



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 10:57 PM UTC

PDB ID : 5WQ9 / pdb_00005wq9
EMDB ID : EMD-6677
Title : CryoEM structure of type II secretion system secretin GspD G453A mutant in *Vibrio cholerae*
Authors : Yan, Z.; Yin, M.; Li, X.
Deposited on : 2016-11-23
Resolution : 4.22 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

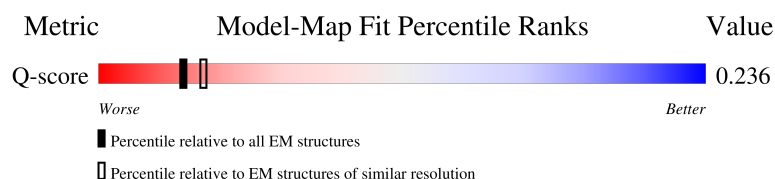
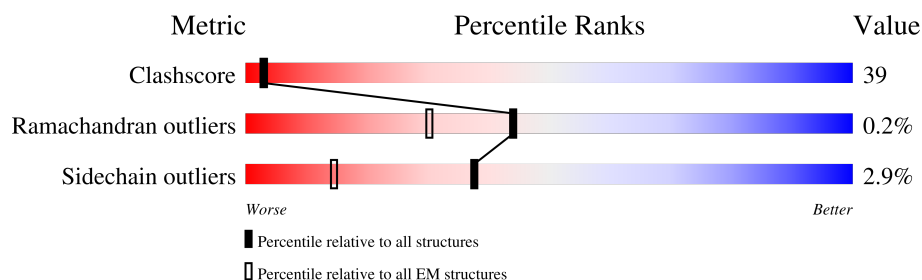
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.22 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	4772 (3.72 - 4.72)

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	A	650	12% 40% 34% 24%
1	B	650	12% 39% 34% 24%
1	C	650	12% 39% 34% 24%
1	D	650	12% 40% 34% 24%

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Mol	Chain	Length	Quality of chain
1	E	650	
1	F	650	
1	G	650	
1	H	650	
1	I	650	
1	J	650	
1	K	650	
1	L	650	
1	M	650	
1	N	650	
1	O	650	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 56340 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 Type II secretion system protein D.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	B	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	C	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	D	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	E	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	F	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	G	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	H	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	I	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	J	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	K	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	L	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	M	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	N	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		
1	O	493	Total	C	N	O	S	0	0
			3756	2347	656	740	13		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	453	ALA	GLY	engineered mutation	UNP P45779
B	453	ALA	GLY	engineered mutation	UNP P45779
C	453	ALA	GLY	engineered mutation	UNP P45779
D	453	ALA	GLY	engineered mutation	UNP P45779
E	453	ALA	GLY	engineered mutation	UNP P45779
F	453	ALA	GLY	engineered mutation	UNP P45779
G	453	ALA	GLY	engineered mutation	UNP P45779
H	453	ALA	GLY	engineered mutation	UNP P45779
I	453	ALA	GLY	engineered mutation	UNP P45779
J	453	ALA	GLY	engineered mutation	UNP P45779
K	453	ALA	GLY	engineered mutation	UNP P45779
L	453	ALA	GLY	engineered mutation	UNP P45779
M	453	ALA	GLY	engineered mutation	UNP P45779
N	453	ALA	GLY	engineered mutation	UNP P45779
O	453	ALA	GLY	engineered mutation	UNP P45779

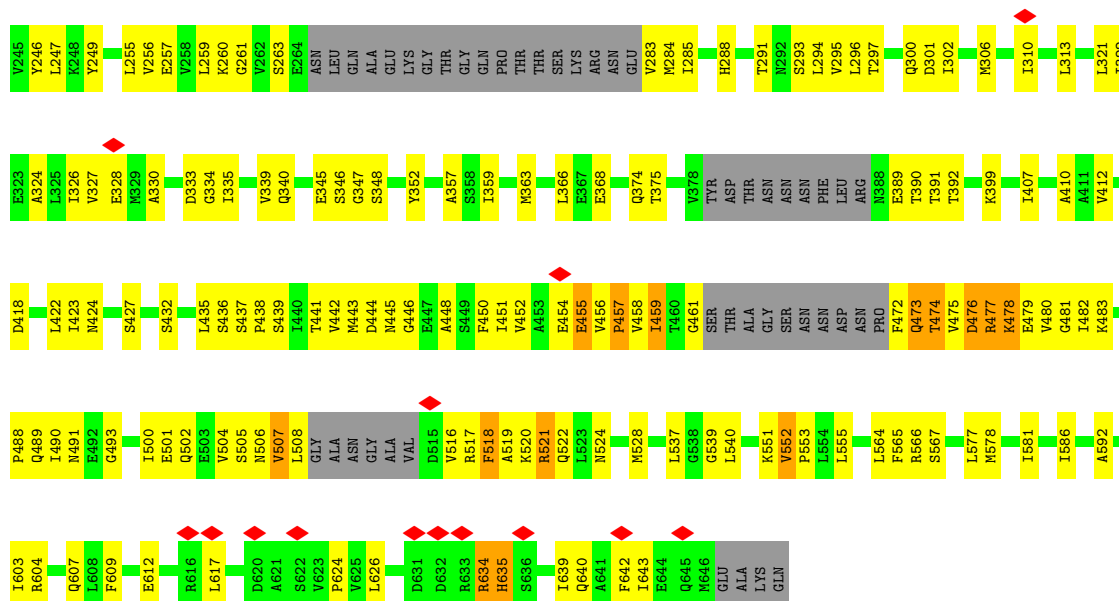


ASN	GLU	PHE	SER	ALA	SER	PHE	LYS	GLY	THR	ASP	ILE	GLN	GLU	PHE	ILE	ASN	ILE	VAL	GLY	ARG	ASN	LEU	GLU	LYS	THR	ILE	ILE	VAL	ASP	PRO	SER	VAL	GLY	ASN	LEU	GLU	LYS	THR	ASN	VAL	GLY	ASP	THR	ASP	THR	LEU	ASN	GLU	GLN	TYR	THR	SER	PHE	PHE	LEU	SER	VAL	LEU	GLU	VAL
Q121	L122	I123	D124	N125	A126	G127	A128	G129	N130	V131	V132	H133	Y134	D135	P136	A137	N138	I139	I140	L141	I142	T143	G144	R145	A146	A147	V148	V149	N150	R151	L152	A153	E154	I155	I156	R157	V158	V159	D160	Q161	A162	G163	D164	K165	E166	I167	E168	V169	E171	P171	L118	L119	N173	N174	A175	S176	A177	A178	E179	M180
V181	R182	I183	V184	E185	A186	L187	N188	LYS	THR	THR	ASP	ALA	GLN	ASN	THR	PRO	GLU	PHE	LEU	LEU	PRO	K203	F204	V205	A206	D207	E208	R209	T210	N211	S212	I213	L214	L215	S216	G217	D218	P219	K220	V221	R222	E223	R224	L225	K226	R227	L228	I229	K230	Q231	L232	D233	V234	E235	A238	K239	V244			
V245	Y246	L247	K248	Y249	L255	V256	E257	L259	K260	G261	V262	S263	E264	ASN	LEU	GLN	ALA	GLU	LYS	THR	GLY	THR	GLY	THR	GLY	GLN	PRO	THR	ARG	ASN	GLU	M284	L285	H288	T291	N292	S293	L294	V295	L296	T297	Q300	D301	I302	M306	I310	L313	L321	I322											
E323	A324	L325	I326	V327	E328	M329	A330	D333	G334	I335	V339	Q340	E345	S346	G347	S348	V352	A357	S358	I359	M363	L366	E367	E368	Q374	T375	V378	TYR	ASP	THR	ASN	ASN	ASN	PHE	LEU	ARG	N388	E389	T390	T391	T392	K399	T407	A410	A411	V412														
D418	L422	I423	N424	S427	S432	L436	S436	S437	P438	S439	I440	T441	V442	M443	D444	N445	G446	A448	S449	F450	I451	V452	A453	E454	O455	V456	P457	V458	I459	T460	G461	SER	THR	ALA	GLY	SER	ASN	ASN	ASN	ASN	PRO	F472	Q473	T474	V475	D476	K477	E479	V480	G481	I482	K483								
P488	Q489	T490	N491	E492	G493	T500	E501	Q502	V504	S505	R506	V507	L508	GLY	ALA	ASN	GLY	ALA	VAL	D515	V516	R517	F518	A519	K520	R521	Q522	L523	N524	M528	L537	G538	G539	L540	K551	V552	P553	L554	L555	L564	F565	R566	S567	L577	M578	I581	L586	A592												
I603	R604	Q607	L608	F609	E612	R616	L617	D620	A621	S622	V623	P624	V625	L626	D631	D632	R633	R634	H635	S636	T639	Q640	F642	T643	E644	D645	N646	GLU	ALA	LYS	GLN																													

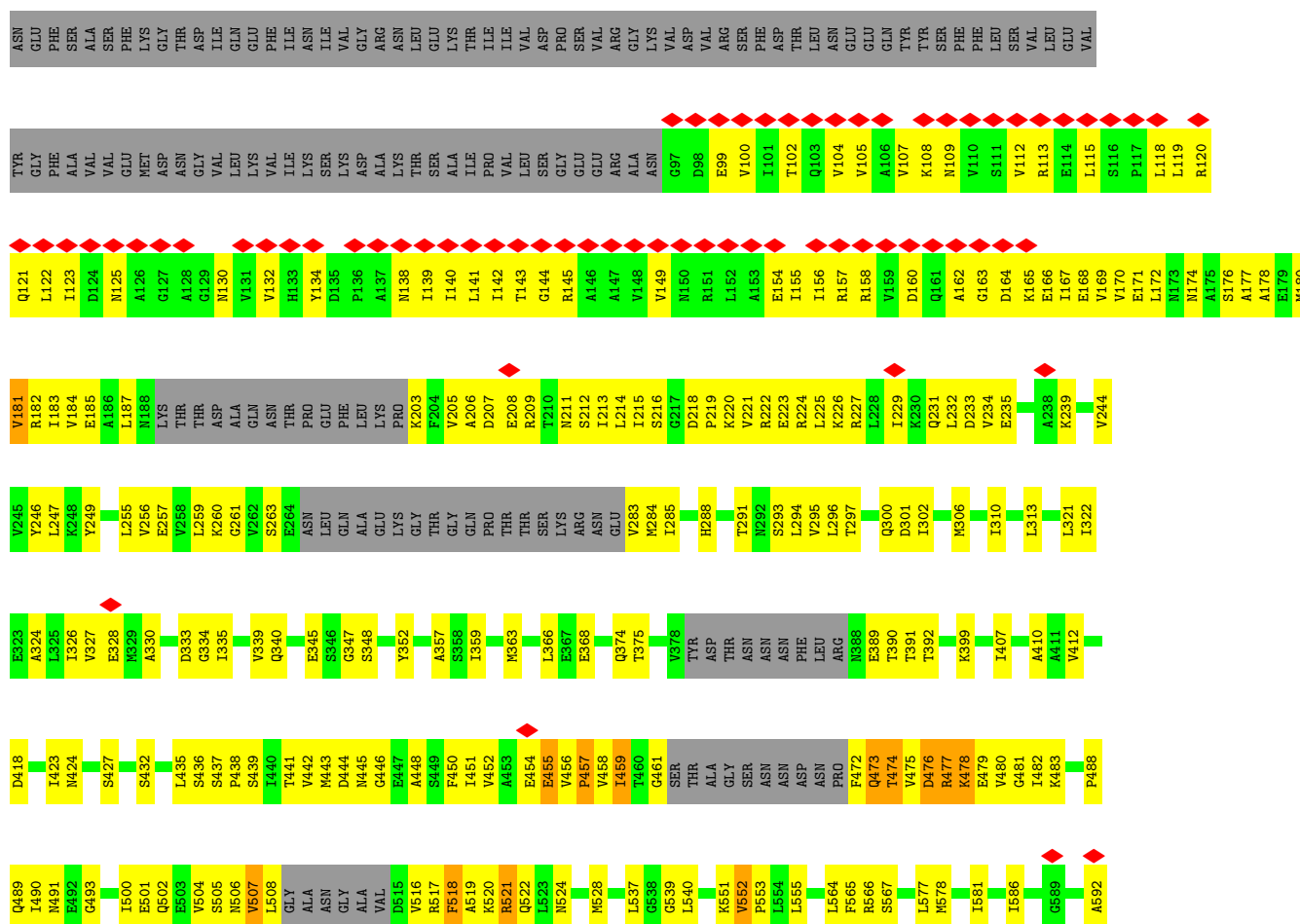
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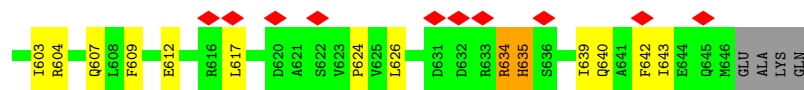


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Q121	L122	I123	D124	N125	A126	G127	A128	G129	N130	V131	V132	H133	Y134	D135	P136	A137	N138	I139	I140	L141	I142	T143	G144	R145	A146	A147	V148	V149	N150	R151	L152	A153	E154	I155	I156	R157	R158	V159	D160	Q161	A162	G163	D164	K165	E166	I167	E168	V169	E171	P170	I171	L172	N173	M174	A175	S176	A177	A178	E179	M180
V181	R182	I183	V184	E185	A186	L187	N188	LYS	THR	THR	ASP	ALA	GLN	ASN	THR	PRO	GLU	PHE	LEU	LEU	PRO	K203	F204	V205	A206	D207	E208	R209	T210	N211	S212	I213	L214	L215	S216	G217	D218	P219	K220	V221	R222	E223	R224	L225	K226	R227	L228	I229	K230	Q231	L232	D233	V234	E235	A236	K238	K239	V244		
V245	Y246	K247	K248	Y249	L255	V256	E257	L259	K260	G261	V262	S263	E264	ASN	LEU	GLN	ALA	GLU	LYS	THR	GLY	THR	GLY	GLY	GLN	PRO	THR	ARG	ASN	GLU	M284	L285	H288	T291	N292	S293	L294	V296	L296	T297	Q300	D301	I302	M306	I310	L313	L321	I322												
E323	A324	L325	I326	V327	E328	M329	A330	D333	G334	I335	V339	Q340	E345	S346	G347	S348	V352	A357	S358	I359	M363	L366	E367	E368	Q374	T375	V378	TYR	ASP	THR	ASN	ASN	ASN	PHE	LEU	ARG	N388	E389	T390	T392	K399	T407	A410	A411	V412															
D418	L422	I423	N424	S427	S432	L436	S436	S437	P438	S439	I440	T441	V442	M443	D444	N445	G446	A448	S449	F450	I451	V452	A453	E454	O455	V456	P457	V458	I459	T460	G461	SER	THR	ALA	GLY	SER	ASN	ASN	PRO	F472	Q473	T474	V475	D476	K477	E479	V480	G481	I482	K483										
P488	Q489	T490	N491	E492	G493	T500	E501	D502	V504	S505	R506	V507	L508	GLY	ALA	ASN	GLY	ALA	VAL	D515	V516	R517	F518	A519	K520	R521	Q522	L523	N524	M528	L537	G538	G539	L540	K551	V552	P553	L554	L555	L564	F565	R566	S567	L577	M578	I581	L586	A592												

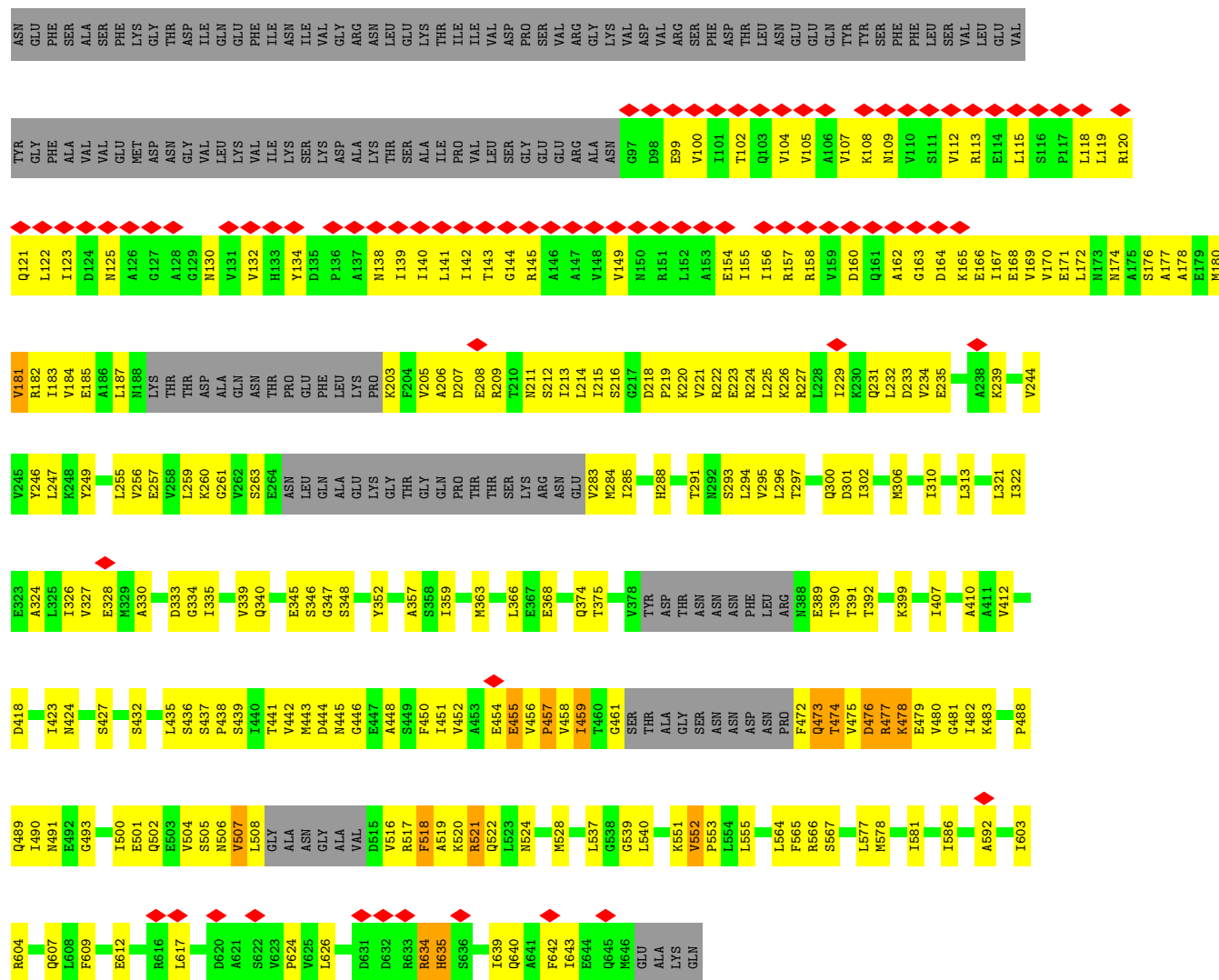


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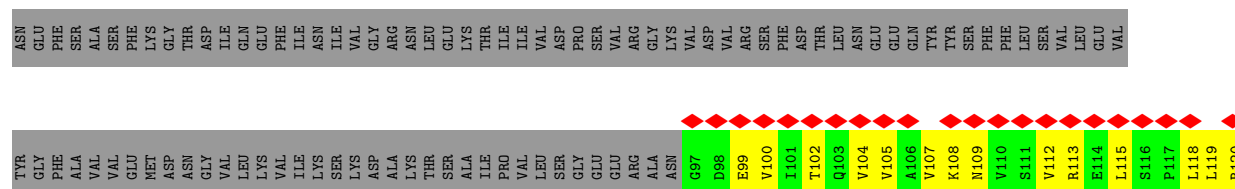
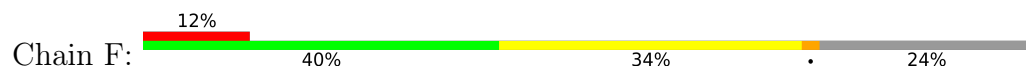


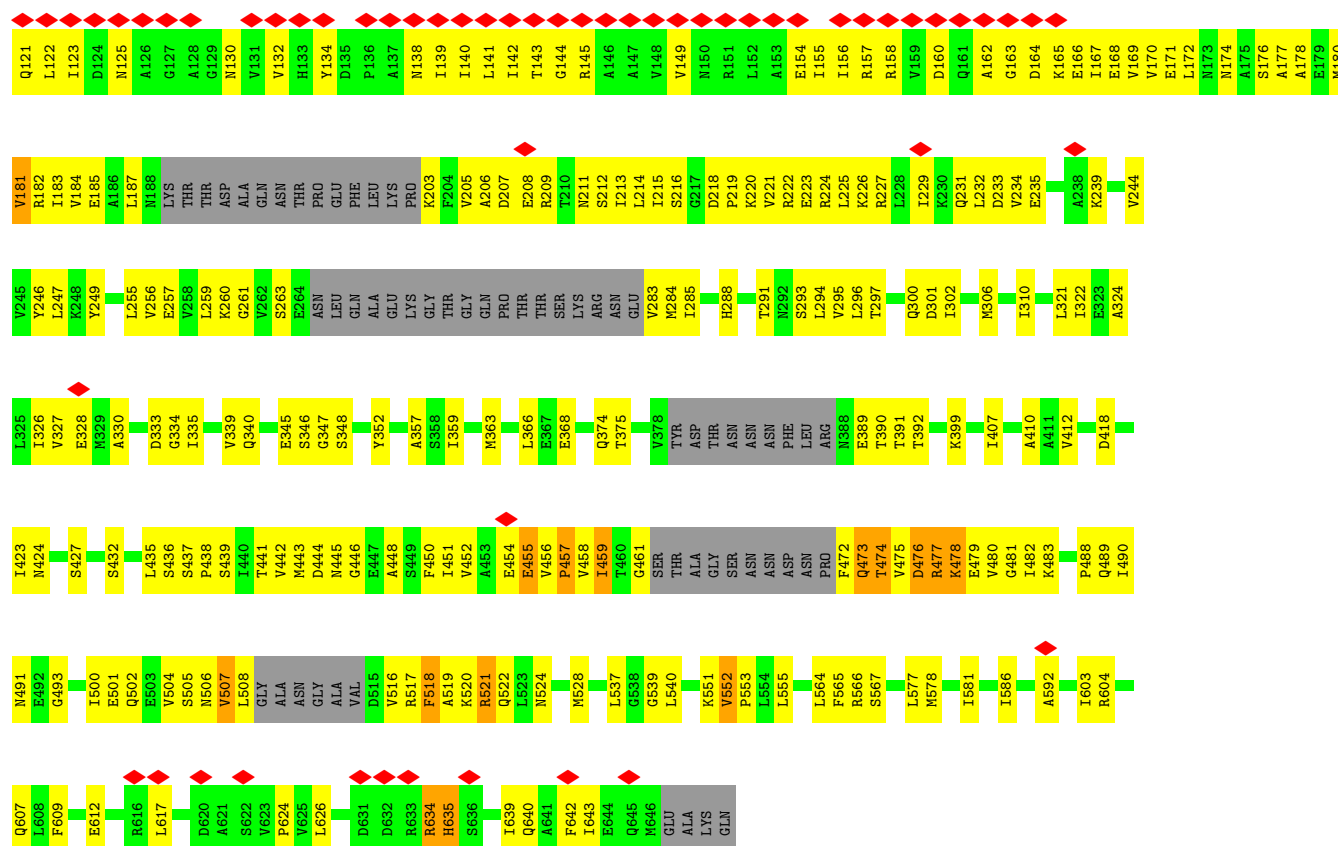


• Molecule 1: Type II secretion system protein D

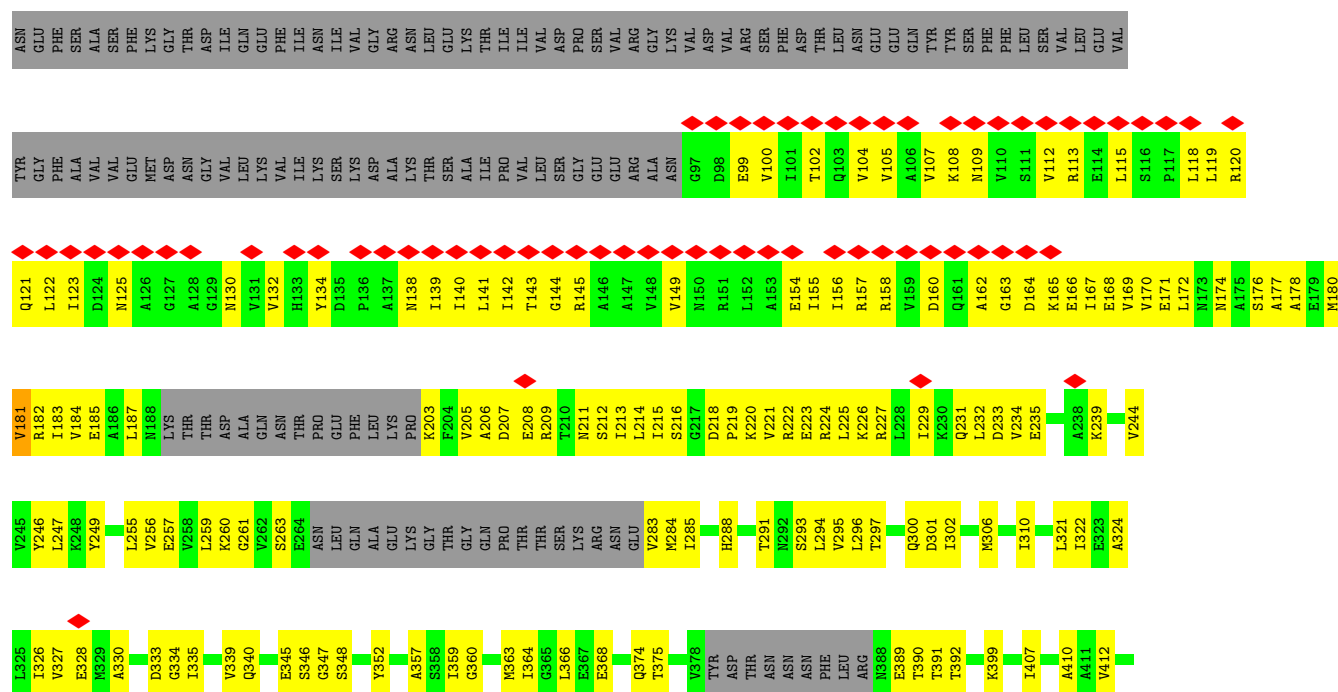
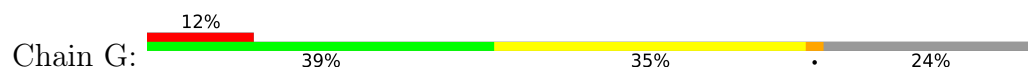


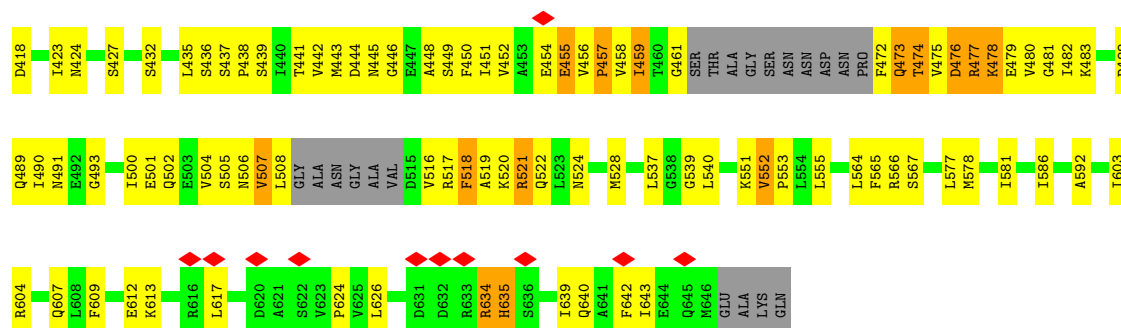
• Molecule 1: Type II secretion system protein D



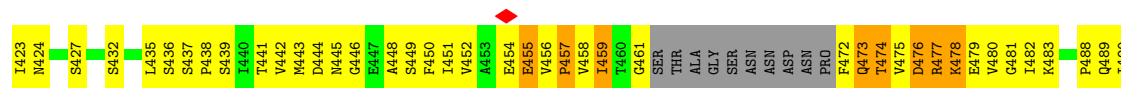
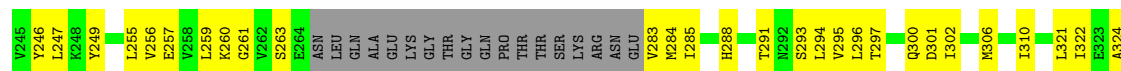
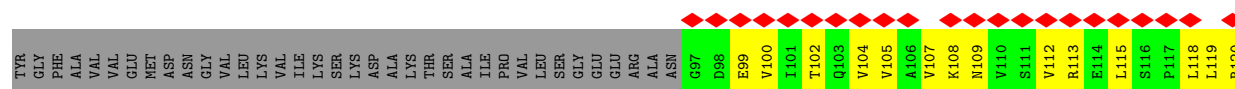
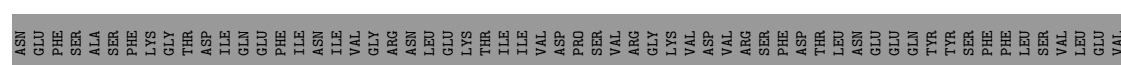


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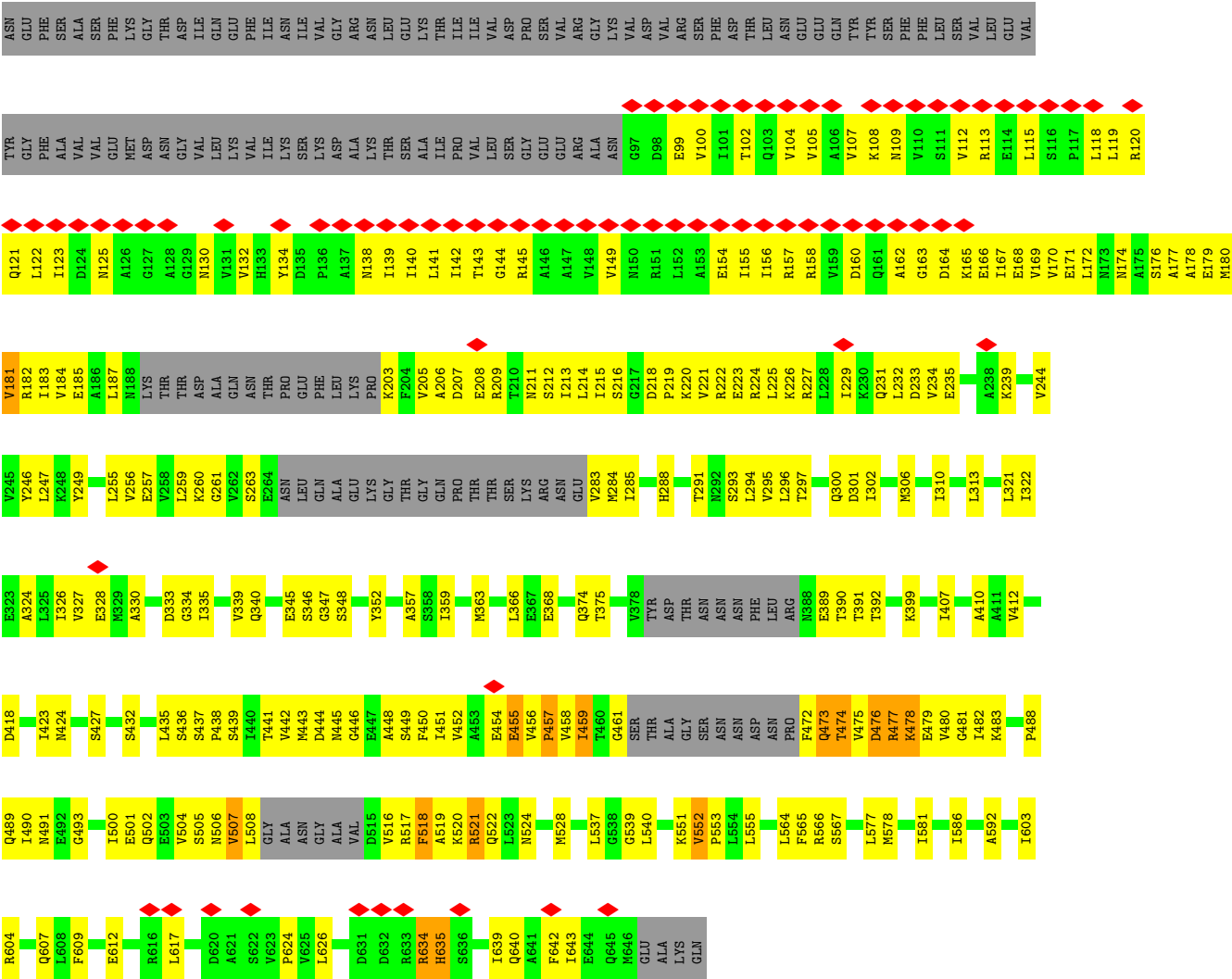


• Molecule 1: Type II secretion system protein D

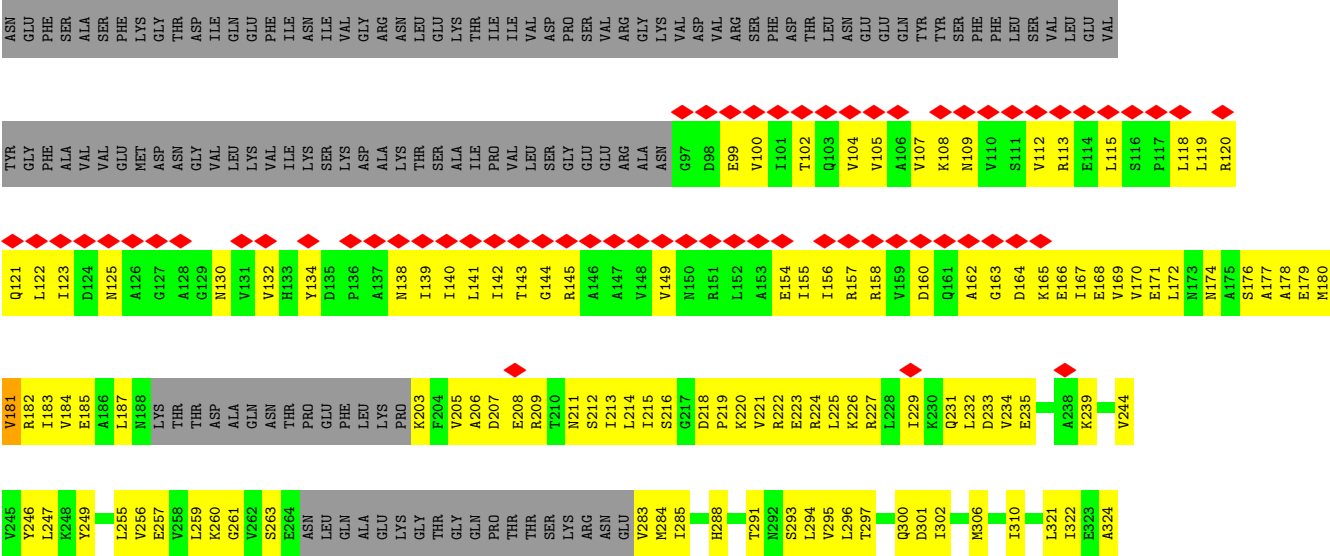


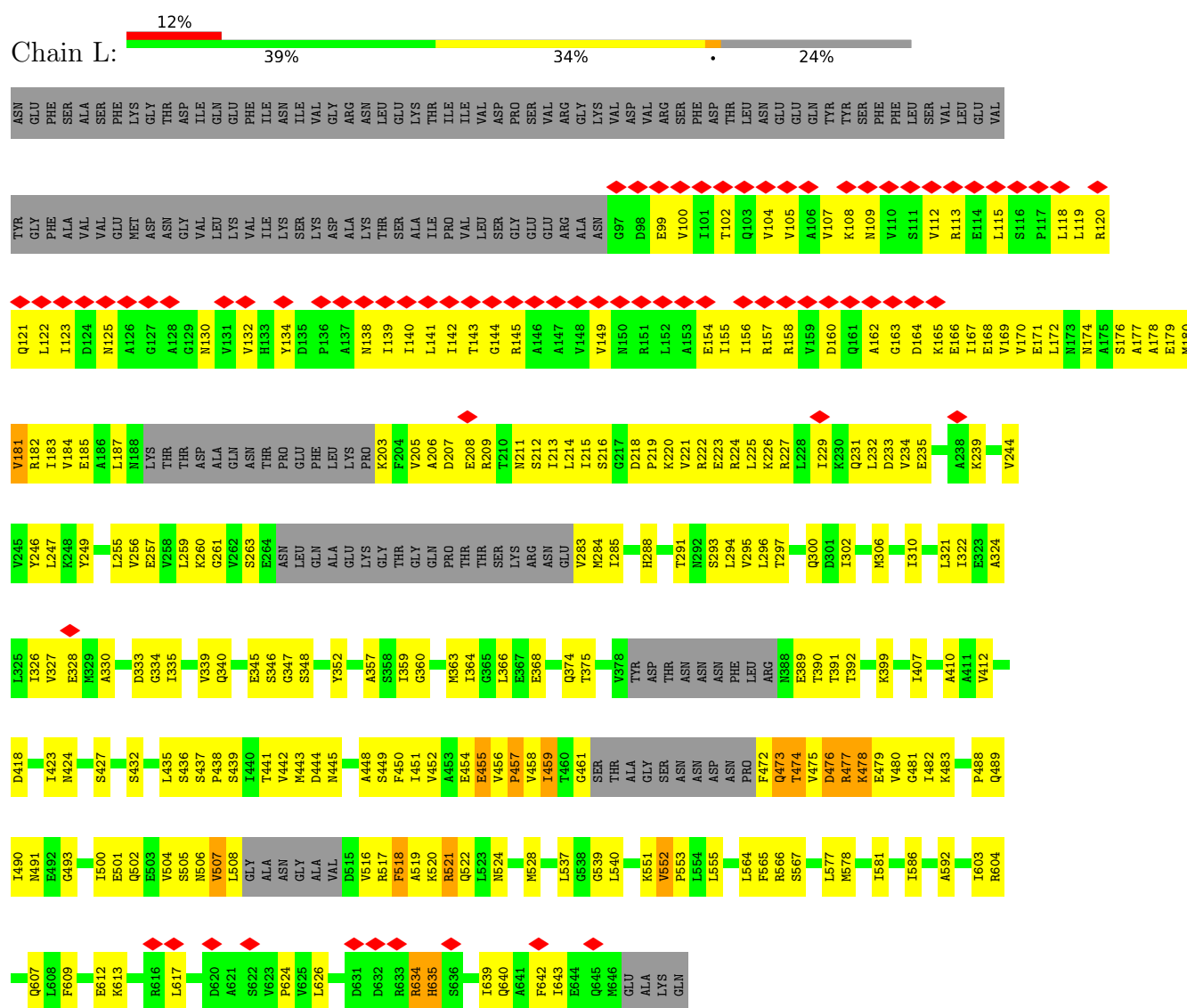
• Molecule 1: Type II secretion system protein D



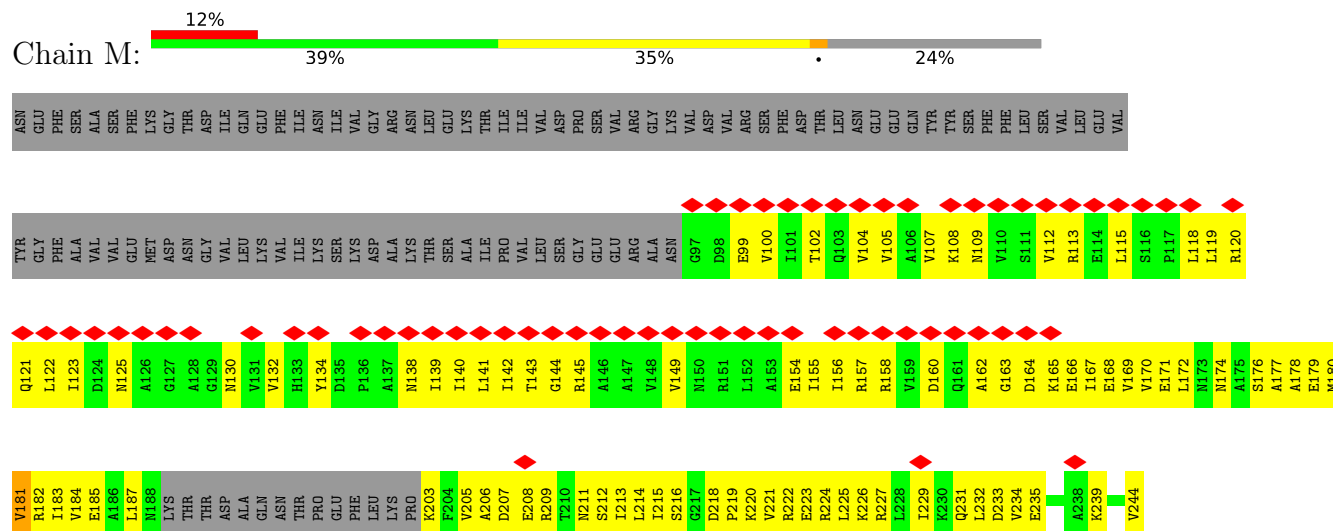


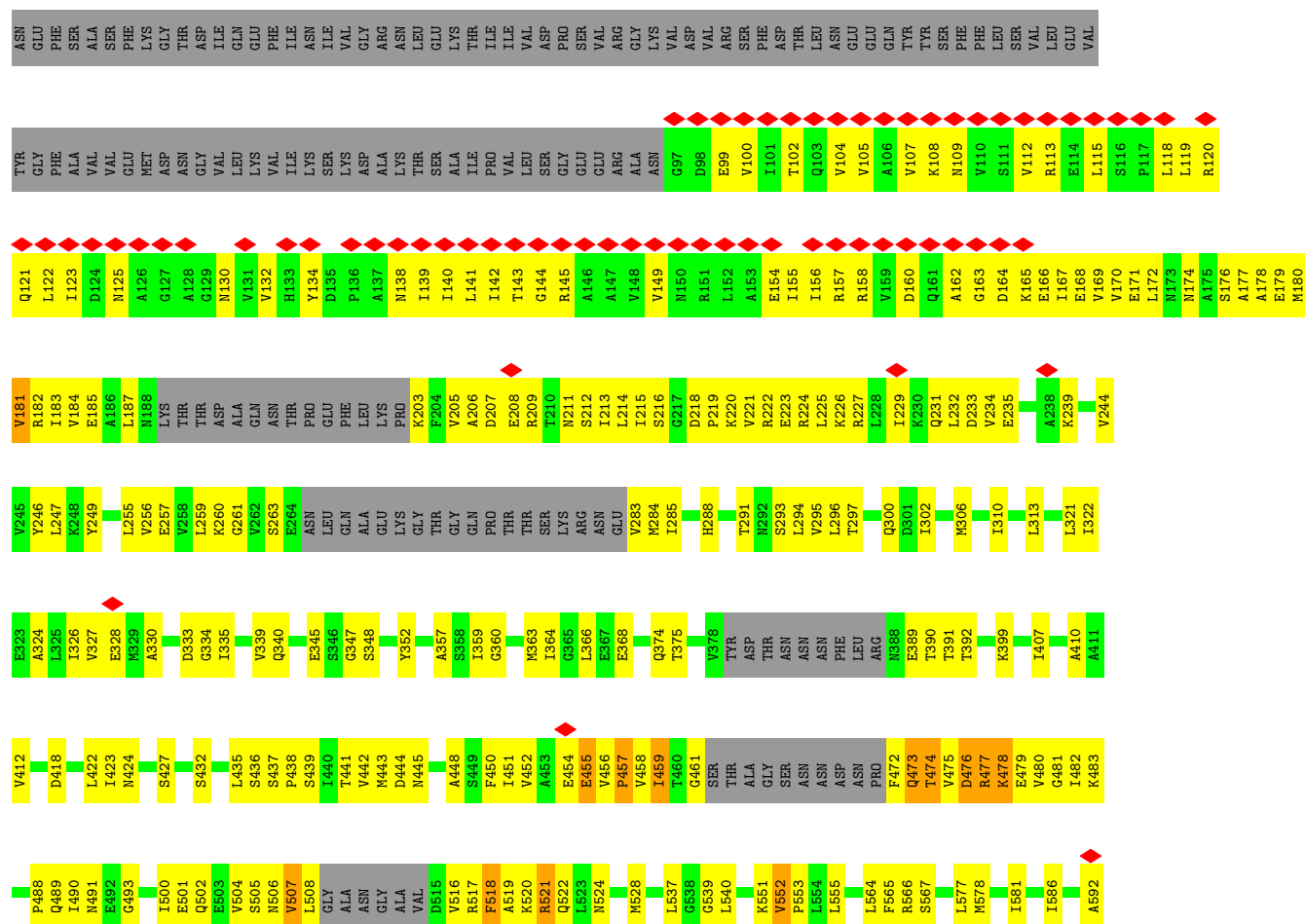
• Molecule 1: Type II secretion system protein D

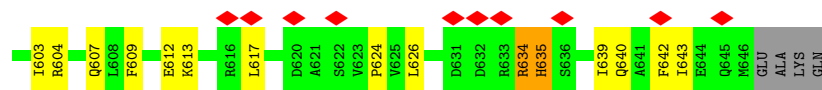




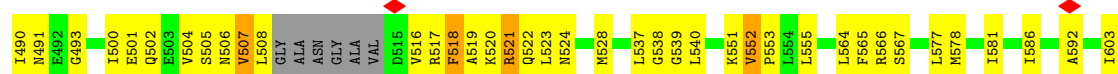
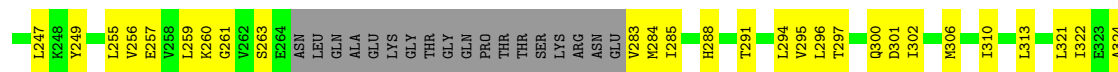
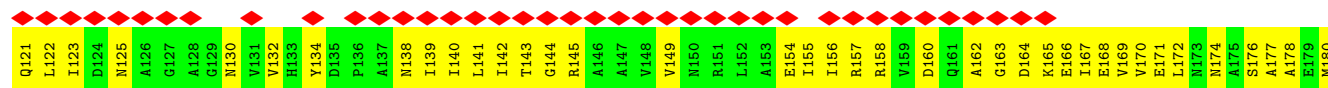
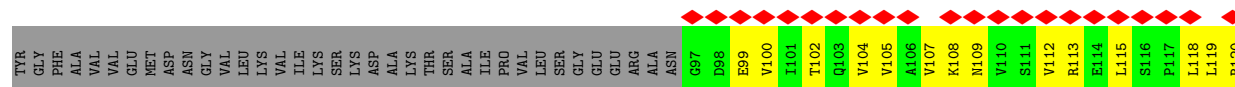
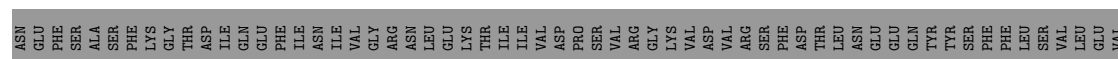
- Molecule 1: Type II secretion system protein D







• Molecule 1: Type II secretion system protein D



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C15	Depositor
Number of particles used	26955	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.046	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	501.6, 501.6, 501.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	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	A	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	B	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	C	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
1	D	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	E	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	F	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	G	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	H	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
1	I	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	J	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
1	K	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
1	L	0.41	1/3786 (0.0%)	0.74	7/5117 (0.1%)
1	M	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
1	N	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
1	O	0.41	1/3786 (0.0%)	0.74	8/5117 (0.2%)
All	All	0.41	15/56790 (0.0%)	0.74	112/76755 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	457	PRO	N-CD	5.31	1.55	1.47
1	E	457	PRO	N-CD	5.30	1.55	1.47
1	J	457	PRO	N-CD	5.30	1.55	1.47
1	C	457	PRO	N-CD	5.29	1.55	1.47
1	B	457	PRO	N-CD	5.28	1.55	1.47

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	507	VAL	CB-CA-C	-12.16	91.07	110.28
1	B	507	VAL	CB-CA-C	-12.16	91.07	110.28
1	C	507	VAL	CB-CA-C	-12.16	91.07	110.28
1	I	507	VAL	CB-CA-C	-12.15	91.08	110.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	507	VAL	CB-CA-C	-12.15	91.08	110.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3756	0	3858	333	0
1	B	3756	0	3858	336	0
1	C	3756	0	3858	332	0
1	D	3756	0	3858	328	0
1	E	3756	0	3858	329	0
1	F	3756	0	3858	328	0
1	G	3756	0	3858	330	0
1	H	3756	0	3858	330	0
1	I	3756	0	3858	330	0
1	J	3756	0	3858	333	0
1	K	3756	0	3858	332	0
1	L	3756	0	3858	327	0
1	M	3756	0	3858	328	0
1	N	3756	0	3858	331	0
1	O	3756	0	3858	334	0
All	All	56340	0	57870	4433	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 39.

The worst 5 of 4433 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:481:GLY:H	1:G:505:SER:CB	1.22	1.53
1:I:481:GLY:H	1:I:505:SER:CB	1.22	1.53
1:L:481:GLY:H	1:L:505:SER:CB	1.22	1.52
1:N:481:GLY:H	1:N:505:SER:CB	1.22	1.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:481:GLY:H	1:D:505:SER:CB	1.22	1.52

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	A	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	B	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	C	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	D	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	E	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	F	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	G	481/650 (74%)	458 (95%)	22 (5%)	1 (0%)	43	77
1	H	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	I	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	J	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	K	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	L	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	M	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	N	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
1	O	481/650 (74%)	459 (95%)	21 (4%)	1 (0%)	43	77
All	All	7215/9750 (74%)	6884 (95%)	316 (4%)	15 (0%)	44	77

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	VAL
1	B	181	VAL
1	C	181	VAL
1	E	181	VAL
1	F	181	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	B	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	C	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	D	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	E	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	F	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	G	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	H	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	I	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	J	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	K	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	L	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	M	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	N	415/550 (76%)	403 (97%)	12 (3%)	37	58
1	O	415/550 (76%)	403 (97%)	12 (3%)	37	58
All	All	6225/8250 (76%)	6045 (97%)	180 (3%)	38	58

5 of 180 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	478	LYS
1	L	521	ARG

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Mol	Chain	Res	Type
1	J	521	ARG
1	K	520	LYS
1	M	477	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 174 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	645	GLN
1	M	340	GLN
1	K	340	GLN
1	L	288	HIS
1	M	640	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

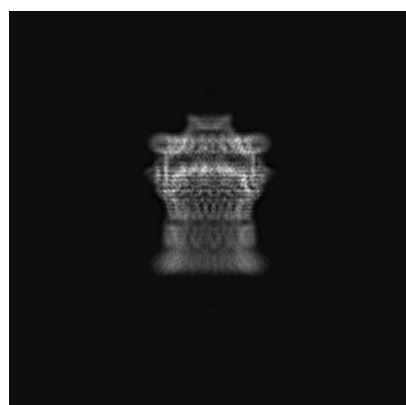
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6677. These allow visual inspection of the internal detail of the map and identification of artifacts.

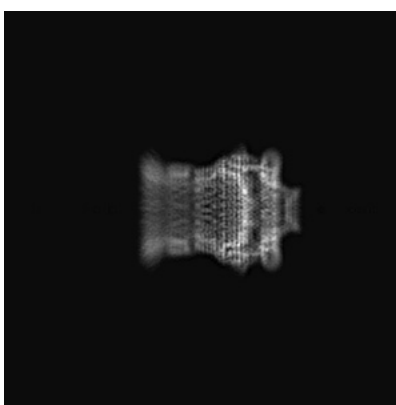
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

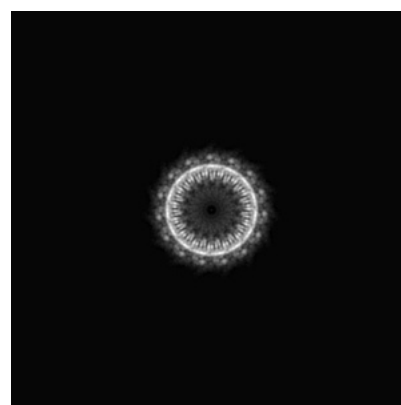
6.1.1 Primary map



X



Y

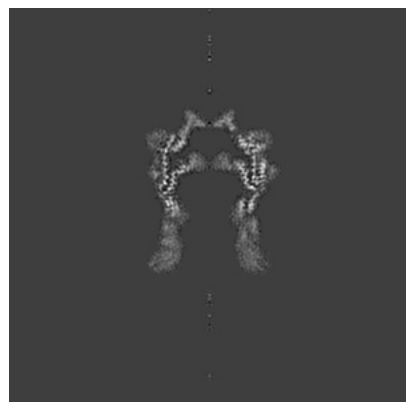


Z

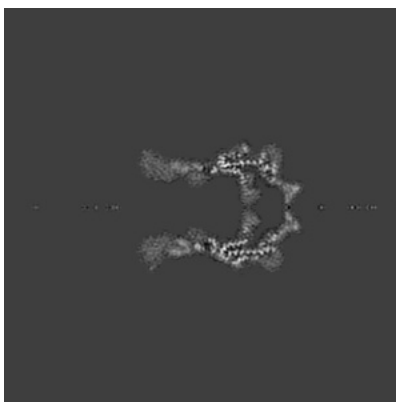
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

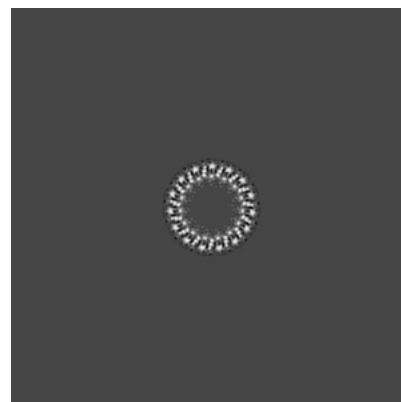
6.2.1 Primary map



X Index: 190



Y Index: 190



Z Index: 190

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

6.3 Largest variance slices [i](#)

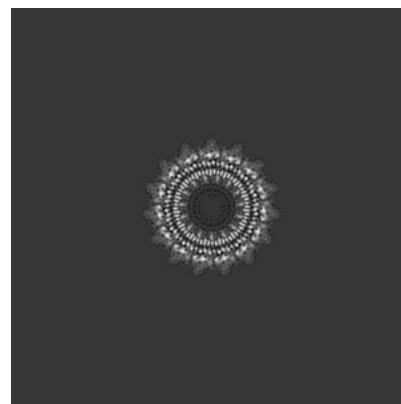
6.3.1 Primary map



X Index: 224



Y Index: 224

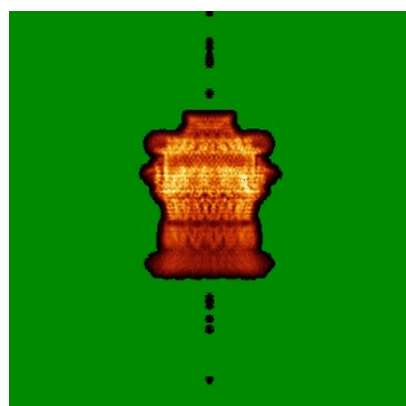


Z Index: 223

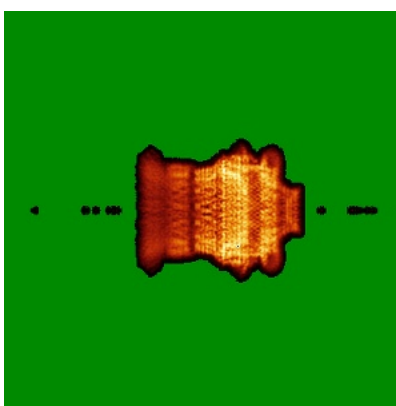
The images above show the largest variance slices of the map in three orthogonal directions.

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

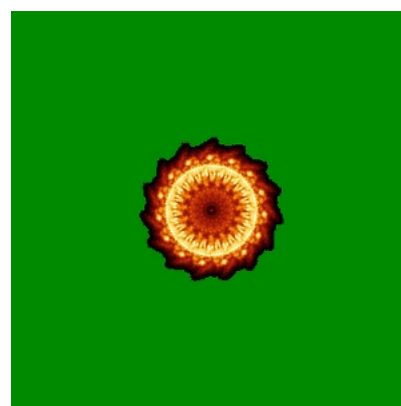
6.4.1 Primary map



X



Y

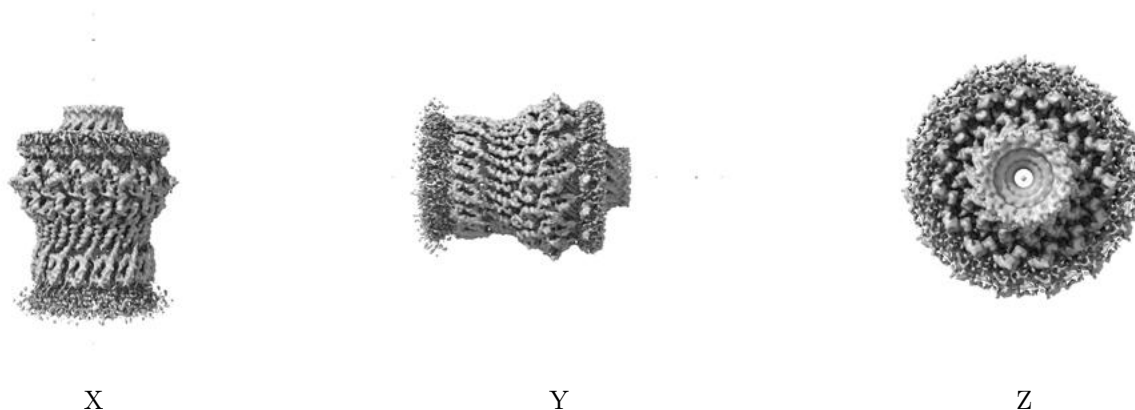


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

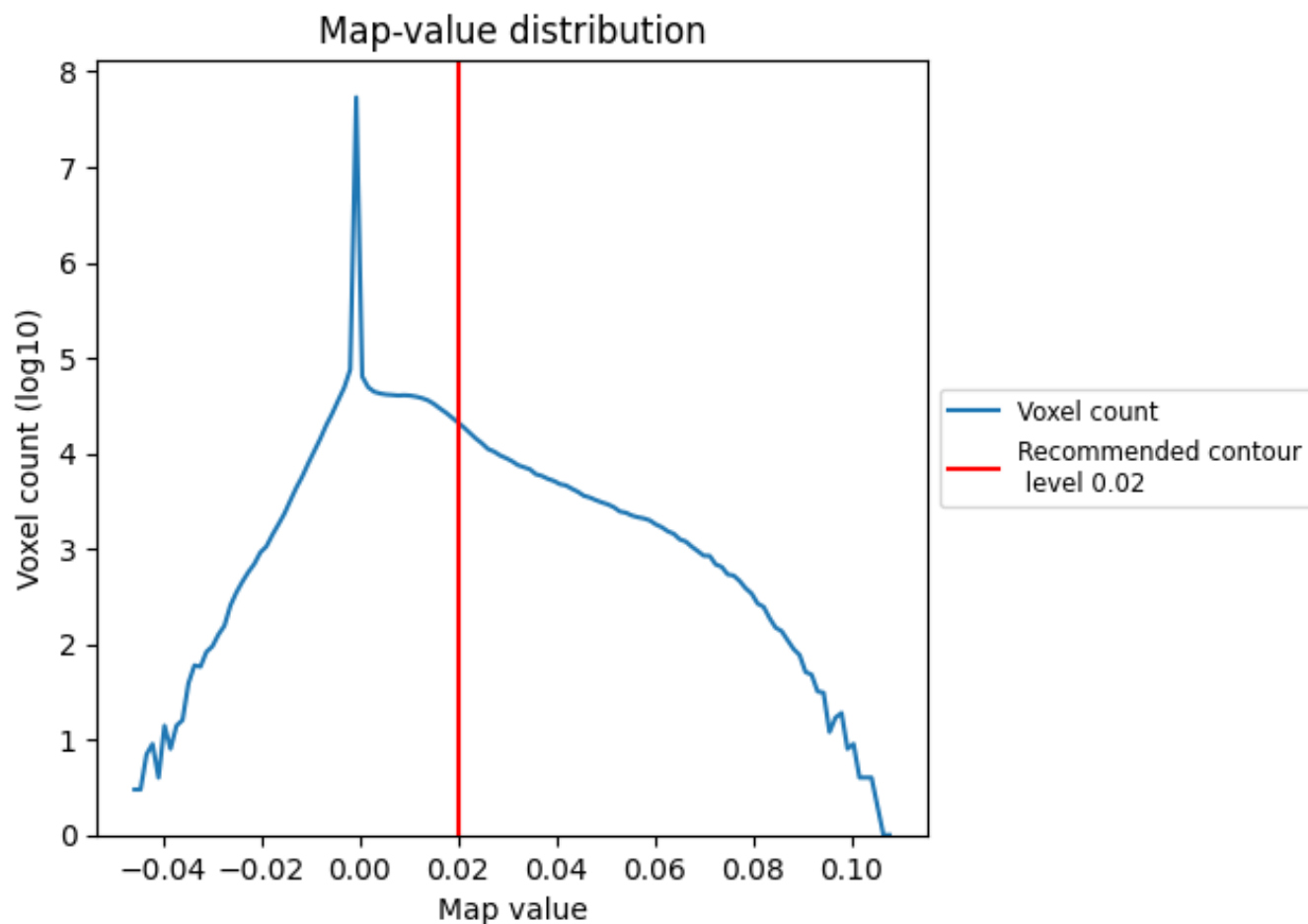
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

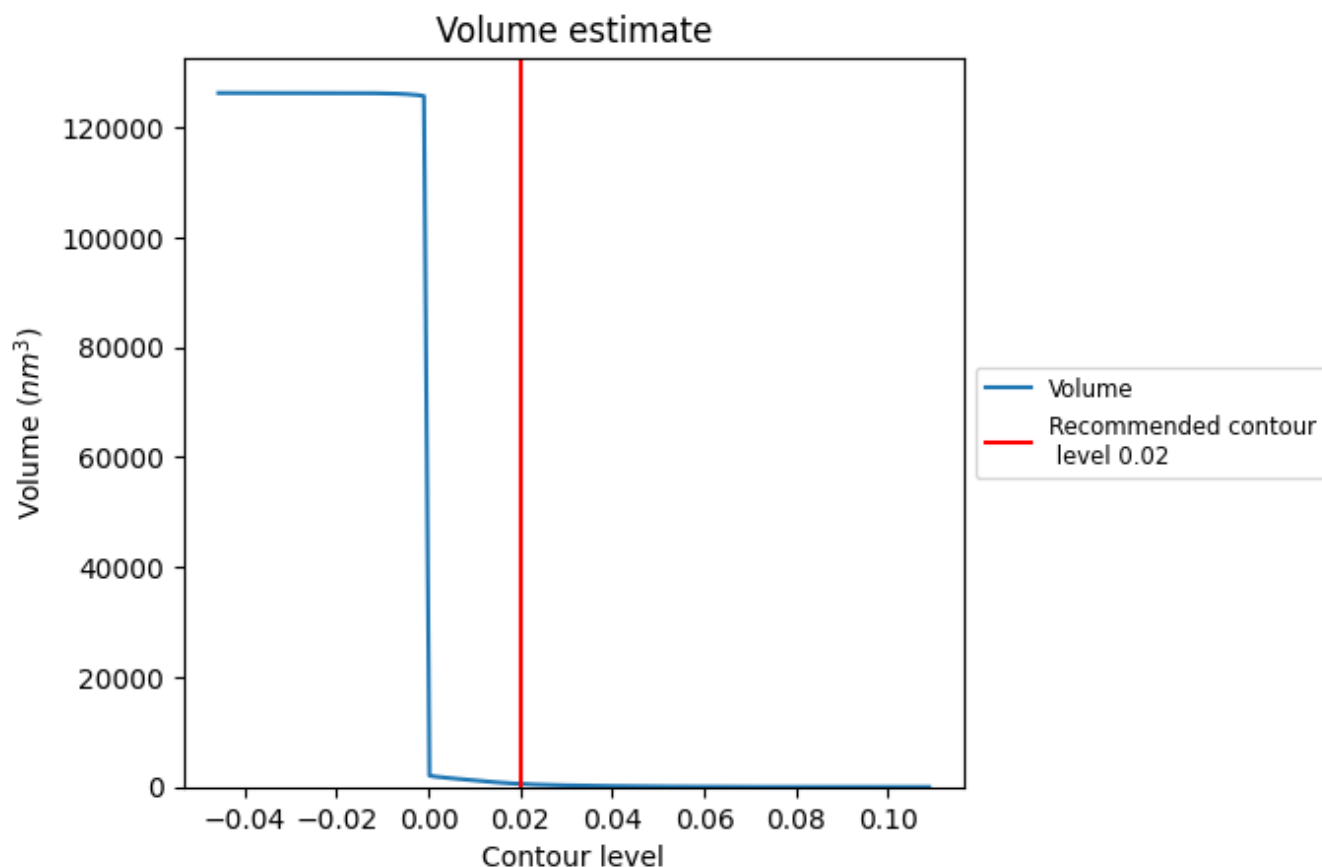
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

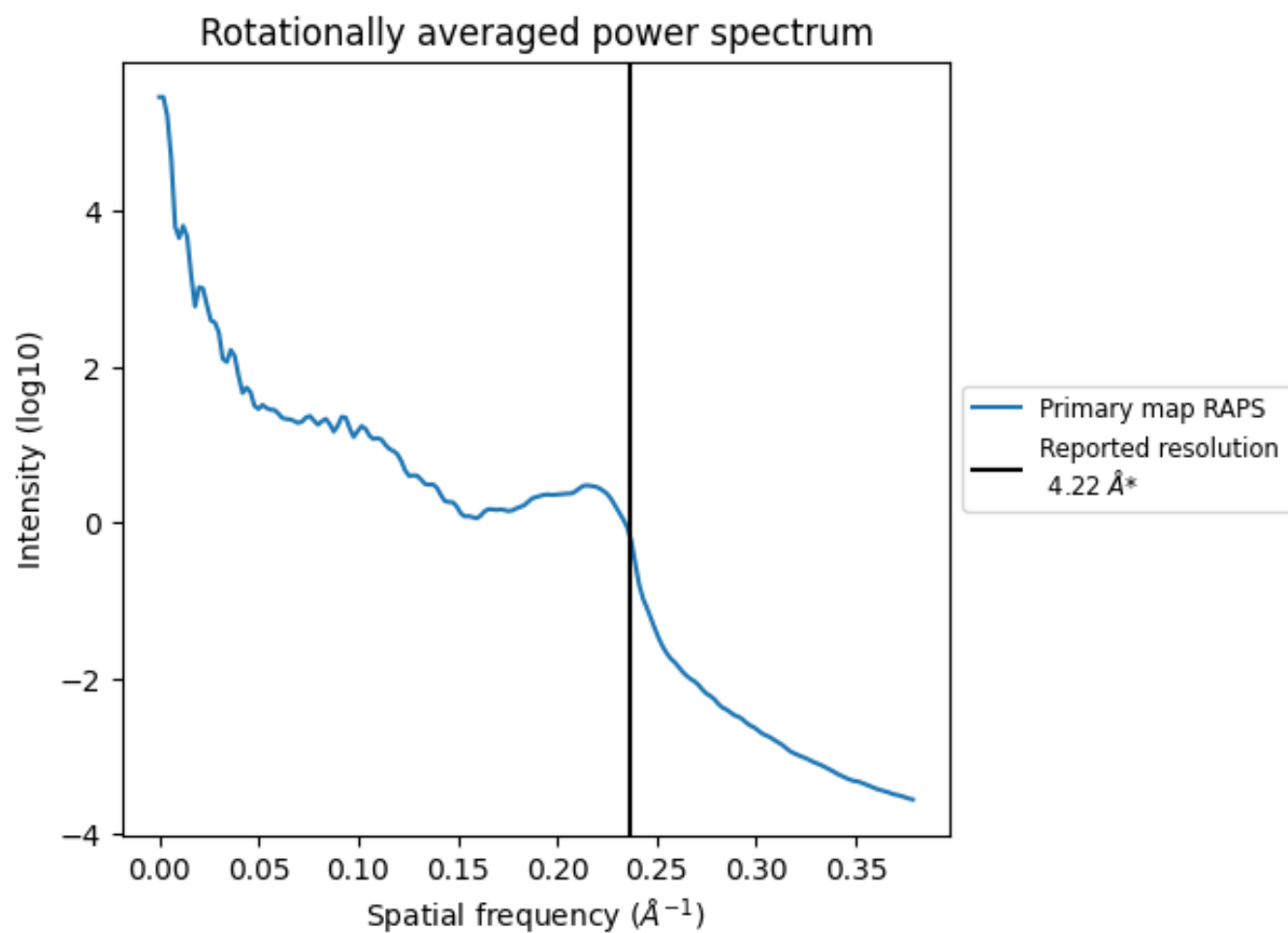
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 559 nm³; this corresponds to an approximate mass of 505 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 0.237 Å⁻¹

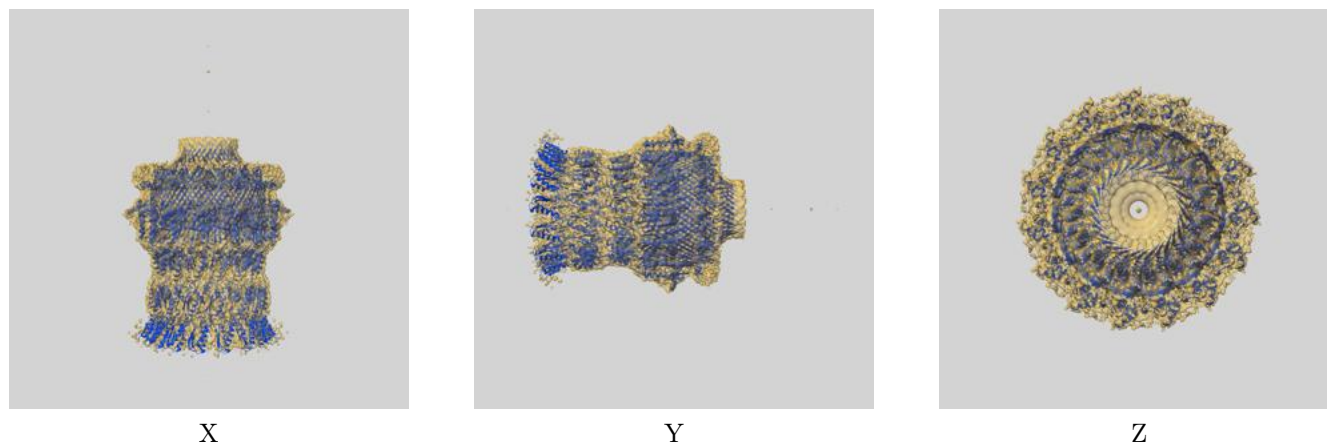
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

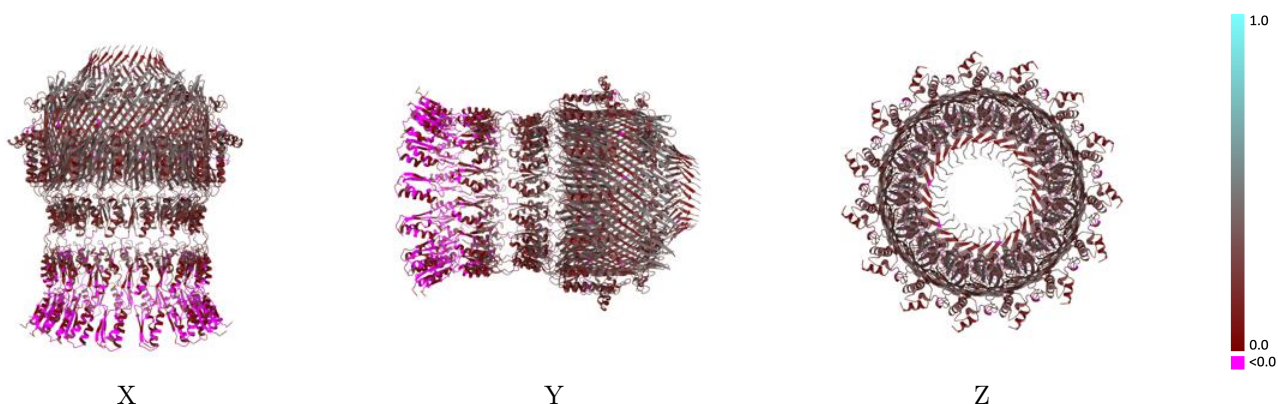
This section contains information regarding the fit between EMDB map EMD-6677 and PDB model 5WQ9. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



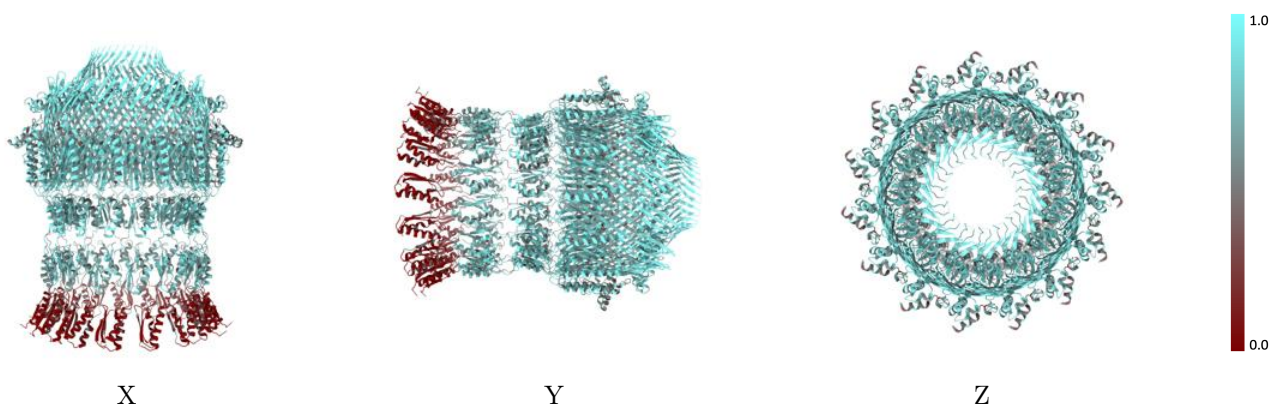
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



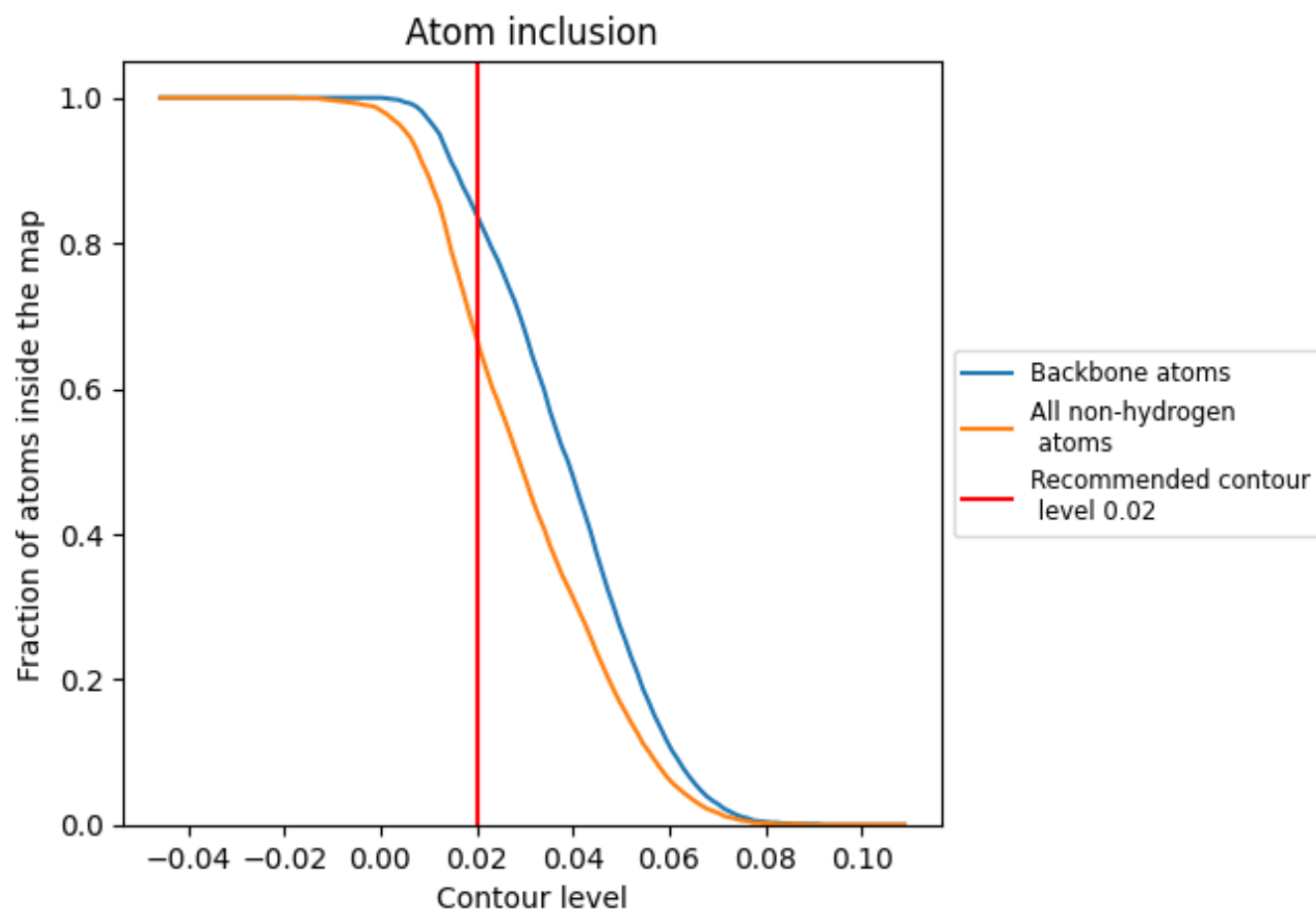
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 67% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6680	0.2360
A	0.6690	0.2340
B	0.6700	0.2350
C	0.6680	0.2340
D	0.6700	0.2350
E	0.6680	0.2360
F	0.6670	0.2370
G	0.6680	0.2360
H	0.6700	0.2390
I	0.6690	0.2390
J	0.6680	0.2390
K	0.6680	0.2370
L	0.6700	0.2360
M	0.6660	0.2360
N	0.6680	0.2340
O	0.6680	0.2350

1.0

0.0

<0.0