



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:32 AM UTC

PDB ID : 9H2H / pdb_00009h2h
EMDB ID : EMD-51803
Title : AcMNPV apical cap - composite map of the C2 plug
Authors : Effantin, G.; Kandiah, E.; Pelosse, M.
Deposited on : 2024-10-11
Resolution : 6.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

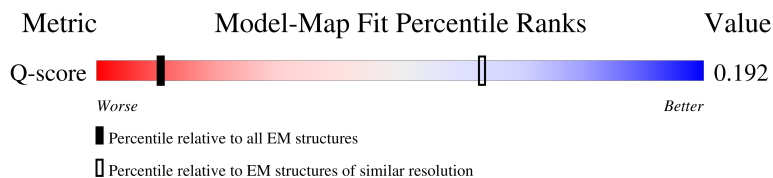
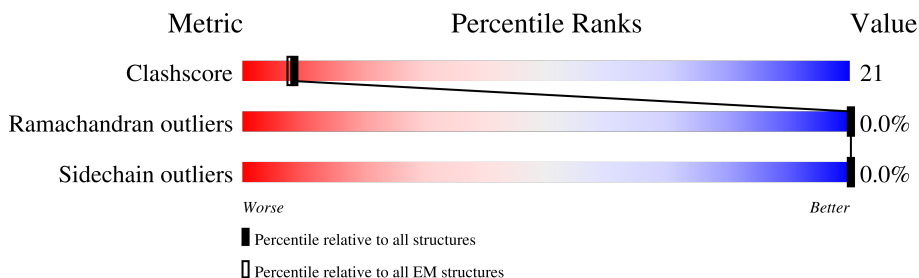
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.10 Å.

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



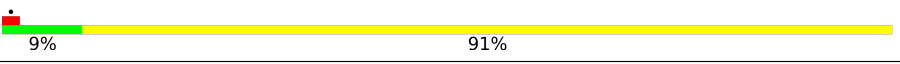
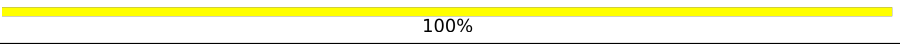
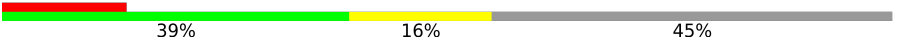
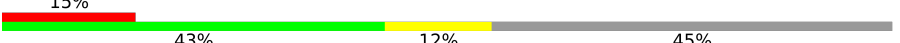
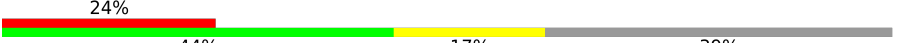
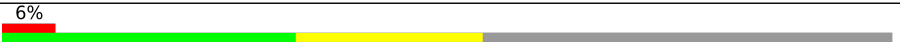
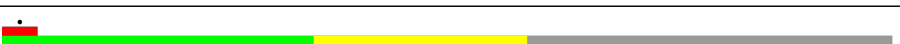
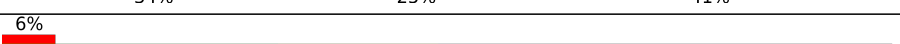
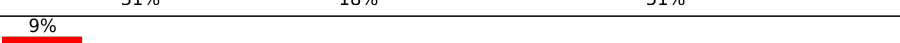
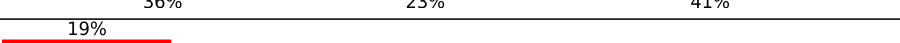
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	531 (5.60 - 6.60)

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	365	 6% 56% 35% 9%
1	B	365	 5% 54% 39% 8%
1	C	365	 1% 52% 37% 11%
1	D	365	 1% 50% 39% 11%

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Mol	Chain	Length	Quality of chain
2	E	58	
3	F	58	
4	G	290	
4	H	290	
4	K	290	
4	L	290	
4	O	290	
4	P	290	
4	S	290	
4	T	290	
5	I	361	
5	J	361	
5	M	361	
5	N	361	
5	Q	361	
5	R	361	
5	U	361	
5	V	361	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 39098 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 Protein AC54.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	332	Total	C	N	O	S	0	0
			2717	1723	479	497	18		
1	B	337	Total	C	N	O	S	0	0
			2757	1752	484	502	19		
1	C	324	Total	C	N	O	S	0	0
			2660	1691	468	483	18		
1	D	325	Total	C	N	O	S	0	0
			2666	1700	469	478	19		

- Molecule 2 is a DNA chain called DNA (58-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	58	Total	C	N	O	P	0	0
			1198	574	233	333	58		

- Molecule 3 is a DNA chain called DNA (58-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	58	Total	C	N	O	P	0	0
			1177	573	186	361	57		

- Molecule 4 is a protein called Occlusion-derived virus envelope protein E27.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	240	Total	C	N	O	S	0	0
			1941	1247	312	373	9		
4	H	160	Total	C	N	O	S	0	0
			1301	844	215	234	8		
4	K	228	Total	C	N	O	S	0	0
			1850	1191	296	354	9		
4	L	130	Total	C	N	O	S	0	0
			1061	692	172	190	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	238	Total	C	N	O	S	0	0
			1926	1238	309	370	9		
4	P	160	Total	C	N	O	S	0	0
			1302	847	212	235	8		
4	S	222	Total	C	N	O	S	0	0
			1805	1164	284	349	8		
4	T	178	Total	C	N	O	S	0	0
			1440	938	234	260	8		

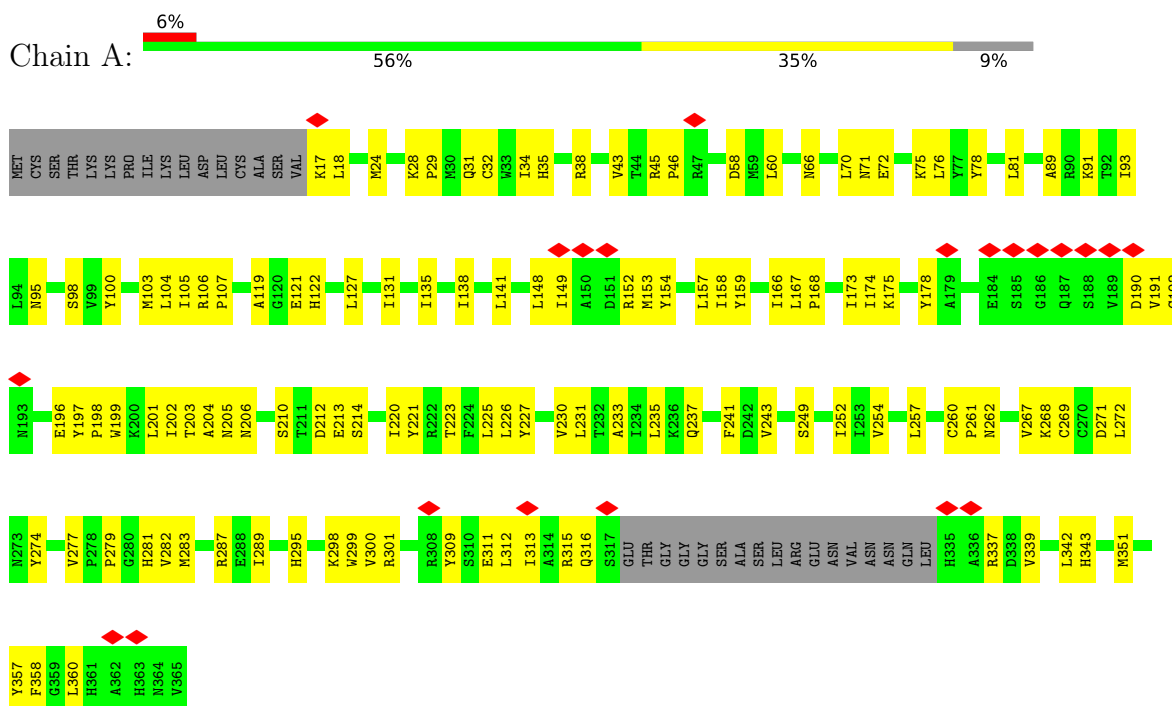
- Molecule 5 is a protein called Protein C42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	J	194	Total	C	N	O	S	0	0
			1622	1033	275	301	13		
5	M	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	N	181	Total	C	N	O	S	0	0
			1517	966	257	282	12		
5	Q	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	R	178	Total	C	N	O	S	0	0
			1488	943	253	279	13		
5	U	213	Total	C	N	O	S	0	0
			1760	1117	296	331	16		
5	V	196	Total	C	N	O	S	0	0
			1630	1036	276	306	12		

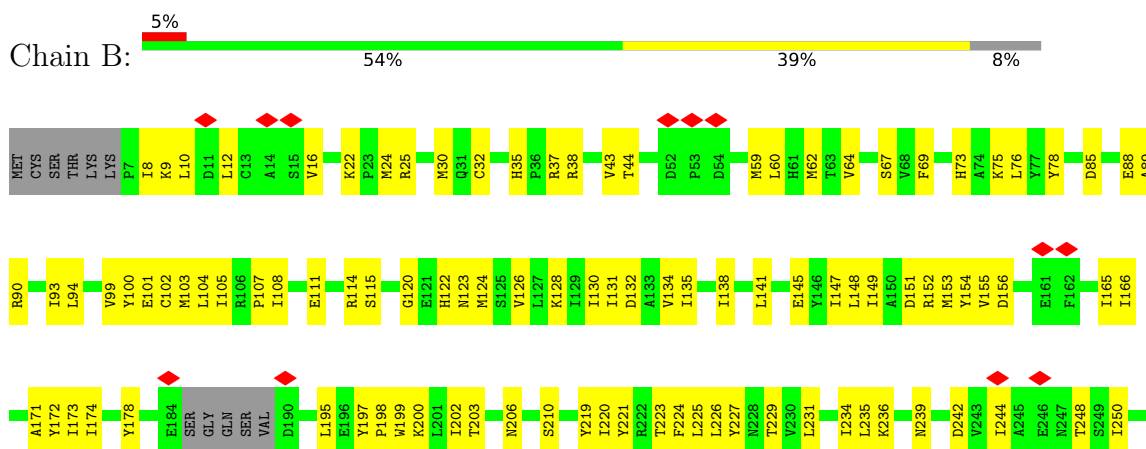
3 Residue-property plots

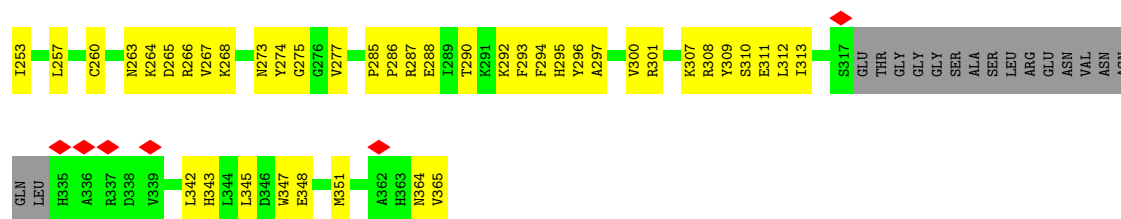
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Protein AC54



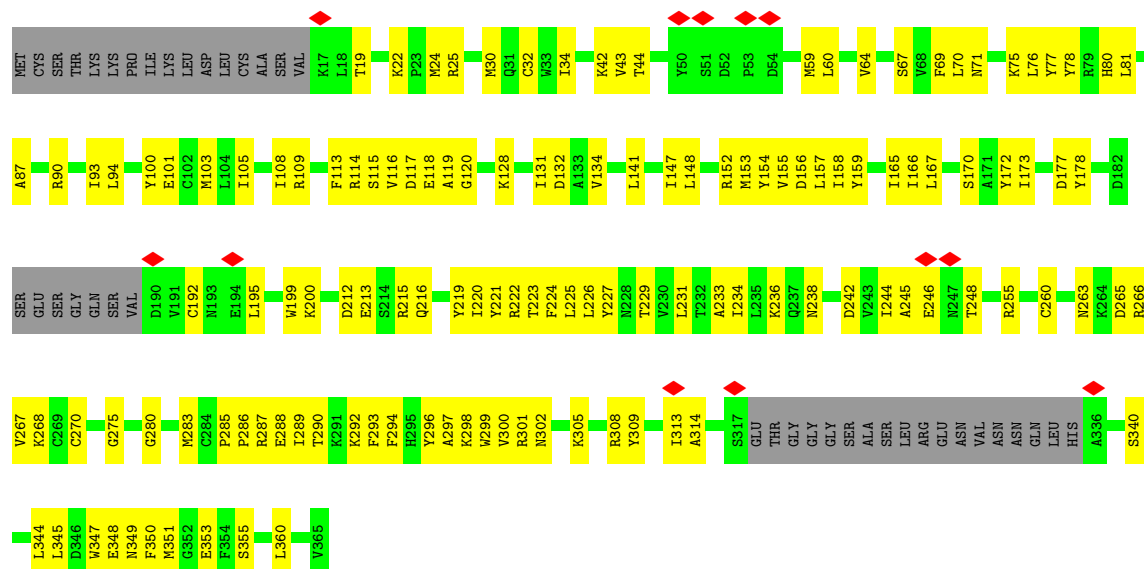
• Molecule 1: Protein AC54





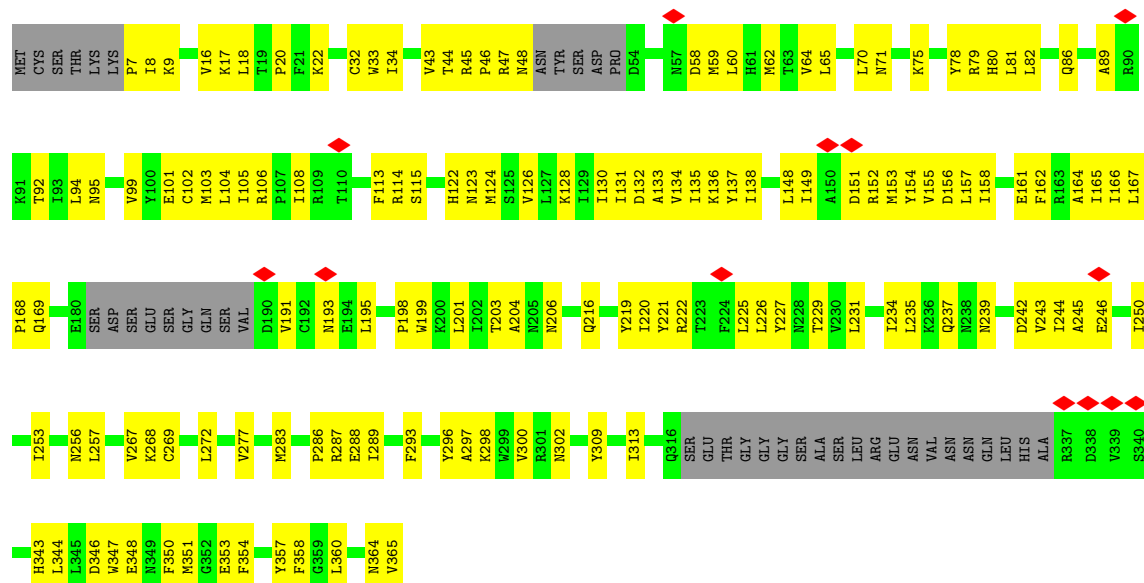
• Molecule 1: Protein AC54

Chain C: 52% 37% 11%



• Molecule 1: Protein AC54

Chain D: 50% 39% 11%



• Molecule 2: DNA (58-MER)

T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11	T12	T13	T14	T15	T16	T17	T18	T19	T20	T21	T22	T23	T24	T25	T26	T27	T28	T29	T30	T31	T32	T33	T34	T35	T36	T37	T38	T39	T40	T41	T42	T43	T44	T45	T46	T47	T48	T49	T50	T51	T52	T53	T54	T55	T56	T57	T58	T59	T60	T61	T62	T63	T64	T65	T66	T67	T68	T69	T70	T71	T72	T73	T74	T75	T76	T77	T78	T79	T80	T81	T82	T83	T84	T85	T86	T87	T88	T89	T90	T91	T92	T93	T94	T95	T96	T97	T98	T99	T100	T101	T102	T103	T104	T105	T106	T107	T108	T109	T110	T111	T112	T113	T114	T115	T116	T117	T118	T119	T120	T121	T122	T123	T124	T125	T126	T127	T128	T129	T130	T131	T132	T133	T134	T135	T136	T137	T138	T139	T140	T141	T142	T143	T144	T145	T146	T147	T148	T149	T150	T151	T152	T153	T154	T155	T156	T157	T158	T159	T160	T161	T162	T163	T164	T165	T166	T167	T168	T169	T170	T171	T172	T173	T174	T175	T176	T177	T178	T179	T180	T181	T182	T183	T184	T185	T186	T187	T188	T189	T190	T191	T192	T193	T194	T195	T196	T197	T198	T199	T200	T201	T202	T203	T204	T205	T206	T207	T208	T209	T210	T211	T212	T213	T214	T215	T216	T217	T218	T219	T220	T221	T222	T223	T224	T225	T226	T227	T228	T229	T230	T231	T232	T233	T234	T235	T236	T237	T238	T239	T240	T241	T242	T243	T244	T245	T246	T247	T248	T249	T250	T251	T252	T253	T254	T255	T256	T257	T258	T259	T260	T261	T262	T263	T264	T265	T266	T267	T268	T269	T270	T271	T272	T273	T274	T275	T276	T277	T278	T279	T280	T281	T282	T283	T284	T285	T286	T287	T288	T289	T290	T291	T292	T293	T294	T295	T296	T297	T298	T299	T300	T301	T302	T303	T304	T305	T306	T307	T308	T309	T310	T311	T312	T313	T314	T315	T316	T317	T318	T319	T320	T321	T322	T323	T324	T325	T326	T327	T328	T329	T330	T331	T332	T333	T334	T335	T336	T337	T338	T339	T340	T341	T342	T343	T344	T345	T346	T347	T348	T349	T350	T351	T352	T353	T354	T355	T356	T357	T358	T359	T360	T361	T362	T363	T364	T365	T366	T367	T368	T369	T370	T371	T372	T373	T374	T375	T376	T377	T378	T379	T380	T381	T382	T383	T384	T385	T386	T387	T388	T389	T390	T391	T392	T393	T394	T395	T396	T397	T398	T399	T400	T401	T402	T403	T404	T405	T406	T407	T408	T409	T410	T411	T412	T413	T414	T415	T416	T417	T418	T419	T420	T421	T422	T423	T424	T425	T426	T427	T428	T429	T430	T431	T432	T433	T434	T435	T436	T437	T438	T439	T440	T441	T442	T443	T444	T445	T446	T447	T448	T449	T450	T451	T452	T453	T454	T455	T456	T457	T458	T459	T460	T461	T462	T463	T464	T465	T466	T467	T468	T469	T470	T471	T472	T473	T474	T475	T476	T477	T478	T479	T480	T481	T482	T483	T484	T485	T486	T487	T488	T489	T490	T491	T492	T493	T494	T495	T496	T497	T498	T499	T500	T501	T502	T503	T504	T505	T506	T507	T508	T509	T510	T511	T512	T513	T514	T515	T516	T517	T518	T519	T520	T521	T522	T523	T524	T5
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Chain F: 100%

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30	C31	C32	C33	C34	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49	C50	C51	C52	C53	C54	C55	C56	C57	C58	C59	C60	C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	C72	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100
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Chain G:

Protein	Residue	Score	Category
Protein 1	F226	0.85	High
	V231	0.78	High
	F232	0.82	High
	E233	0.75	High
	Y234	0.88	High
	C235	0.72	High
	K236	0.80	High
	K237	0.70	High
	L238	0.85	High
	H241	0.75	High
Protein 2	F244	0.80	High
	T245	0.78	High
	K246	0.85	High
	K247	0.72	High
	L248	0.88	High
	R249	0.75	High
	M252	0.82	High
	S253	0.70	High
	T254	0.85	High
	L259	0.78	High
Protein 3	L260	0.80	High
	L261	0.75	High
	S262	0.88	High
	K263	0.72	High
	F266	0.85	High
	D272	0.78	High
	K273	0.82	High
	L274	0.70	High
	N275	0.85	High
	S276	0.75	High
Protein 4	ASN	0.80	High
	SER	0.78	High
	VAL	0.85	High
	THR	0.72	High
	SER	0.88	High
	GLY	0.75	High
	PHE	0.82	High
	ASN	0.70	High
	ASN	0.85	High
	LYS	0.78	High
Protein 5	F85	0.80	High
	S86	0.75	High
	T87	0.88	High
	L88	0.72	High
	A89	0.85	High
	F90	0.70	High
	I91	0.82	High
	H92	0.78	High
	H93	0.85	High
	R94	0.75	High
Protein 6	F95	0.80	High
	H96	0.78	High
	P97	0.85	High
	L98	0.72	High
	V99	0.88	High
	T100	0.75	High
	N101	0.82	High
	F102	0.70	High
	T103	0.85	High
	N104	0.78	High
Protein 7	E107	0.80	High
	F108	0.75	High
	V109	0.88	High
	V110	0.72	High
	T111	0.85	High
	E112	0.70	High
	T113	0.82	High
	N114	0.78	High
	T118	0.85	High
	P119	0.75	High
Protein 8	G120	0.80	High
	E121	0.78	High
	F122	0.85	High
	I123	0.72	High
	L124	0.88	High
	F125	0.75	High
	N128	0.82	High
	E129	0.70	High
	G130	0.85	High
	V131	0.78	High
Protein 9	L132	0.80	High
	L133	0.75	High
	G134	0.88	High
	S135	0.72	High
	V136	0.85	High
	D137	0.70	High
	R138	0.82	High
	P139	0.78	High
	S140	0.85	High
	T141	0.75	High
Protein 10	V142	0.80	High
	K143	0.78	High
	M144	0.85	High
	L145	0.72	High
	S146	0.88	High
	T147	0.75	High
	A175	0.82	High
	A81	0.70	High
	A82	0.85	High
	T147	0.78	High

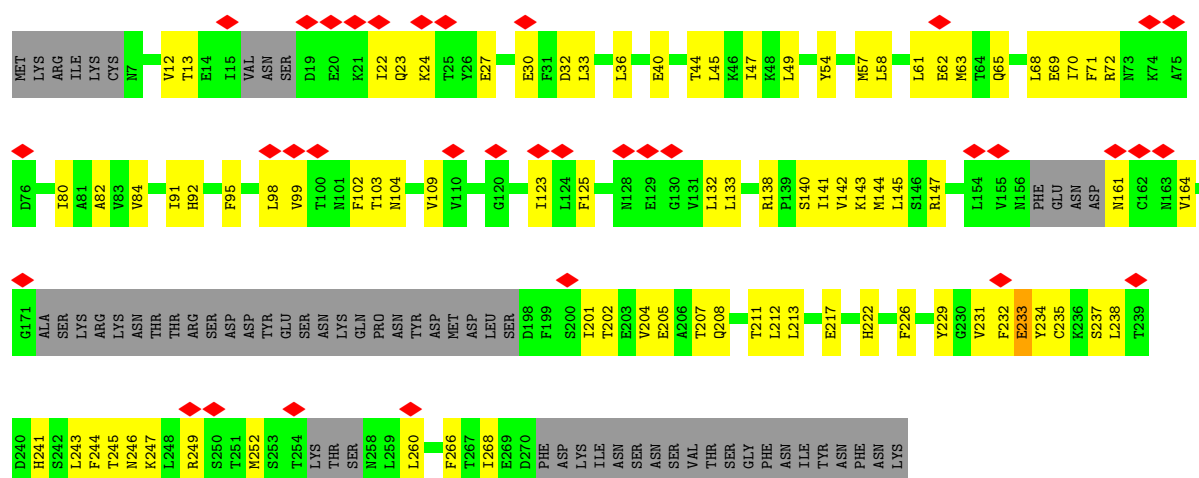
Chain H:

[illegible]

PHE
ASN
ILE
TYR
ASN
PHE
ASN
LYS

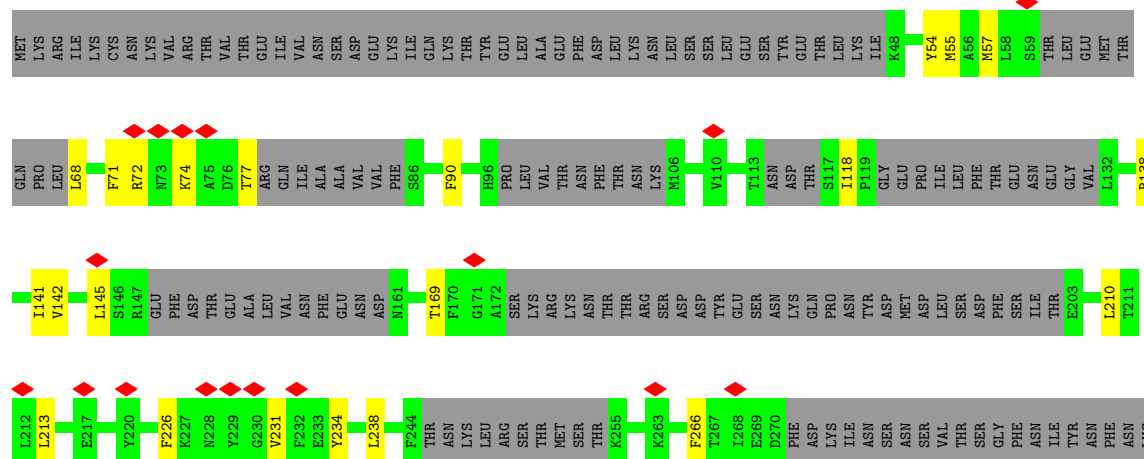
• Molecule 4: Occlusion-derived virus envelope protein E27

Chain K: 12% 50% 29% 21%



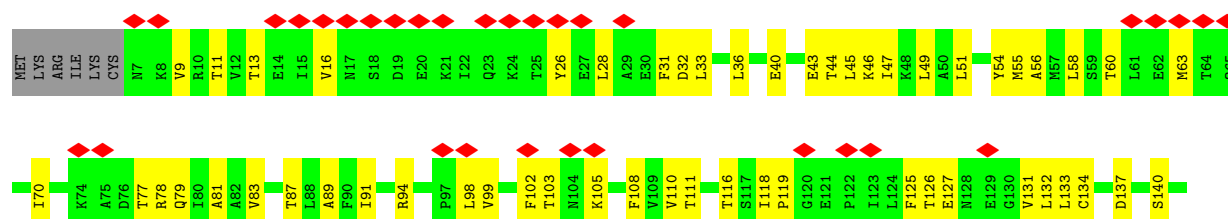
• Molecule 4: Occlusion-derived virus envelope protein E27

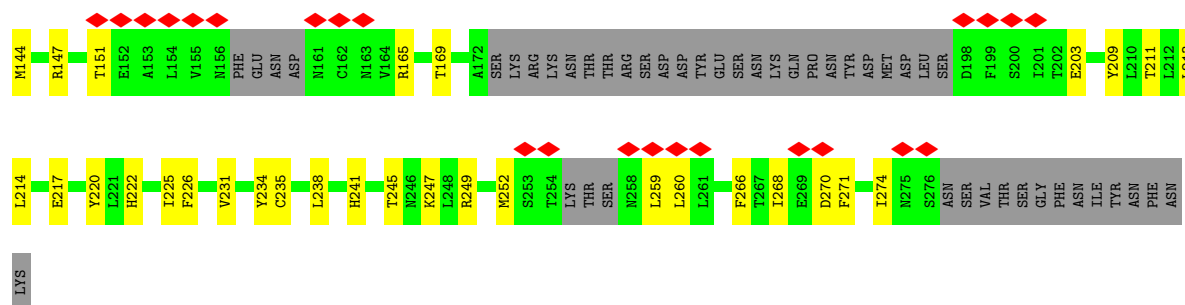
Chain L: 6% 37% 8% 55%



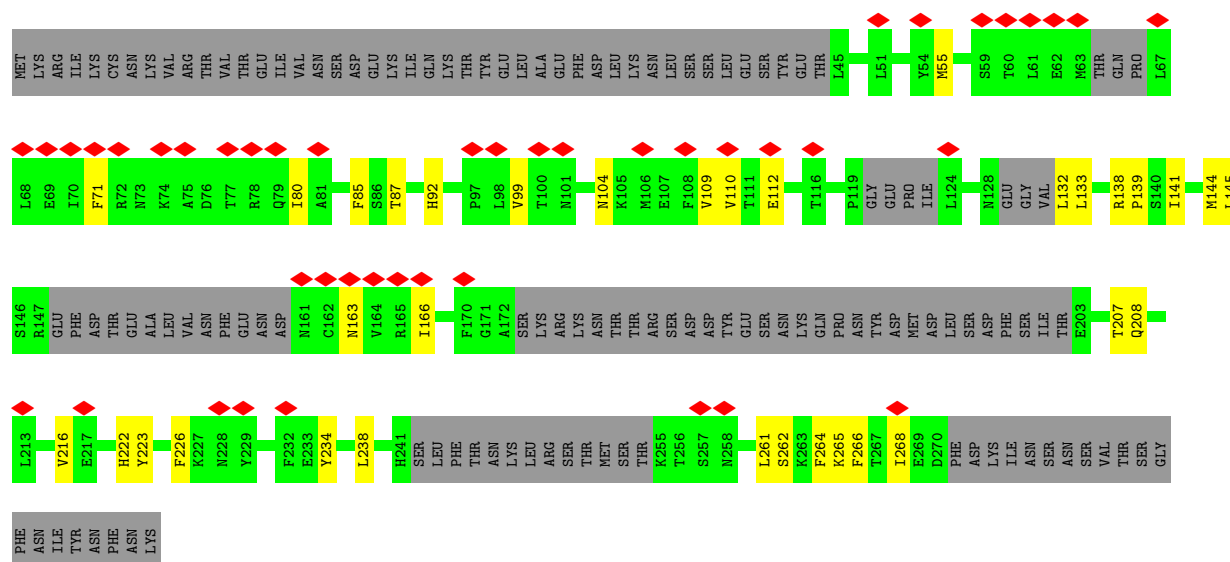
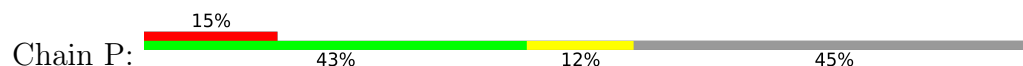
• Molecule 4: Occlusion-derived virus envelope protein E27

Chain O: 19% 53% 29% 18%

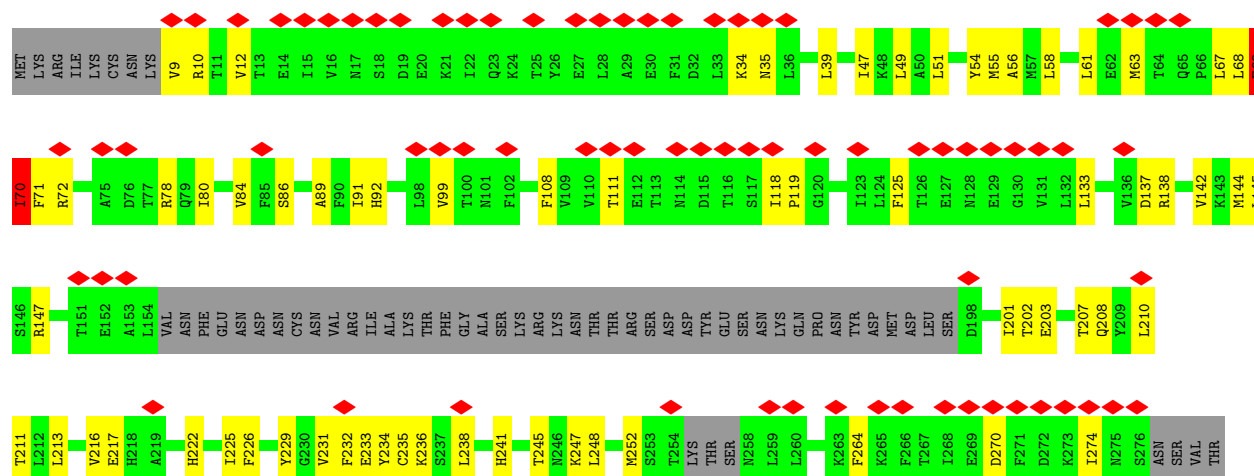




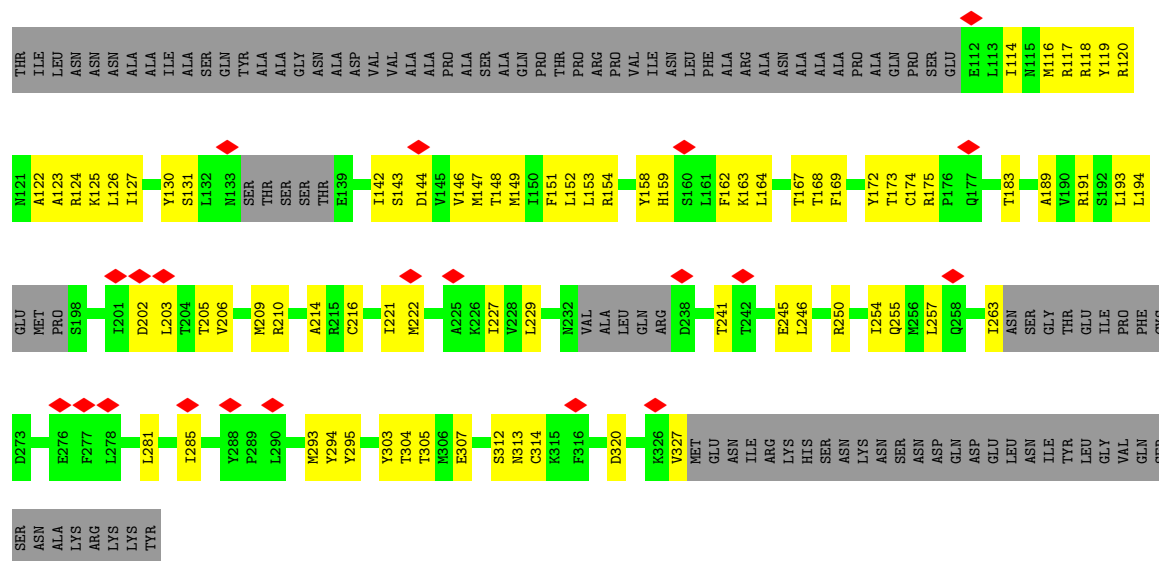
• Molecule 4: Occlusion-derived virus envelope protein E27



• Molecule 4: Occlusion-derived virus envelope protein E27

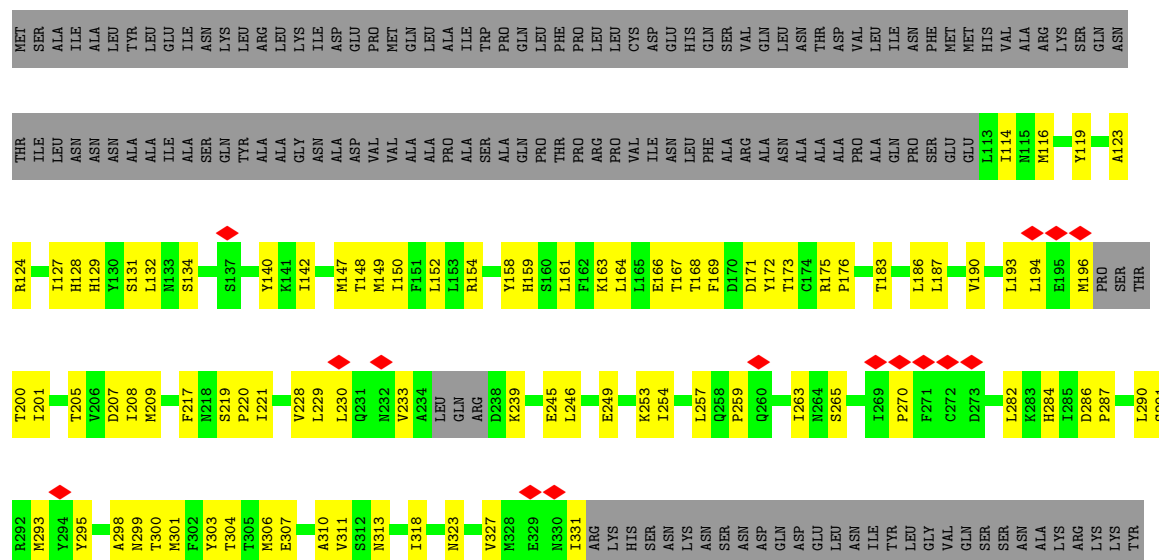


MET	SER	ALA	ILE	ALA	LEU	TYR	GLU	ILE	ASN	LYS	LEU	LEU	ARG	LEU	LYS	ASP	GLU	ILE	ILE	TRP	PRO	PRO	GLN	LEU	PHE	LEU	PRO	LEU	CYS	ASP	GLU	HIS	GLN	SER	VAL	VAL	GLN	LEU	ILE	ASN	ASN	PHE	MET	MET	HIS	VAL	ALA	ARG	LYS	LYS	SER	GLN
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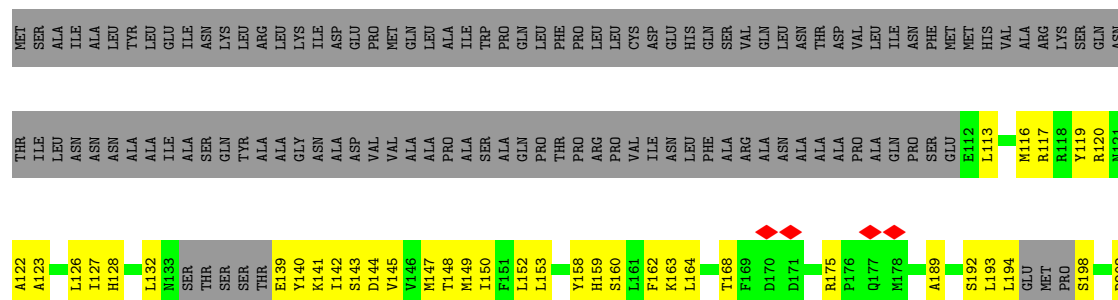
• Molecule 5: Protein C42

Chain M: 35% 24% 41%

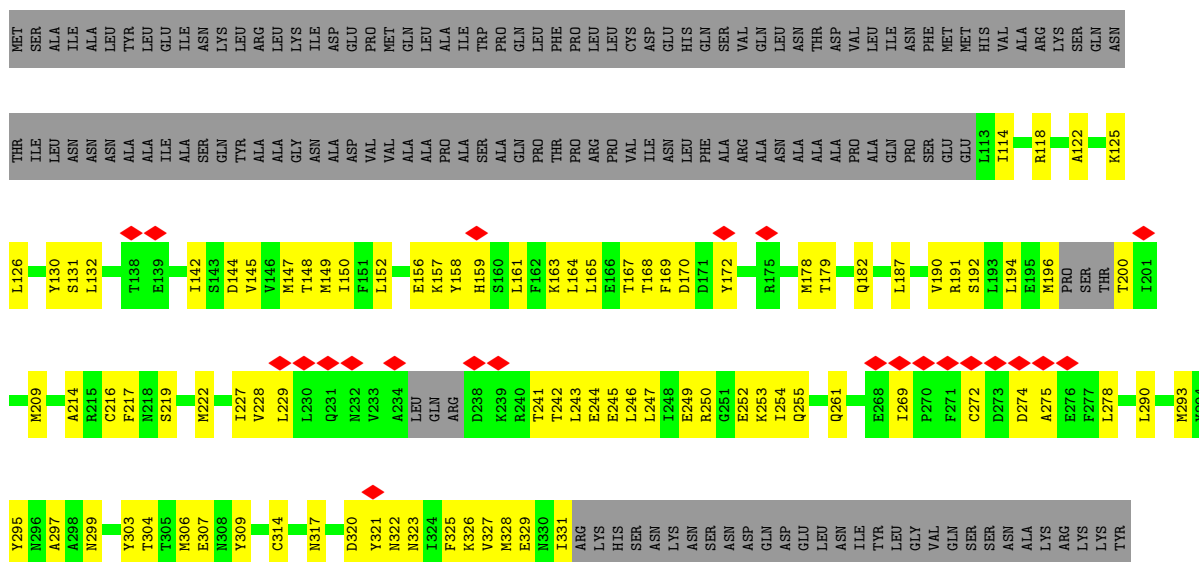
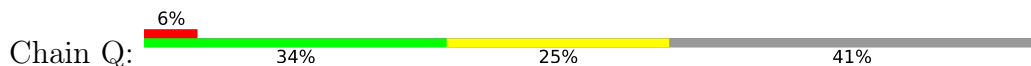


• Molecule 5: Protein C42

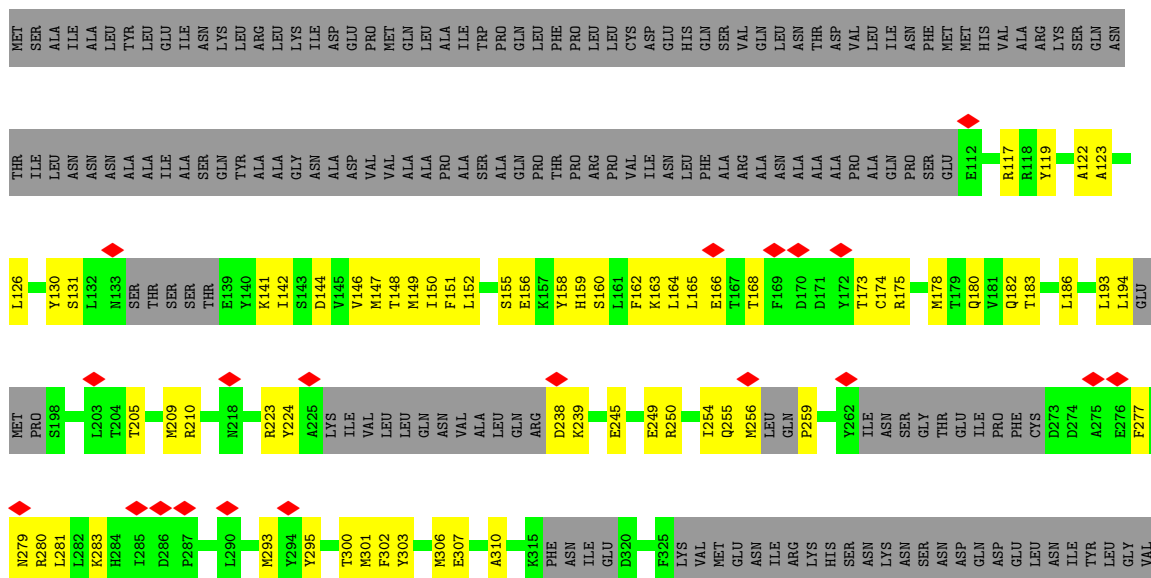
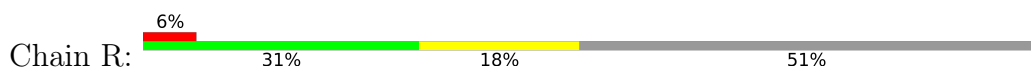
Chain N: 6% 33% 17% 50%



- Molecule 5: Protein C42



- Molecule 5: Protein C42



GLN
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● Molecule 5: Protein C42



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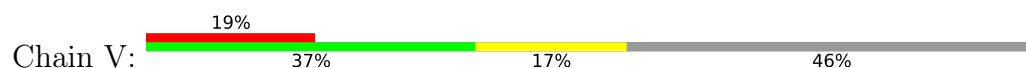
R124
H128
S131
L132
T135
S136
S137
T138
E139
Y140
K141
I142
S143
D144
V145
V146
M147
T148
M149
I150
F151
L152
L153
Y158
H159
S160
L161
F162
K163
L164
L165
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F169
D170
D171
Y172
T173
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R175
P176
T183
A189
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L194
E195
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M209
R210
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M222
Y224
A225
K226
I227
V228
L229
L230
A234
LEU
GLN
ARG
D238
K239
R240
L243
E244
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L246
E249
R250
G251
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K253
Q254
Q255
P259
Q260
Q261
Y262
L263
N264
S265
E268
I269
P270
F271
C272
D273
E277
L278
N279
R280
L281

L282
I285
D286
P287
P288
L289
S291
M292
K293
Y294
A297
A298
N299
T300
K301
F302
Y303
T304
T305
K306
E307
V311
I318
Y321
K326
V327
E328
N330
I331
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● Molecule 5: Protein C42



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Y119
A123
I127
H128
H129

L132
M133
S134
T135
S136
S137
T138
I142
S143
D144
V145
V146
M147
T148
M149
I150
F151
L152
L153
K157
Y158
L161
F162
K163
L164
L165
E166
T167
T168
F169
D170
P176
GLN
MET
THR
Q180
L187
D188
A189
V190
L194
GLU
MET
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S198
T199
T200
I201
D202
L203
T204
T205
V206

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F217
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A225
K226
I227
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I285
D286
P287
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P289
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S291
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M301
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12477	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.027	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0065	Depositor
Map size (Å)	405.0, 405.0, 405.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.15	0/2783	0.37	0/3772
1	B	0.16	0/2823	0.37	0/3825
1	C	0.16	0/2724	0.41	0/3691
1	D	0.17	0/2728	0.42	0/3693
2	E	0.19	0/1350	0.34	0/2081
3	F	0.19	0/1313	0.40	0/2025
4	G	0.14	0/1973	0.34	0/2664
4	H	0.13	0/1321	0.32	0/1774
4	K	0.16	0/1880	0.42	2/2538 (0.1%)
4	L	0.11	0/1076	0.25	0/1439
4	O	0.15	0/1958	0.37	0/2645
4	P	0.13	0/1322	0.31	0/1778
4	S	0.17	0/1837	0.40	2/2484 (0.1%)
4	T	0.12	0/1464	0.29	0/1972
5	I	0.14	0/1790	0.35	0/2415
5	J	0.16	0/1648	0.36	0/2219
5	M	0.16	0/1790	0.38	0/2415
5	N	0.14	0/1539	0.37	0/2065
5	Q	0.17	0/1790	0.40	0/2415
5	R	0.14	0/1511	0.36	0/2030
5	U	0.16	0/1790	0.35	0/2415
5	V	0.12	0/1656	0.30	0/2231
All	All	0.15	0/40066	0.37	4/54586 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	233	GLU	CA-C-N	-5.48	112.51	120.29
4	K	233	GLU	C-N-CA	-5.48	112.51	120.29
4	S	69	GLU	N-CA-C	-5.43	106.49	113.23
4	S	70	ILE	N-CA-C	-5.34	104.20	111.89

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	A	2717	0	2673	112	0
1	B	2757	0	2724	139	0
1	C	2660	0	2624	124	0
1	D	2666	0	2655	135	0
2	E	1198	0	654	113	0
3	F	1177	0	670	156	0
4	G	1941	0	1954	114	0
4	H	1301	0	1330	46	0
4	K	1850	0	1862	84	0
4	L	1061	0	1072	20	0
4	O	1926	0	1936	86	0
4	P	1302	0	1328	27	0
4	S	1805	0	1811	72	0
4	T	1440	0	1476	46	0
5	I	1760	0	1756	74	0
5	J	1622	0	1623	89	0
5	M	1760	0	1756	84	0
5	N	1517	0	1507	65	0
5	Q	1760	0	1756	89	0
5	R	1488	0	1469	74	0
5	U	1760	0	1756	92	0
5	V	1630	0	1628	65	0
All	All	39098	0	38020	1633	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 21.

The worst 5 of 1633 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)
4:K:47:ILE:HD12	4:K:260:LEU:HD12	1.46	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:220:ILE:HD11	1:C:313:ILE:HG21	1.43	0.96
5:V:152:LEU:HD12	5:V:161:LEU:HD11	1.57	0.85
4:G:248:LEU:HD12	4:G:252:MET:HB2	1.59	0.85
4:O:54:TYR:OH	4:O:87:THR:HG22	1.78	0.83

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	328/365 (90%)	296 (90%)	32 (10%)	0	100	100
1	B	331/365 (91%)	305 (92%)	26 (8%)	0	100	100
1	C	318/365 (87%)	283 (89%)	35 (11%)	0	100	100
1	D	317/365 (87%)	286 (90%)	31 (10%)	0	100	100
4	G	232/290 (80%)	219 (94%)	13 (6%)	0	100	100
4	H	146/290 (50%)	141 (97%)	5 (3%)	0	100	100
4	K	218/290 (75%)	206 (94%)	12 (6%)	0	100	100
4	L	112/290 (39%)	111 (99%)	1 (1%)	0	100	100
4	O	230/290 (79%)	216 (94%)	14 (6%)	0	100	100
4	P	146/290 (50%)	140 (96%)	6 (4%)	0	100	100
4	S	216/290 (74%)	204 (94%)	12 (6%)	0	100	100
4	T	166/290 (57%)	161 (97%)	4 (2%)	1 (1%)	21	59
5	I	207/361 (57%)	196 (95%)	11 (5%)	0	100	100
5	J	184/361 (51%)	172 (94%)	12 (6%)	0	100	100
5	M	207/361 (57%)	194 (94%)	13 (6%)	0	100	100
5	N	165/361 (46%)	159 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Q	207/361 (57%)	195 (94%)	12 (6%)	0	100	100
5	R	164/361 (45%)	156 (95%)	8 (5%)	0	100	100
5	U	207/361 (57%)	194 (94%)	13 (6%)	0	100	100
5	V	186/361 (52%)	174 (94%)	12 (6%)	0	100	100
All	All	4287/6668 (64%)	4008 (94%)	278 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	T	247	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	303/331 (92%)	303 (100%)	0	100	100
1	B	308/331 (93%)	308 (100%)	0	100	100
1	C	296/331 (89%)	296 (100%)	0	100	100
1	D	297/331 (90%)	297 (100%)	0	100	100
4	G	224/273 (82%)	224 (100%)	0	100	100
4	H	148/273 (54%)	148 (100%)	0	100	100
4	K	213/273 (78%)	213 (100%)	0	100	100
4	L	120/273 (44%)	120 (100%)	0	100	100
4	O	222/273 (81%)	222 (100%)	0	100	100
4	P	148/273 (54%)	148 (100%)	0	100	100
4	S	209/273 (77%)	207 (99%)	2 (1%)	68	78
4	T	164/273 (60%)	164 (100%)	0	100	100
5	I	201/326 (62%)	201 (100%)	0	100	100
5	J	184/326 (56%)	184 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	M	201/326 (62%)	201 (100%)	0	100	100
5	N	171/326 (52%)	171 (100%)	0	100	100
5	Q	201/326 (62%)	201 (100%)	0	100	100
5	R	168/326 (52%)	168 (100%)	0	100	100
5	U	201/326 (62%)	201 (100%)	0	100	100
5	V	186/326 (57%)	186 (100%)	0	100	100
All	All	4165/6116 (68%)	4163 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	S	69	GLU
4	S	70	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
5	N	159	HIS
5	R	129	HIS
4	O	92	HIS
4	O	258	ASN
4	T	93	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

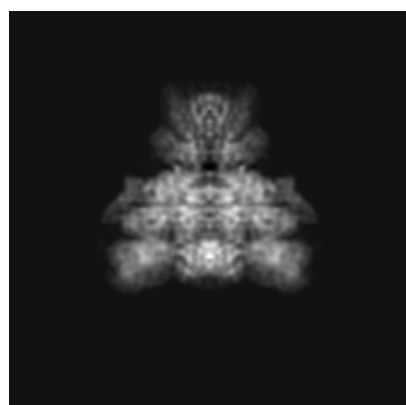
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51803. These allow visual inspection of the internal detail of the map and identification of artifacts.

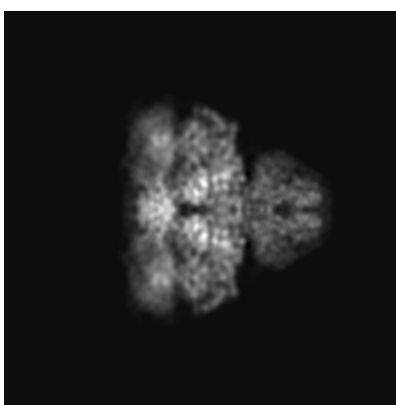
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

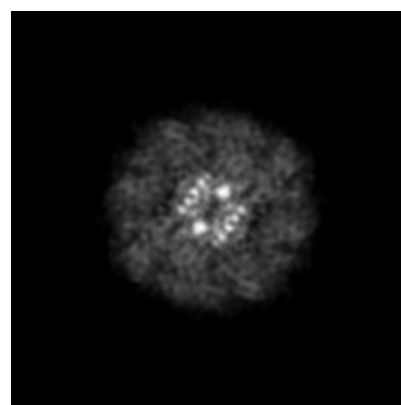
6.1.1 Primary map



X



Y

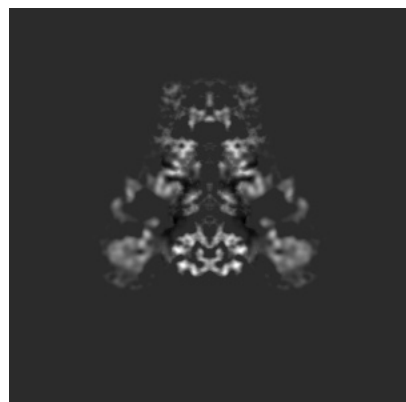


Z

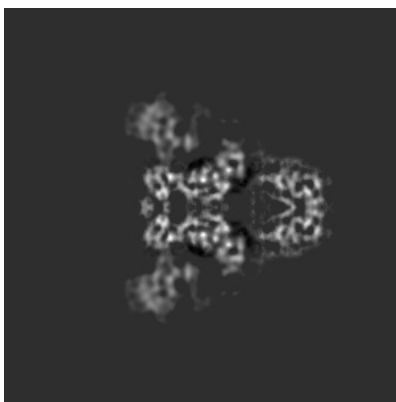
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

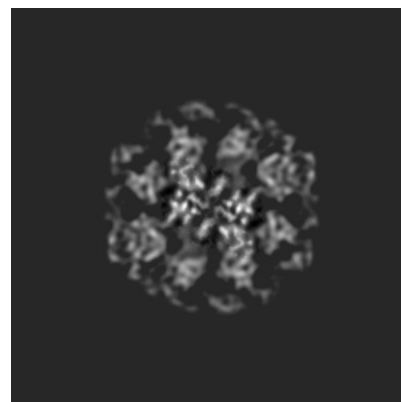
6.2.1 Primary map



X Index: 150



Y Index: 150

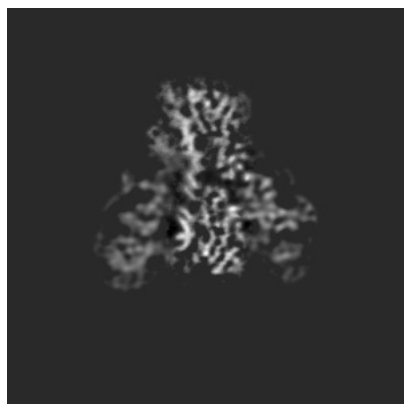


Z Index: 150

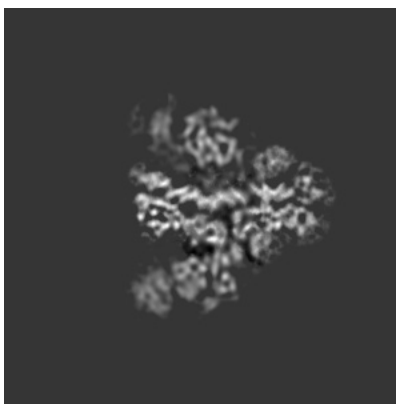
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

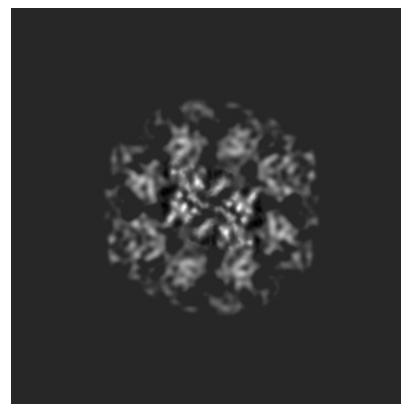
6.3.1 Primary map



X Index: 139



Y Index: 164

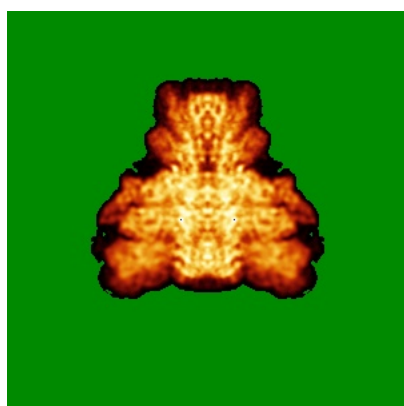


Z Index: 149

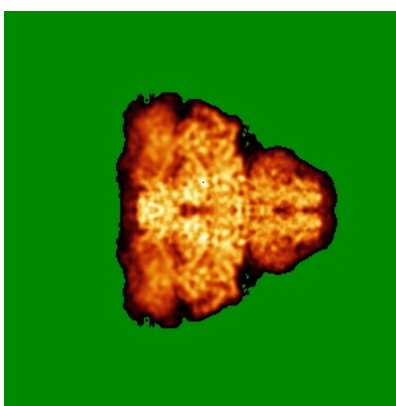
The images above show the largest variance slices of the map in three orthogonal directions.

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

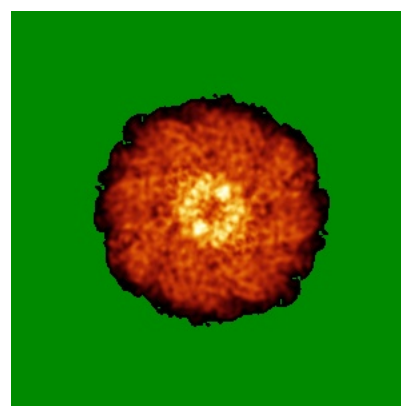
6.4.1 Primary map



X



Y

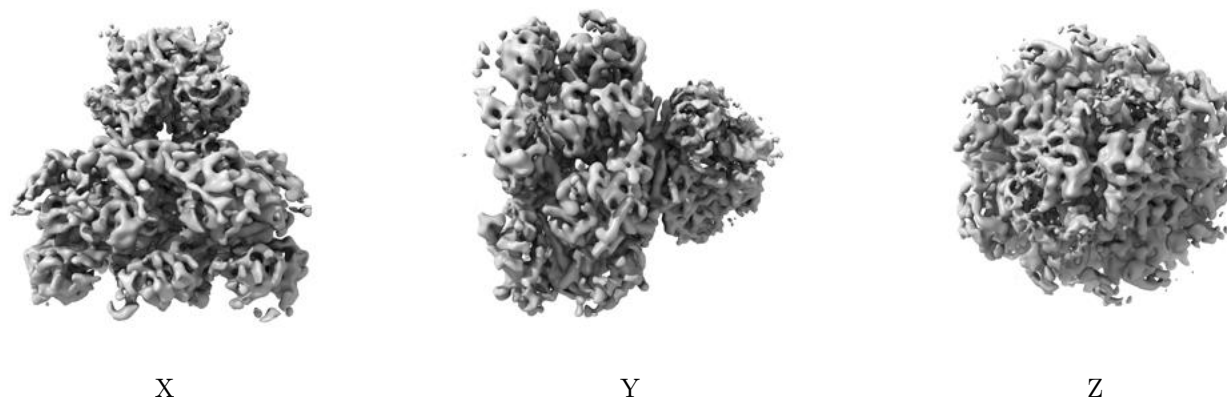


Z

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 0.0065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

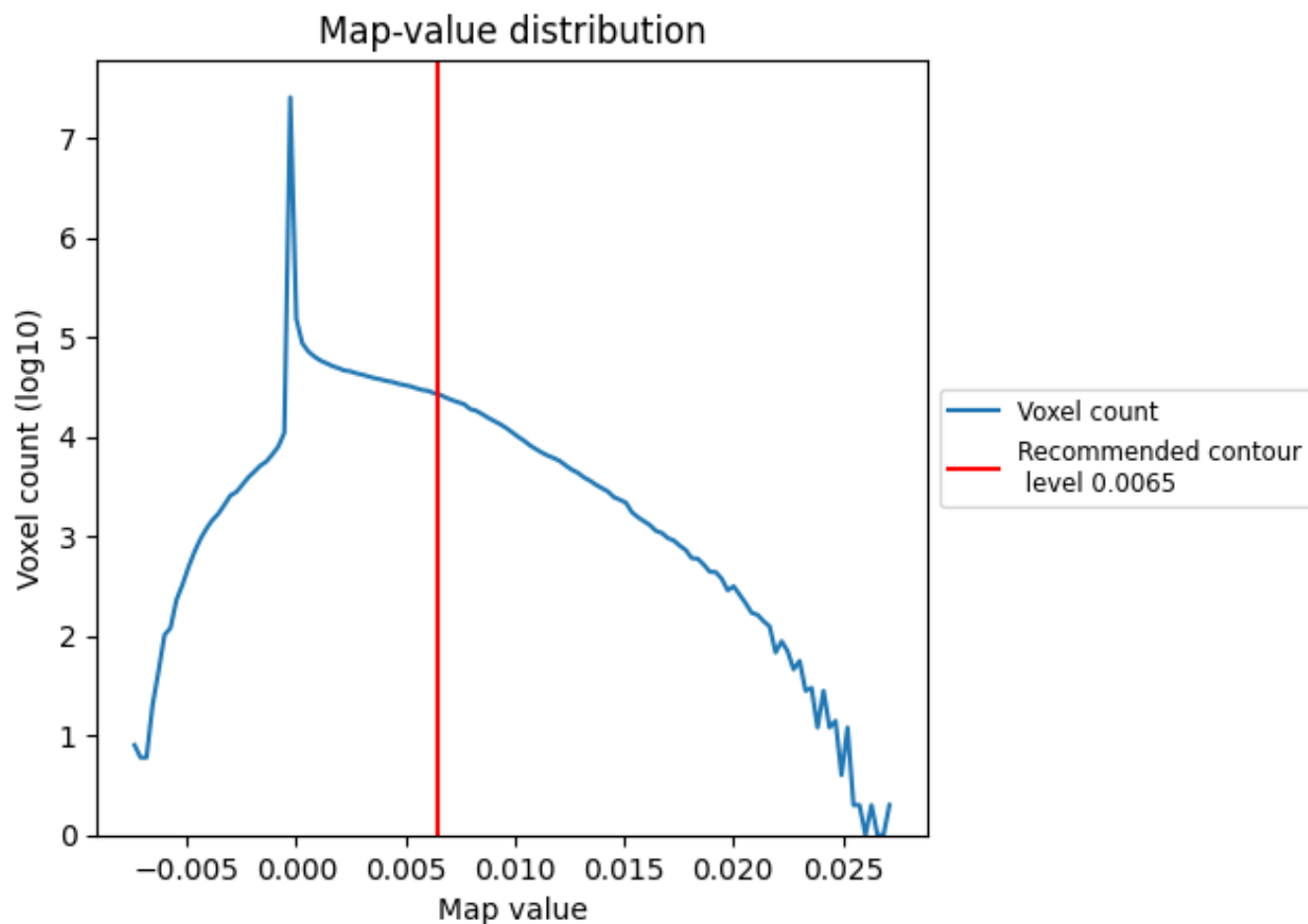
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

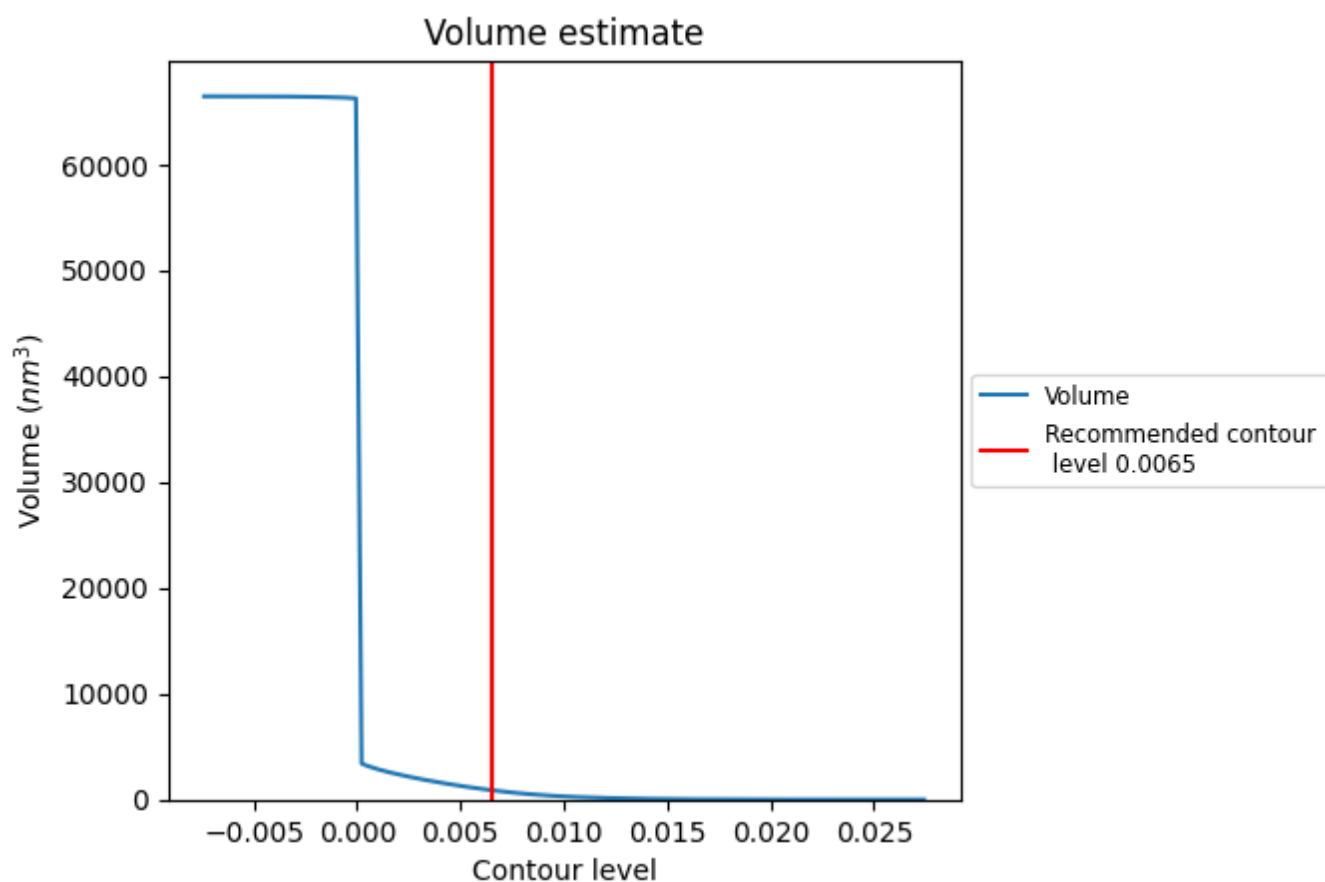
This section contains the results of statistical analysis of the map.

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.

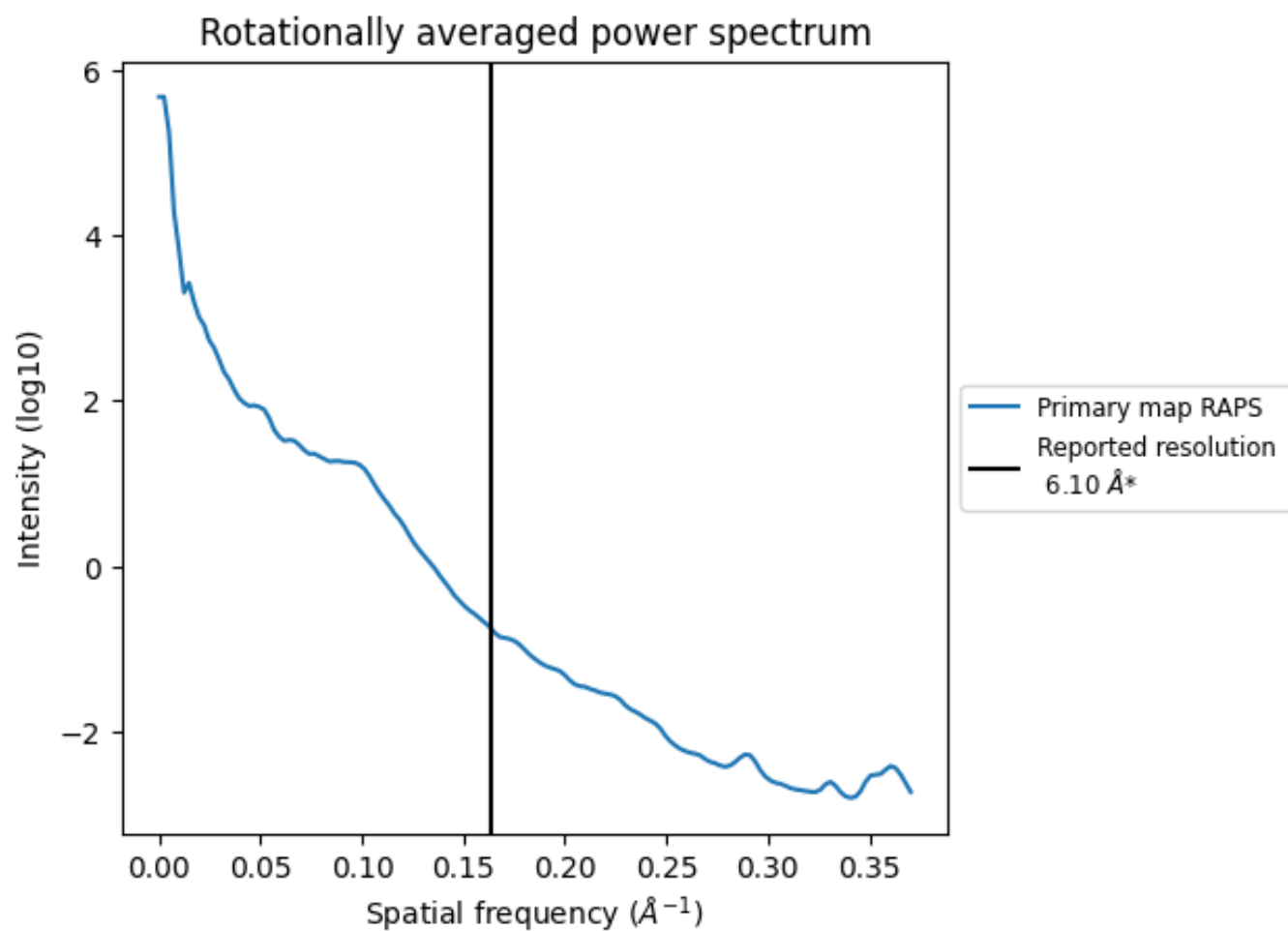
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 886 nm³; this corresponds to an approximate mass of 800 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 0.164 Å⁻¹

8 Fourier-Shell correlation

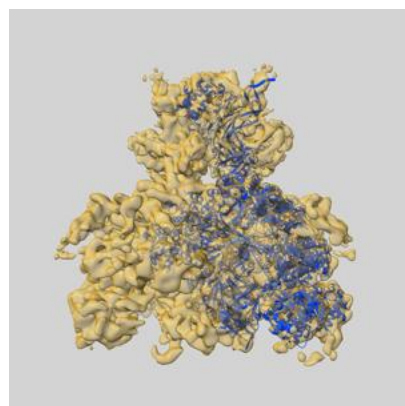
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

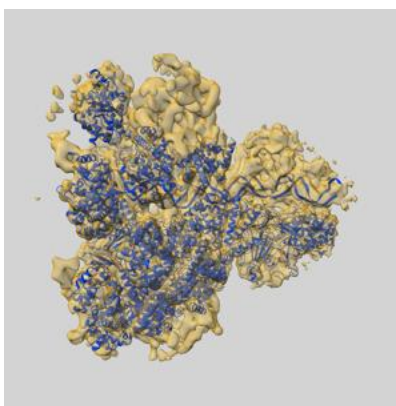
This section contains information regarding the fit between EMDB map EMD-51803 and PDB model 9H2H. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

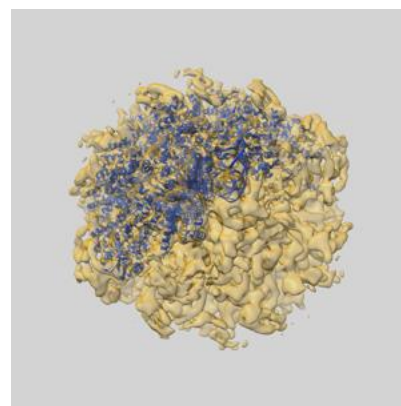
9.1.1 Map-model overlay [i](#)



X

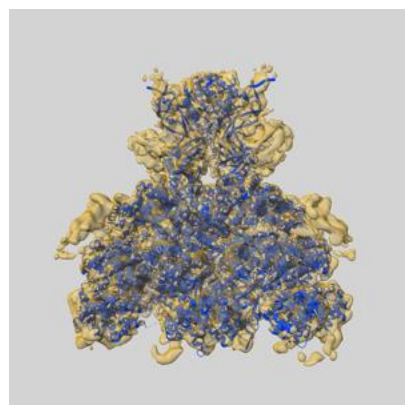


Y

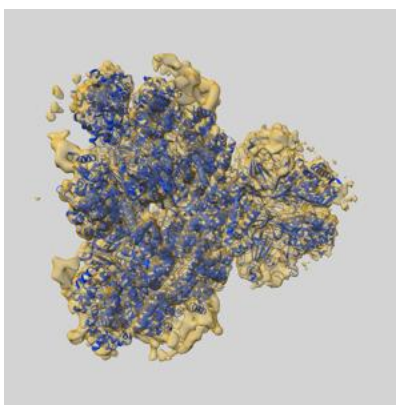


Z

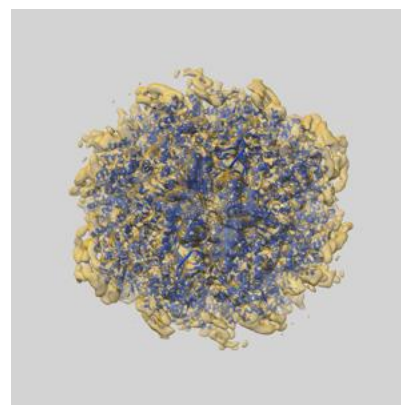
9.1.2 Map-model assembly overlay [i](#)



X



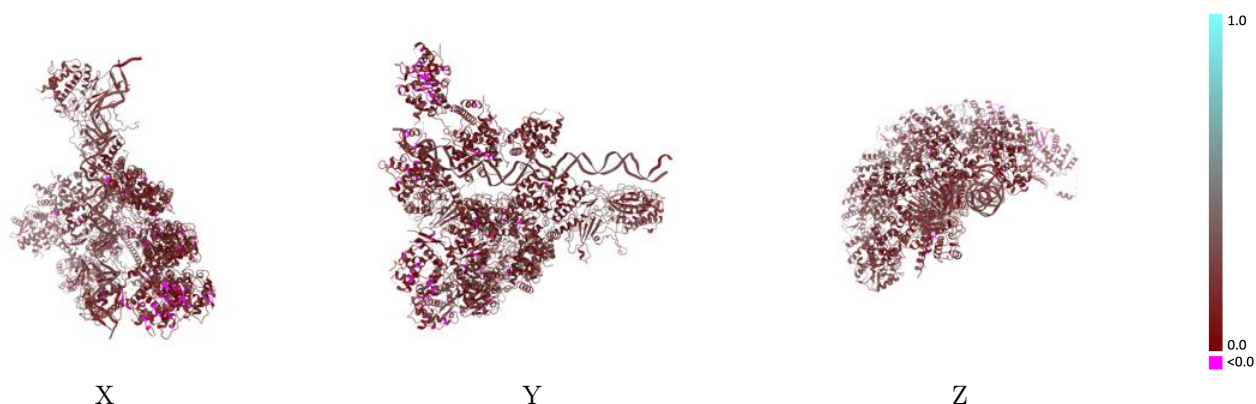
Y



Z

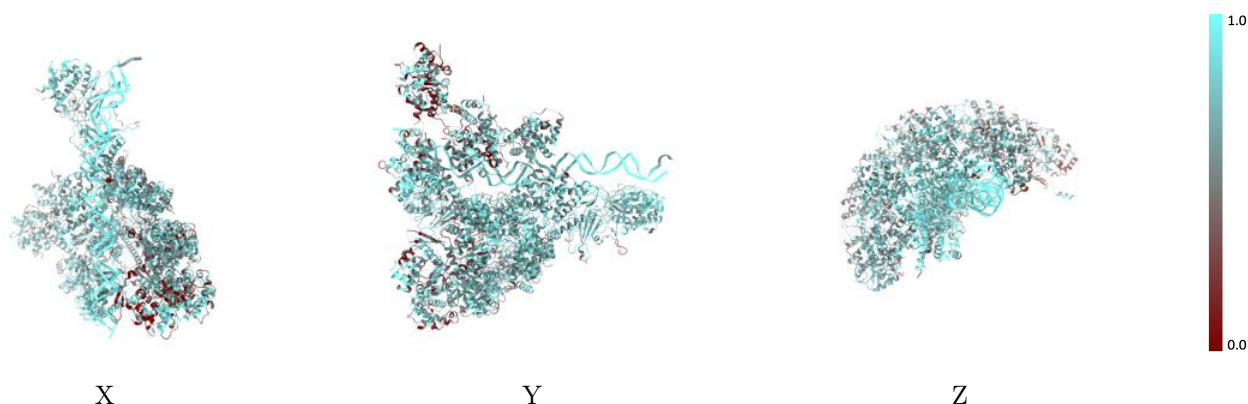
The images above show the 3D surface view of the map at the recommended contour level 0.0065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



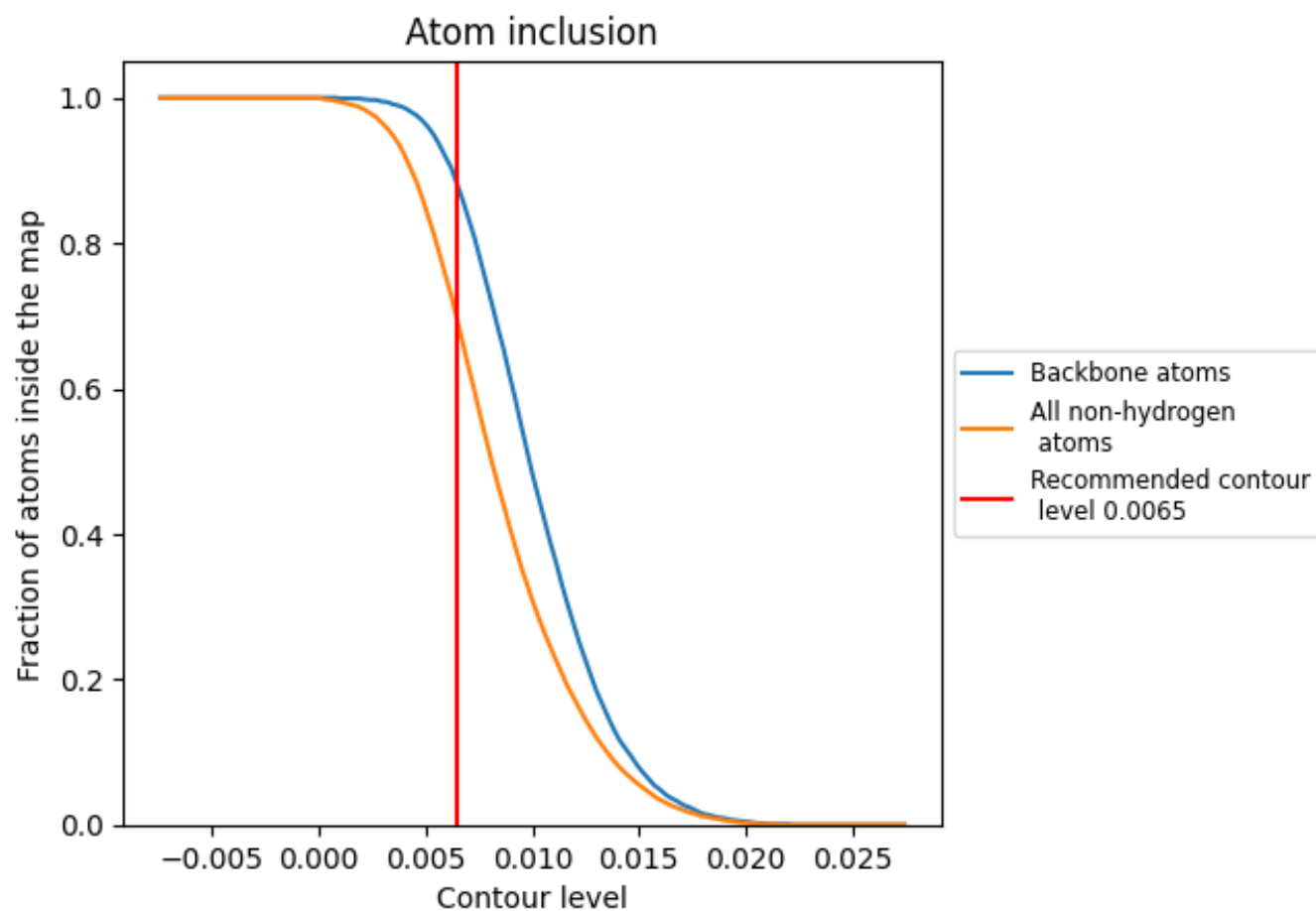
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 69% 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 (0.0065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6930	 0.1920
A	 0.7500	 0.2170
B	 0.7680	 0.2250
C	 0.7900	 0.2300
D	 0.7850	 0.2170
E	 0.9240	 0.2670
F	 0.9520	 0.2780
G	 0.6420	 0.1770
H	 0.6240	 0.1580
I	 0.7220	 0.1970
J	 0.7100	 0.1790
K	 0.6480	 0.1760
L	 0.7210	 0.1580
M	 0.7060	 0.1870
N	 0.7010	 0.1780
O	 0.5770	 0.1710
P	 0.6370	 0.1540
Q	 0.6640	 0.1880
R	 0.6730	 0.1840
S	 0.4990	 0.1580
T	 0.5360	 0.1260
U	 0.6310	 0.1760
V	 0.5370	 0.1650

