



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:41 AM UTC

PDB ID : 3GZU / pdb_00003gzu
EMDB ID : EMD-1571
Title : VP7 recoated rotavirus DLP
Authors : Chen, J.Z.; Settembre, E.C.; Harrison, S.C.; Grigorieff, N.
Deposited on : 2009-04-07
Resolution : 3.80 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:

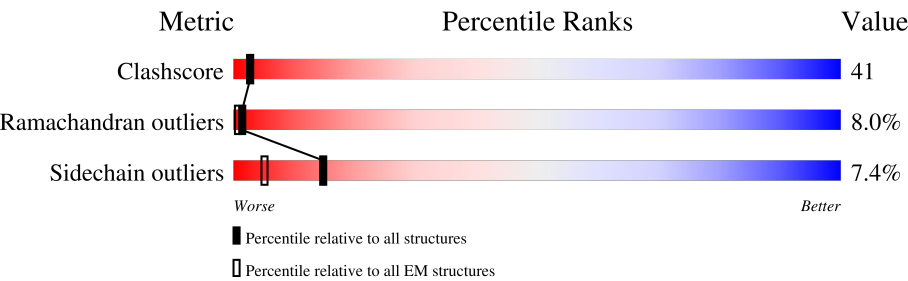
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	800	98% 14% 54% 24% 5% .
1	B	800	100% 17% 54% 26% .
2	C	397	100% 58% 35% 7% .
2	D	397	100% 58% 32% 9% .
2	E	397	100% 58% 34% 7% .
2	F	397	100% 58% 35% 6% .
2	G	397	100% 58% 32% 9% .
2	H	397	100% 56% 35% 8% .

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Mol	Chain	Length	Quality of chain
2	I	397	100% 58%35%7%
2	J	397	100% 58%32%9%
2	K	397	100% 58%33%8%
2	L	397	100% 58%35%7%
2	M	397	100% 58%33%9%
2	N	397	100% 58%34%8%
2	O	397	100% 60%31%9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 53996 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 Inner capsid protein VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	781	Total	C	N	O	S	1	0
			6383	4054	1099	1194	36		
1	B	800	Total	C	N	O	S	0	0
			6541	4157	1124	1224	36		

- Molecule 2 is a protein called Intermediate capsid protein VP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	D	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	E	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	F	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	G	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	H	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	I	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	J	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	K	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	L	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	M	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	N	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		
2	O	397	Total	C	N	O	S	0	0
			3159	2002	546	596	15		

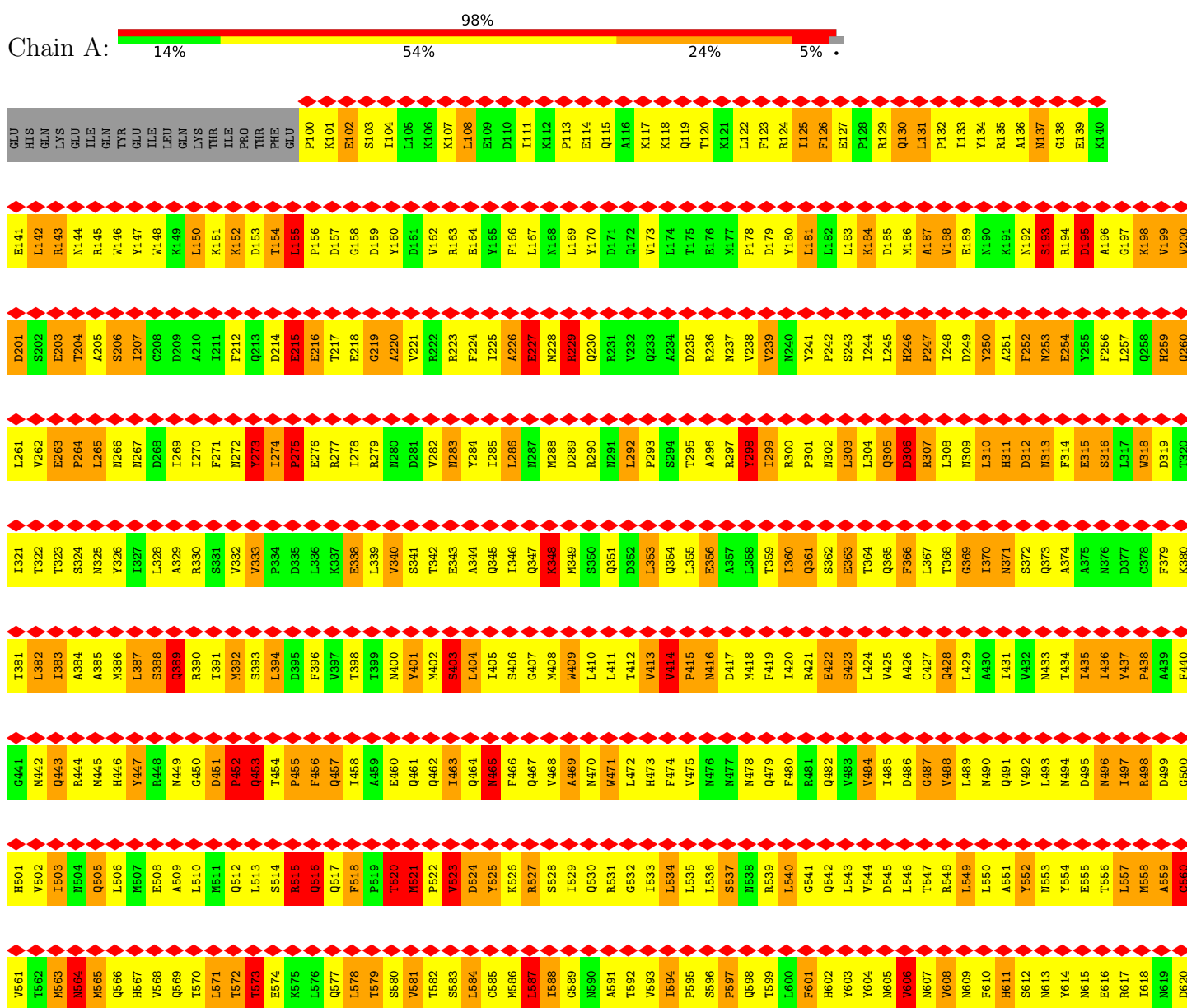
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

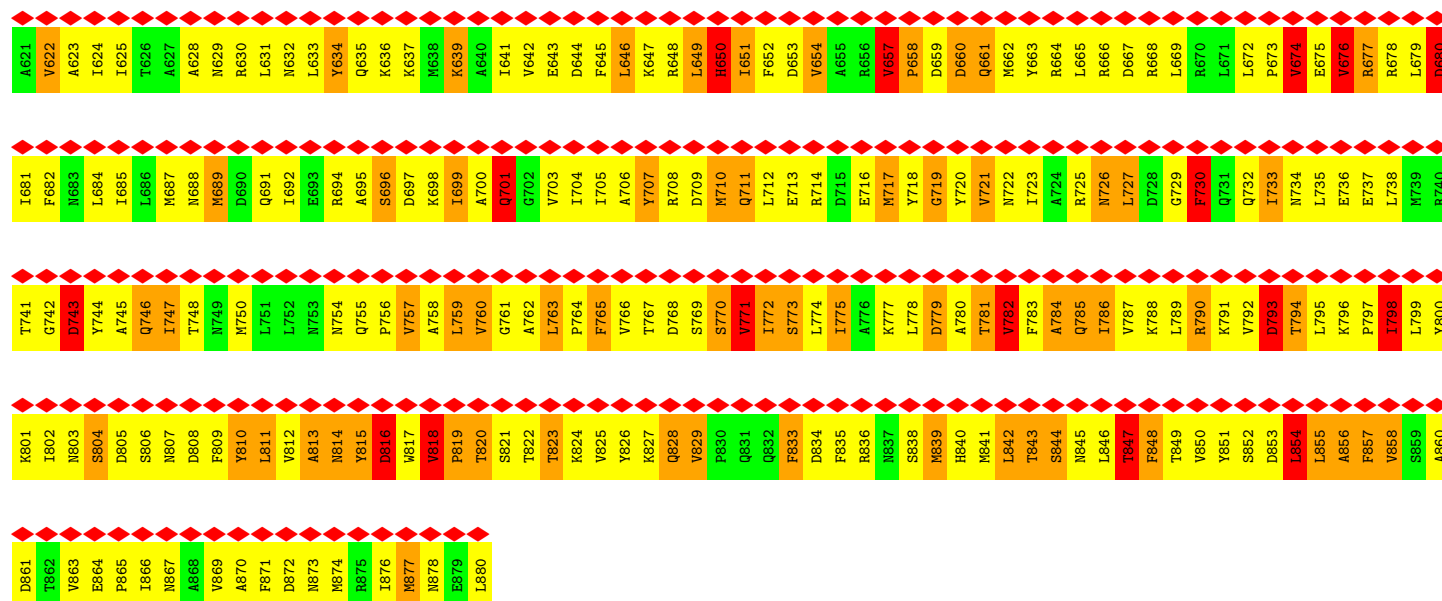
Mol	Chain	Residues	Atoms		AltConf
3	C	1	Total 1	Zn 1	0
3	G	1	Total 1	Zn 1	0
3	J	1	Total 1	Zn 1	0
3	N	1	Total 1	Zn 1	0
3	O	1	Total 1	Zn 1	0

3 Residue-property plots

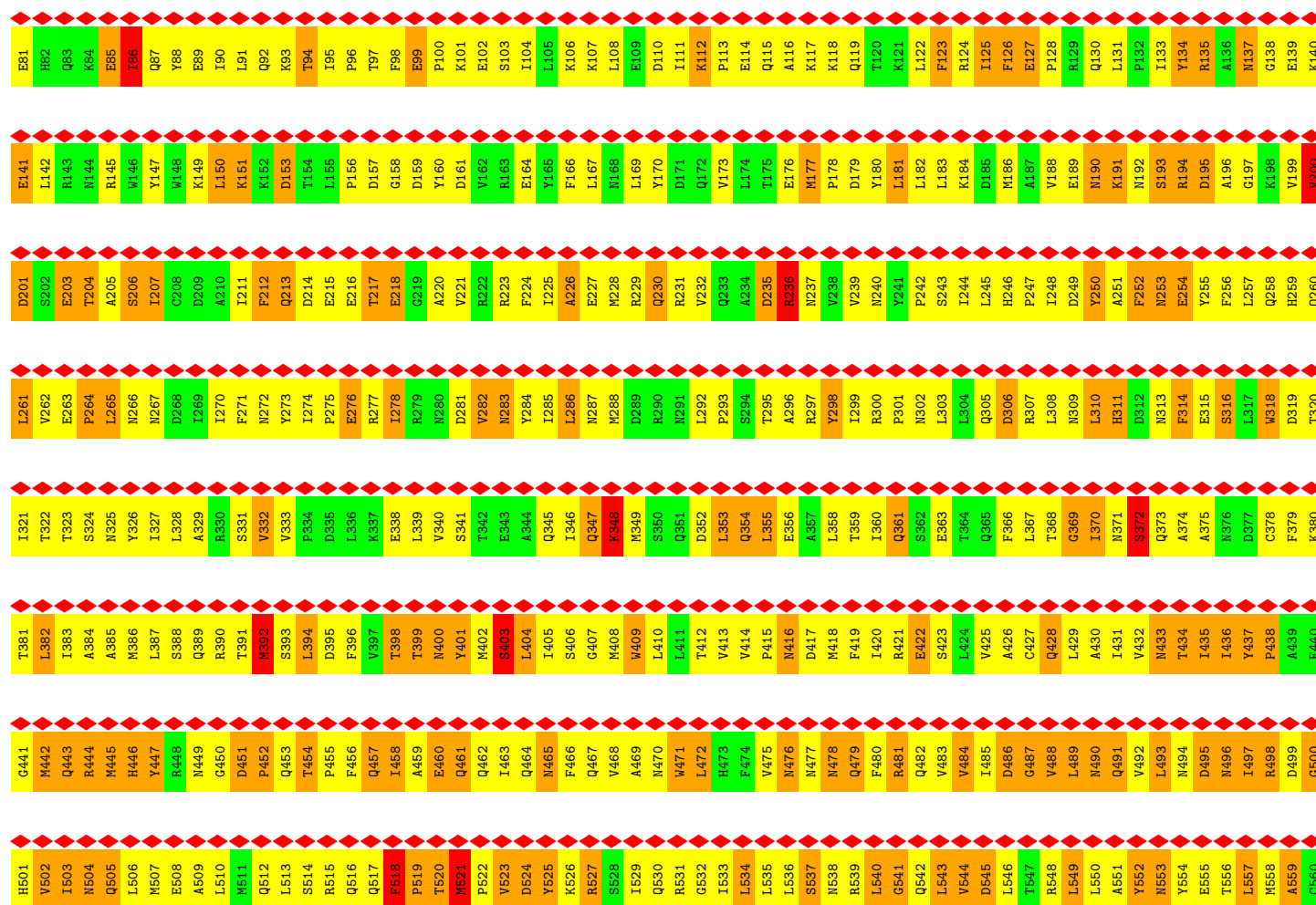
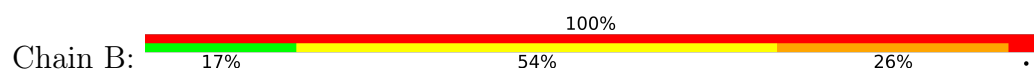
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

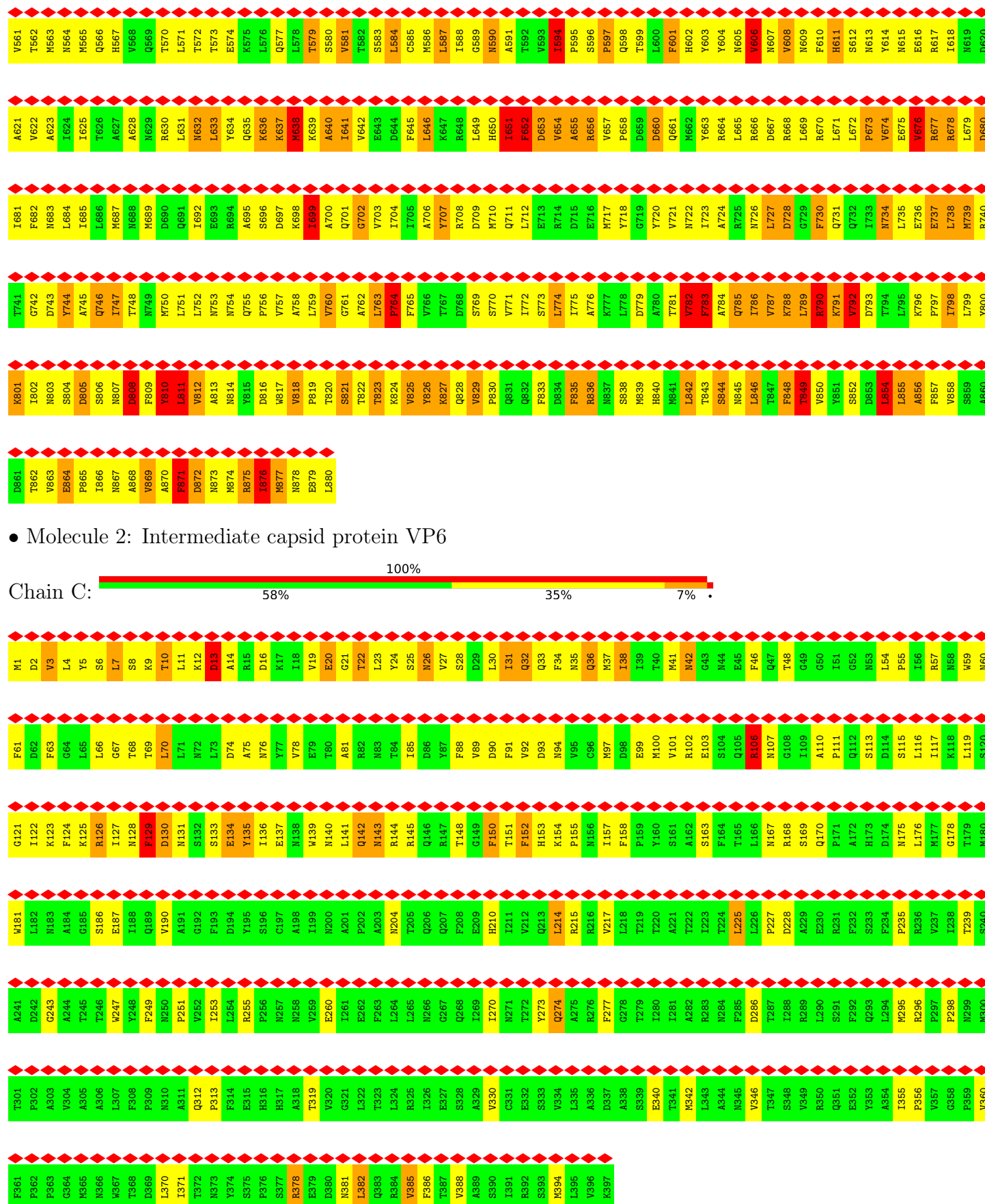
• Molecule 1: Inner capsid protein VP2



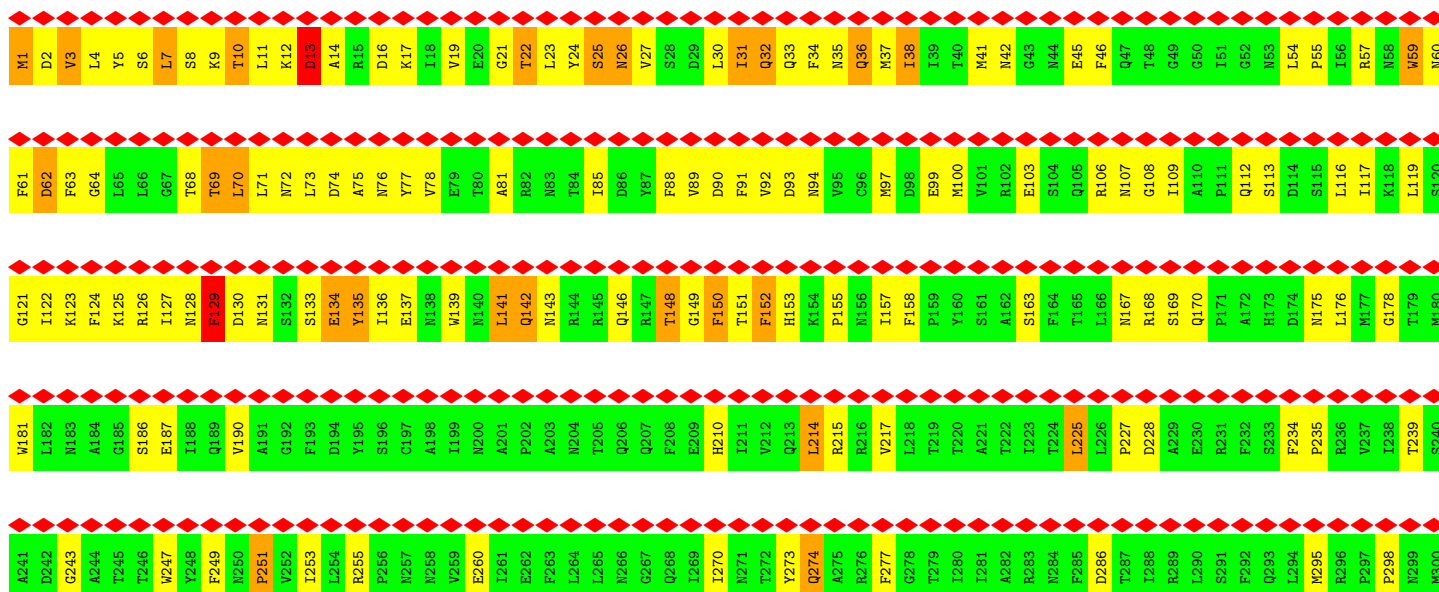


• Molecule 1: Inner capsid protein VP2



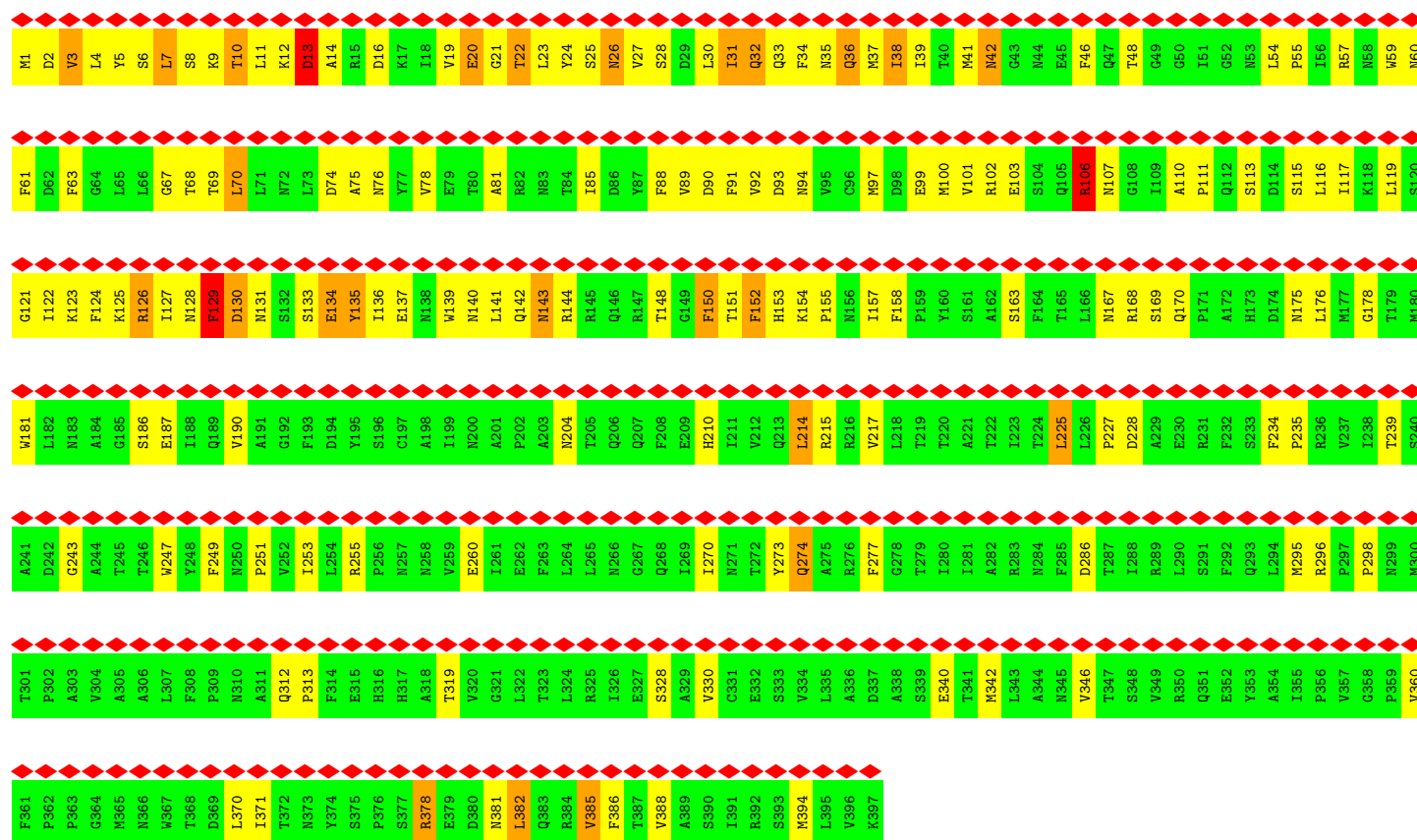


Chain D: 100% 58% 32% 9%

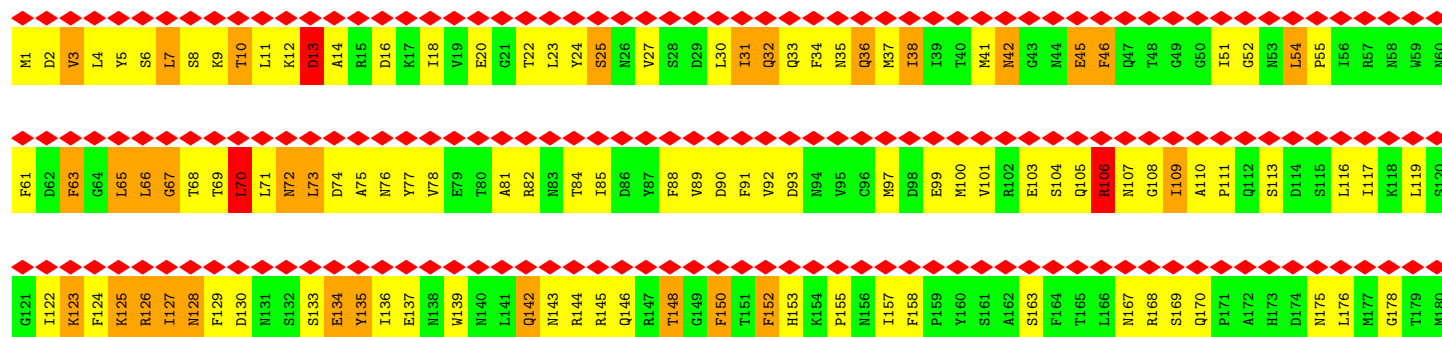


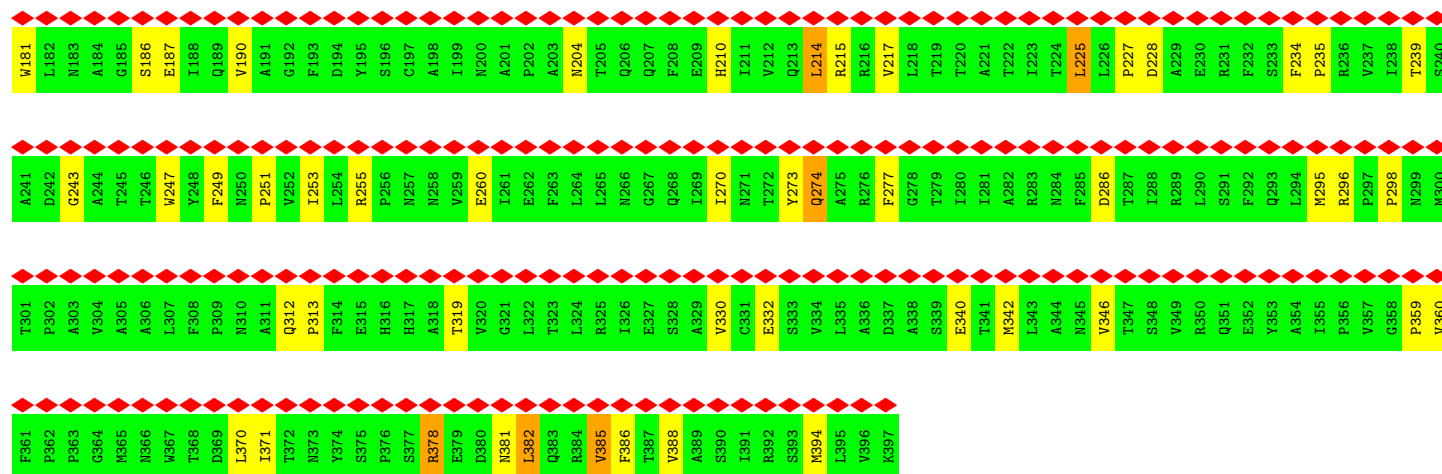


• Molecule 2: Intermediate capsid protein VP6

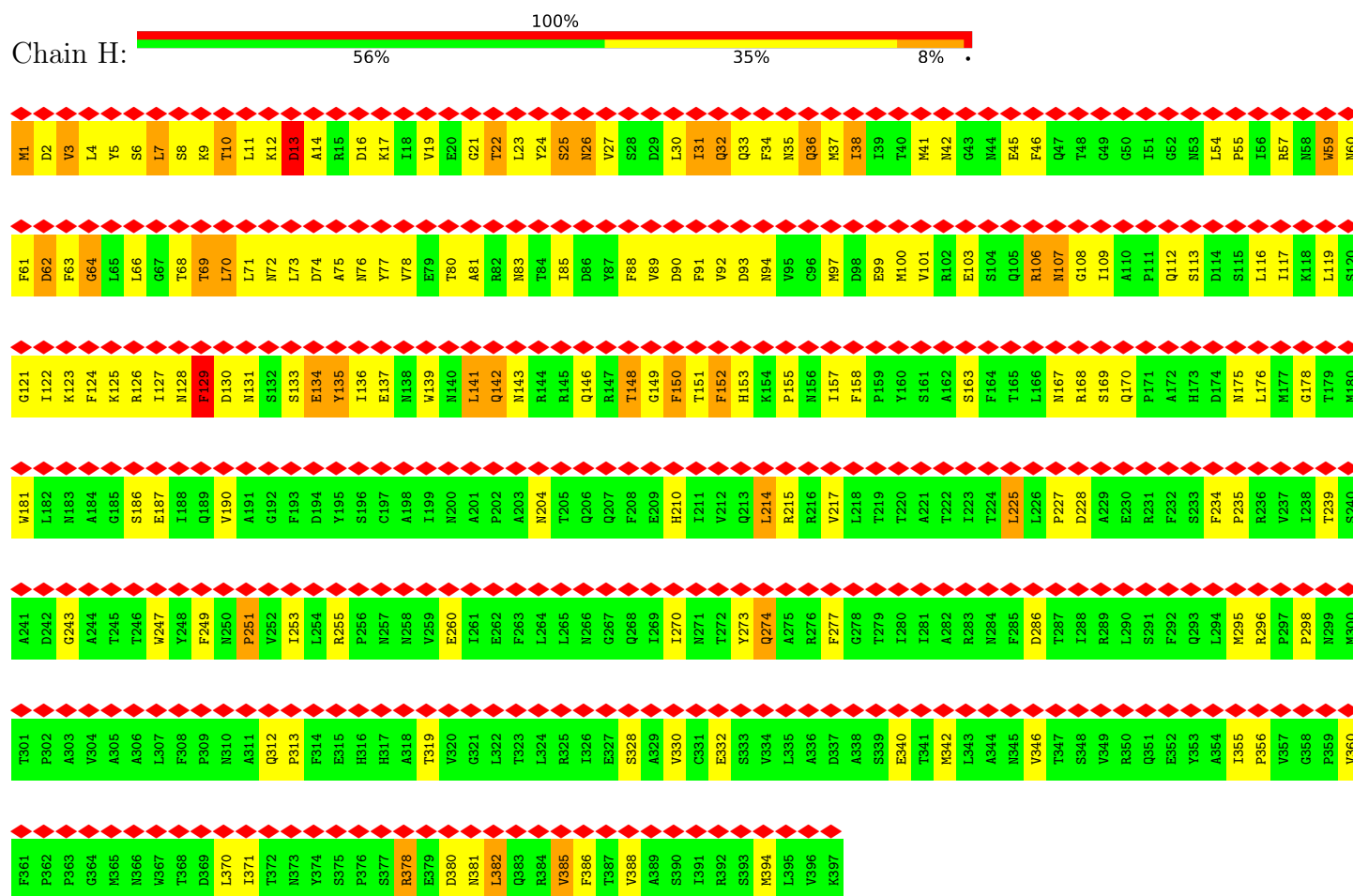


• Molecule 2: Intermediate capsid protein VP6

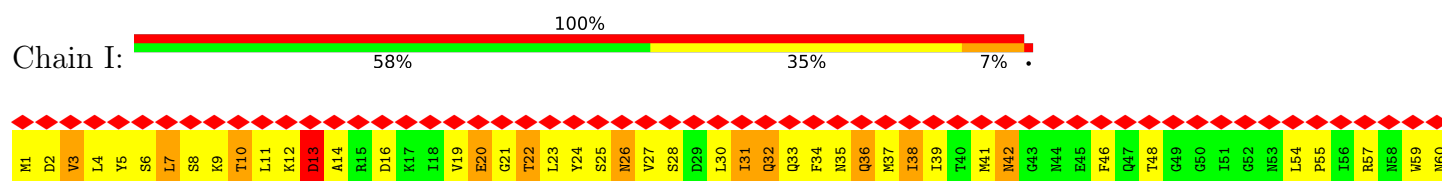




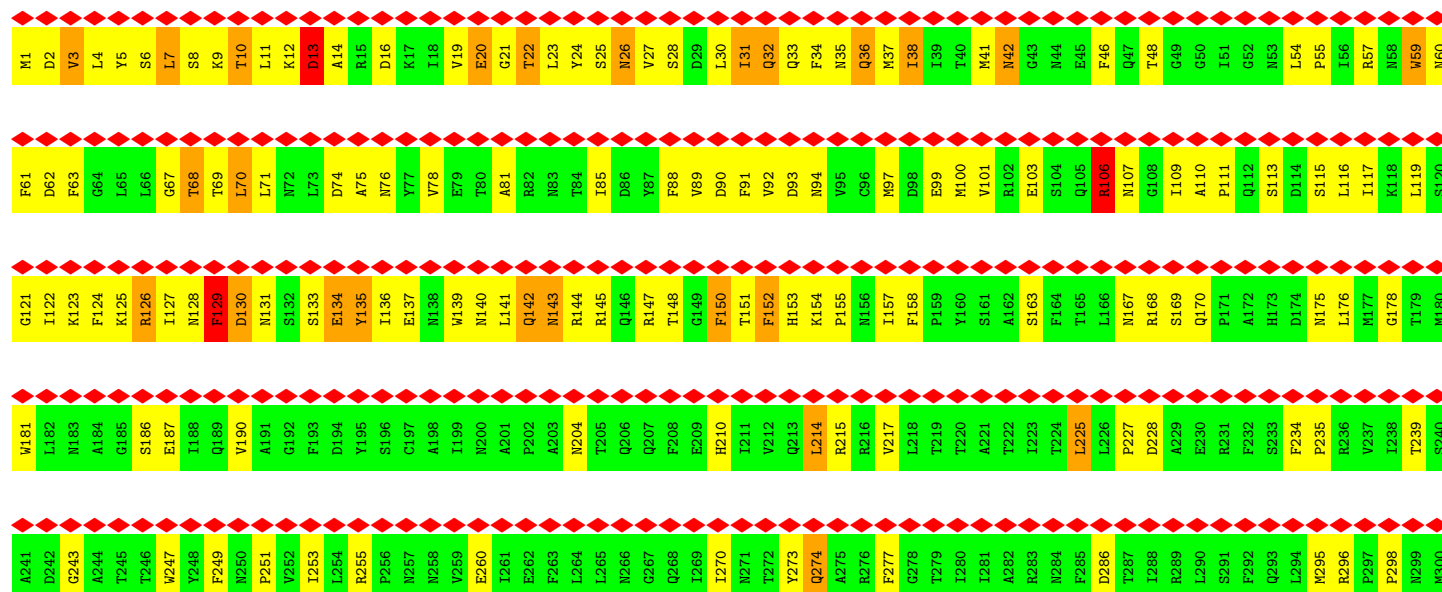
• Molecule 2: Intermediate capsid protein VP6

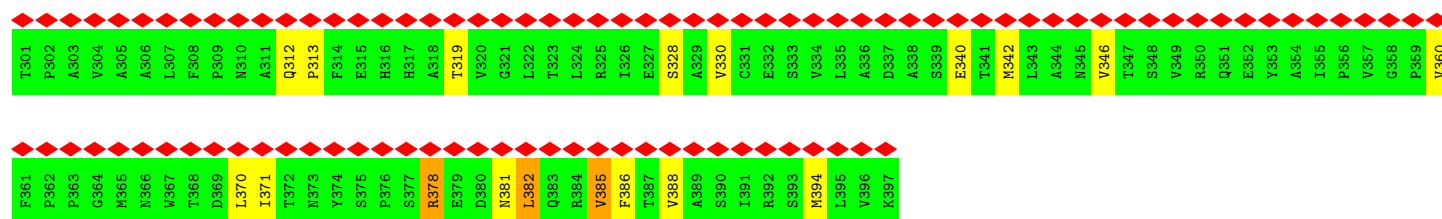


• Molecule 2: Intermediate capsid protein VP6

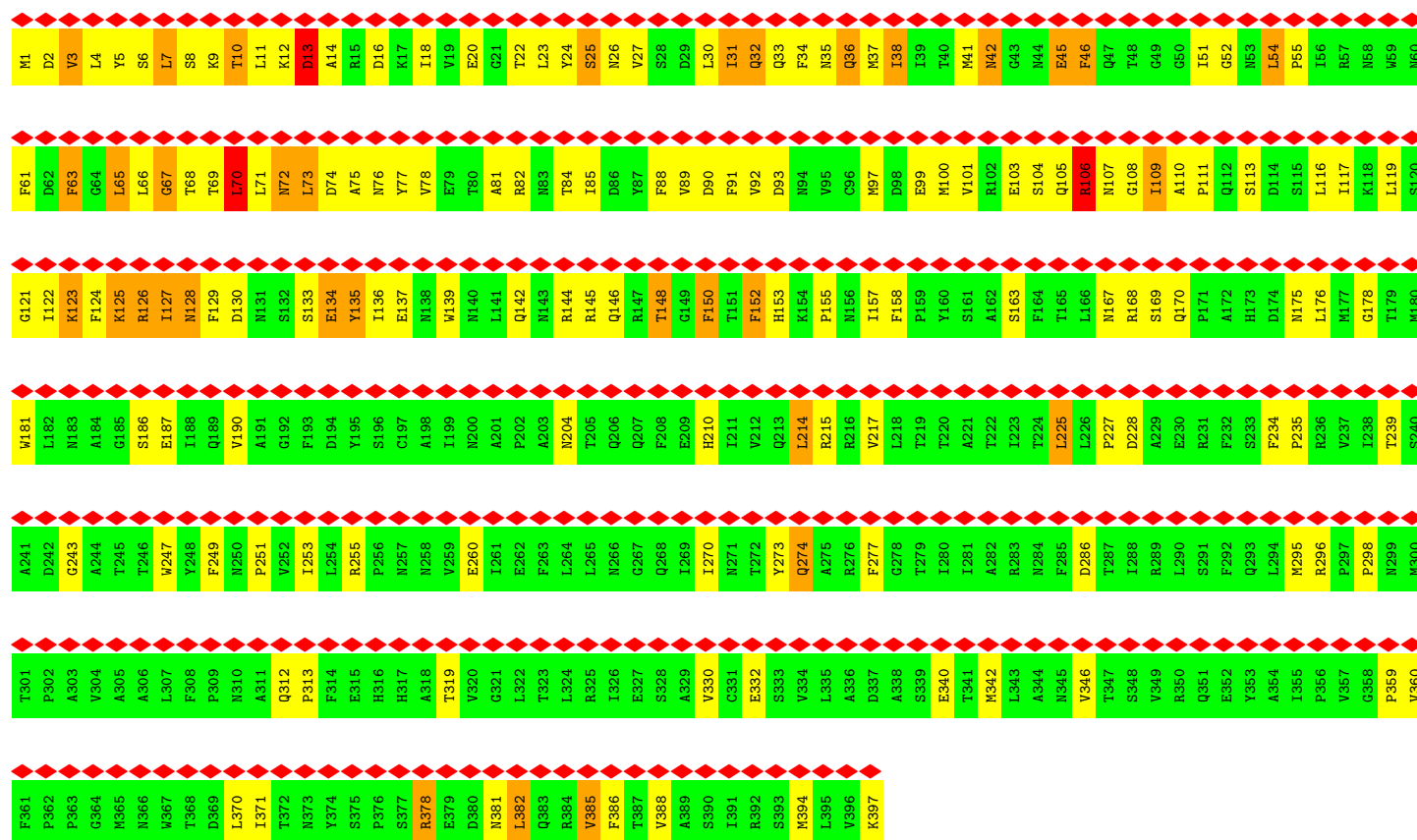


Chain K:

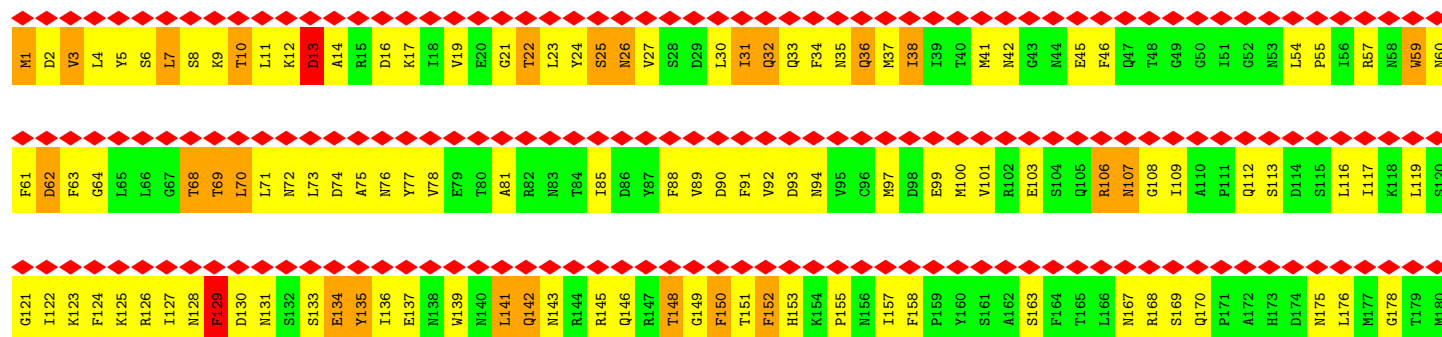




• Molecule 2: Intermediate capsid protein VP6



• Molecule 2: Intermediate capsid protein VP6



W181	A241	T301	F361
L182	D242	P302	P362
N183	G243	A303	P363
A184	A244	V304	G364
A185	T245	A305	M365
S186	T246	A306	N366
E187	W247	L307	W367
I188	Y248	F308	T368
Q189	F249	P309	D369
V190	N250	N310	L370
A191	P251	A311	I371
G192	V252	Q312	T372
F193	I253	P313	N373
D194	L254	F314	Y374
Y195	R255	E315	S375
S196	P256	H316	P376
C197	N257	H317	S377
A198	N258	A318	R378
I199	V259	T319	E379
N200	E260	V320	D380
A201	I261	G321	N381
P202	E262	L322	L382
A203	F263	T323	Q383
N204	L264	L324	R384
T205	L265	R325	V385
Q206	N266	I326	F386
Q207	G267	E327	T387
F208	Q268	S328	V388
E209	I269	A329	A389
H210	I270	V330	S390
I211	N271	C331	I391
V212	T272	E332	R392
Q213	Y273	S333	S393
L214	Q274	V334	M394
R215	A275	L335	L395
R216	R276	A336	V396
V217	F277	D337	K397
L218	G278	A338	
T219	T279	S339	
T220	I280	E340	
A221	I281	T341	
T222	A282	M342	
I223	R283	L343	
T224	N284	A344	
L225	F285	N345	
L226	D286	V346	
P227	T287	T347	
D228	I288	S348	
A229	R289	V349	
E230	L290	R350	
R231	S291	Q351	
F232	F292	E352	
S233	Q293	Y353	
F234	L294	A354	
P235	M295	I355	
R236	R296	P356	
V237	P297	V357	
I238	P298	G358	
T239	N299	P359	
S240	M300	V360	

• Molecule 2: Intermediate capsid protein VP6



M1	F61	G121	W181	A241	T301	F361
D2	D62	I122	L182	D242	P302	P362
V3	F63	K123	N183	G243	A303	P363
L4	G64	F124	A184	A244	V304	G364
Y5	L65	K125	A185	T245	A305	M365
S6	L66	R126	S186	T246	A306	N366
L7	G67	I127	E187	W247	L307	W367
S8	T68	N128	I188	Y248	F308	T368
K9	T69	F129	Q189	F249	P309	D369
T10	L70	D130	V190	N250	N310	L370
L11	L71	M131	A191	P251	A311	I371
K12	N72	S132	G192	V252	Q312	T372
D13	L73	E133	F193	I253	P313	N373
A14	D74	E134	D194	L254	F314	Y374
R15	A75	Y135	Y195	R255	E315	S375
D16	N76	I136	S196	P256	H316	P376
K17	Y77	E137	C197	N257	H317	S377
I18	V78	N138	A198	N258	A318	R378
V19	E79	W139	I199	V259	T319	E379
E20	T80	N140	N200	E260	V320	D380
G21	A81	L141	A201	I261	G321	N381
T22	R82	Q142	P202	E262	L322	L382
L23	N83	M143	A203	F263	T323	Q383
Y24	T84	R144	N204	L264	L324	R384
S25	I85	R145	T205	L265	R325	V385
N26	D86	Q146	Q206	N266	I326	F386
V27	N87	R147	Q207	G267	E327	T387
S28	F88	T148	F208	Q268	S328	V388
D29	N89	G149	E209	I269	A329	A389
L30	D90	F150	H210	I270	V330	S390
I31	F91	T151	I211	N271	C331	I391
Q32	V92	F152	V212	T272	E332	R392
Q33	D93	H153	Q213	Y273	S333	S393
F34	N94	K154	L214	Q274	V334	M394
N35	V95	P155	R215	A275	L335	L395
Q36	C96	N156	R216	R276	A336	V396
K37	N97	I157	V217	F277	D337	K397
I38	D98	F158	L218	G278	A338	
E99	E99	P159	T219	T279	S339	
M100	T40	V160	T220	I280	E340	
V101	V101	S161	A221	I281	T341	
R102	R102	A162	T222	A282	M342	
E103	E103	S163	I223	R283	L343	
S104	S104	F164	T224	N284	A344	
Q105	Q105	T165	L225	F285	N345	
R106	R106	L166	L226	D286	V346	
N107	N107	M167	P227	T287	T347	
G108	G108	R168	D228	I288	S348	
I109	I109	S169	A229	R289	V349	
A110	A110	Q170	E230	L290	R350	
I51	P111	F171	R231	S291	Q351	
G52	Q112	A172	F232	F292	E352	
N53	S113	H173	S233	Q293	Y353	
L54	D114	D174	F234	L294	A354	
S115	S115	N175	P235	M295	I355	
L116	L116	L176	R236	R296	P356	
I117	I117	M177	V237	P297	V357	
K118	K118	G178	I238	P298	G358	
L119	L119	T179	T239	N299	P359	
S120	S120	M180	S240	M300	V360	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	3780	Depositor
Resolution determination method	Not provided	
CTF correction method	individual particle CTF	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	58168	Depositor
Image detector	GENERIC FILM	Depositor
Maximum map value	6.849	Depositor
Minimum map value	-4.636	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	108.504005, 108.504005, 133.164	wwPDB
Map dimensions	88, 88, 108	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.233, 1.233, 1.233	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.62	1/6500 (0.0%)	1.23	81/8819 (0.9%)
1	B	0.74	3/6662 (0.0%)	1.25	78/9038 (0.9%)
2	C	0.62	1/3229 (0.0%)	1.01	9/4394 (0.2%)
2	D	0.62	1/3229 (0.0%)	1.00	14/4394 (0.3%)
2	E	0.62	1/3229 (0.0%)	1.01	11/4394 (0.3%)
2	F	0.62	1/3229 (0.0%)	1.01	9/4394 (0.2%)
2	G	0.62	1/3229 (0.0%)	1.00	14/4394 (0.3%)
2	H	0.62	1/3229 (0.0%)	1.00	11/4394 (0.3%)
2	I	0.62	1/3229 (0.0%)	1.01	9/4394 (0.2%)
2	J	0.62	1/3229 (0.0%)	1.00	14/4394 (0.3%)
2	K	0.62	1/3229 (0.0%)	1.01	11/4394 (0.3%)
2	L	0.62	1/3229 (0.0%)	1.01	9/4394 (0.2%)
2	M	0.62	1/3229 (0.0%)	1.00	14/4394 (0.3%)
2	N	0.62	1/3229 (0.0%)	1.00	10/4394 (0.2%)
2	O	0.62	1/3229 (0.0%)	1.01	11/4394 (0.3%)
All	All	0.64	17/55139 (0.0%)	1.07	305/74979 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
All	All	0	4

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	848	PHE	C-N	-28.58	0.93	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	116	ALA	C-N	-14.21	1.09	1.33
1	A	114	GLU	C-N	-7.72	1.23	1.33
1	B	674	VAL	C-N	-5.98	1.25	1.33
2	E	247	TRP	NE1-CE2	-5.54	1.31	1.37

The worst 5 of 305 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	497	ILE	N-CA-C	-15.20	95.83	110.42
1	A	367	LEU	N-CA-C	-14.12	96.98	113.21
1	B	518	PHE	N-CA-C	13.90	120.44	108.07
1	B	116	ALA	CA-C-N	-13.83	103.47	123.11
1	B	116	ALA	C-N-CA	-13.83	103.47	123.11

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	263[A]	GLU	Mainchain
1	A	273	TYR	Sidechain
1	A	674	VAL	Mainchain
1	B	810	TYR	Sidechain

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	A	6383	0	6398	1086	0
1	B	6541	0	6551	1318	0
2	C	3159	0	3102	158	0
2	D	3159	0	3102	172	0
2	E	3159	0	3102	157	0
2	F	3159	0	3100	158	0
2	G	3159	0	3102	201	0
2	H	3159	0	3101	216	0
2	I	3159	0	3100	230	0
2	J	3159	0	3102	204	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	3159	0	3101	177	0
2	L	3159	0	3099	195	0
2	M	3159	0	3102	179	0
2	N	3159	0	3101	195	0
2	O	3159	0	3102	154	0
3	C	1	0	0	0	0
3	G	1	0	0	0	0
3	J	1	0	0	0	0
3	N	1	0	0	0	0
3	O	1	0	0	0	0
All	All	53996	0	53265	4398	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 41.

The worst 5 of 4398 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:B:498:ARG:HH12	2:J:25:SER:CB	1.22	1.46
1:B:498:ARG:NH1	2:J:25:SER:HB3	1.24	1.46
2:K:145:ARG:CD	2:L:143:ASN:HA	1.45	1.44
1:B:630:ARG:HD3	2:L:71:LEU:CB	1.07	1.44
1:A:473:HIS:CD2	2:G:70:LEU:CD1	2.01	1.44

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	780/800 (98%)	433 (56%)	201 (26%)	146 (19%)	0	1
1	B	798/800 (100%)	460 (58%)	210 (26%)	128 (16%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	395/397 (100%)	326 (82%)	49 (12%)	20 (5%)	1	17
2	D	395/397 (100%)	330 (84%)	43 (11%)	22 (6%)	1	15
2	E	395/397 (100%)	331 (84%)	45 (11%)	19 (5%)	2	17
2	F	395/397 (100%)	326 (82%)	49 (12%)	20 (5%)	1	17
2	G	395/397 (100%)	329 (83%)	45 (11%)	21 (5%)	1	16
2	H	395/397 (100%)	331 (84%)	45 (11%)	19 (5%)	2	17
2	I	395/397 (100%)	326 (82%)	49 (12%)	20 (5%)	1	17
2	J	395/397 (100%)	329 (83%)	45 (11%)	21 (5%)	1	16
2	K	395/397 (100%)	331 (84%)	45 (11%)	19 (5%)	2	17
2	L	395/397 (100%)	326 (82%)	49 (12%)	20 (5%)	1	17
2	M	395/397 (100%)	330 (84%)	44 (11%)	21 (5%)	1	16
2	N	395/397 (100%)	331 (84%)	45 (11%)	19 (5%)	2	17
2	O	395/397 (100%)	320 (81%)	52 (13%)	23 (6%)	1	15
All	All	6713/6761 (99%)	5159 (77%)	1016 (15%)	538 (8%)	1	10

5 of 538 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	GLU
1	A	131	LEU
1	A	154	THR
1	A	187	ALA
1	A	198	LYS

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	716/734 (98%)	617 (86%)	99 (14%)	3	18
1	B	734/734 (100%)	639 (87%)	95 (13%)	4	20
2	C	350/350 (100%)	331 (95%)	19 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	350/350 (100%)	330 (94%)	20 (6%)	18	44
2	E	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	F	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	G	350/350 (100%)	330 (94%)	20 (6%)	18	44
2	H	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	I	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	J	350/350 (100%)	330 (94%)	20 (6%)	18	44
2	K	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	L	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	M	350/350 (100%)	330 (94%)	20 (6%)	18	44
2	N	350/350 (100%)	331 (95%)	19 (5%)	20	45
2	O	350/350 (100%)	332 (95%)	18 (5%)	21	46
All	All	6000/6018 (100%)	5556 (93%)	444 (7%)	15	38

5 of 444 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	382	LEU
2	O	385	VAL
2	G	274	GLN
2	O	255	ARG
2	M	214	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 214 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	142	GLN
2	I	35	ASN
2	N	142	GLN
2	F	284	ASN
2	H	26	ASN

5.3.3 RNA ⓘ

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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
1	B	2
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	262:VAL	C	263[B]:GLU	N	1.63
1	B	116:ALA	C	117:LYS	N	1.09
1	B	848:PHE	C	849:THR	N	0.93

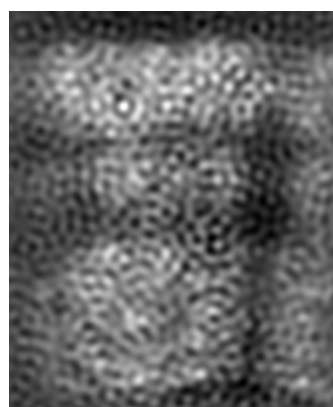
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1571. These allow visual inspection of the internal detail of the map and identification of artifacts.

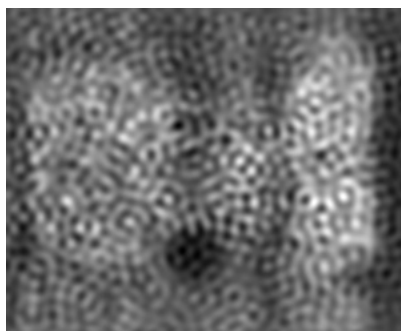
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

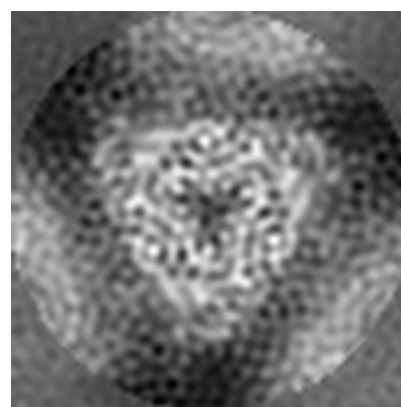
6.1.1 Primary map



X



Y

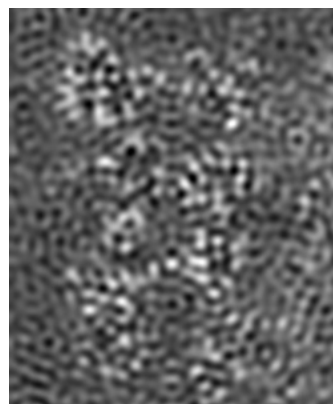


Z

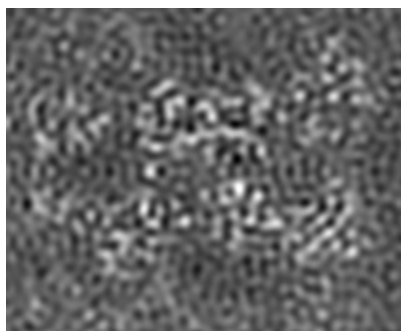
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

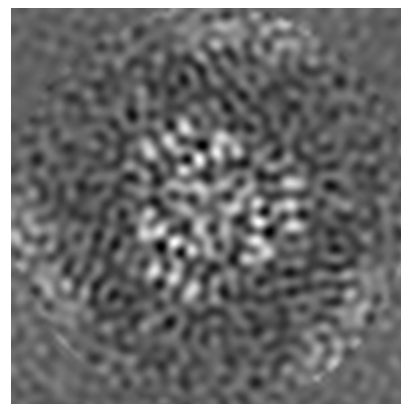
6.2.1 Primary map



X Index: 44



Y Index: 44

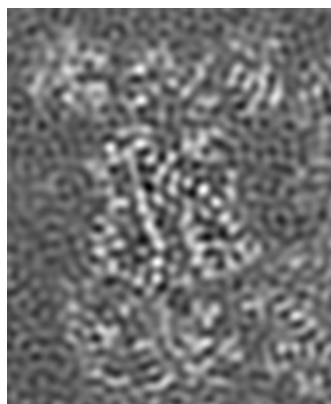


Z Index: 54

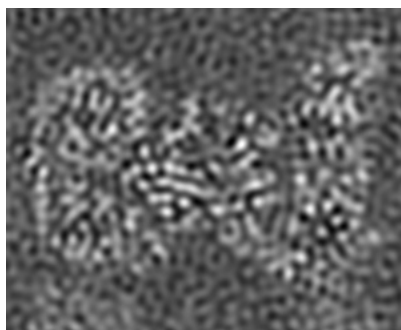
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

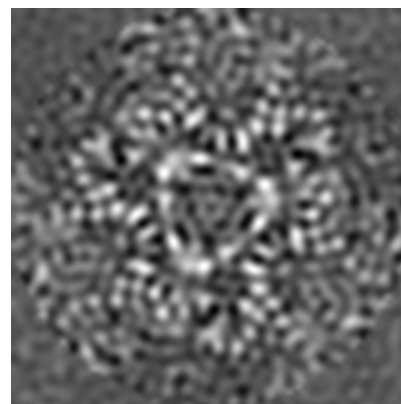
6.3.1 Primary map



X Index: 36



Y Index: 51

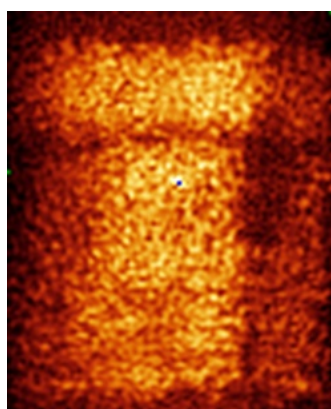


Z Index: 82

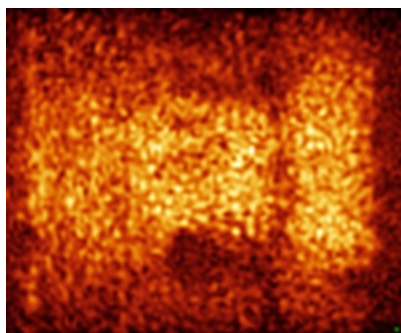
The images above show the largest variance slices of the map in three orthogonal directions.

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

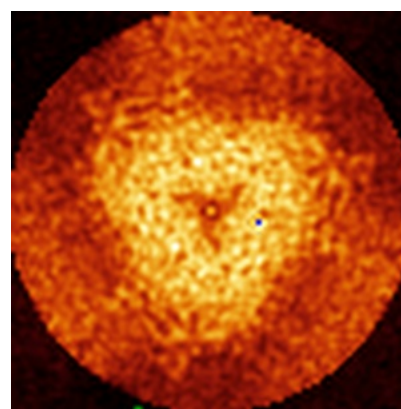
6.4.1 Primary map



X



Y

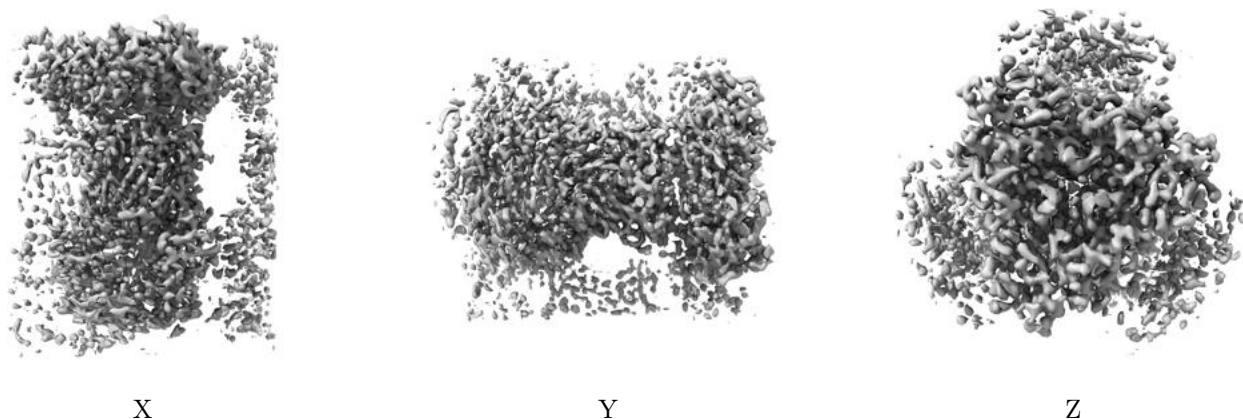


Z

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

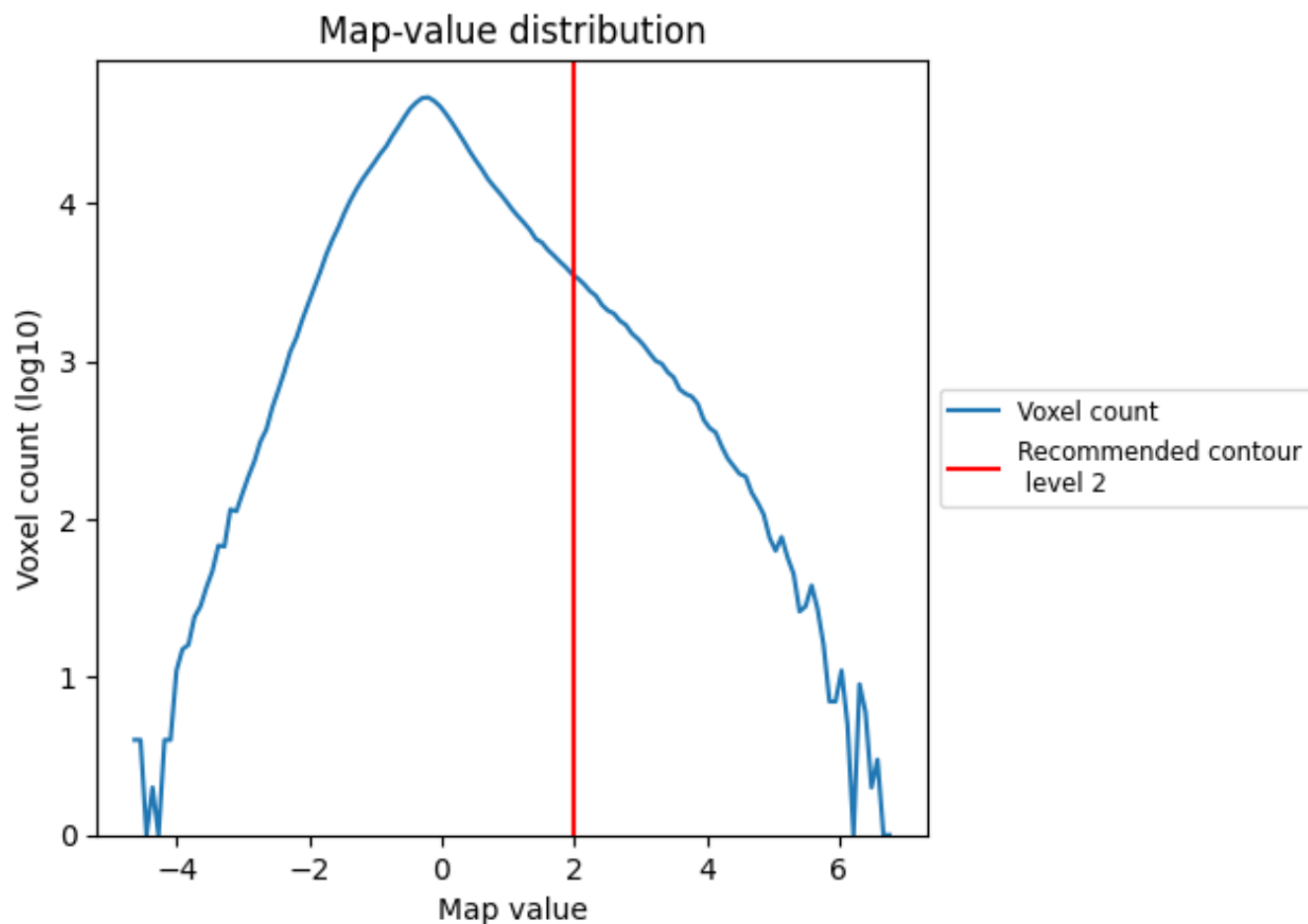
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

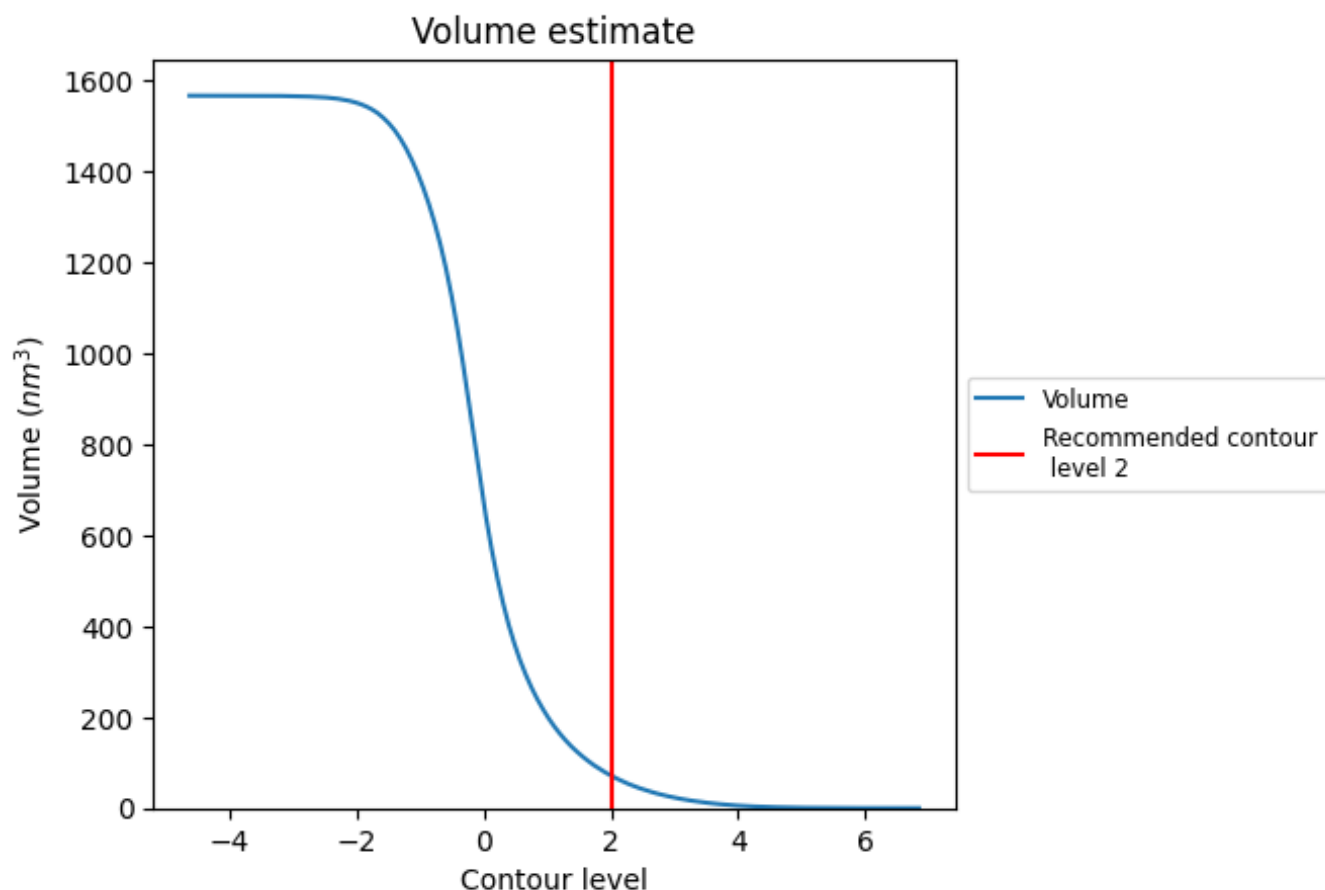
This section contains the results of statistical analysis of the map.

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 72 nm³; this corresponds to an approximate mass of 65 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

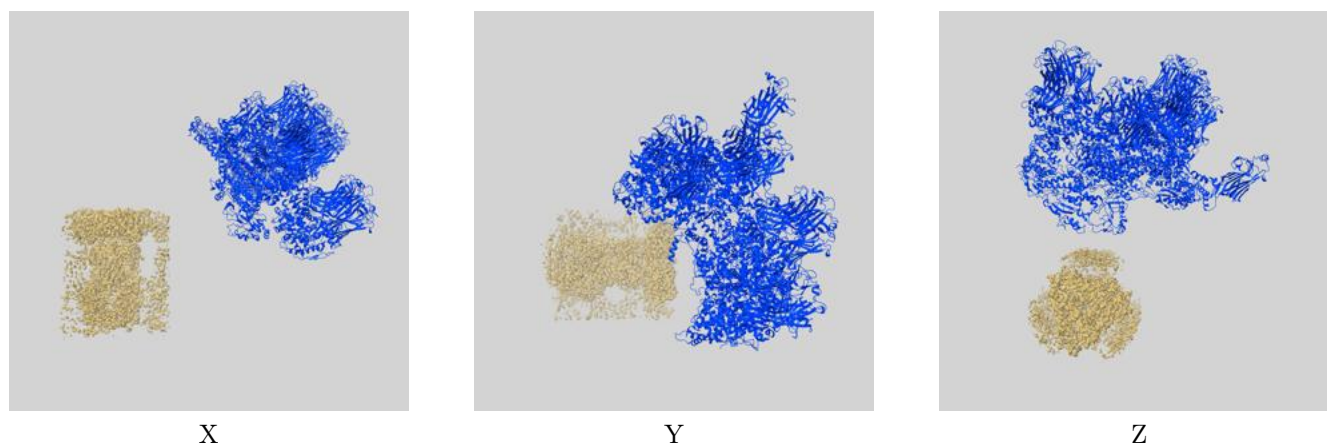
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1571 and PDB model 3GZU. Per-residue inclusion information can be found in section 3 on page 6.

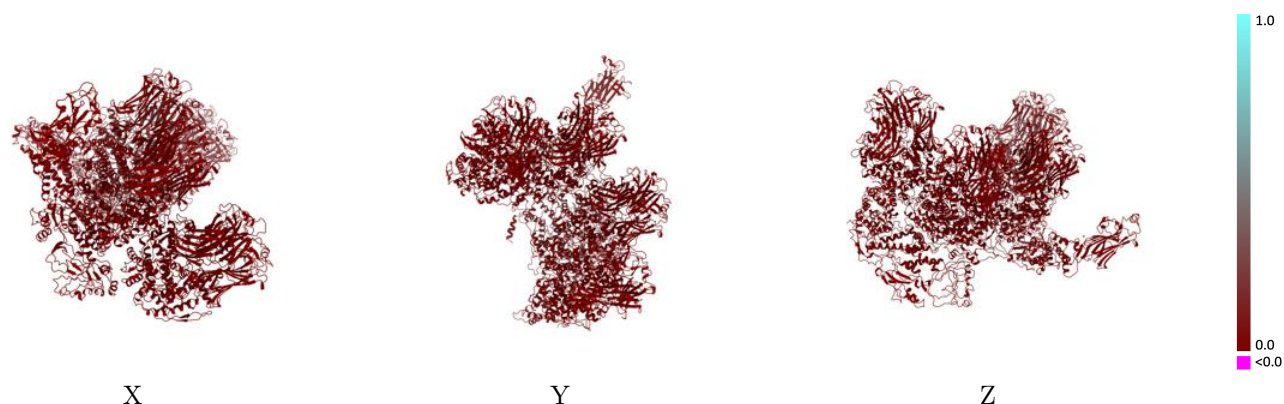
9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



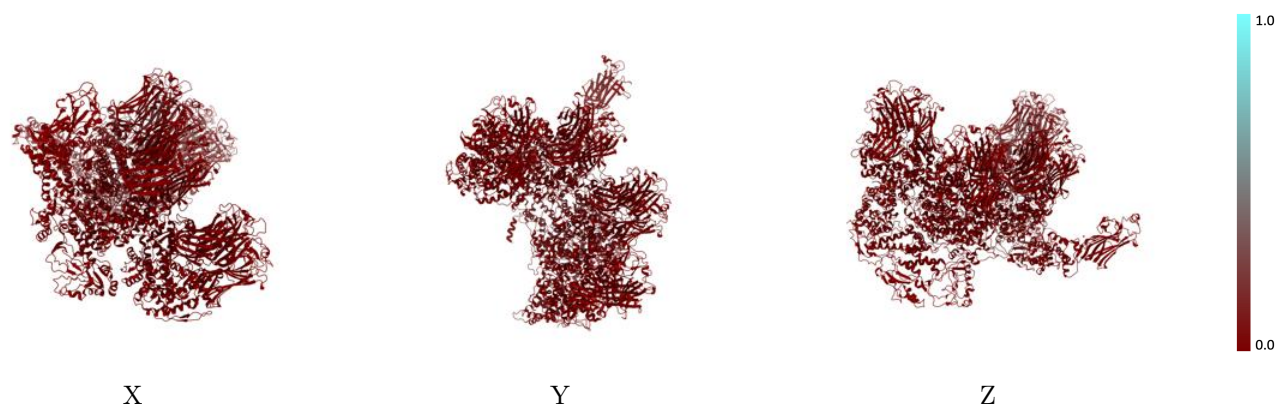
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



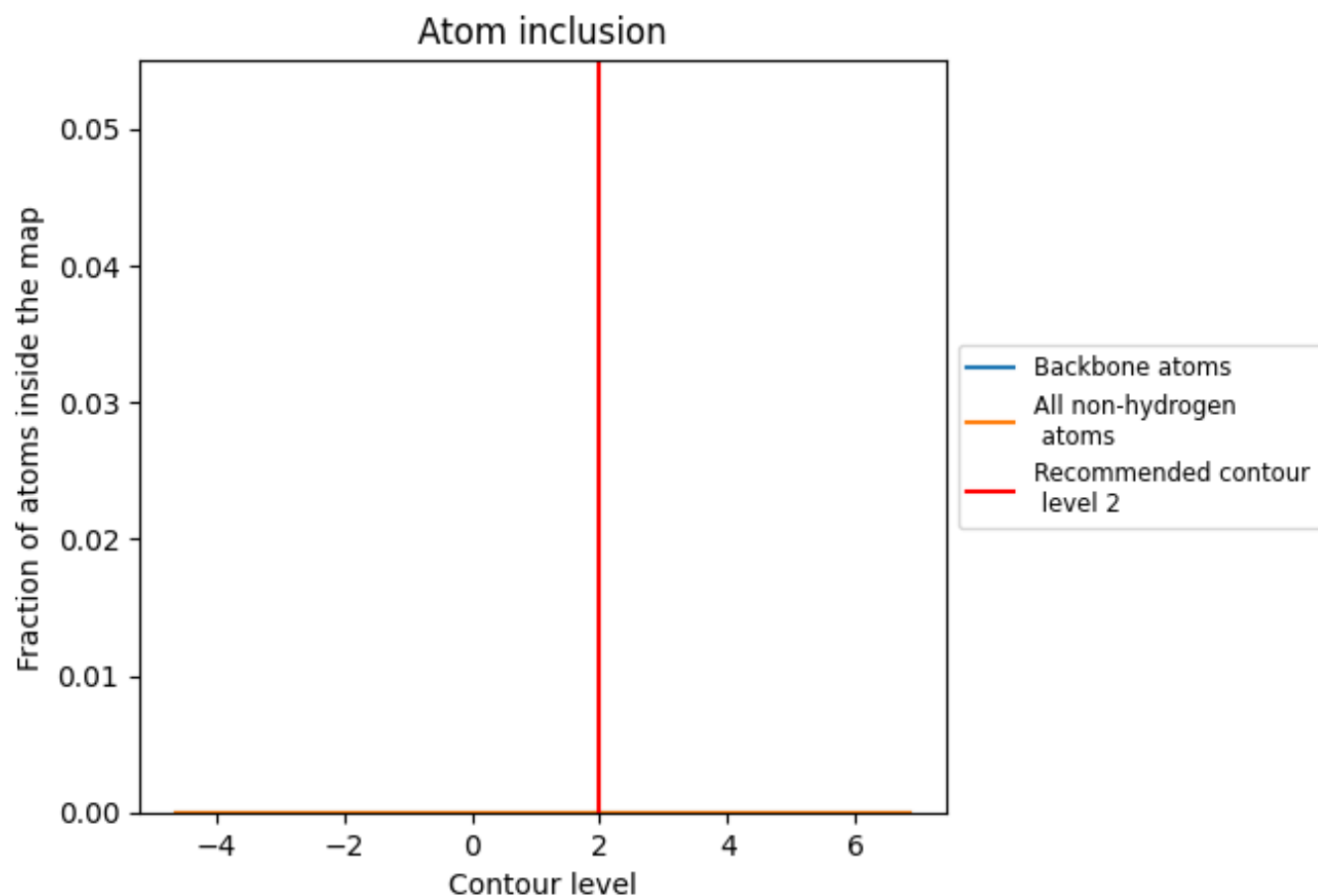
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.0000
A	0.0000	0.0000
B	0.0000	0.0000
C	0.0000	0.0000
D	0.0000	0.0000
E	0.0000	0.0000
F	0.0000	0.0000
G	0.0000	0.0000
H	0.0000	0.0000
I	0.0000	0.0000
J	0.0000	0.0000
K	0.0000	0.0000
L	0.0000	0.0000
M	0.0000	0.0000
N	0.0000	0.0000
O	0.0000	0.0000

1.0
0.0
<0.0