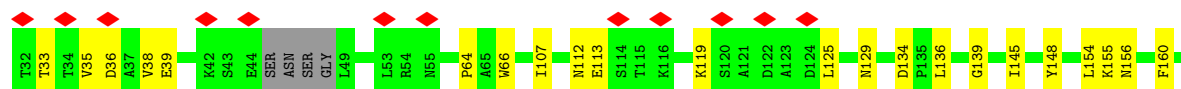
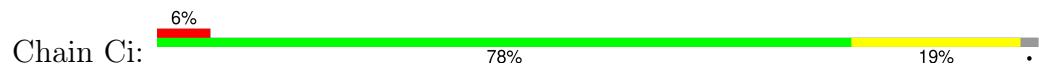
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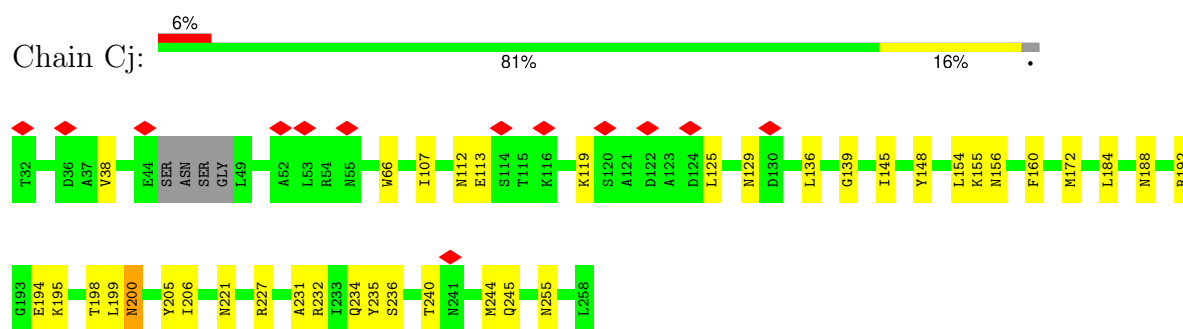
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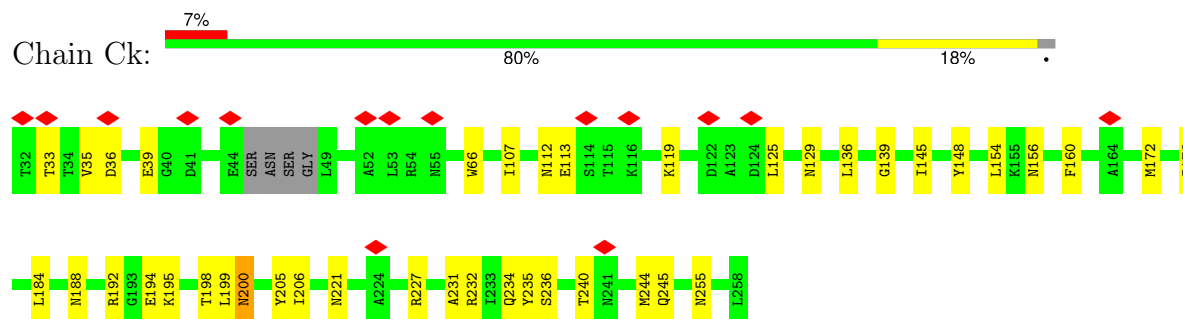
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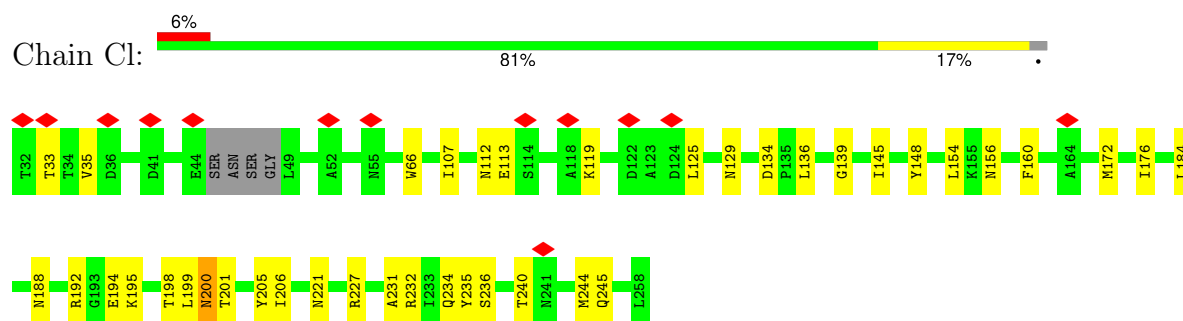
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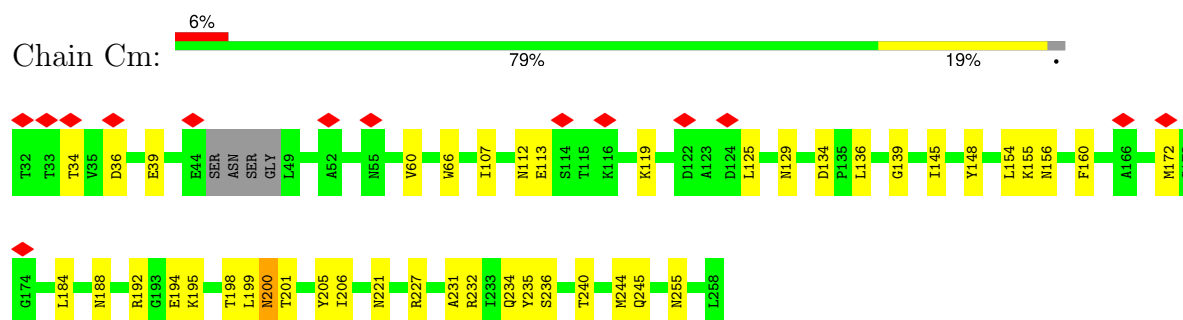
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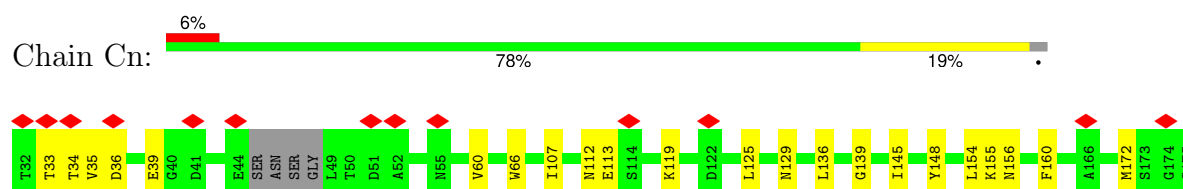
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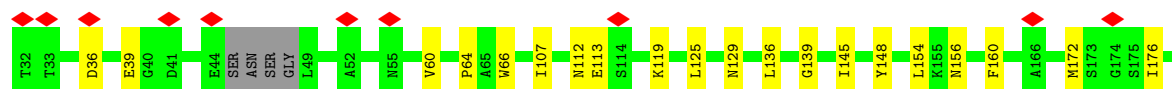
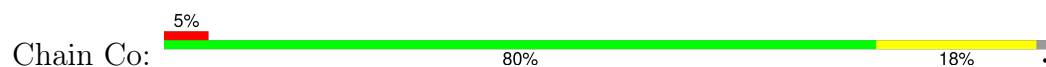


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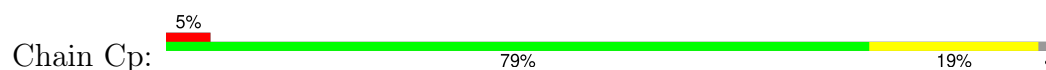




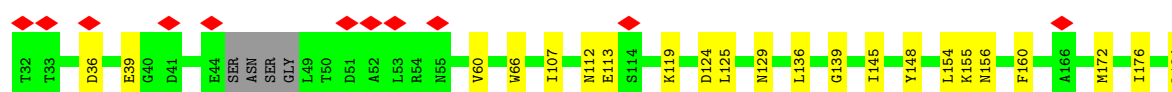
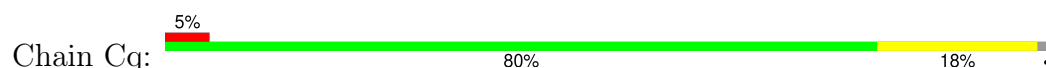
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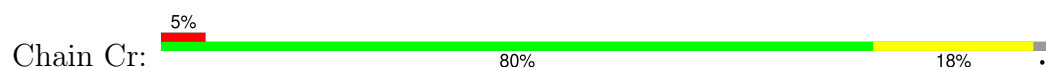
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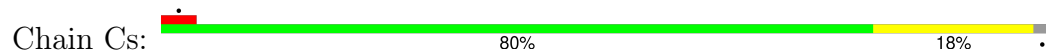
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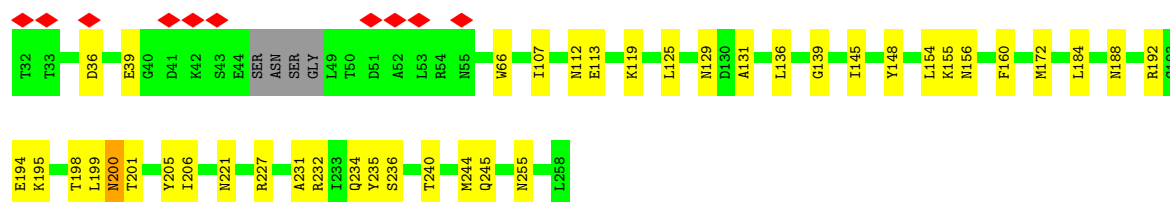


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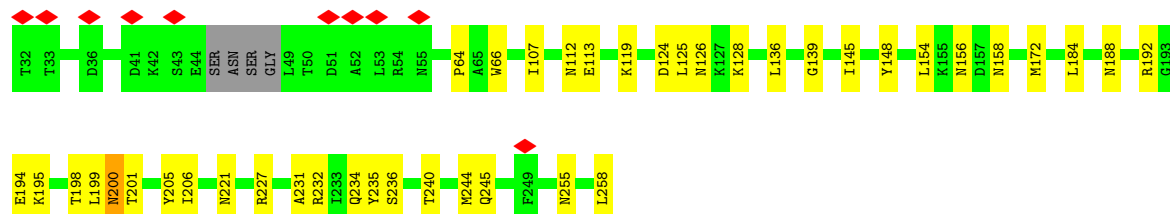
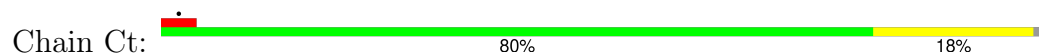


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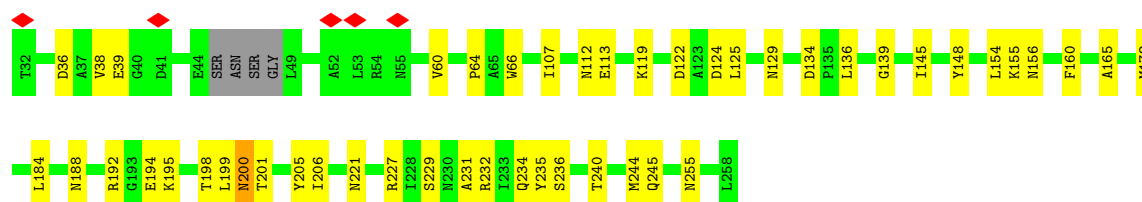
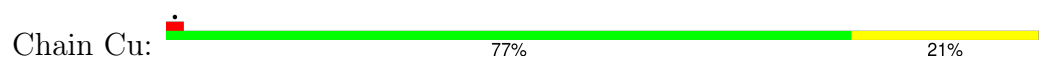




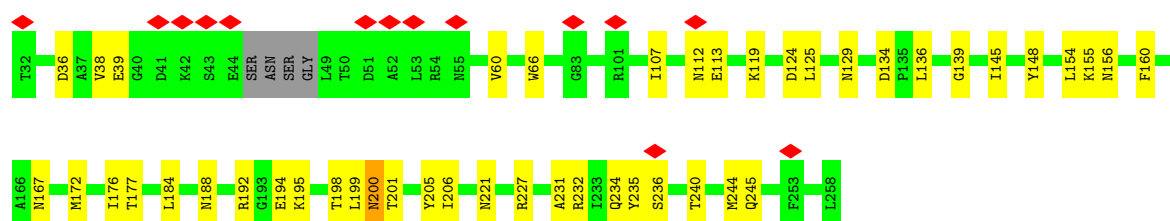
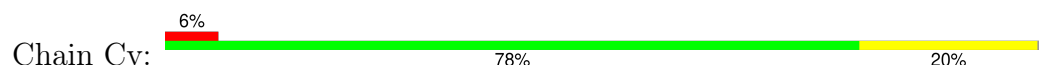
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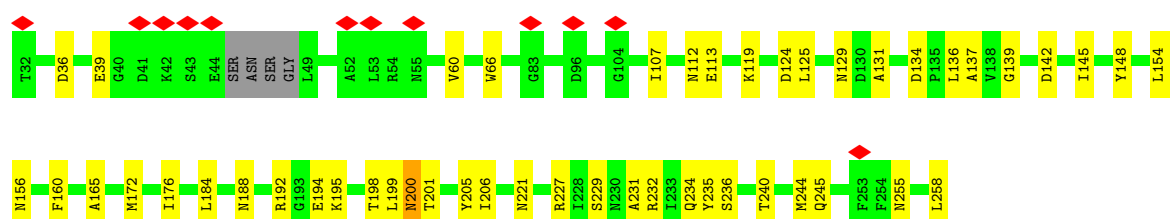
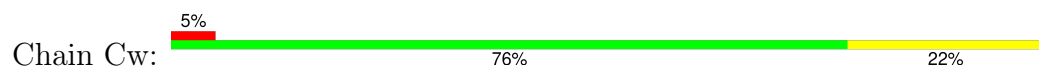
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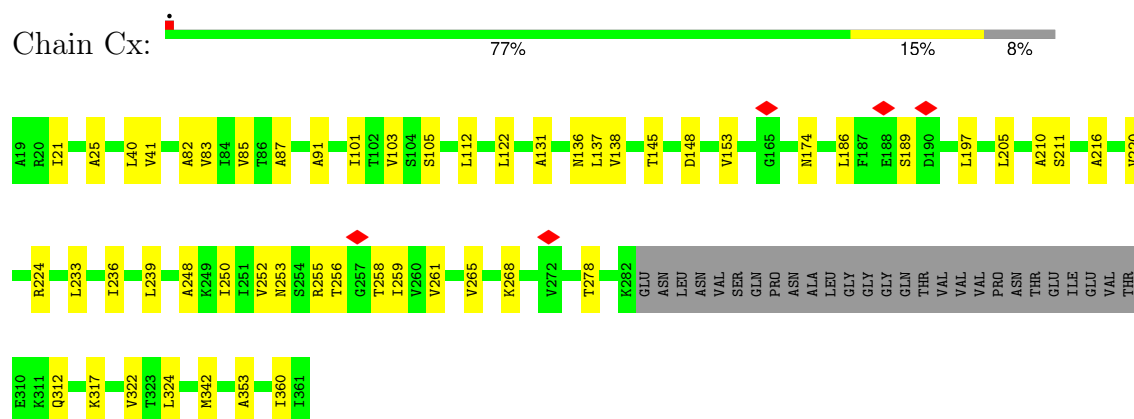
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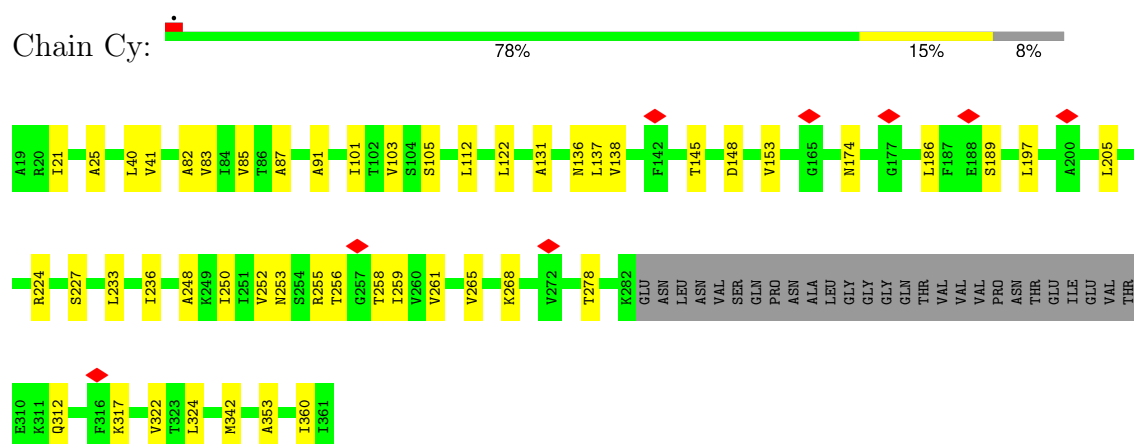
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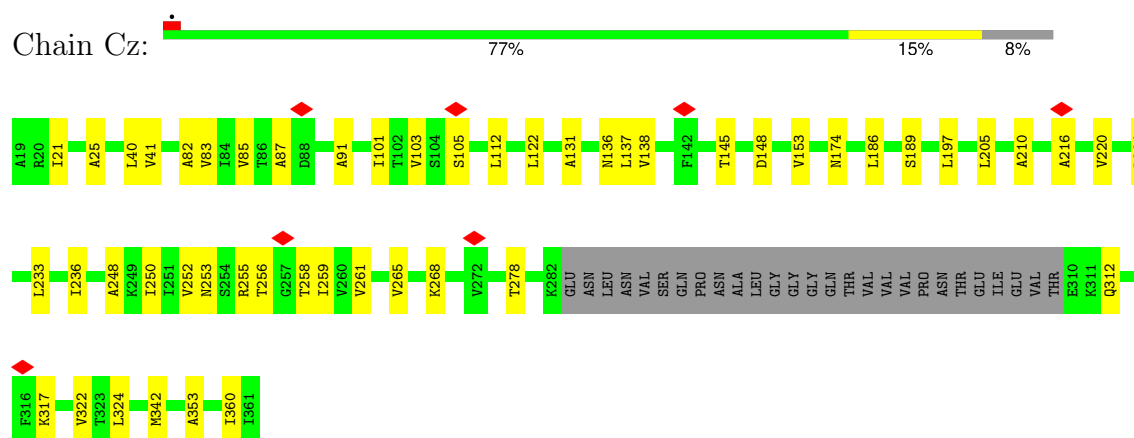
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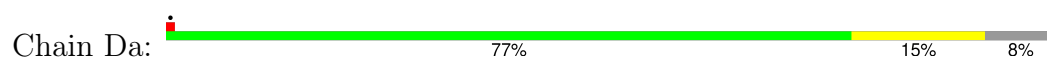
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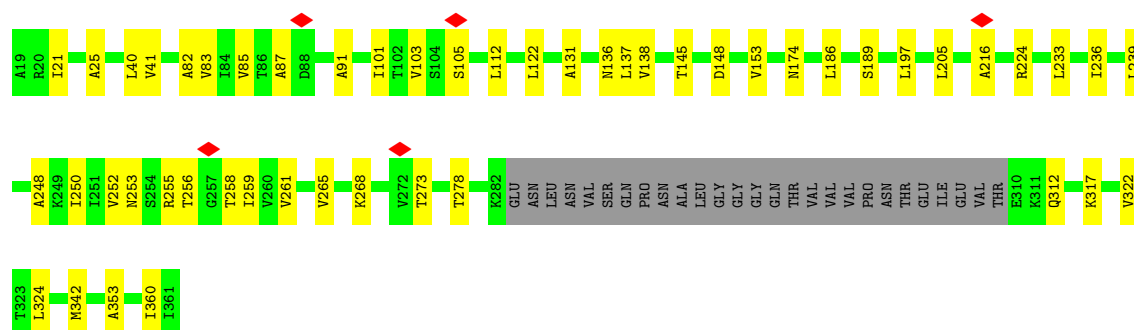


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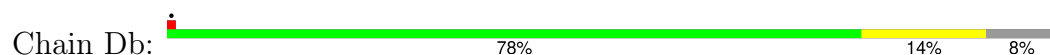


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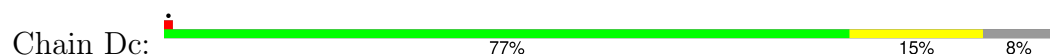




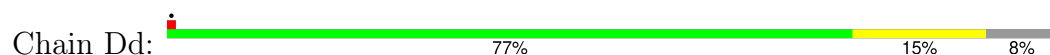
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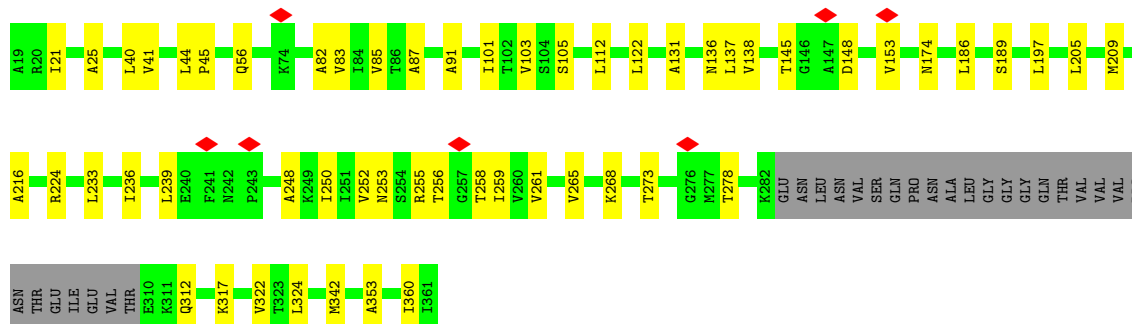
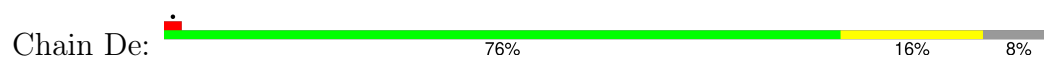


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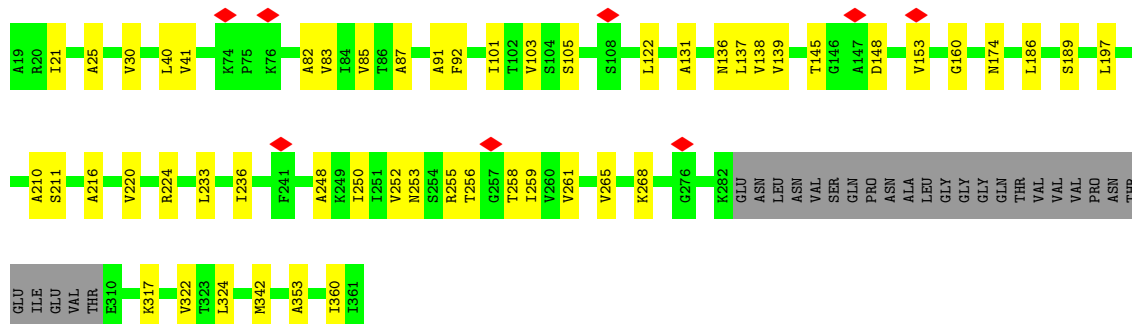
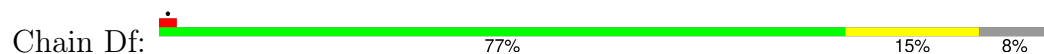




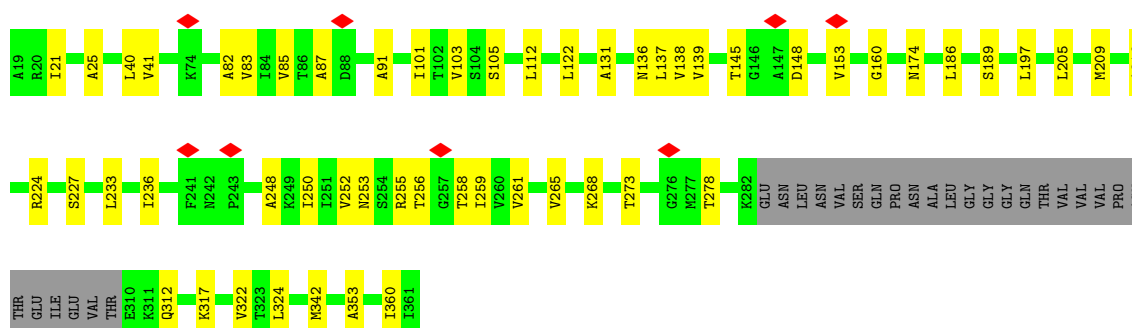
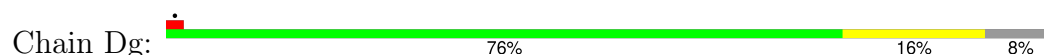
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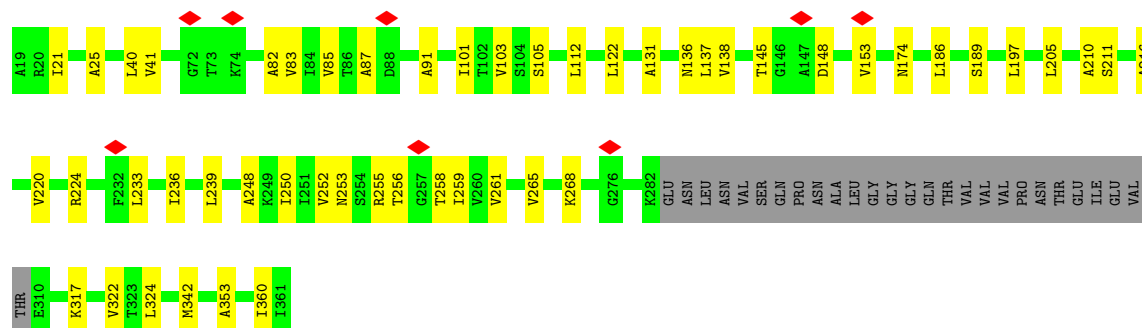


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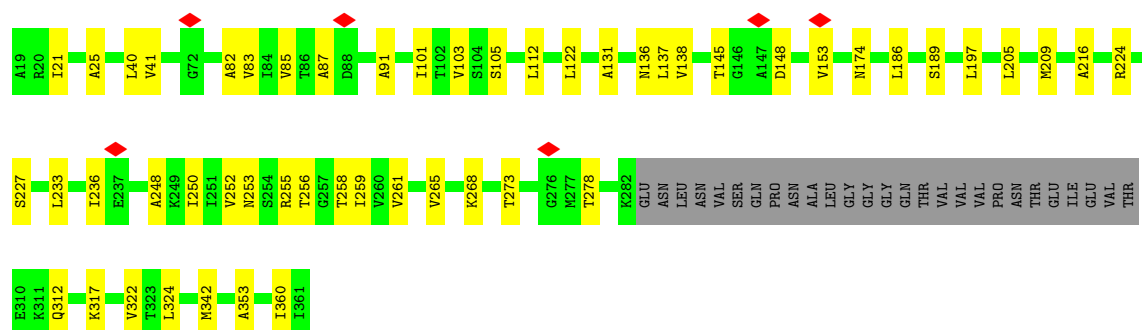
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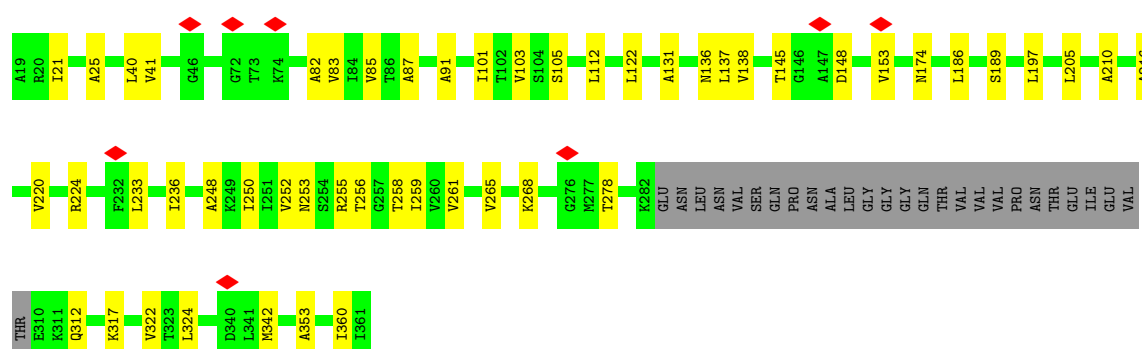
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Chain Di: 77% 15% 8%



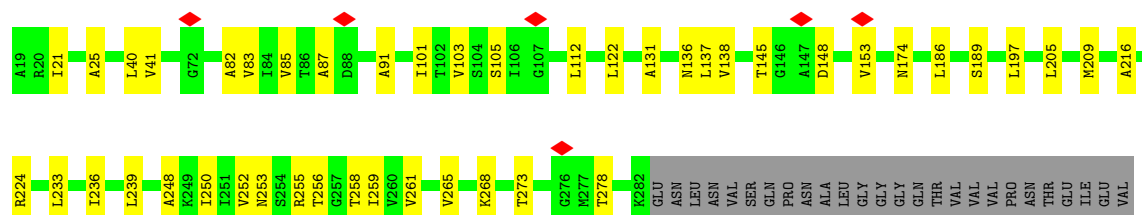
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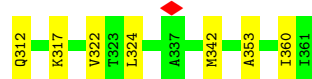
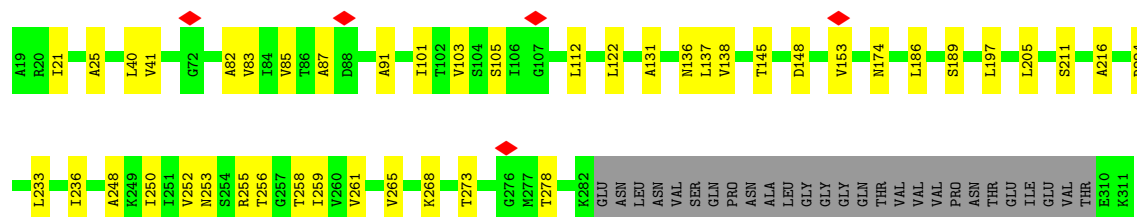
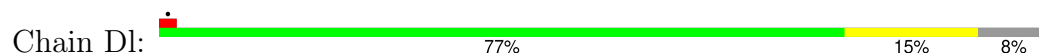
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Chain Dk: 77% 15% 8%

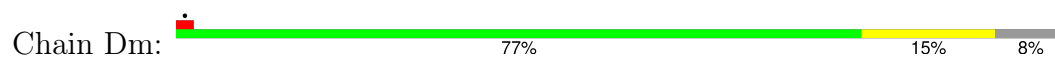




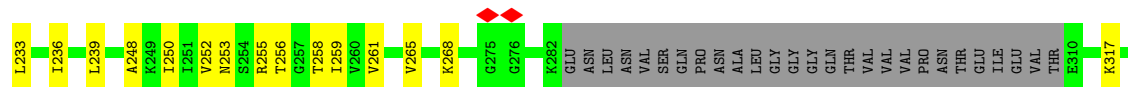
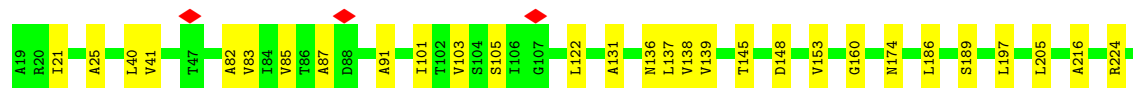
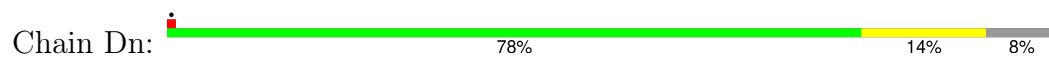
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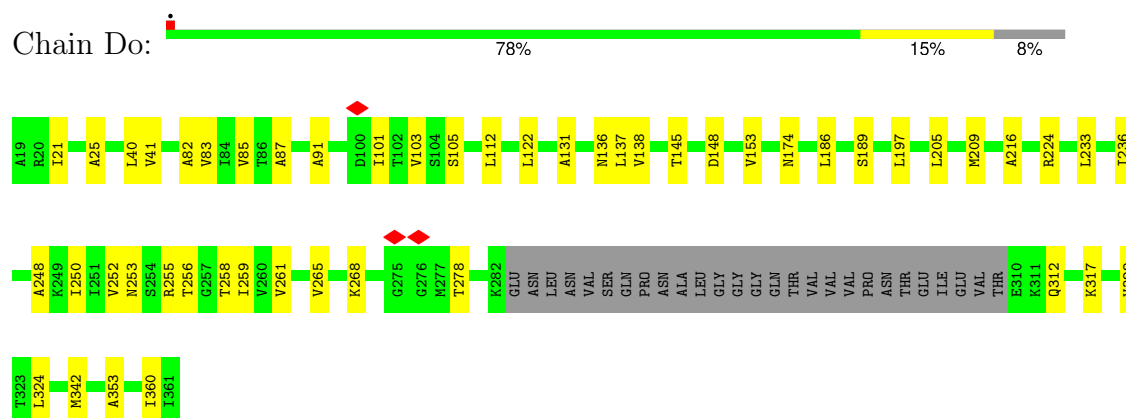
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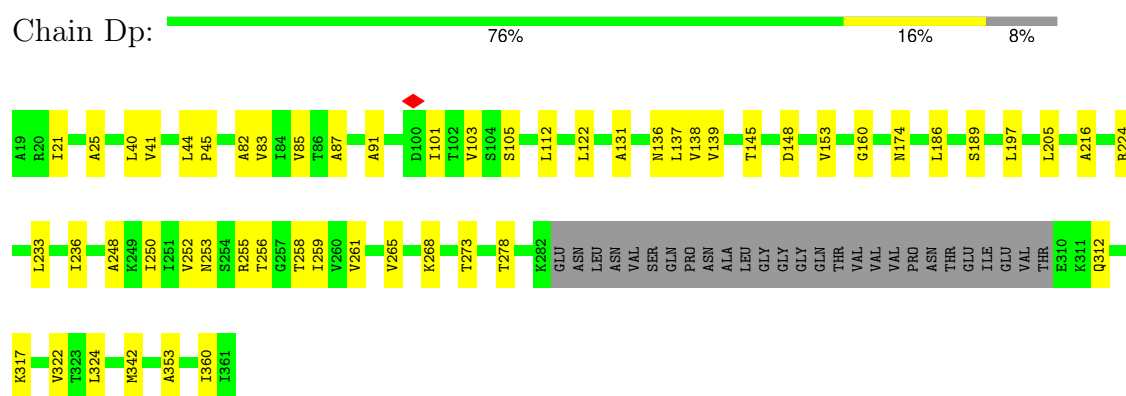
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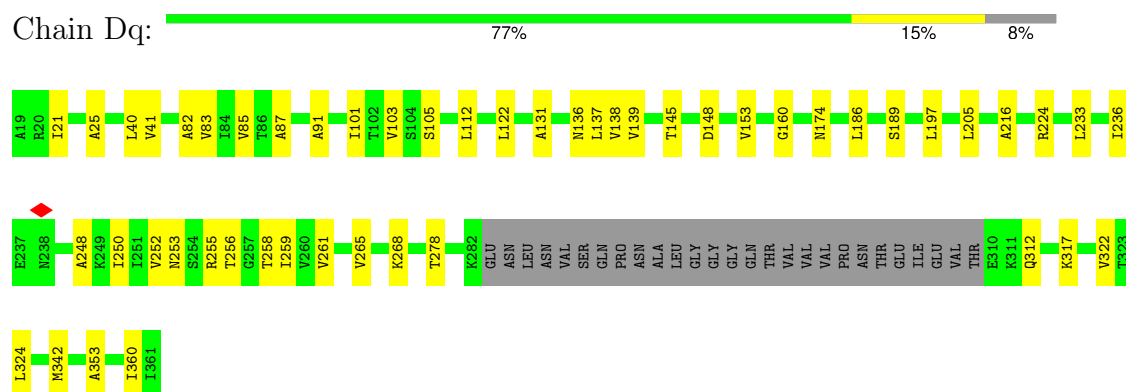
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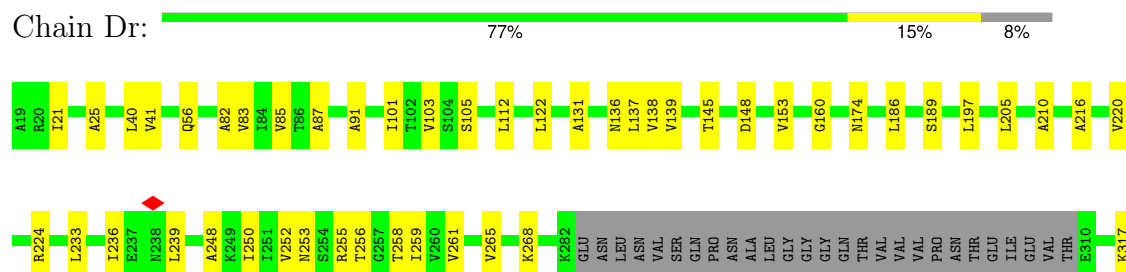
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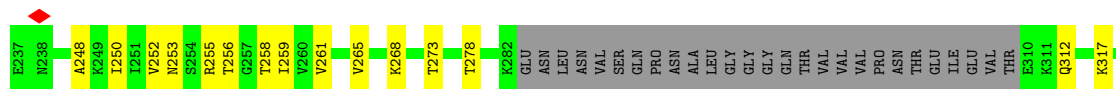
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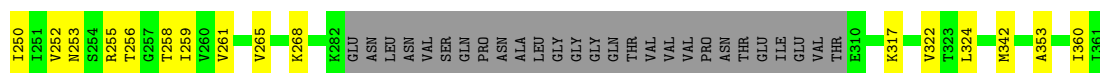
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Chain Ds: 77% 15% 8%



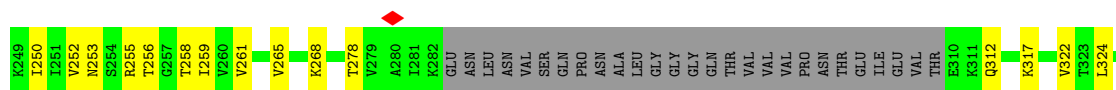
• Molecule 5: Flagellar P-ring protein

Chain Dt: 78% 14% 8%



• Molecule 5: Flagellar P-ring protein

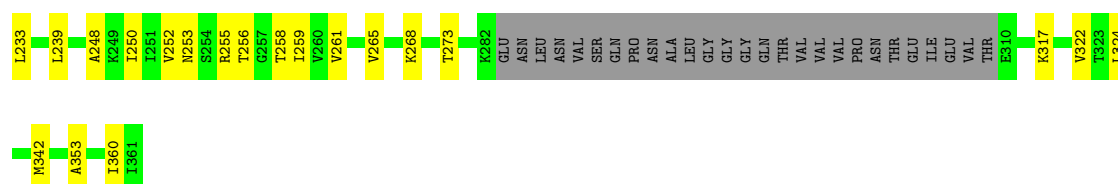
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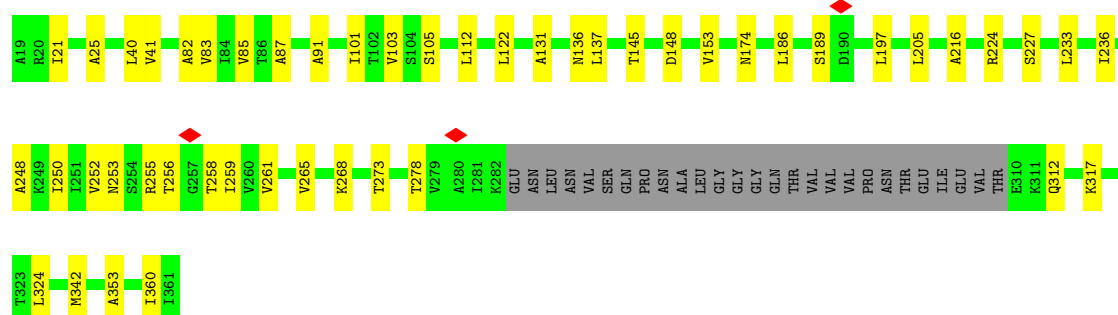
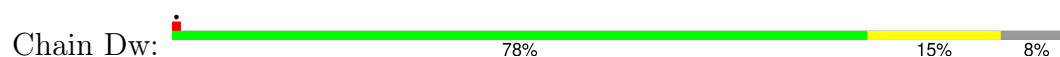
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Chain Dv: 77% 15% 8%

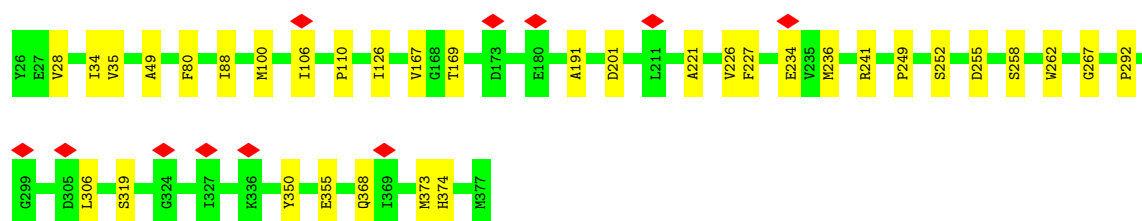




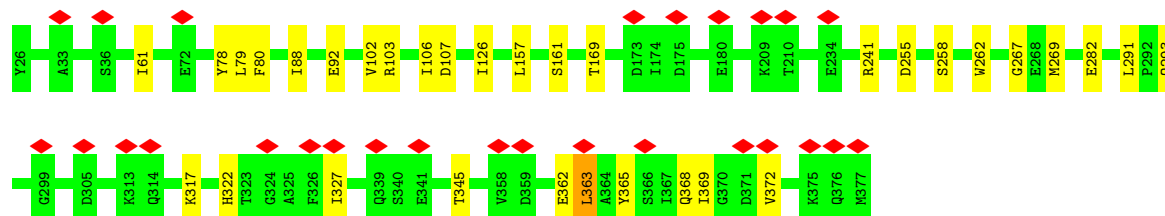
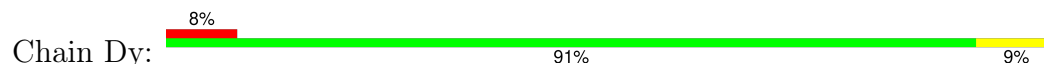
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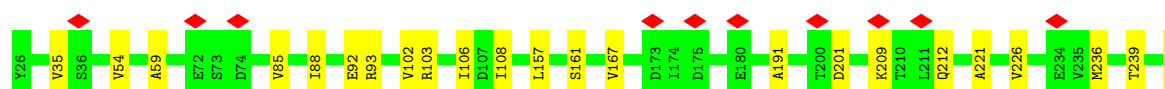
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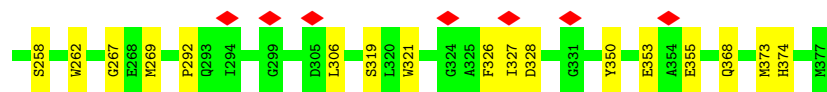


• Molecule 6: Flagellar protein FlgT

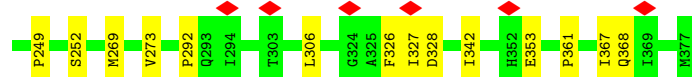
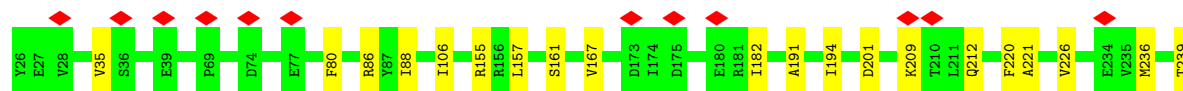
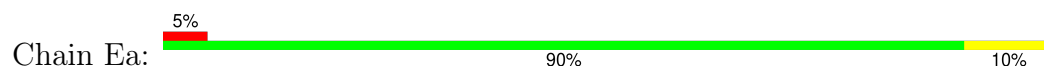


• Molecule 6: Flagellar protein FlgT

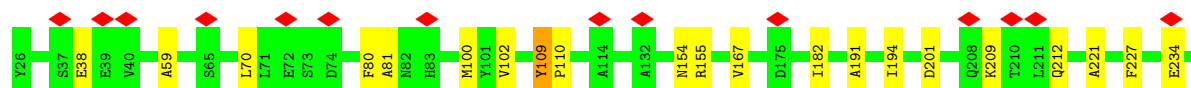
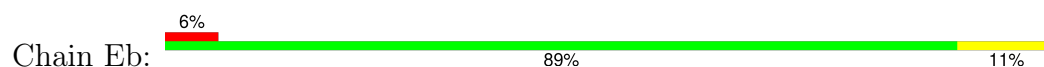




• Molecule 6: Flagellar protein FlgT



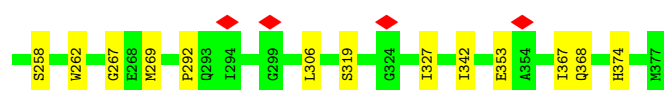
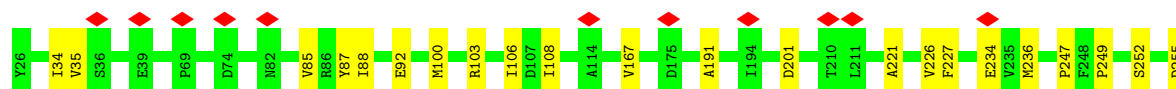
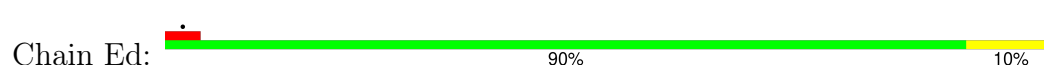
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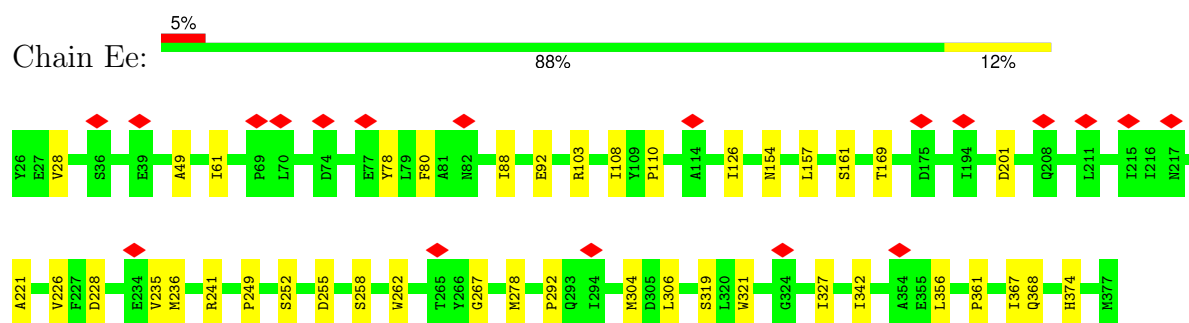
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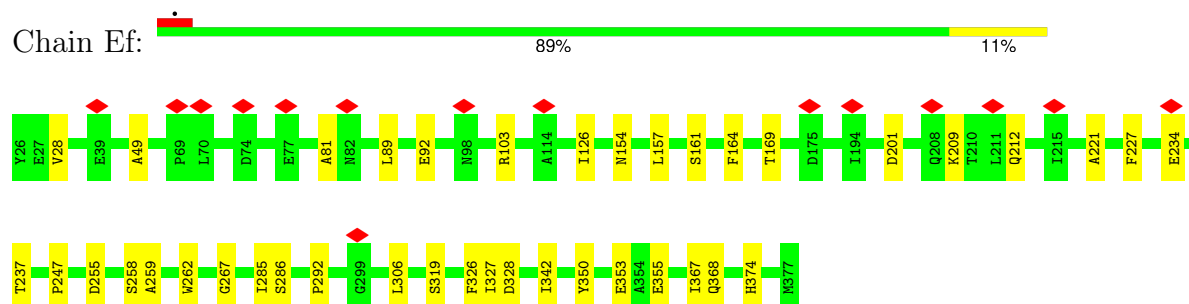
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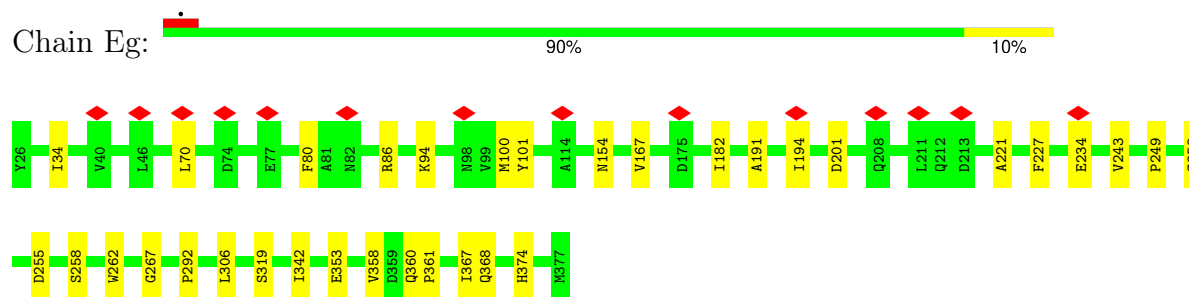
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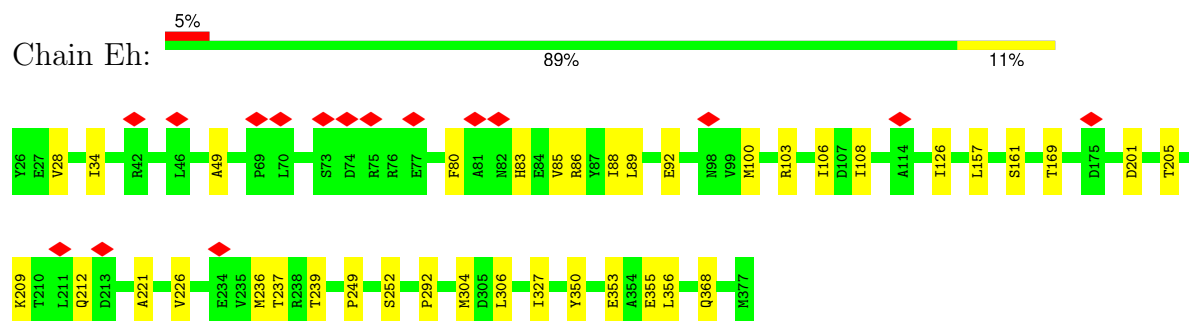
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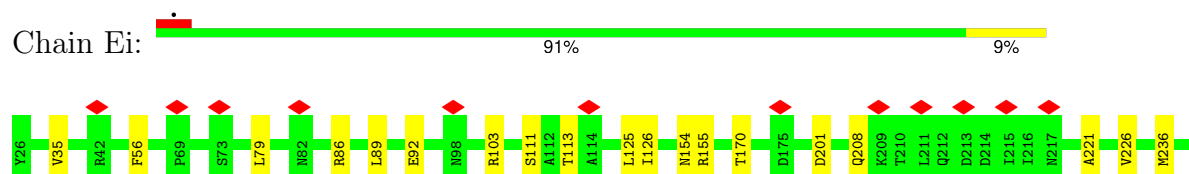
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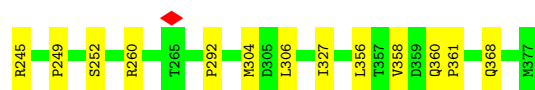


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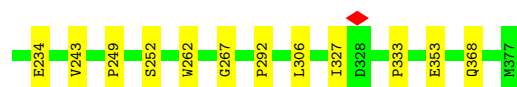
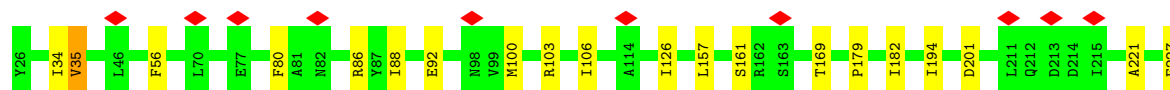


• Molecule 6: Flagellar protein FlgT





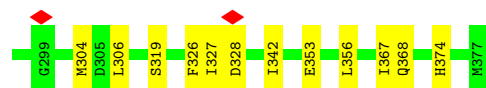
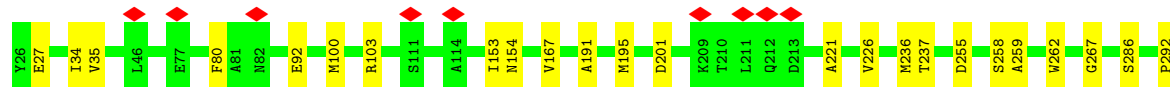
- Molecule 6: Flagellar protein FlgT



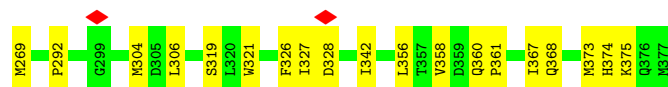
- Molecule 6: Flagellar protein FlgT



- Molecule 6: Flagellar protein FlgT

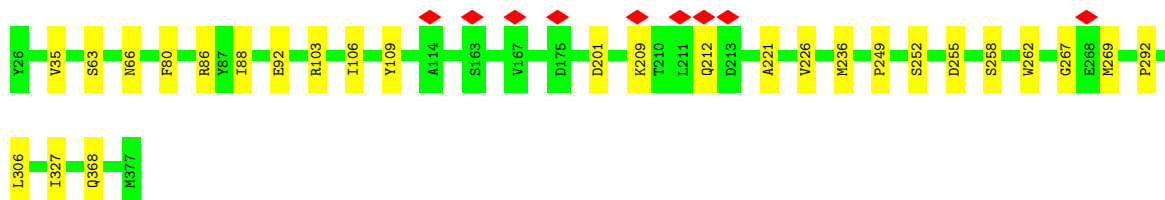


- Molecule 6: Flagellar protein FlgT



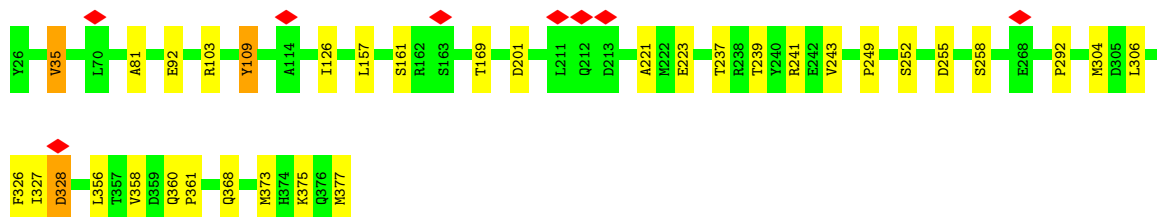
- Molecule 6: Flagellar protein FlgT

Chain En:  92% 8%




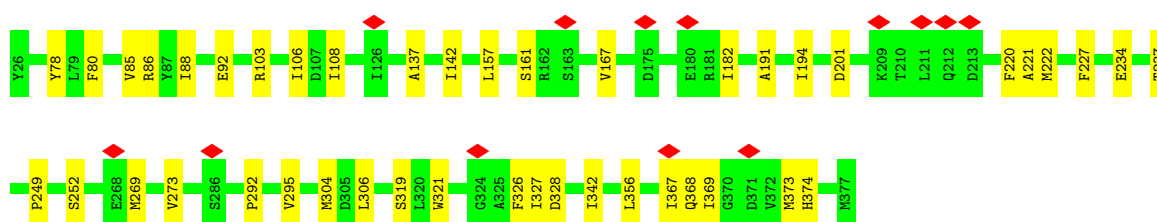
• Molecule 6: Flagellar protein FlgT

Chain Eo:  90% 9%




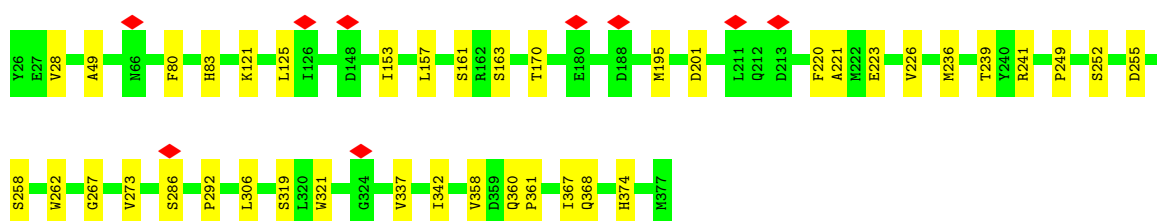
• Molecule 6: Flagellar protein FlgT

Chain Ep:  88% 13%




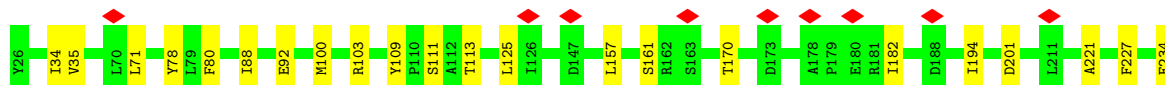
• Molecule 6: Flagellar protein FlgT

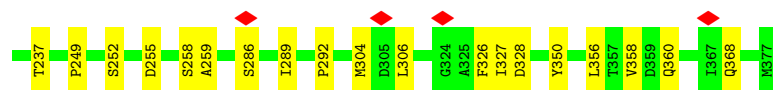
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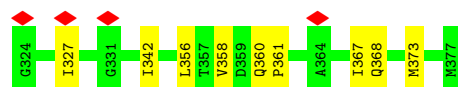
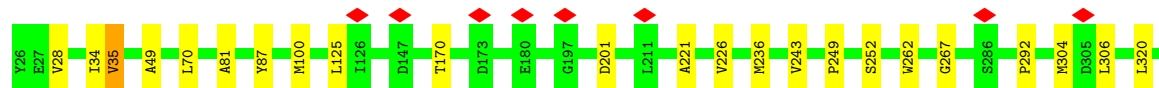
• Molecule 6: Flagellar protein FlgT

Chain Er:  88% 12%

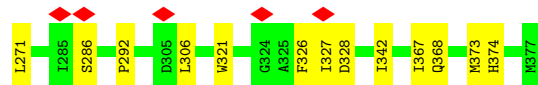
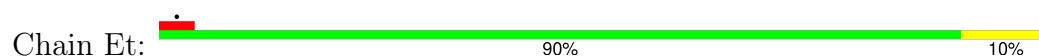




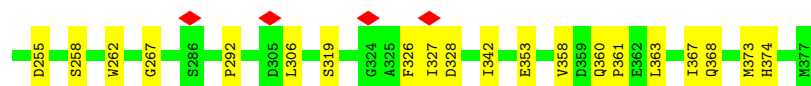
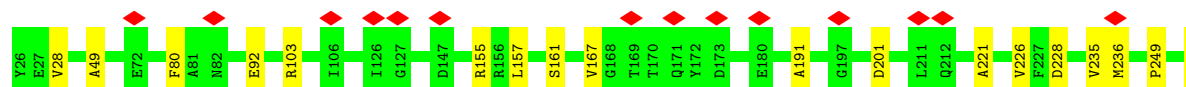
• Molecule 6: Flagellar protein FlgT



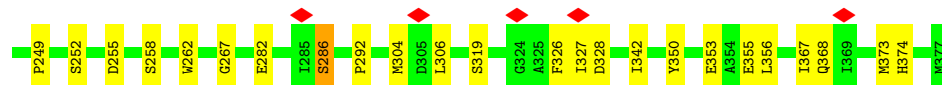
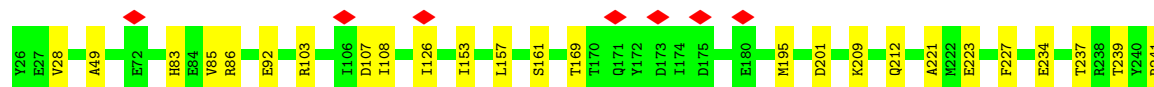
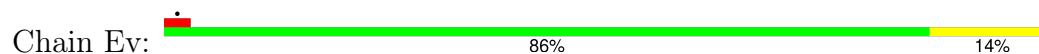
• Molecule 6: Flagellar protein FlgT



• Molecule 6: Flagellar protein FlgT

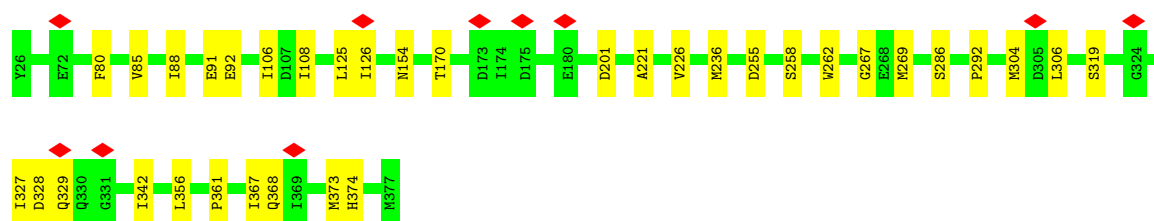


• Molecule 6: Flagellar protein FlgT




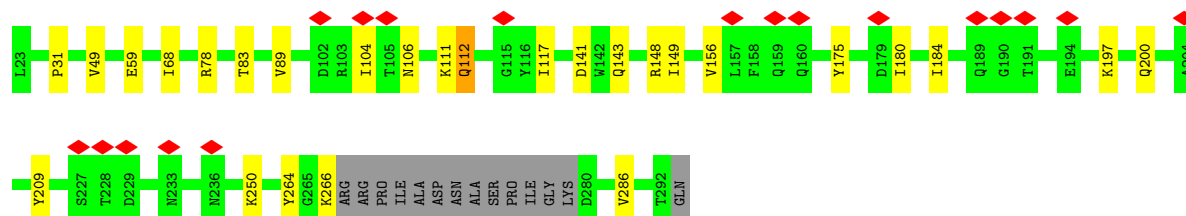
• Molecule 6: Flagellar protein FlgT

Chain Ew: 




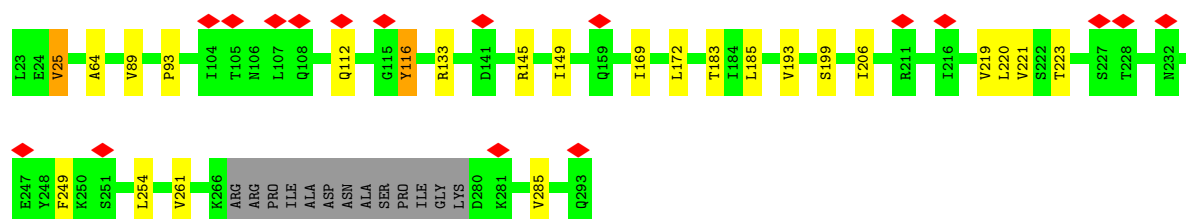
• Molecule 7: Sodium-type flagellar protein MotY

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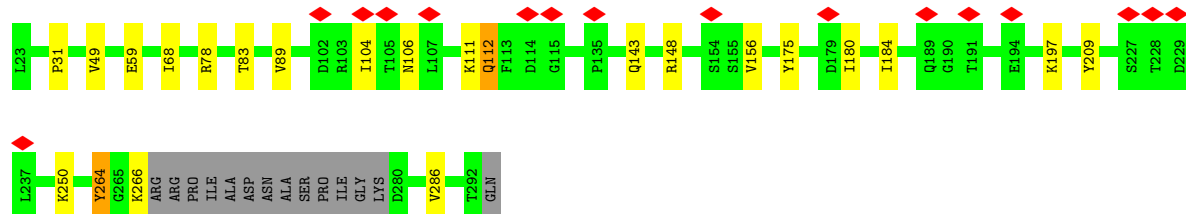
• Molecule 7: Sodium-type flagellar protein MotY

Chain Ey: 




• Molecule 7: Sodium-type flagellar protein MotY

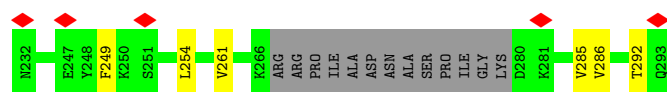
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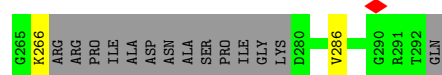
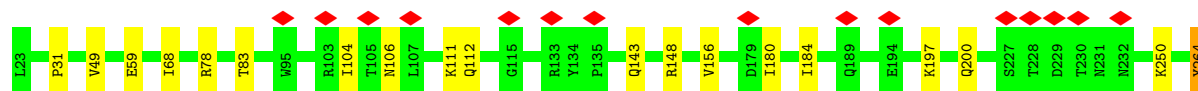
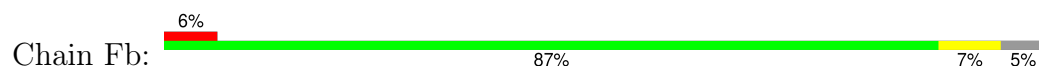
• Molecule 7: Sodium-type flagellar protein MotY

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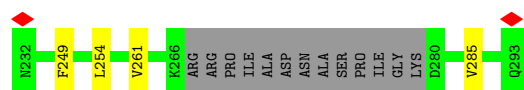
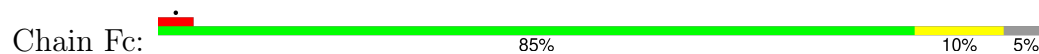




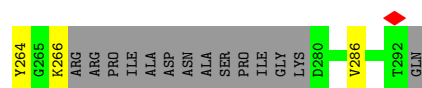
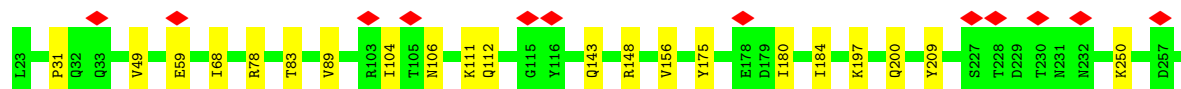
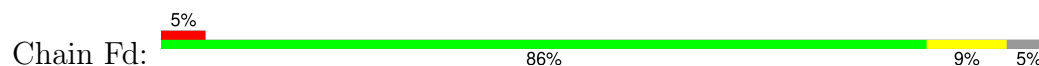
- Molecule 7: Sodium-type flagellar protein MotY



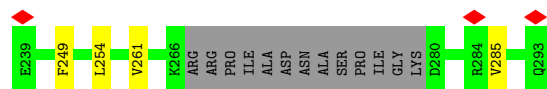
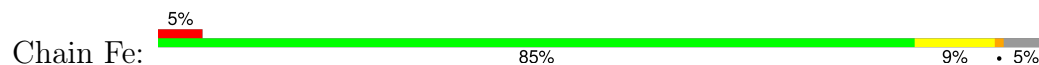
- Molecule 7: Sodium-type flagellar protein MotY




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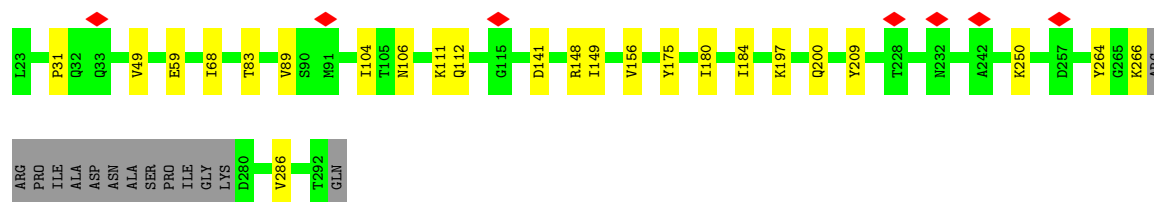


- Molecule 7: Sodium-type flagellar protein MotY




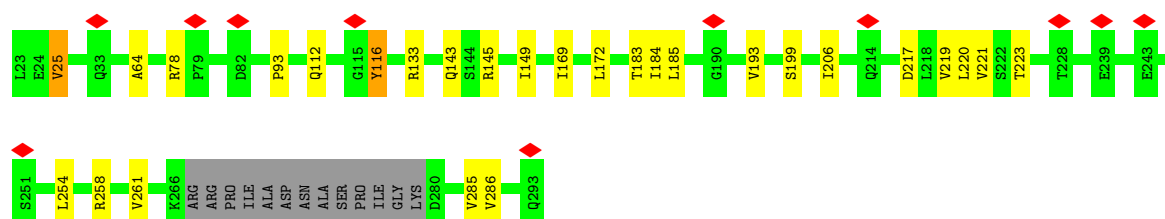
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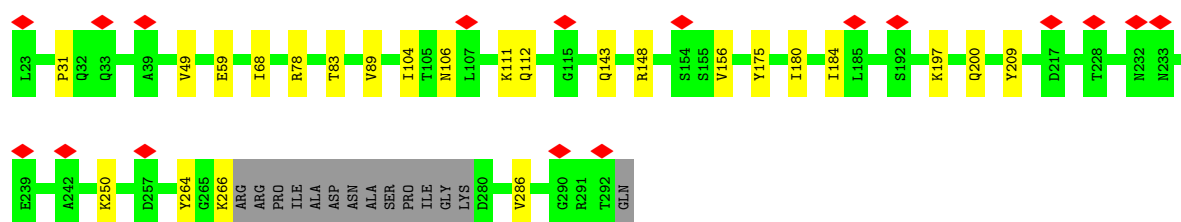
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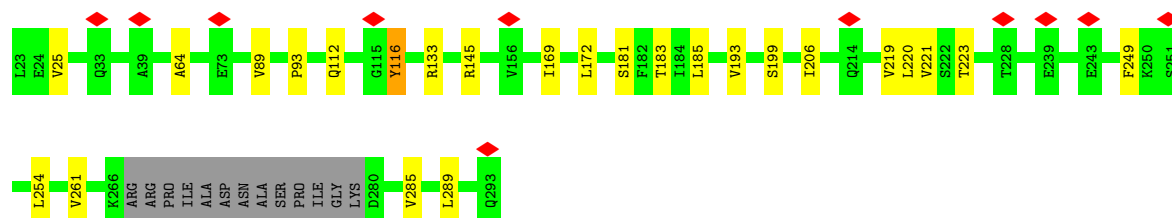
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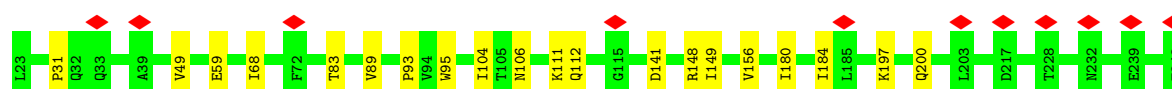
• Molecule 7: Sodium-type flagellar protein MotY

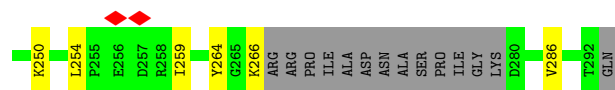
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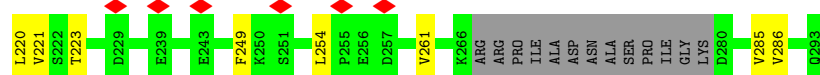
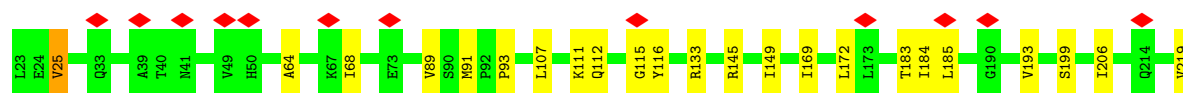
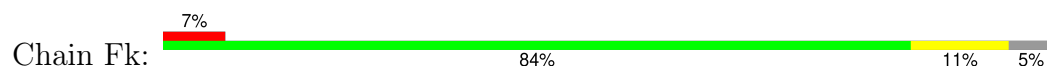
• Molecule 7: Sodium-type flagellar protein MotY

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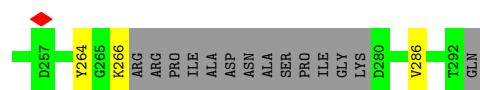
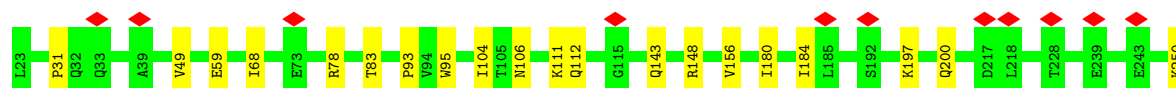
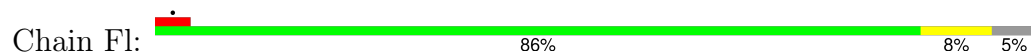




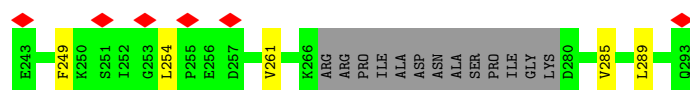
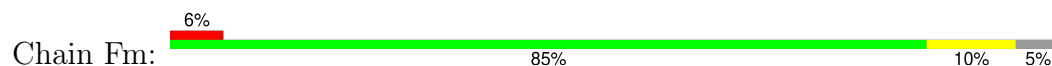
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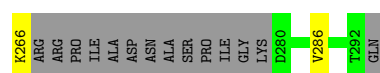
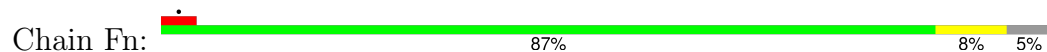
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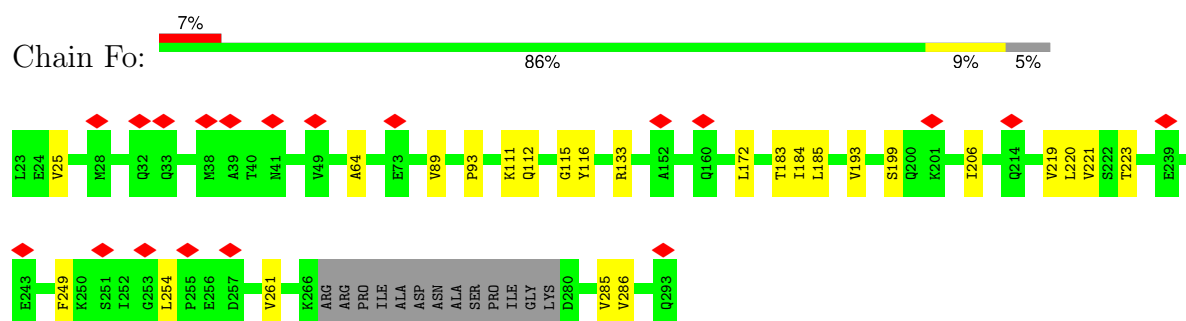
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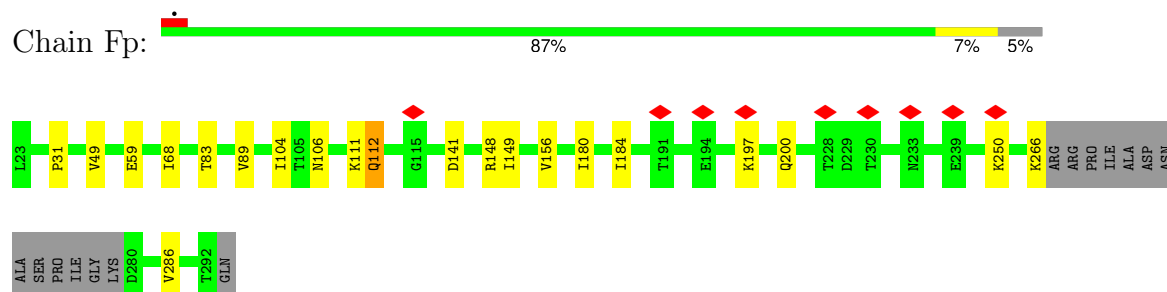
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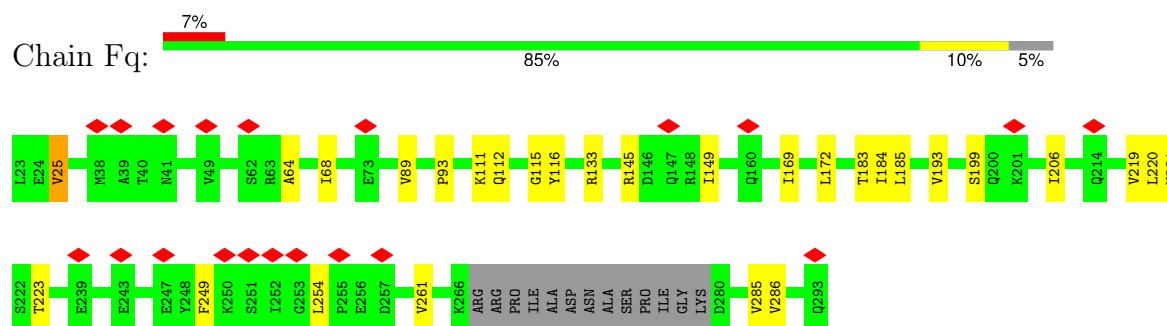
- Molecule 7: Sodium-type flagellar protein MotY



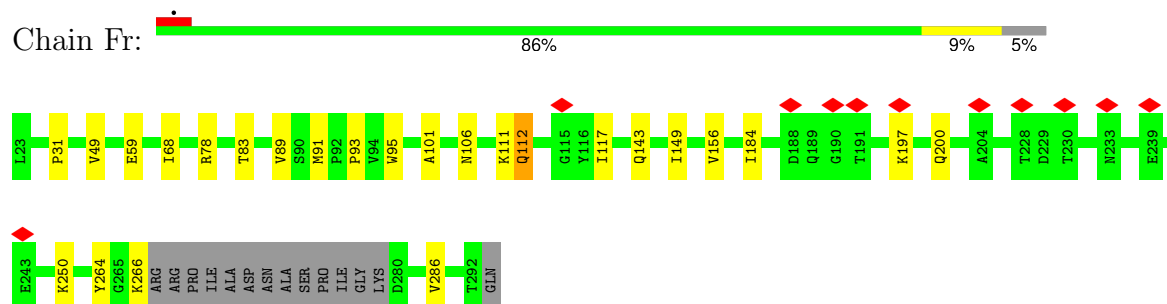
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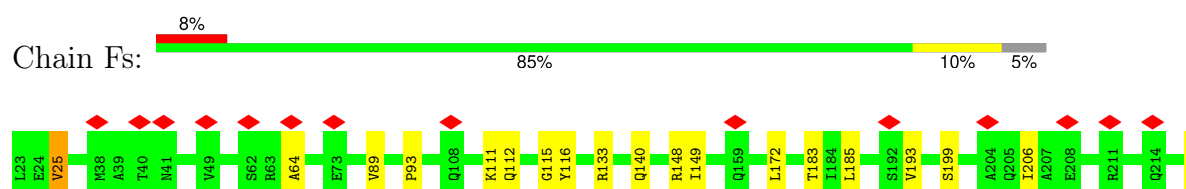
• Molecule 7: Sodium-type flagellar protein MotY

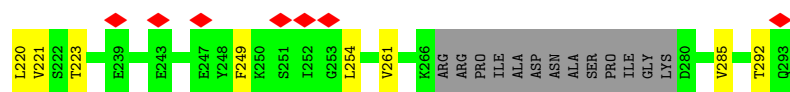


• Molecule 7: Sodium-type flagellar protein MotY

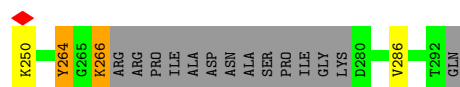
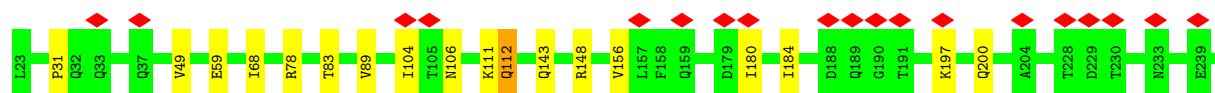
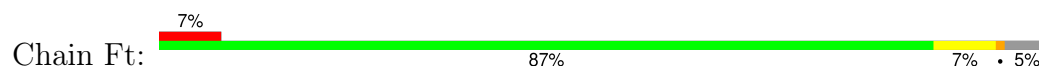


• Molecule 7: Sodium-type flagellar protein MotY

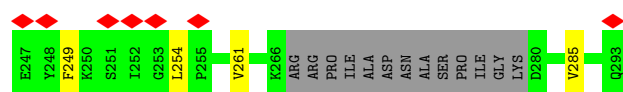
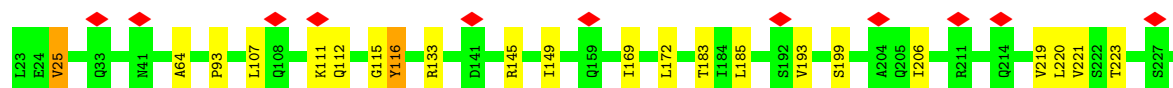
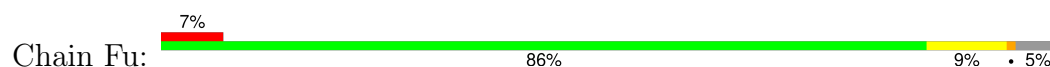




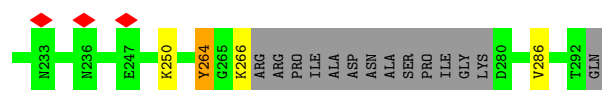
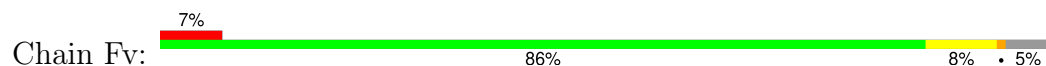
- Molecule 7: Sodium-type flagellar protein MotY



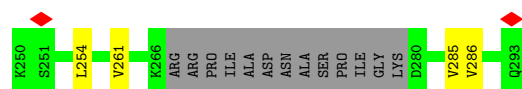
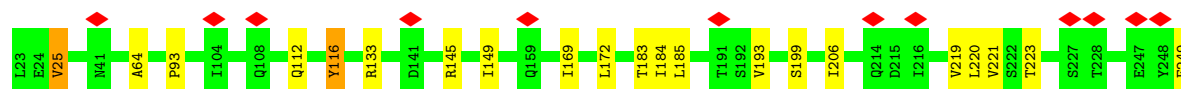
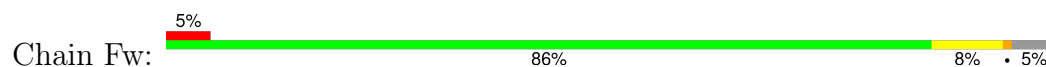
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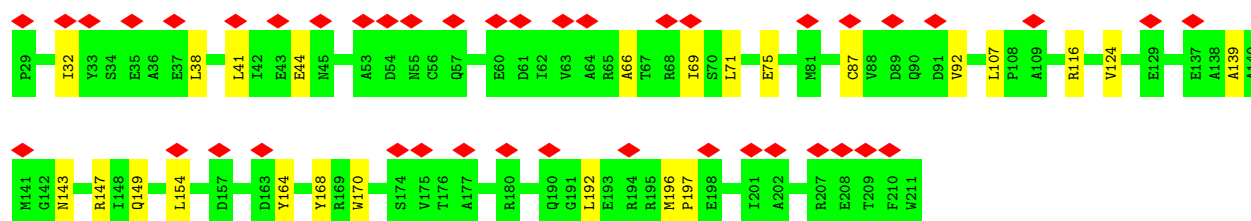
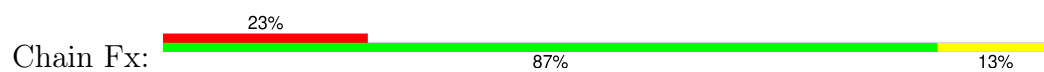
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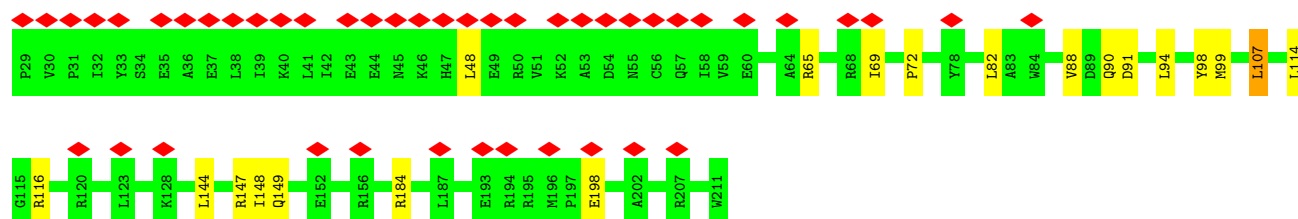
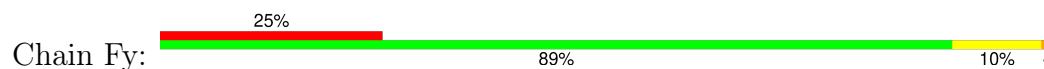
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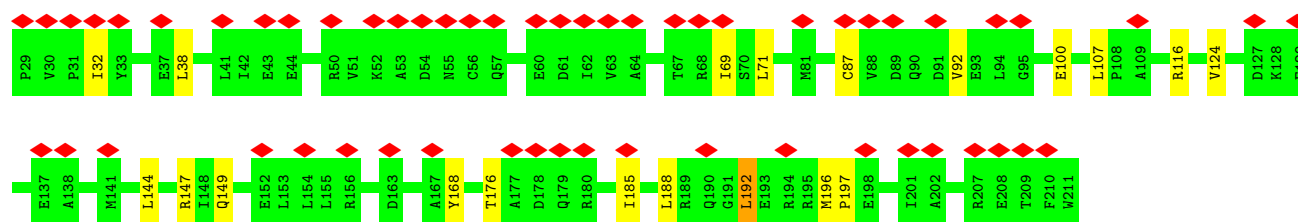
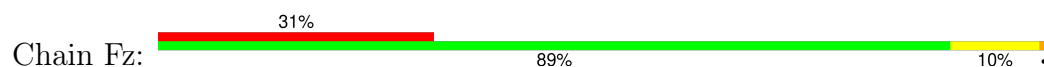
- Molecule 8: Sodium-type flagellar protein MotX



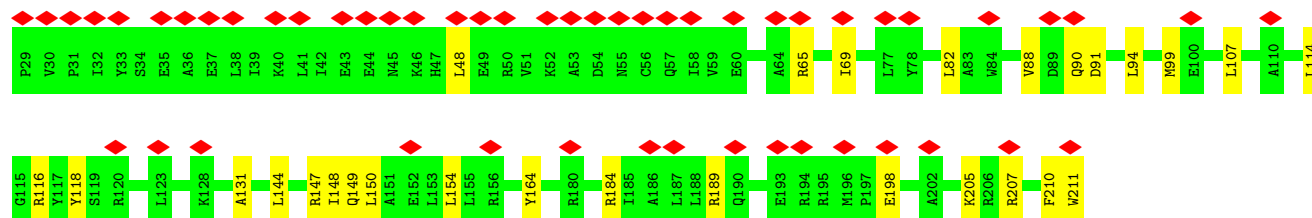
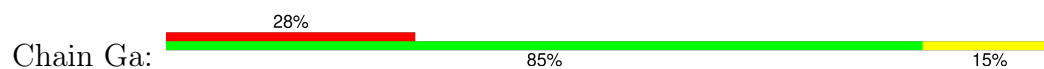
• Molecule 8: Sodium-type flagellar protein MotX



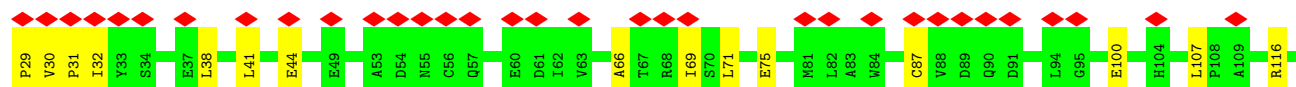
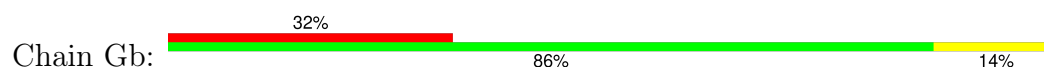
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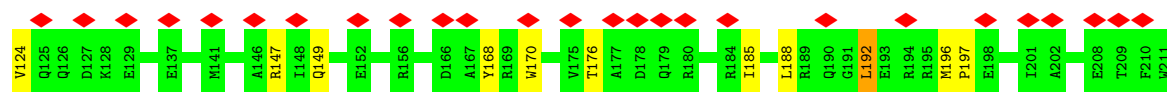


• Molecule 8: Sodium-type flagellar protein MotX

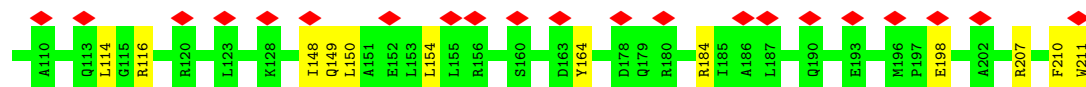
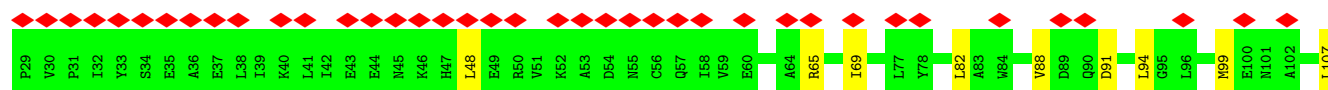
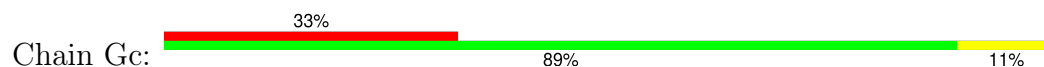


• Molecule 8: Sodium-type flagellar protein MotX

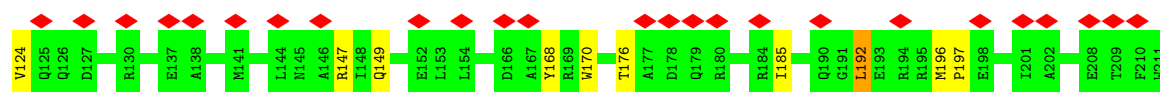
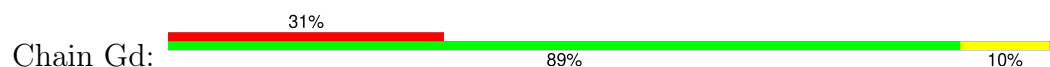




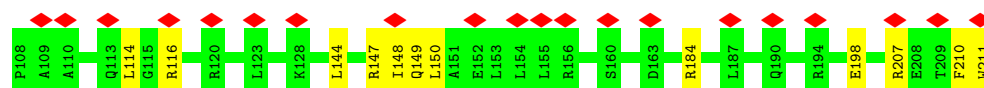
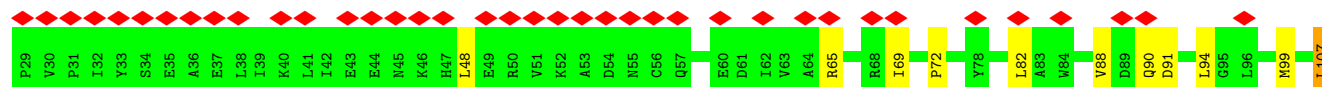
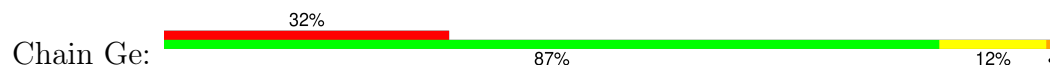
• Molecule 8: Sodium-type flagellar protein MotX



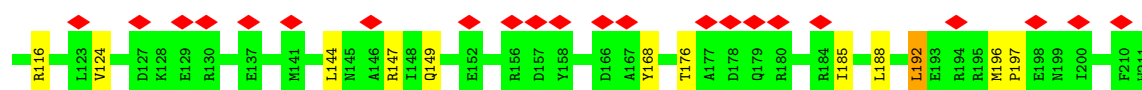
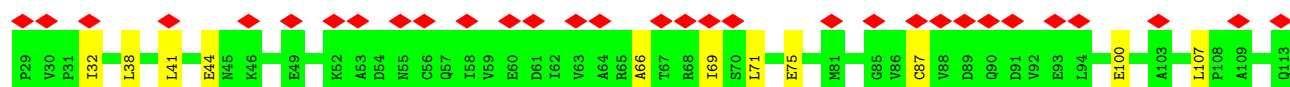
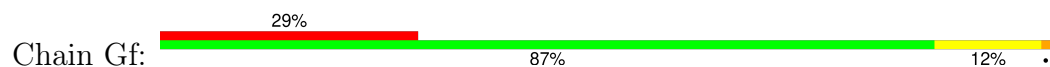
• Molecule 8: Sodium-type flagellar protein MotX



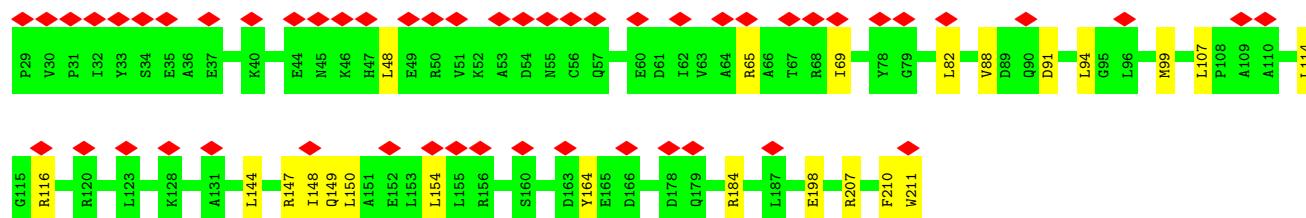
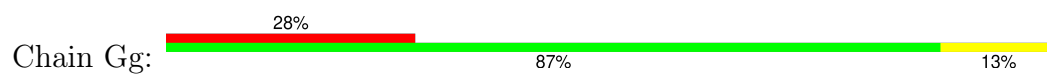
• Molecule 8: Sodium-type flagellar protein MotX



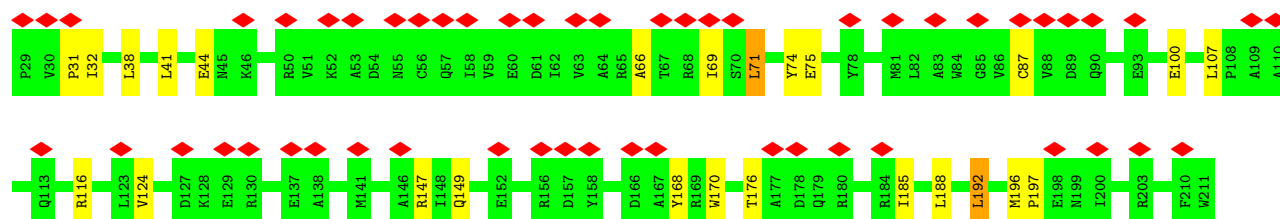
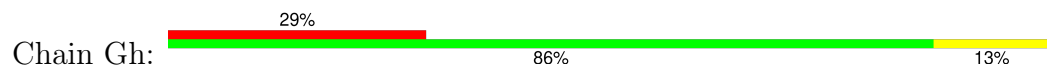
• Molecule 8: Sodium-type flagellar protein MotX



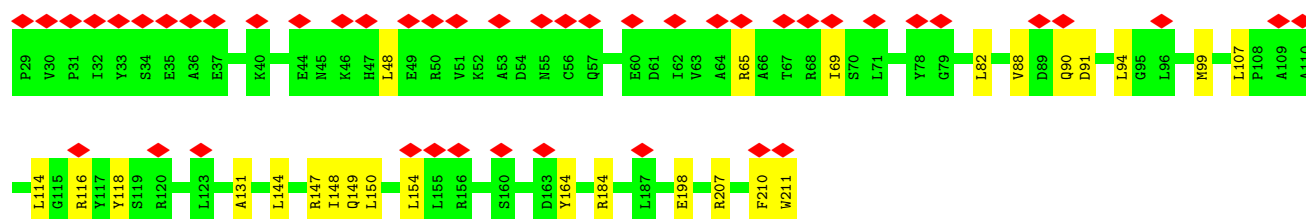
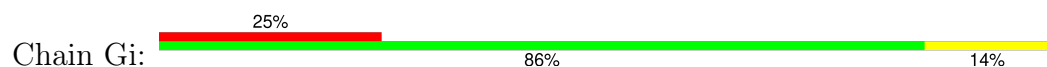
• Molecule 8: Sodium-type flagellar protein MotX



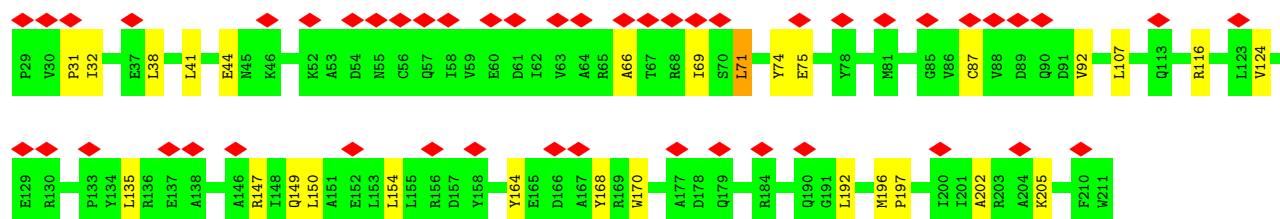
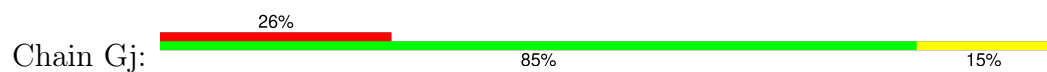
• Molecule 8: Sodium-type flagellar protein MotX



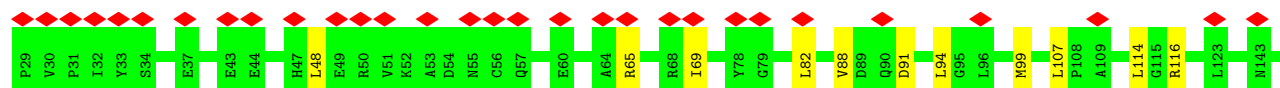
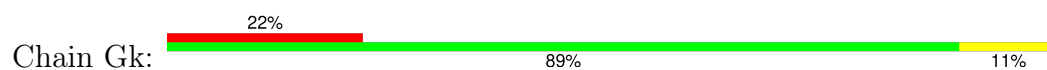
• Molecule 8: Sodium-type flagellar protein MotX

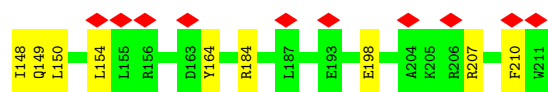


• Molecule 8: Sodium-type flagellar protein MotX

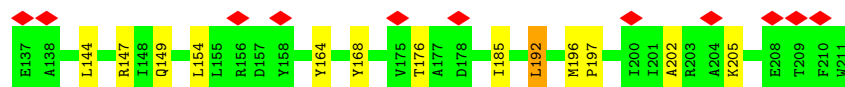
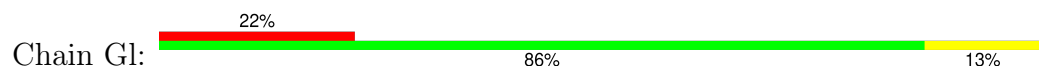


• Molecule 8: Sodium-type flagellar protein MotX

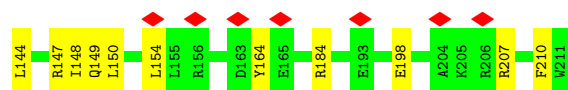
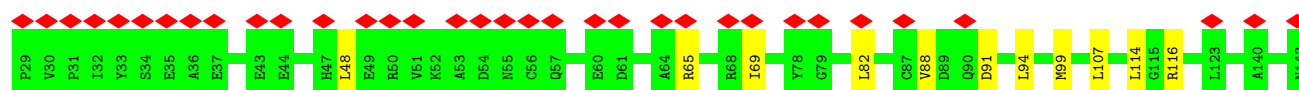
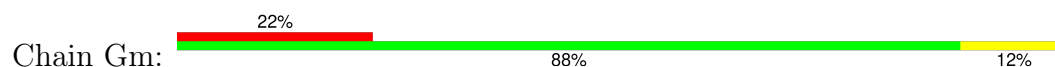




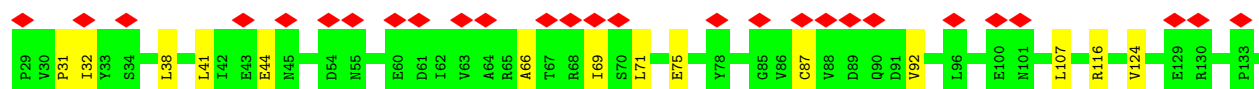
• Molecule 8: Sodium-type flagellar protein MotX



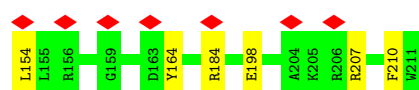
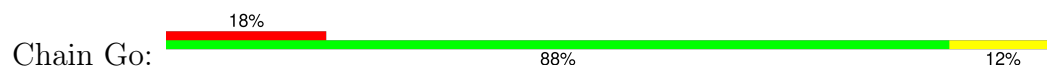
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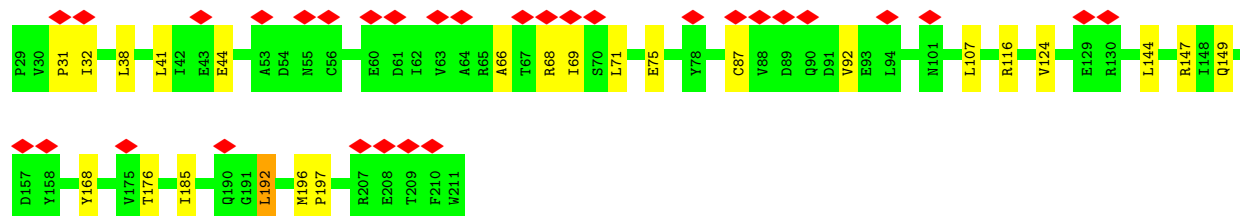
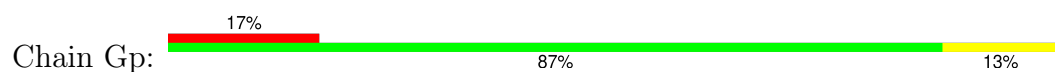
• Molecule 8: Sodium-type flagellar protein MotX



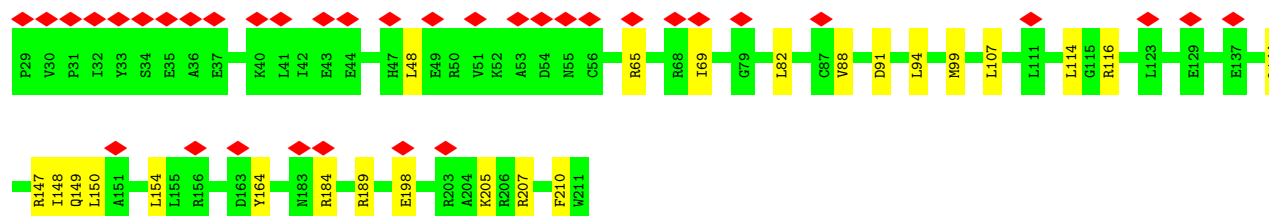
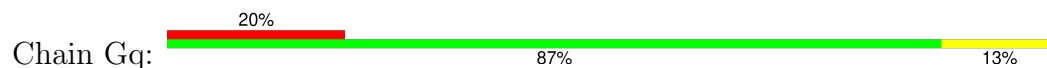
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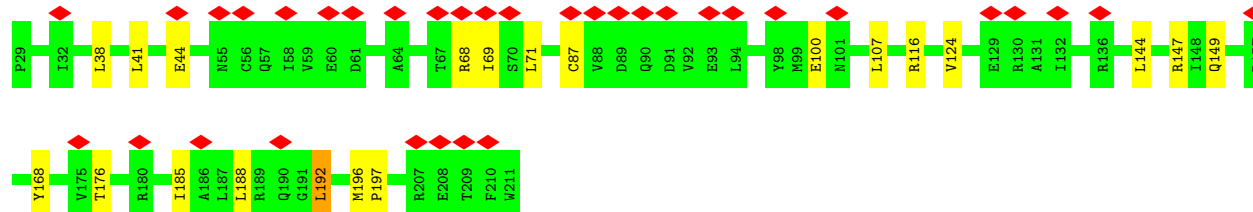
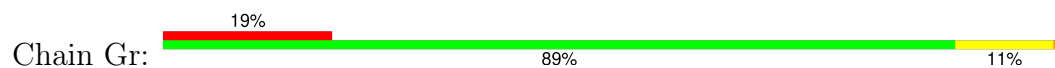
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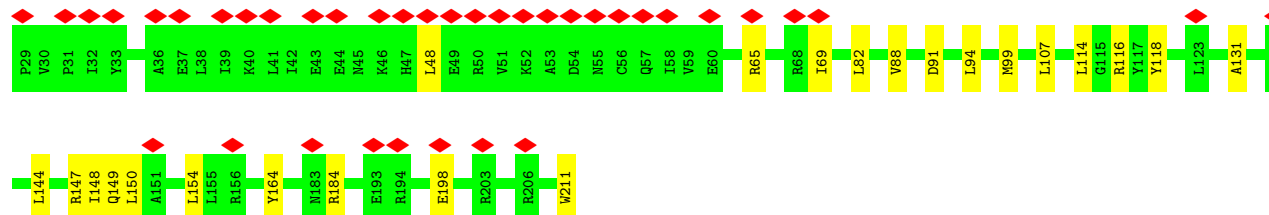
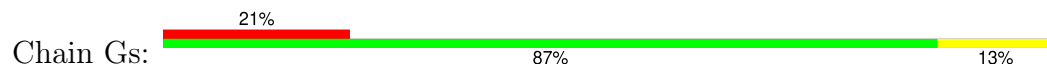
- Molecule 8: Sodium-type flagellar protein MotX



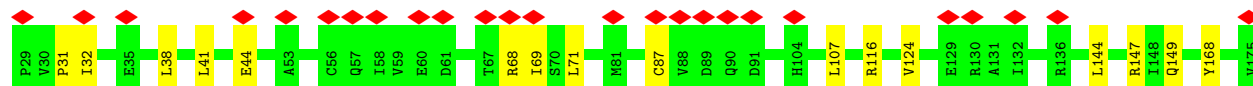
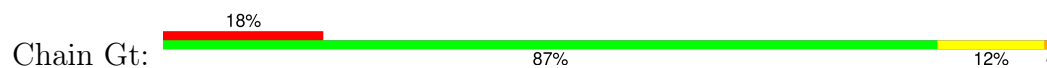
- Molecule 8: Sodium-type flagellar protein MotX



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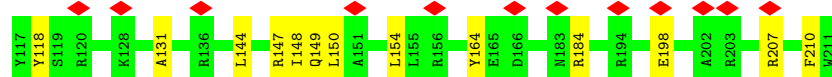
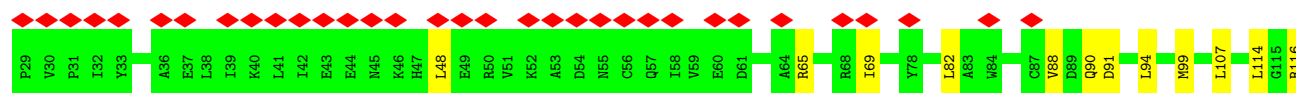
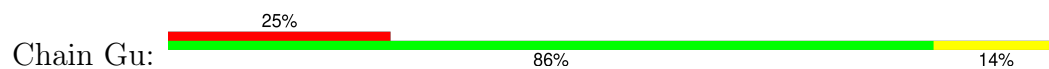


- Molecule 8: Sodium-type flagellar protein MotX

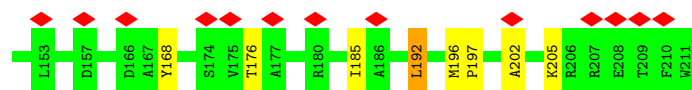
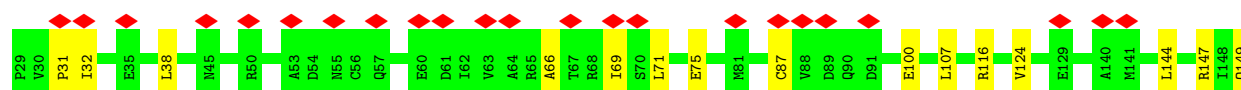
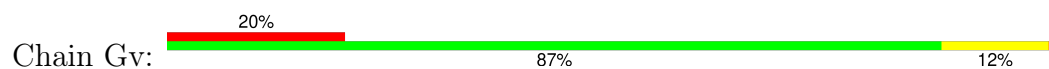




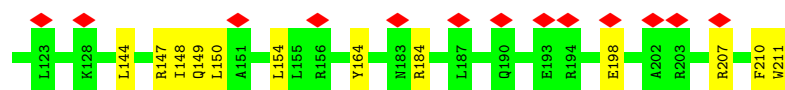
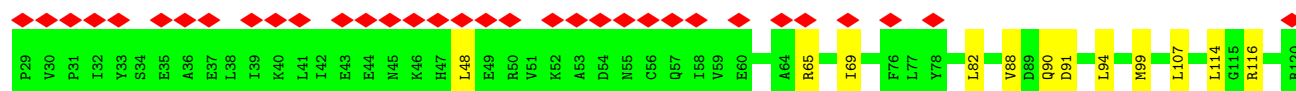
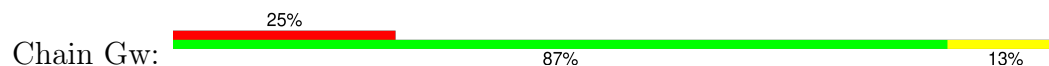
- Molecule 8: Sodium-type flagellar protein MotX



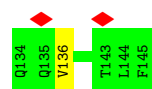
- Molecule 8: Sodium-type flagellar protein MotX



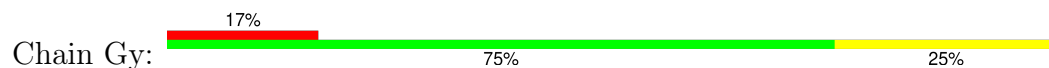
- Molecule 8: Sodium-type flagellar protein MotX

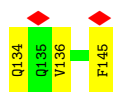


- Molecule 9: FlgP

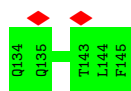


- Molecule 9: FlgP

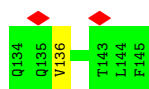




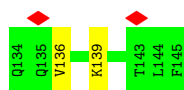
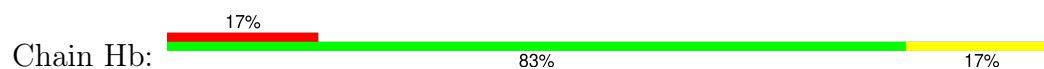
• Molecule 9: FlgP



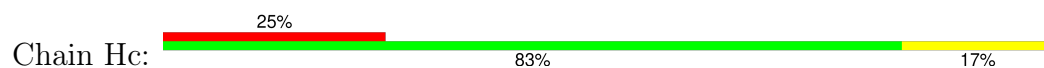
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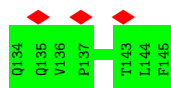
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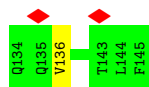
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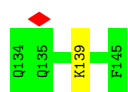
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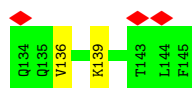
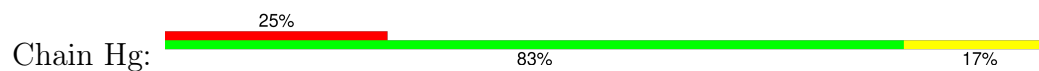
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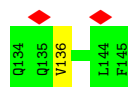
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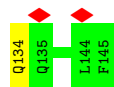
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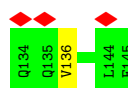
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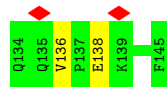
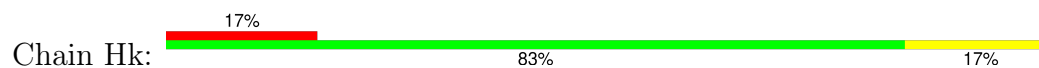
- Molecule 9: FlgP



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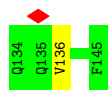


- Molecule 9: FlgP



- Molecule 9: FlgP





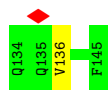
- Molecule 9: FlgP

Chain Hm: 100%

There are no outlier residues recorded for this chain.

- Molecule 9: FlgP

Chain Hn: 8% 92% 8%



- Molecule 9: FlgP

Chain Ho: 8% 100%



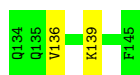
- Molecule 9: FlgP

Chain Hp: 17% 83% 17%



- Molecule 9: FlgP

Chain Hq: 83% 17%



- Molecule 9: FlgP

Chain Hr: 17% 83% 17%

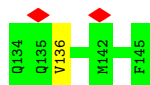
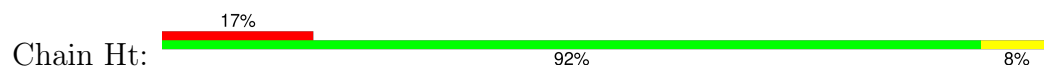


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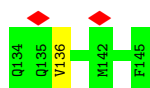
Chain Hs: 92% 8%



- Molecule 9: FlgP



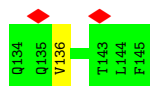
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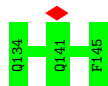
- Molecule 9: FlgP



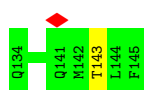
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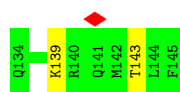
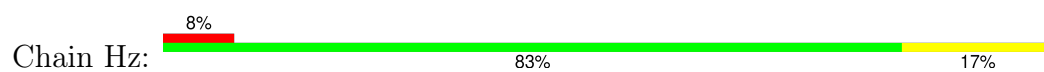
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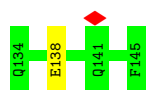
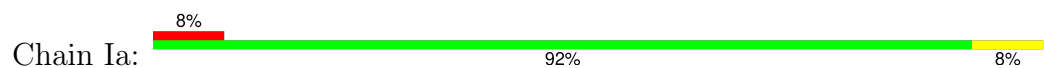
- Molecule 9: FlgP



- Molecule 9: FlgP



- Molecule 9: FlgP

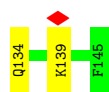
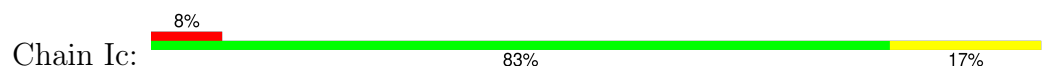


- Molecule 9: FlgP

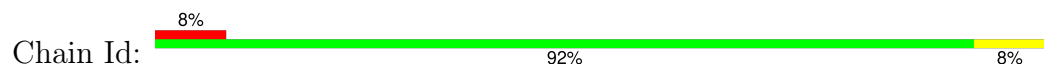


There are no outlier residues recorded for this chain.

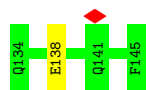
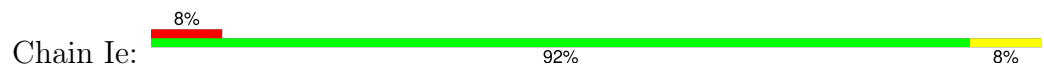
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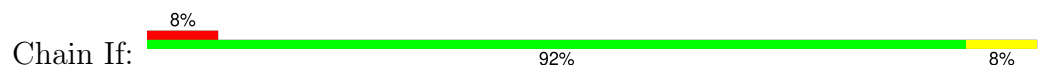
- Molecule 9: FlgP



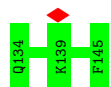
- Molecule 9: FlgP



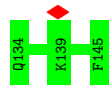
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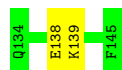
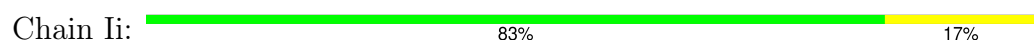
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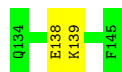
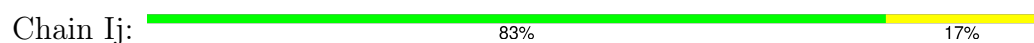
- Molecule 9: FlgP



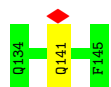
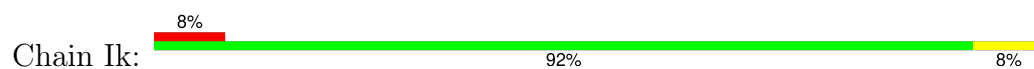
- Molecule 9: FlgP



- Molecule 9: FlgP



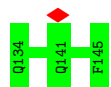
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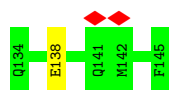
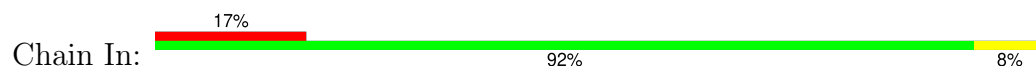
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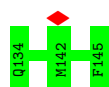
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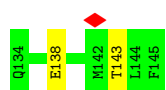
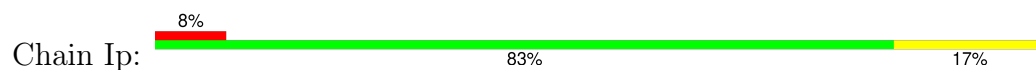
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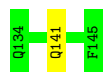
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• Molecule 9: FlgP



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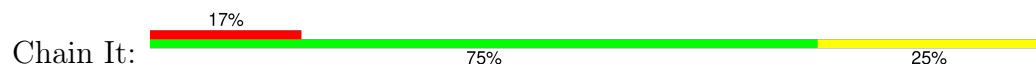
• Molecule 9: FlgP



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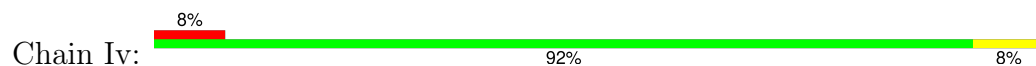




• Molecule 9: FlgP



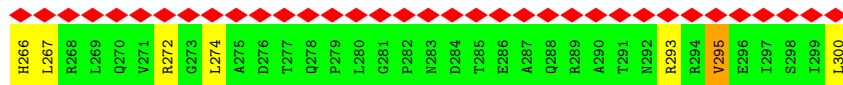
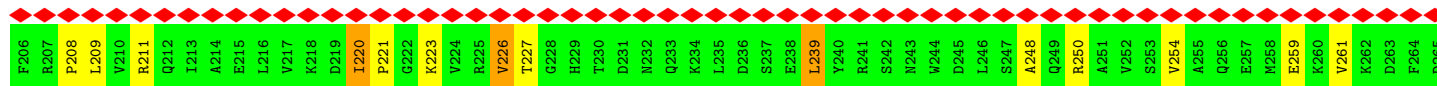
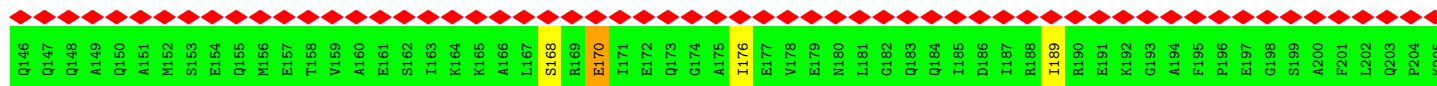
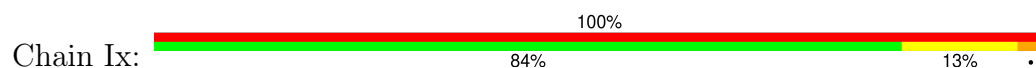
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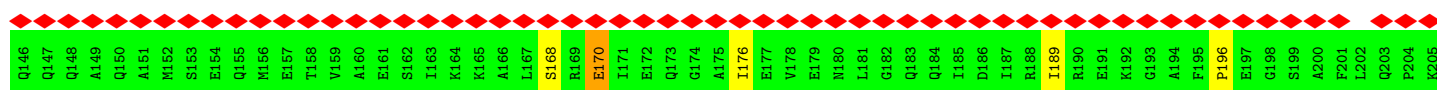
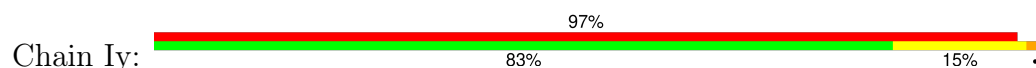
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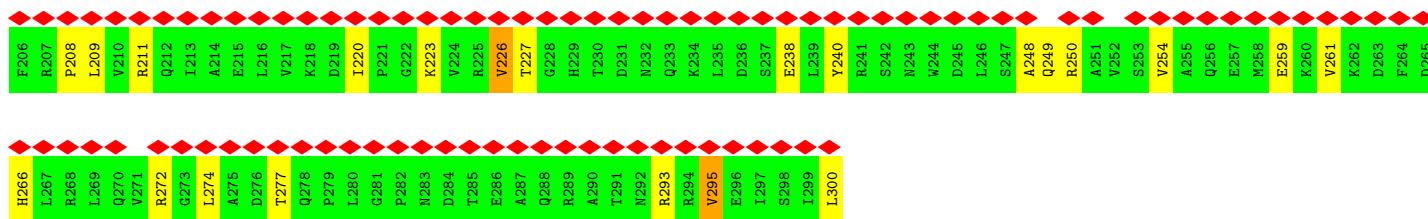


• Molecule 10: Chemotaxis protein PomB

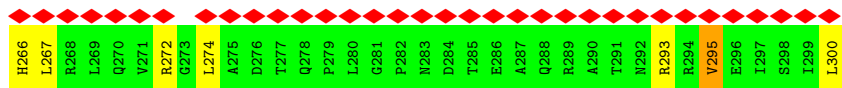
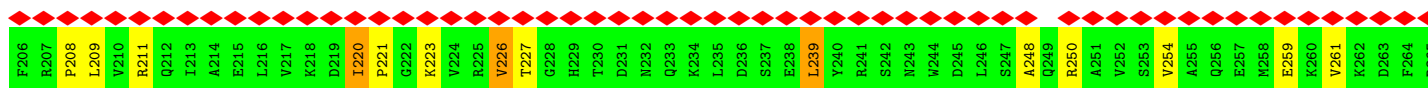
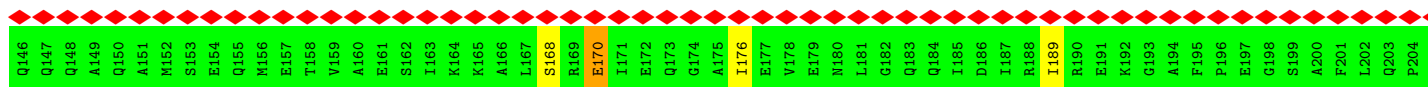
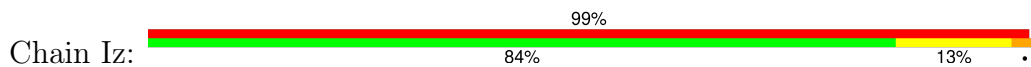


• Molecule 10: Chemotaxis protein PomB

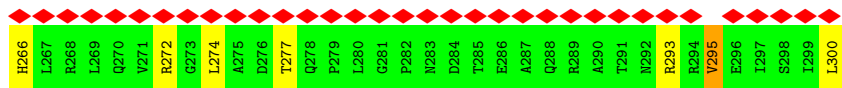
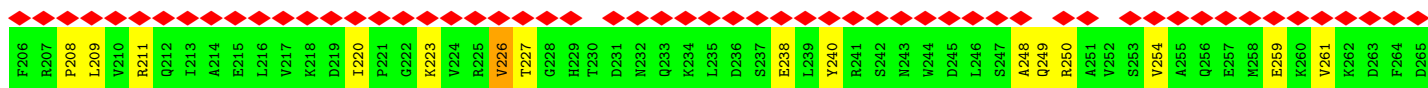
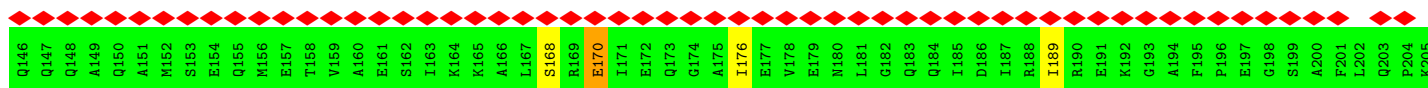
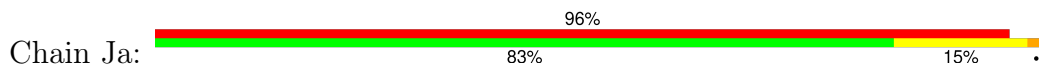




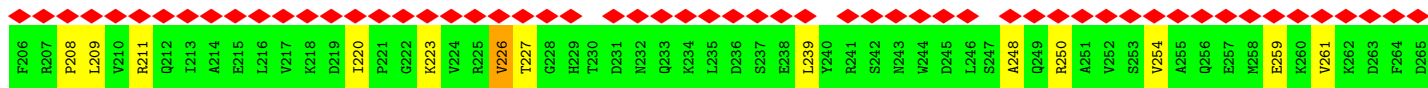
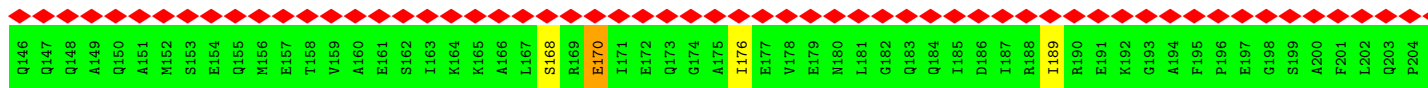
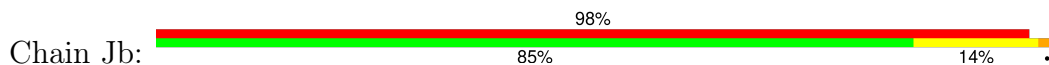
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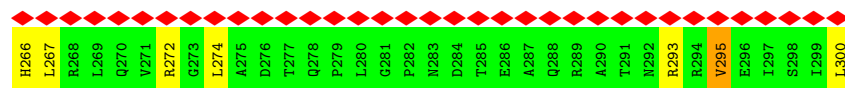


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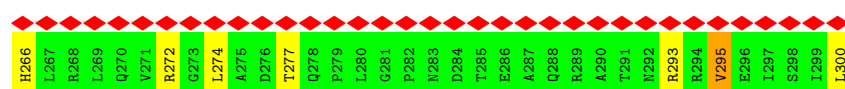
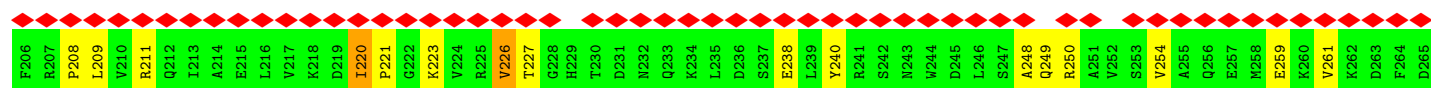
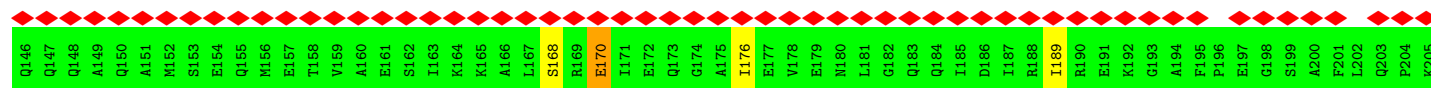
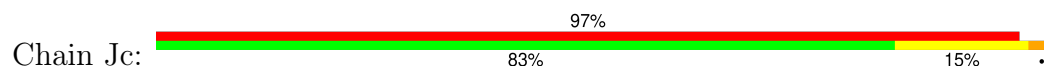


• Molecule 10: Chemotaxis protein PomB

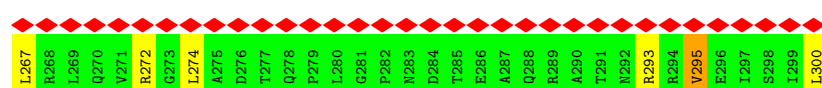
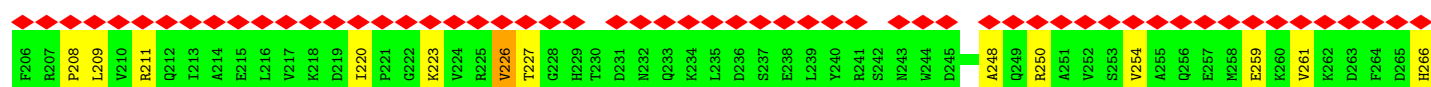
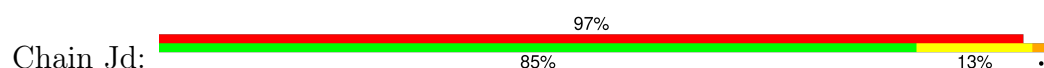




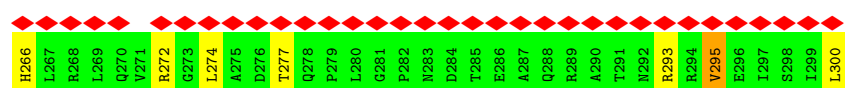
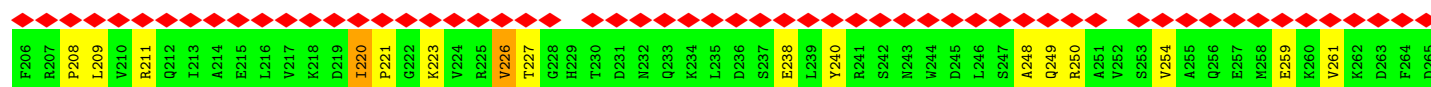
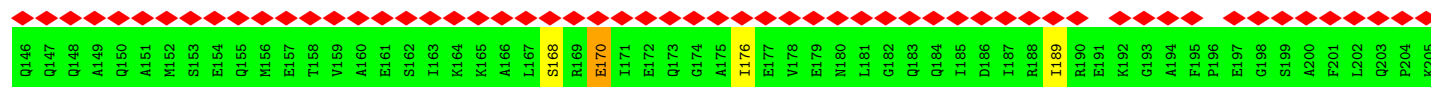
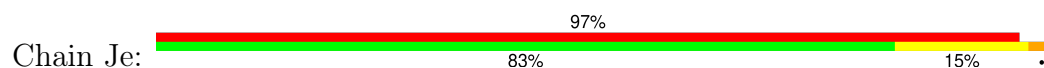
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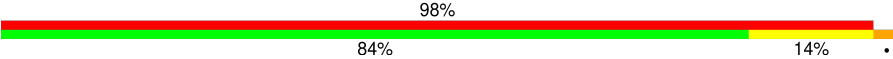
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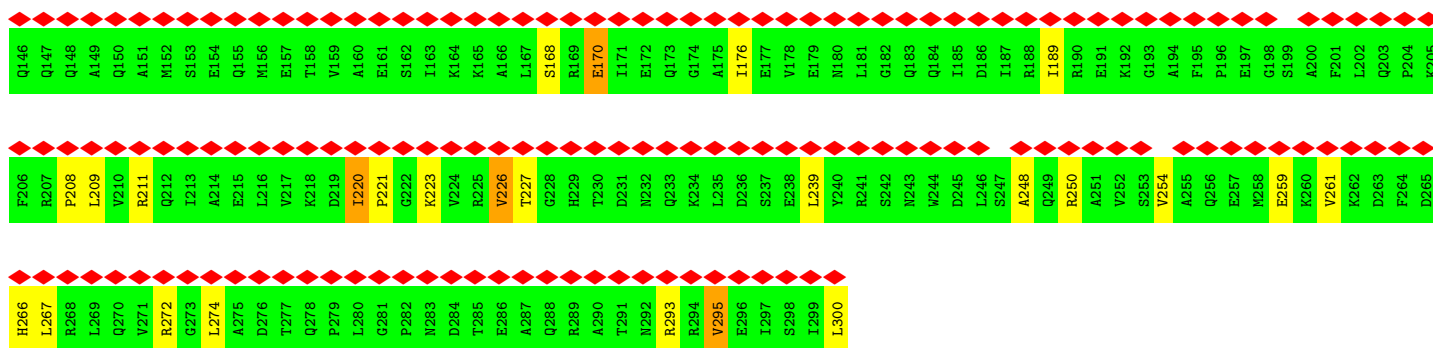


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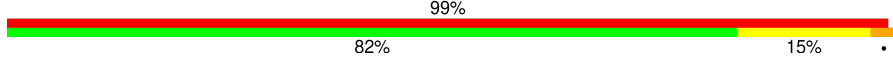


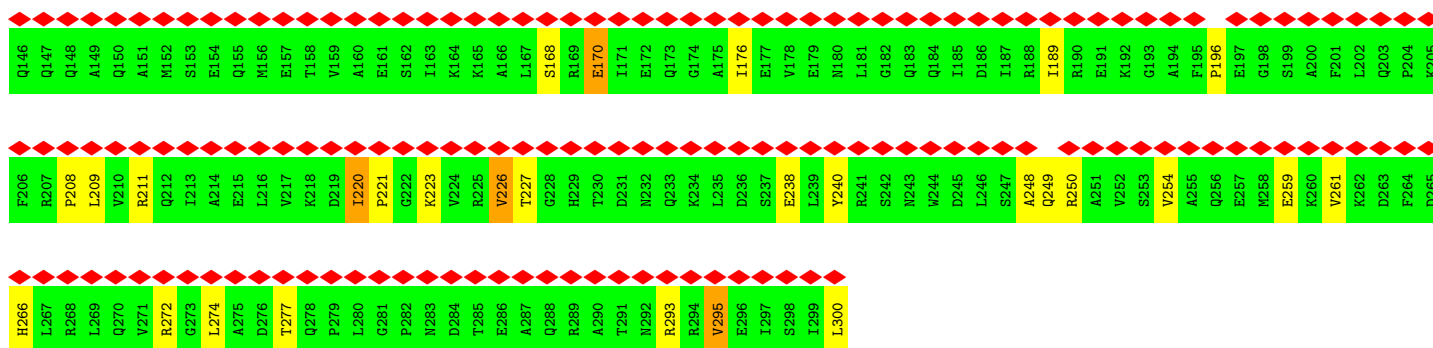
• Molecule 10: Chemotaxis protein PomB

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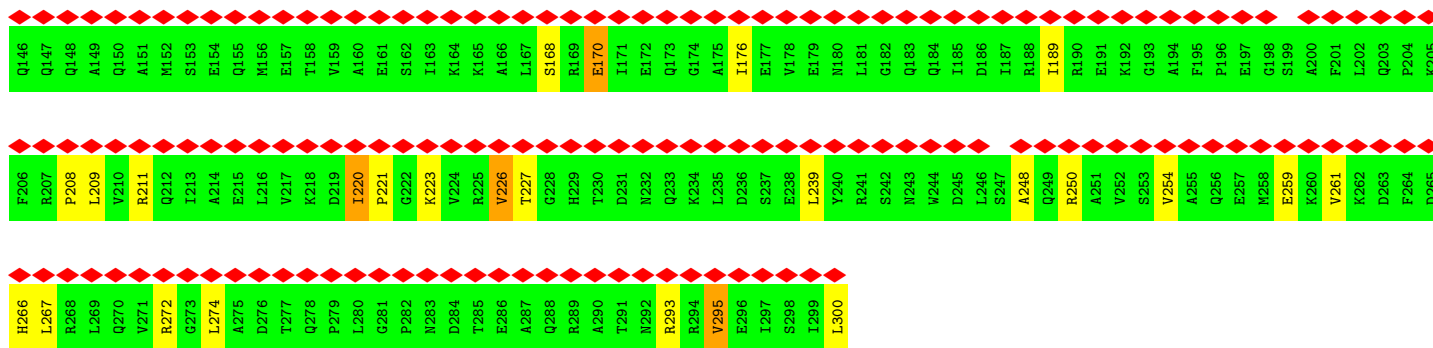
• Molecule 10: Chemotaxis protein PomB

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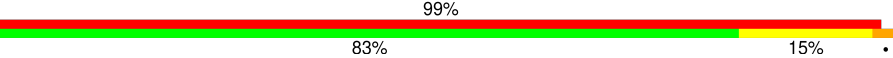


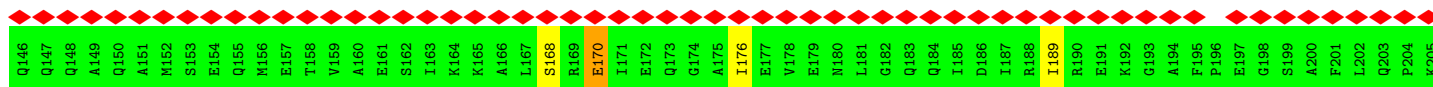
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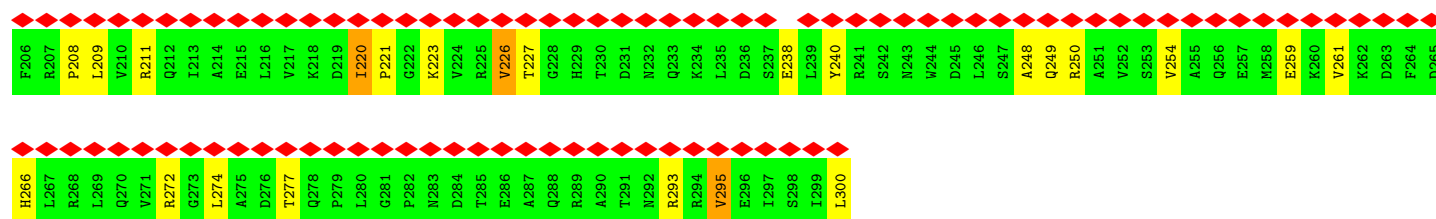
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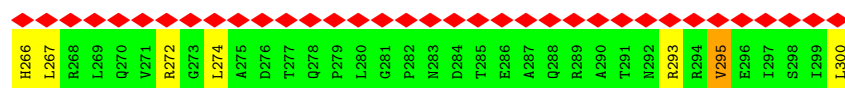
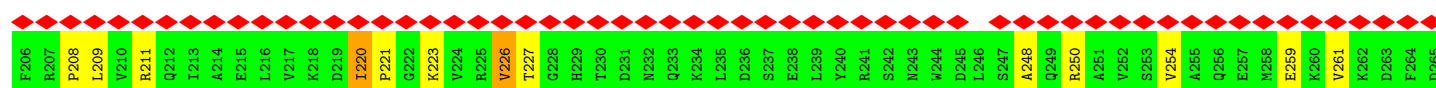
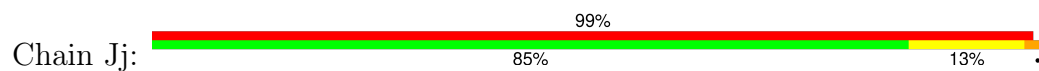
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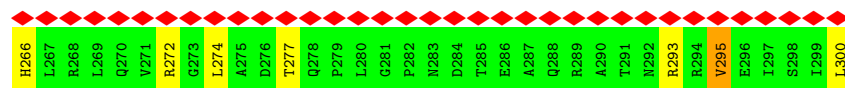
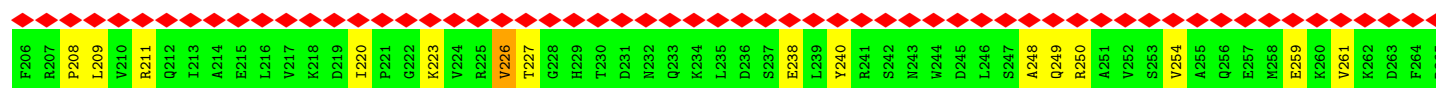
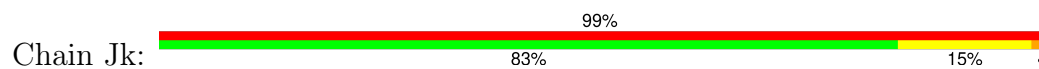




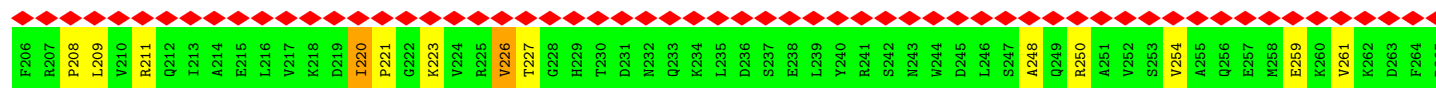
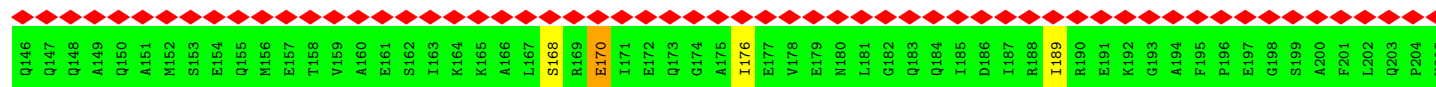
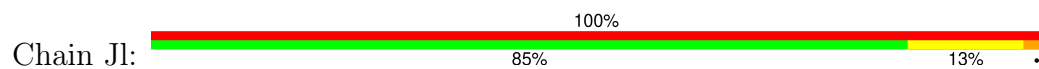
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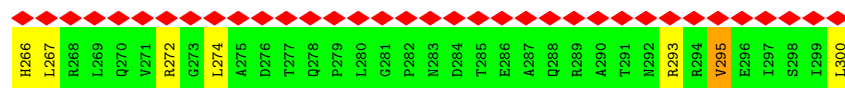


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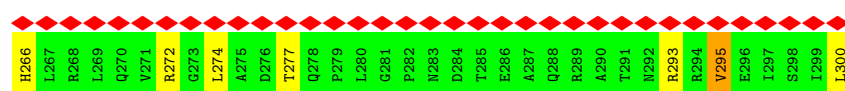
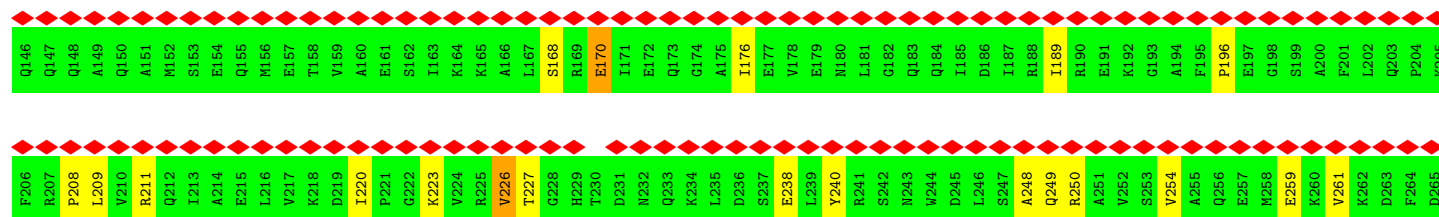
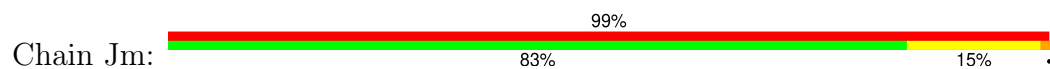


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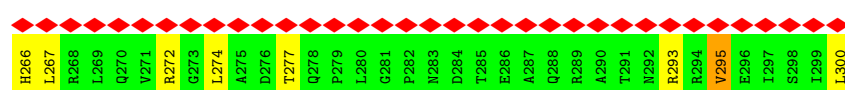
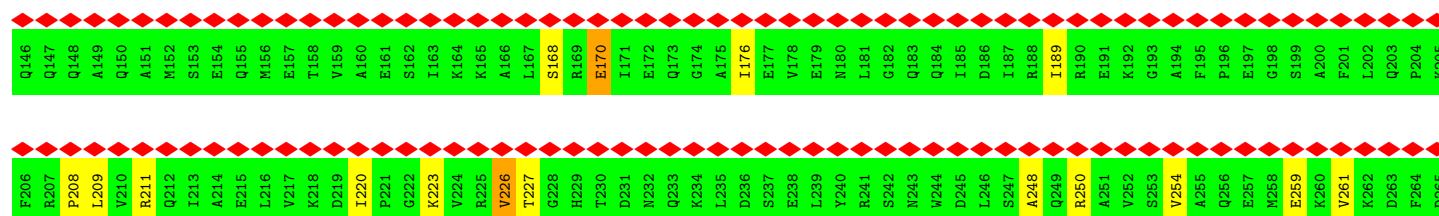
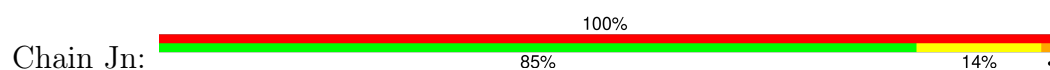




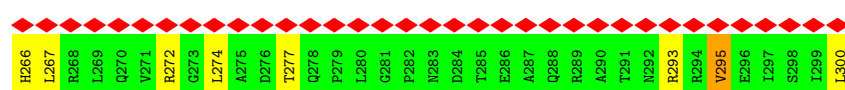
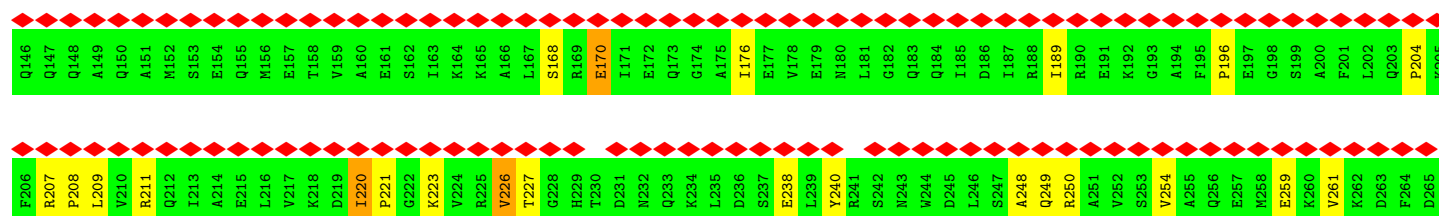
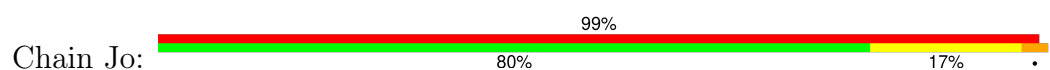
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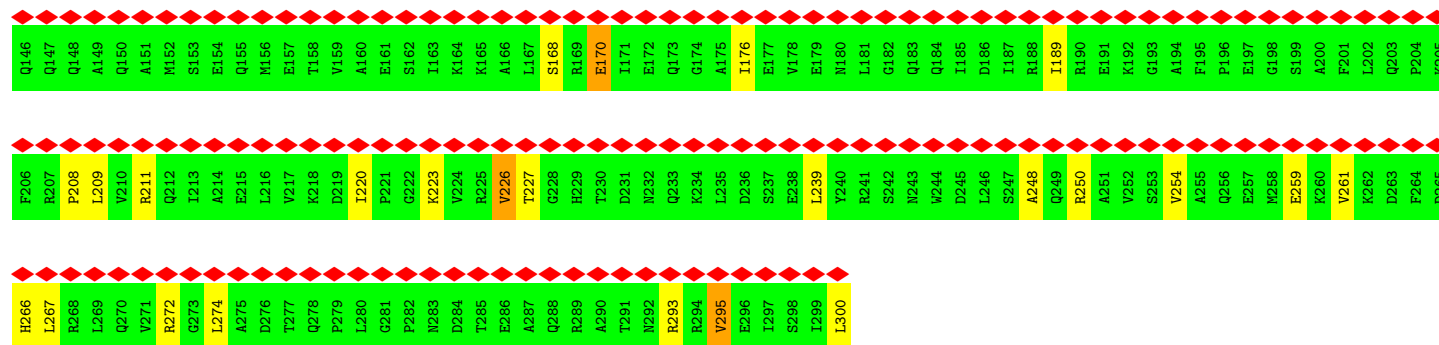
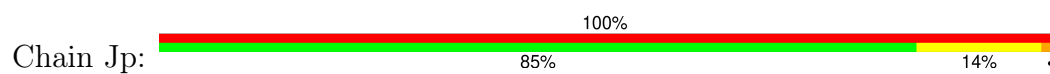
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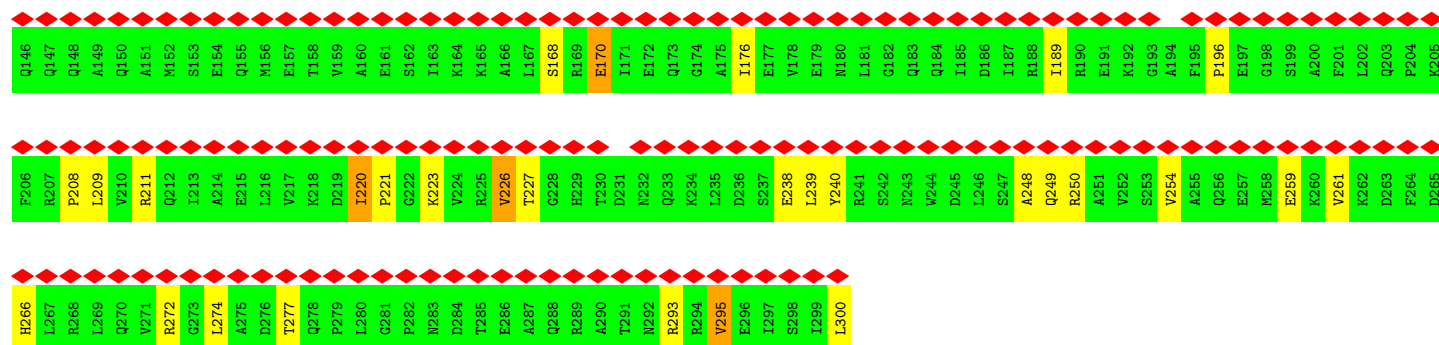
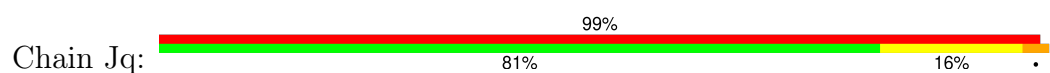
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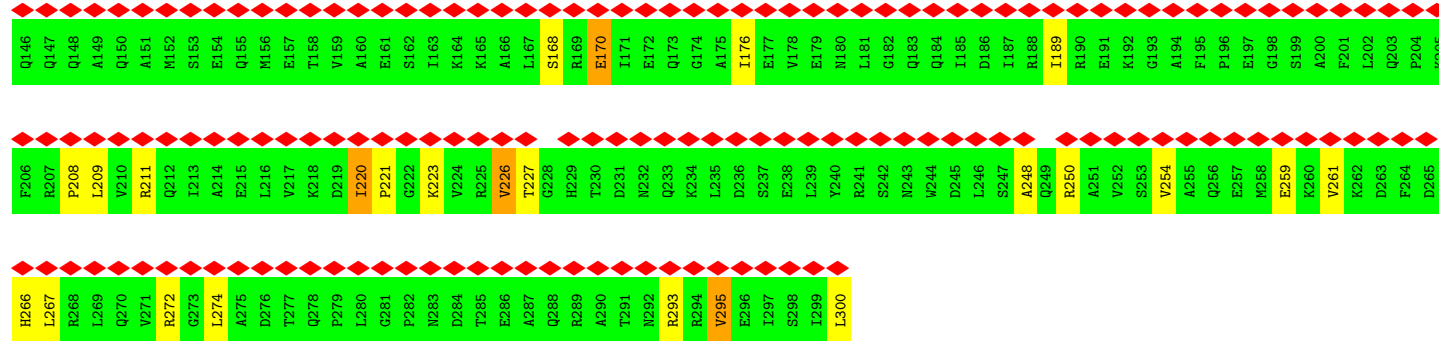
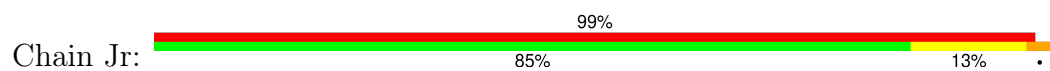
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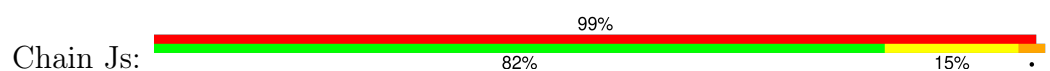
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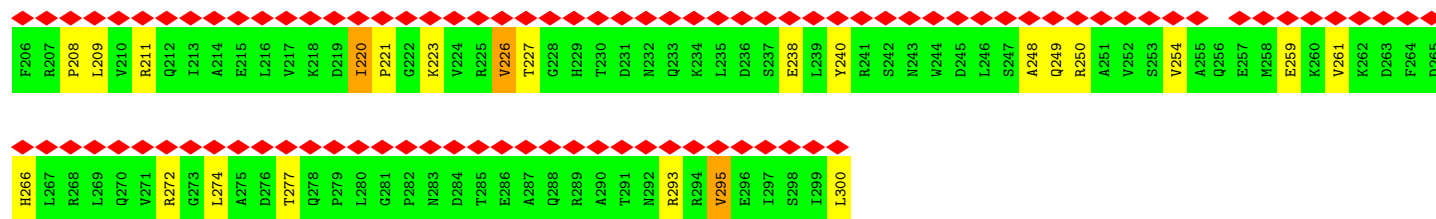


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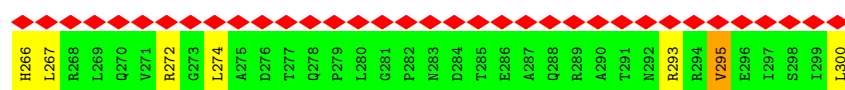
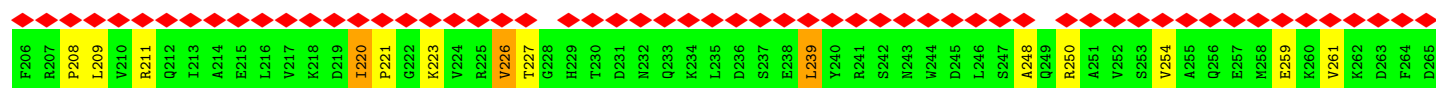
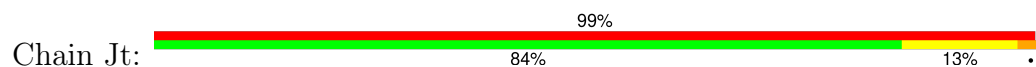


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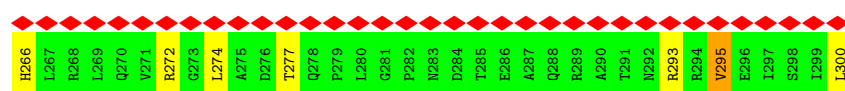
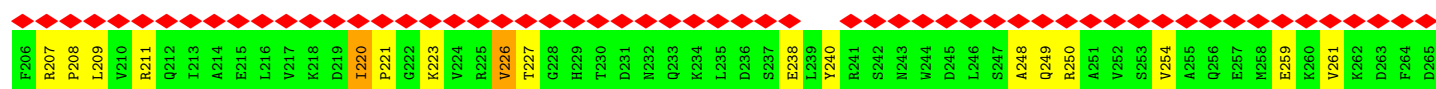
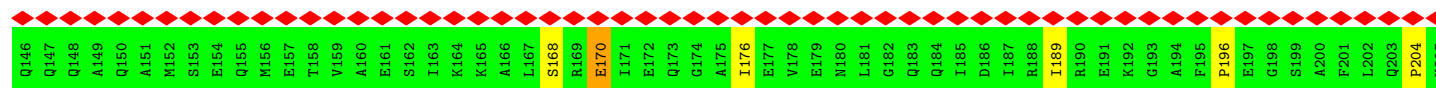
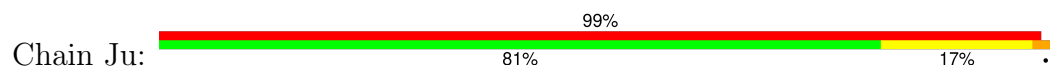




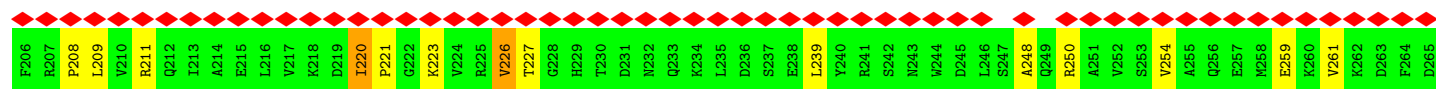
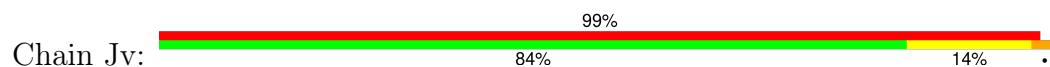
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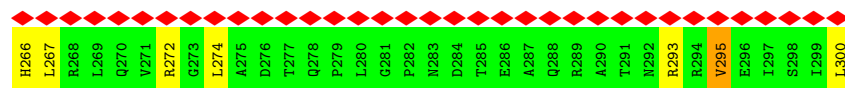


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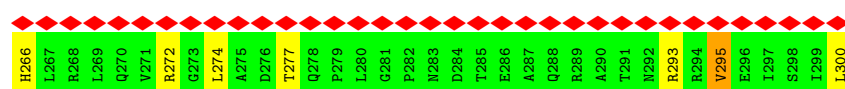
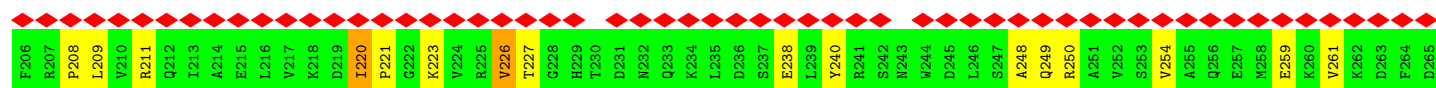
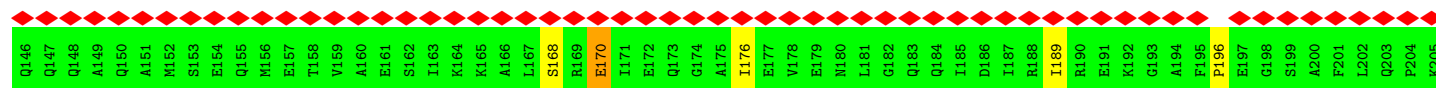
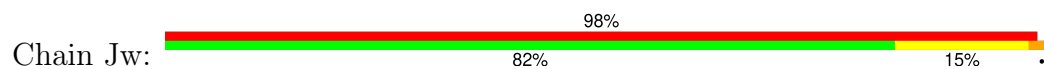


• Molecule 10: Chemotaxis protein PomB

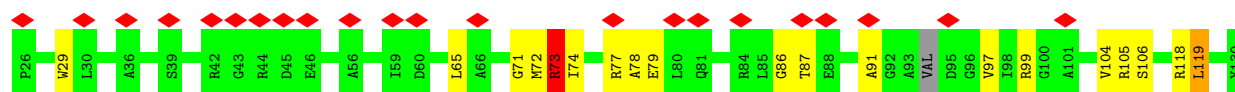
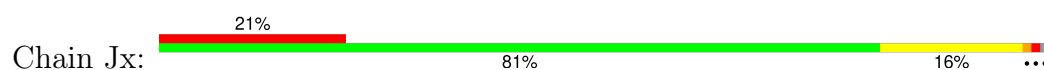




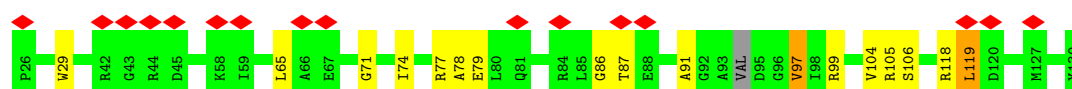
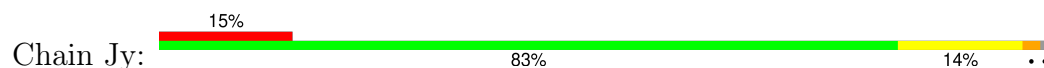
• Molecule 10: Chemotaxis protein PomB



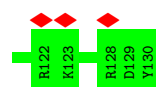
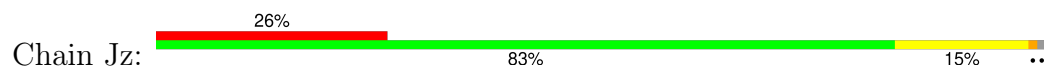
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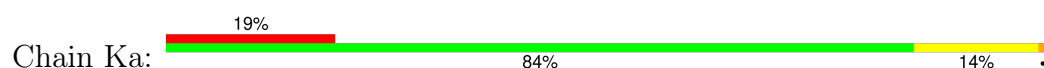
• Molecule 11: Lipoprotein



• Molecule 11: Lipoprotein

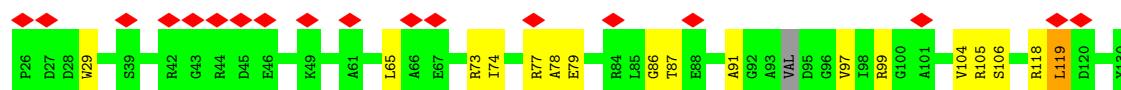
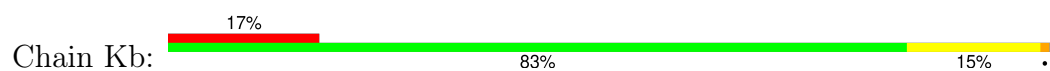


• Molecule 11: Lipoprotein

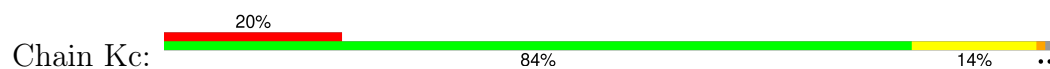




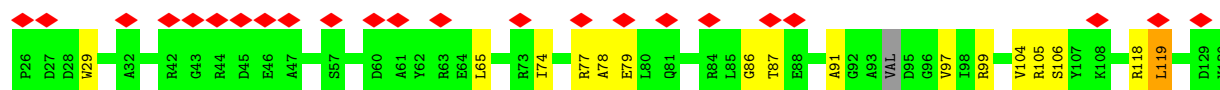
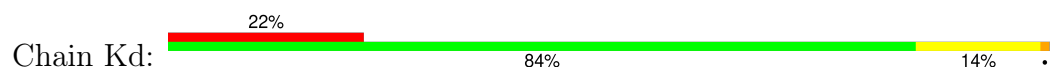
- Molecule 11: Lipoprotein



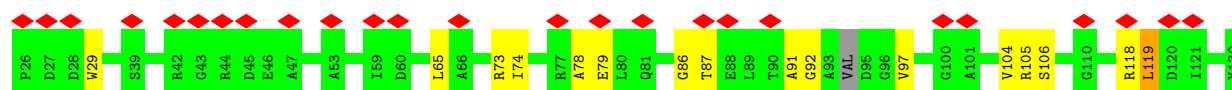
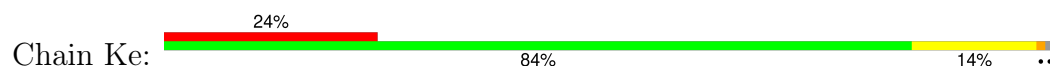
- Molecule 11: Lipoprotein



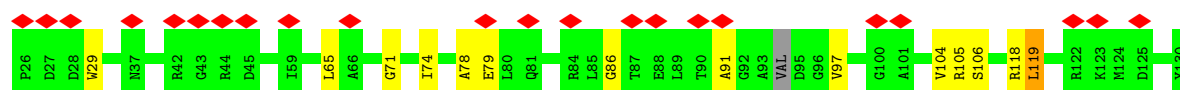
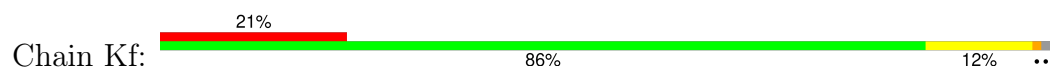
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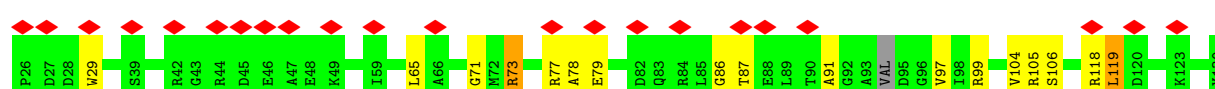
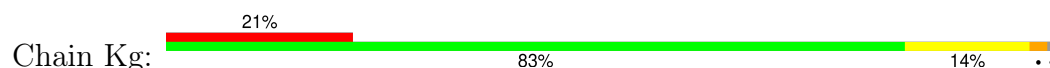
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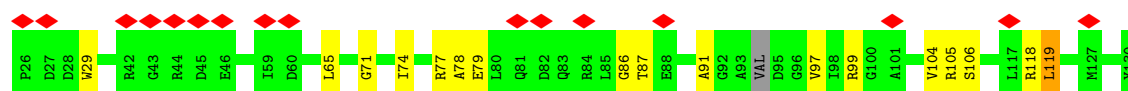
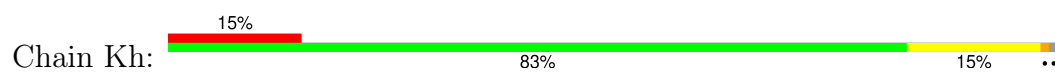
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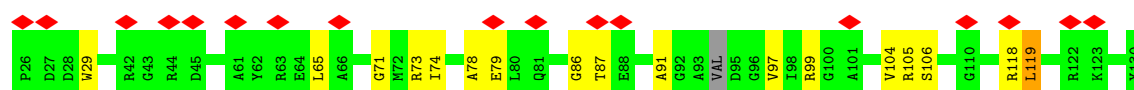
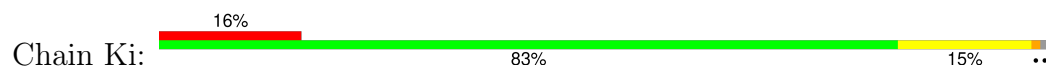
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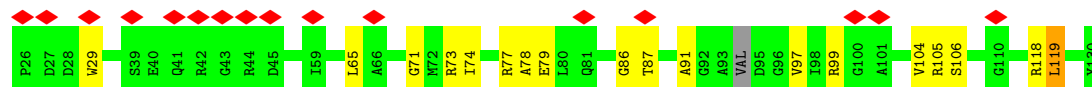
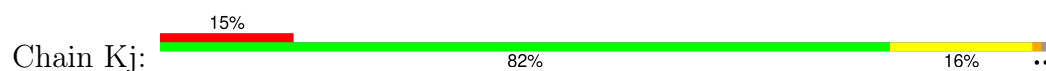
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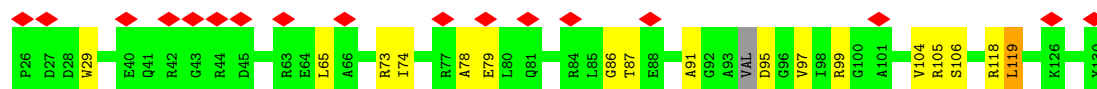
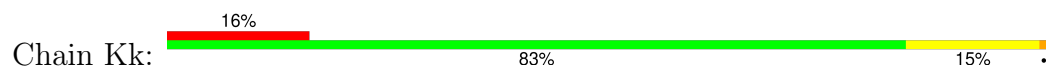
• Molecule 11: Lipoprotein



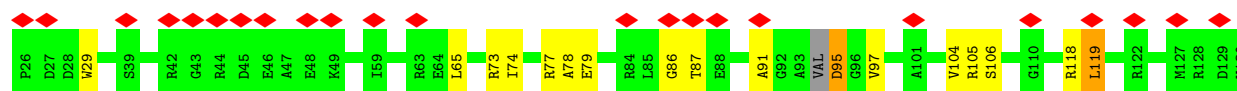
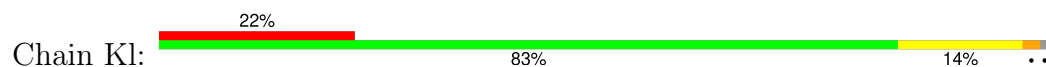
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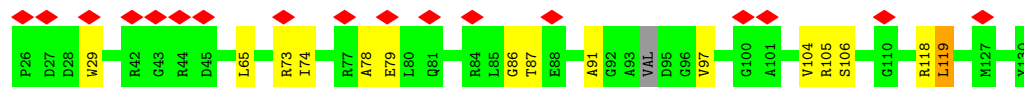
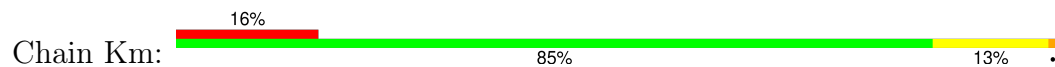
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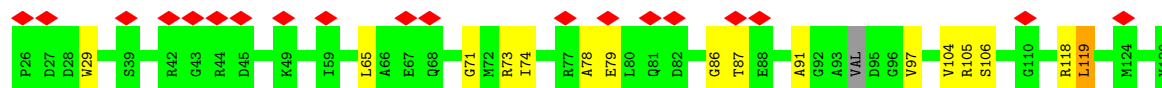
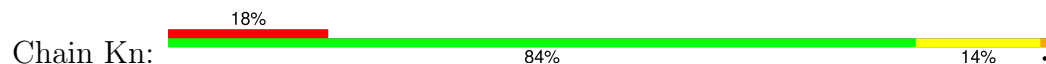
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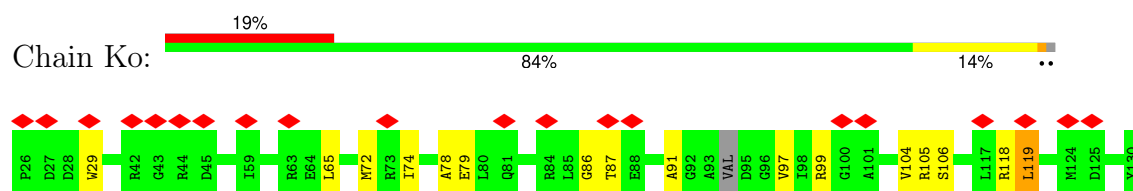
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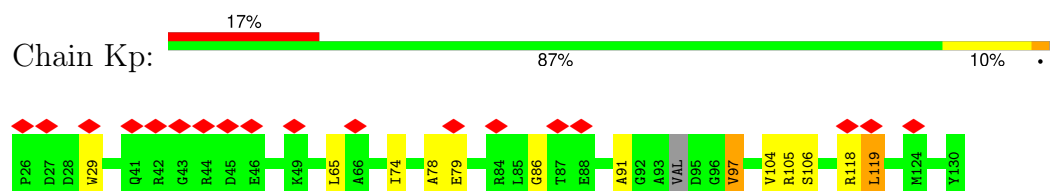
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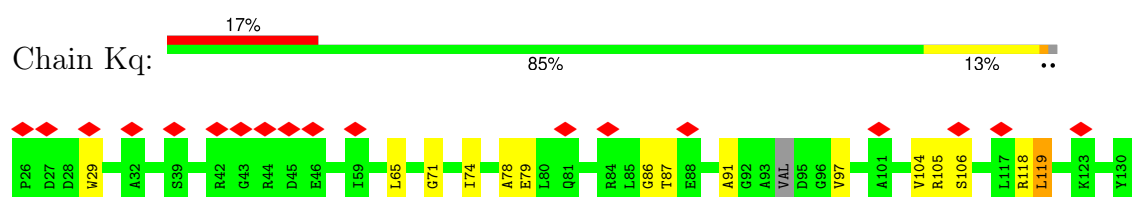
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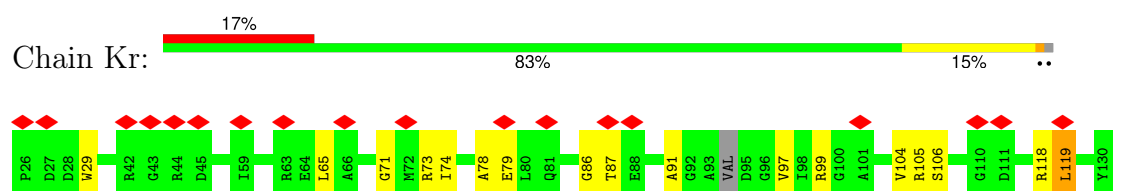
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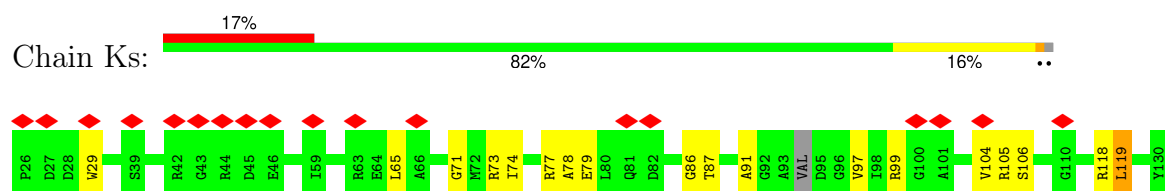
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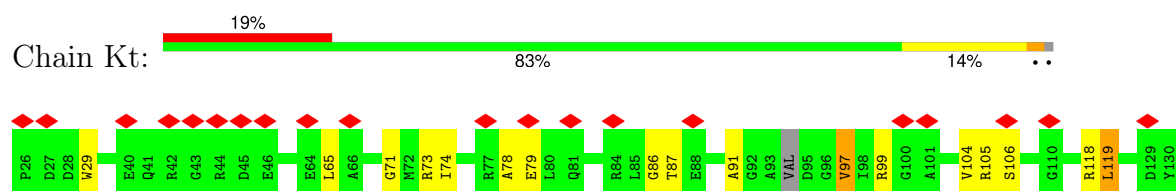
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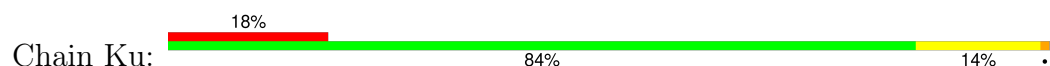
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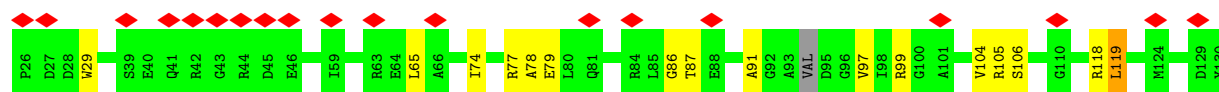


● Molecule 11: Lipoprotein

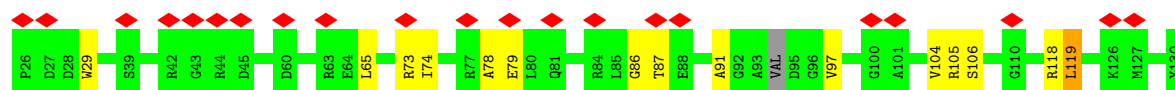
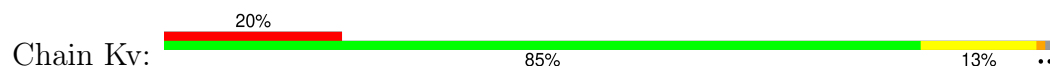


● Molecule 11: Lipoprotein

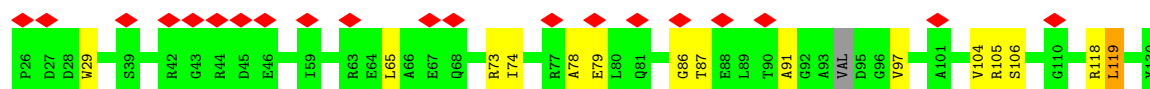
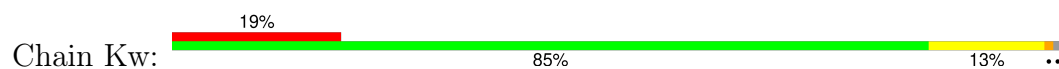




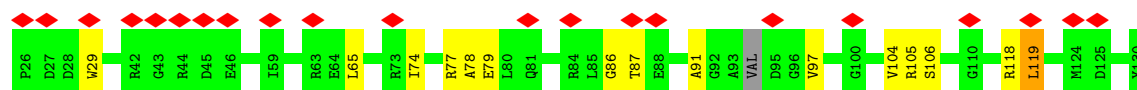
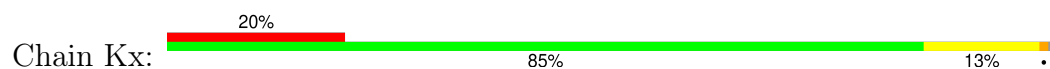
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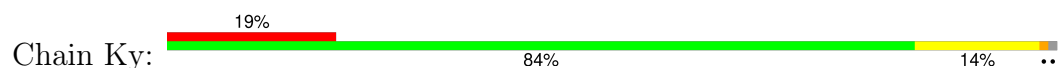
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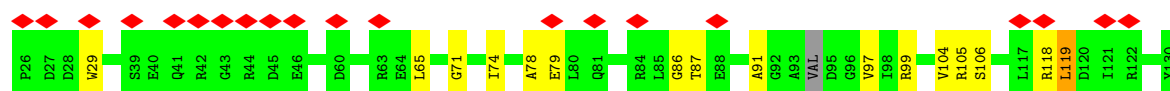
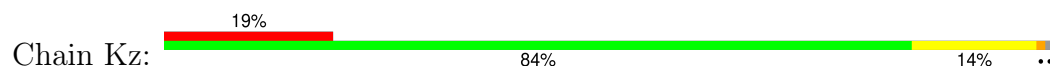
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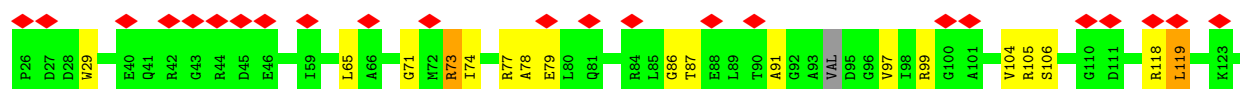
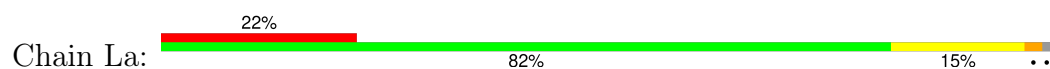
• Molecule 11: Lipoprotein



• Molecule 11: Lipoprotein



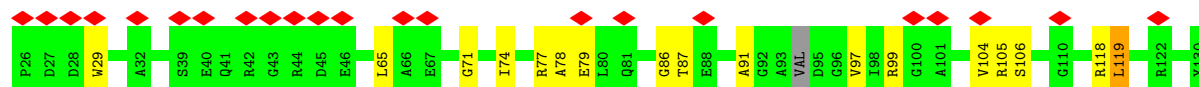
• Molecule 11: Lipoprotein



Y130

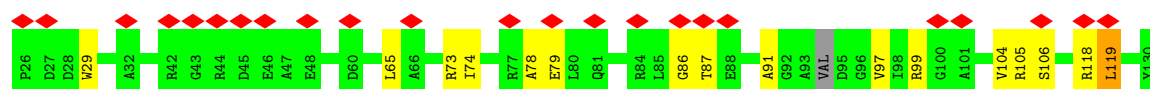
• Molecule 11: Lipoprotein

Chain Lb: 21% 83% 15% ..



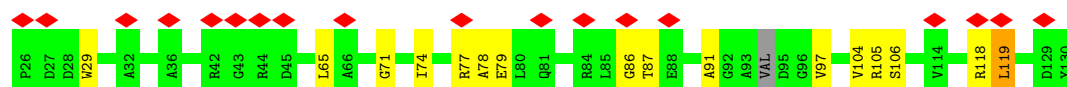
• Molecule 11: Lipoprotein

Chain Lc: 22% 84% 14% ..



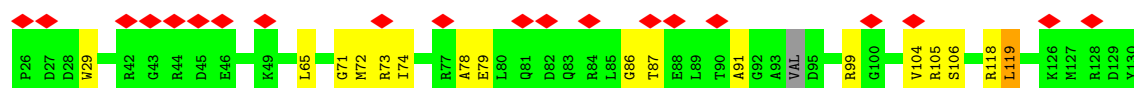
• Molecule 11: Lipoprotein

Chain Ld: 17% 84% 14% ..



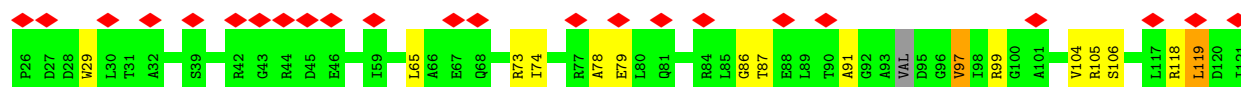
• Molecule 11: Lipoprotein

Chain Le: 19% 83% 15% ..



• Molecule 11: Lipoprotein

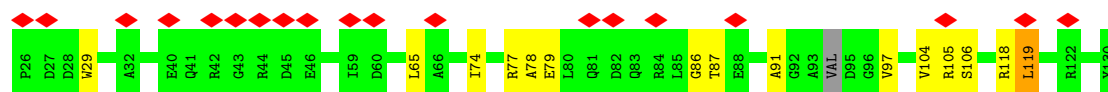
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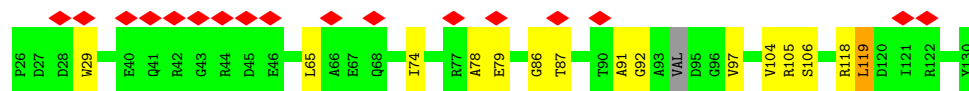
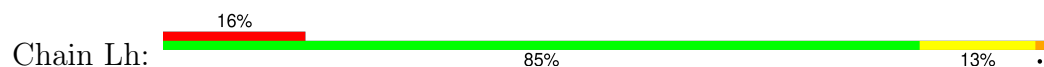
R122 Y130

• Molecule 11: Lipoprotein

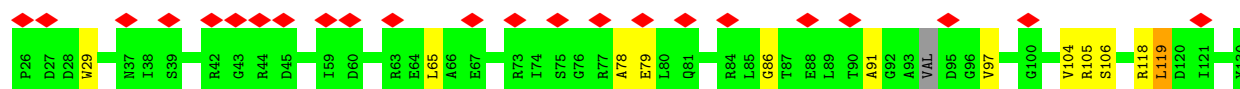
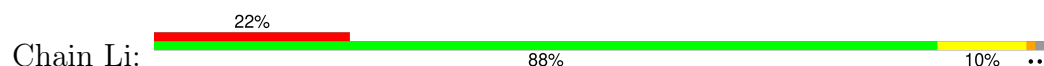
Chain Lg: 18% 85% 13% ..



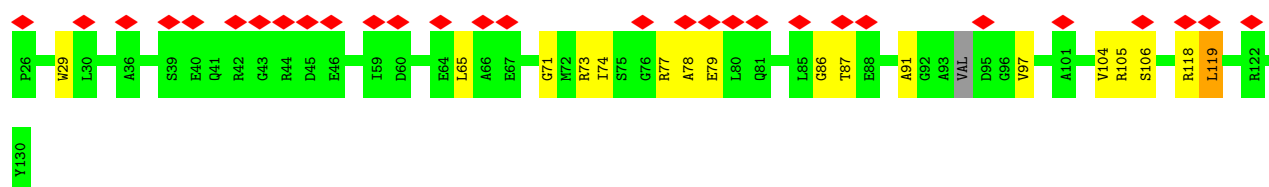
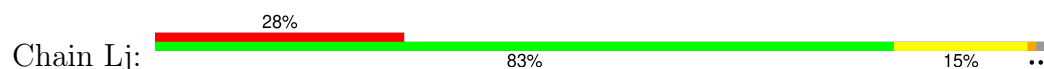
- Molecule 11: Lipoprotein



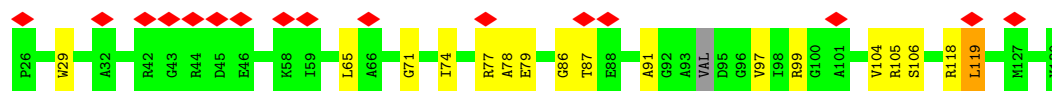
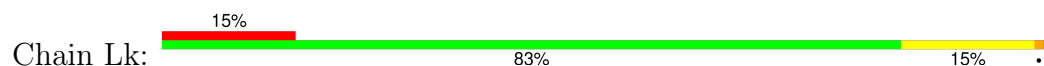
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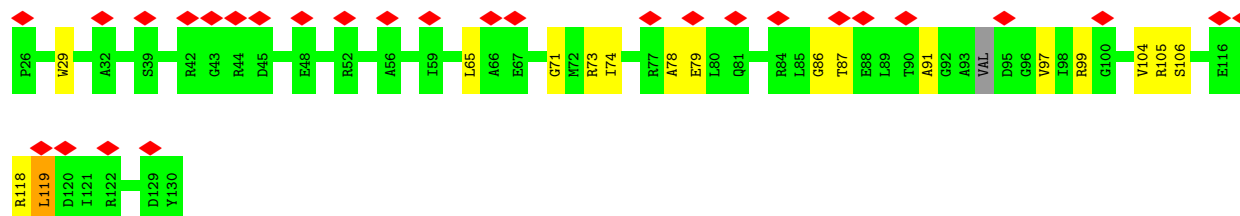
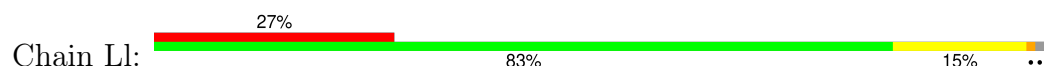
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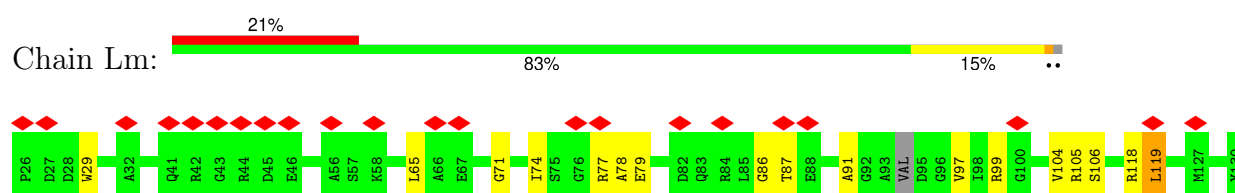
- Molecule 11: Lipoprotein



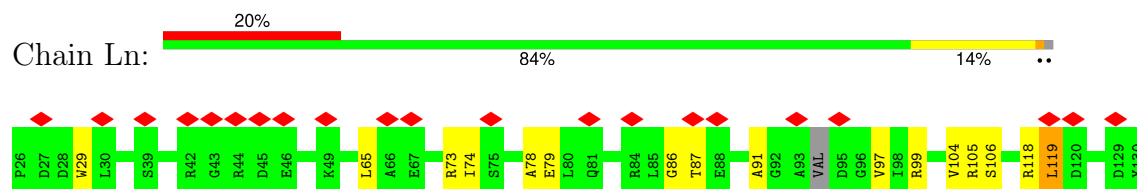
- Molecule 11: Lipoprotein



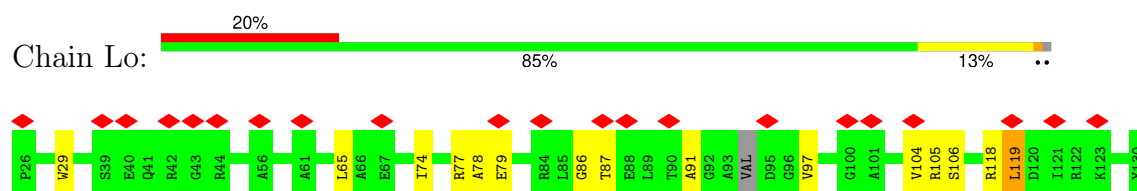
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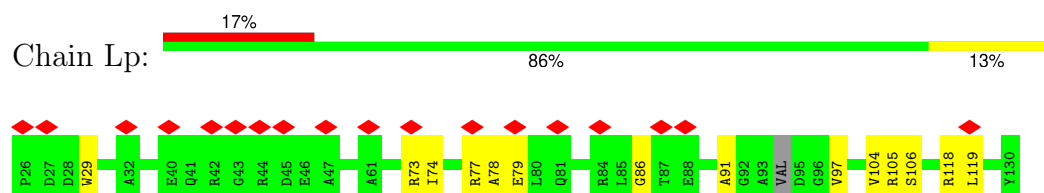
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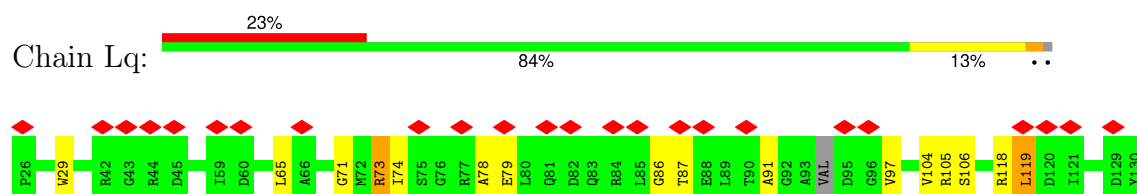
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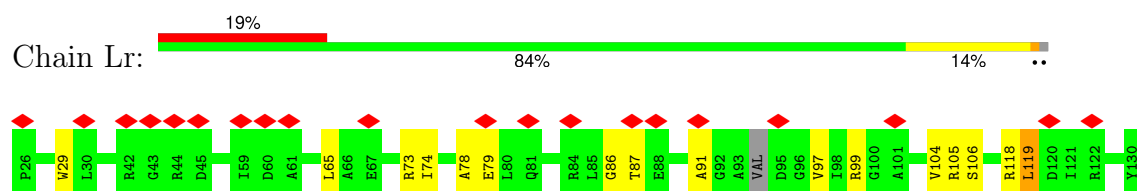
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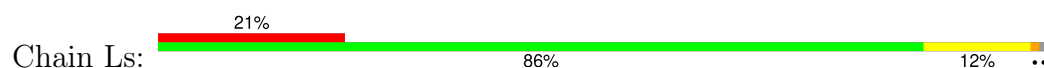
- Molecule 11: Lipoprotein



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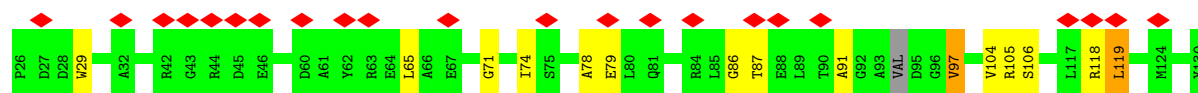
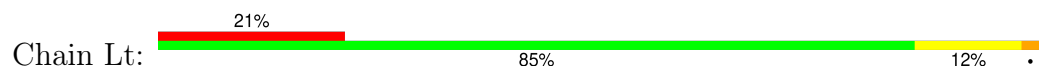


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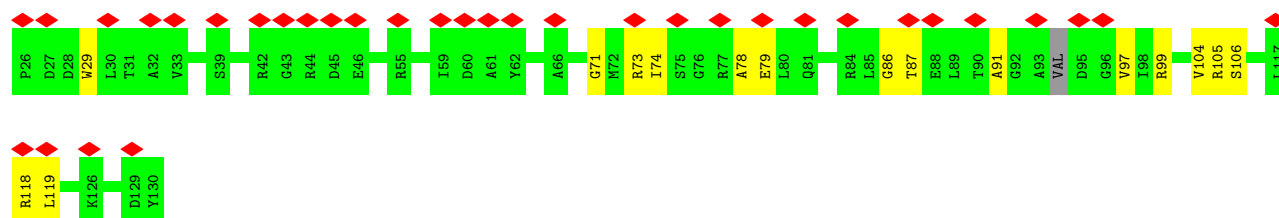
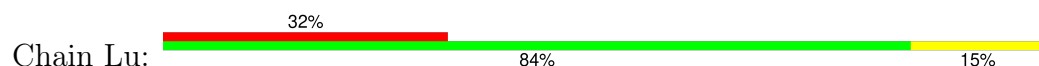




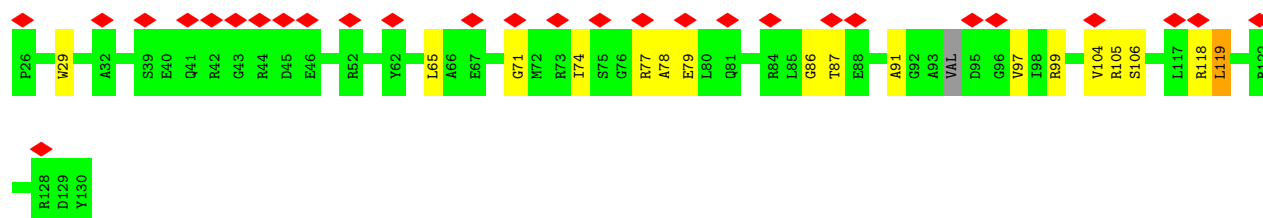
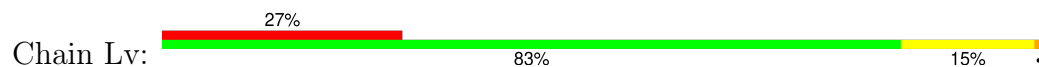
• Molecule 11: Lipoprotein



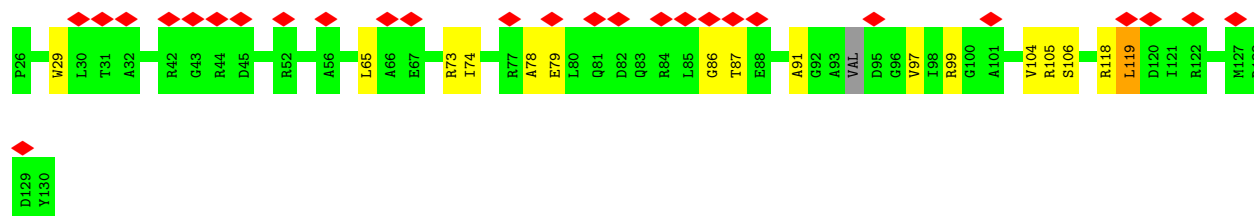
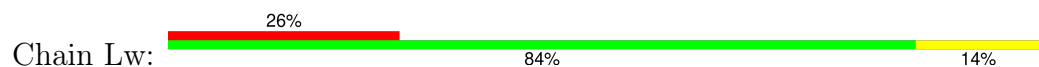
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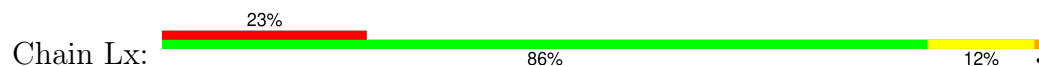
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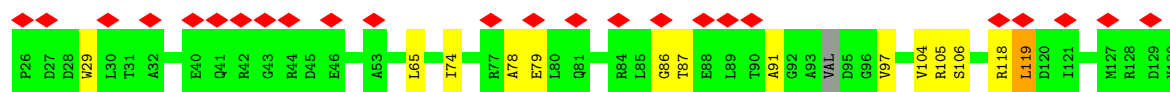


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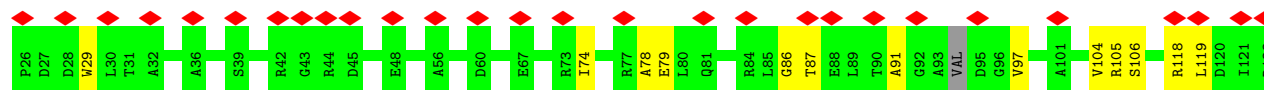
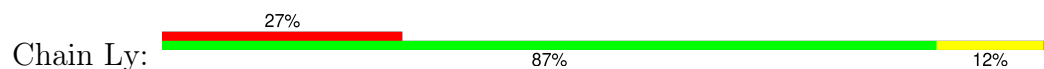


• Molecule 11: Lipoprotein

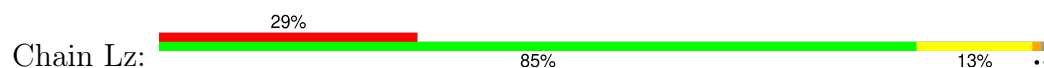




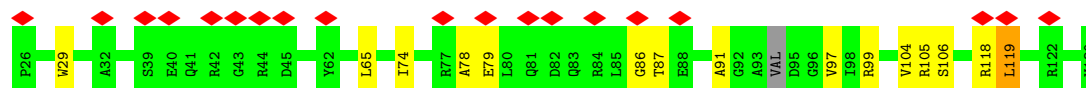
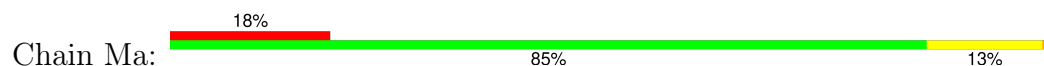
- Molecule 11: Lipoprotein



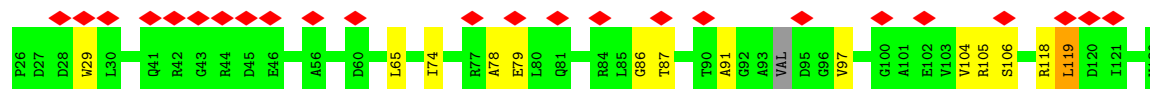
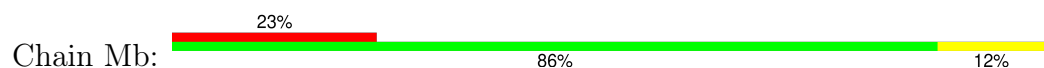
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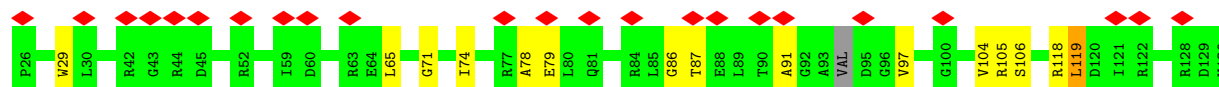
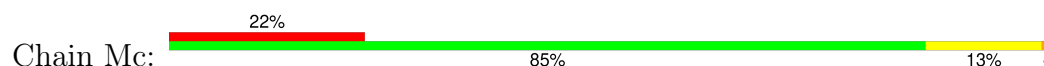
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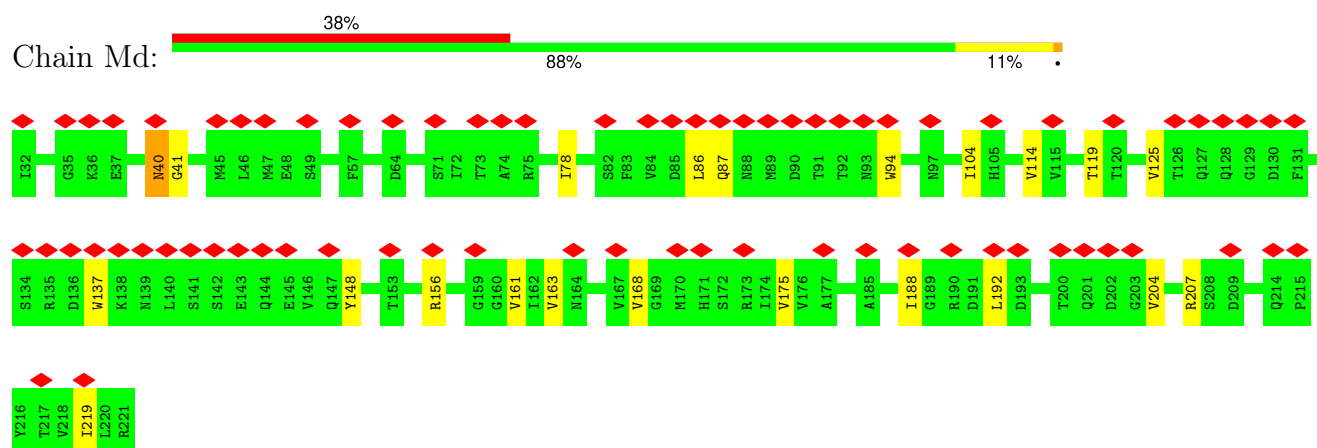
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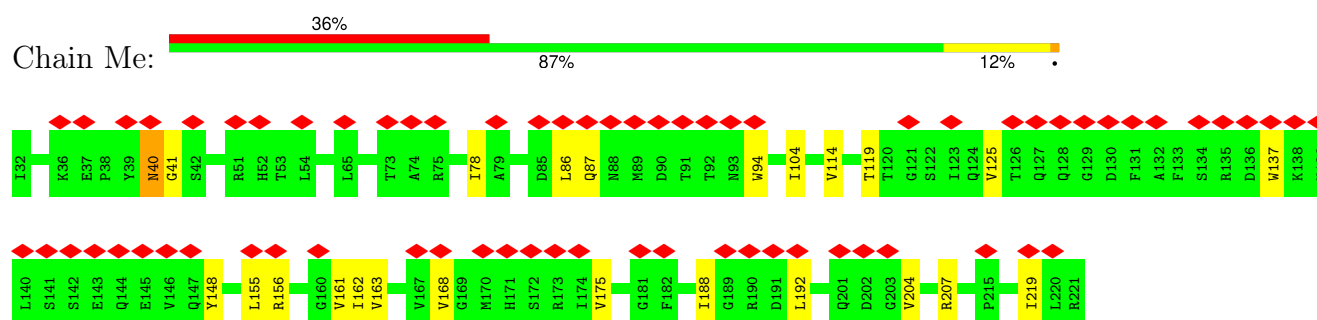
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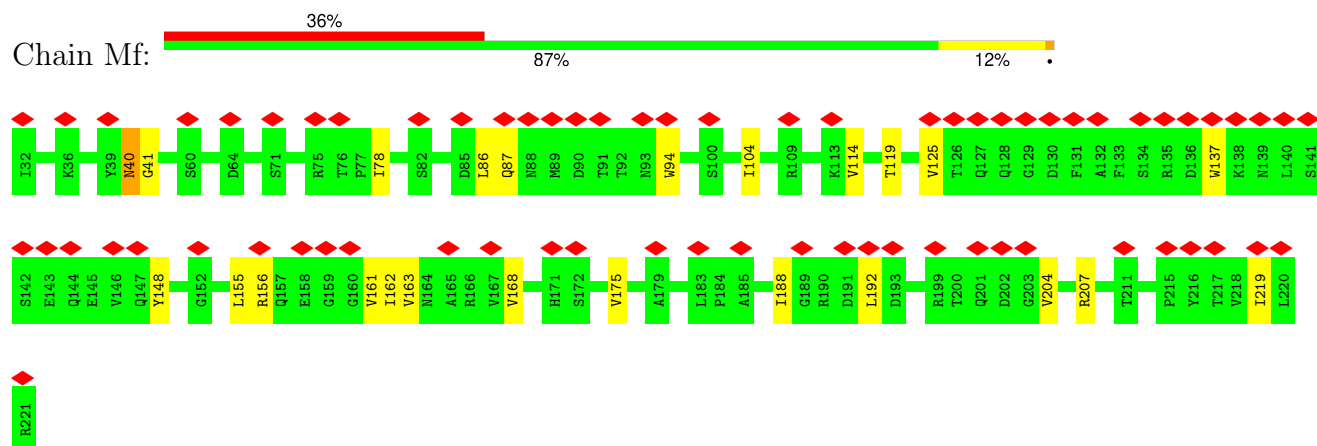
- Molecule 12: FlgO domain-containing protein



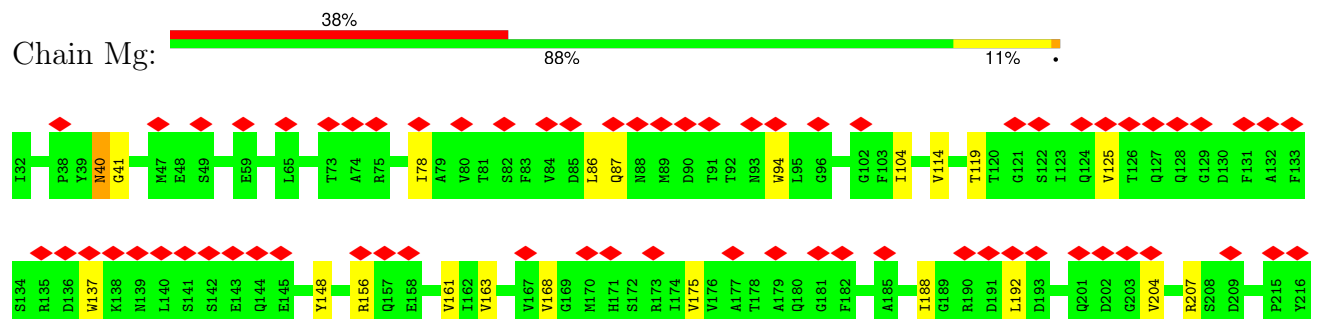
• Molecule 12: FlgO domain-containing protein



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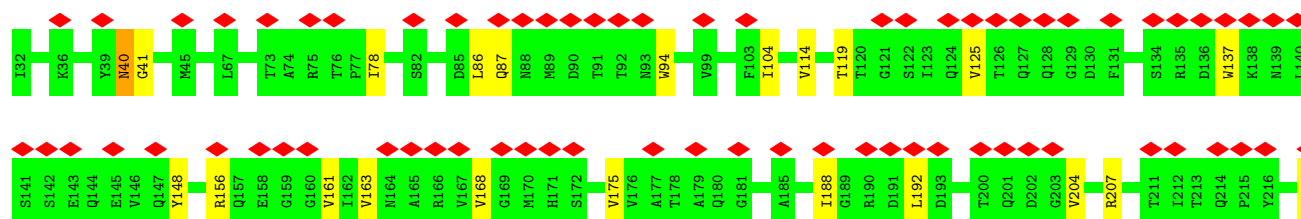
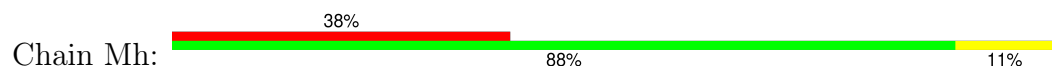


• Molecule 12: FlgO domain-containing protein

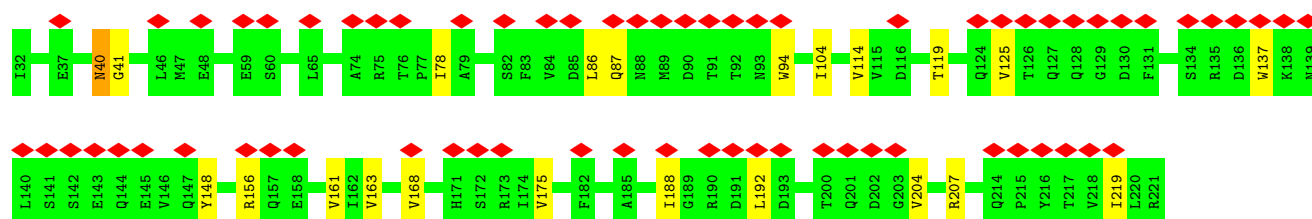
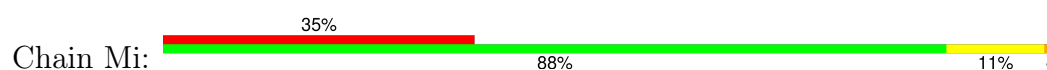




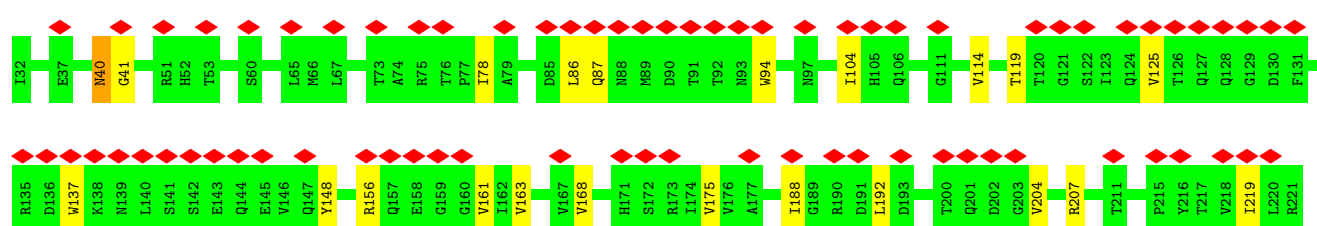
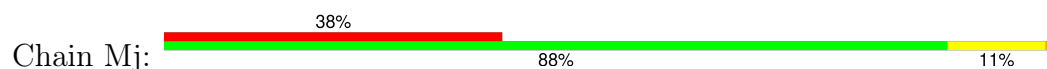
- Molecule 12: FlgO domain-containing protein



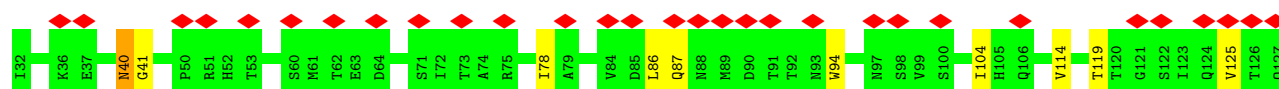
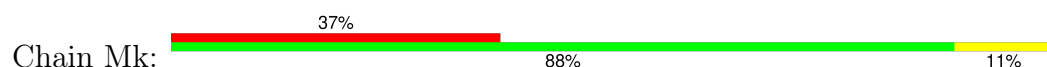
- Molecule 12: FlgO domain-containing protein

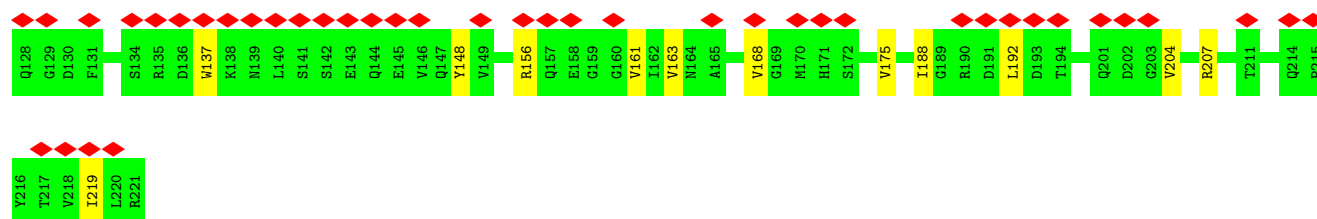


- Molecule 12: FlgO domain-containing protein

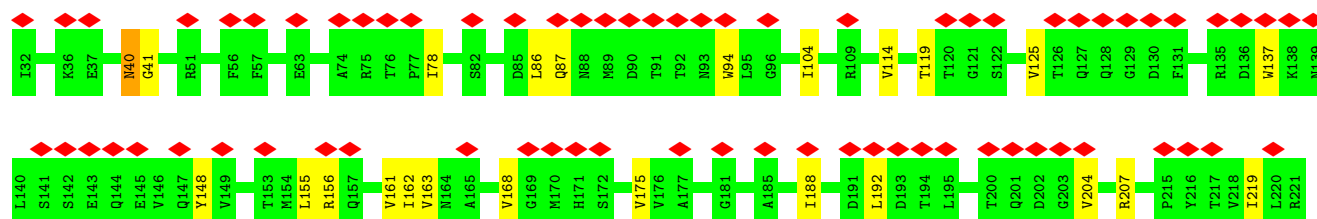
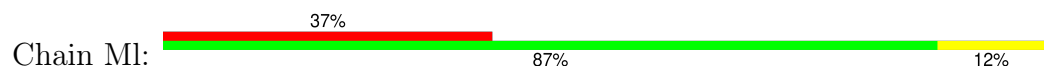


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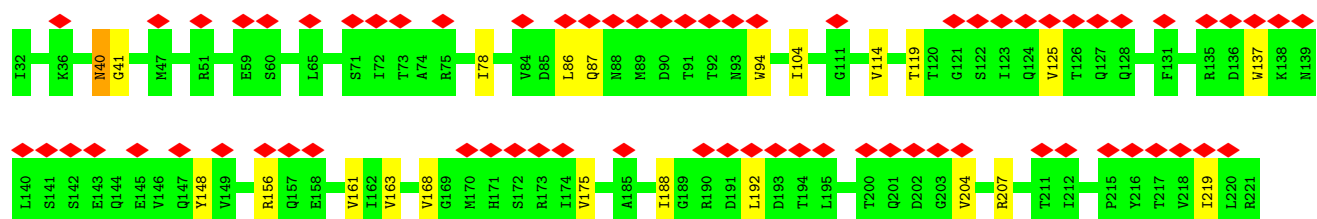
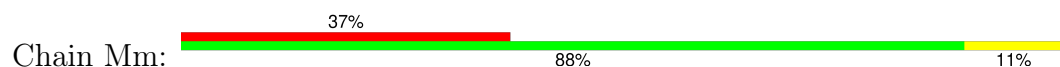




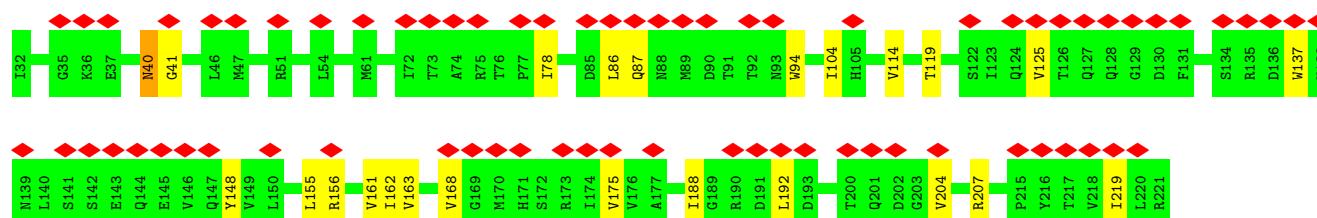
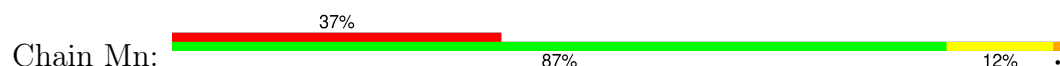
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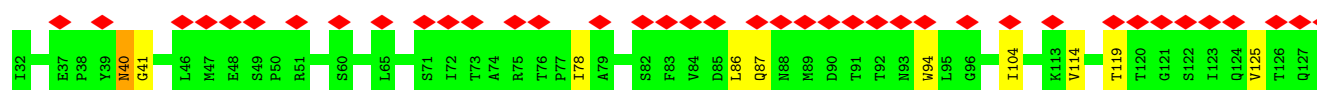
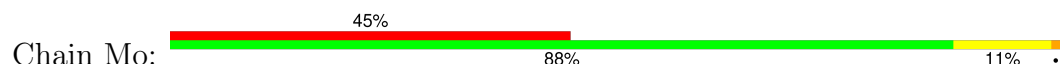
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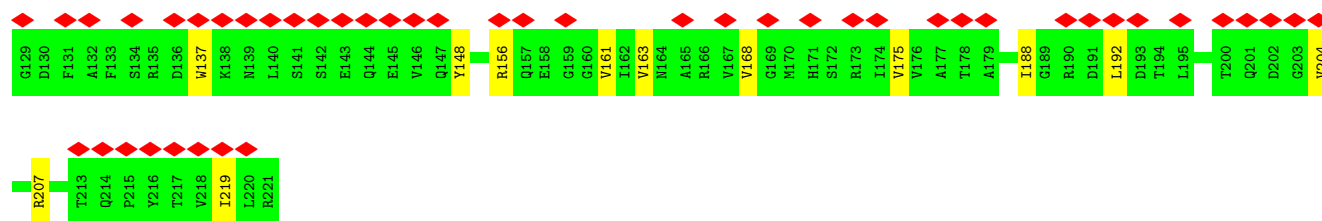


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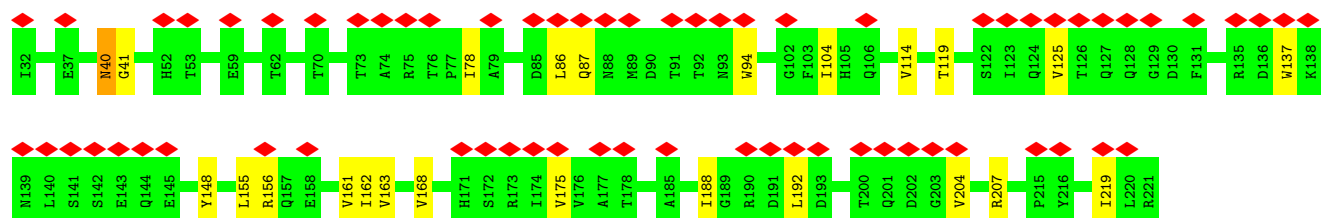
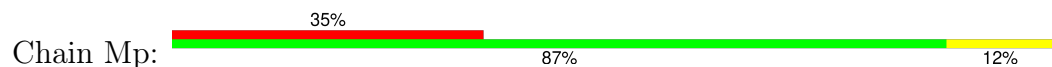


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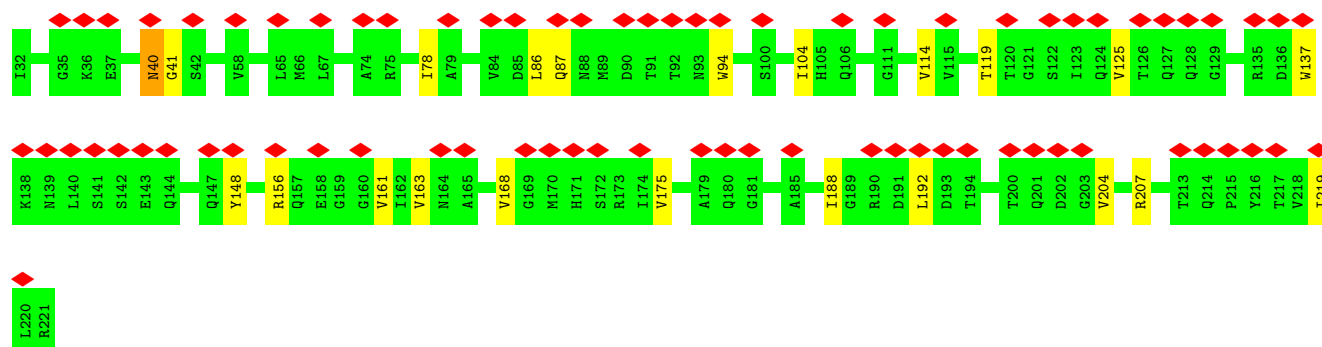
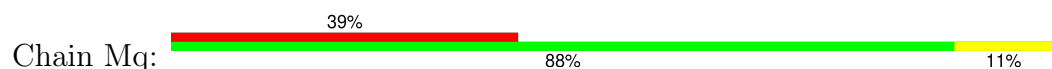




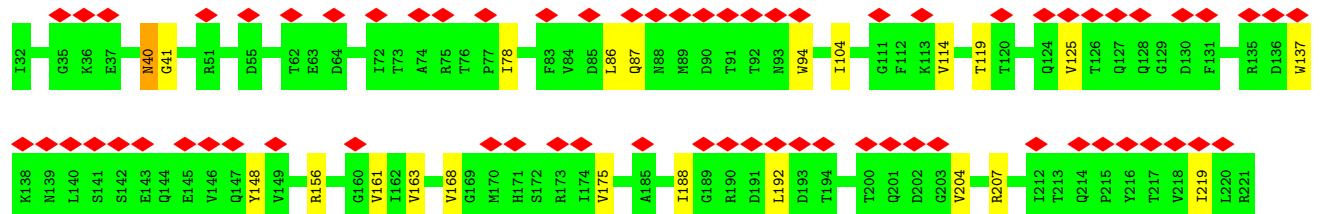
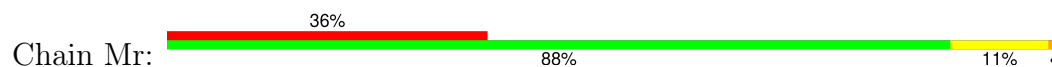
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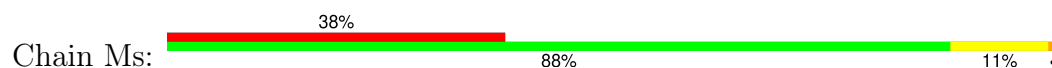
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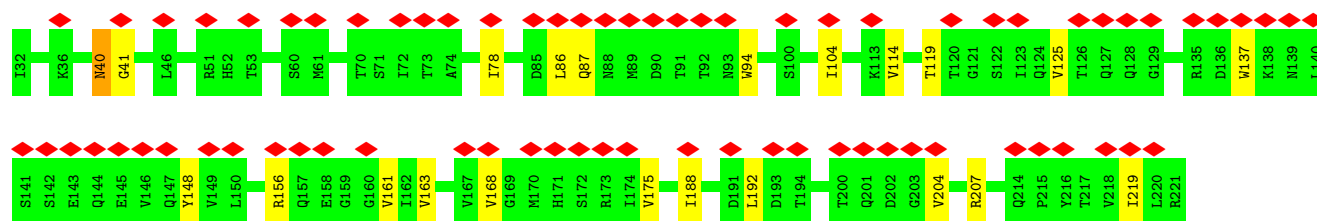


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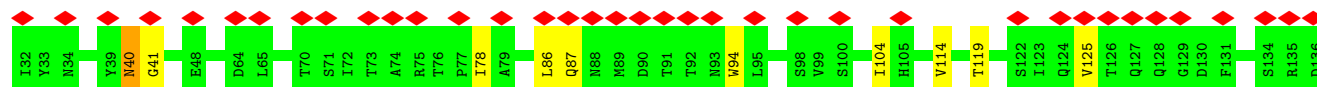
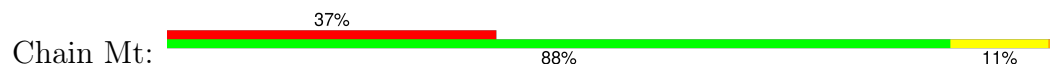


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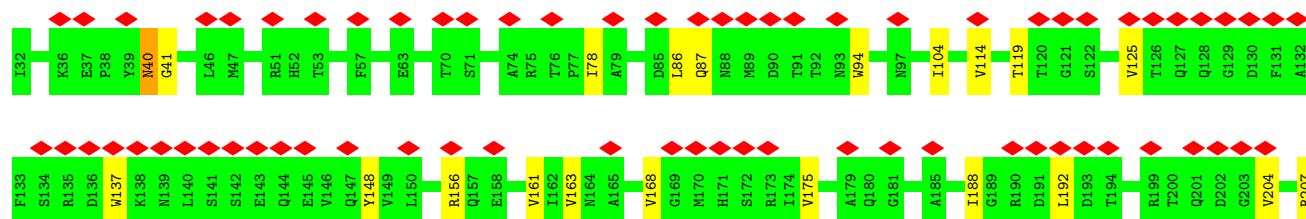
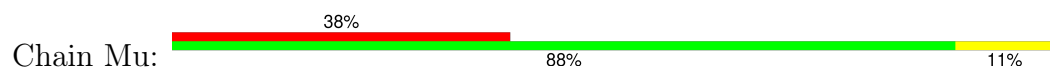




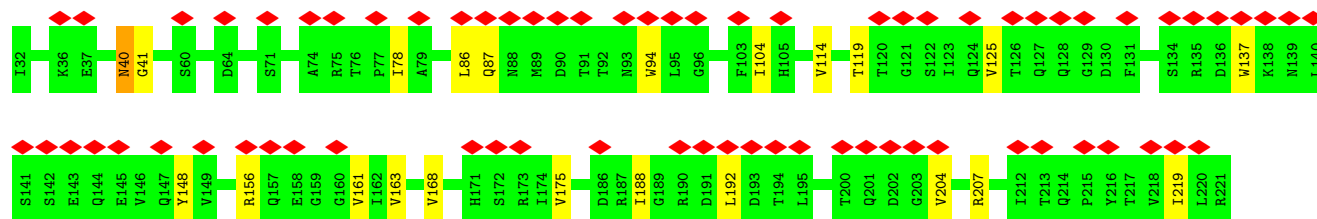
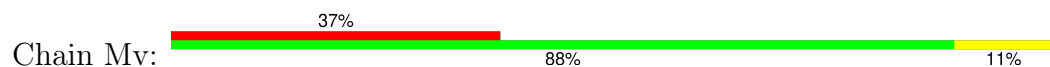
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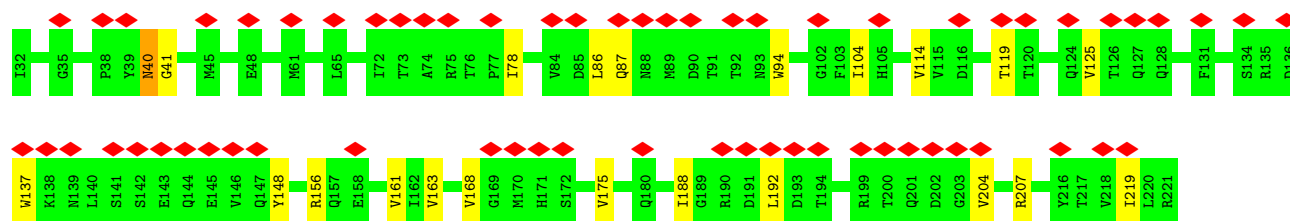


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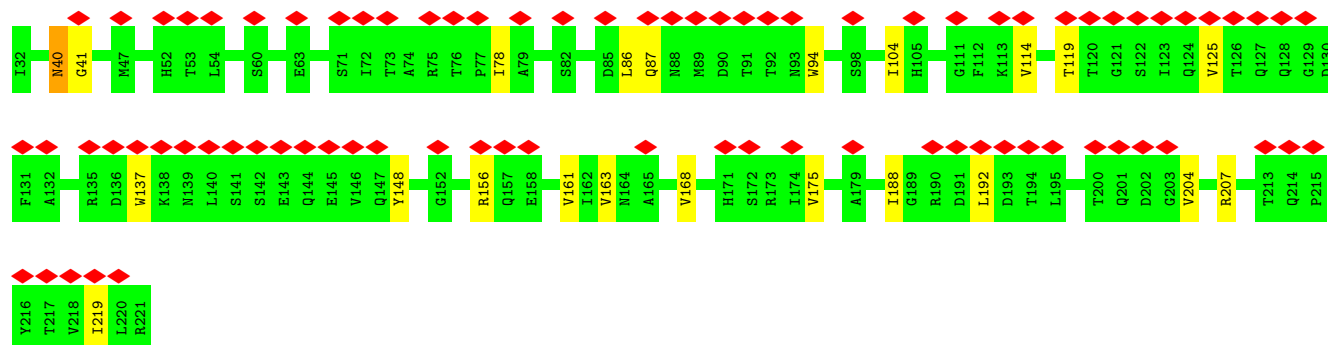
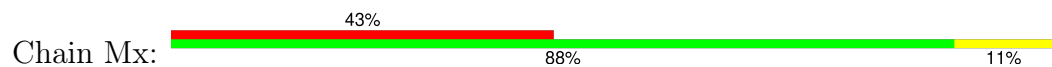


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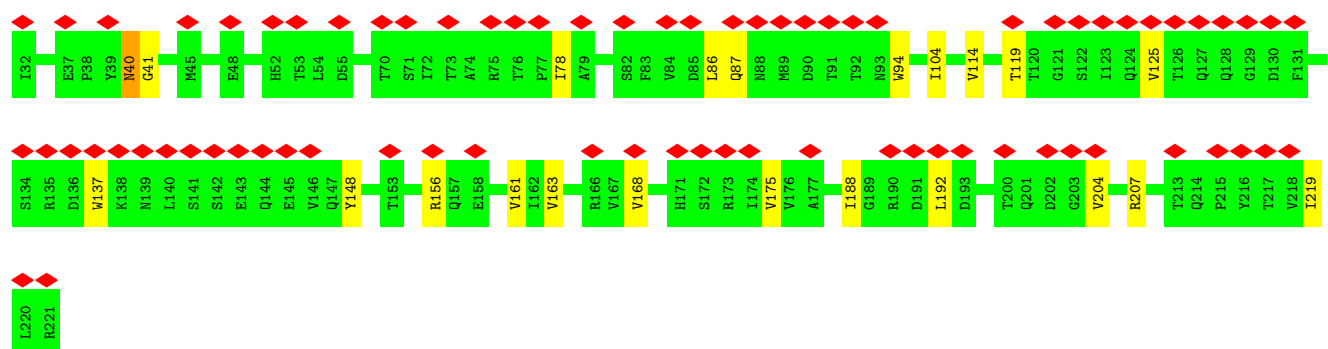
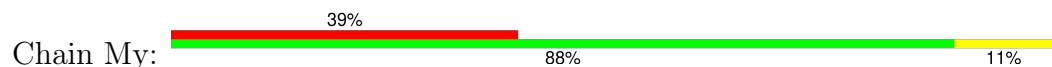




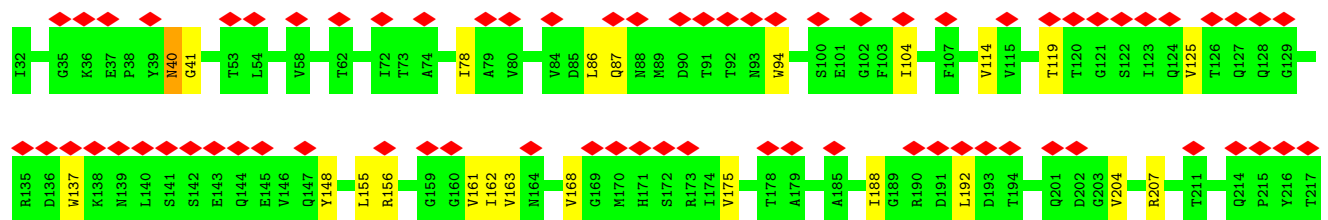
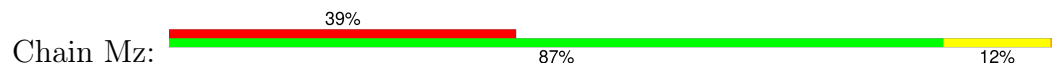
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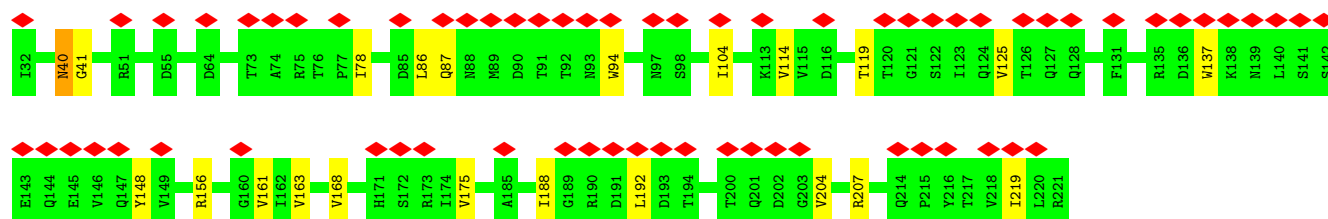
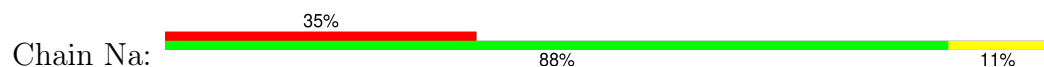


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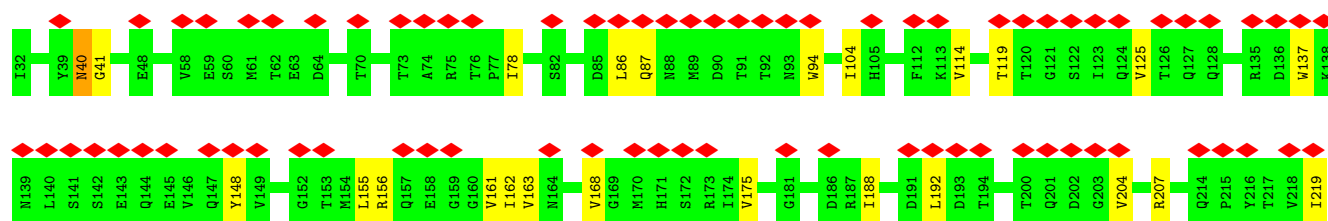
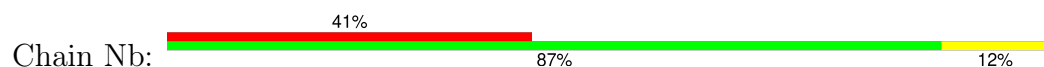




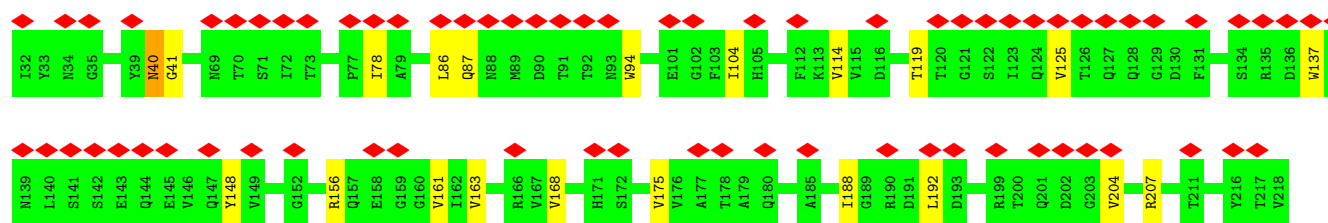
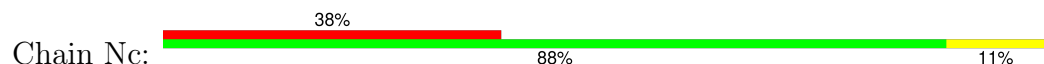
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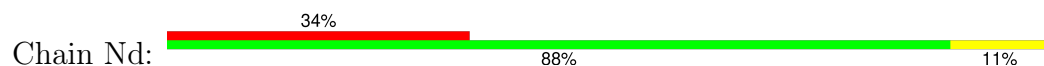
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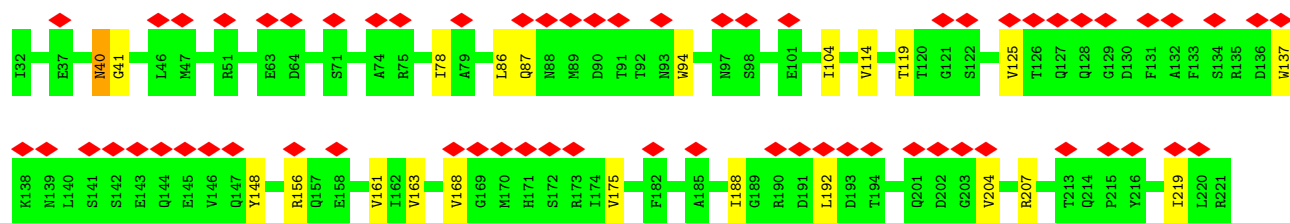


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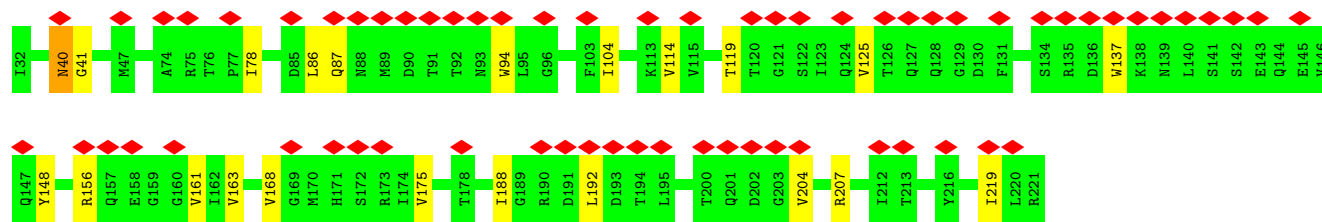
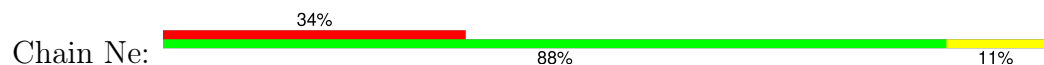


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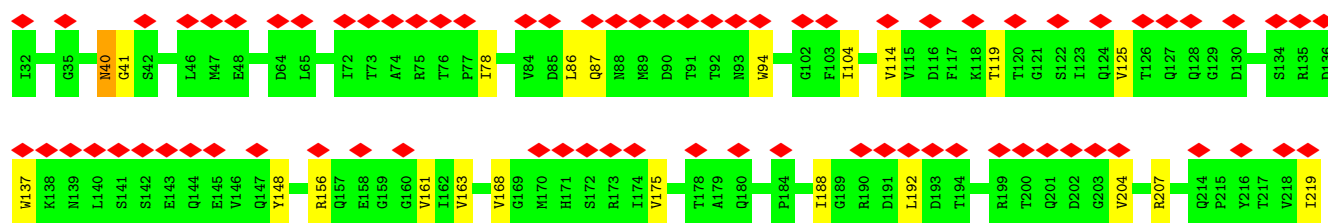
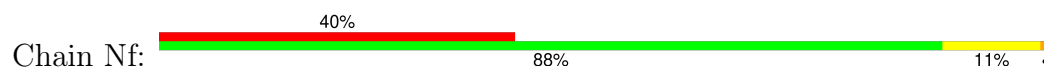




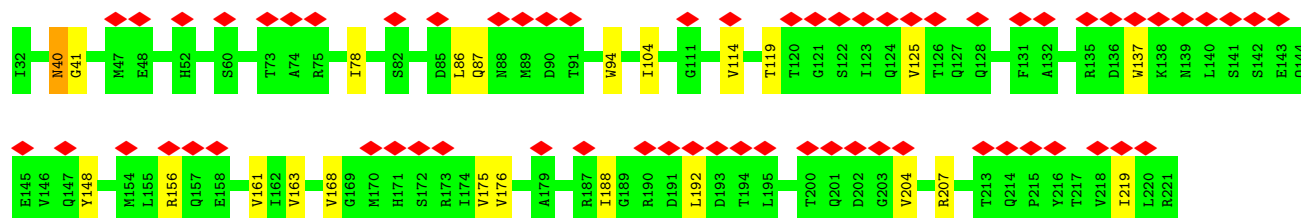
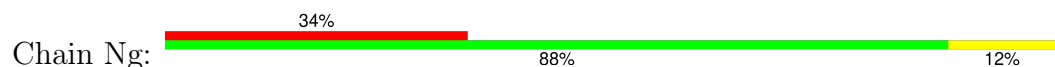
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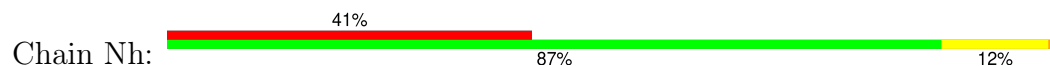
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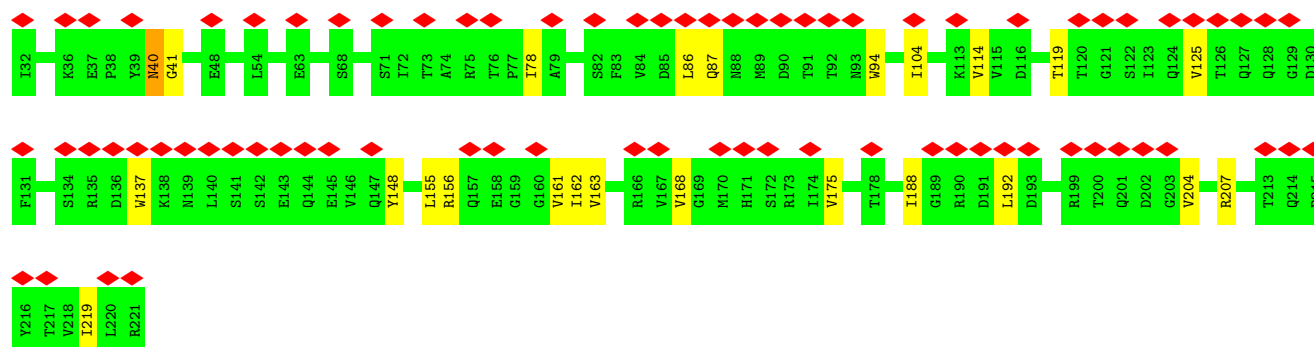


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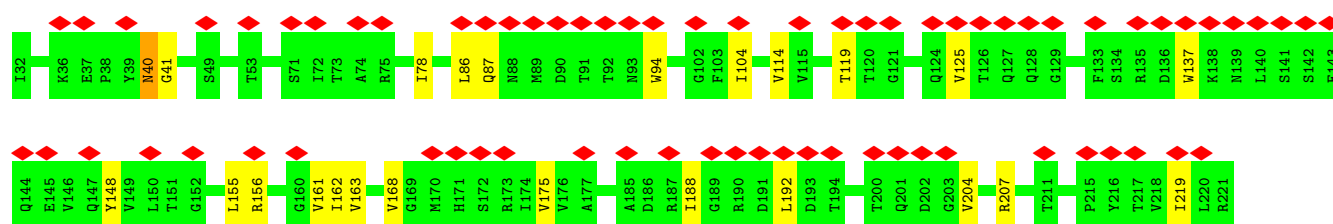
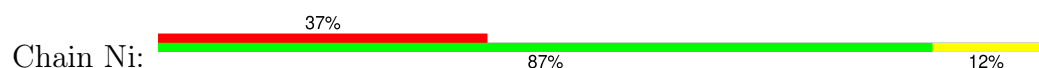


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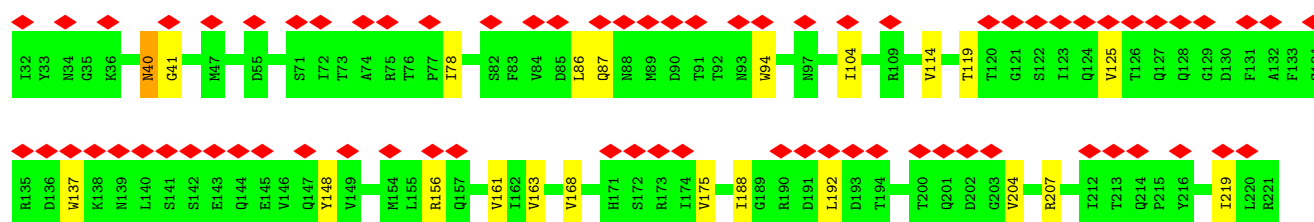
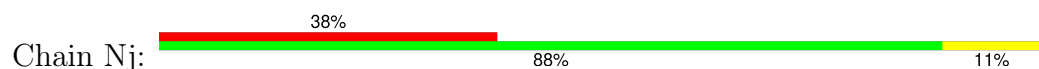




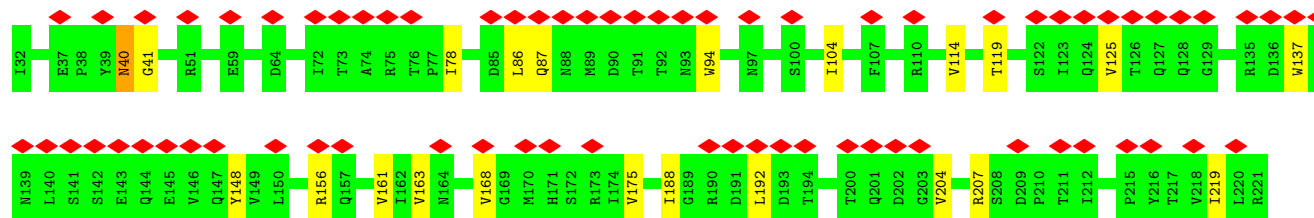
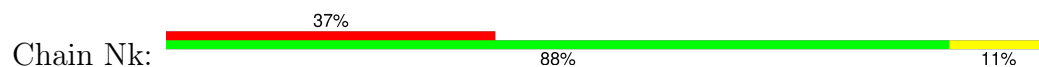
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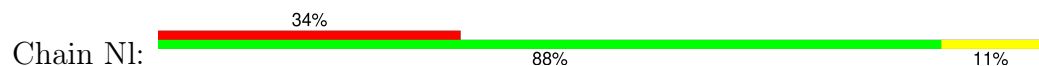
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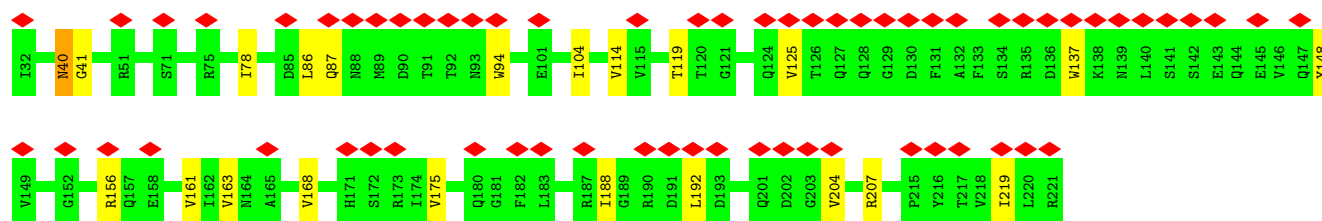


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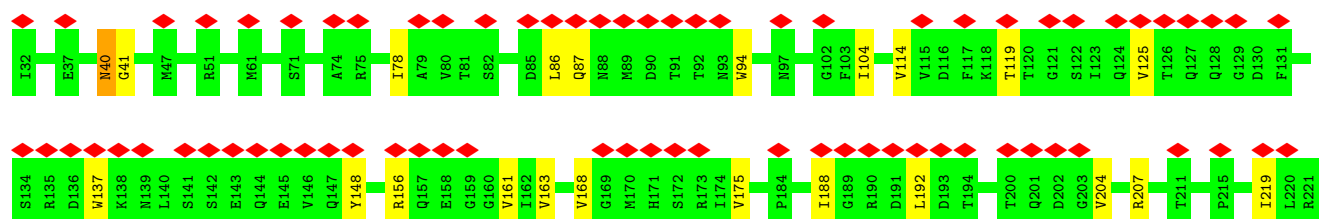
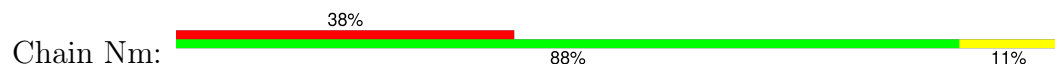


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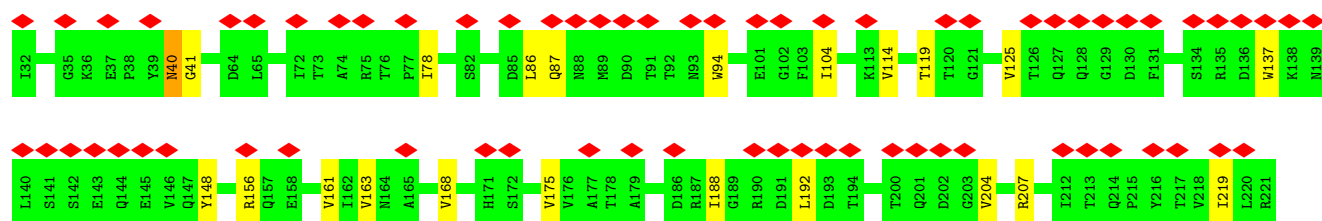
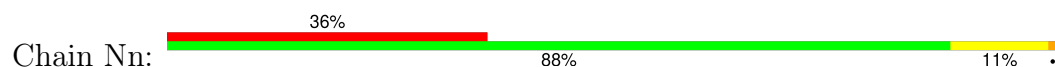




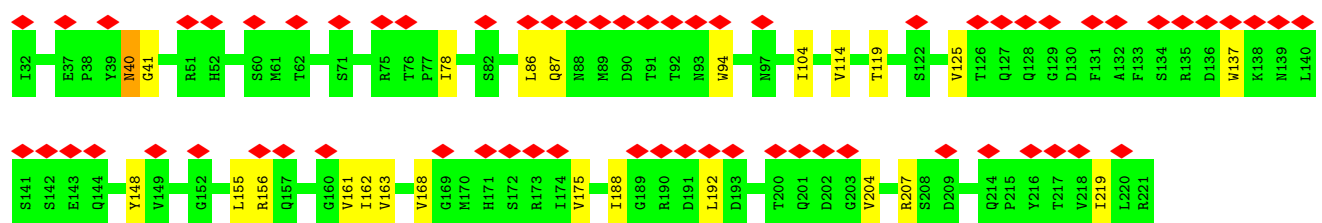
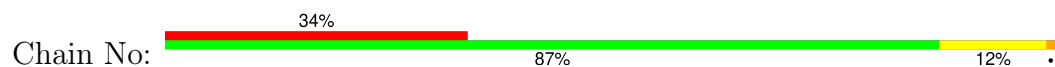
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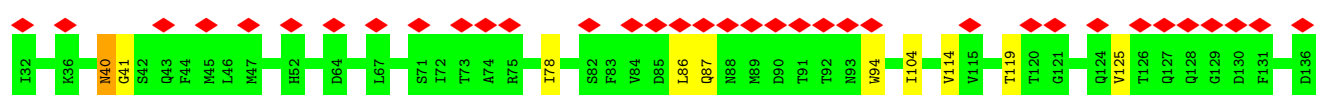
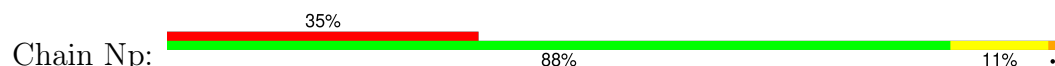
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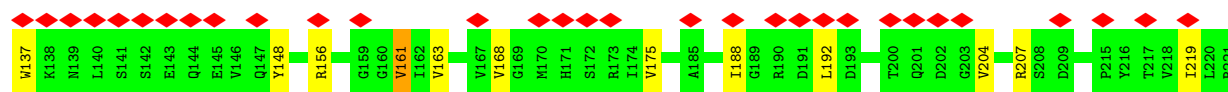


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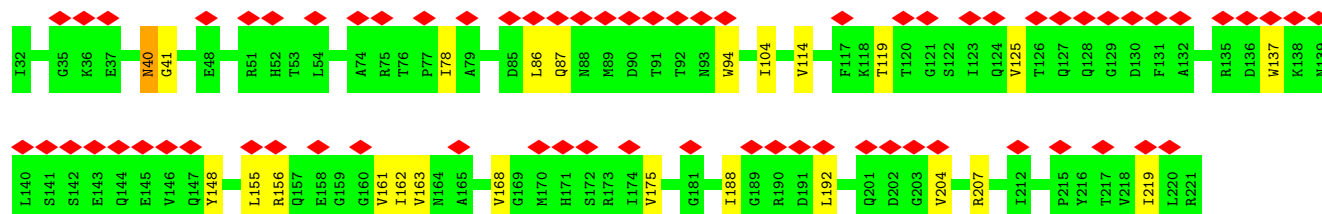
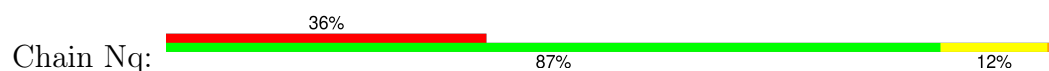


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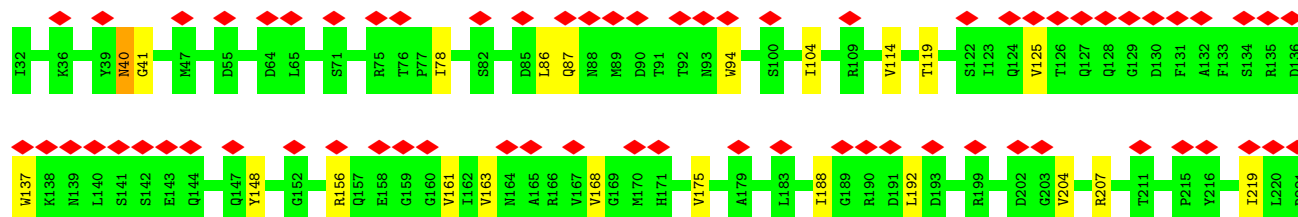
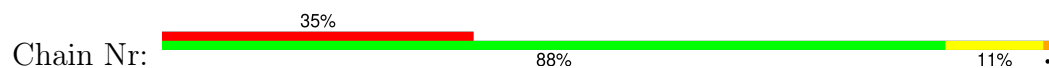




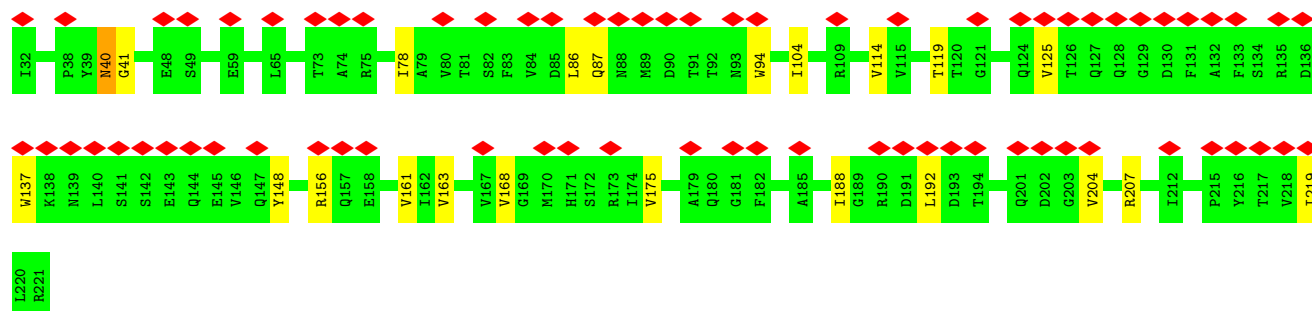
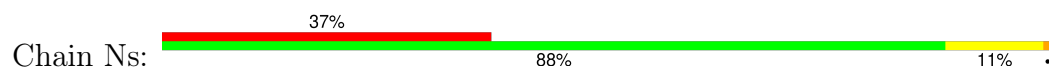
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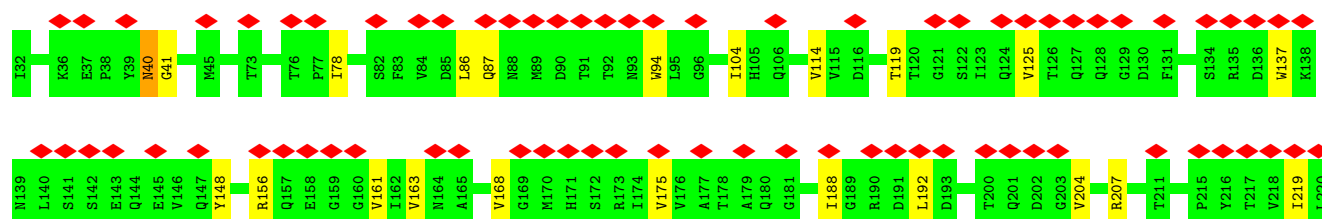
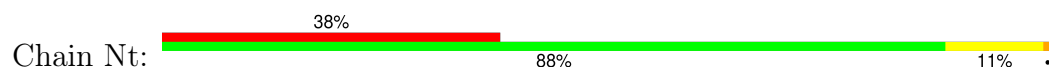
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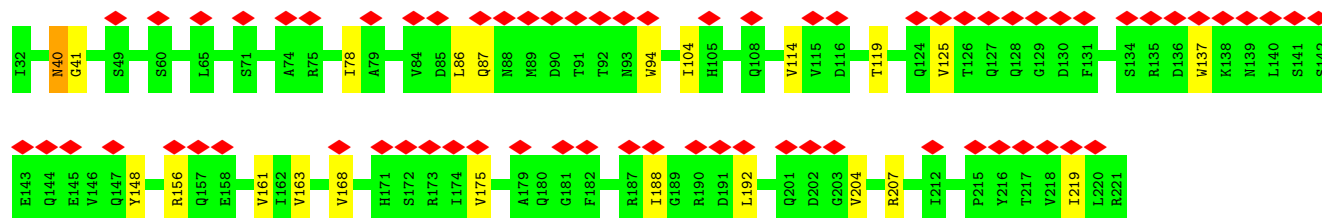
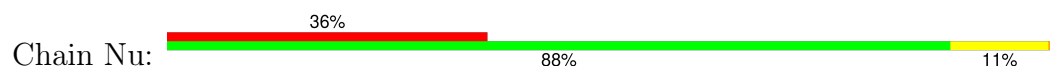


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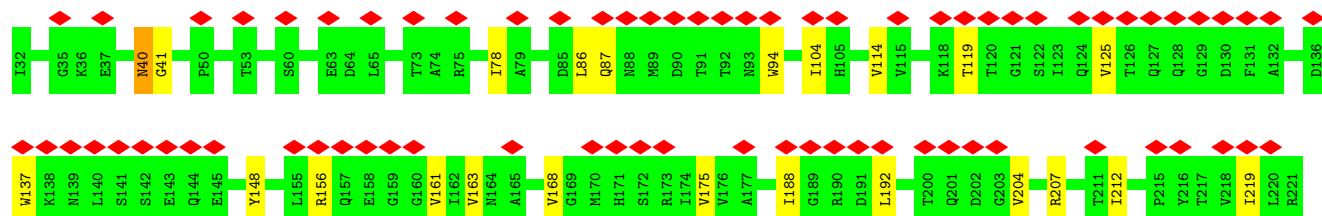
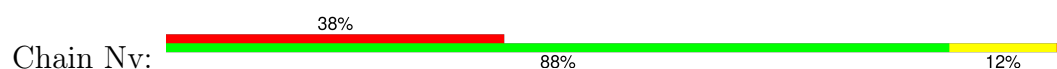


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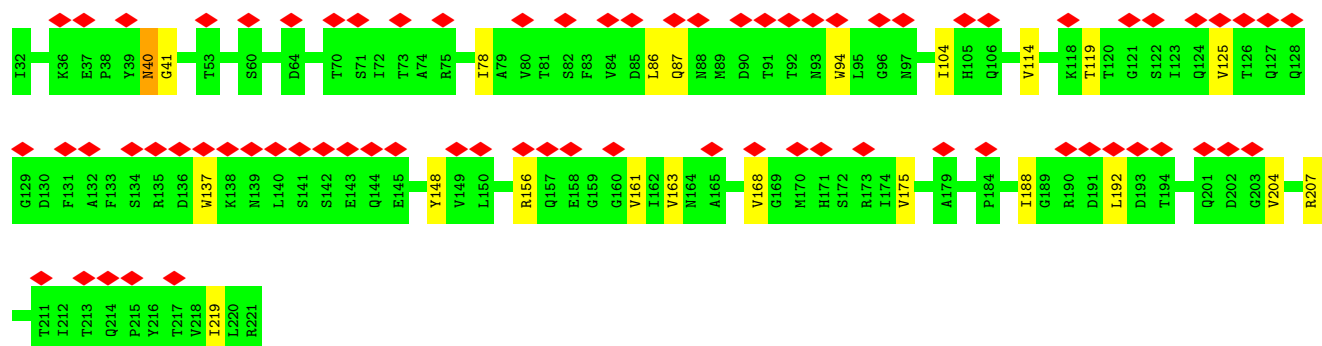
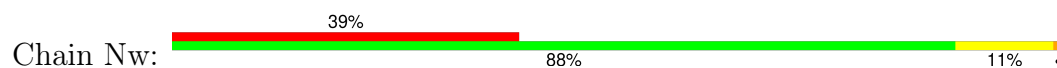
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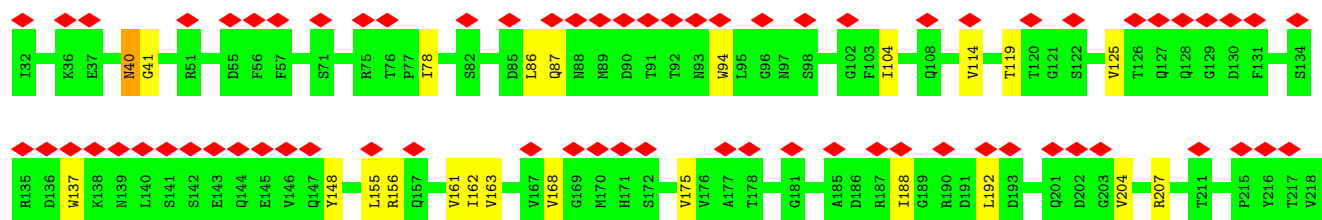
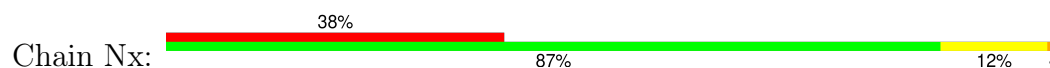
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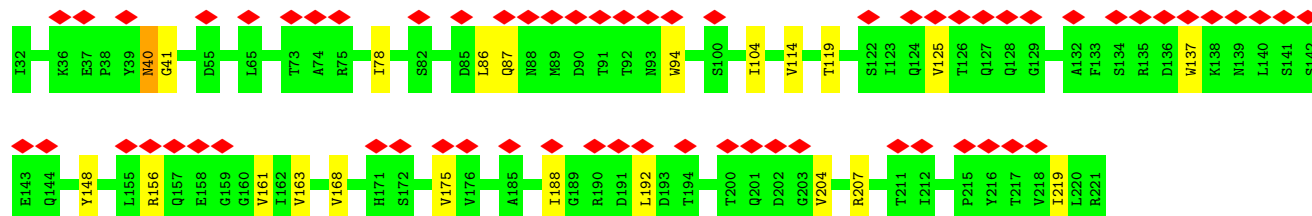
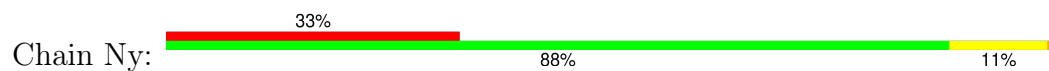


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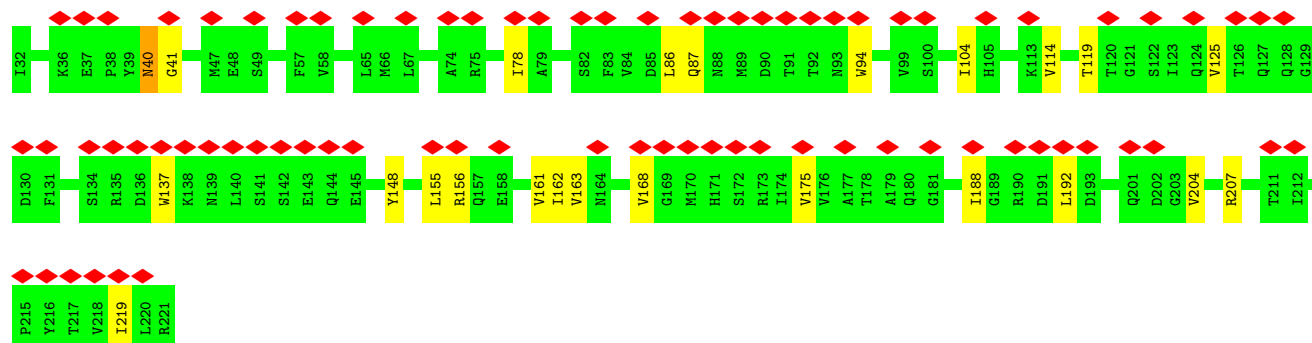
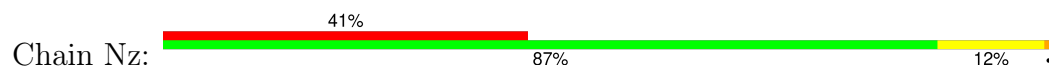




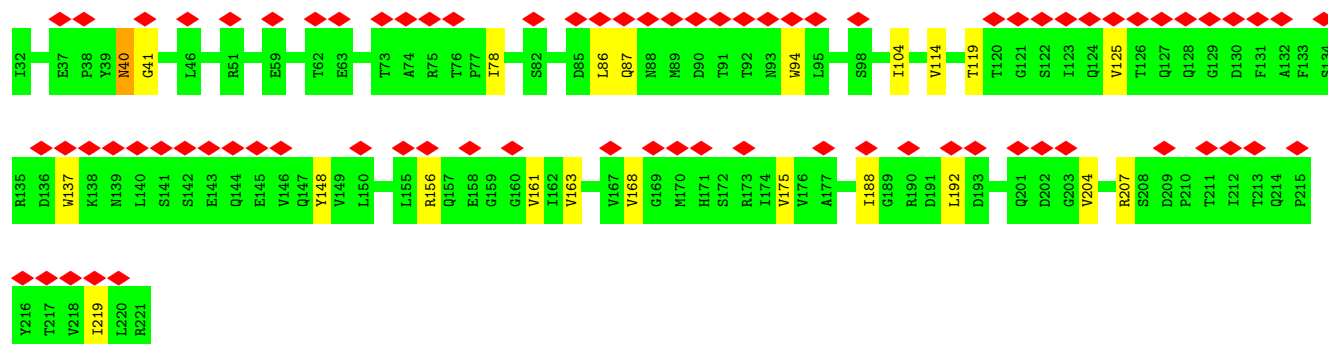
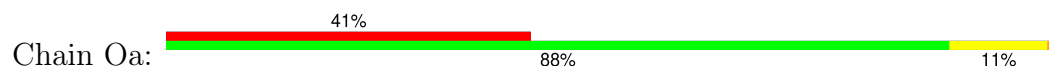
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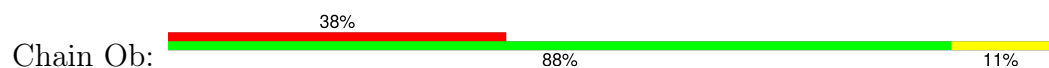
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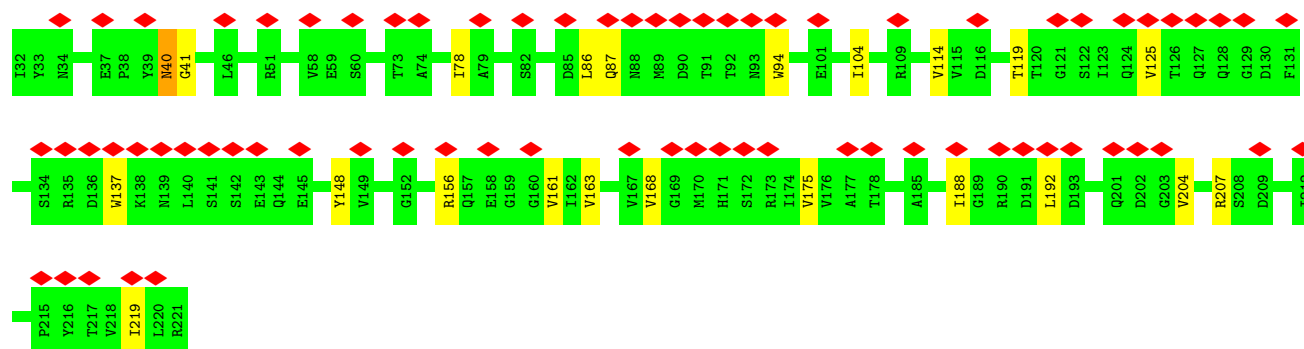


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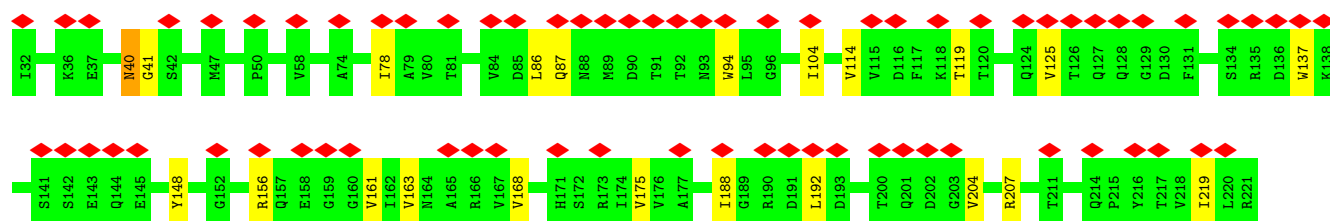
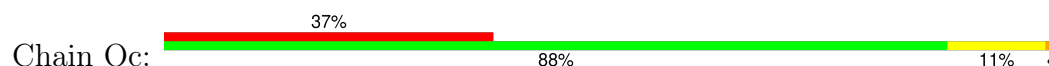


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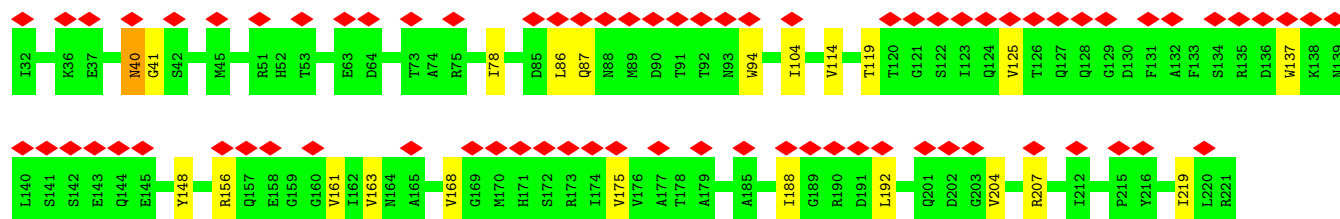
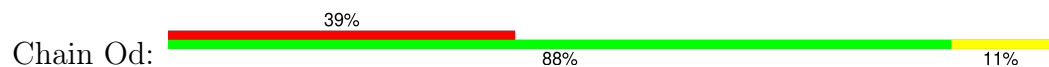




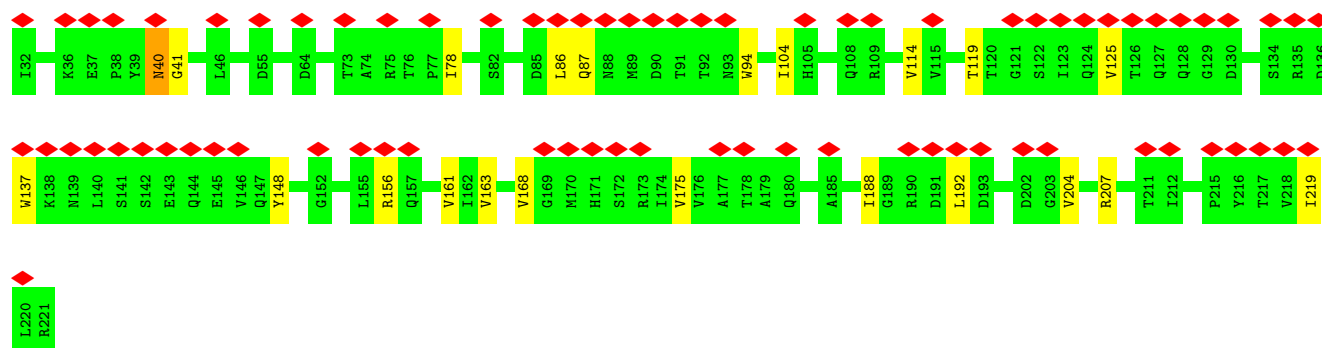
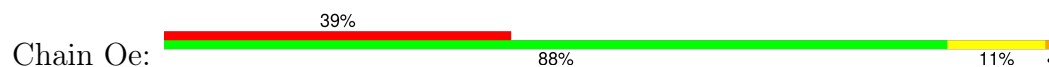
- Molecule 12: FlgO domain-containing protein



- Molecule 12: FlgO domain-containing protein

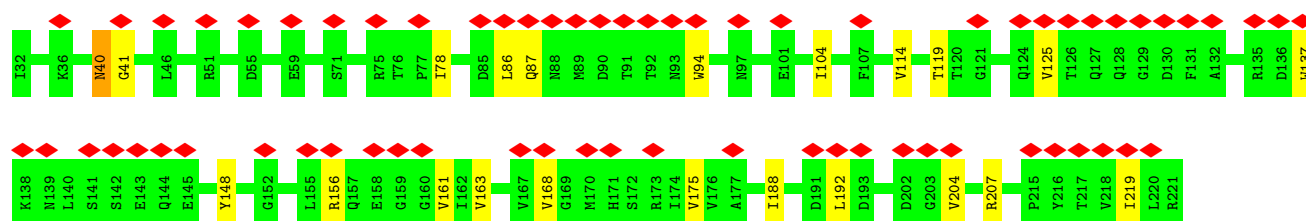


- Molecule 12: FlgO domain-containing protein



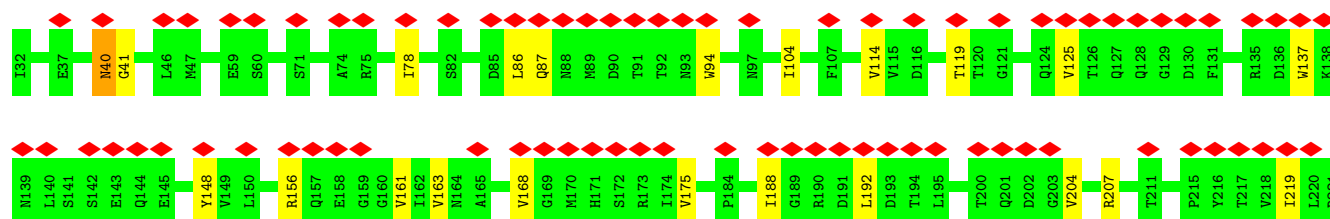
- Molecule 12: FlgO domain-containing protein

Chain Of:



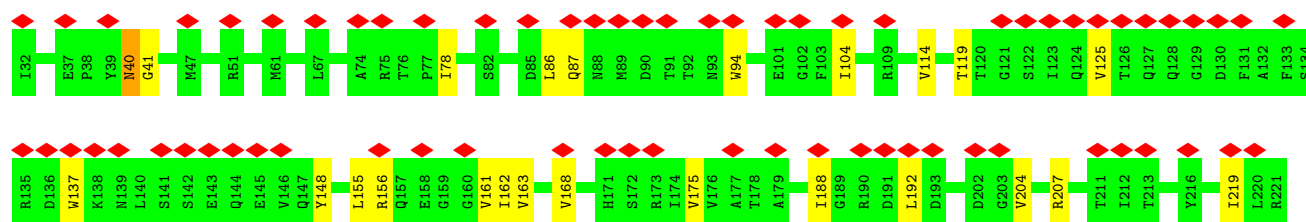
• Molecule 12: FlgO domain-containing protein

Chain Og:



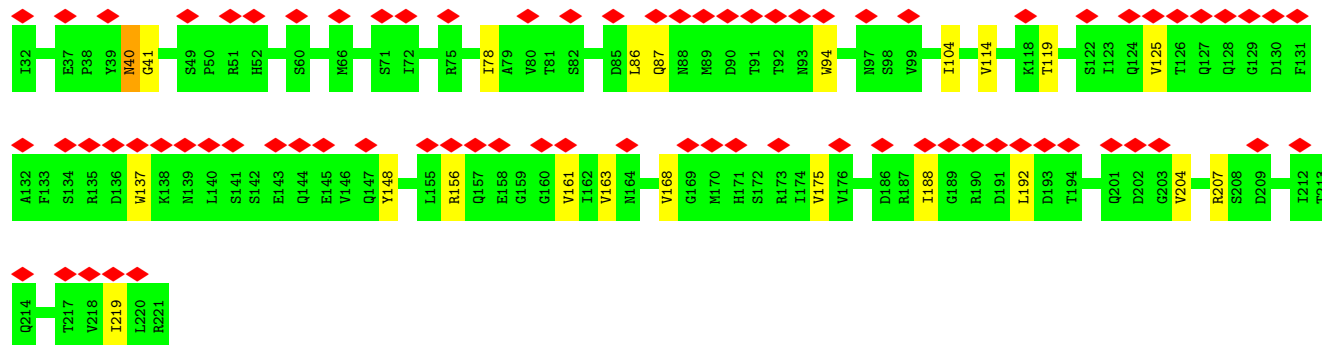
• Molecule 12: FlgO domain-containing protein

Chain Oh:



• Molecule 12: FlgO domain-containing protein

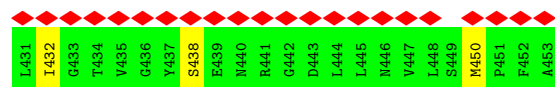
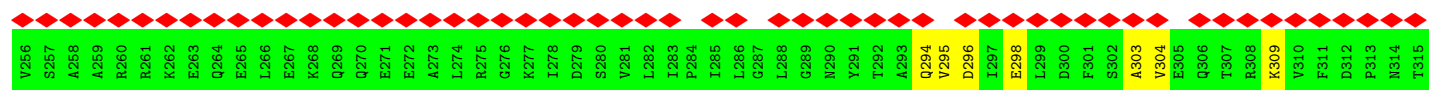
Chain Oi:



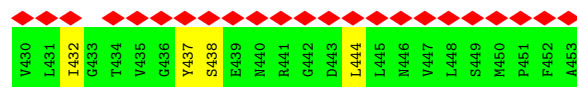
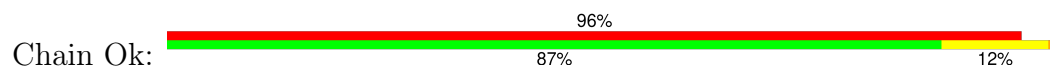
• Molecule 13: FlhF

Chain Oj:

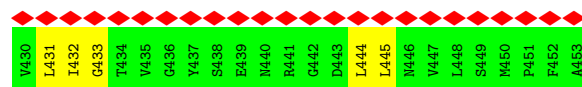
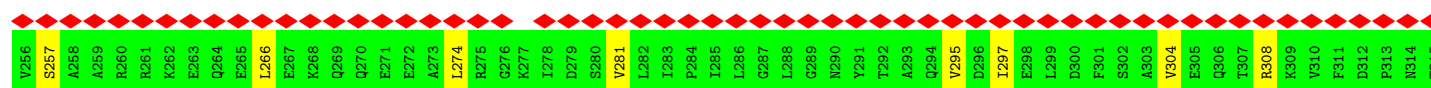
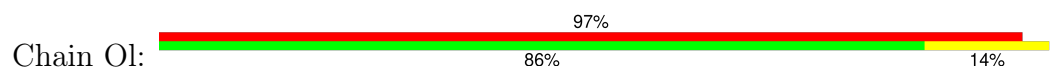




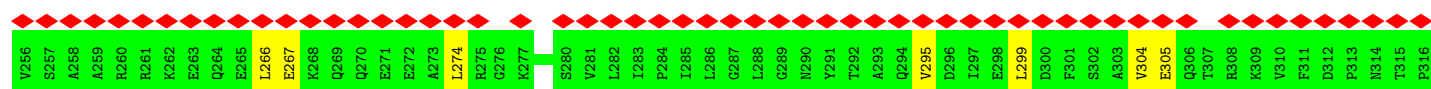
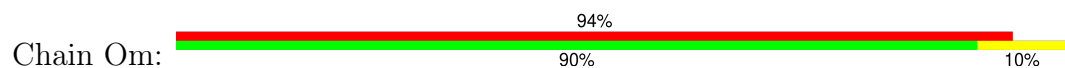
• Molecule 13: FliF

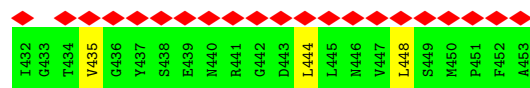


• Molecule 13: FliF

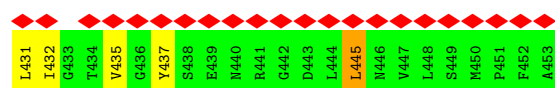
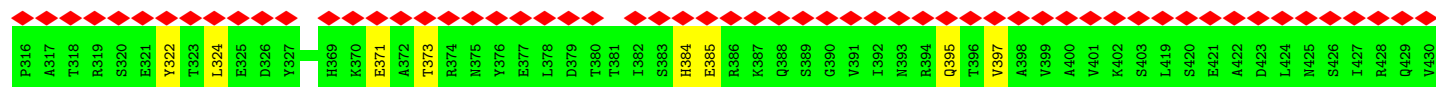
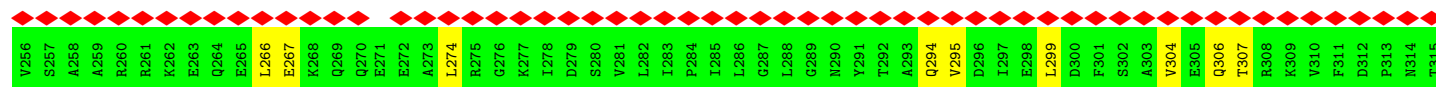
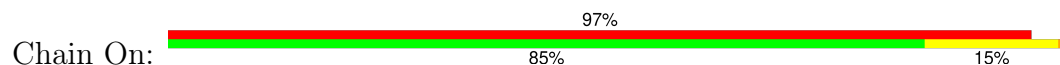


• Molecule 13: FliF

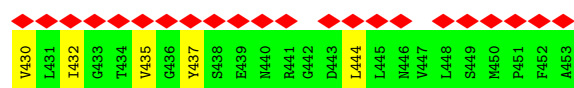
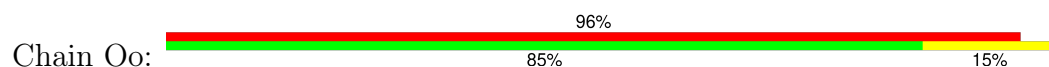




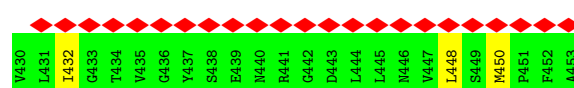
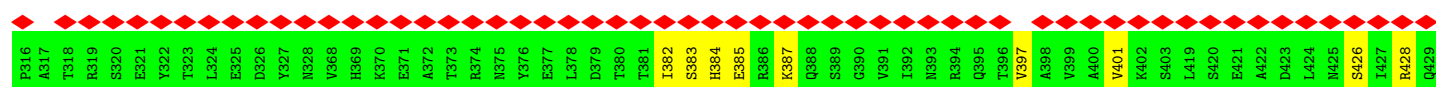
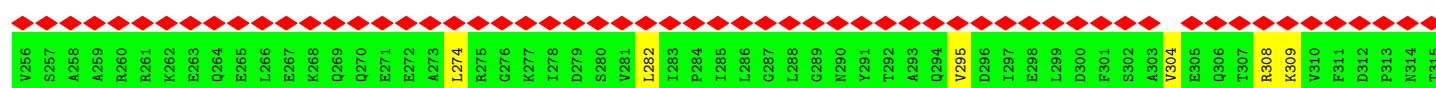
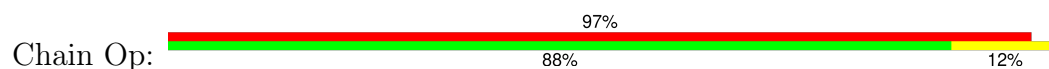
• Molecule 13: FliF



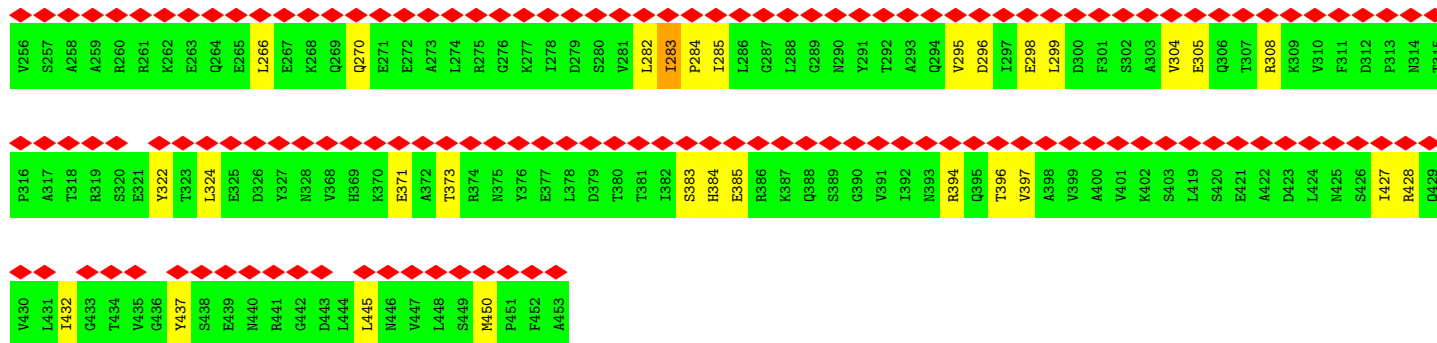
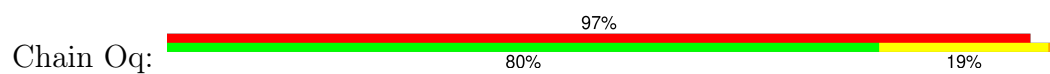
• Molecule 13: FliF



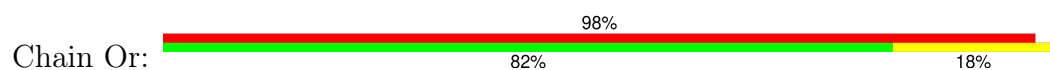
• Molecule 13: FliF



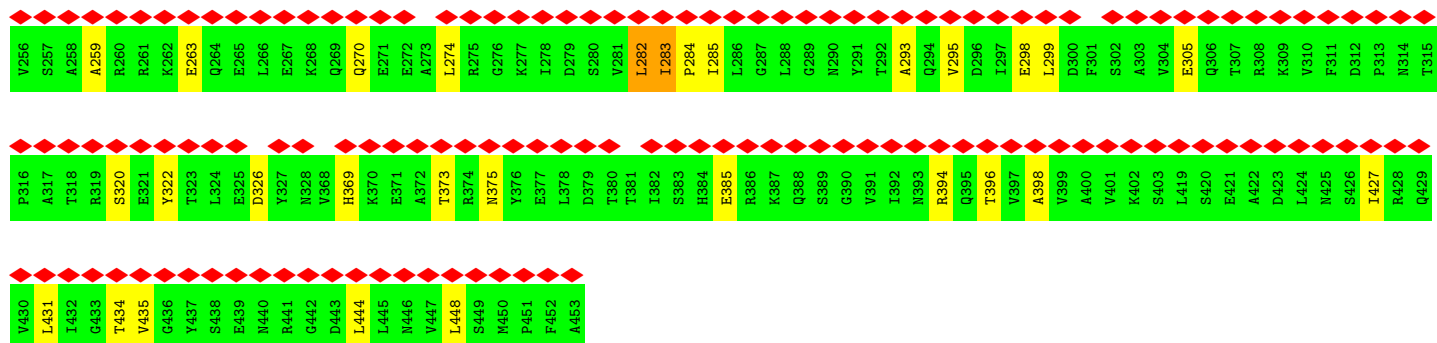
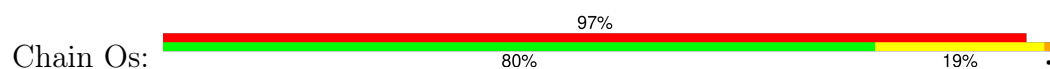
• Molecule 13: FliF



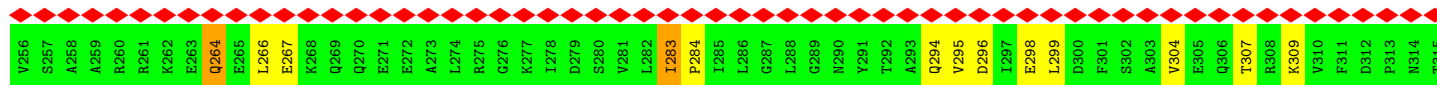
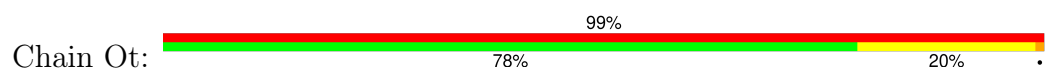
● Molecule 13: FliF



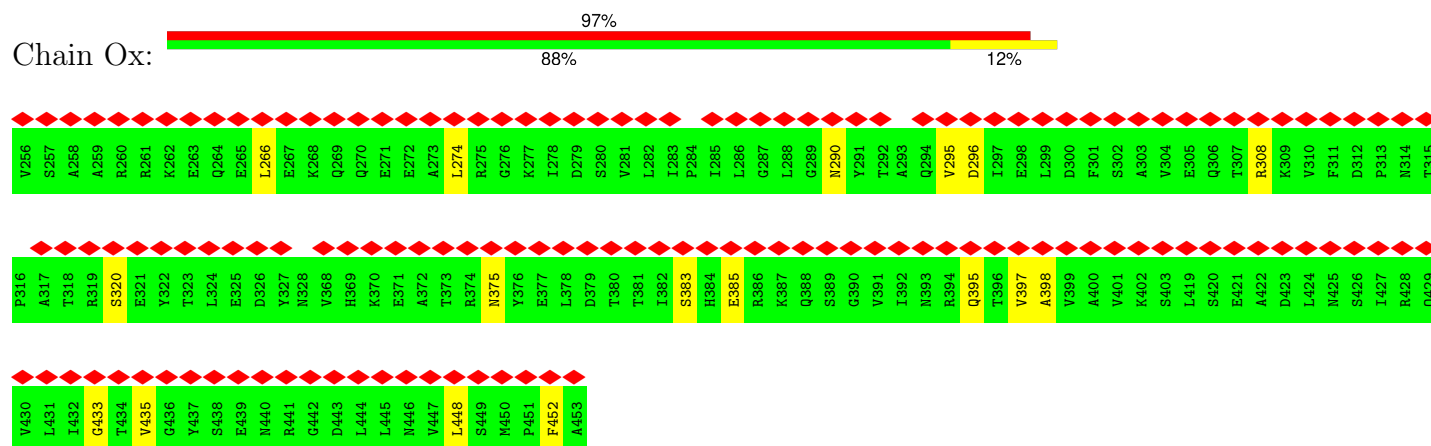
● Molecule 13: FliF



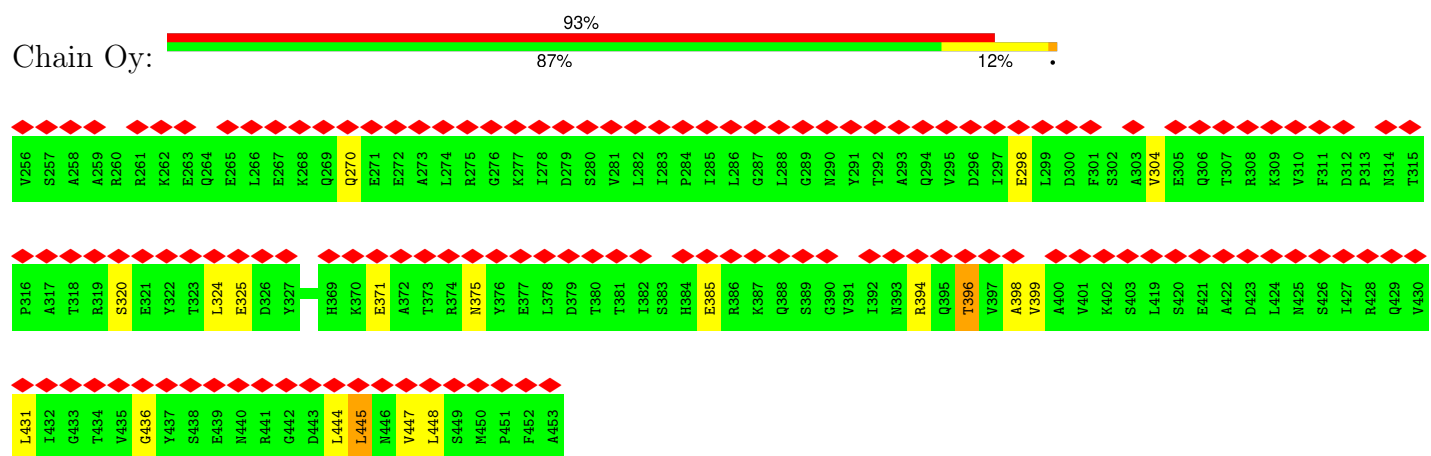
● Molecule 13: FliF



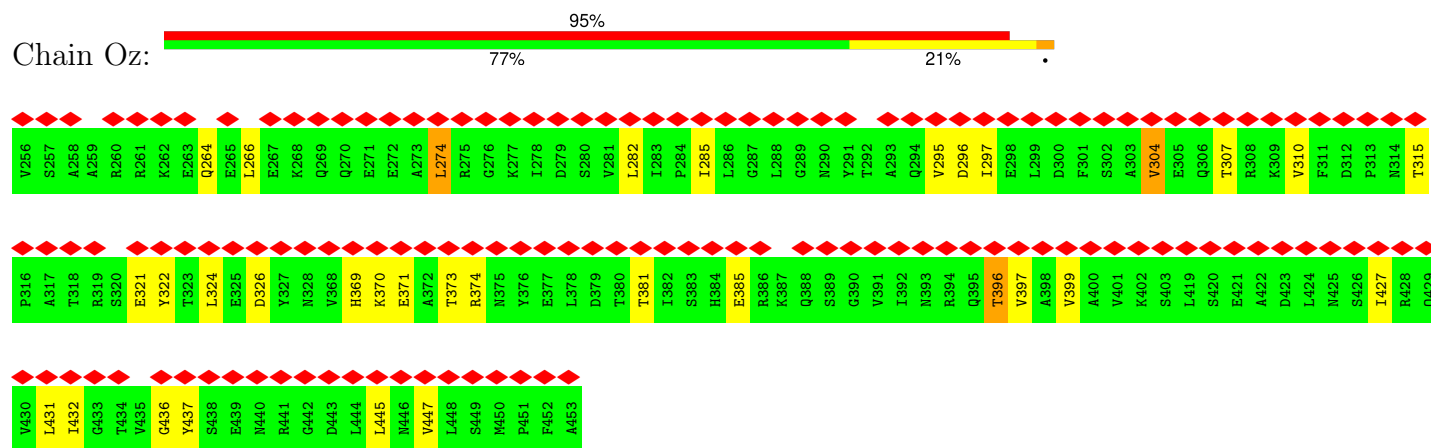
● Molecule 13: FliF



● Molecule 13: FliF

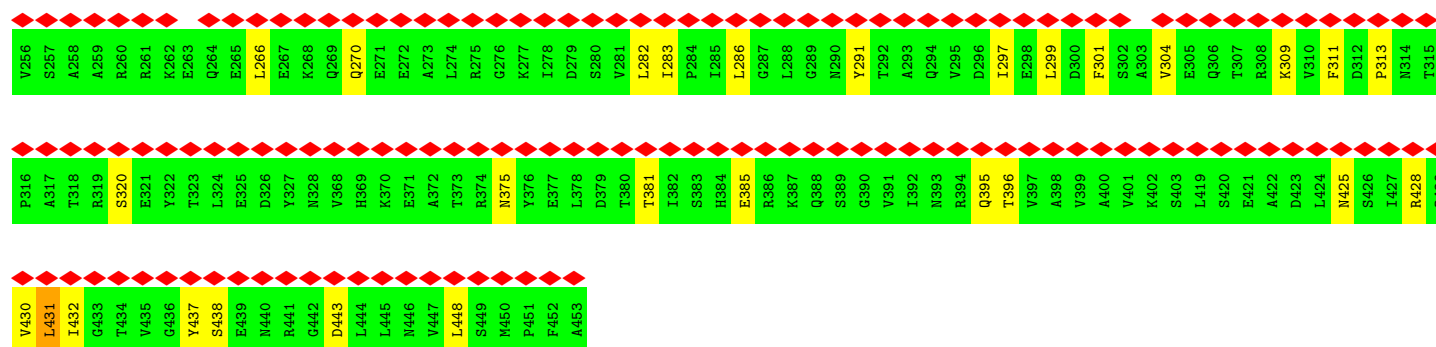


● Molecule 13: FliF

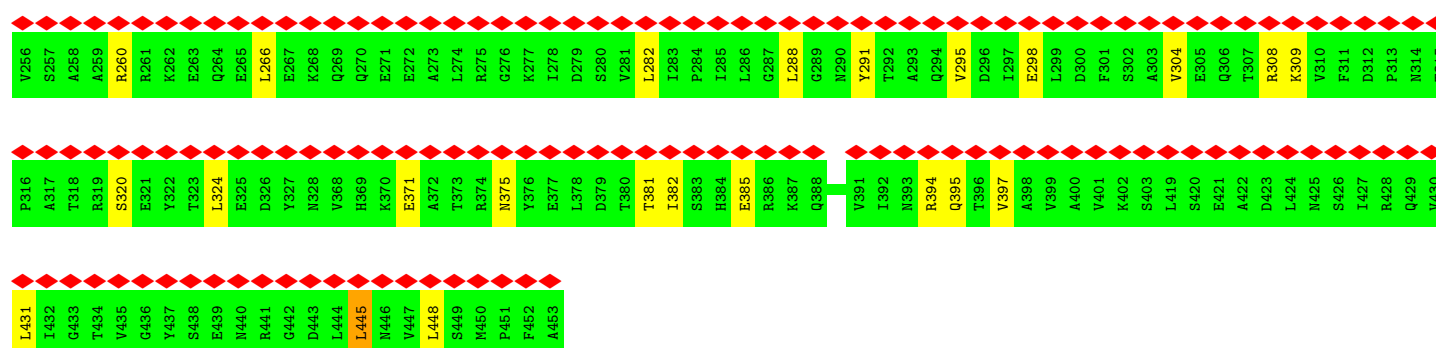
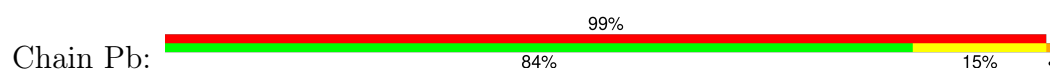


● Molecule 13: FliF

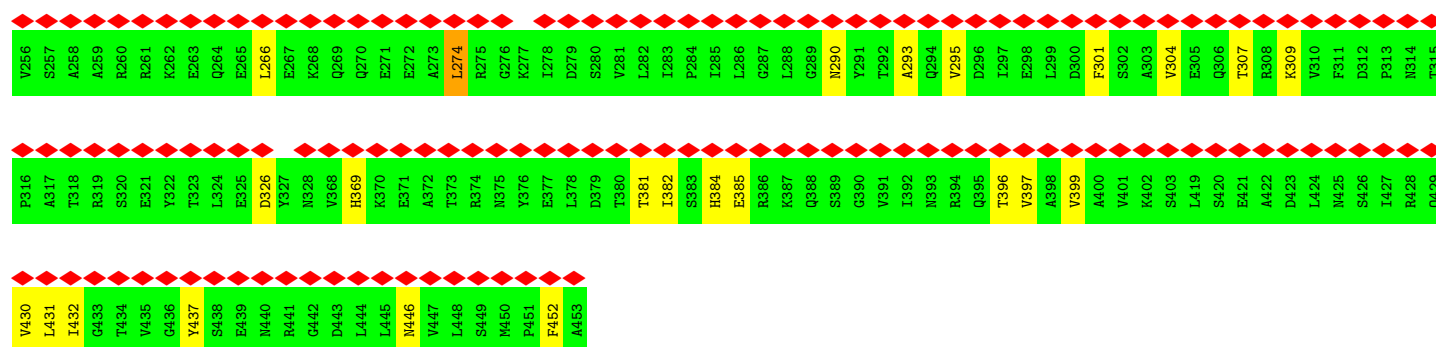
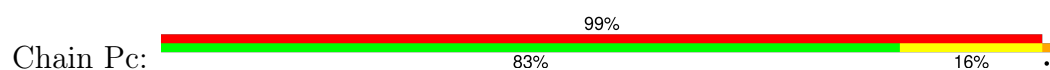




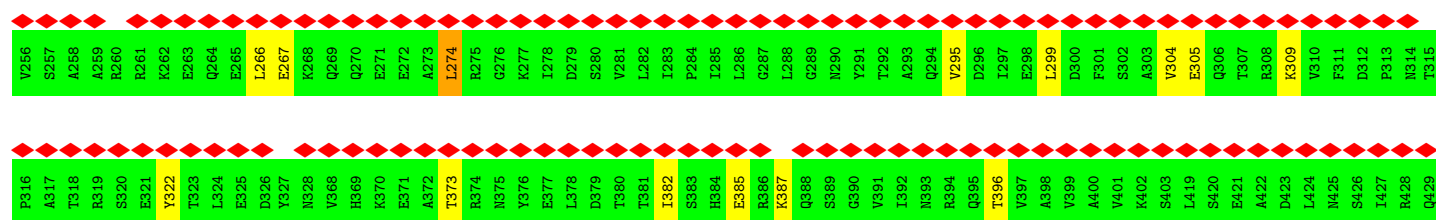
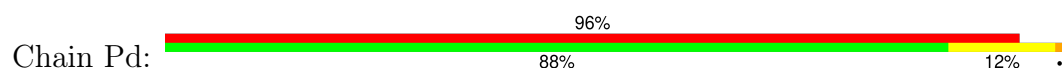
• Molecule 13: FliF



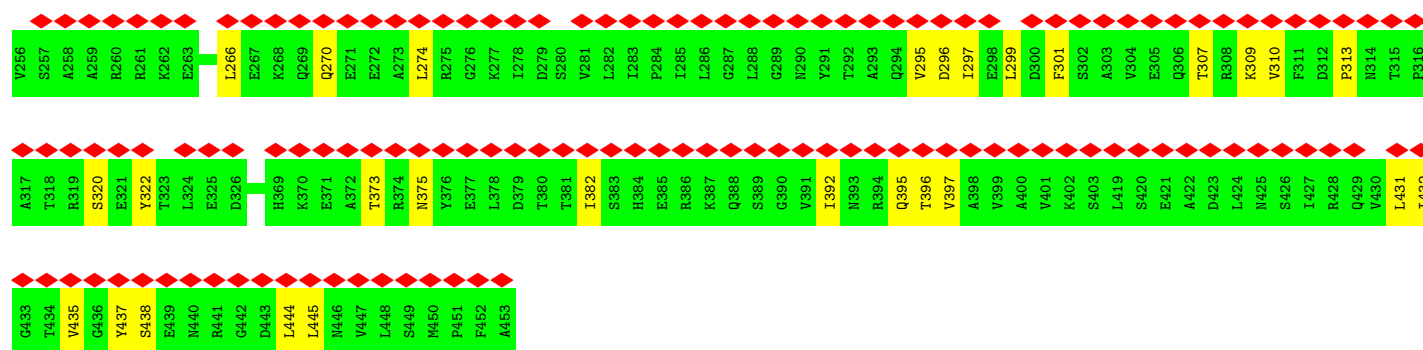
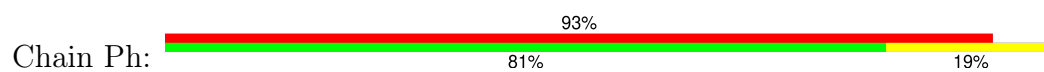
• Molecule 13: FliF



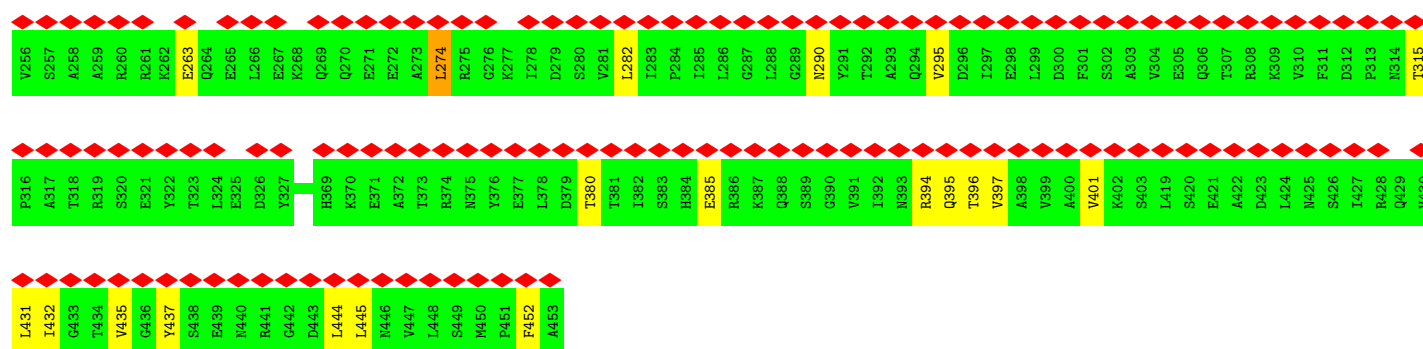
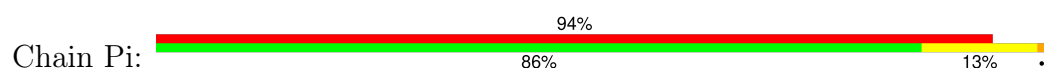
• Molecule 13: FliF



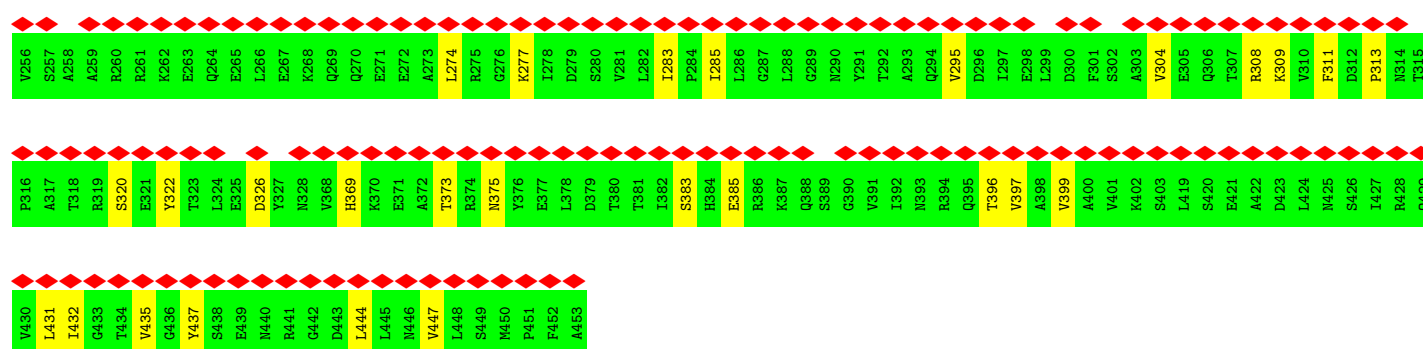
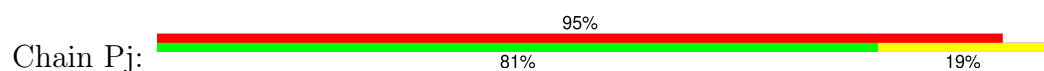




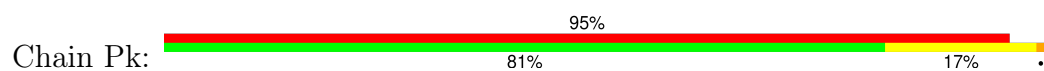
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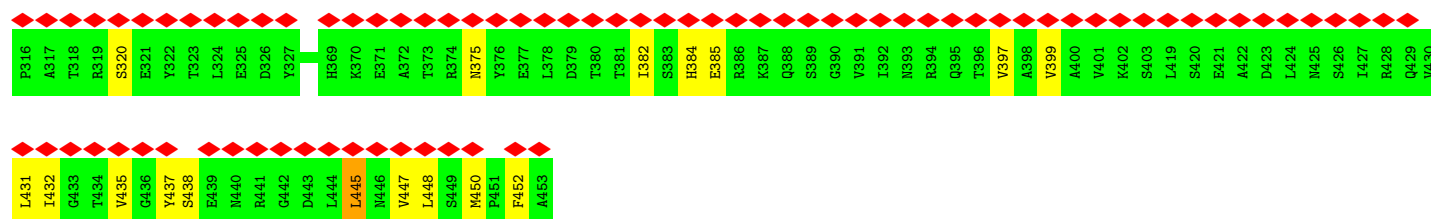


• Molecule 13: FlIF

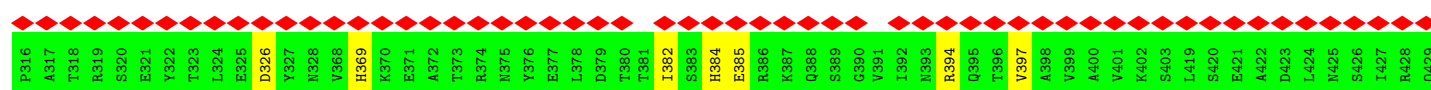
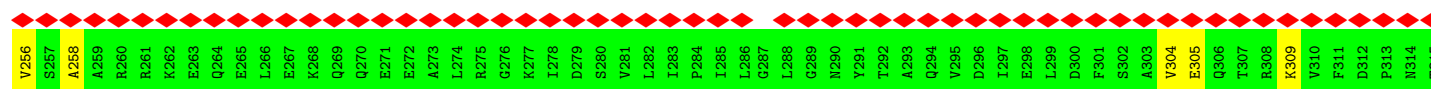
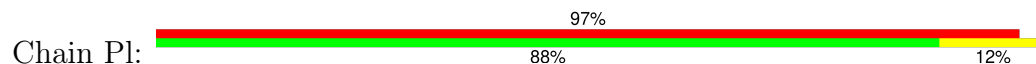


• Molecule 13: FlIF

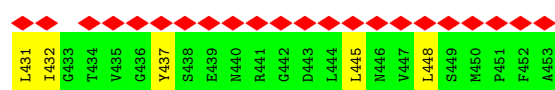
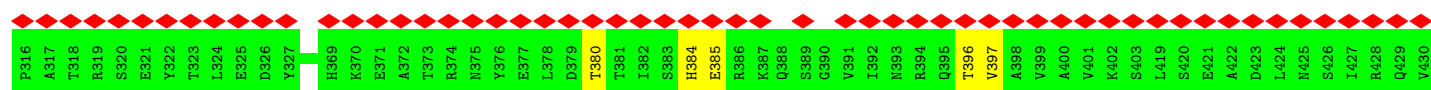
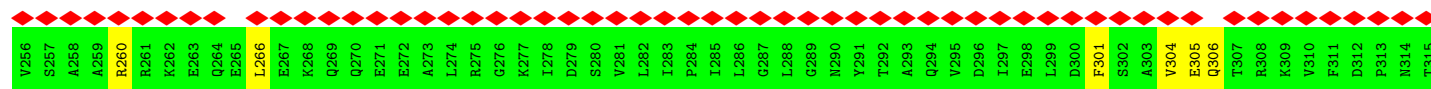




• Molecule 13: FliF

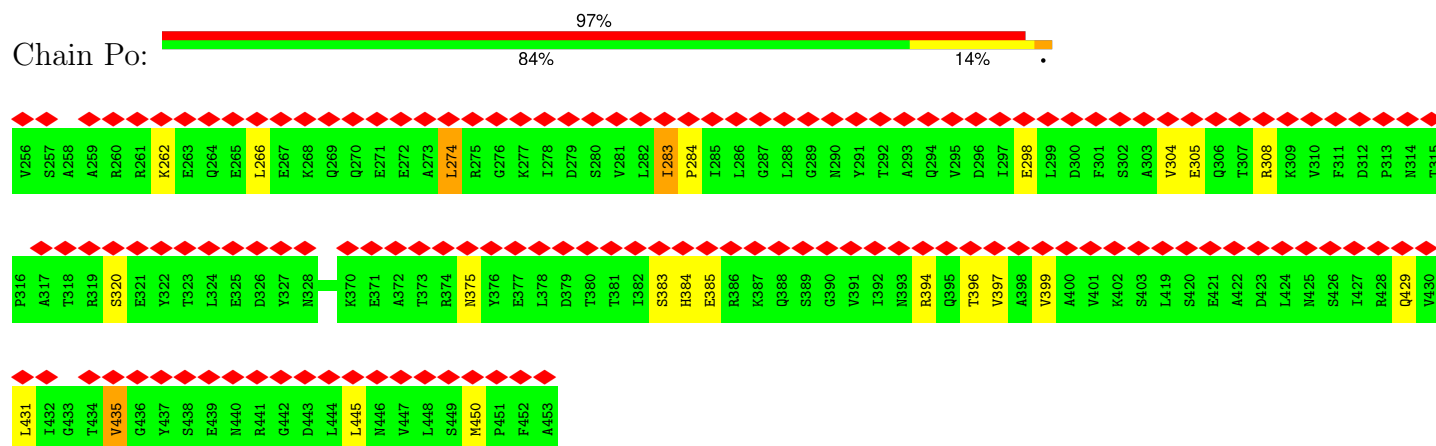


• Molecule 13: FliF



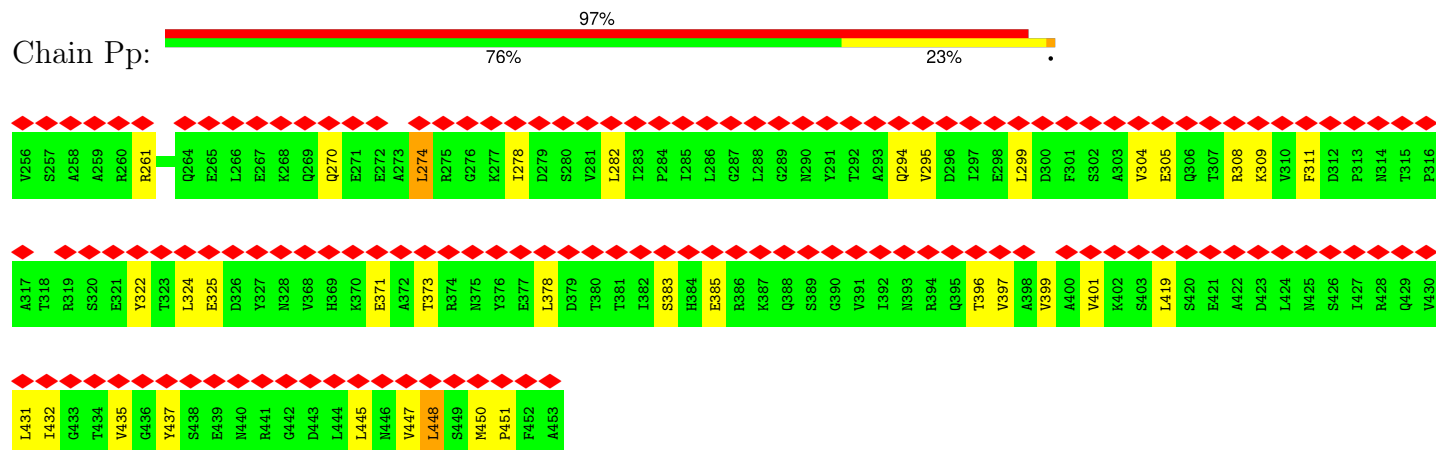
- Molecule 13: FliF

Chain Po:



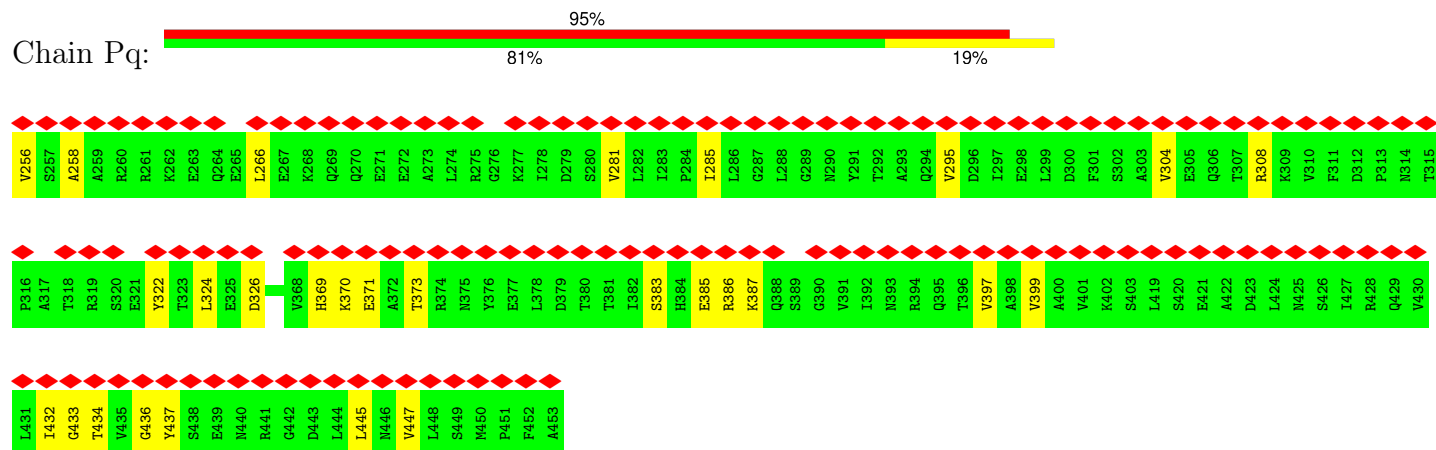
- Molecule 13: FliF

Chain Pp:



- Molecule 13: FliF

Chain Pq:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C13	Depositor
Number of particles used	53628	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	1.105	Depositor
Minimum map value	-0.764	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.046	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 ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Aa	0.10	0/1995	0.26	0/2704
1	Ab	0.11	0/1995	0.27	0/2704
1	Ac	0.10	0/1995	0.25	0/2704
1	Ad	0.10	0/1995	0.24	0/2704
1	Ae	0.11	0/1995	0.28	0/2704
1	Af	0.10	0/1995	0.25	0/2704
1	Ag	0.11	0/1995	0.29	0/2704
1	Ah	0.11	0/1995	0.27	0/2704
1	Ai	0.11	0/1995	0.26	0/2704
1	Aj	0.11	0/1995	0.26	0/2704
1	Ak	0.11	0/1995	0.26	0/2704
1	Al	0.10	0/1995	0.26	0/2704
1	Am	0.12	0/1992	0.30	0/2701
1	An	0.12	0/1995	0.26	0/2704
1	Ao	0.10	0/1995	0.26	0/2704
1	Ap	0.13	0/1917	0.26	0/2596
1	Aq	0.11	0/1995	0.28	0/2704
1	Ar	0.10	0/1886	0.26	0/2554
1	As	0.12	0/1995	0.29	0/2704
1	At	0.12	0/1913	0.27	0/2591
1	Au	0.11	0/1995	0.29	0/2704
1	Av	0.11	0/1882	0.27	0/2548
1	Aw	0.11	0/1995	0.27	0/2704
1	Ax	0.11	0/1899	0.28	0/2571
1	Ay	0.11	0/1888	0.27	0/2557
1	Az	0.10	0/1896	0.26	0/2567
1	Bb	0.11	0/1925	0.27	0/2607
2	Ba	0.09	0/1830	0.22	0/2466
2	Bc	0.09	0/1891	0.22	0/2550
2	Bd	0.09	0/1852	0.22	0/2495
2	Bv	0.09	0/1753	0.25	0/2363
2	Bw	0.08	0/1888	0.22	0/2545
3	Be	0.09	0/2080	0.24	0/2817
3	Bf	0.09	0/2080	0.24	0/2817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	Bg	0.08	0/2100	0.23	0/2842
3	Bh	0.09	0/2080	0.23	0/2817
3	Bi	0.08	0/2100	0.21	0/2842
3	Bj	0.09	0/2100	0.23	0/2842
3	Bk	0.08	0/2100	0.22	0/2842
3	Bl	0.08	0/2100	0.22	0/2842
3	Bm	0.09	0/2100	0.23	0/2842
3	Bn	0.09	0/2100	0.25	0/2842
3	Bo	0.08	0/2100	0.22	0/2842
3	Bp	0.08	0/2100	0.23	0/2842
3	Bq	0.09	0/2100	0.25	0/2842
3	Br	0.10	0/2100	0.25	0/2842
3	Bs	0.09	0/2100	0.24	0/2842
3	Bt	0.09	0/2100	0.23	0/2842
3	Bu	0.09	0/2100	0.22	0/2842
4	Bx	0.09	0/1699	0.24	0/2303
4	By	0.09	0/1699	0.24	0/2303
4	Bz	0.09	0/1699	0.24	0/2303
4	Ca	0.09	0/1699	0.24	0/2303
4	Cb	0.08	0/1699	0.24	0/2303
4	Cc	0.08	0/1699	0.24	0/2303
4	Cd	0.09	0/1699	0.24	0/2303
4	Ce	0.08	0/1699	0.25	0/2303
4	Cf	0.08	0/1699	0.24	0/2303
4	Cg	0.08	0/1699	0.24	0/2303
4	Ch	0.09	0/1699	0.24	0/2303
4	Ci	0.08	0/1699	0.24	0/2303
4	Cj	0.09	0/1699	0.24	0/2303
4	Ck	0.09	0/1699	0.24	0/2303
4	Cl	0.08	0/1699	0.24	0/2303
4	Cm	0.09	0/1699	0.24	0/2303
4	Cn	0.09	0/1699	0.24	0/2303
4	Co	0.09	0/1699	0.24	0/2303
4	Cp	0.08	0/1699	0.24	0/2303
4	Cq	0.08	0/1699	0.24	0/2303
4	Cr	0.09	0/1699	0.24	0/2303
4	Cs	0.09	0/1699	0.24	0/2303
4	Ct	0.09	0/1699	0.25	0/2303
4	Cu	0.09	0/1699	0.25	0/2303
4	Cv	0.08	0/1699	0.25	0/2303
4	Cw	0.09	0/1699	0.24	0/2303
5	Cx	0.09	0/2345	0.27	0/3177
5	Cy	0.09	0/2345	0.27	0/3177

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	Cz	0.09	0/2345	0.26	0/3177
5	Da	0.09	0/2345	0.27	0/3177
5	Db	0.09	0/2345	0.27	0/3177
5	Dc	0.10	0/2345	0.27	0/3177
5	Dd	0.09	0/2345	0.26	0/3177
5	De	0.09	0/2345	0.27	0/3177
5	Df	0.10	0/2345	0.27	0/3177
5	Dg	0.10	0/2345	0.27	0/3177
5	Dh	0.10	0/2345	0.27	0/3177
5	Di	0.09	0/2345	0.26	0/3177
5	Dj	0.10	0/2345	0.27	0/3177
5	Dk	0.09	0/2345	0.27	0/3177
5	Dl	0.10	0/2345	0.27	0/3177
5	Dm	0.10	0/2345	0.27	0/3177
5	Dn	0.10	0/2345	0.27	0/3177
5	Do	0.10	0/2345	0.27	0/3177
5	Dp	0.10	0/2345	0.26	0/3177
5	Dq	0.09	0/2345	0.27	0/3177
5	Dr	0.09	0/2345	0.27	0/3177
5	Ds	0.10	0/2345	0.27	0/3177
5	Dt	0.09	0/2345	0.27	0/3177
5	Du	0.09	0/2345	0.27	0/3177
5	Dv	0.10	0/2345	0.27	0/3177
5	Dw	0.10	0/2345	0.26	0/3177
6	Dx	0.10	0/2816	0.27	0/3809
6	Dy	0.13	0/2816	0.27	0/3809
6	Dz	0.10	0/2816	0.26	0/3809
6	Ea	0.11	0/2816	0.27	0/3809
6	Eb	0.98	6/2816 (0.2%)	0.28	0/3809
6	Ec	0.10	0/2816	0.27	0/3809
6	Ed	0.11	0/2816	0.27	0/3809
6	Ee	0.10	0/2816	0.28	0/3809
6	Ef	0.10	0/2816	0.27	0/3809
6	Eg	0.11	0/2816	0.26	0/3809
6	Uh	0.10	0/2816	0.27	0/3809
6	Ei	0.10	0/2816	0.28	0/3809
6	Ej	0.10	0/2816	0.26	0/3809
6	Ek	0.10	0/2816	0.27	0/3809
6	El	0.10	0/2816	0.27	0/3809
6	Em	0.10	0/2816	0.27	0/3809
6	En	0.10	0/2816	0.27	0/3809
6	Eo	1.67	6/2816 (0.2%)	0.29	1/3809 (0.0%)
6	Ep	0.10	0/2816	0.28	0/3809

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	Eq	0.11	0/2816	0.29	0/3809
6	Er	0.10	0/2816	0.27	0/3809
6	Es	0.10	0/2816	0.28	0/3809
6	Et	0.10	0/2816	0.27	0/3809
6	Eu	0.10	0/2816	0.26	0/3809
6	Ev	0.10	0/2816	0.27	0/3809
6	Ew	0.10	0/2816	0.27	0/3809
7	Ex	0.12	0/2129	0.29	0/2882
7	Ey	0.12	0/2124	0.32	0/2877
7	Ez	0.11	0/2129	0.28	0/2882
7	Fa	0.12	0/2124	0.32	0/2877
7	Fb	0.11	0/2129	0.28	0/2882
7	Fc	0.12	0/2124	0.32	0/2877
7	Fd	0.12	0/2129	0.28	0/2882
7	Fe	0.12	0/2124	0.33	0/2877
7	Ff	0.11	0/2129	0.28	0/2882
7	Fg	0.12	0/2124	0.31	0/2877
7	Fh	0.12	0/2129	0.29	0/2882
7	Fi	0.12	0/2124	0.32	0/2877
7	Fj	0.11	0/2129	0.28	0/2882
7	Fk	0.12	0/2124	0.32	0/2877
7	Fl	0.11	0/2129	0.28	0/2882
7	Fm	0.12	0/2124	0.32	0/2877
7	Fn	0.11	0/2129	0.28	0/2882
7	Fo	0.12	0/2124	0.32	0/2877
7	Fp	0.11	0/2129	0.28	0/2882
7	Fq	0.12	0/2124	0.32	0/2877
7	Fr	0.12	0/2129	0.30	0/2882
7	Fs	0.12	0/2124	0.32	0/2877
7	Ft	0.11	0/2129	0.28	0/2882
7	Fu	0.12	0/2124	0.32	0/2877
7	Fv	0.11	0/2129	0.30	0/2882
7	Fw	0.12	0/2124	0.32	0/2877
8	Fx	0.11	0/1494	0.31	0/2027
8	Fy	0.11	0/1523	0.30	0/2062
8	Fz	0.11	0/1494	0.31	0/2027
8	Ga	0.12	0/1523	0.31	0/2062
8	Gb	0.11	0/1494	0.31	0/2027
8	Gc	0.11	0/1523	0.30	0/2062
8	Gd	0.12	0/1494	0.31	0/2027
8	Ge	0.11	0/1523	0.31	0/2062
8	Gf	0.12	0/1494	0.31	0/2027
8	Gg	0.11	0/1523	0.30	0/2062

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	Gh	0.11	0/1494	0.31	0/2027
8	Gi	0.11	0/1523	0.30	0/2062
8	Gj	0.11	0/1494	0.31	0/2027
8	Gk	0.12	0/1523	0.31	0/2062
8	Gl	0.11	0/1494	0.31	0/2027
8	Gm	0.12	0/1523	0.31	0/2062
8	Gn	0.12	0/1494	0.31	0/2027
8	Go	0.11	0/1523	0.31	0/2062
8	Gp	0.11	0/1494	0.31	0/2027
8	Gq	0.11	0/1523	0.31	0/2062
8	Gr	0.12	0/1494	0.31	0/2027
8	Gs	0.12	0/1523	0.31	0/2062
8	Gt	0.11	0/1494	0.30	0/2027
8	Gu	0.11	0/1523	0.30	0/2062
8	Gv	0.12	0/1494	0.31	0/2027
8	Gw	0.11	0/1523	0.30	0/2062
9	Gx	0.13	0/106	0.35	0/139
9	Gy	0.13	0/106	0.32	0/139
9	Gz	0.15	0/106	0.39	0/139
9	Ha	0.16	0/106	0.41	0/139
9	Hb	0.14	0/106	0.36	0/139
9	Hc	0.14	0/106	0.37	0/139
9	Hd	0.12	0/106	0.36	0/139
9	He	0.18	0/106	0.40	0/139
9	Hf	0.16	0/106	0.40	0/139
9	Hg	0.15	0/106	0.36	0/139
9	Hh	0.17	0/106	0.39	0/139
9	Hi	0.15	0/106	0.40	0/139
9	Hj	0.16	0/106	0.43	0/139
9	Hk	0.12	0/106	0.35	0/139
9	Hl	0.15	0/106	0.39	0/139
9	Hm	0.15	0/106	0.36	0/139
9	Hn	0.16	0/106	0.38	0/139
9	Ho	0.14	0/106	0.34	0/139
9	Hp	0.14	0/106	0.36	0/139
9	Hq	0.17	0/106	0.40	0/139
9	Hr	0.14	0/106	0.42	0/139
9	Hs	0.16	0/106	0.40	0/139
9	Ht	0.13	0/106	0.36	0/139
9	Hu	0.15	0/106	0.39	0/139
9	Hv	0.18	0/106	0.41	0/139
9	Hw	0.13	0/106	0.41	0/139
9	Hx	0.14	0/106	0.39	0/139

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	Hy	0.14	0/106	0.40	0/139
9	Hx	0.15	0/106	0.40	0/139
9	Ia	0.12	0/106	0.36	0/139
9	Ib	0.14	0/106	0.37	0/139
9	Ic	0.14	0/106	0.37	0/139
9	Id	0.16	0/106	0.39	0/139
9	Ie	0.14	0/106	0.38	0/139
9	If	0.12	0/106	0.39	0/139
9	Ig	0.11	0/106	0.37	0/139
9	Ih	0.15	0/106	0.41	0/139
9	Ii	0.13	0/106	0.38	0/139
9	Ij	0.14	0/106	0.38	0/139
9	Ik	0.15	0/106	0.39	0/139
9	Il	0.12	0/106	0.38	0/139
9	Im	0.12	0/106	0.40	0/139
9	In	0.12	0/106	0.39	0/139
9	Io	0.15	0/106	0.39	0/139
9	Ip	0.13	0/106	0.36	0/139
9	Iq	0.14	0/106	0.41	0/139
9	Ir	0.11	0/106	0.37	0/139
9	Is	0.12	0/106	0.44	0/139
9	It	0.19	0/106	0.54	0/139
9	Iu	0.15	0/106	0.38	0/139
9	Iv	0.12	0/106	0.38	0/139
9	Iw	0.15	0/106	0.38	0/139
10	Ix	0.11	0/1245	0.27	0/1674
10	Iy	0.11	0/1245	0.27	0/1674
10	Iz	0.11	0/1245	0.27	0/1674
10	Ja	0.11	0/1245	0.27	0/1674
10	Jb	0.11	0/1245	0.27	0/1674
10	Jc	0.11	0/1245	0.27	0/1674
10	Jd	0.12	0/1245	0.27	0/1674
10	Je	0.11	0/1245	0.27	0/1674
10	Jf	0.11	0/1245	0.27	0/1674
10	Jg	0.11	0/1245	0.27	0/1674
10	Jh	0.11	0/1245	0.27	0/1674
10	Ji	0.11	0/1245	0.27	0/1674
10	Jj	0.11	0/1245	0.27	0/1674
10	Jk	0.11	0/1245	0.27	0/1674
10	Jl	0.11	0/1245	0.27	0/1674
10	Jm	0.11	0/1245	0.27	0/1674
10	Jn	0.11	0/1245	0.27	0/1674
10	Jo	0.11	0/1245	0.27	0/1674

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
10	Jp	0.11	0/1245	0.27	0/1674
10	Jq	0.11	0/1245	0.28	0/1674
10	Jr	0.11	0/1245	0.27	0/1674
10	Js	0.11	0/1245	0.27	0/1674
10	Jt	0.11	0/1245	0.27	0/1674
10	Ju	0.11	0/1245	0.27	0/1674
10	Jv	0.11	0/1245	0.27	0/1674
10	Jw	0.11	0/1245	0.27	0/1674
11	Jx	2.72	1/836 (0.1%)	0.42	2/1119 (0.2%)
11	Jy	0.11	0/836	0.28	0/1119
11	Jz	0.11	0/836	0.29	0/1119
11	Ka	0.11	0/836	0.27	0/1119
11	Kb	0.11	0/836	0.27	0/1119
11	Kc	0.11	0/836	0.29	0/1119
11	Kd	0.10	0/836	0.27	0/1119
11	Ke	0.11	0/836	0.27	0/1119
11	Kf	0.10	0/836	0.29	0/1119
11	Kg	0.11	0/836	0.28	0/1119
11	Kh	0.10	0/836	0.28	0/1119
11	Ki	0.10	0/836	0.27	0/1119
11	Kj	0.10	0/836	0.27	0/1119
11	Kk	0.11	0/836	0.27	0/1119
11	Kl	0.11	0/836	0.28	0/1119
11	Km	0.11	0/836	0.28	0/1119
11	Kn	0.11	0/836	0.30	0/1119
11	Ko	0.10	0/836	0.27	0/1119
11	Kp	0.10	0/836	0.28	0/1119
11	Kq	0.10	0/836	0.30	0/1119
11	Kr	0.11	0/836	0.28	0/1119
11	Ks	0.11	0/836	0.28	0/1119
11	Kt	0.10	0/836	0.27	0/1119
11	Ku	0.11	0/836	0.27	0/1119
11	Kv	0.11	0/836	0.27	0/1119
11	Kw	0.11	0/836	0.28	0/1119
11	Kx	0.10	0/836	0.29	0/1119
11	Ky	0.11	0/836	0.27	0/1119
11	Kz	0.10	0/836	0.27	0/1119
11	La	0.93	2/836 (0.2%)	0.86	3/1119 (0.3%)
11	Lb	0.11	0/836	0.28	0/1119
11	Lc	0.11	0/836	0.30	0/1119
11	Ld	0.11	0/836	0.31	0/1119
11	Le	0.11	0/836	0.27	0/1119
11	Lf	0.11	0/836	0.30	0/1119

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	Lg	0.10	0/836	0.27	0/1119
11	Lh	0.10	0/836	0.27	0/1119
11	Li	0.11	0/836	0.28	0/1119
11	Lj	0.10	0/836	0.29	0/1119
11	Lk	0.11	0/836	0.30	0/1119
11	Ll	0.11	0/836	0.27	0/1119
11	Lm	0.10	0/836	0.28	0/1119
11	Ln	0.10	0/836	0.30	0/1119
11	Lo	0.11	0/836	0.28	0/1119
11	Lp	0.11	0/836	0.27	0/1119
11	Lq	0.11	0/836	0.30	0/1119
11	Lr	0.11	0/836	0.28	0/1119
11	Ls	0.11	0/836	0.28	0/1119
11	Lt	0.11	0/836	0.27	0/1119
11	Lu	0.10	0/836	0.27	0/1119
11	Lv	0.11	0/836	0.28	0/1119
11	Lw	0.10	0/836	0.27	0/1119
11	Lx	0.11	0/836	0.27	0/1119
11	Ly	0.11	0/836	0.28	0/1119
11	Lz	0.11	0/836	0.28	0/1119
11	Ma	0.10	0/836	0.27	0/1119
11	Mb	0.11	0/836	0.27	0/1119
11	Mc	0.10	0/836	0.29	0/1119
12	Md	0.10	0/1508	0.28	0/2045
12	Me	0.10	0/1508	0.28	0/2045
12	Mf	0.10	0/1508	0.28	0/2045
12	Mg	0.10	0/1508	0.28	0/2045
12	Mh	0.10	0/1508	0.28	0/2045
12	Mi	0.10	0/1508	0.28	0/2045
12	Mj	0.10	0/1508	0.28	0/2045
12	Mk	0.10	0/1508	0.29	0/2045
12	Ml	0.10	0/1508	0.28	0/2045
12	Mm	0.10	0/1508	0.28	0/2045
12	Mn	0.10	0/1508	0.28	0/2045
12	Mo	0.10	0/1508	0.28	0/2045
12	Mp	0.10	0/1508	0.28	0/2045
12	Mq	0.10	0/1508	0.28	0/2045
12	Mr	0.10	0/1508	0.28	0/2045
12	Ms	0.10	0/1508	0.28	0/2045
12	Mt	0.10	0/1508	0.28	0/2045
12	Mu	0.10	0/1508	0.28	0/2045
12	Mv	0.10	0/1508	0.28	0/2045
12	Mw	0.10	0/1508	0.28	0/2045

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
12	Mx	0.10	0/1508	0.28	0/2045
12	My	0.10	0/1508	0.28	0/2045
12	Mz	0.10	0/1508	0.28	0/2045
12	Na	0.10	0/1508	0.28	0/2045
12	Nb	0.10	0/1508	0.28	0/2045
12	Nc	0.10	0/1508	0.28	0/2045
12	Nd	0.10	0/1508	0.28	0/2045
12	Ne	0.10	0/1508	0.28	0/2045
12	Nf	0.10	0/1508	0.28	0/2045
12	Ng	0.10	0/1508	0.28	0/2045
12	Nh	0.10	0/1508	0.28	0/2045
12	Ni	0.10	0/1508	0.28	0/2045
12	Nj	0.10	0/1508	0.28	0/2045
12	Nk	0.10	0/1508	0.28	0/2045
12	Nl	0.10	0/1508	0.28	0/2045
12	Nm	0.10	0/1508	0.28	0/2045
12	Nn	0.10	0/1508	0.28	0/2045
12	No	0.10	0/1508	0.28	0/2045
12	Np	0.10	0/1508	0.28	0/2045
12	Nq	0.10	0/1508	0.28	0/2045
12	Nr	0.10	0/1508	0.28	0/2045
12	Ns	0.10	0/1508	0.28	0/2045
12	Nt	0.10	0/1508	0.28	0/2045
12	Nu	0.10	0/1508	0.28	0/2045
12	Nv	0.10	0/1508	0.28	0/2045
12	Nw	0.10	0/1508	0.28	0/2045
12	Nx	0.10	0/1508	0.28	0/2045
12	Ny	0.10	0/1508	0.28	0/2045
12	Nz	0.10	0/1508	0.28	0/2045
12	Oa	0.10	0/1508	0.28	0/2045
12	Ob	0.10	0/1508	0.28	0/2045
12	Oc	0.10	0/1508	0.28	0/2045
12	Od	0.10	0/1508	0.28	0/2045
12	Oe	0.10	0/1508	0.28	0/2045
12	Of	0.10	0/1508	0.28	0/2045
12	Og	0.10	0/1508	0.28	0/2045
12	Oh	0.10	0/1508	0.28	0/2045
12	Oi	0.10	0/1508	0.28	0/2045
13	Oj	0.11	0/1145	0.30	0/1546
13	Ok	0.12	0/1145	0.30	0/1546
13	Ol	0.12	0/1145	0.29	0/1546
13	Om	0.11	0/1145	0.28	0/1546
13	On	0.10	0/1145	0.27	0/1546

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	Oo	0.12	0/1145	0.32	0/1546
13	Op	0.11	0/1145	0.28	0/1546
13	Oq	0.11	0/1145	0.31	0/1546
13	Or	0.11	0/1145	0.27	0/1546
13	Os	0.12	0/1145	0.28	0/1546
13	Ot	0.12	0/1145	0.29	0/1546
13	Ou	0.11	0/1145	0.30	0/1546
13	Ov	0.11	0/1145	0.28	0/1546
13	Ow	0.12	0/1145	0.28	0/1546
13	Ox	0.11	0/1145	0.27	0/1546
13	Oy	0.13	0/1145	0.30	0/1546
13	Oz	0.11	0/1145	0.27	0/1546
13	Pa	0.11	0/1145	0.29	0/1546
13	Pb	0.11	0/1145	0.28	0/1546
13	Pc	0.11	0/1145	0.28	0/1546
13	Pd	0.13	0/1145	0.29	0/1546
13	Pe	0.11	0/1145	0.27	0/1546
13	Pf	0.11	0/1145	0.29	0/1546
13	Pg	0.11	0/1145	0.29	0/1546
13	Ph	0.13	0/1145	0.28	0/1546
13	Pi	0.11	0/1145	0.26	0/1546
13	Pj	0.13	0/1145	0.29	0/1546
13	Pk	0.11	0/1145	0.28	0/1546
13	Pl	0.12	0/1145	0.28	0/1546
13	Pm	0.12	0/1145	0.30	0/1546
13	Pn	0.12	0/1145	0.28	0/1546
13	Po	0.11	0/1145	0.32	0/1546
13	Pp	0.13	0/1145	0.27	0/1546
13	Pq	0.11	0/1145	0.33	0/1546
All	All	0.20	15/583596 (0.0%)	0.28	6/788988 (0.0%)

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	Jx	73	ARG	CG-CD	78.42	3.87	1.52
6	Eo	109	TYR	CD1-CE1	47.31	2.80	1.38
6	Eo	109	TYR	CD2-CE2	44.19	2.71	1.38
6	Eo	109	TYR	CE2-CZ	32.46	2.16	1.38
6	Eo	109	TYR	CE1-CZ	31.94	2.15	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	La	73	ARG	CD-NE-CZ	25.17	159.63	124.40
11	Jx	73	ARG	CB-CG-CD	8.80	131.53	111.30
11	La	73	ARG	CG-CD-NE	7.36	128.20	112.00
11	La	73	ARG	NE-CZ-NH1	5.94	127.44	121.50
11	Jx	73	ARG	CG-CD-NE	5.28	123.61	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Aa	1969	0	1936	24	0
1	Ab	1969	0	1936	27	0
1	Ac	1969	0	1936	24	0
1	Ad	1969	0	1936	27	0
1	Ae	1969	0	1936	23	0
1	Af	1969	0	1936	22	0
1	Ag	1969	0	1936	20	0
1	Ah	1969	0	1936	31	0
1	Ai	1969	0	1936	25	0
1	Aj	1969	0	1936	29	0
1	Ak	1969	0	1936	28	0
1	Al	1969	0	1936	27	0
1	Am	1966	0	1929	20	0
1	An	1969	0	1936	18	0
1	Ao	1969	0	1936	25	0
1	Ap	1893	0	1860	15	0
1	Aq	1969	0	1936	27	0
1	Ar	1863	0	1834	27	0
1	As	1969	0	1936	28	0
1	At	1889	0	1857	27	0
1	Au	1969	0	1936	16	0
1	Av	1859	0	1831	16	0
1	Aw	1969	0	1936	30	0
1	Ax	1876	0	1845	22	0
1	Ay	1864	0	1837	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Az	1873	0	1842	19	0
1	Bb	1900	0	1868	18	0
2	Ba	1811	0	1818	15	0
2	Bc	1870	0	1872	12	0
2	Bd	1833	0	1840	14	0
2	Bv	1737	0	1738	14	0
2	Bw	1868	0	1866	17	0
3	Be	2045	0	1967	15	0
3	Bf	2045	0	1967	18	0
3	Bg	2065	0	1991	13	0
3	Bh	2045	0	1967	7	0
3	Bi	2065	0	1991	7	0
3	Bj	2065	0	1991	16	0
3	Bk	2065	0	1991	11	0
3	Bl	2065	0	1991	17	0
3	Bm	2065	0	1991	22	0
3	Bn	2065	0	1991	14	0
3	Bo	2065	0	1991	16	0
3	Bp	2065	0	1991	10	0
3	Bq	2065	0	1991	21	0
3	Br	2065	0	1991	26	0
3	Bs	2065	0	1991	16	0
3	Bt	2065	0	1991	19	0
3	Bu	2065	0	1991	14	0
4	Bx	1674	0	1609	38	0
4	By	1674	0	1609	35	0
4	Bz	1674	0	1609	36	0
4	Ca	1674	0	1609	36	0
4	Cb	1674	0	1609	34	0
4	Cc	1674	0	1609	34	0
4	Cd	1674	0	1609	33	0
4	Ce	1674	0	1609	35	0
4	Cf	1674	0	1609	36	0
4	Cg	1674	0	1609	31	0
4	Ch	1674	0	1609	34	0
4	Ci	1674	0	1609	35	0
4	Cj	1674	0	1609	30	0
4	Ck	1674	0	1609	31	0
4	Cl	1674	0	1609	31	0
4	Cm	1674	0	1609	34	0
4	Cn	1674	0	1609	34	0
4	Co	1674	0	1609	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Cp	1674	0	1609	34	0
4	Cq	1674	0	1609	32	0
4	Cr	1674	0	1609	34	0
4	Cs	1674	0	1609	33	0
4	Ct	1674	0	1609	36	0
4	Cu	1674	0	1609	41	0
4	Cv	1674	0	1609	37	0
4	Cw	1674	0	1609	39	0
5	Cx	2314	0	2373	35	0
5	Cy	2314	0	2373	32	0
5	Cz	2314	0	2373	33	0
5	Da	2314	0	2373	33	0
5	Db	2314	0	2373	32	0
5	Dc	2314	0	2373	34	0
5	Dd	2314	0	2373	33	0
5	De	2314	0	2373	35	0
5	Df	2314	0	2373	34	0
5	Dg	2314	0	2373	34	0
5	Dh	2314	0	2373	34	0
5	Di	2314	0	2373	33	0
5	Dj	2314	0	2373	33	0
5	Dk	2314	0	2373	34	0
5	Dl	2314	0	2373	33	0
5	Dm	2314	0	2373	34	0
5	Dn	2314	0	2373	32	0
5	Do	2314	0	2373	33	0
5	Dp	2314	0	2373	34	0
5	Dq	2314	0	2373	33	0
5	Dr	2314	0	2373	35	0
5	Ds	2314	0	2373	33	0
5	Dt	2314	0	2373	31	0
5	Du	2314	0	2373	31	0
5	Dv	2314	0	2373	33	0
5	Dw	2314	0	2373	32	0
6	Dx	2770	0	2749	19	0
6	Dy	2770	0	2749	19	0
6	Dz	2770	0	2749	22	0
6	Ea	2770	0	2749	19	0
6	Eb	2770	0	2749	47	0
6	Ec	2770	0	2749	24	0
6	Ed	2770	0	2749	18	0
6	Ee	2770	0	2749	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Ef	2770	0	2749	19	0
6	Eg	2770	0	2749	19	0
6	Uh	2770	0	2749	21	0
6	Ei	2770	0	2749	18	0
6	Ej	2770	0	2749	17	0
6	Ek	2770	0	2749	25	0
6	El	2770	0	2749	17	0
6	Em	2770	0	2749	23	0
6	En	2770	0	2749	16	0
6	Uo	2770	0	2749	48	0
6	Ep	2770	0	2749	24	0
6	Eq	2770	0	2749	23	0
6	Er	2770	0	2749	21	0
6	Es	2770	0	2749	17	0
6	Et	2770	0	2749	20	0
6	Eu	2770	0	2749	20	0
6	Ev	2770	0	2749	24	0
6	Uw	2770	0	2749	19	0
7	Ex	2085	0	2022	13	0
7	Ey	2080	0	2003	13	0
7	Ez	2085	0	2022	13	0
7	Fa	2080	0	2003	16	0
7	Fb	2085	0	2022	11	0
7	Fc	2080	0	2003	15	0
7	Fd	2085	0	2022	11	0
7	Fe	2080	0	2003	14	0
7	Ff	2085	0	2022	11	0
7	Fg	2080	0	2003	15	0
7	Fh	2085	0	2022	11	0
7	Fi	2080	0	2003	13	0
7	Fj	2085	0	2022	12	0
7	Fk	2080	0	2003	17	0
7	Fl	2085	0	2022	11	0
7	Fm	2080	0	2003	15	0
7	Fn	2085	0	2022	9	0
7	Fo	2080	0	2003	12	0
7	Fp	2085	0	2022	11	0
7	Fq	2080	0	2003	15	0
7	Fr	2085	0	2022	14	0
7	Fs	2080	0	2003	14	0
7	Ft	2085	0	2022	13	0
7	Fu	2080	0	2003	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Fv	2085	0	2022	12	0
7	Fw	2080	0	2003	14	0
8	Fx	1466	0	1434	10	0
8	Fy	1494	0	1478	9	0
8	Fz	1466	0	1434	8	0
8	Ga	1494	0	1478	12	0
8	Gb	1466	0	1434	13	0
8	Gc	1494	0	1478	9	0
8	Gd	1466	0	1434	10	0
8	Ge	1494	0	1478	10	0
8	Gf	1466	0	1434	10	0
8	Gg	1494	0	1478	10	0
8	Gh	1466	0	1434	12	0
8	Gi	1494	0	1478	11	0
8	Gj	1466	0	1434	13	0
8	Gk	1494	0	1478	8	0
8	Gl	1466	0	1434	13	0
8	Gm	1494	0	1478	9	0
8	Gn	1466	0	1434	11	0
8	Go	1494	0	1478	9	0
8	Gp	1466	0	1434	11	0
8	Gq	1494	0	1478	10	0
8	Gr	1466	0	1434	10	0
8	Gs	1494	0	1478	10	0
8	Gt	1466	0	1434	11	0
8	Gu	1494	0	1478	10	0
8	Gv	1466	0	1434	11	0
8	Gw	1494	0	1478	10	0
9	Gx	105	0	107	1	0
9	Gy	105	0	107	2	0
9	Gz	105	0	107	0	0
9	Ha	105	0	107	1	0
9	Hb	105	0	107	2	0
9	Hc	105	0	107	1	0
9	Hd	105	0	107	0	0
9	He	105	0	107	1	0
9	Hf	105	0	107	0	0
9	Hg	105	0	107	2	0
9	Hh	105	0	107	1	0
9	Hi	105	0	107	1	0
9	Hj	105	0	107	1	0
9	Hk	105	0	107	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	Hl	105	0	107	1	0
9	Hm	105	0	107	0	0
9	Hn	105	0	107	1	0
9	Ho	105	0	107	0	0
9	Hp	105	0	107	2	0
9	Hq	105	0	107	1	0
9	Hr	105	0	107	1	0
9	Hs	105	0	107	1	0
9	Ht	105	0	107	1	0
9	Hu	105	0	107	1	0
9	Hv	105	0	107	1	0
9	Hw	105	0	107	1	0
9	Hx	105	0	107	0	0
9	Hy	105	0	107	1	0
9	Hz	105	0	107	2	0
9	Ia	105	0	107	0	0
9	Ib	105	0	107	0	0
9	Ic	105	0	107	2	0
9	Id	105	0	107	1	0
9	Ie	105	0	107	0	0
9	If	105	0	107	0	0
9	Ig	105	0	107	0	0
9	Ih	105	0	107	0	0
9	Ii	105	0	107	1	0
9	Ij	105	0	107	1	0
9	Ik	105	0	107	0	0
9	Il	105	0	107	1	0
9	Im	105	0	107	0	0
9	In	105	0	107	0	0
9	Io	105	0	107	0	0
9	Ip	105	0	107	1	0
9	Iq	105	0	107	0	0
9	Ir	105	0	107	0	0
9	Is	105	0	107	0	0
9	It	105	0	107	3	0
9	Iu	105	0	107	1	0
9	Iv	105	0	107	0	0
9	Iw	105	0	107	1	0
10	Ix	1231	0	1240	15	0
10	Iy	1231	0	1240	16	0
10	Iz	1231	0	1240	15	0
10	Ja	1231	0	1240	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	Jb	1231	0	1240	13	0
10	Jc	1231	0	1240	16	0
10	Jd	1231	0	1240	12	0
10	Je	1231	0	1240	15	0
10	Jf	1231	0	1240	13	0
10	Jg	1231	0	1240	16	0
10	Jh	1231	0	1240	14	0
10	Ji	1231	0	1240	16	0
10	Jj	1231	0	1240	14	0
10	Jk	1231	0	1240	15	0
10	Jl	1231	0	1240	14	0
10	Jm	1231	0	1240	16	0
10	Jn	1231	0	1240	14	0
10	Jo	1231	0	1240	19	0
10	Jp	1231	0	1240	13	0
10	Jq	1231	0	1240	18	0
10	Jr	1231	0	1240	14	0
10	Js	1231	0	1240	17	0
10	Jt	1231	0	1240	14	0
10	Ju	1231	0	1240	17	0
10	Jv	1231	0	1240	14	0
10	Jw	1231	0	1240	17	0
11	Jx	828	0	820	30	0
11	Jy	828	0	820	11	0
11	Jz	828	0	820	10	0
11	Ka	828	0	820	9	0
11	Kb	828	0	820	11	0
11	Kc	828	0	820	9	0
11	Kd	828	0	820	9	0
11	Ke	828	0	820	8	0
11	Kf	828	0	820	8	0
11	Kg	828	0	820	11	0
11	Kh	828	0	820	10	0
11	Ki	828	0	820	10	0
11	Kj	828	0	820	12	0
11	Kk	828	0	820	9	0
11	Kl	828	0	820	10	0
11	Km	828	0	820	8	0
11	Kn	828	0	820	8	0
11	Ko	828	0	820	9	0
11	Kp	828	0	820	8	0
11	Kq	828	0	820	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Kr	828	0	820	10	0
11	Ks	828	0	820	11	0
11	Kt	828	0	820	11	0
11	Ku	828	0	820	9	0
11	Kv	828	0	820	8	0
11	Kw	828	0	820	8	0
11	Kx	828	0	820	8	0
11	Ky	828	0	820	9	0
11	Kz	828	0	820	9	0
11	La	828	0	820	36	0
11	Lb	828	0	820	10	0
11	Lc	828	0	820	9	0
11	Ld	828	0	820	9	0
11	Le	828	0	820	11	0
11	Lf	828	0	820	10	0
11	Lg	828	0	820	9	0
11	Lh	828	0	820	8	0
11	Li	828	0	820	7	0
11	Lj	828	0	820	9	0
11	Lk	828	0	820	10	0
11	Ll	828	0	820	10	0
11	Lm	828	0	820	10	0
11	Ln	828	0	820	9	0
11	Lo	828	0	820	8	0
11	Lp	828	0	820	9	0
11	Lq	828	0	820	9	0
11	Lr	828	0	820	9	0
11	Ls	828	0	820	8	0
11	Lt	828	0	820	9	0
11	Lu	828	0	820	9	0
11	Lv	828	0	820	10	0
11	Lw	828	0	820	9	0
11	Lx	828	0	820	7	0
11	Ly	828	0	820	6	0
11	Lz	828	0	820	8	0
11	Ma	828	0	820	8	0
11	Mb	828	0	820	7	0
11	Mc	828	0	820	8	0
12	Md	1482	0	1448	13	0
12	Me	1482	0	1448	14	0
12	Mf	1482	0	1448	14	0
12	Mg	1482	0	1448	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	Mh	1482	0	1448	13	0
12	Mi	1482	0	1448	13	0
12	Mj	1482	0	1448	13	0
12	Mk	1482	0	1448	13	0
12	Ml	1482	0	1448	14	0
12	Mm	1482	0	1448	13	0
12	Mn	1482	0	1448	14	0
12	Mo	1482	0	1448	13	0
12	Mp	1482	0	1448	14	0
12	Mq	1482	0	1448	13	0
12	Mr	1482	0	1448	13	0
12	Ms	1482	0	1448	13	0
12	Mt	1482	0	1448	13	0
12	Mu	1482	0	1448	13	0
12	Mv	1482	0	1448	13	0
12	Mw	1482	0	1448	13	0
12	Mx	1482	0	1448	13	0
12	My	1482	0	1448	13	0
12	Mz	1482	0	1448	14	0
12	Na	1482	0	1448	13	0
12	Nb	1482	0	1448	14	0
12	Nc	1482	0	1448	13	0
12	Nd	1482	0	1448	13	0
12	Ne	1482	0	1448	13	0
12	Nf	1482	0	1448	13	0
12	Ng	1482	0	1448	14	0
12	Nh	1482	0	1448	14	0
12	Ni	1482	0	1448	14	0
12	Nj	1482	0	1448	13	0
12	Nk	1482	0	1448	13	0
12	Nl	1482	0	1448	13	0
12	Nm	1482	0	1448	13	0
12	Nn	1482	0	1448	13	0
12	No	1482	0	1448	14	0
12	Np	1482	0	1448	13	0
12	Nq	1482	0	1448	14	0
12	Nr	1482	0	1448	13	0
12	Ns	1482	0	1448	13	0
12	Nt	1482	0	1448	13	0
12	Nu	1482	0	1448	13	0
12	Nv	1482	0	1448	14	0
12	Nw	1482	0	1448	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	Nx	1482	0	1448	14	0
12	Ny	1482	0	1448	13	0
12	Nz	1482	0	1448	14	0
12	Oa	1482	0	1448	13	0
12	Ob	1482	0	1448	13	0
12	Oc	1482	0	1448	13	0
12	Od	1482	0	1448	13	0
12	Oe	1482	0	1448	13	0
12	Of	1482	0	1448	13	0
12	Og	1482	0	1448	13	0
12	Oh	1482	0	1448	14	0
12	Oi	1482	0	1448	13	0
13	Oj	1134	0	1129	17	0
13	Ok	1134	0	1129	13	0
13	Ol	1134	0	1129	12	0
13	Om	1134	0	1129	9	0
13	On	1134	0	1129	11	0
13	Oo	1134	0	1129	13	0
13	Op	1134	0	1129	12	0
13	Oq	1134	0	1129	16	0
13	Or	1134	0	1129	16	0
13	Os	1134	0	1129	17	0
13	Ot	1134	0	1129	17	0
13	Ou	1134	0	1129	11	0
13	Ov	1134	0	1129	6	0
13	Ow	1134	0	1129	12	0
13	Ox	1134	0	1129	11	0
13	Oy	1134	0	1129	12	0
13	Oz	1134	0	1129	20	0
13	Pa	1134	0	1129	16	0
13	Pb	1134	0	1129	14	0
13	Pc	1134	0	1129	12	0
13	Pd	1134	0	1129	11	0
13	Pe	1134	0	1129	14	0
13	Pf	1134	0	1129	17	0
13	Pg	1134	0	1129	18	0
13	Ph	1134	0	1129	15	0
13	Pi	1134	0	1129	12	0
13	Pj	1134	0	1129	18	0
13	Pk	1134	0	1129	17	0
13	Pl	1134	0	1129	11	0
13	Pm	1134	0	1129	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	Pn	1134	0	1129	14	0
13	Po	1134	0	1129	14	0
13	Pp	1134	0	1129	22	0
13	Pq	1134	0	1129	20	0
All	All	574924	0	567381	4800	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 4800 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Eb:109:TYR:CD1	6:Eb:109:TYR:CG	1.75	1.72
6:Eb:109:TYR:CE2	6:Eb:109:TYR:CZ	1.84	1.66
6:Eb:109:TYR:CG	6:Eb:109:TYR:CD2	1.75	1.65
6:Eb:109:TYR:CZ	6:Eb:109:TYR:CE1	1.84	1.62
6:Eo:109:TYR:CG	6:Eo:109:TYR:CD1	1.98	1.51

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	260/262 (99%)	260 (100%)	0	0	100	100
1	Ab	260/262 (99%)	255 (98%)	5 (2%)	0	100	100
1	Ac	260/262 (99%)	258 (99%)	2 (1%)	0	100	100
1	Ad	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
1	Ae	260/262 (99%)	250 (96%)	10 (4%)	0	100	100
1	Af	260/262 (99%)	258 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ag	260/262 (99%)	256 (98%)	4 (2%)	0	100	100
1	Ah	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
1	Ai	260/262 (99%)	255 (98%)	5 (2%)	0	100	100
1	Aj	260/262 (99%)	256 (98%)	4 (2%)	0	100	100
1	Ak	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
1	Al	260/262 (99%)	259 (100%)	1 (0%)	0	100	100
1	Am	260/262 (99%)	256 (98%)	3 (1%)	1 (0%)	30	61
1	An	260/262 (99%)	255 (98%)	5 (2%)	0	100	100
1	Ao	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
1	Ap	248/262 (95%)	247 (100%)	1 (0%)	0	100	100
1	Aq	260/262 (99%)	256 (98%)	4 (2%)	0	100	100
1	Ar	243/262 (93%)	239 (98%)	4 (2%)	0	100	100
1	As	260/262 (99%)	253 (97%)	6 (2%)	1 (0%)	30	61
1	At	247/262 (94%)	242 (98%)	5 (2%)	0	100	100
1	Au	260/262 (99%)	251 (96%)	9 (4%)	0	100	100
1	Av	243/262 (93%)	241 (99%)	1 (0%)	1 (0%)	30	61
1	Aw	260/262 (99%)	256 (98%)	4 (2%)	0	100	100
1	Ax	245/262 (94%)	242 (99%)	3 (1%)	0	100	100
1	Ay	244/262 (93%)	241 (99%)	3 (1%)	0	100	100
1	Az	245/262 (94%)	244 (100%)	1 (0%)	0	100	100
1	Bb	249/262 (95%)	249 (100%)	0	0	100	100
2	Ba	237/249 (95%)	232 (98%)	5 (2%)	0	100	100
2	Bc	247/249 (99%)	245 (99%)	2 (1%)	0	100	100
2	Bd	240/249 (96%)	237 (99%)	3 (1%)	0	100	100
2	Bv	228/249 (92%)	219 (96%)	8 (4%)	1 (0%)	30	61
2	Bw	247/249 (99%)	244 (99%)	3 (1%)	0	100	100
3	Be	264/434 (61%)	260 (98%)	4 (2%)	0	100	100
3	Bf	264/434 (61%)	256 (97%)	8 (3%)	0	100	100
3	Bg	266/434 (61%)	265 (100%)	1 (0%)	0	100	100
3	Bh	264/434 (61%)	259 (98%)	5 (2%)	0	100	100
3	Bi	266/434 (61%)	262 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Bj	266/434 (61%)	263 (99%)	3 (1%)	0	100	100
3	Bk	266/434 (61%)	262 (98%)	4 (2%)	0	100	100
3	Bl	266/434 (61%)	263 (99%)	3 (1%)	0	100	100
3	Bm	266/434 (61%)	262 (98%)	4 (2%)	0	100	100
3	Bn	266/434 (61%)	262 (98%)	4 (2%)	0	100	100
3	Bo	266/434 (61%)	260 (98%)	6 (2%)	0	100	100
3	Bp	266/434 (61%)	262 (98%)	4 (2%)	0	100	100
3	Bq	266/434 (61%)	257 (97%)	9 (3%)	0	100	100
3	Br	266/434 (61%)	260 (98%)	6 (2%)	0	100	100
3	Bs	266/434 (61%)	261 (98%)	5 (2%)	0	100	100
3	Bt	266/434 (61%)	263 (99%)	3 (1%)	0	100	100
3	Bu	266/434 (61%)	264 (99%)	2 (1%)	0	100	100
4	Bx	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	By	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
4	Bz	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Ca	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cb	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cc	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cd	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
4	Ce	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cf	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cg	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
4	Ch	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Ci	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cj	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Ck	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cl	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cm	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cn	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Co	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
4	Cp	219/227 (96%)	213 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Cq	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cr	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
4	Cs	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Ct	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cu	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cv	219/227 (96%)	214 (98%)	5 (2%)	0	100	100
4	Cw	219/227 (96%)	215 (98%)	4 (2%)	0	100	100
5	Cx	312/343 (91%)	304 (97%)	8 (3%)	0	100	100
5	Cy	312/343 (91%)	307 (98%)	5 (2%)	0	100	100
5	Cz	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Da	312/343 (91%)	307 (98%)	5 (2%)	0	100	100
5	Db	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Dc	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	Dd	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	De	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Df	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	Dg	312/343 (91%)	307 (98%)	5 (2%)	0	100	100
5	Dh	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Di	312/343 (91%)	307 (98%)	5 (2%)	0	100	100
5	Dj	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	Dk	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	Dl	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Dm	312/343 (91%)	307 (98%)	5 (2%)	0	100	100
5	Dn	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Do	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	Dp	312/343 (91%)	306 (98%)	6 (2%)	0	100	100
5	Dq	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Dr	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Ds	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Dt	312/343 (91%)	304 (97%)	8 (3%)	0	100	100
5	Du	312/343 (91%)	306 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Dv	312/343 (91%)	305 (98%)	7 (2%)	0	100	100
5	Dw	312/343 (91%)	307 (98%)	5 (2%)	0	100	100
6	Dx	350/352 (99%)	344 (98%)	6 (2%)	0	100	100
6	Dy	350/352 (99%)	336 (96%)	14 (4%)	0	100	100
6	Dz	350/352 (99%)	346 (99%)	4 (1%)	0	100	100
6	Ea	350/352 (99%)	345 (99%)	5 (1%)	0	100	100
6	Eb	350/352 (99%)	343 (98%)	7 (2%)	0	100	100
6	Ec	350/352 (99%)	344 (98%)	6 (2%)	0	100	100
6	Ed	350/352 (99%)	344 (98%)	6 (2%)	0	100	100
6	Ee	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
6	Ef	350/352 (99%)	343 (98%)	7 (2%)	0	100	100
6	Eg	350/352 (99%)	344 (98%)	6 (2%)	0	100	100
6	Eh	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
6	Ei	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
6	Ej	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
6	Ek	350/352 (99%)	343 (98%)	7 (2%)	0	100	100
6	El	350/352 (99%)	343 (98%)	7 (2%)	0	100	100
6	Em	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
6	En	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
6	Eo	350/352 (99%)	344 (98%)	6 (2%)	0	100	100
6	Ep	350/352 (99%)	343 (98%)	7 (2%)	0	100	100
6	Eq	350/352 (99%)	339 (97%)	11 (3%)	0	100	100
6	Er	350/352 (99%)	340 (97%)	10 (3%)	0	100	100
6	Es	350/352 (99%)	346 (99%)	4 (1%)	0	100	100
6	Et	350/352 (99%)	339 (97%)	11 (3%)	0	100	100
6	Eu	350/352 (99%)	344 (98%)	6 (2%)	0	100	100
6	Ev	350/352 (99%)	341 (97%)	9 (3%)	0	100	100
6	Ew	350/352 (99%)	342 (98%)	8 (2%)	0	100	100
7	Ex	253/271 (93%)	235 (93%)	18 (7%)	0	100	100
7	Ey	254/271 (94%)	230 (91%)	22 (9%)	2 (1%)	16	49
7	Ez	253/271 (93%)	235 (93%)	18 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	Fa	254/271 (94%)	232 (91%)	21 (8%)	1 (0%)	30	61
7	Fb	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fc	254/271 (94%)	233 (92%)	20 (8%)	1 (0%)	30	61
7	Fd	253/271 (93%)	235 (93%)	18 (7%)	0	100	100
7	Fe	254/271 (94%)	232 (91%)	20 (8%)	2 (1%)	16	49
7	Ff	253/271 (93%)	236 (93%)	17 (7%)	0	100	100
7	Fg	254/271 (94%)	231 (91%)	21 (8%)	2 (1%)	16	49
7	Fh	253/271 (93%)	232 (92%)	21 (8%)	0	100	100
7	Fi	254/271 (94%)	231 (91%)	21 (8%)	2 (1%)	16	49
7	Fj	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fk	254/271 (94%)	232 (91%)	21 (8%)	1 (0%)	30	61
7	Fl	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fm	254/271 (94%)	230 (91%)	23 (9%)	1 (0%)	30	61
7	Fn	253/271 (93%)	234 (92%)	19 (8%)	0	100	100
7	Fo	254/271 (94%)	232 (91%)	21 (8%)	1 (0%)	30	61
7	Fp	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fq	254/271 (94%)	231 (91%)	22 (9%)	1 (0%)	30	61
7	Fr	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fs	254/271 (94%)	230 (91%)	23 (9%)	1 (0%)	30	61
7	Ft	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fu	254/271 (94%)	231 (91%)	21 (8%)	2 (1%)	16	49
7	Fv	253/271 (93%)	237 (94%)	16 (6%)	0	100	100
7	Fw	254/271 (94%)	230 (91%)	22 (9%)	2 (1%)	16	49
8	Fx	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Fy	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Fz	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Ga	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gb	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Gc	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gd	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
8	Ge	181/183 (99%)	176 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	Gf	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Gg	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gh	181/183 (99%)	172 (95%)	8 (4%)	1 (1%)	21	54
8	Gi	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gj	181/183 (99%)	173 (96%)	7 (4%)	1 (1%)	21	54
8	Gk	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gl	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Gm	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gn	181/183 (99%)	172 (95%)	8 (4%)	1 (1%)	21	54
8	Go	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gp	181/183 (99%)	172 (95%)	8 (4%)	1 (1%)	21	54
8	Gq	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gr	181/183 (99%)	172 (95%)	8 (4%)	1 (1%)	21	54
8	Gs	181/183 (99%)	178 (98%)	3 (2%)	0	100	100
8	Gt	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Gu	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
8	Gv	181/183 (99%)	171 (94%)	9 (5%)	1 (1%)	21	54
8	Gw	181/183 (99%)	177 (98%)	4 (2%)	0	100	100
9	Gx	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Gy	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Gz	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Ha	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hb	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hc	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hd	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	He	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Hf	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hg	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hh	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hi	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hj	10/12 (83%)	9 (90%)	1 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	Hk	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hl	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hm	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hn	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ho	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hp	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hq	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hr	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hs	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Ht	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hu	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hv	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
9	Hw	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Hx	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Hy	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Hz	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
9	Ia	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
9	Ib	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ic	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Id	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ie	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	If	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ig	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ih	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
9	Ii	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ij	10/12 (83%)	7 (70%)	3 (30%)	0	100	100
9	Ik	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Il	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Im	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	In	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Io	10/12 (83%)	7 (70%)	3 (30%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	Ip	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Iq	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Ir	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Is	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	It	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Iu	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Iv	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
9	Iw	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
10	Ix	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Iy	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Iz	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Ja	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jb	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jc	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jd	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Je	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jf	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jg	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jh	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Ji	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jj	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jk	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jl	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jm	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jn	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jo	153/155 (99%)	149 (97%)	4 (3%)	0	100	100
10	Jp	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jq	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jr	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Js	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jt	153/155 (99%)	150 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	Ju	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jv	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
10	Jw	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
11	Jx	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Jy	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Jz	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ka	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kb	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kc	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kd	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ke	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kf	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Kg	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kh	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Ki	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Kj	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kk	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kl	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Km	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kn	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ko	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kp	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Kq	102/105 (97%)	96 (94%)	6 (6%)	0	100	100
11	Kr	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Ks	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kt	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ku	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kv	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kw	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Kx	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ky	102/105 (97%)	97 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	Kz	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	La	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lb	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lc	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Ld	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Le	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Lf	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lg	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lh	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Li	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Lj	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Lk	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Ll	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Lm	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ln	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lo	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lp	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Lq	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lr	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ls	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Lt	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lu	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lv	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lw	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lx	102/105 (97%)	97 (95%)	5 (5%)	0	100	100
11	Ly	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Lz	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Ma	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Mb	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
11	Mc	102/105 (97%)	98 (96%)	4 (4%)	0	100	100
12	Md	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Me	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mf	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mg	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mh	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mi	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mj	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mk	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	ML	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mm	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mn	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mo	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mp	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mq	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mr	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ms	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mt	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mu	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mv	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mw	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
12	Mx	188/190 (99%)	179 (95%)	8 (4%)	1 (0%)	24	57
12	My	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Mz	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Na	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nb	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nc	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nd	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ne	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nf	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ng	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nh	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ni	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Nj	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nk	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nl	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nm	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nn	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	No	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Np	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nq	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nr	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ns	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nt	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nu	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nv	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nw	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nx	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ny	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Nz	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Oa	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Ob	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Oc	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Od	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Oe	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Of	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Og	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Oh	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
12	Oi	188/190 (99%)	180 (96%)	7 (4%)	1 (0%)	24	57
13	Oj	138/144 (96%)	138 (100%)	0	0	100	100
13	Ok	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Ol	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Om	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	On	138/144 (96%)	138 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Oo	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Op	138/144 (96%)	138 (100%)	0	0	100	100
13	Oq	138/144 (96%)	138 (100%)	0	0	100	100
13	Or	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Os	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Ot	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Ou	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Ov	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Ow	138/144 (96%)	135 (98%)	3 (2%)	0	100	100
13	Ox	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Oy	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Oz	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Pa	138/144 (96%)	131 (95%)	7 (5%)	0	100	100
13	Pb	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Pc	138/144 (96%)	138 (100%)	0	0	100	100
13	Pd	138/144 (96%)	135 (98%)	3 (2%)	0	100	100
13	Pe	138/144 (96%)	135 (98%)	3 (2%)	0	100	100
13	Pf	138/144 (96%)	135 (98%)	3 (2%)	0	100	100
13	Pg	138/144 (96%)	138 (100%)	0	0	100	100
13	Ph	138/144 (96%)	138 (100%)	0	0	100	100
13	Pi	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Pj	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Pk	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Pl	138/144 (96%)	137 (99%)	1 (1%)	0	100	100
13	Pm	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Pn	138/144 (96%)	138 (100%)	0	0	100	100
13	Po	138/144 (96%)	135 (98%)	3 (2%)	0	100	100
13	Pp	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
13	Pq	138/144 (96%)	135 (98%)	3 (2%)	0	100	100
All	All	72832/78133 (93%)	70519 (97%)	2220 (3%)	93 (0%)	49	79

5 of 93 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	As	138	GLN
2	Bv	134	PRO
1	Av	138	GLN
1	Am	141	ILE
7	Ey	116	TYR

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	218/218 (100%)	216 (99%)	2 (1%)	70	76
1	Ab	218/218 (100%)	213 (98%)	5 (2%)	44	64
1	Ac	218/218 (100%)	213 (98%)	5 (2%)	44	64
1	Ad	218/218 (100%)	214 (98%)	4 (2%)	51	68
1	Ae	218/218 (100%)	216 (99%)	2 (1%)	70	76
1	Af	218/218 (100%)	215 (99%)	3 (1%)	59	71
1	Ag	218/218 (100%)	215 (99%)	3 (1%)	59	71
1	Ah	218/218 (100%)	212 (97%)	6 (3%)	38	60
1	Ai	218/218 (100%)	217 (100%)	1 (0%)	81	80
1	Aj	218/218 (100%)	216 (99%)	2 (1%)	70	76
1	Ak	218/218 (100%)	214 (98%)	4 (2%)	51	68
1	Al	218/218 (100%)	213 (98%)	5 (2%)	44	64
1	Am	217/218 (100%)	216 (100%)	1 (0%)	81	80
1	An	218/218 (100%)	213 (98%)	5 (2%)	44	64
1	Ao	218/218 (100%)	217 (100%)	1 (0%)	81	80
1	Ap	209/218 (96%)	206 (99%)	3 (1%)	59	71
1	Aq	218/218 (100%)	216 (99%)	2 (1%)	70	76
1	Ar	206/218 (94%)	202 (98%)	4 (2%)	50	67
1	As	218/218 (100%)	216 (99%)	2 (1%)	70	76
1	At	209/218 (96%)	204 (98%)	5 (2%)	43	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Au	218/218 (100%)	214 (98%)	4 (2%)	51	68
1	Av	205/218 (94%)	199 (97%)	6 (3%)	37	60
1	Aw	218/218 (100%)	213 (98%)	5 (2%)	44	64
1	Ax	207/218 (95%)	202 (98%)	5 (2%)	43	63
1	Ay	206/218 (94%)	205 (100%)	1 (0%)	81	80
1	Az	207/218 (95%)	203 (98%)	4 (2%)	50	67
1	Bb	210/218 (96%)	207 (99%)	3 (1%)	59	71
2	Ba	197/202 (98%)	195 (99%)	2 (1%)	68	75
2	Bc	202/202 (100%)	199 (98%)	3 (2%)	57	70
2	Bd	199/202 (98%)	195 (98%)	4 (2%)	48	66
2	Bv	187/202 (93%)	183 (98%)	4 (2%)	47	65
2	Bw	201/202 (100%)	198 (98%)	3 (2%)	57	70
3	Be	221/359 (62%)	219 (99%)	2 (1%)	70	76
3	Bf	221/359 (62%)	218 (99%)	3 (1%)	59	71
3	Bg	223/359 (62%)	221 (99%)	2 (1%)	70	76
3	Bh	221/359 (62%)	215 (97%)	6 (3%)	39	61
3	Bi	223/359 (62%)	221 (99%)	2 (1%)	70	76
3	Bj	223/359 (62%)	220 (99%)	3 (1%)	61	72
3	Bk	223/359 (62%)	221 (99%)	2 (1%)	70	76
3	Bl	223/359 (62%)	220 (99%)	3 (1%)	61	72
3	Bm	223/359 (62%)	215 (96%)	8 (4%)	31	56
3	Bn	223/359 (62%)	221 (99%)	2 (1%)	70	76
3	Bo	223/359 (62%)	220 (99%)	3 (1%)	61	72
3	Bp	223/359 (62%)	219 (98%)	4 (2%)	51	68
3	Bq	223/359 (62%)	219 (98%)	4 (2%)	51	68
3	Br	223/359 (62%)	223 (100%)	0	100	100
3	Bs	223/359 (62%)	220 (99%)	3 (1%)	61	72
3	Bt	223/359 (62%)	220 (99%)	3 (1%)	61	72
3	Bu	223/359 (62%)	221 (99%)	2 (1%)	70	76
4	Bx	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	By	182/186 (98%)	177 (97%)	5 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Bz	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Ca	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cb	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cc	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cd	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Ce	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cf	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cg	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Ch	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Ci	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cj	182/186 (98%)	179 (98%)	3 (2%)	55	69
4	Ck	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cl	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cm	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cn	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Co	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cp	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cq	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cr	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cs	182/186 (98%)	179 (98%)	3 (2%)	55	69
4	Ct	182/186 (98%)	179 (98%)	3 (2%)	55	69
4	Cu	182/186 (98%)	178 (98%)	4 (2%)	45	65
4	Cv	182/186 (98%)	177 (97%)	5 (3%)	39	61
4	Cw	182/186 (98%)	177 (97%)	5 (3%)	39	61
5	Cx	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Cy	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Cz	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Da	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Db	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dc	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dd	246/269 (91%)	240 (98%)	6 (2%)	43	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	De	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Df	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dg	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dh	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Di	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dj	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dk	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	DI	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dm	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dn	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Do	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dp	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dq	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dr	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Ds	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dt	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Du	246/269 (91%)	240 (98%)	6 (2%)	43	63
5	Dv	246/269 (91%)	239 (97%)	7 (3%)	38	60
5	Dw	246/269 (91%)	239 (97%)	7 (3%)	38	60
6	Dx	299/303 (99%)	298 (100%)	1 (0%)	86	83
6	Dy	299/303 (99%)	294 (98%)	5 (2%)	53	69
6	Dz	299/303 (99%)	297 (99%)	2 (1%)	76	78
6	Ea	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	Eb	299/303 (99%)	294 (98%)	5 (2%)	53	69
6	Ec	299/303 (99%)	297 (99%)	2 (1%)	76	78
6	Ed	299/303 (99%)	295 (99%)	4 (1%)	61	72
6	Ee	299/303 (99%)	297 (99%)	2 (1%)	76	78
6	Ef	299/303 (99%)	293 (98%)	6 (2%)	48	66
6	Eg	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	Eh	299/303 (99%)	295 (99%)	4 (1%)	61	72
6	Ei	299/303 (99%)	296 (99%)	3 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Ej	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	Ek	299/303 (99%)	297 (99%)	2 (1%)	76	78
6	El	299/303 (99%)	293 (98%)	6 (2%)	48	66
6	Em	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	En	299/303 (99%)	297 (99%)	2 (1%)	76	78
6	Eo	299/303 (99%)	295 (99%)	4 (1%)	61	72
6	Ep	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	Eq	299/303 (99%)	298 (100%)	1 (0%)	86	83
6	Er	299/303 (99%)	295 (99%)	4 (1%)	61	72
6	Es	299/303 (99%)	295 (99%)	4 (1%)	61	72
6	Et	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	Eu	299/303 (99%)	296 (99%)	3 (1%)	68	75
6	Ev	299/303 (99%)	294 (98%)	5 (2%)	53	69
6	Ew	299/303 (99%)	297 (99%)	2 (1%)	76	78
7	Ex	231/243 (95%)	223 (96%)	8 (4%)	32	57
7	Ey	229/243 (94%)	226 (99%)	3 (1%)	61	72
7	Ez	231/243 (95%)	224 (97%)	7 (3%)	36	59
7	Fa	229/243 (94%)	225 (98%)	4 (2%)	53	69
7	Fb	231/243 (95%)	225 (97%)	6 (3%)	40	62
7	Fc	229/243 (94%)	225 (98%)	4 (2%)	53	69
7	Fd	231/243 (95%)	224 (97%)	7 (3%)	36	59
7	Fe	229/243 (94%)	225 (98%)	4 (2%)	53	69
7	Ff	231/243 (95%)	224 (97%)	7 (3%)	36	59
7	Fg	229/243 (94%)	227 (99%)	2 (1%)	70	76
7	Fh	231/243 (95%)	224 (97%)	7 (3%)	36	59
7	Fi	229/243 (94%)	226 (99%)	3 (1%)	61	72
7	Fj	231/243 (95%)	224 (97%)	7 (3%)	36	59
7	Fk	229/243 (94%)	225 (98%)	4 (2%)	53	69
7	Fl	231/243 (95%)	225 (97%)	6 (3%)	40	62
7	Fm	229/243 (94%)	226 (99%)	3 (1%)	61	72
7	Fn	231/243 (95%)	224 (97%)	7 (3%)	36	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Fo	229/243 (94%)	226 (99%)	3 (1%)	61	72
7	Fp	231/243 (95%)	225 (97%)	6 (3%)	40	62
7	Fq	229/243 (94%)	225 (98%)	4 (2%)	53	69
7	Fr	231/243 (95%)	223 (96%)	8 (4%)	32	57
7	Fs	229/243 (94%)	226 (99%)	3 (1%)	61	72
7	Ft	231/243 (95%)	224 (97%)	7 (3%)	36	59
7	Fu	229/243 (94%)	227 (99%)	2 (1%)	70	76
7	Fv	231/243 (95%)	223 (96%)	8 (4%)	32	57
7	Fw	229/243 (94%)	227 (99%)	2 (1%)	70	76
8	Fx	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Fy	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Fz	149/154 (97%)	141 (95%)	8 (5%)	20	47
8	Ga	154/154 (100%)	148 (96%)	6 (4%)	28	54
8	Gb	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Gc	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Gd	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Ge	154/154 (100%)	148 (96%)	6 (4%)	28	54
8	Gf	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Gg	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Gh	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Gi	154/154 (100%)	148 (96%)	6 (4%)	28	54
8	Gj	149/154 (97%)	143 (96%)	6 (4%)	28	54
8	Gk	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Gl	149/154 (97%)	144 (97%)	5 (3%)	32	57
8	Gm	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Gn	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Go	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Gp	149/154 (97%)	142 (95%)	7 (5%)	23	50
8	Gq	154/154 (100%)	149 (97%)	5 (3%)	34	58
8	Gr	149/154 (97%)	143 (96%)	6 (4%)	28	54
8	Gs	154/154 (100%)	149 (97%)	5 (3%)	34	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	Gt	149/154 (97%)	143 (96%)	6 (4%)	28	54
8	Gu	154/154 (100%)	148 (96%)	6 (4%)	28	54
8	Gv	149/154 (97%)	143 (96%)	6 (4%)	28	54
8	Gw	154/154 (100%)	148 (96%)	6 (4%)	28	54
9	Gx	12/12 (100%)	12 (100%)	0	100	100
9	Gy	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Gz	12/12 (100%)	12 (100%)	0	100	100
9	Ha	12/12 (100%)	12 (100%)	0	100	100
9	Hb	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Hc	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Hd	12/12 (100%)	12 (100%)	0	100	100
9	He	12/12 (100%)	12 (100%)	0	100	100
9	Hf	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Hg	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Hh	12/12 (100%)	12 (100%)	0	100	100
9	Hi	12/12 (100%)	12 (100%)	0	100	100
9	Hj	12/12 (100%)	12 (100%)	0	100	100
9	Hk	12/12 (100%)	12 (100%)	0	100	100
9	Hl	12/12 (100%)	12 (100%)	0	100	100
9	Hm	12/12 (100%)	12 (100%)	0	100	100
9	Hn	12/12 (100%)	12 (100%)	0	100	100
9	Ho	12/12 (100%)	12 (100%)	0	100	100
9	Hp	12/12 (100%)	12 (100%)	0	100	100
9	Hq	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Hr	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Hs	12/12 (100%)	12 (100%)	0	100	100
9	Ht	12/12 (100%)	12 (100%)	0	100	100
9	Hu	12/12 (100%)	12 (100%)	0	100	100
9	Hv	12/12 (100%)	12 (100%)	0	100	100
9	Hw	12/12 (100%)	12 (100%)	0	100	100
9	Hx	12/12 (100%)	12 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Hy	12/12 (100%)	12 (100%)	0	100	100
9	H _z	12/12 (100%)	12 (100%)	0	100	100
9	Ia	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Ib	12/12 (100%)	12 (100%)	0	100	100
9	Ic	12/12 (100%)	12 (100%)	0	100	100
9	Id	12/12 (100%)	12 (100%)	0	100	100
9	Ie	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	If	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Ig	12/12 (100%)	12 (100%)	0	100	100
9	Ih	12/12 (100%)	12 (100%)	0	100	100
9	Ii	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Ij	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Ik	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Il	12/12 (100%)	12 (100%)	0	100	100
9	Im	12/12 (100%)	12 (100%)	0	100	100
9	In	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Io	12/12 (100%)	12 (100%)	0	100	100
9	Ip	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Iq	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Ir	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Is	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	It	12/12 (100%)	12 (100%)	0	100	100
9	Iu	12/12 (100%)	12 (100%)	0	100	100
9	Iv	12/12 (100%)	11 (92%)	1 (8%)	10	35
9	Iw	12/12 (100%)	12 (100%)	0	100	100
10	Ix	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Iy	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Iz	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Ja	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jb	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Jc	133/133 (100%)	125 (94%)	8 (6%)	17	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Jd	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Je	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jf	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Jg	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jh	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Ji	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jj	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jk	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jl	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jm	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jn	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jo	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jp	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Jq	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Jr	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Js	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jt	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Ju	133/133 (100%)	125 (94%)	8 (6%)	17	45
10	Jv	133/133 (100%)	124 (93%)	9 (7%)	14	42
10	Jw	133/133 (100%)	125 (94%)	8 (6%)	17	45
11	Jx	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Jy	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Jz	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ka	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kb	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kc	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kd	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ke	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Kf	84/85 (99%)	81 (96%)	3 (4%)	31	56
11	Kg	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kh	84/85 (99%)	80 (95%)	4 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Ki	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kj	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kk	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Kl	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Km	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kn	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Ko	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kp	84/85 (99%)	81 (96%)	3 (4%)	31	56
11	Kq	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kr	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ks	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kt	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ku	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kv	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kw	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kx	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ky	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Kz	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	La	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lb	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lc	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ld	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Le	84/85 (99%)	81 (96%)	3 (4%)	31	56
11	Lf	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lg	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lh	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Li	84/85 (99%)	82 (98%)	2 (2%)	43	63
11	Lj	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Lk	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ll	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lm	84/85 (99%)	80 (95%)	4 (5%)	23	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Ln	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lo	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lp	84/85 (99%)	81 (96%)	3 (4%)	31	56
11	Lq	84/85 (99%)	79 (94%)	5 (6%)	17	45
11	Lr	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ls	84/85 (99%)	81 (96%)	3 (4%)	31	56
11	Lt	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lu	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lv	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lw	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lx	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ly	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Lz	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Ma	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Mb	84/85 (99%)	80 (95%)	4 (5%)	23	50
11	Mc	84/85 (99%)	80 (95%)	4 (5%)	23	50
12	Md	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Me	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mf	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mg	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mh	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mi	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mj	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mk	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ml	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mm	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mn	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mo	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mp	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mq	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mr	165/169 (98%)	161 (98%)	4 (2%)	43	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Ms	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mt	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mu	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mv	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mw	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mx	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	My	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Mz	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Na	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nb	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nc	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nd	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ne	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nf	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ng	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nh	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ni	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nj	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nk	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nl	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nm	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nn	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	No	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Np	165/169 (98%)	160 (97%)	5 (3%)	36	59
12	Nq	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nr	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ns	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nt	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nu	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nv	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nw	165/169 (98%)	161 (98%)	4 (2%)	43	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Nx	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ny	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Nz	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Oa	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Ob	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Oc	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Od	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Oe	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Of	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Og	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Oh	165/169 (98%)	161 (98%)	4 (2%)	43	63
12	Oi	165/169 (98%)	161 (98%)	4 (2%)	43	63
13	Oj	126/126 (100%)	126 (100%)	0	100	100
13	Ok	126/126 (100%)	124 (98%)	2 (2%)	55	69
13	Ol	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Om	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	On	126/126 (100%)	121 (96%)	5 (4%)	28	54
13	Oo	126/126 (100%)	125 (99%)	1 (1%)	73	77
13	Op	126/126 (100%)	124 (98%)	2 (2%)	55	69
13	Oq	126/126 (100%)	122 (97%)	4 (3%)	34	58
13	Or	126/126 (100%)	126 (100%)	0	100	100
13	Os	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Ot	126/126 (100%)	122 (97%)	4 (3%)	34	58
13	Ou	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Ov	126/126 (100%)	121 (96%)	5 (4%)	28	54
13	Ow	126/126 (100%)	125 (99%)	1 (1%)	73	77
13	Ox	126/126 (100%)	125 (99%)	1 (1%)	73	77
13	Oy	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Oz	126/126 (100%)	120 (95%)	6 (5%)	23	50
13	Pa	126/126 (100%)	121 (96%)	5 (4%)	28	54
13	Pb	126/126 (100%)	122 (97%)	4 (3%)	34	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	Pc	126/126 (100%)	120 (95%)	6 (5%)	23	50
13	Pd	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Pe	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Pf	126/126 (100%)	121 (96%)	5 (4%)	28	54
13	Pg	126/126 (100%)	124 (98%)	2 (2%)	55	69
13	Ph	126/126 (100%)	124 (98%)	2 (2%)	55	69
13	Pi	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Pj	126/126 (100%)	125 (99%)	1 (1%)	73	77
13	Pk	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Pl	126/126 (100%)	125 (99%)	1 (1%)	73	77
13	Pm	126/126 (100%)	123 (98%)	3 (2%)	43	63
13	Pn	126/126 (100%)	122 (97%)	4 (3%)	34	58
13	Po	126/126 (100%)	121 (96%)	5 (4%)	28	54
13	Pp	126/126 (100%)	119 (94%)	7 (6%)	19	47
13	Pq	126/126 (100%)	125 (99%)	1 (1%)	73	77
All	All	62200/66127 (94%)	60581 (97%)	1619 (3%)	41	62

5 of 1619 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	Ji	168	SER
11	Ku	87	THR
13	Pm	380	THR
10	Jl	220	ILE
10	Jh	295	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1665 such sidechains are listed below:

Mol	Chain	Res	Type
8	Fx	149	GLN
10	Jm	147	GLN
13	Ov	294	GLN
8	Ge	57	GLN
8	Fx	145	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
13	Ox	2
13	Or	2
13	Ow	2
13	Pd	2
13	Pi	2
13	Ph	2
13	Op	2
13	Om	2
13	Ov	2
13	Pe	2
13	Os	2
13	Oo	2
13	Pn	2
13	Pq	2
13	Po	2
13	Oy	2

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Mol	Chain	Number of breaks
13	Oq	2
13	Pl	2
13	Pp	2
13	Oz	2
13	Pm	2
13	Ok	2
13	Ol	2
13	Pa	2
13	Pj	2
13	Pf	2
13	Pg	2
13	On	2
13	Ou	2
13	Ot	2
13	Pc	2
13	Pk	2
13	Pb	2
13	Oj	2

The worst 5 of 68 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Ox	328:ASN	C	368:VAL	N	7.31
1	Or	328:ASN	C	368:VAL	N	7.21
1	Ow	328:ASN	C	368:VAL	N	6.70
1	Pd	328:ASN	C	368:VAL	N	6.62
1	Pi	328:ASN	C	368:VAL	N	6.43

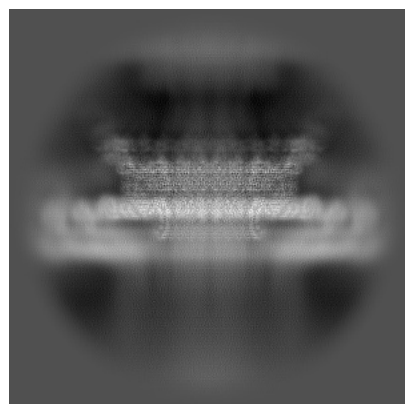
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72961. These allow visual inspection of the internal detail of the map and identification of artifacts.

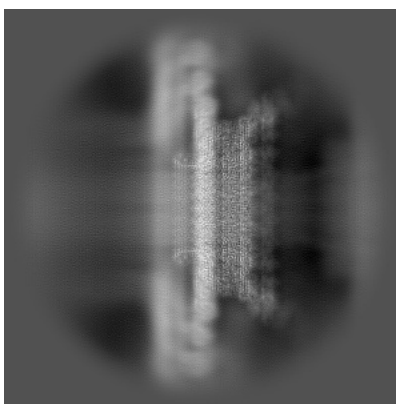
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

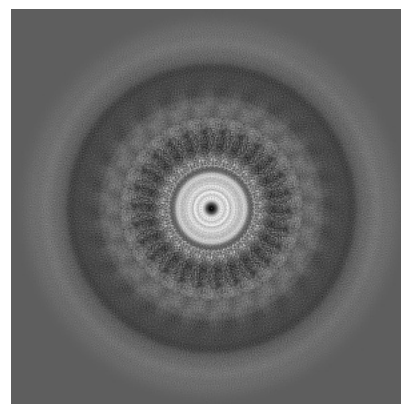
6.1.1 Primary map



X

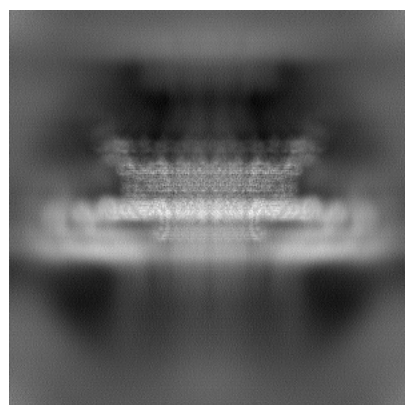


Y

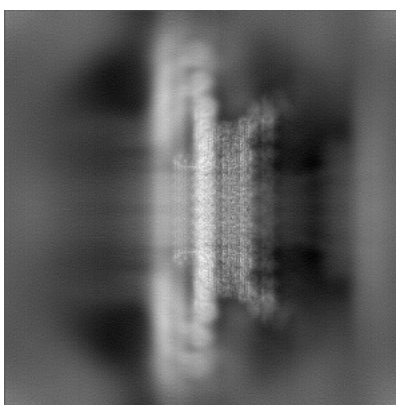


Z

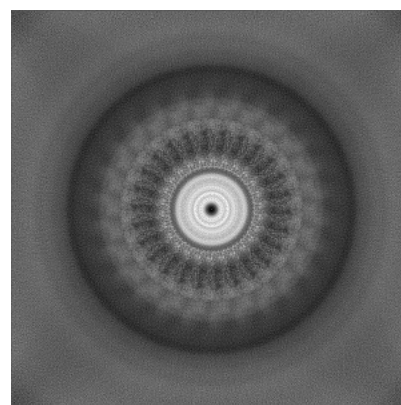
6.1.2 Raw map



X



Y

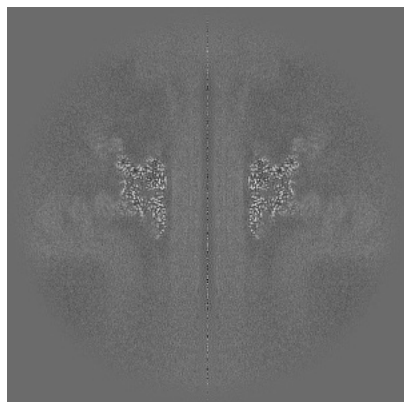


Z

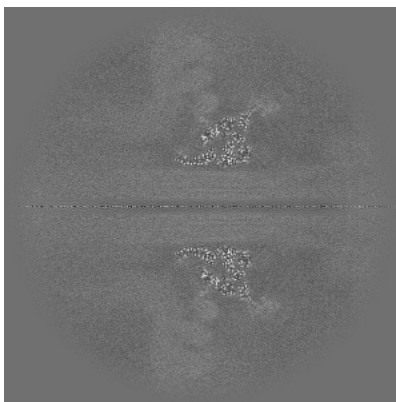
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

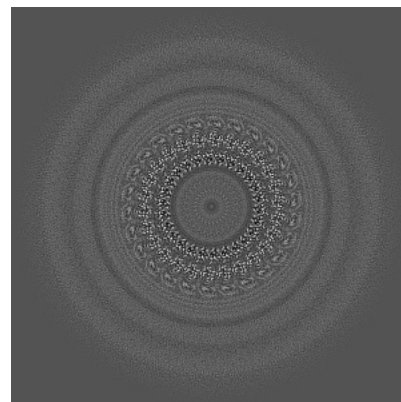
6.2.1 Primary map



X Index: 224

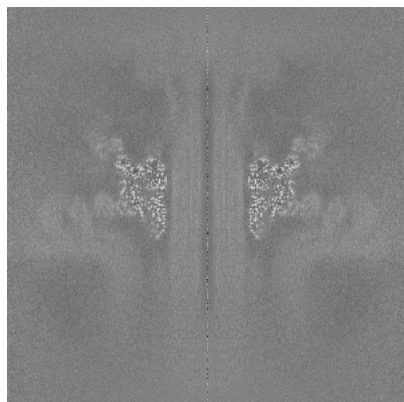


Y Index: 224

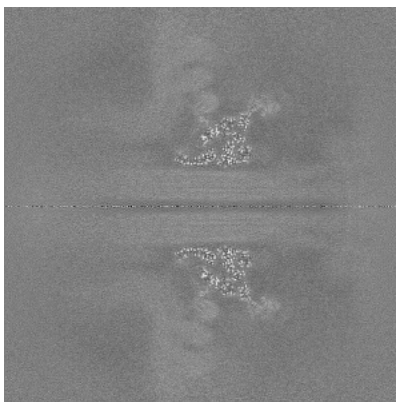


Z Index: 224

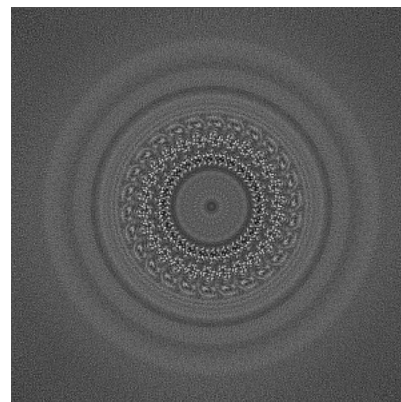
6.2.2 Raw map



X Index: 224



Y Index: 224

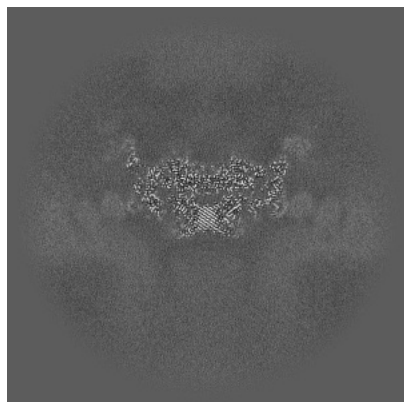


Z Index: 224

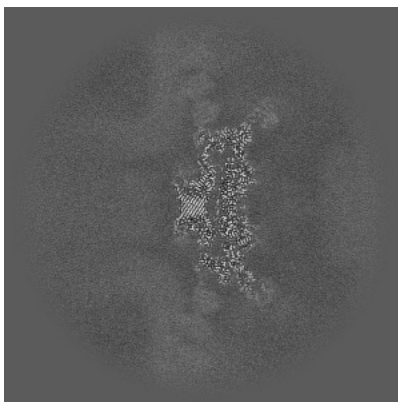
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

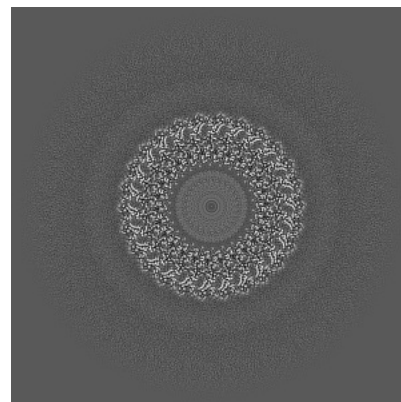
6.3.1 Primary map



X Index: 272

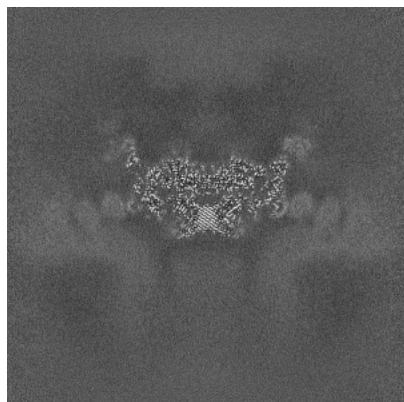


Y Index: 272

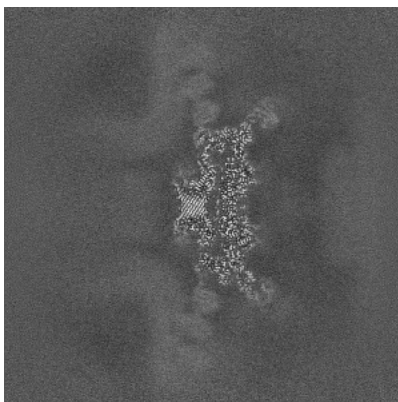


Z Index: 267

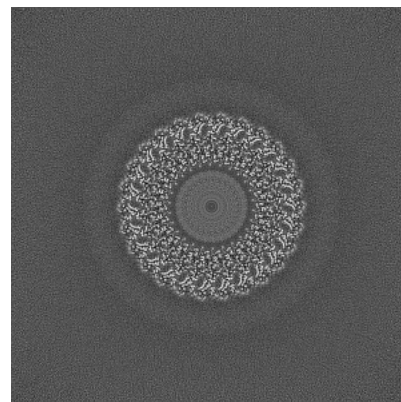
6.3.2 Raw map



X Index: 272



Y Index: 272

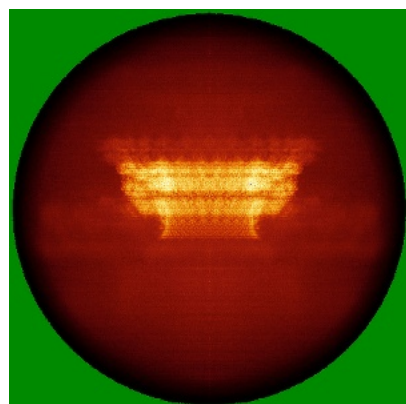


Z Index: 267

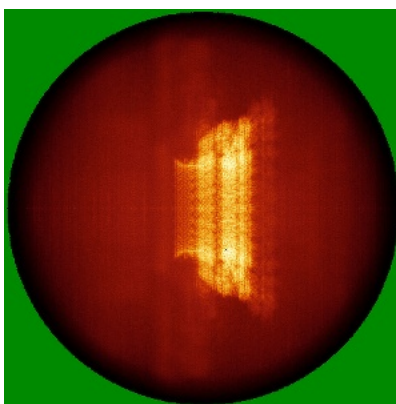
The images above show the largest variance slices of the map in three orthogonal directions.

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

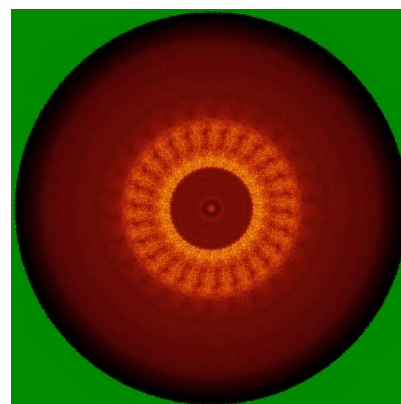
6.4.1 Primary map



X

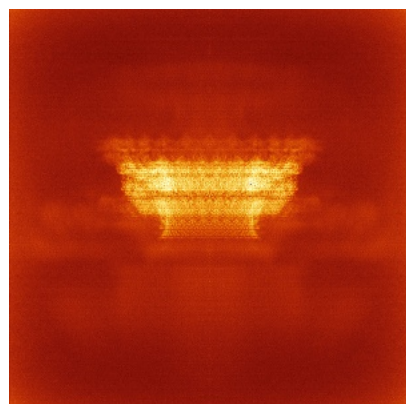


Y

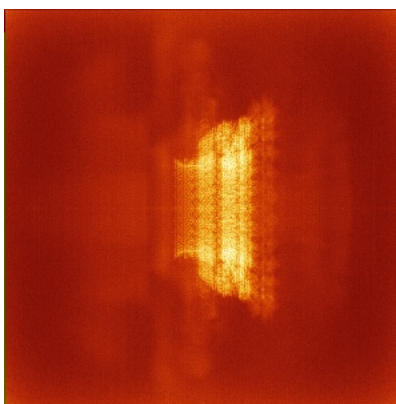


Z

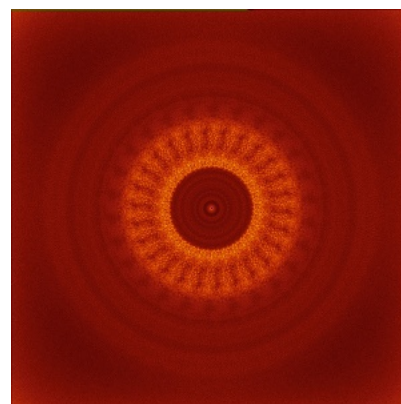
6.4.2 Raw map



X



Y

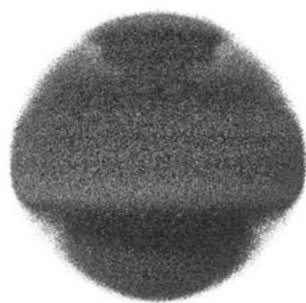


Z

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



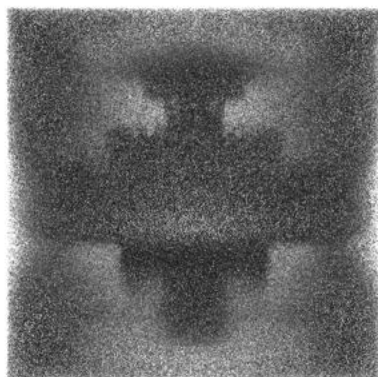
Y



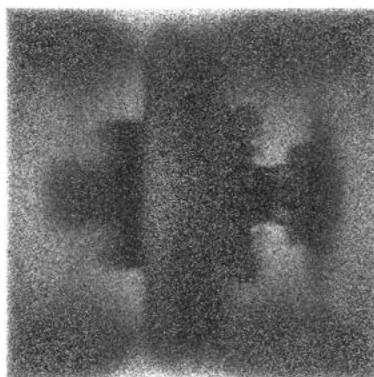
Z

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.

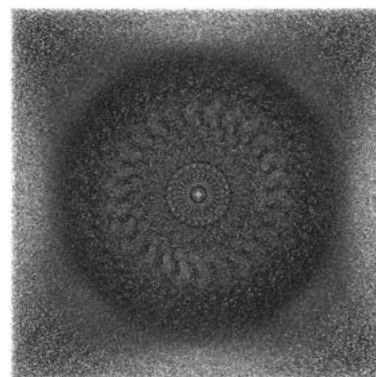
6.5.2 Raw map



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_72961_msk_1.map [i](#)



X



Y

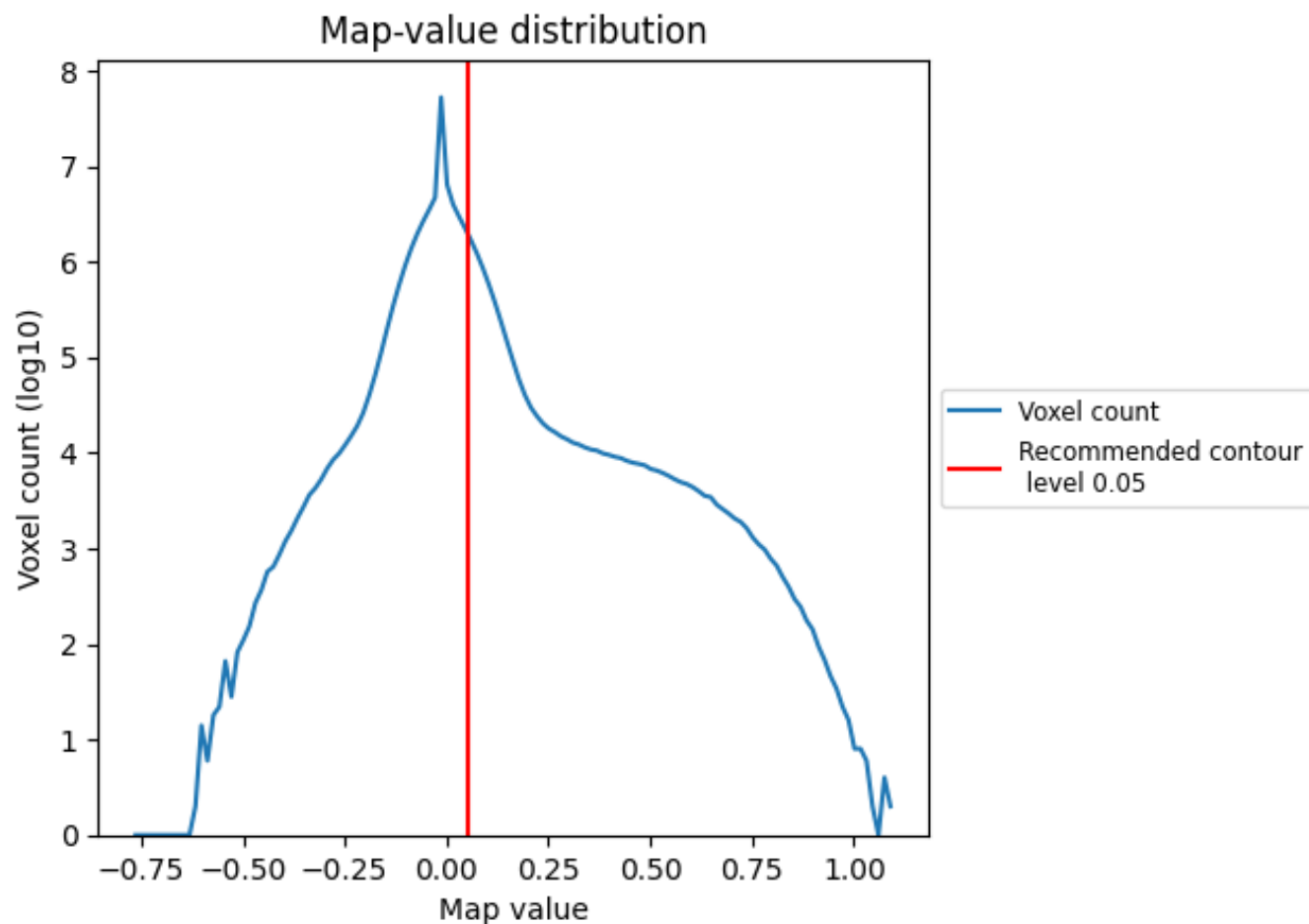


Z

7 Map analysis [i](#)

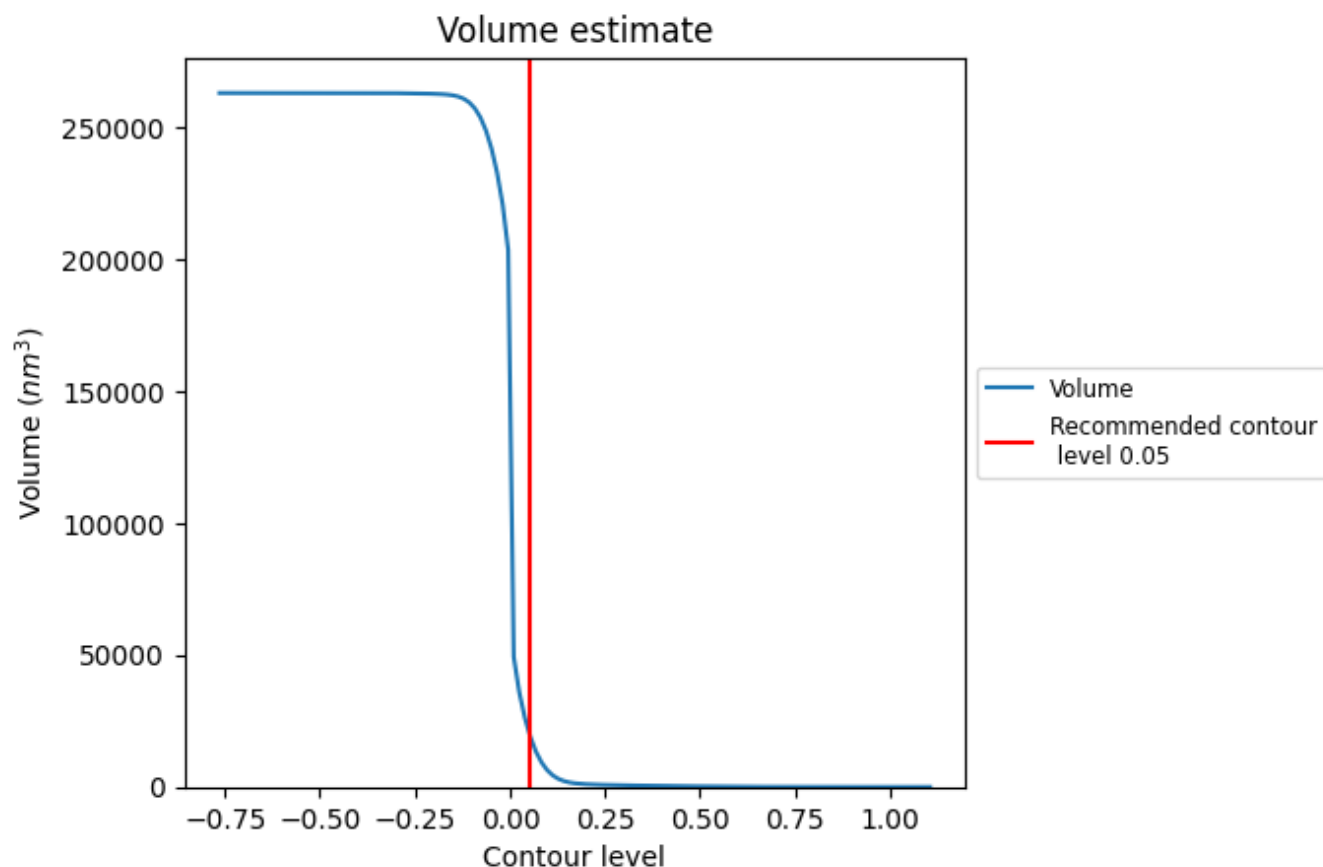
This section contains the results of statistical analysis of the map.

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.

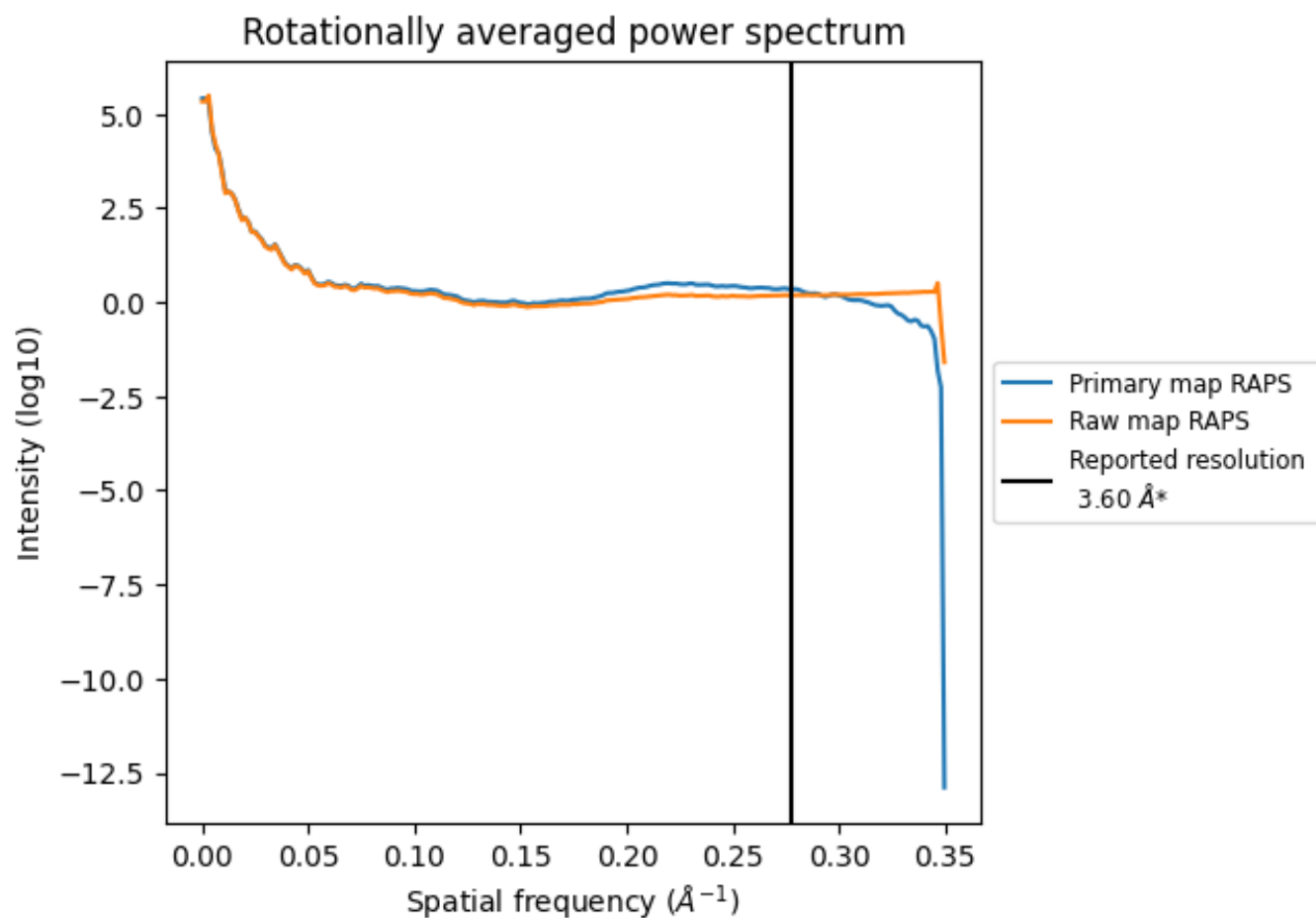
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 20850 nm^3 ; this corresponds to an approximate mass of 18834 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 ⓘ

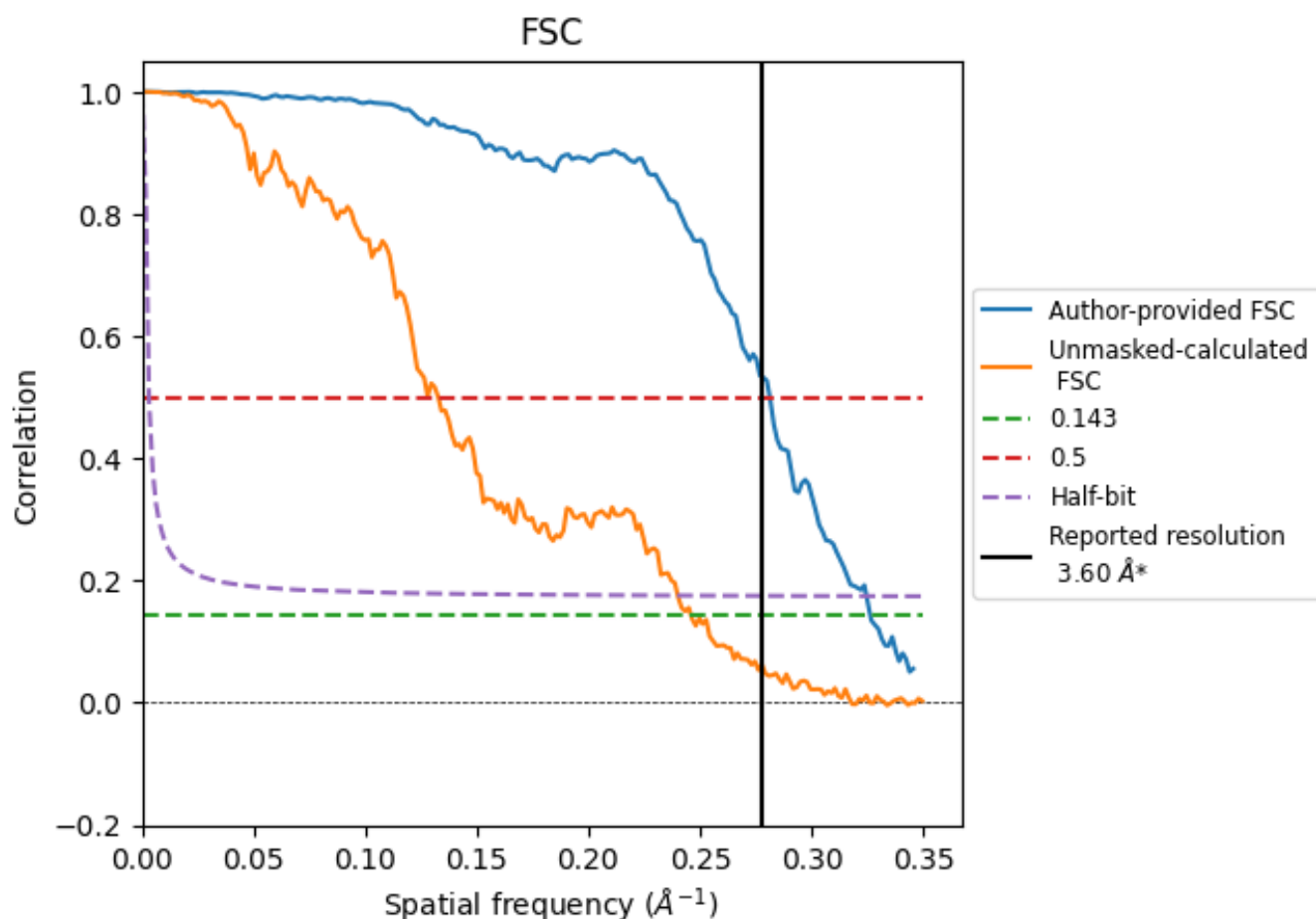


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.06	3.55	3.08
Unmasked-calculated*	4.06	7.54	4.16

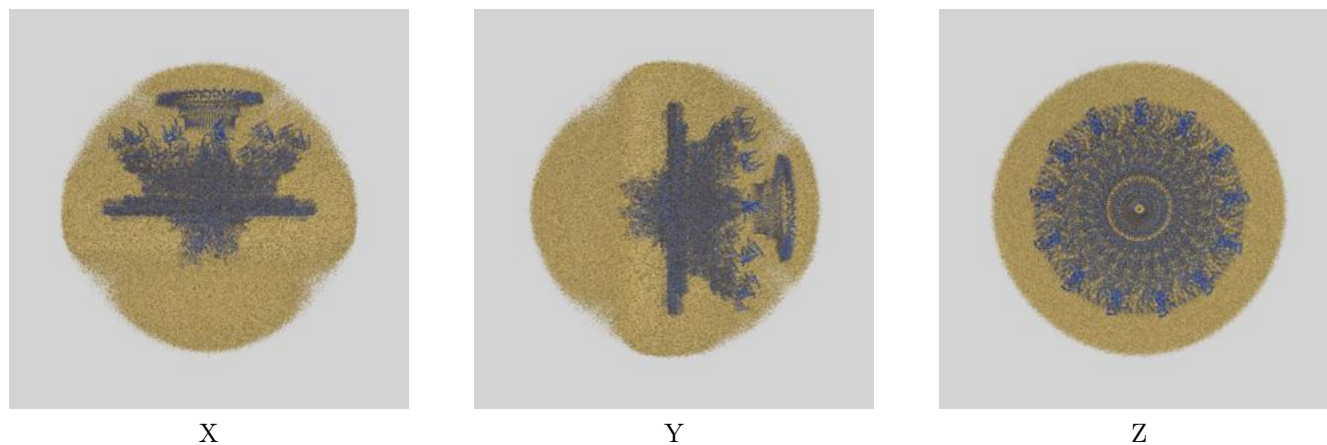
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.06 differs from the reported value 3.6 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.06 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

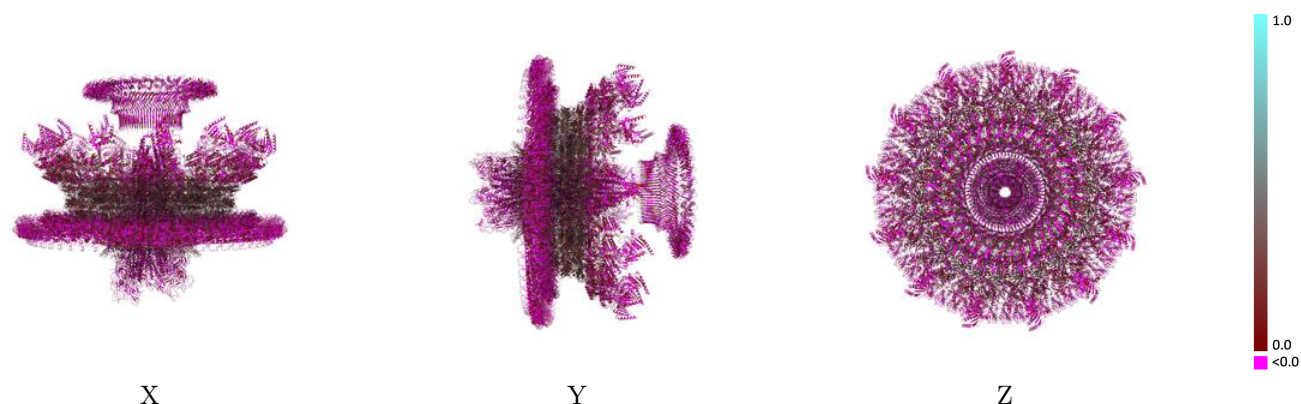
This section contains information regarding the fit between EMDB map EMD-72961 and PDB model 9YH6. Per-residue inclusion information can be found in [section 3](#) on [page 41](#).

9.1 Map-model overlay [i](#)



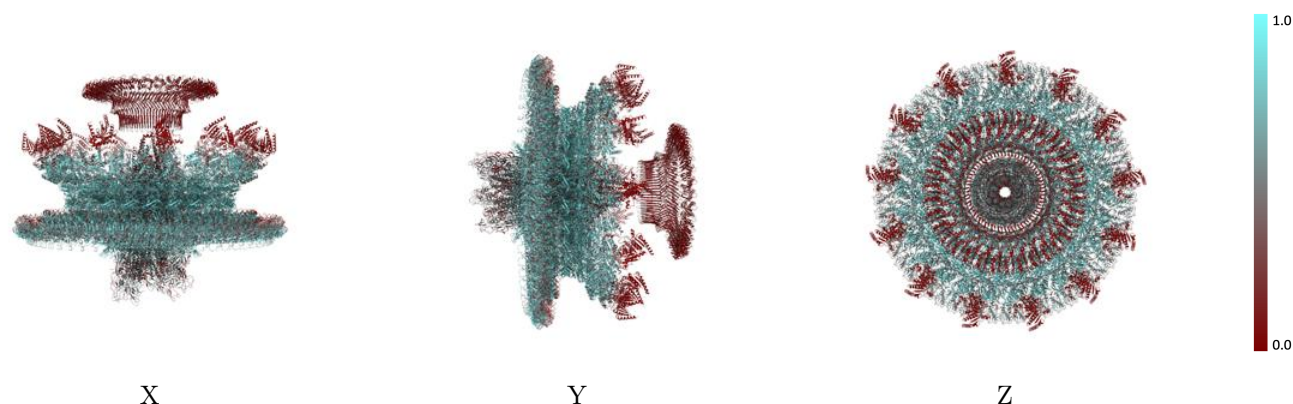
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



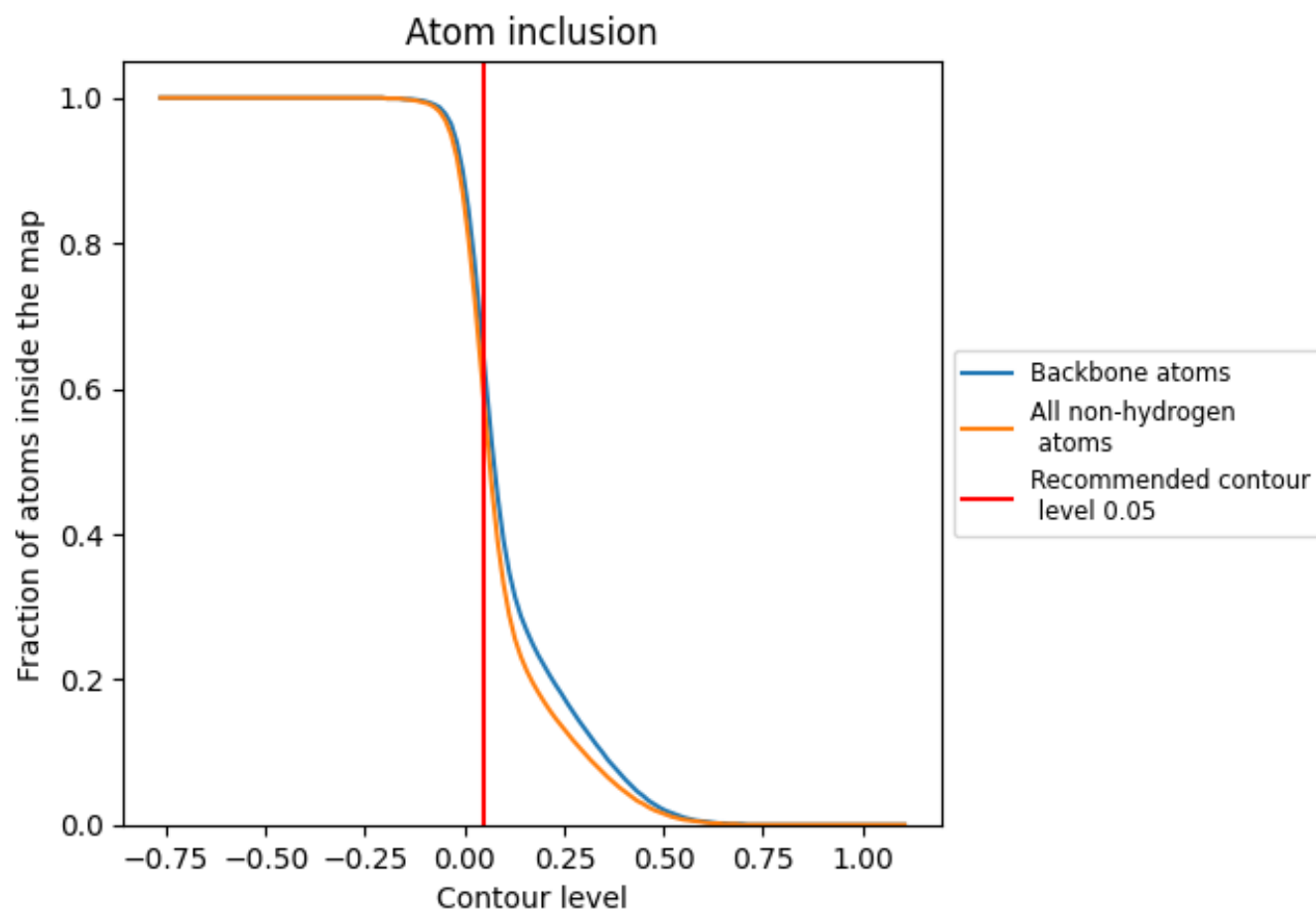
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 57% 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	 0.5740	 0.1060
Aa	 0.4890	 -0.0060
Ab	 0.5100	 -0.0140
Ac	 0.5420	 -0.0040
Ad	 0.5530	 0.0140
Ae	 0.5440	 0.0100
Af	 0.5520	 0.0260
Ag	 0.4830	 -0.0070
Ah	 0.5550	 0.0160
Ai	 0.5660	 0.0090
Aj	 0.5860	 0.0150
Ak	 0.5410	 0.0100
Al	 0.5830	 0.0180
Am	 0.5300	 0.0130
An	 0.5090	 -0.0060
Ao	 0.5160	 0.0070
Ap	 0.4820	 0.0120
Aq	 0.5610	 0.0160
Ar	 0.4980	 -0.0040
As	 0.5660	 0.0130
At	 0.5240	 0.0100
Au	 0.5760	 0.0210
Av	 0.5230	 -0.0050
Aw	 0.5710	 0.0130
Ax	 0.5360	 0.0070
Ay	 0.4350	 0.0130
Az	 0.4450	 -0.0070
Ba	 0.3630	 0.0130
Bb	 0.4150	 -0.0170
Bc	 0.3260	 0.0030
Bd	 0.3230	 -0.0290
Be	 0.4390	 0.0130
Bf	 0.4480	 0.0040
Bg	 0.4020	 0.0130
Bh	 0.4340	 0.0100























































































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Chain	Atom inclusion	Q-score
Bi	0.4390	0.0280
Bj	0.4360	0.0120
Bk	0.4200	-0.0000
Bl	0.4790	0.0150
Bm	0.4780	0.0150
Bn	0.4430	0.0130
Bo	0.4390	-0.0070
Bp	0.4130	0.0010
Bq	0.4930	0.0170
Br	0.4520	-0.0090
Bs	0.4440	0.0010
Bt	0.4620	-0.0040
Bu	0.4100	0.0020
Bv	0.3870	-0.0160
Bw	0.3820	-0.0050
Bx	0.7490	0.2340
By	0.7470	0.2440
Bz	0.7480	0.2470
Ca	0.7540	0.2540
Cb	0.7590	0.2590
Cc	0.7610	0.2600
Cd	0.7690	0.2710
Ce	0.7770	0.2730
Cf	0.7810	0.2680
Cg	0.7720	0.2690
Ch	0.7640	0.2640
Ci	0.7600	0.2640
Cj	0.7550	0.2590
Ck	0.7630	0.2560
Cl	0.7630	0.2550
Cm	0.7550	0.2530
Cn	0.7660	0.2510
Co	0.7630	0.2490
Cp	0.7690	0.2450
Cq	0.7580	0.2490
Cr	0.7570	0.2490
Cs	0.7570	0.2510
Ct	0.7460	0.2470
Cu	0.7450	0.2370
Cv	0.7370	0.2370
Cw	0.7420	0.2330
Cx	0.7790	0.2660





















































































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Chain	Atom inclusion	Q-score
Cy	 0.7710	 0.2620
Cz	 0.7810	 0.2640
Da	 0.7840	 0.2630
Db	 0.7780	 0.2660
Dc	 0.7890	 0.2700
Dd	 0.7900	 0.2720
De	 0.7920	 0.2810
Df	 0.7990	 0.2800
Dg	 0.7980	 0.2810
Dh	 0.7940	 0.2790
Di	 0.7950	 0.2750
Dj	 0.7840	 0.2660
Dk	 0.7890	 0.2660
Dl	 0.7900	 0.2620
Dm	 0.7850	 0.2620
Dn	 0.7850	 0.2600
Do	 0.7870	 0.2690
Dp	 0.7980	 0.2720
Dq	 0.8030	 0.2790
Dr	 0.8040	 0.2800
Ds	 0.8050	 0.2850
Dt	 0.8050	 0.2890
Du	 0.8000	 0.2860
Dv	 0.7940	 0.2730
Dw	 0.7890	 0.2720
Dx	 0.7660	 0.2220
Dy	 0.7400	 0.2140
Dz	 0.7640	 0.2330
Ea	 0.7510	 0.2240
Eb	 0.7550	 0.2230
Ec	 0.7630	 0.2310
Ed	 0.7600	 0.2360
Ee	 0.7640	 0.2360
Ef	 0.7730	 0.2420
Eg	 0.7800	 0.2520
Eh	 0.7890	 0.2570
Ei	 0.7930	 0.2640
Ej	 0.7920	 0.2660
Ek	 0.7990	 0.2720
El	 0.8000	 0.2690
Em	 0.7920	 0.2630
En	 0.7950	 0.2590





















































































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Chain	Atom inclusion	Q-score
Eo	 0.7820	 0.2490
Ep	 0.7720	 0.2360
Eq	 0.7660	 0.2260
Er	 0.7720	 0.2310
Es	 0.7720	 0.2230
Et	 0.7600	 0.2220
Eu	 0.7630	 0.2230
Ev	 0.7740	 0.2280
Ew	 0.7720	 0.2290
Ex	 0.7390	 0.1570
Ey	 0.7550	 0.1940
Ez	 0.7300	 0.1440
Fa	 0.7570	 0.1990
Fb	 0.7310	 0.1470
Fc	 0.7720	 0.2040
Fd	 0.7340	 0.1450
Fe	 0.7810	 0.2050
Ff	 0.7400	 0.1440
Fg	 0.7650	 0.1890
Fh	 0.7310	 0.1410
Fi	 0.7540	 0.1830
Fj	 0.7410	 0.1530
Fk	 0.7450	 0.1780
Fl	 0.7570	 0.1740
Fm	 0.7480	 0.1900
Fn	 0.7630	 0.2010
Fo	 0.7560	 0.2040
Fp	 0.7780	 0.2250
Fq	 0.7560	 0.2070
Fr	 0.7780	 0.2220
Fs	 0.7480	 0.2020
Ft	 0.7610	 0.2050
Fu	 0.7540	 0.1930
Fv	 0.7550	 0.1800
Fw	 0.7540	 0.1910
Fx	 0.6030	 0.0760
Fy	 0.5880	 0.0850
Fz	 0.5760	 0.0610
Ga	 0.5650	 0.0670
Gb	 0.5600	 0.0560
Gc	 0.5610	 0.0590
Gd	 0.5520	 0.0560





















































































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Chain	Atom inclusion	Q-score
Ge	 0.5660	 0.0630
Gf	 0.5590	 0.0630
Gg	 0.5700	 0.0680
Gh	 0.5720	 0.0780
Gi	 0.5840	 0.0860
Gj	 0.5940	 0.0970
Gk	 0.6210	 0.0970
Gl	 0.6210	 0.1170
Gm	 0.6280	 0.1050
Gn	 0.6510	 0.1470
Go	 0.6350	 0.1340
Gp	 0.6560	 0.1560
Gq	 0.6490	 0.1390
Gr	 0.6570	 0.1530
Gs	 0.6330	 0.1370
Gt	 0.6530	 0.1350
Gu	 0.6150	 0.1200
Gv	 0.6150	 0.1080
Gw	 0.5920	 0.0990
Gx	 0.6210	 0.0940
Gy	 0.5830	 0.1370
Gz	 0.6120	 0.1200
Ha	 0.5530	 0.0880
Hb	 0.5920	 0.0740
Hc	 0.5730	 0.0880
Hd	 0.5630	 0.0790
He	 0.5340	 0.0870
Hf	 0.5730	 0.1070
Hg	 0.5920	 0.0880
Hh	 0.6500	 0.1260
Hi	 0.6120	 0.1340
Hj	 0.6410	 0.1160
Hk	 0.6120	 0.0900
Hl	 0.6500	 0.0950
Hm	 0.6600	 0.0980
Hn	 0.6600	 0.1050
Ho	 0.6500	 0.0970
Hp	 0.6600	 0.1590
Hq	 0.6600	 0.0980
Hr	 0.6410	 0.0930
HS	 0.6700	 0.1200
Ht	 0.6120	 0.1140

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Chain	Atom inclusion	Q-score
Hu	 0.6310	 0.1250
Hv	 0.6500	 0.0970
Hw	 0.6120	 0.1100
Hx	 0.8160	 0.2100
Hy	 0.7770	 0.2090
Hz	 0.7480	 0.1790
Ia	 0.7670	 0.1640
Ib	 0.7770	 0.1500
Ic	 0.7860	 0.1650
Id	 0.7380	 0.1530
Ie	 0.7280	 0.1530
If	 0.7380	 0.1300
Ig	 0.7570	 0.2100
Ih	 0.7380	 0.1910
Ii	 0.7570	 0.1870
Ij	 0.7570	 0.1940
Ik	 0.7480	 0.1660
Il	 0.7770	 0.1740
Im	 0.7180	 0.1120
In	 0.6890	 0.0880
Io	 0.7180	 0.1240
Ip	 0.6990	 0.1470
Iq	 0.7770	 0.2030
Ir	 0.6890	 0.1460
Is	 0.7670	 0.1770
It	 0.7380	 0.1690
Iu	 0.7770	 0.2470
Iv	 0.7860	 0.2490
Iw	 0.7960	 0.2740
Ix	 0.0550	 -0.0110
Iy	 0.0820	 0.0160
Iz	 0.0610	 -0.0040
Ja	 0.0910	 0.0230
Jb	 0.0720	 -0.0150
Jc	 0.0780	 0.0040
Jd	 0.0800	 -0.0010
Je	 0.0820	 0.0090
Jf	 0.0680	 0.0020
Jg	 0.0810	 0.0110
Jh	 0.0590	 0.0150
Ji	 0.0710	 -0.0010
Jj	 0.0590	 0.0110





















































































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Chain	Atom inclusion	Q-score
Jk	0.0620	-0.0090
Jl	0.0570	0.0090
Jm	0.0610	-0.0040
Jn	0.0540	0.0030
Jo	0.0690	-0.0070
Jp	0.0620	0.0110
Jq	0.0750	0.0010
Jr	0.0570	0.0040
Js	0.0880	0.0150
Jt	0.0540	-0.0010
Ju	0.0820	0.0250
Jv	0.0610	-0.0190
Jw	0.0780	0.0100
Jx	0.6240	0.0080
Jy	0.6340	0.0330
Jz	0.5960	0.0070
Ka	0.6440	0.0290
Kb	0.6340	0.0100
Kc	0.6500	0.0480
Kd	0.6190	-0.0140
Ke	0.6500	0.0180
Kf	0.6450	0.0080
Kg	0.6330	0.0120
Kh	0.6550	0.0430
Ki	0.6600	0.0310
Kj	0.6440	0.0200
Kk	0.6240	-0.0000
Kl	0.6450	0.0350
Km	0.6590	0.0100
Kn	0.6520	0.0330
Ko	0.6380	0.0150
Kp	0.6620	0.0080
Kq	0.6600	0.0300
Kr	0.6380	0.0130
Ks	0.6280	0.0010
Kt	0.6360	0.0110
Ku	0.6350	0.0210
Kv	0.6720	0.0190
Kw	0.6350	0.0200
Kx	0.6450	0.0140
Ky	0.6460	0.0180
Kz	0.6400	0.0200

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Chain	Atom inclusion	Q-score
La	 0.6330	 -0.0030
Lb	 0.6200	 0.0070
Lc	 0.6240	 -0.0060
Ld	 0.6400	 0.0320
Le	 0.6600	 0.0390
Lf	 0.6240	 -0.0130
Lg	 0.6340	 0.0010
Lh	 0.6210	 -0.0060
Li	 0.6300	 -0.0080
Lj	 0.5930	 -0.0090
Lk	 0.6390	 0.0360
Ll	 0.5900	 -0.0090
Lm	 0.6340	 0.0120
Ln	 0.6250	 0.0170
Lo	 0.6390	 0.0320
Lp	 0.6210	 -0.0060
Lq	 0.6100	 -0.0190
Lr	 0.6330	 0.0190
Ls	 0.6340	 0.0280
Lt	 0.6160	 0.0030
Lu	 0.5940	 -0.0060
Lv	 0.5860	 -0.0170
Lw	 0.5860	 -0.0230
Lx	 0.6200	 0.0090
Ly	 0.6360	 0.0180
Lz	 0.6040	 0.0010
Ma	 0.6250	 0.0230
Mb	 0.5870	 -0.0160
Mc	 0.6200	 -0.0100
Md	 0.4850	 0.0090
Me	 0.5050	 -0.0010
Mf	 0.4950	 0.0060
Mg	 0.4840	 -0.0070
Mh	 0.5060	 0.0240
Mi	 0.4930	 0.0000
Mj	 0.4980	 -0.0090
Mk	 0.4990	 0.0130
Ml	 0.4940	 -0.0000
Mm	 0.4890	 -0.0030
Mn	 0.4930	 0.0120
Mo	 0.4800	 -0.0080
Mp	 0.4980	 0.0150











































































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Chain	Atom inclusion	Q-score
Mq	0.4780	-0.0100
Mr	0.4980	0.0100
Ms	0.4710	-0.0060
Mt	0.4790	-0.0050
Mu	0.4700	-0.0060
Mv	0.4930	0.0100
Mw	0.5060	0.0040
Mx	0.4840	0.0070
My	0.4870	-0.0030
Mz	0.4860	-0.0080
Na	0.5070	0.0080
Nb	0.4710	-0.0160
Nc	0.4770	-0.0020
Nd	0.4870	0.0020
Ne	0.4930	0.0160
Nf	0.4940	0.0020
Ng	0.5140	0.0380
Nh	0.4870	0.0040
Ni	0.5040	0.0090
Nj	0.4870	0.0100
Nk	0.4630	-0.0180
Nl	0.5060	0.0150
Nm	0.5010	0.0130
Nn	0.5010	0.0150
No	0.5090	0.0320
Np	0.5100	0.0170
Nq	0.4760	-0.0110
Nr	0.5060	0.0080
Ns	0.4900	-0.0090
Nt	0.5090	0.0200
Nu	0.5080	0.0040
Nv	0.4790	-0.0100
Nw	0.5070	0.0240
Nx	0.4770	0.0040
Ny	0.4970	0.0050
Nz	0.4910	0.0040
Oa	0.4730	-0.0120
Ob	0.4940	0.0080
Oc	0.4800	-0.0030
Od	0.4860	-0.0040
Oe	0.4950	-0.0270
Of	0.5100	0.0270

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Chain	Atom inclusion	Q-score
Og	 0.4800	 -0.0090
Oh	 0.5000	 0.0130
Oi	 0.4790	 0.0190
Oj	 0.1380	 0.0270
Ok	 0.1460	 0.0340
Ol	 0.1160	 -0.0100
Om	 0.1140	 0.0070
On	 0.1210	 -0.0100
Oo	 0.1290	 0.0240
Op	 0.1320	 0.0260
Oq	 0.1250	 0.0070
Or	 0.1020	 -0.0070
Os	 0.1130	 -0.0100
Ot	 0.1280	 0.0140
Ou	 0.1140	 0.0040
Ov	 0.1030	 -0.0040
Ow	 0.1230	 0.0040
Ox	 0.1250	 0.0090
Oy	 0.1330	 0.0100
Oz	 0.1320	 0.0110
Pa	 0.1080	 -0.0180
Pb	 0.1110	 -0.0130
Pc	 0.1190	 0.0150
Pd	 0.1210	 0.0220
Pe	 0.1190	 -0.0130
Pf	 0.0950	 -0.0170
Pg	 0.1170	 0.0210
Ph	 0.1340	 0.0170
Pi	 0.1080	 -0.0110
Pj	 0.1220	 0.0080
Pk	 0.1340	 -0.0150
Pl	 0.1140	 -0.0100
Pm	 0.1140	 -0.0090
Pn	 0.1250	 0.0000
Po	 0.1270	 0.0080
Pp	 0.1100	 -0.0170
Pq	 0.1170	 0.0110