



wwPDB EM Validation Summary Report ⓘ

Oct 21, 2024 – 05:27 PM JST

PDB ID : 8GZN
EMDB ID : EMD-34399
Title : IgM-var2CSA complex
Authors : Akhouri, R.R.; Goel, S.; Skoglund, U.
Deposited on : 2022-09-27
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

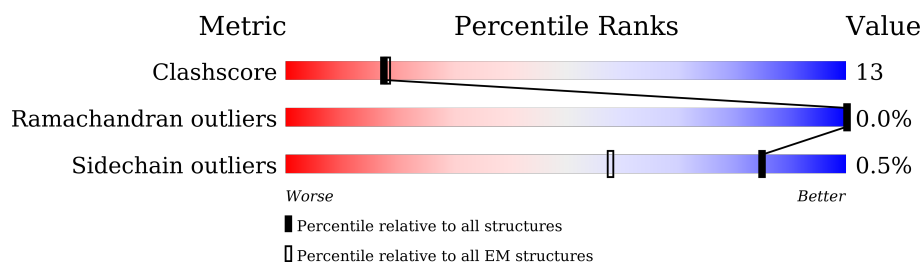
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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





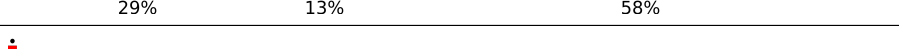


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	453	 19% 10% 71%
1	B	453	 33% 17% 50%
1	C	453	 34% 16% 50%
1	D	453	 35% 14% 51%
1	E	453	 33% 17% 51%
1	F	453	 35% 14% 51%
1	G	453	 31% 18% 51%
1	H	453	 38% 13% 49%

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Mol	Chain	Length	Quality of chain
1	K	453	
1	L	453	
2	I	2680	
2	M	2680	
3	J	136	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 35322 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 Immunoglobulin heavy constant mu.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	132	Total	C	N	O	S	0	0
			1026	648	174	198	6		
1	B	227	Total	C	N	O	S	0	0
			1764	1111	299	346	8		
1	C	225	Total	C	N	O	S	0	0
			1749	1103	297	341	8		
1	D	224	Total	C	N	O	S	0	0
			1743	1100	296	339	8		
1	E	224	Total	C	N	O	S	0	0
			1743	1100	296	339	8		
1	F	221	Total	C	N	O	S	0	0
			1723	1087	292	336	8		
1	G	224	Total	C	N	O	S	0	0
			1743	1100	296	339	8		
1	H	230	Total	C	N	O	S	0	0
			1785	1124	301	351	9		
1	K	230	Total	C	N	O	S	0	0
			1786	1124	302	351	9		
1	L	127	Total	C	N	O	S	0	0
			993	626	168	193	6		

- Molecule 2 is a protein called Erythrocyte membrane protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	1115	Total	C	N	O	S	0	0
			9208	5813	1571	1758	66		
2	M	1115	Total	C	N	O	S	0	0
			9208	5813	1571	1758	66		

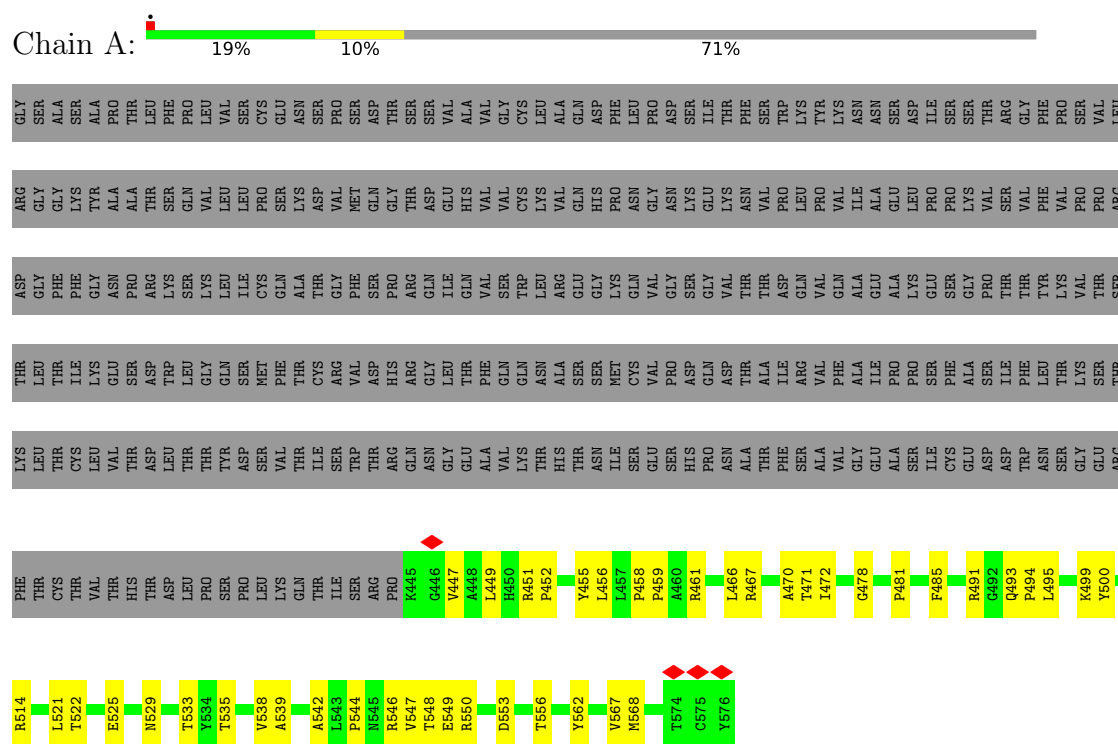
- Molecule 3 is a protein called Immunoglobulin J chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	106	Total	C	N	O	S	0	0
			851	528	150	166	7		

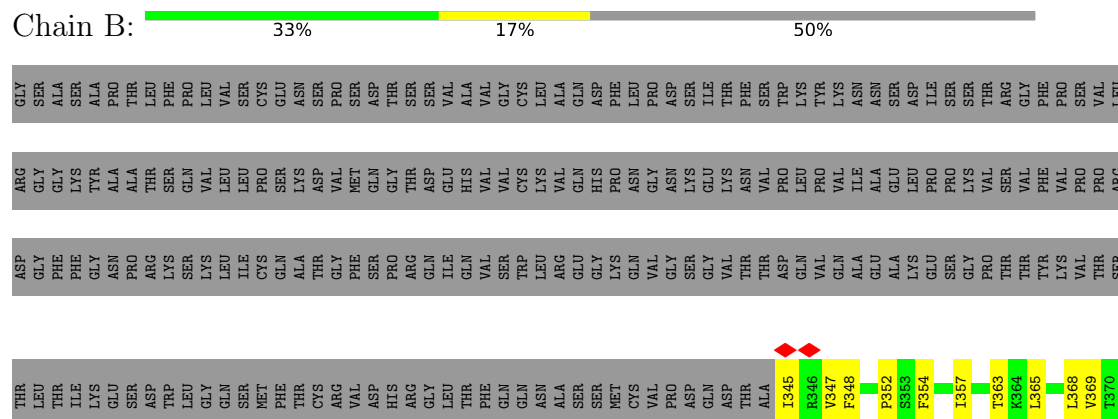
3 Residue-property plots

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: Immunoglobulin heavy constant mu



• Molecule 1: Immunoglobulin heavy constant mu



Chain E:

33%

17%

51%

R461	N465	L466	R467	I472	T473	C474	L475	V476	F479	V484	M489	S496	F497	E498	P509	P512	H518	S519	I520	S524	E525	E526	N529	T530	G531	E532	T533	F534	T535	H540	T551	V552	D553	K554	S555	T556	M568	SER	ASP	THR	ALA	GLY	THR	CYS	TYR											
V378	T379	I380	T383	R384	Q385	E388	A389	V390	K391	T392	H393	I396	S397	E398	S399	H400	A403	T404	F405	S406	A407	V408	G409	E410	D416	D417	W418	N419	S420	G421	E422	R423	F424	T425	V428	T429	H430	T440	I441	S442	R443	P444	K445	P452	D453	V454	L457	P458	A460							
THR	LEU	THR	ILE	LYS	GLY	SER	ASP	TRP	GLY	GLN	SER	MET	PHE	THR	CYS	ARG	VAL	ASP	HIS	ARG	GLY	LEU	THR	PHE	GLN	GLN	ASN	ALA	ALA	SER	SER	GLY	VAL	THR	ALA	I345	R346	V347	F348	S356	T360	K364	C367	L368	V369	L372	T373	T374	SER							
ASP	GLY	PHE	GLY	ASN	PRO	ARG	LYS	VAL	ILE	CYS	GLN	ALA	THR	GLY	VAL	PHE	SER	PRO	ARG	GLN	ILE	GLY	VAL	ARG	GLY	GLY	LYS	GLN	VAL	GLY	ASN	ASP	THR	ASP	GLN	VAL	GLN	ALA	GLY	ALA	GLY	LEU	PRO	GLY	GLY	VAL	SER	THR	ARG	GLY	PHE	VAL	PRO	VAL	THR	ASP

- Molecule 1: Immunoglobulin heavy constant mu

Chain F:

35%

14%

51%

V484	M489	V501	E508	P509	Q510	A511	R514	H518	N529	T530	G531	E532	T533	Y534	T535	C536	V537	V538	A539	H540	T551	V552	D553	S554	S555	T556	H568	SER	ASP	THR	THR	ALA	GLY	THR	CYS	TYR																
K382	T383	R384	E388	H393	H400	F405	S406	A407	V408	G409	E410	A411	S412	D416	D417	W418	N419	C426	H430	T431	D432	Q439	R443	P444	LYS	GLY	VAL	A448	P452	V454	L455	L456	L457	P458	P459	R467	F468	S469	A470	T471	T472	T473	L474	L475	V476	F479						
THR	LEU	THR	ILE	LYS	GLY	GLY	SER	ASP	TRP	LEU	GLN	GLY	SER	MET	PHE	THR	CYS	ARG	VAL	ASP	HIS	ARG	GLY	LEU	THR	PHE	GLN	GLN	ASN	ALA	SER	SER	GLN	ASP	THR	THR	ALA	I345	R346	V347	F348	I357	T363	K364	V369	T370	D371	L372	T373	T374	I380	S381
ASP	GLY	PHE	GLY	ASN	PRO	ARG	ARG	LYS	THR	THR	GLY	PHE	SER	PRO	ARG	GLN	ILE	GLN	VAL	SER	TRP	LEU	ARG	GLY	GLY	VAL	VAL	THR	THR	ASP	GLN	VAL	GLN	ALA	GLY	ALA	LYS	GLY	SER	GLY	PRO	THR	THR	THR	LYS	VAL	PRO	THR	SER	ASP		

- Molecule 1: Immunoglobulin heavy constant mu

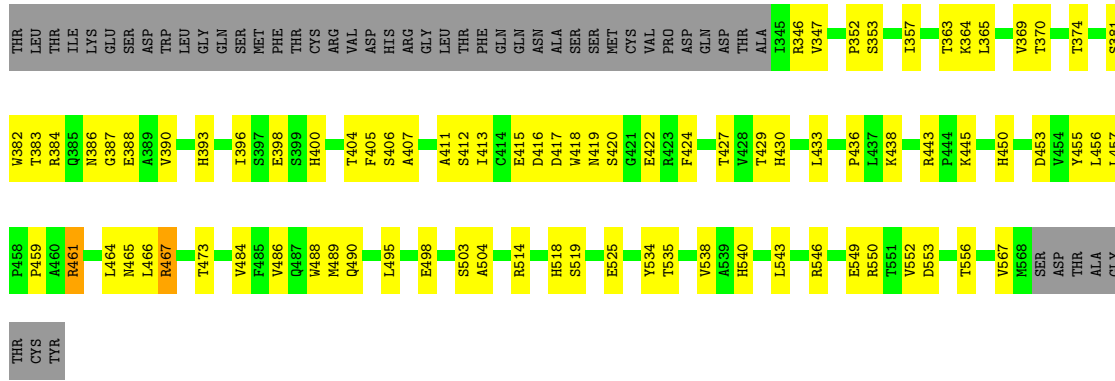
Chain G:

31%

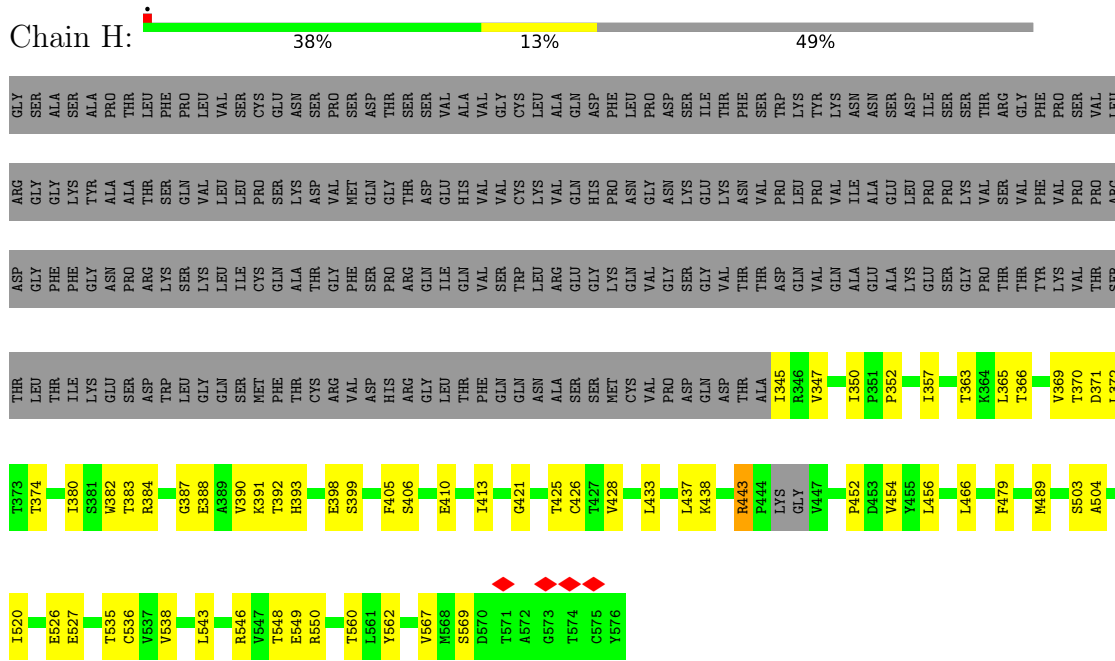
18%

51%

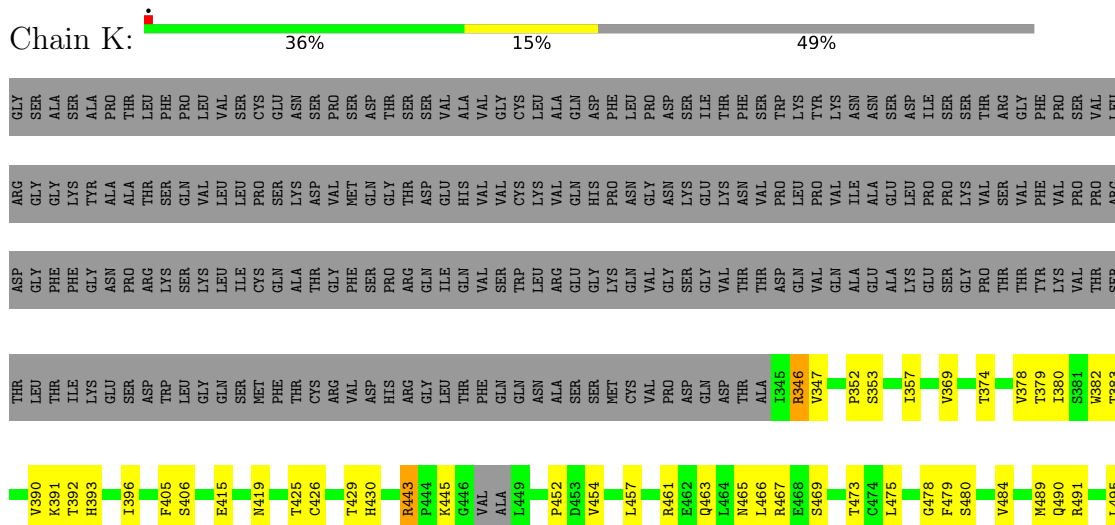
ASP	GLY	PHE	GLY	ASN	PRO	ARG	THR	LYS	SER	LEU	ILE	CYS	GLN	GLY	THR	GLY	THR	ALA	ASP	THR	ASP	GLY	GLN	VAL	SER	TRP	LEU	ARG	ALA	ALA	GLY	GLY	VAL	GLN	ASP	THR	THR	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GL
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• Molecule 1: Immunoglobulin heavy constant mu



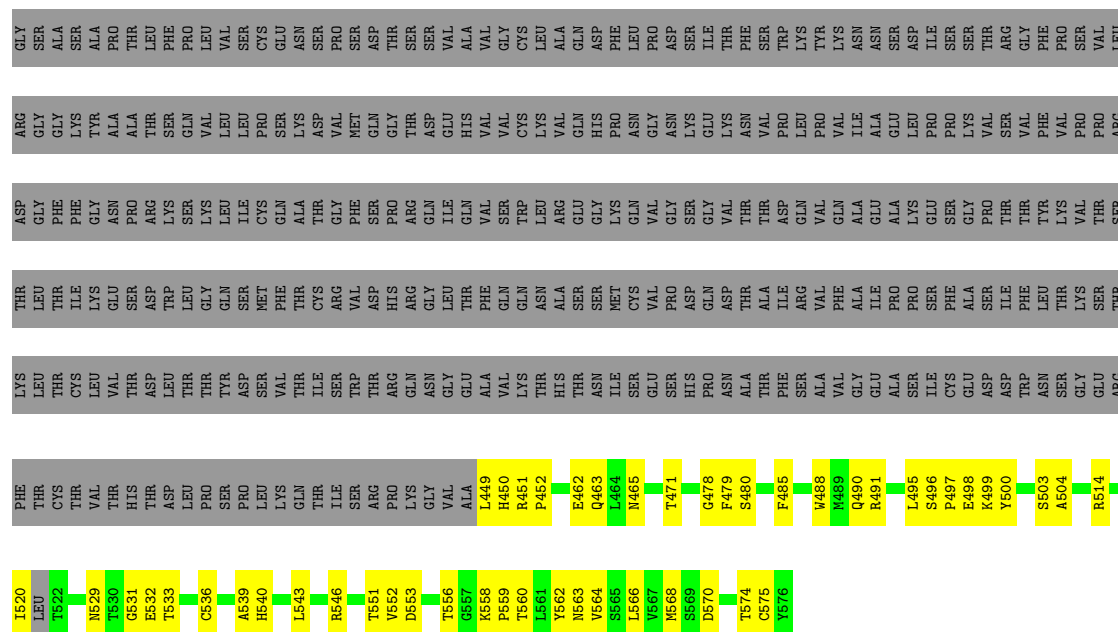
• Molecule 1: Immunoglobulin heavy constant mu





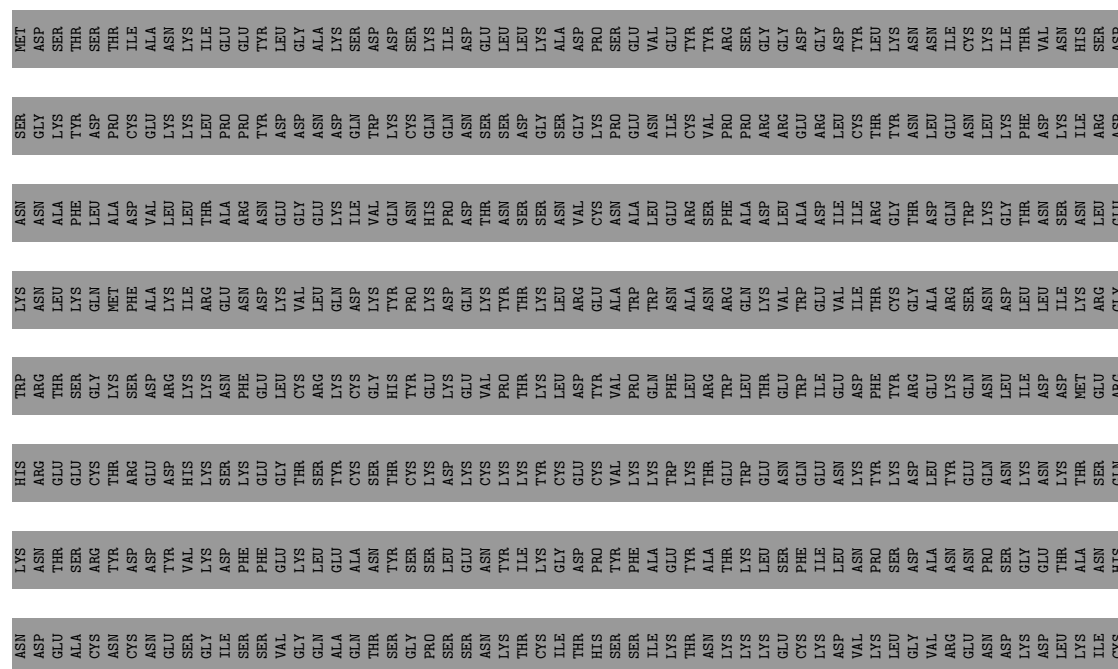
• Molecule 1: Immunoglobulin heavy constant mu

Chain L: 17% 11% 72%

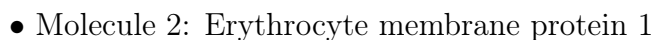


• Molecule 2: Erythrocyte membrane protein 1

Chain I: 29% 13% 58%



Q1629	P1544	C1437	H1345	G1J	N1117	Y1044	LYS	THR	VAL	THR	GLY	ASP	GLY	VAL
I1639	E1545	P1441	A1346	THR	R1122	Q1045	TYR	ALA	ILE	ALA	THR	VAL	TYR	ILE
N1643	C1546	G1444	V1347	ASP	R1125	Q1048	CYS	GLN	ASN	THR	MET	VAL	CYS	ASP
E1644	I1547	G1444	R1349	THR	Q1126	A1063	ASN	ILE	ASN	GLY	GLY	ASP	ASP	THR
E1645	F1551	E1447	Y1354	ILE	Y1127	ASN	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
G1646	F1553	D1448	K1355	ASN	ALA	ILE	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
K1649	F1554	Q1449	N1356	LYS	ASP	CYS	PRO	ILE	ILE	ILE	GLY	GLY	GLY	GLY
L1655	F1555	S1452	N1364	THR	GLY	ILE	TYR70	E972	ASN	ASN	THR	THR	THR	THR
N1656	N1558	W1453	I1365	S1218	GLN	LYS	N971	E973	LYS	LYS	GLY	GLY	GLY	GLY
I1657	I1559	F1454	Y1366	GLU	ASN	VAL	E974	TYR74	ASN	ASN	THR	THR	THR	THR
L1658	E1456	K1455	E1367	VAL	ASN	VAL	R978	R979	LYS	LYS	ASN	ASN	ASN	ASN
Q1659	Y1561	W1457	H1368	LEU	LYS	ASP	K979	E980	GLY	GLY	THR	THR	THR	THR
I1660	K1562	F1461	K1371	ASP	VAL	SER	Y981	Y981	THR	THR	THR	THR	THR	THR
V1661	T1563	C1462	I1379	THR	VAL	THR	C987	C988	THR	THR	THR	THR	THR	THR
R1664	Y1564	E1463	I1380	GLY	S1142	SER	S988	S988	THR	THR	THR	THR	THR	THR
R1671	Y1570	E1464	E1381	ASP	N1143	GLY	ALA	ALA	THR	THR	THR	THR	THR	THR
Q1672	S1571	I1478	K1382	K1252	F1147	THR	ARG	ARG	THR	THR	THR	THR	THR	THR
K1678	S1572	ASN	F1385	D1253	E1151	PRO	SER	SER	THR	THR	THR	THR	THR	THR
D1681	I1573	LYS	GLN	T1254	I1154	VAL	ALA	ALA	THR	THR	THR	THR	THR	THR
K1685	K1580	ASN	LYS	I1255	N1159	ARG	GLY	GLY	THR	THR	THR	THR	THR	THR
I1691	Y1581	GLY	GLN	H1256	GLY	GLY	TYR	TYR	THR	THR	THR	THR	THR	THR
R1692	Y1582	C1486	GLY	H1257	ASP	ASP	LYS	LYS	THR	THR	THR	THR	THR	THR
D1697	Y1584	G1491	VAL	T1260	TRP	THR	ASN	ASN	THR	THR	THR	THR	THR	THR
V1708	N1585	S1491	GLY	H1261	ASP	GLY	D1000	D1000	THR	THR	THR	THR	THR	THR
H1709	N1586	G1494	THR	I1262	K1163	GLY	L1004	L1004	THR	THR	THR	THR	THR	THR
T1713	N1591	D1495	E1399	K1263	K1173	ASN	C1005	C1005	THR	THR	THR	THR	THR	THR
K1714	N1592	K1496	M1400	C1264	K1179	ASN	T1016	T1016	THR	THR	THR	THR	THR	THR
Y1715	L1595	Q1498	V1401	T1269	C1180	THR	V1017	V1017	THR	THR	THR	THR	THR	THR
K1719	K1599	K1504	N1402	S1281	N1183	GLN	R1018	R1018	THR	THR	THR	THR	THR	THR
D1600	D1600	C1505	R1410	D1291	H1186	THR	SER	SER	THR	THR	THR	THR	THR	THR
N1601	N1601	E1506	E1411	T1292	G1187	ASN	ASN	ASN	THR	THR	THR	THR	THR	THR
D1602	D1602	K1507	M1412	K1293	E1188	ASN	THR	THR	THR	THR	THR	THR	THR	THR
W1605	W1605	K1510	W1413	L1295	E1189	THR	S1022	S1022	THR	THR	THR	THR	THR	THR
K1611	K1611	E1514	I1420	T1300	I1190	GLY	D1025	D1025	THR	THR	THR	THR	THR	THR
E1614	E1614	K1515	T1421	H1304	F1191	THR	F1031	F1031	THR	THR	THR	THR	THR	THR
N1615	N1615	Q1516	K1422	H1305	S1192	THR	F1032	F1032	THR	THR	THR	THR	THR	THR
Q1616	Q1616	Q1517	I1423	H1306	E1193	THR	N1033	N1033	THR	THR	THR	THR	THR	THR
R1617	R1617	E1518	N1424	H1307	K1194	THR	E1036	E1036	THR	THR	THR	THR	THR	THR
S1618	S1618	W1519	K1425	L1311	L1195	THR	Q1037	Q1037	THR	THR	THR	THR	THR	THR
P1625	P1625	D1520	I1431	K1328	W1103	THR	W1038	W1038	THR	THR	THR	THR	THR	THR
P1626	P1626	K1521	F1432	N1334	K1106	THR	K1040	K1040	THR	THR	THR	THR	THR	THR
R1627	R1627	K1525	N1433	E1434	Q1114	THR	E1041	E1041	THR	THR	THR	THR	THR	THR
R1628	R1628	A1535	D1435	L1339	Q1114	THR	I1042	I1042	THR	THR	THR	THR	THR	THR
			E1436				Q1043	Q1043	THR	THR	THR	THR	THR	THR

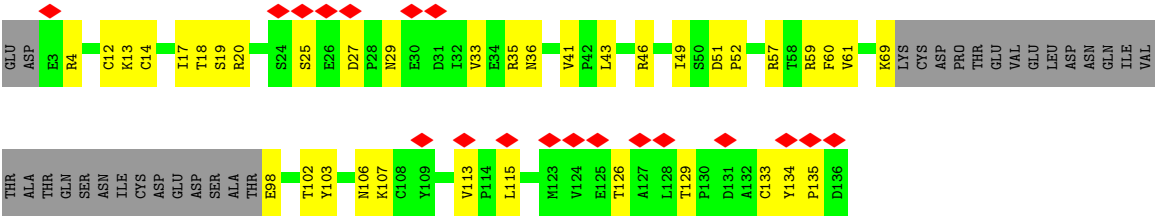


Y1366	E1367	I1368	I1369	L1372	Q1373	I1376	I1379	I1380	E1381	K1382	P1385	GLN	GLN	GLN	LYS	ASP	T1254	I1255	I1256	I1257	G1258	I1265	L1272	E1276	L1277	W1278	T1292	K1293	E1294	L1295	N1302	E1309	H1345	A1346	V1347	G1437	G1438	V1439	P1442	T1443	G1444	N1445	D1446	E1447	D1448	Q1449	S1452	W1453				
ASN	ILE	ASN	SER	GLU	THR	S1218	C1219	ALA	ASN	LYS	LYS	LYS	LYS	VAL	V1139	S1142	N1143	F1146	F1147	S1148	C1149	W1150	E1151	I1154	F1158	N1159	GLY	ASP	TRP	S1163	K1164	N1182	H1186	G1187	E1188	E1193	K1194	N1197	A1198	K1203	GLU	ASN	GLU	SER	THR	ASP	THR					
LYS	THR	ALA	CYS	GLN	CYS	LYS	PRO	T970	R978	Y981	C987	G988	ALA	ALA	ARG	ARG	S1142	N1143	F1146	F1147	S1148	C1149	W1150	E1151	I1154	F1158	N1159	GLY	ASP	TRP	S1163	K1164	N1182	H1186	G1187	E1188	E1193	K1194	N1197	A1198	K1203	GLU	ASN	GLU	SER	THR	ASP	THR				
LEU	SER	ASN	VAL	LEU	ASP	ASN	ASN	ALA	ALA	LYS	PRO	TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			
ARG	THR	THR	LYS	HIS	LYS	ILE	GLU	ASP	GLU	ASP	ASN	GLY	ARG	ASN	ARG	LYS	ALA	ALA	LYS	THR	GLY	THR	GLY	THR	ASN	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
VAL	ILE	GLU	ASP	THR	SER	LEU	SER	GLY	THR	ASP	ASN	GLY	ARG	ASN	ARG	LYS	ALA	ALA	LYS	THR	GLY	THR	GLY	THR	ASN	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
ASN	ASP	GLU	ALA	CYS	ASN	ASP	ASN	ASP	PHE	ASP	ASN	VAL	GLY	ASN	GLY	CYS	LEU	ALA	GLY	CYS	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			
LYS	ASN	THR	ARG	TYR	ASP	ASP	ASP	THR	PHE	PHE	ASP	GLY	THR	LEU	ALA	GLY	ASN	GLY	THR	GLY	THR	GLY	THR	ASN	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
HIS	ARG	GLU	THR	THR	THR	GLU	GLY	THR	THR	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
TRP	ARG	THR	SER	GLY	LYS	SER	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
LYS	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

PHE	GLU	PRO	ASN	ILE	GLU	LYS	I2175	F2080	CYS	THR	ARG	D1706	Y1585	F1454
SER	TYR	GLN	SER	CYS	THR	GLU	P2176	L2081	ASP	GLU	ALA	D1707	Y1570	K1455
GLY	ILE	PHE	ASP	GLU	ASP	PRO	T2177	G2082	LEU	CYS	THR	H1709	Y1457	E1456
ASP	LYS	GLY	LYS	TYR	ALA	ASP	T2178	N2083	ILE	GLU	CYS	D1710	S1571	G1458
TRP	ASN	TRP	ILE	LYS	ASN	ASP	P2181	K2086	ALA	GLY	GLY	T1713	S1572	R1473
PHE	ASP	PHE	GLY	ASP	THR	ALA	P2182	K2089	ASP	ASN	ASP	T1717	I1573	Y1477
GLU	PRO	GLU	LYS	PRO	TYR	ILE	Q2183	Y2103	ILE	SER	SER	D1718	C1574	Y1478
LEU	ILE	LEU	ARG	GLU	LEU	G2011	R2186	L2095	G2011	ASN	ASN	K1719	S1575	ASN
GLY	LYS	GLY	GLY	GLY	GLY	K2015	W2187	M2098	K2015	ILE	ILE	E1582	Y1582	GLY
ASP	LYS	ASP	ASN	ASN	HIS	T2016	K2188	K2098	T2016	GLY	GLY	K1583	Y1584	LYS
THR	LYS	THR	LYS	TYR	CYS	K2017	K2189	Y2103	K2017	GLY	GLY	E1584	Y1584	ASN
ASP	LYS	ASP	LYS	LYS	SER	L2018	E2190	Y2103	L2018	GLY	GLY	I1723	Y1584	ASN
GLY	ASN	GLY	ASN	ASN	CYS	L2021	W2191	D2107	L2021	GLY	GLY	F1724	A1587	GLU
ASN	ILE	ASN	LYS	ILE	CYS	D2022	G2192	D2107	D2022	PRO	PRO	G1725	A1587	LYS
ASP	TRP	ASP	LYS	TRP	PRO	E2023	T2193	T2112	E2023	ASN	ASN	S1726	K1590	LYS
ARG	HIS	ARG	ASN	HIS	ASN	W2024	C2196	T2112	W2024	GLY	GLY	S1727	K1590	C1486
GLY	ARG	GLY	CYS	ARG	CYS	N2025	Y2200	D2113	N2025	ASN	ASN	N1728	D1600	GLY
PHE	MET	PHE	GLY	MET	PHE	D2026	Q2200	E2119	D2026	THR	THR	E1491	S1491	GLY
ASN	LYS	ASN	ASN	LYS	ASN	M2027	E2201	E2119	M2027	GLY	GLY	K1611	S1491	GLN
VAL	LYS	VAL	LYS	LYS	VAL	D2028	H2202	T2123	D2028	GLY	GLY	L1612	K1611	GLN
ALA	ASN	ALA	ASN	ASN	ASN	K2124	E2203	K2123	K2124	ASP	ASP	L1613	K1612	GLN
GLY	GLY	GLY	GLY	GLY	GLY	L2125	E2204	K2124	L2029	THR	THR	E1614	K1613	GLY
LEU	ASN	LEU	ASN	ASN	ASN	K2126	Y2205	L2125	M1959	ARG	ARG	N1615	E1614	GLY
ASN	ASN	ASN	ASN	ASN	ASN	D2127	Y2205	K2126	K1960	THR	THR	I1497	E1498	GLY
PRO	PRO	PRO	ASN	PHE	ASN	L2128	V2213	D2127	E1963	THR	THR	I1498	E1498	GLY
LYS	LYS	LYS	LYS	LYS	LYS	D2129	T2214	L2128	V1965	GLY	GLY	A1500	E1499	GLY
GLY	GLY	GLY	GLY	GLY	GLY	R2130	T2214	L2130	L1966	GLY	GLY	C1501	A1500	GLY
ASN	ASN	ASN	ASN	ASN	ASN	L2131	E2222	L2131	L1966	THR	THR	R1617	C1501	GLY
GLY	GLY	GLY	GLY	GLY	GLY	K2139	S2223	K2139	V1969	THR	THR	S1618	K1502	GLY
VAL	VAL	VAL	VAL	VAL	VAL	N2224	N2225	E2142	Q1972	THR	THR	P1626	E1506	GLY
ALA	ALA	ALA	ALA	ALA	ALA	N2225	N2225	D2143	L1973	ASN	ASN	R1627	E1506	GLY
GLY	GLY	GLY	GLY	GLY	GLY	E2229	E2229	W2144	N1974	GLY	GLY	R1628	K1510	GLY
GLY	GLY	GLY	GLY	GLY	GLY	Y2233	Y2233	W2145	E1975	THR	THR	Q1629	E1514	GLY
VAL	VAL	VAL	VAL	VAL	VAL	W2236	W2236	K2146	N1976	ASP	ASP	Q1630	K1515	GLY
ASN	ASN	ASN	ASN	ASN	ASN	R2240	R2240	N2148	I1980	ARG	ARG	I1639	K1516	GLY
ASP	ASP	ASP	ASP	ASP	ASP	S2241	S2241	K2149	K1981	LYS	LYS	T1687	Q1517	GLY
GLY	GLY	GLY	GLY	GLY	GLY	Q2243	Q2243	S2151	I1984	LYS	LYS	P1687	E1518	GLY
THR	THR	THR	THR	THR	THR	W2244	W2244	L2152	K1984	THR	THR	A1662	Q1522	GLY
LYS	LYS	LYS	LYS	LYS	LYS	I2247	I2247	W2153	L1985	THR	THR	E1663	Q1522	GLY
ALA	ALA	ALA	ALA	ALA	ALA	N2154	N2154	N2153	TYR	ASN	ASN	R1664	K1529	GLY
GLY	GLY	GLY	GLY	GLY	GLY	S2248	S2248	L2063	PRO	THR	THR	E1665	Y1530	GLY
ASN	ASN	ASN	ASN	ASN	ASN	A2155	A2155	N2064	LEU	THR	THR	Y1668	L1539	GLY
GLY	GLY	GLY	GLY	GLY	GLY	M2156	M2156	E2065	ASP	THR	THR	L1669	L1539	GLY
ASN	ASN	ASN	ASN	ASN	ASN	L2157	L2157	F2066	ARG	THR	THR	P1671	P1544	GLY
ASN	ASN	ASN	ASN	ASN	ASN	C2158	C2158	K2067	CYS	THR	THR	Q1672	I1547	GLY
CYS	CYS	CYS	CYS	CYS	CYS	K2162	K2162	T2070	PHE	VAL	VAL	Y1673	T1547	GLY
ASP	ASP	ASP	ASP	ASP	ASP	D2169	D2169	L2071	ASP	ASN	ASN	D1681	F1551	GLY
ILE	ILE	ILE	ILE	ILE	ILE	S2171	S2171	L2071	ASP	LYS	LYS	D1682	F1551	GLY
ASP	ASP	ASP	ASP	ASP	ASP	W2172	W2172	Q2075	GLN	LYS	LYS	F1554	F1554	GLY
PRO	PRO	PRO	PRO	PRO	PRO	T2174	T2174	S2076	LEU	LYS	LYS	K1686	F1555	GLY
LYS	LYS	LYS	LYS	LYS	LYS	VAL	VAL	E2077	GLY	LYS	LYS	L1688	N1556	GLY
HIS	HIS	HIS	HIS	HIS	HIS	VAL	VAL	G2078	VAL	LYS	LYS	I1701	Y1561	GLY
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	K2079	VAL	VAL	VAL	I1702	Y1561	GLY

• Molecule 3: Immunoglobulin J chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	371049	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 ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.018	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00805	Depositor
Map size (Å)	594.0, 594.0, 594.0	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	0.24	0/1053	0.51	0/1442
1	B	0.25	0/1809	0.54	0/2478
1	C	0.24	0/1794	0.52	0/2457
1	D	0.25	0/1788	0.53	0/2449
1	E	0.25	0/1788	0.53	0/2449
1	F	0.25	0/1767	0.52	0/2420
1	G	0.25	0/1788	0.52	0/2449
1	H	0.25	0/1830	0.52	0/2507
1	K	0.25	0/1831	0.52	0/2506
1	L	0.25	0/1019	0.55	0/1395
2	I	0.24	0/9392	0.46	0/12593
2	M	0.25	0/9392	0.47	0/12593
3	J	0.23	0/864	0.55	0/1173
All	All	0.25	0/36115	0.49	0/48911

There are no bond length outliers.

There are no bond angle outliers.

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	1026	0	1001	33	0
1	B	1764	0	1724	61	0
1	C	1749	0	1713	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1743	0	1709	40	0
1	E	1743	0	1709	48	0
1	F	1723	0	1682	41	0
1	G	1743	0	1708	57	0
1	H	1785	0	1735	42	0
1	K	1786	0	1737	43	0
1	L	993	0	959	39	0
2	I	9208	0	8976	235	0
2	M	9208	0	8974	240	0
3	J	851	0	843	37	0
All	All	35322	0	34470	927	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 13.

The worst 5 of 927 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:K:369:VAL:O	1:K:406:SER:HA	1.58	1.04
2:I:1191:PHE:O	2:I:1194:LYS:HB2	1.66	0.93
3:J:4:ARG:HH22	3:J:36:ASN:H	1.23	0.87
1:B:490:GLN:HG2	1:B:491:ARG:HG2	1.60	0.83
1:C:452:PRO:HB3	1:C:479:PHE:HB3	1.61	0.81

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	130/453 (29%)	123 (95%)	7 (5%)	0	100	100
1	B	225/453 (50%)	206 (92%)	19 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	223/453 (49%)	195 (87%)	28 (13%)	0	100	100
1	D	222/453 (49%)	204 (92%)	18 (8%)	0	100	100
1	E	222/453 (49%)	206 (93%)	16 (7%)	0	100	100
1	F	217/453 (48%)	198 (91%)	19 (9%)	0	100	100
1	G	222/453 (49%)	203 (91%)	19 (9%)	0	100	100
1	H	226/453 (50%)	206 (91%)	20 (9%)	0	100	100
1	K	226/453 (50%)	206 (91%)	20 (9%)	0	100	100
1	L	123/453 (27%)	112 (91%)	11 (9%)	0	100	100
2	I	1085/2680 (40%)	991 (91%)	94 (9%)	0	100	100
2	M	1085/2680 (40%)	976 (90%)	108 (10%)	1 (0%)	48	79
3	J	102/136 (75%)	89 (87%)	13 (13%)	0	100	100
All	All	4308/10026 (43%)	3915 (91%)	392 (9%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	1367	GLU

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	115/399 (29%)	114 (99%)	1 (1%)	75	87
1	B	203/399 (51%)	203 (100%)	0	100	100
1	C	201/399 (50%)	201 (100%)	0	100	100
1	D	200/399 (50%)	199 (100%)	1 (0%)	86	93
1	E	200/399 (50%)	200 (100%)	0	100	100
1	F	198/399 (50%)	198 (100%)	0	100	100
1	G	200/399 (50%)	198 (99%)	2 (1%)	73	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	205/399 (51%)	204 (100%)	1 (0%)	86	93
1	K	205/399 (51%)	203 (99%)	2 (1%)	73	85
1	L	112/399 (28%)	112 (100%)	0	100	100
2	I	1013/2431 (42%)	1004 (99%)	9 (1%)	75	87
2	M	1013/2431 (42%)	1009 (100%)	4 (0%)	89	95
3	J	100/128 (78%)	100 (100%)	0	100	100
All	All	3965/8980 (44%)	3945 (100%)	20 (0%)	85	93

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	346	ARG
2	M	1840	LYS
2	M	2186	ARG
2	M	2139	LYS
2	I	1349	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	2075	GLN
2	M	2036	HIS
2	I	1629	GLN
2	M	1850	ASN
2	I	1305	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

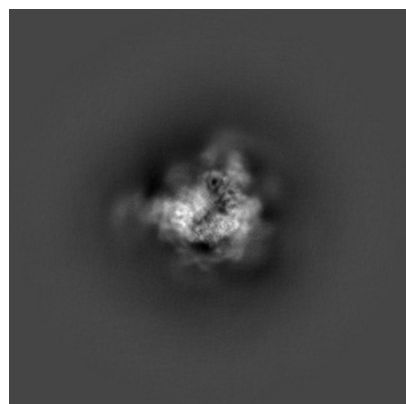
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34399. These allow visual inspection of the internal detail of the map and identification of artifacts.

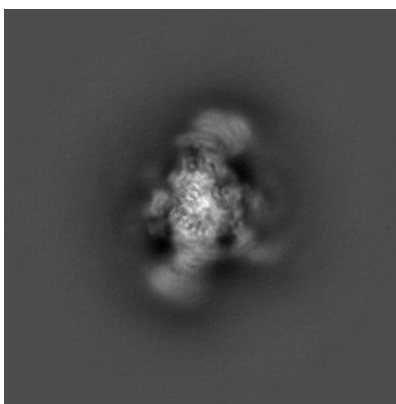
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

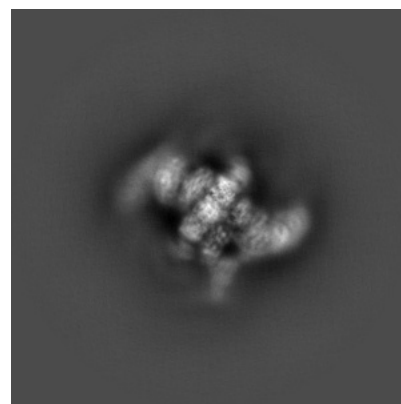
6.1.1 Primary map



X

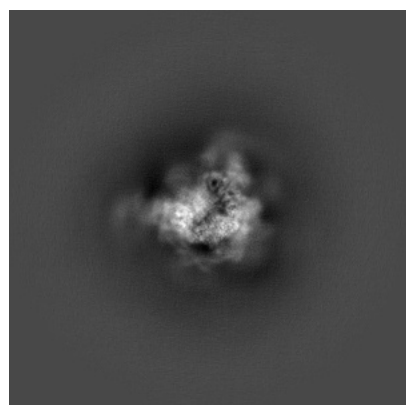


Y

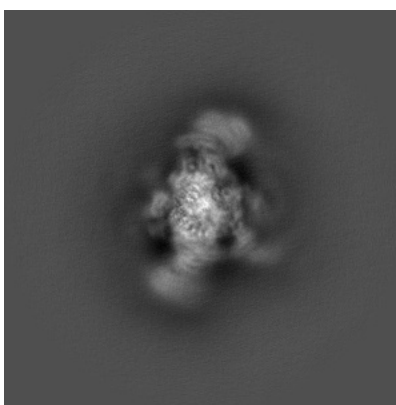


Z

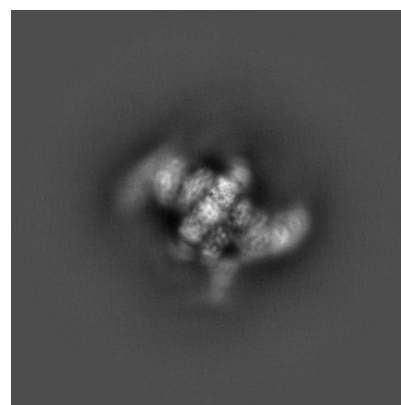
6.1.2 Raw map



X



Y

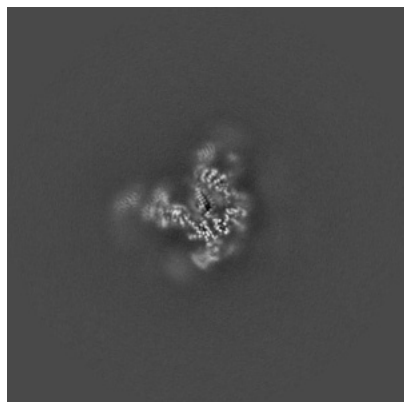


Z

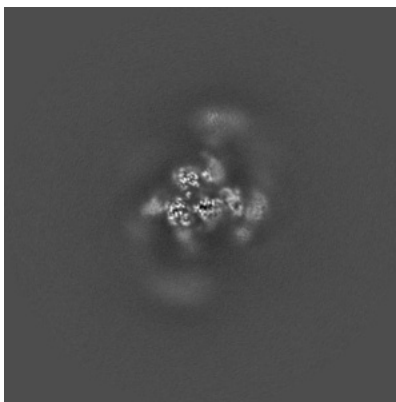
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

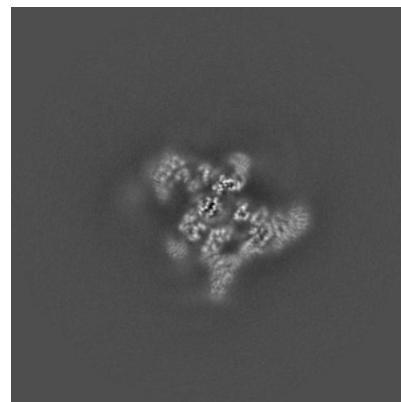
6.2.1 Primary map



X Index: 270

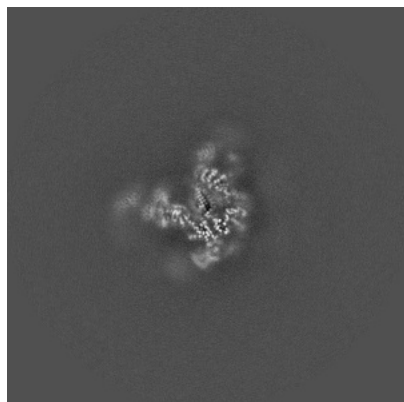


Y Index: 270

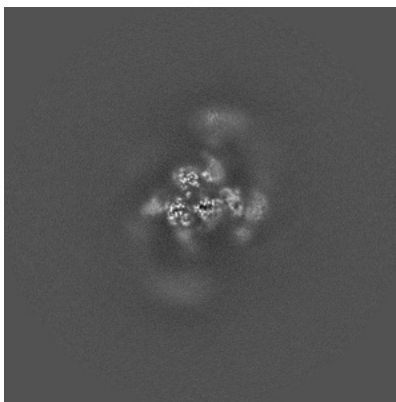


Z Index: 270

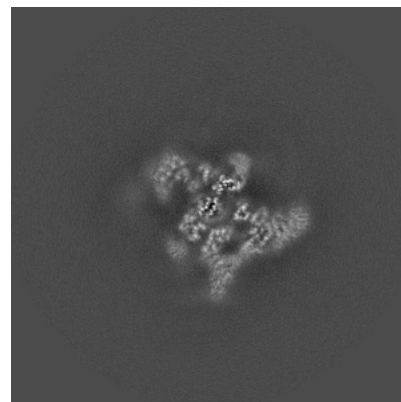
6.2.2 Raw map



X Index: 270



Y Index: 270

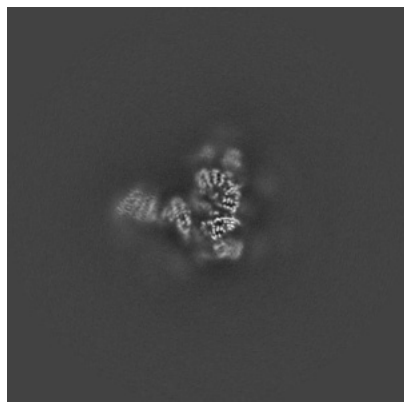


Z Index: 270

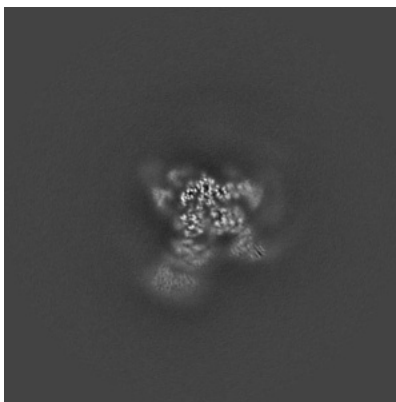
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

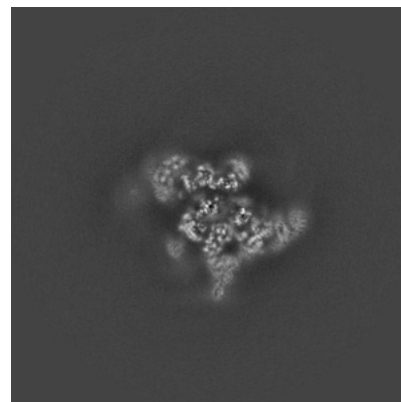
6.3.1 Primary map



X Index: 283

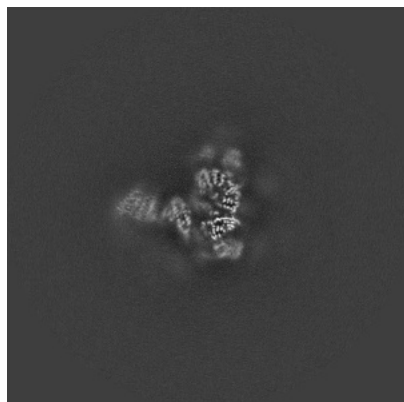


Y Index: 301

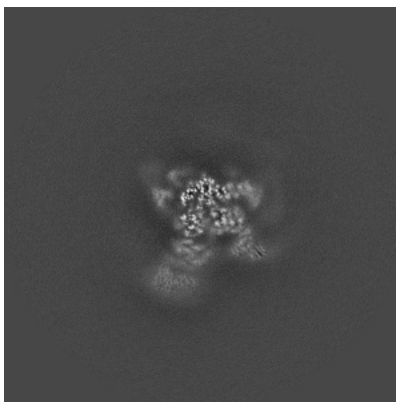


Z Index: 265

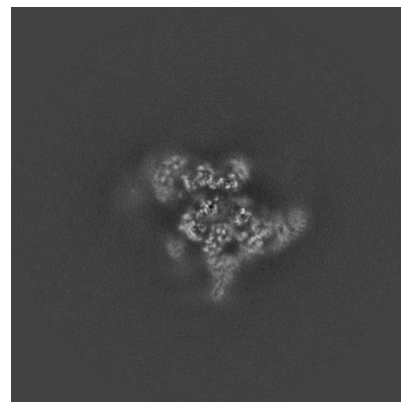
6.3.2 Raw map



X Index: 283



Y Index: 301

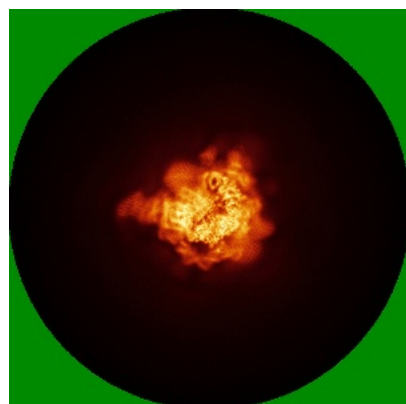


Z Index: 265

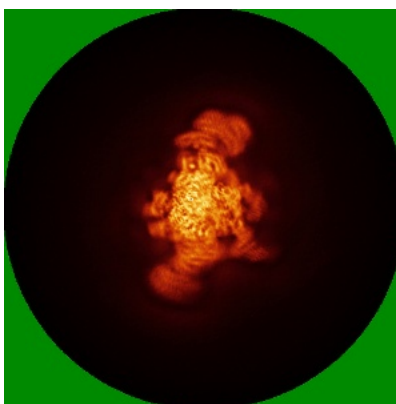
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

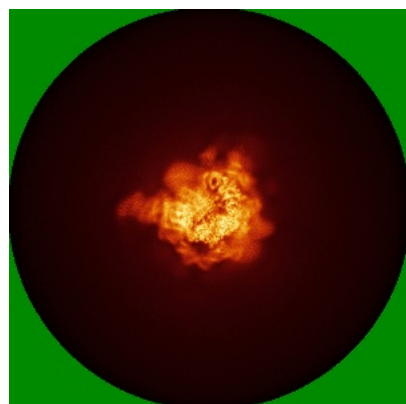


Y

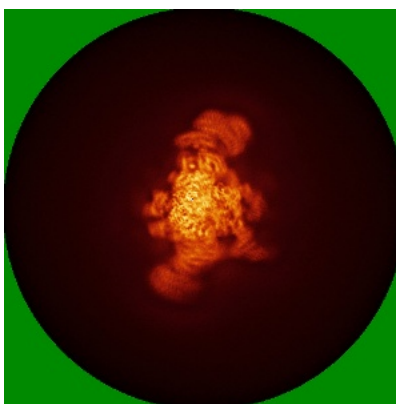


Z

6.4.2 Raw map



X



Y

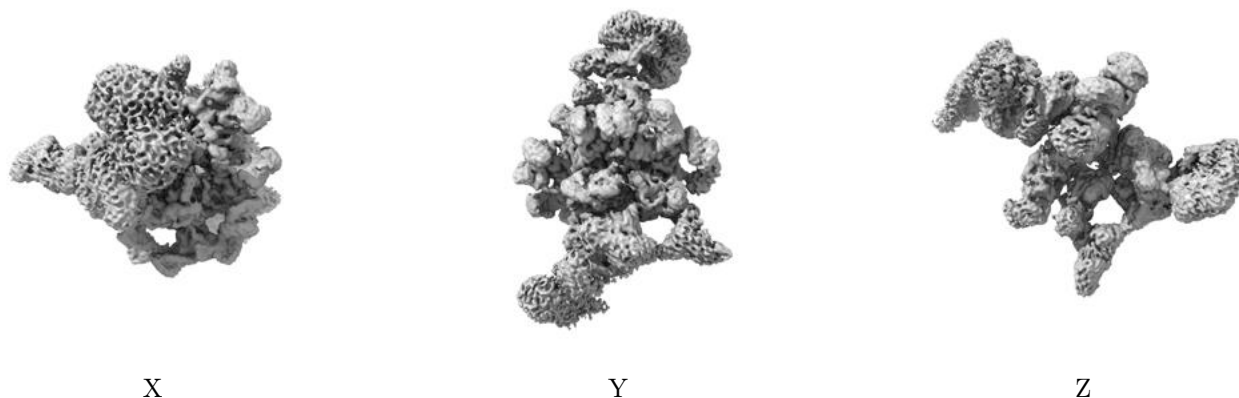


Z

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

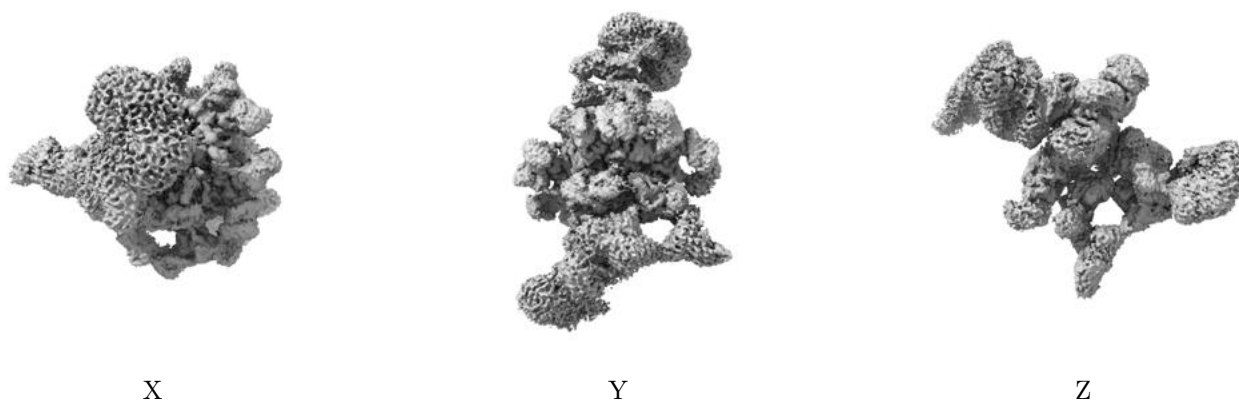
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00805. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

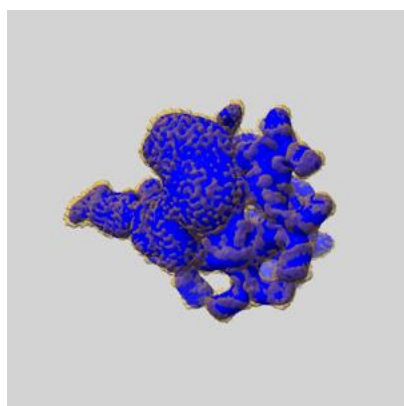
6.6 Mask visualisation [i](#)

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

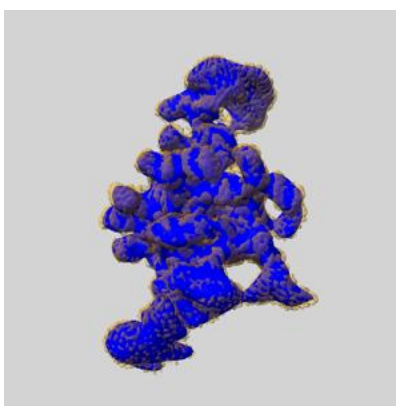
A mask typically either:

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

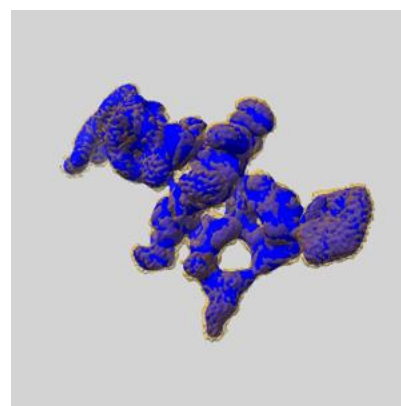
6.6.1 emd_34399_msk_1.map [i](#)



X



Y

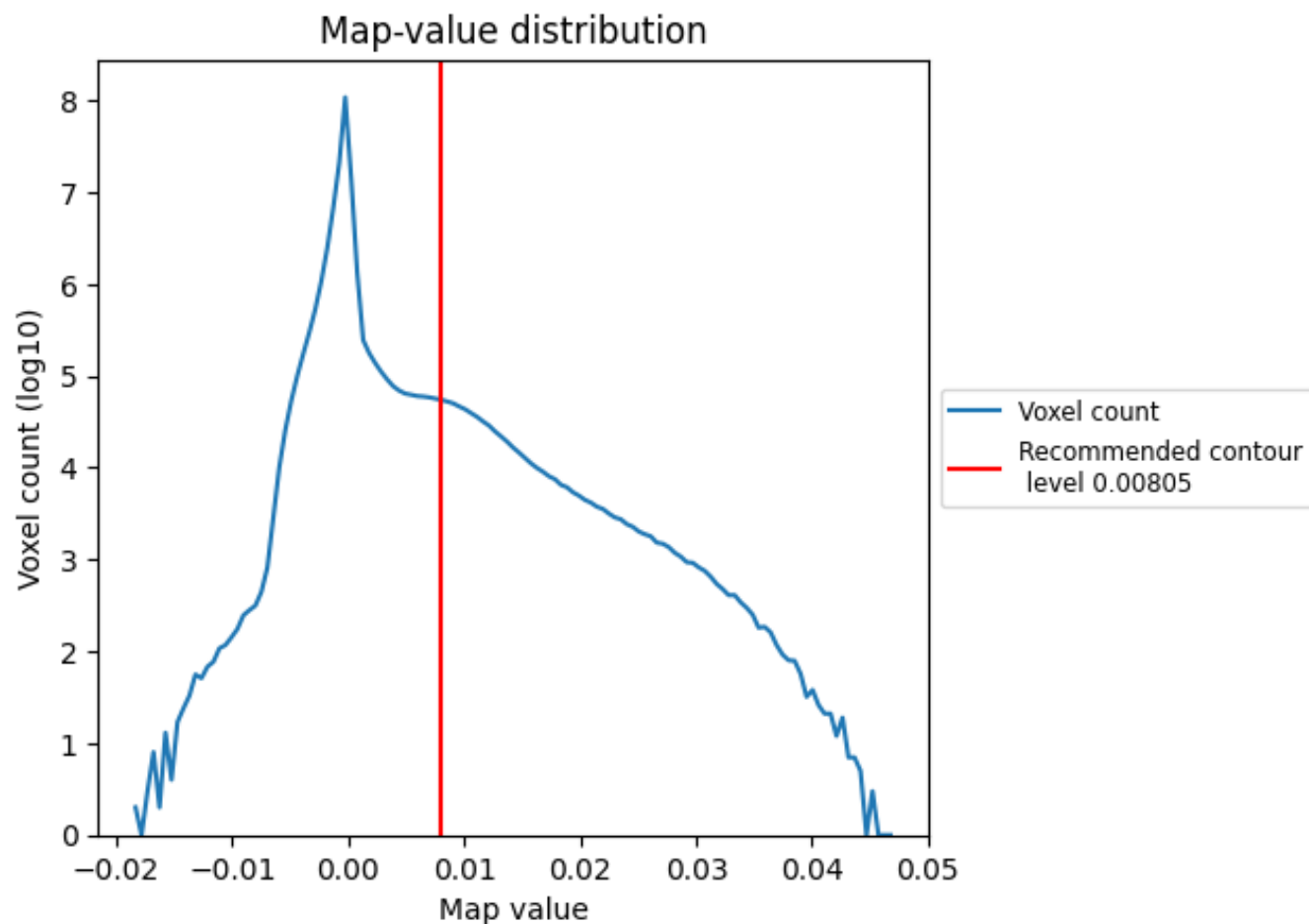


Z

7 Map analysis [i](#)

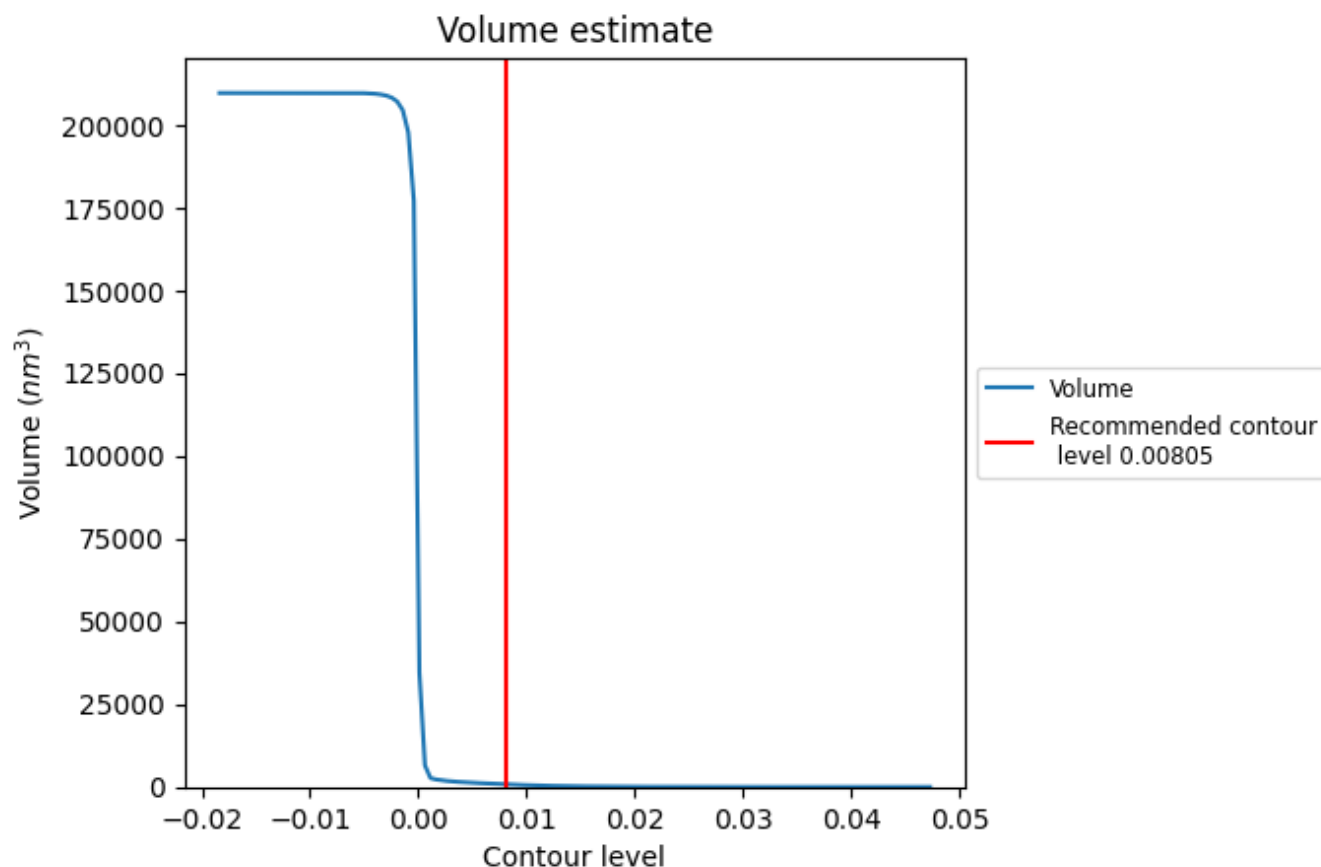
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

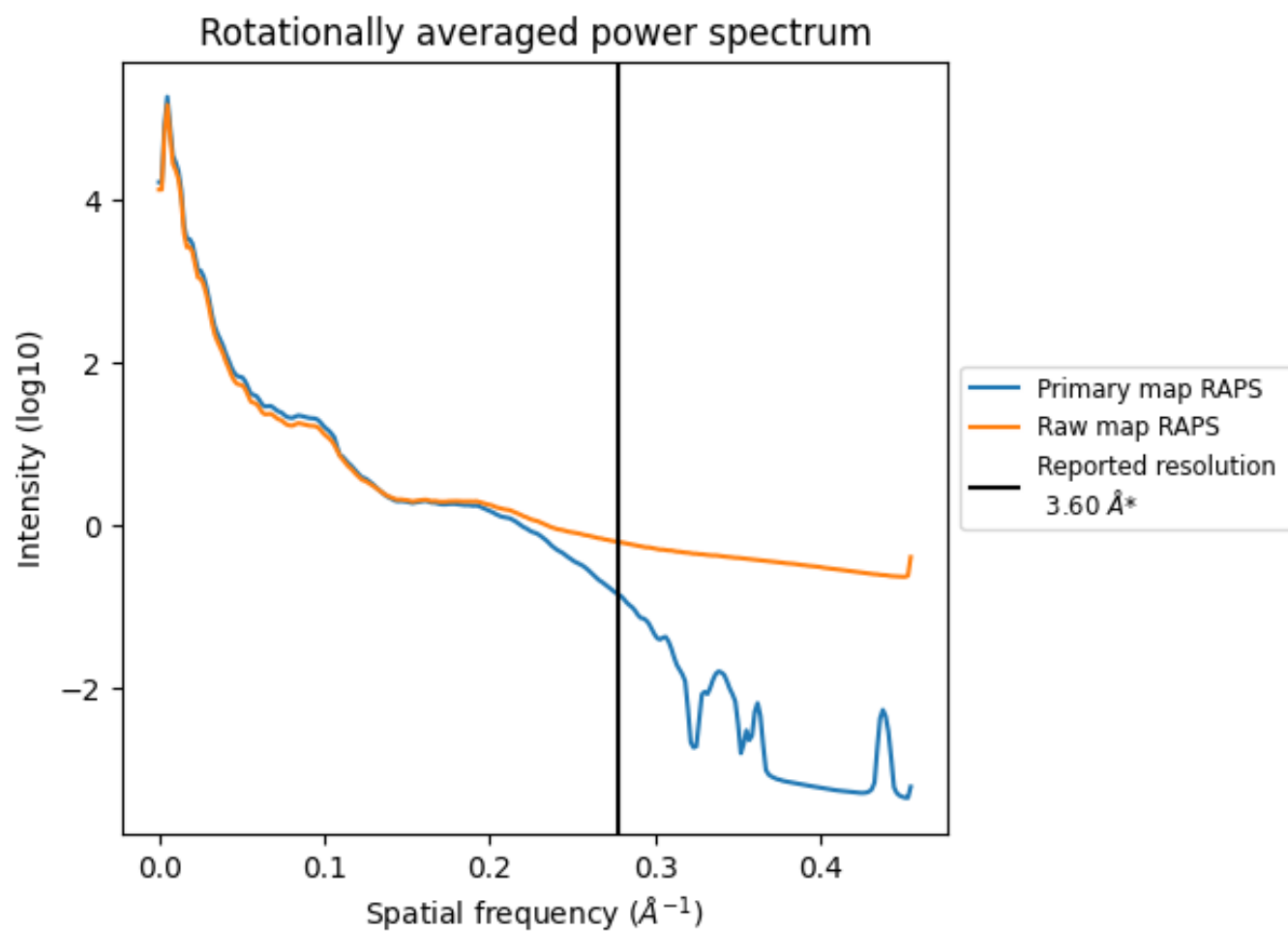
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 809 nm^3 ; this corresponds to an approximate mass of 731 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

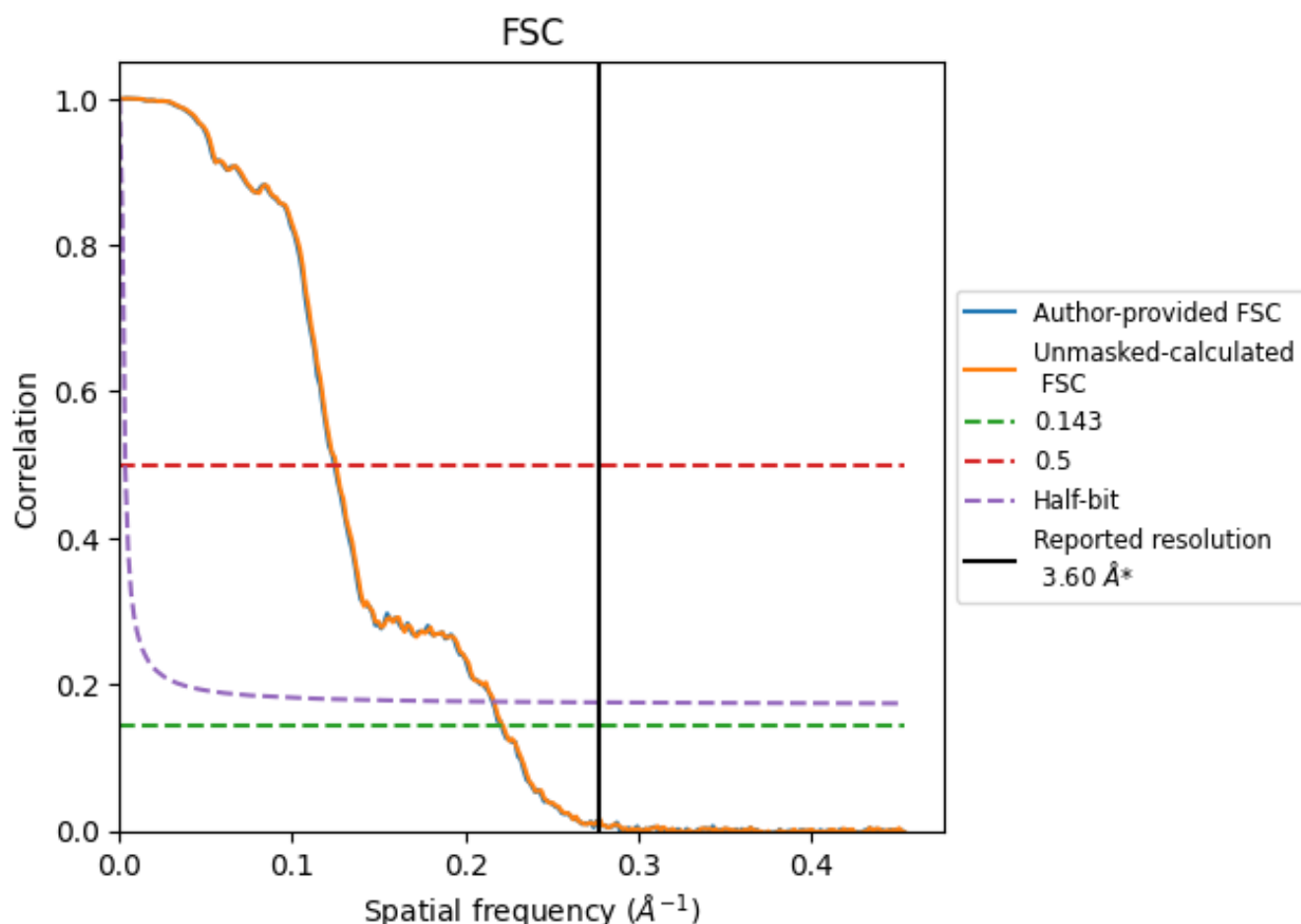


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	4.52	8.05	4.63
Unmasked-calculated*	4.50	7.98	4.61

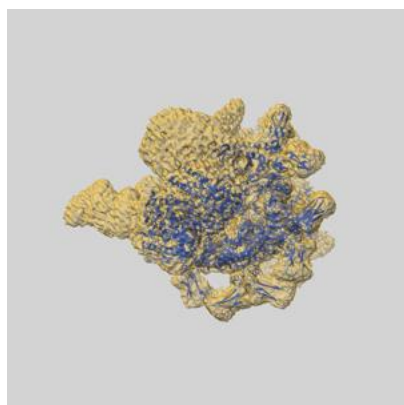
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.52 differs from the reported value 3.6 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.50 differs from the reported value 3.6 by more than 10 %

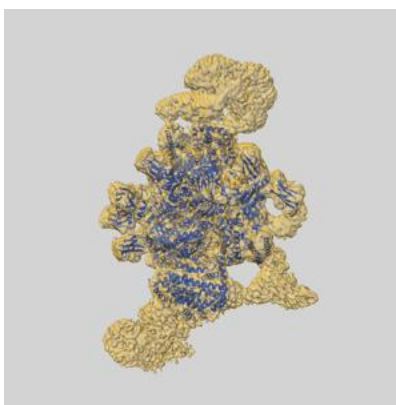
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34399 and PDB model 8GZN. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

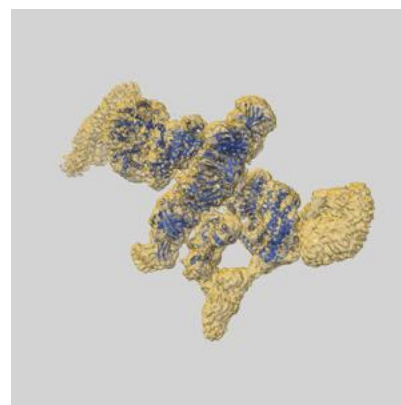
9.1 Map-model overlay [i](#)



X



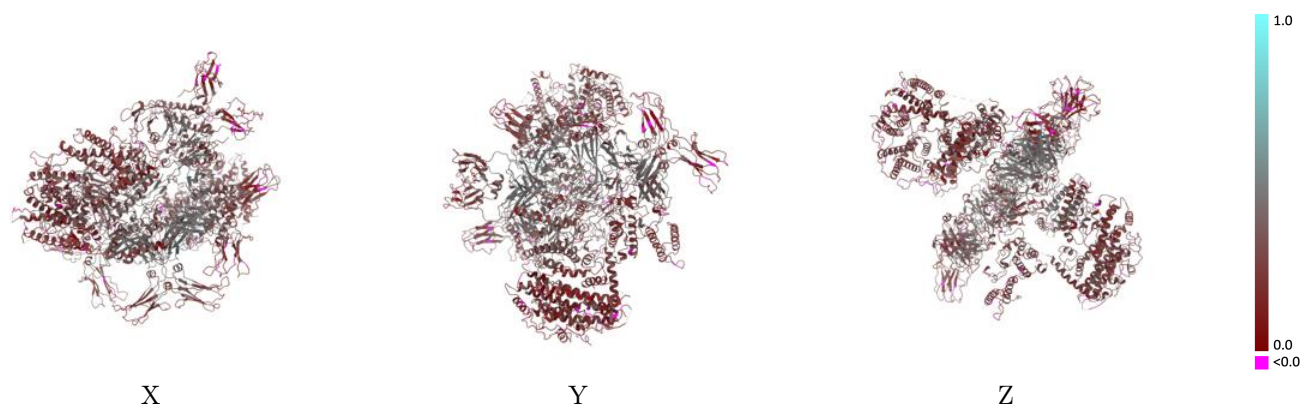
Y



Z

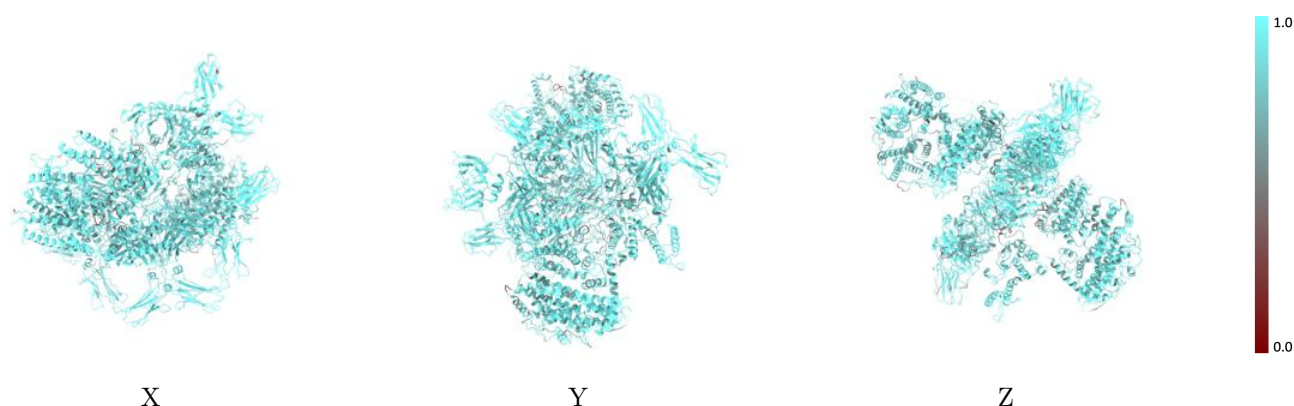
The images above show the 3D surface view of the map at the recommended contour level 0.00805 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



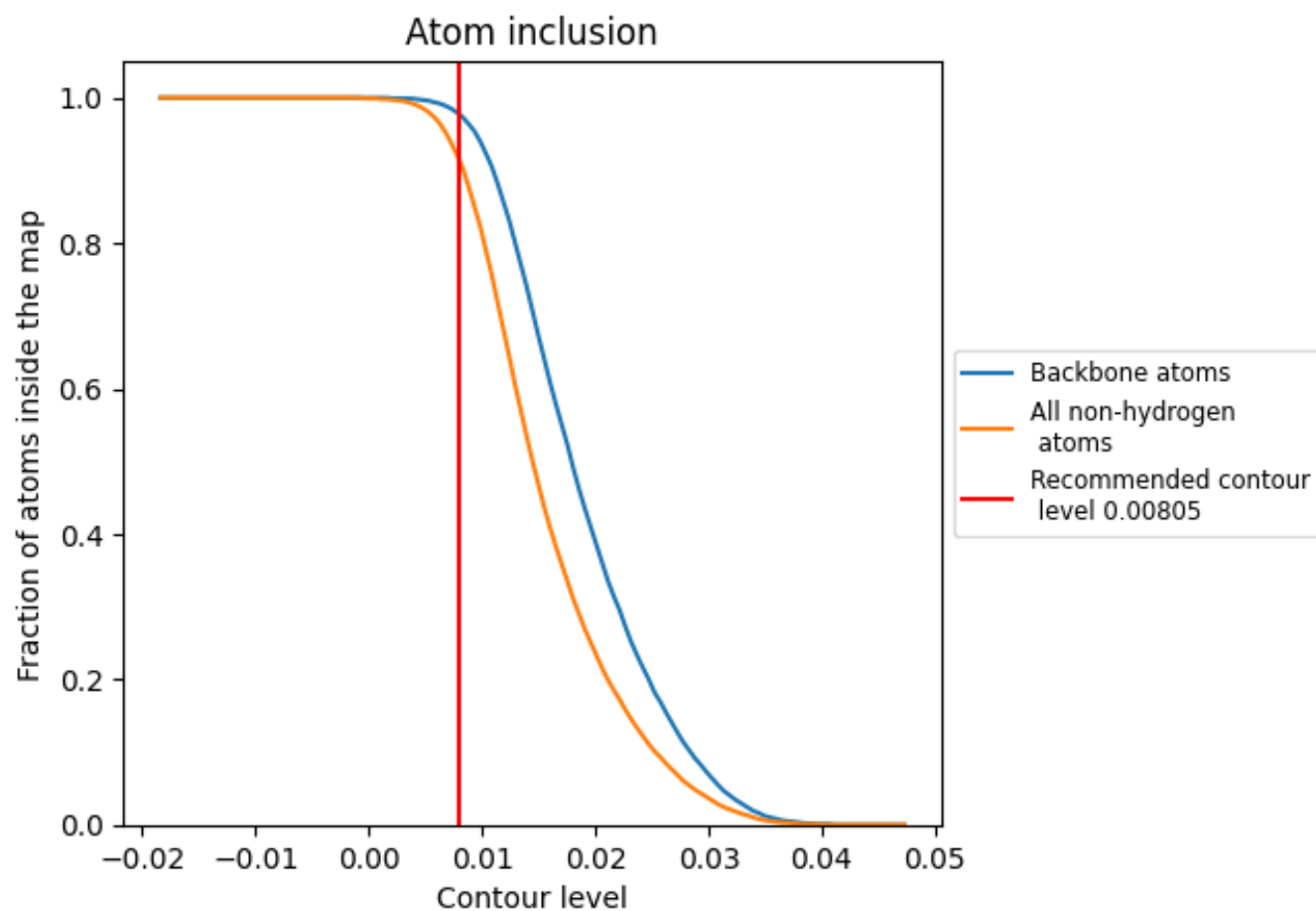
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00805).





























9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 91% 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 (0.00805) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9130	 0.3040
A	 0.9120	 0.3280
B	 0.9120	 0.3300
C	 0.9560	 0.3410
D	 0.9550	 0.3630
E	 0.9590	 0.3830
F	 0.9510	 0.3730
G	 0.9400	 0.3620
H	 0.9450	 0.3300
I	 0.8870	 0.2540
J	 0.7250	 0.2720
K	 0.9210	 0.3080
L	 0.9550	 0.3170
M	 0.9070	 0.2840

