



Full wwPDB EM Validation Report ⓘ

Aug 17, 2026 – 04:09 PM JST

PDB ID : 9X74 / pdb_00009x74
EMDB ID : EMD-66632
Title : Human GPR30 -Gq complex
Authors : Kaneda, S.; Oshima, H.S.; Akasaka, H.; Shihoya, W.; Nureki, O.
Deposited on : 2025-10-16
Resolution : 3.15 Å(reported)

This is a Full wwPDB EM Validation 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:

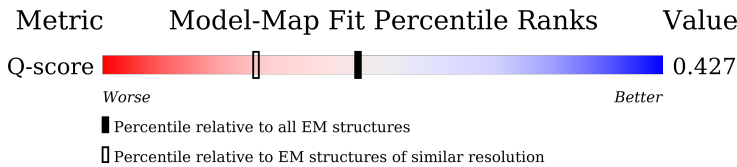
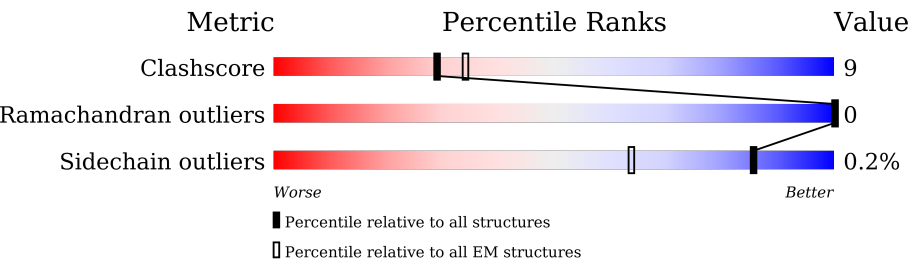
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.15 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	14486 (2.65 - 3.65)

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	B	374	10% 74% 16% 10%
2	G	68	44% 69% 6% 25%
3	A	258	9% 71% 13% 16%
4	R	850	26% 6% 68%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	S	260	75% 14% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8468 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 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	337	2473	1541	439	473	20	0	0

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P54311
B	-2	SER	-	expression tag	UNP P54311
B	-1	GLN	-	expression tag	UNP P54311
B	0	LEU	-	expression tag	UNP P54311
B	1	GLN	-	expression tag	UNP P54311
B	341	GLY	-	expression tag	UNP P54311
B	342	ALA	-	expression tag	UNP P54311
B	343	SER	-	expression tag	UNP P54311
B	344	GLY	-	expression tag	UNP P54311
B	345	GLY	-	expression tag	UNP P54311
B	346	GLY	-	expression tag	UNP P54311
B	347	SER	-	expression tag	UNP P54311
B	348	GLY	-	expression tag	UNP P54311
B	349	GLY	-	expression tag	UNP P54311
B	350	ASN	-	expression tag	UNP P54311
B	351	SER	-	expression tag	UNP P54311
B	352	GLY	-	expression tag	UNP P54311
B	353	SER	-	expression tag	UNP P54311
B	354	SER	-	expression tag	UNP P54311
B	355	GLY	-	expression tag	UNP P54311
B	356	GLY	-	expression tag	UNP P54311
B	357	SER	-	expression tag	UNP P54311
B	358	SER	-	expression tag	UNP P54311
B	359	GLY	-	expression tag	UNP P54311
B	360	VAL	-	expression tag	UNP P54311
B	361	SER	-	expression tag	UNP P54311
B	362	GLY	-	expression tag	UNP P54311

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	363	TRP	-	expression tag	UNP P54311
B	364	ARG	-	expression tag	UNP P54311
B	365	LEU	-	expression tag	UNP P54311
B	366	PHE	-	expression tag	UNP P54311
B	367	LYS	-	expression tag	UNP P54311
B	368	LYS	-	expression tag	UNP P54311
B	369	ILE	-	expression tag	UNP P54311
B	370	SER	-	expression tag	UNP P54311

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	51	Total	C	N	O	S	0	0
			350	221	60	67	2		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-2, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	218	Total	C	N	O	S	0	0
			1710	1086	302	315	7		

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	ALA	-	expression tag	UNP P04899
A	-10	ILE	-	expression tag	UNP P04899
A	-9	LEU	-	expression tag	UNP P04899
A	-8	GLY	-	expression tag	UNP P04899
A	-7	SER	-	expression tag	UNP P04899
A	-6	ALA	-	expression tag	UNP P04899
A	-5	GLY	-	expression tag	UNP P04899
A	-4	SER	-	expression tag	UNP P04899
A	-3	ALA	-	expression tag	UNP P04899
A	-2	GLY	-	expression tag	UNP P04899
A	-1	SER	-	expression tag	UNP P04899
A	0	ALA	-	expression tag	UNP P04899
A	3	SER	CYS	engineered mutation	UNP P04899
A	31	ARG	ALA	engineered mutation	UNP P04899
A	33	THR	GLU	engineered mutation	UNP P04899
A	34	LEU	VAL	engineered mutation	UNP P04899

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	ARG	LYS	engineered mutation	UNP P04899
A	42	ASP	GLY	engineered mutation	UNP P04899
A	43	ASN	GLU	engineered mutation	UNP P04899
A	54	ARG	LYS	engineered mutation	UNP P04899
A	56	LEU	ILE	engineered mutation	UNP P04899
A	58	GLY	-	linker	UNP P04899
A	59	GLY	-	linker	UNP P04899
A	60	SER	-	linker	UNP P04899
A	61	GLY	-	linker	UNP P04899
A	62	GLY	-	linker	UNP P04899
A	63	SER	-	linker	UNP P04899
A	64	GLY	-	linker	UNP P04899
A	65	GLY	-	linker	UNP P04899
A	111	ASP	ALA	engineered mutation	UNP P04896
A	114	ASP	SER	engineered mutation	UNP P04896
A	?	-	ASN	deletion	UNP P04896
A	?	-	MET	deletion	UNP P04896
A	?	-	VAL	deletion	UNP P04896
A	?	-	ILE	deletion	UNP P04896
A	?	-	ARG	deletion	UNP P04896
A	?	-	GLU	deletion	UNP P04896
A	?	-	ASP	deletion	UNP P04896
A	?	-	ASN	deletion	UNP P04896
A	?	-	GLN	deletion	UNP P04896
A	?	-	THR	deletion	UNP P04896
A	124	ASP	LEU	engineered mutation	UNP P04896
A	195	LYS	ASP	engineered mutation	UNP P04896
A	198	VAL	LEU	engineered mutation	UNP P04896
A	199	ASP	ARG	engineered mutation	UNP P04896
A	210	ILE	TYR	engineered mutation	UNP P04896
A	224	ALA	ILE	engineered mutation	UNP P04896
A	227	ILE	VAL	engineered mutation	UNP P04896
A	232	LYS	ARG	engineered mutation	UNP P04896
A	236	LEU	GLN	engineered mutation	UNP P04896
A	237	GLN	ARG	engineered mutation	UNP P04896
A	239	ASN	HIS	engineered mutation	UNP P04896
A	242	GLU	GLN	engineered mutation	UNP P04896
A	244	ASN	GLU	engineered mutation	UNP P04896
A	246	VAL	LEU	engineered mutation	UNP P04896

- Molecule 4 is a protein called G-protein coupled estrogen receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	271	Total	C	N	O	S	0	0
			2208	1463	374	356	15		

There are 476 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-22	MET	-	initiating methionine	UNP Q99527
R	-21	LYS	-	expression tag	UNP Q99527
R	-20	THR	-	expression tag	UNP Q99527
R	-19	ILE	-	expression tag	UNP Q99527
R	-18	ILE	-	expression tag	UNP Q99527
R	-17	ALA	-	expression tag	UNP Q99527
R	-16	LEU	-	expression tag	UNP Q99527
R	-15	SER	-	expression tag	UNP Q99527
R	-14	TYR	-	expression tag	UNP Q99527
R	-13	ILE	-	expression tag	UNP Q99527
R	-12	PHE	-	expression tag	UNP Q99527
R	-11	CYS	-	expression tag	UNP Q99527
R	-10	LEU	-	expression tag	UNP Q99527
R	-9	VAL	-	expression tag	UNP Q99527
R	-8	PHE	-	expression tag	UNP Q99527
R	-7	ALA	-	expression tag	UNP Q99527
R	-6	ASP	-	expression tag	UNP Q99527
R	-5	TYR	-	expression tag	UNP Q99527
R	-4	LYS	-	expression tag	UNP Q99527
R	-3	ASP	-	expression tag	UNP Q99527
R	-2	ASP	-	expression tag	UNP Q99527
R	-1	ASP	-	expression tag	UNP Q99527
R	0	ASP	-	expression tag	UNP Q99527
R	1	LYS	-	expression tag	UNP Q99527
R	376	GLY	-	expression tag	UNP Q99527
R	377	SER	-	expression tag	UNP Q99527
R	378	GLY	-	expression tag	UNP Q99527
R	379	GLY	-	expression tag	UNP Q99527
R	380	GLY	-	expression tag	UNP Q99527
R	381	GLY	-	expression tag	UNP Q99527
R	382	SER	-	expression tag	UNP Q99527
R	383	GLY	-	expression tag	UNP Q99527
R	384	GLY	-	expression tag	UNP Q99527
R	385	SER	-	expression tag	UNP Q99527
R	386	SER	-	expression tag	UNP Q99527
R	387	SER	-	expression tag	UNP Q99527
R	388	GLY	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	389	GLY	-	expression tag	UNP Q99527
R	390	VAL	-	expression tag	UNP Q99527
R	391	PHE	-	expression tag	UNP Q99527
R	392	THR	-	expression tag	UNP Q99527
R	393	LEU	-	expression tag	UNP Q99527
R	394	GLU	-	expression tag	UNP Q99527
R	395	ASP	-	expression tag	UNP Q99527
R	396	PHE	-	expression tag	UNP Q99527
R	397	VAL	-	expression tag	UNP Q99527
R	398	GLY	-	expression tag	UNP Q99527
R	399	ASP	-	expression tag	UNP Q99527
R	400	TRP	-	expression tag	UNP Q99527
R	401	GLU	-	expression tag	UNP Q99527
R	402	GLN	-	expression tag	UNP Q99527
R	403	THR	-	expression tag	UNP Q99527
R	404	ALA	-	expression tag	UNP Q99527
R	405	ALA	-	expression tag	UNP Q99527
R	406	TYR	-	expression tag	UNP Q99527
R	407	ASN	-	expression tag	UNP Q99527
R	408	LEU	-	expression tag	UNP Q99527
R	409	ASP	-	expression tag	UNP Q99527
R	410	GLN	-	expression tag	UNP Q99527
R	411	VAL	-	expression tag	UNP Q99527
R	412	LEU	-	expression tag	UNP Q99527
R	413	GLU	-	expression tag	UNP Q99527
R	414	GLN	-	expression tag	UNP Q99527
R	415	GLY	-	expression tag	UNP Q99527
R	416	GLY	-	expression tag	UNP Q99527
R	417	VAL	-	expression tag	UNP Q99527
R	418	SER	-	expression tag	UNP Q99527
R	419	SER	-	expression tag	UNP Q99527
R	420	LEU	-	expression tag	UNP Q99527
R	421	LEU	-	expression tag	UNP Q99527
R	422	GLN	-	expression tag	UNP Q99527
R	423	ASN	-	expression tag	UNP Q99527
R	424	LEU	-	expression tag	UNP Q99527
R	425	ALA	-	expression tag	UNP Q99527
R	426	VAL	-	expression tag	UNP Q99527
R	427	SER	-	expression tag	UNP Q99527
R	428	VAL	-	expression tag	UNP Q99527
R	429	THR	-	expression tag	UNP Q99527
R	430	PRO	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	431	ILE	-	expression tag	UNP Q99527
R	432	GLN	-	expression tag	UNP Q99527
R	433	ARG	-	expression tag	UNP Q99527
R	434	ILE	-	expression tag	UNP Q99527
R	435	VAL	-	expression tag	UNP Q99527
R	436	ARG	-	expression tag	UNP Q99527
R	437	SER	-	expression tag	UNP Q99527
R	438	GLY	-	expression tag	UNP Q99527
R	439	GLU	-	expression tag	UNP Q99527
R	440	ASN	-	expression tag	UNP Q99527
R	441	ALA	-	expression tag	UNP Q99527
R	442	LEU	-	expression tag	UNP Q99527
R	443	LYS	-	expression tag	UNP Q99527
R	444	ILE	-	expression tag	UNP Q99527
R	445	ASP	-	expression tag	UNP Q99527
R	446	ILE	-	expression tag	UNP Q99527
R	447	HIS	-	expression tag	UNP Q99527
R	448	VAL	-	expression tag	UNP Q99527
R	449	ILE	-	expression tag	UNP Q99527
R	450	ILE	-	expression tag	UNP Q99527
R	451	PRO	-	expression tag	UNP Q99527
R	452	TYR	-	expression tag	UNP Q99527
R	453	GLU	-	expression tag	UNP Q99527
R	454	GLY	-	expression tag	UNP Q99527
R	455	LEU	-	expression tag	UNP Q99527
R	456	SER	-	expression tag	UNP Q99527
R	457	ALA	-	expression tag	UNP Q99527
R	458	ASP	-	expression tag	UNP Q99527
R	459	GLN	-	expression tag	UNP Q99527
R	460	MET	-	expression tag	UNP Q99527
R	461	ALA	-	expression tag	UNP Q99527
R	462	GLN	-	expression tag	UNP Q99527
R	463	ILE	-	expression tag	UNP Q99527
R	464	GLU	-	expression tag	UNP Q99527
R	465	GLU	-	expression tag	UNP Q99527
R	466	VAL	-	expression tag	UNP Q99527
R	467	PHE	-	expression tag	UNP Q99527
R	468	LYS	-	expression tag	UNP Q99527
R	469	VAL	-	expression tag	UNP Q99527
R	470	VAL	-	expression tag	UNP Q99527
R	471	TYR	-	expression tag	UNP Q99527
R	472	PRO	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	473	VAL	-	expression tag	UNP Q99527
R	474	ASP	-	expression tag	UNP Q99527
R	475	ASP	-	expression tag	UNP Q99527
R	476	HIS	-	expression tag	UNP Q99527
R	477	HIS	-	expression tag	UNP Q99527
R	478	PHE	-	expression tag	UNP Q99527
R	479	LYS	-	expression tag	UNP Q99527
R	480	VAL	-	expression tag	UNP Q99527
R	481	ILE	-	expression tag	UNP Q99527
R	482	LEU	-	expression tag	UNP Q99527
R	483	PRO	-	expression tag	UNP Q99527
R	484	TYR	-	expression tag	UNP Q99527
R	485	GLY	-	expression tag	UNP Q99527
R	486	THR	-	expression tag	UNP Q99527
R	487	LEU	-	expression tag	UNP Q99527
R	488	VAL	-	expression tag	UNP Q99527
R	489	ILE	-	expression tag	UNP Q99527
R	490	ASP	-	expression tag	UNP Q99527
R	491	GLY	-	expression tag	UNP Q99527
R	492	VAL	-	expression tag	UNP Q99527
R	493	THR	-	expression tag	UNP Q99527
R	494	PRO	-	expression tag	UNP Q99527
R	495	ASN	-	expression tag	UNP Q99527
R	496	MET	-	expression tag	UNP Q99527
R	497	LEU	-	expression tag	UNP Q99527
R	498	ASN	-	expression tag	UNP Q99527
R	499	TYR	-	expression tag	UNP Q99527
R	500	PHE	-	expression tag	UNP Q99527
R	501	GLY	-	expression tag	UNP Q99527
R	502	ARG	-	expression tag	UNP Q99527
R	503	PRO	-	expression tag	UNP Q99527
R	504	TYR	-	expression tag	UNP Q99527
R	505	GLU	-	expression tag	UNP Q99527
R	506	GLY	-	expression tag	UNP Q99527
R	507	ILE	-	expression tag	UNP Q99527
R	508	ALA	-	expression tag	UNP Q99527
R	509	VAL	-	expression tag	UNP Q99527
R	510	PHE	-	expression tag	UNP Q99527
R	511	ASP	-	expression tag	UNP Q99527
R	512	GLY	-	expression tag	UNP Q99527
R	513	LYS	-	expression tag	UNP Q99527
R	514	LYS	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	515	ILE	-	expression tag	UNP Q99527
R	516	THR	-	expression tag	UNP Q99527
R	517	VAL	-	expression tag	UNP Q99527
R	518	THR	-	expression tag	UNP Q99527
R	519	GLY	-	expression tag	UNP Q99527
R	520	THR	-	expression tag	UNP Q99527
R	521	LEU	-	expression tag	UNP Q99527
R	522	TRP	-	expression tag	UNP Q99527
R	523	ASN	-	expression tag	UNP Q99527
R	524	GLY	-	expression tag	UNP Q99527
R	525	ASN	-	expression tag	UNP Q99527
R	526	LYS	-	expression tag	UNP Q99527
R	527	ILE	-	expression tag	UNP Q99527
R	528	ILE	-	expression tag	UNP Q99527
R	529	ASP	-	expression tag	UNP Q99527
R	530	GLU	-	expression tag	UNP Q99527
R	531	ARG	-	expression tag	UNP Q99527
R	532	LEU	-	expression tag	UNP Q99527
R	533	ILE	-	expression tag	UNP Q99527
R	534	THR	-	expression tag	UNP Q99527
R	535	PRO	-	expression tag	UNP Q99527
R	536	ASP	-	expression tag	UNP Q99527
R	537	GLY	-	expression tag	UNP Q99527
R	538	SER	-	expression tag	UNP Q99527
R	539	MET	-	expression tag	UNP Q99527
R	540	LEU	-	expression tag	UNP Q99527
R	541	PHE	-	expression tag	UNP Q99527
R	542	ARG	-	expression tag	UNP Q99527
R	543	VAL	-	expression tag	UNP Q99527
R	544	THR	-	expression tag	UNP Q99527
R	545	ILE	-	expression tag	UNP Q99527
R	546	ASN	-	expression tag	UNP Q99527
R	547	SER	-	expression tag	UNP Q99527
R	548	GLY	-	expression tag	UNP Q99527
R	549	GLY	-	expression tag	UNP Q99527
R	550	SER	-	expression tag	UNP Q99527
R	551	GLY	-	expression tag	UNP Q99527
R	552	GLY	-	expression tag	UNP Q99527
R	553	GLY	-	expression tag	UNP Q99527
R	554	GLY	-	expression tag	UNP Q99527
R	555	SER	-	expression tag	UNP Q99527
R	556	GLY	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	557	GLY	-	expression tag	UNP Q99527
R	558	SER	-	expression tag	UNP Q99527
R	559	SER	-	expression tag	UNP Q99527
R	560	SER	-	expression tag	UNP Q99527
R	561	GLY	-	expression tag	UNP Q99527
R	562	GLY	-	expression tag	UNP Q99527
R	563	LEU	-	expression tag	UNP Q99527
R	564	GLU	-	expression tag	UNP Q99527
R	565	VAL	-	expression tag	UNP Q99527
R	566	LEU	-	expression tag	UNP Q99527
R	567	PHE	-	expression tag	UNP Q99527
R	568	GLN	-	expression tag	UNP Q99527
R	569	GLY	-	expression tag	UNP Q99527
R	570	PRO	-	expression tag	UNP Q99527
R	571	GLY	-	expression tag	UNP Q99527
R	572	SER	-	expression tag	UNP Q99527
R	573	ALA	-	expression tag	UNP Q99527
R	574	ALA	-	expression tag	UNP Q99527
R	575	ALA	-	expression tag	UNP Q99527
R	576	ALA	-	expression tag	UNP Q99527
R	577	VAL	-	expression tag	UNP Q99527
R	578	SER	-	expression tag	UNP Q99527
R	579	LYS	-	expression tag	UNP Q99527
R	580	GLY	-	expression tag	UNP Q99527
R	581	GLU	-	expression tag	UNP Q99527
R	582	GLU	-	expression tag	UNP Q99527
R	583	LEU	-	expression tag	UNP Q99527
R	584	PHE	-	expression tag	UNP Q99527
R	585	THR	-	expression tag	UNP Q99527
R	586	GLY	-	expression tag	UNP Q99527
R	587	VAL	-	expression tag	UNP Q99527
R	588	VAL	-	expression tag	UNP Q99527
R	589	PRO	-	expression tag	UNP Q99527
R	590	ILE	-	expression tag	UNP Q99527
R	591	LEU	-	expression tag	UNP Q99527
R	592	VAL	-	expression tag	UNP Q99527
R	593	GLU	-	expression tag	UNP Q99527
R	594	LEU	-	expression tag	UNP Q99527
R	595	ASP	-	expression tag	UNP Q99527
R	596	GLY	-	expression tag	UNP Q99527
R	597	ASP	-	expression tag	UNP Q99527
R	598	VAL	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	599	ASN	-	expression tag	UNP Q99527
R	600	GLY	-	expression tag	UNP Q99527
R	601	HIS	-	expression tag	UNP Q99527
R	602	LYS	-	expression tag	UNP Q99527
R	603	PHE	-	expression tag	UNP Q99527
R	604	SER	-	expression tag	UNP Q99527
R	605	VAL	-	expression tag	UNP Q99527
R	606	SER	-	expression tag	UNP Q99527
R	607	GLY	-	expression tag	UNP Q99527
R	608	GLU	-	expression tag	UNP Q99527
R	609	GLY	-	expression tag	UNP Q99527
R	610	GLU	-	expression tag	UNP Q99527
R	611	GLY	-	expression tag	UNP Q99527
R	612	ASP	-	expression tag	UNP Q99527
R	613	ALA	-	expression tag	UNP Q99527
R	614	THR	-	expression tag	UNP Q99527
R	615	TYR	-	expression tag	UNP Q99527
R	616	GLY	-	expression tag	UNP Q99527
R	617	LYS	-	expression tag	UNP Q99527
R	618	LEU	-	expression tag	UNP Q99527
R	619	THR	-	expression tag	UNP Q99527
R	620	LEU	-	expression tag	UNP Q99527
R	621	LYS	-	expression tag	UNP Q99527
R	622	PHE	-	expression tag	UNP Q99527
R	623	ILE	-	expression tag	UNP Q99527
R	624	CYS	-	expression tag	UNP Q99527
R	625	THR	-	expression tag	UNP Q99527
R	626	THR	-	expression tag	UNP Q99527
R	627	GLY	-	expression tag	UNP Q99527
R	628	LYS	-	expression tag	UNP Q99527
R	629	LEU	-	expression tag	UNP Q99527
R	630	PRO	-	expression tag	UNP Q99527
R	631	VAL	-	expression tag	UNP Q99527
R	632	PRO	-	expression tag	UNP Q99527
R	633	TRP	-	expression tag	UNP Q99527
R	634	PRO	-	expression tag	UNP Q99527
R	635	THR	-	expression tag	UNP Q99527
R	636	LEU	-	expression tag	UNP Q99527
R	637	VAL	-	expression tag	UNP Q99527
R	638	THR	-	expression tag	UNP Q99527
R	639	THR	-	expression tag	UNP Q99527
R	640	LEU	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	641	THR	-	expression tag	UNP Q99527
R	642	TYR	-	expression tag	UNP Q99527
R	643	GLY	-	expression tag	UNP Q99527
R	644	VAL	-	expression tag	UNP Q99527
R	645	GLN	-	expression tag	UNP Q99527
R	646	CYS	-	expression tag	UNP Q99527
R	647	PHE	-	expression tag	UNP Q99527
R	648	SER	-	expression tag	UNP Q99527
R	649	ARG	-	expression tag	UNP Q99527
R	650	TYR	-	expression tag	UNP Q99527
R	651	PRO	-	expression tag	UNP Q99527
R	652	ASP	-	expression tag	UNP Q99527
R	653	HIS	-	expression tag	UNP Q99527
R	654	MET	-	expression tag	UNP Q99527
R	655	LYS	-	expression tag	UNP Q99527
R	656	GLN	-	expression tag	UNP Q99527
R	657	HIS	-	expression tag	UNP Q99527
R	658	ASP	-	expression tag	UNP Q99527
R	659	PHE	-	expression tag	UNP Q99527
R	660	PHE	-	expression tag	UNP Q99527
R	661	LYS	-	expression tag	UNP Q99527
R	662	SER	-	expression tag	UNP Q99527
R	663	ALA	-	expression tag	UNP Q99527
R	664	MET	-	expression tag	UNP Q99527
R	665	PRO	-	expression tag	UNP Q99527
R	666	GLU	-	expression tag	UNP Q99527
R	667	GLY	-	expression tag	UNP Q99527
R	668	TYR	-	expression tag	UNP Q99527
R	669	VAL	-	expression tag	UNP Q99527
R	670	GLN	-	expression tag	UNP Q99527
R	671	GLU	-	expression tag	UNP Q99527
R	672	ARG	-	expression tag	UNP Q99527
R	673	THR	-	expression tag	UNP Q99527
R	674	ILE	-	expression tag	UNP Q99527
R	675	PHE	-	expression tag	UNP Q99527
R	676	PHE	-	expression tag	UNP Q99527
R	677	LYS	-	expression tag	UNP Q99527
R	678	ASP	-	expression tag	UNP Q99527
R	679	ASP	-	expression tag	UNP Q99527
R	680	GLY	-	expression tag	UNP Q99527
R	681	ASN	-	expression tag	UNP Q99527
R	682	TYR	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	683	LYS	-	expression tag	UNP Q99527
R	684	THR	-	expression tag	UNP Q99527
R	685	ARG	-	expression tag	UNP Q99527
R	686	ALA	-	expression tag	UNP Q99527
R	687	GLU	-	expression tag	UNP Q99527
R	688	VAL	-	expression tag	UNP Q99527
R	689	LYS	-	expression tag	UNP Q99527
R	690	PHE	-	expression tag	UNP Q99527
R	691	GLU	-	expression tag	UNP Q99527
R	692	GLY	-	expression tag	UNP Q99527
R	693	ASP	-	expression tag	UNP Q99527
R	694	THR	-	expression tag	UNP Q99527
R	695	LEU	-	expression tag	UNP Q99527
R	696	VAL	-	expression tag	UNP Q99527
R	697	ASN	-	expression tag	UNP Q99527
R	698	ARG	-	expression tag	UNP Q99527
R	699	ILE	-	expression tag	UNP Q99527
R	700	GLU	-	expression tag	UNP Q99527
R	701	LEU	-	expression tag	UNP Q99527
R	702	LYS	-	expression tag	UNP Q99527
R	703	GLY	-	expression tag	UNP Q99527
R	704	ILE	-	expression tag	UNP Q99527
R	705	ASP	-	expression tag	UNP Q99527
R	706	PHE	-	expression tag	UNP Q99527
R	707	LYS	-	expression tag	UNP Q99527
R	708	GLU	-	expression tag	UNP Q99527
R	709	ASP	-	expression tag	UNP Q99527
R	710	GLY	-	expression tag	UNP Q99527
R	711	ASN	-	expression tag	UNP Q99527
R	712	ILE	-	expression tag	UNP Q99527
R	713	LEU	-	expression tag	UNP Q99527
R	714	GLY	-	expression tag	UNP Q99527
R	715	HIS	-	expression tag	UNP Q99527
R	716	LYS	-	expression tag	UNP Q99527
R	717	LEU	-	expression tag	UNP Q99527
R	718	GLU	-	expression tag	UNP Q99527
R	719	TYR	-	expression tag	UNP Q99527
R	720	ASN	-	expression tag	UNP Q99527
R	721	TYR	-	expression tag	UNP Q99527
R	722	ASN	-	expression tag	UNP Q99527
R	723	SER	-	expression tag	UNP Q99527
R	724	HIS	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	725	ASN	-	expression tag	UNP Q99527
R	726	VAL	-	expression tag	UNP Q99527
R	727	TYR	-	expression tag	UNP Q99527
R	728	ILE	-	expression tag	UNP Q99527
R	729	MET	-	expression tag	UNP Q99527
R	730	ALA	-	expression tag	UNP Q99527
R	731	ASP	-	expression tag	UNP Q99527
R	732	LYS	-	expression tag	UNP Q99527
R	733	GLN	-	expression tag	UNP Q99527
R	734	LYS	-	expression tag	UNP Q99527
R	735	ASN	-	expression tag	UNP Q99527
R	736	GLY	-	expression tag	UNP Q99527
R	737	ILE	-	expression tag	UNP Q99527
R	738	LYS	-	expression tag	UNP Q99527
R	739	VAL	-	expression tag	UNP Q99527
R	740	ASN	-	expression tag	UNP Q99527
R	741	PHE	-	expression tag	UNP Q99527
R	742	LYS	-	expression tag	UNP Q99527
R	743	ILE	-	expression tag	UNP Q99527
R	744	ARG	-	expression tag	UNP Q99527
R	745	HIS	-	expression tag	UNP Q99527
R	746	ASN	-	expression tag	UNP Q99527
R	747	ILE	-	expression tag	UNP Q99527
R	748	GLU	-	expression tag	UNP Q99527
R	749	ASP	-	expression tag	UNP Q99527
R	750	GLY	-	expression tag	UNP Q99527
R	751	SER	-	expression tag	UNP Q99527
R	752	VAL	-	expression tag	UNP Q99527
R	753	GLN	-	expression tag	UNP Q99527
R	754	LEU	-	expression tag	UNP Q99527
R	755	ALA	-	expression tag	UNP Q99527
R	756	ASP	-	expression tag	UNP Q99527
R	757	HIS	-	expression tag	UNP Q99527
R	758	TYR	-	expression tag	UNP Q99527
R	759	GLN	-	expression tag	UNP Q99527
R	760	GLN	-	expression tag	UNP Q99527
R	761	ASN	-	expression tag	UNP Q99527
R	762	THR	-	expression tag	UNP Q99527
R	763	PRO	-	expression tag	UNP Q99527
R	764	ILE	-	expression tag	UNP Q99527
R	765	GLY	-	expression tag	UNP Q99527
R	766	ASP	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	767	GLY	-	expression tag	UNP Q99527
R	768	PRO	-	expression tag	UNP Q99527
R	769	VAL	-	expression tag	UNP Q99527
R	770	LEU	-	expression tag	UNP Q99527
R	771	LEU	-	expression tag	UNP Q99527
R	772	PRO	-	expression tag	UNP Q99527
R	773	ASP	-	expression tag	UNP Q99527
R	774	ASN	-	expression tag	UNP Q99527
R	775	HIS	-	expression tag	UNP Q99527
R	776	TYR	-	expression tag	UNP Q99527
R	777	LEU	-	expression tag	UNP Q99527
R	778	SER	-	expression tag	UNP Q99527
R	779	THR	-	expression tag	UNP Q99527
R	780	GLN	-	expression tag	UNP Q99527
R	781	SER	-	expression tag	UNP Q99527
R	782	LYS	-	expression tag	UNP Q99527
R	783	LEU	-	expression tag	UNP Q99527
R	784	SER	-	expression tag	UNP Q99527
R	785	LYS	-	expression tag	UNP Q99527
R	786	ASP	-	expression tag	UNP Q99527
R	787	PRO	-	expression tag	UNP Q99527
R	788	ASN	-	expression tag	UNP Q99527
R	789	GLU	-	expression tag	UNP Q99527
R	790	LYS	-	expression tag	UNP Q99527
R	791	ARG	-	expression tag	UNP Q99527
R	792	ASP	-	expression tag	UNP Q99527
R	793	HIS	-	expression tag	UNP Q99527
R	794	MET	-	expression tag	UNP Q99527
R	795	VAL	-	expression tag	UNP Q99527
R	796	LEU	-	expression tag	UNP Q99527
R	797	LEU	-	expression tag	UNP Q99527
R	798	GLU	-	expression tag	UNP Q99527
R	799	PHE	-	expression tag	UNP Q99527
R	800	VAL	-	expression tag	UNP Q99527
R	801	THR	-	expression tag	UNP Q99527
R	802	ALA	-	expression tag	UNP Q99527
R	803	ALA	-	expression tag	UNP Q99527
R	804	GLY	-	expression tag	UNP Q99527
R	805	ILE	-	expression tag	UNP Q99527
R	806	THR	-	expression tag	UNP Q99527
R	807	LEU	-	expression tag	UNP Q99527
R	808	GLY	-	expression tag	UNP Q99527

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	809	MET	-	expression tag	UNP Q99527
R	810	ASP	-	expression tag	UNP Q99527
R	811	GLU	-	expression tag	UNP Q99527
R	812	LEU	-	expression tag	UNP Q99527
R	813	TYR	-	expression tag	UNP Q99527
R	814	LYS	-	expression tag	UNP Q99527
R	815	SER	-	expression tag	UNP Q99527
R	816	GLY	-	expression tag	UNP Q99527
R	817	LEU	-	expression tag	UNP Q99527
R	818	ARG	-	expression tag	UNP Q99527
R	819	SER	-	expression tag	UNP Q99527
R	820	HIS	-	expression tag	UNP Q99527
R	821	HIS	-	expression tag	UNP Q99527
R	822	HIS	-	expression tag	UNP Q99527
R	823	HIS	-	expression tag	UNP Q99527
R	824	HIS	-	expression tag	UNP Q99527
R	825	HIS	-	expression tag	UNP Q99527
R	826	HIS	-	expression tag	UNP Q99527
R	827	HIS	-	expression tag	UNP Q99527

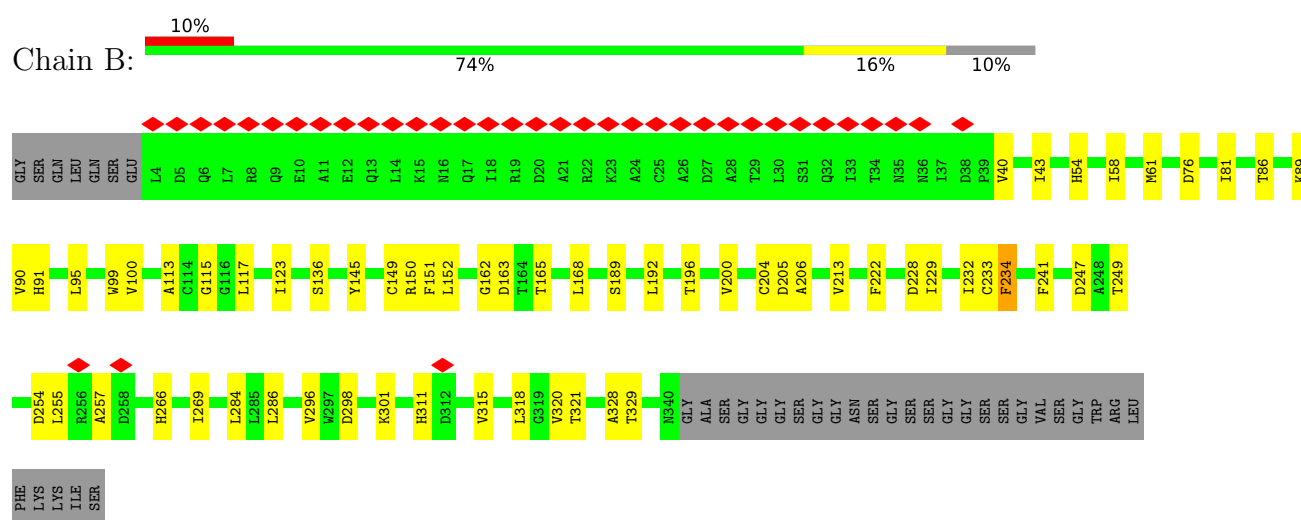
- Molecule 5 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	231	Total	C	N	O	S	0	0
			1727	1099	289	330	9		

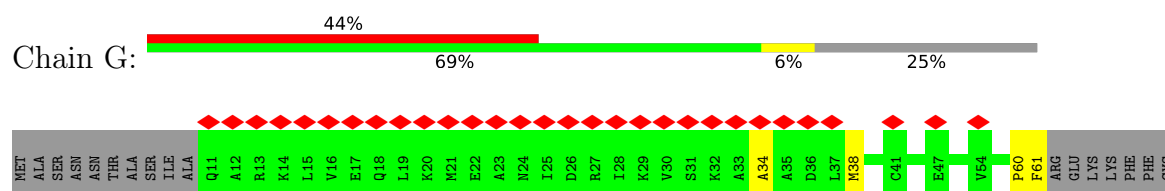
3 Residue-property plots

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.

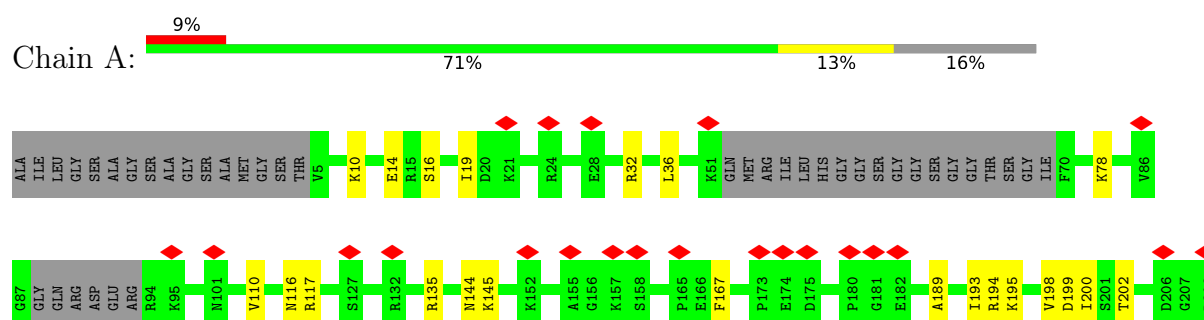
- Molecule 1: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



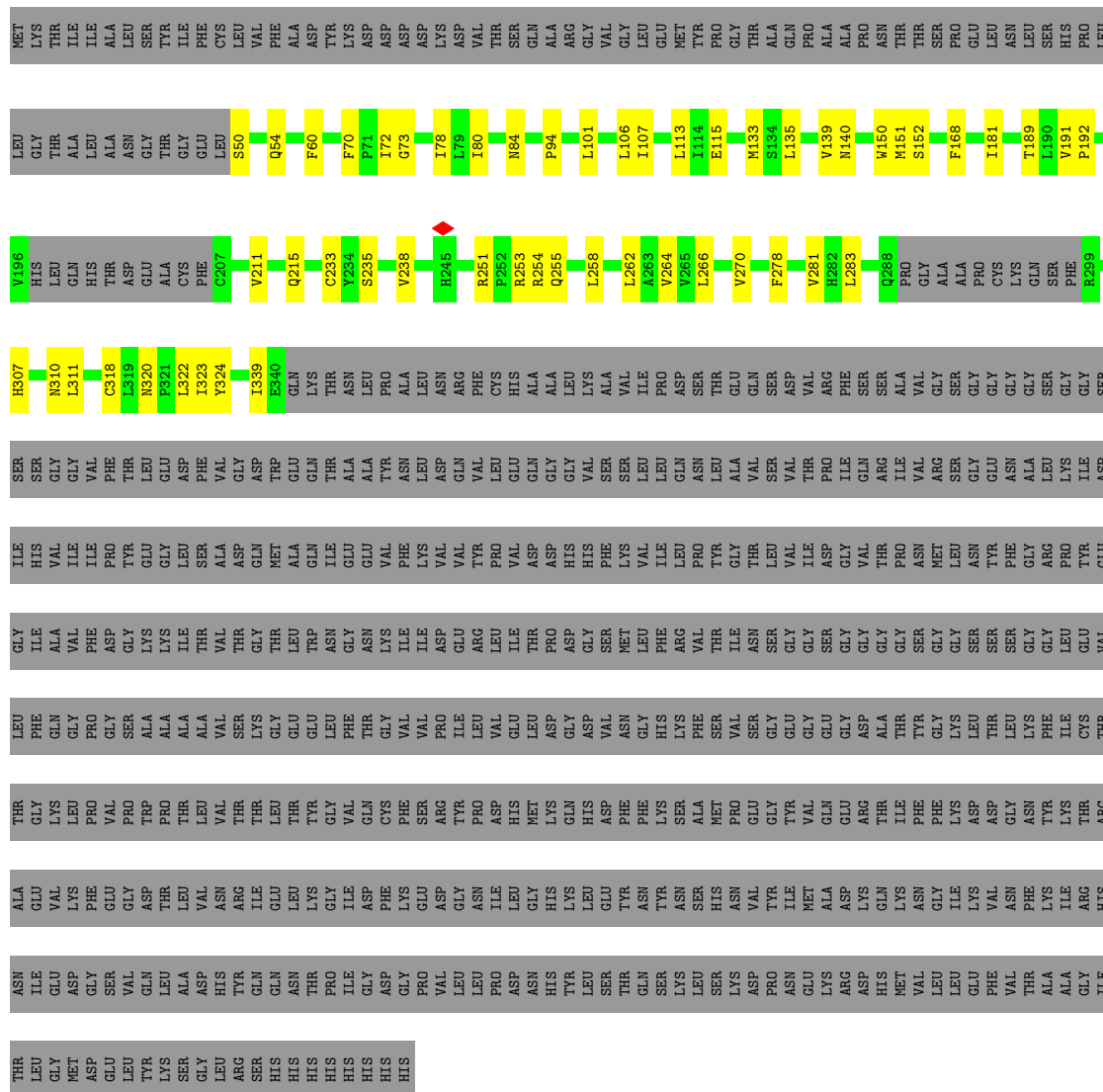
- Molecule 3: Guanine nucleotide-binding protein G(i) subunit alpha-2, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short





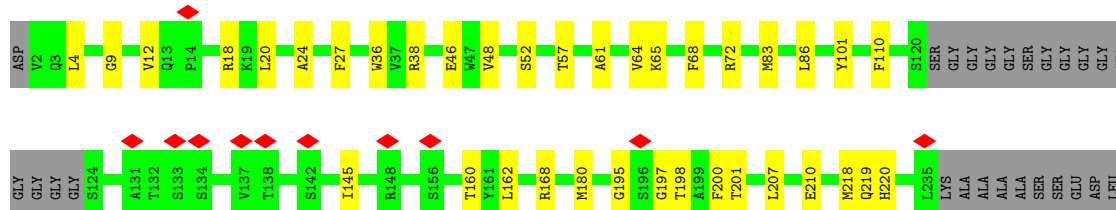
• Molecule 4: G-protein coupled estrogen receptor 1

Chain R: 26% 6% 68%



• Molecule 5: scFv16

Chain S: 75% 14% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	522404	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 ($e^-/\text{\AA}^2$)	50.66	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	56.088	Depositor
Minimum map value	-36.793	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.44	Depositor
Map size (Å)	232.0, 232.0, 232.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	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	B	0.13	0/2520	0.31	0/3432
2	G	0.13	0/356	0.25	0/488
3	A	0.12	0/1741	0.27	0/2354
4	R	0.15	0/2264	0.32	0/3074
5	S	0.12	0/1771	0.30	0/2408
All	All	0.13	0/8652	0.30	0/11756

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	B	2473	0	2303	68	0
2	G	350	0	315	2	0
3	A	1710	0	1649	30	0
4	R	2208	0	2268	37	0
5	S	1727	0	1621	26	0
All	All	8468	0	8156	155	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 9.

All (155) 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:241:PHE:CE2	1:B:255:LEU:HD21	1.69	1.28
1:B:241:PHE:HE2	1:B:255:LEU:CD2	1.63	1.10
1:B:241:PHE:CE2	1:B:255:LEU:CD2	2.37	1.08
1:B:241:PHE:CD2	1:B:255:LEU:HD21	1.91	1.04
1:B:318:LEU:HD13	1:B:329:THR:HG22	1.40	1.00
1:B:189:SER:OG	1:B:232:ILE:HG22	1.69	0.91
1:B:318:LEU:CD1	1:B:329:THR:HG22	2.01	0.90
3:A:144:ASN:ND2	3:A:145:LYS:HD3	1.90	0.87
1:B:189:SER:CB	1:B:232:ILE:HG22	2.06	0.85
1:B:222:PHE:CE2	1:B:241:PHE:HZ	1.97	0.83
1:B:200:VAL:HG11	1:B:241:PHE:CD2	2.20	0.76
1:B:222:PHE:CE2	1:B:241:PHE:CZ	2.75	0.74
1:B:189:SER:OG	1:B:232:ILE:CG2	2.35	0.74
1:B:189:SER:HB2	1:B:232:ILE:HG22	1.71	0.73
1:B:222:PHE:HE2	1:B:241:PHE:CZ	2.07	0.73
3:A:144:ASN:ND2	3:A:145:LYS:CD	2.51	0.72
1:B:298:ASP:OD2	1:B:301:LYS:HG3	1.92	0.69
5:S:38:ARG:O	5:S:46:GLU:N	2.27	0.67
3:A:135:ARG:O	3:A:209:HIS:ND1	2.25	0.66
5:S:145:ILE:O	5:S:201:THR:OG1	2.13	0.65
1:B:163:ASP:OD1	1:B:165:THR:OG1	2.13	0.64
1:B:241:PHE:HE2	1:B:255:LEU:HD22	1.58	0.63
4:R:253:ARG:O	4:R:253:ARG:HD3	2.00	0.62
4:R:50:SER:O	4:R:54:GLN:N	2.32	0.62
4:R:139:VAL:HG23	4:R:189:THR:HG21	1.82	0.61
1:B:117:LEU:HD23	1:B:145:TYR:HB2	1.84	0.60
4:R:253:ARG:NE	4:R:253:ARG:HA	2.17	0.59
1:B:150:ARG:HB2	1:B:192:LEU:HD13	1.85	0.59
1:B:95:LEU:HD13	1:B:100:VAL:HG11	1.85	0.58
3:A:237:GLN:OE1	4:R:254:ARG:NH2	2.37	0.58
1:B:247:ASP:HB2	1:B:249:THR:HG22	1.86	0.57
1:B:200:VAL:HG23	1:B:232:ILE:CD1	2.35	0.57
4:R:107:ILE:HD13	4:R:140:ASN:HD21	1.68	0.57
1:B:189:SER:HG	1:B:232:ILE:HG22	1.69	0.57
1:B:81:ILE:HD12	1:B:91:HIS:HB2	1.87	0.57
1:B:145:TYR:O	1:B:162:GLY:N	2.38	0.56
1:B:168:LEU:HD22	1:B:213:VAL:CG1	2.35	0.56
5:S:198:THR:O	5:S:198:THR:HG22	2.05	0.56
5:S:38:ARG:N	5:S:46:GLU:O	2.37	0.56
1:B:123:ILE:O	1:B:136:SER:N	2.38	0.55
1:B:123:ILE:HG23	1:B:151:PHE:HZ	1.71	0.55
2:G:34:ALA:O	2:G:38:MET:HG3	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:VAL:HG12	1:B:115:GLY:O	2.07	0.54
4:R:133:MET:HA	4:R:133:MET:HE2	1.87	0.54
1:B:40:VAL:HG11	1:B:43:ILE:HD11	1.90	0.54
1:B:89:LYS:O	1:B:89:LYS:HG3	2.08	0.54
5:S:64:VAL:HG21	5:S:68:PHE:CE2	2.42	0.54
3:A:231:CYS:O	3:A:235:ILE:HG12	2.08	0.54
3:A:32:ARG:NH2	3:A:78:LYS:O	2.36	0.53
1:B:254:ASP:OD2	1:B:257:ALA:N	2.37	0.53
1:B:89:LYS:HG2	3:A:19:ILE:HG23	1.90	0.53
1:B:205:ASP:O	1:B:205:ASP:OD1	2.26	0.52
4:R:135:LEU:O	4:R:139:VAL:HG23	2.09	0.52
1:B:86:THR:O	3:A:16:SER:HB2	2.09	0.52
1:B:233:CYS:SG	1:B:234:PHE:N	2.81	0.52
3:A:240:LEU:HB3	3:A:246:VAL:HG12	1.91	0.52
1:B:89:LYS:HG2	3:A:19:ILE:HD12	1.90	0.52
3:A:14:GLU:OE2	5:S:57:THR:OG1	2.19	0.52
3:A:189:ALA:O	3:A:193:ILE:HG13	2.11	0.51
4:R:78:ILE:HG13	4:R:106:LEU:HD11	1.91	0.51
4:R:152:SER:OG	4:R:233:CYS:HB2	2.11	0.51
1:B:152:LEU:HD23	1:B:192:LEU:HD23	1.93	0.50
1:B:286:LEU:HD22	1:B:296:VAL:HG22	1.94	0.50
4:R:115:GLU:OE2	4:R:310:ASN:ND2	2.44	0.50
4:R:339:ILE:HG22	4:R:339:ILE:O	2.12	0.50
5:S:61:ALA:O	5:S:65:LYS:N	2.44	0.50
1:B:168:LEU:HD22	1:B:213:VAL:HG13	1.94	0.50
4:R:101:LEU:HD22	4:R:151:MET:CE	2.42	0.49
4:R:320:ASN:O	4:R:323:ILE:O	2.30	0.49
3:A:144:ASN:CG	3:A:145:LYS:HD2	2.37	0.49
1:B:222:PHE:CD2	1:B:241:PHE:HZ	2.30	0.49
4:R:72:ILE:HD13	4:R:322:LEU:HD11	1.94	0.49
4:R:255:GLN:HA	4:R:258:LEU:HD12	1.94	0.49
3:A:198:VAL:O	3:A:202:THR:N	2.43	0.49
3:A:245:LEU:O	3:A:246:VAL:HB	2.12	0.49
1:B:200:VAL:HG23	1:B:232:ILE:HD11	1.93	0.48
1:B:150:ARG:CB	1:B:192:LEU:HD13	2.43	0.48
5:S:20:LEU:HD13	5:S:83:MET:CE	2.44	0.48
3:A:10:LYS:O	3:A:14:GLU:HG3	2.13	0.48
5:S:160:THR:HG21	5:S:180:MET:HE3	1.94	0.48
1:B:40:VAL:HG23	1:B:298:ASP:OD1	2.14	0.48
1:B:76:ASP:N	1:B:76:ASP:OD1	2.37	0.48
5:S:218:MET:HE3	5:S:219:GLN:O	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:TRP:CG	1:B:117:LEU:HD12	2.49	0.47
3:A:144:ASN:ND2	3:A:145:LYS:HD2	2.29	0.47
5:S:12:VAL:HG11	5:S:86:LEU:HD12	1.97	0.47
1:B:266:HIS:CB	1:B:269:ILE:HD12	2.45	0.47
1:B:204:CYS:HA	1:B:228:ASP:HA	1.96	0.47
5:S:180:MET:HE2	5:S:195:GLY:O	2.15	0.47
1:B:152:LEU:HD22	1:B:196:THR:HB	1.97	0.46
3:A:195:LYS:HA	3:A:198:VAL:HG22	1.98	0.46
4:R:323:ILE:HG22	4:R:324:TYR:N	2.29	0.46
1:B:200:VAL:CG2	1:B:232:ILE:HD11	2.46	0.46
4:R:191:VAL:N	4:R:192:PRO:HD2	2.30	0.46
1:B:43:ILE:HD13	1:B:284:LEU:HD13	1.98	0.46
3:A:110:VAL:O	3:A:144:ASN:N	2.49	0.45
4:R:238:VAL:HG23	4:R:258:LEU:HD23	1.97	0.45
1:B:286:LEU:CB	1:B:318:LEU:HD21	2.47	0.45
1:B:315:VAL:O	1:B:315:VAL:HG23	2.17	0.45
1:B:318:LEU:HD12	1:B:328:ALA:O	2.16	0.45
1:B:205:ASP:O	1:B:206:ALA:HB3	2.17	0.45
5:S:12:VAL:HG11	5:S:86:LEU:CD1	2.47	0.45
3:A:199:ASP:OD1	3:A:200:ILE:N	2.48	0.45
4:R:266:LEU:O	4:R:270:VAL:HG22	2.16	0.44
1:B:149:CYS:O	1:B:150:ARG:NH1	2.49	0.44
1:B:241:PHE:HD2	1:B:255:LEU:HD21	1.69	0.44
4:R:211:VAL:HG23	4:R:211:VAL:O	2.17	0.44
3:A:145:LYS:HD2	3:A:145:LYS:N	2.32	0.44
4:R:70:PHE:CZ	4:R:113:LEU:HD11	2.52	0.44
3:A:210:ILE:HG22	3:A:211:CYS:N	2.33	0.44
5:S:9:GLY:O	5:S:18:ARG:NH1	2.51	0.43
1:B:113:ALA:HB2	1:B:151:PHE:CE1	2.53	0.43
1:B:81:ILE:O	1:B:90:VAL:N	2.51	0.43
5:S:197:GLY:O	5:S:198:THR:HB	2.18	0.43
4:R:101:LEU:HD22	4:R:151:MET:HE1	1.99	0.43
4:R:60:PHE:CD1	4:R:60:PHE:C	2.96	0.43
5:S:168:ARG:NE	5:S:210:GLU:O	2.46	0.43
5:S:52:SER:O	5:S:72:ARG:NH2	2.51	0.43
4:R:339:ILE:O	4:R:339:ILE:CG2	2.67	0.43
5:S:20:LEU:HD13	5:S:83:MET:HE2	2.01	0.43
5:S:162:LEU:O	5:S:180:MET:N	2.52	0.43
1:B:286:LEU:HB3	1:B:318:LEU:HD21	2.00	0.42
3:A:236:LEU:HD12	3:A:236:LEU:O	2.19	0.42
1:B:61:MET:HE3	1:B:328:ALA:HB3	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:194:ARG:O	3:A:198:VAL:HG22	2.19	0.42
4:R:73:GLY:HA3	4:R:318:CYS:HA	2.02	0.42
4:R:191:VAL:HG12	4:R:192:PRO:HD3	2.02	0.42
4:R:215:GLN:HB3	4:R:283:LEU:HD11	2.01	0.42
4:R:80:ILE:O	4:R:84:ASN:ND2	2.36	0.42
5:S:4:LEU:HD12	5:S:110:PHE:HD2	1.83	0.42
5:S:162:LEU:HD13	5:S:200:PHE:CD2	2.54	0.42
5:S:38:ARG:NH2	5:S:46:GLU:OE2	2.50	0.42
2:G:60:PRO:O	2:G:61:PHE:C	2.63	0.42
3:A:116:ASN:OD1	3:A:117:ARG:N	2.53	0.42
4:R:235:SER:O	4:R:238:VAL:HG12	2.20	0.42
1:B:229:ILE:O	1:B:229:ILE:HG22	2.20	0.41
3:A:36:LEU:HD13	3:A:227:ILE:HG21	2.01	0.41
4:R:258:LEU:O	4:R:262:LEU:HD12	2.19	0.41
4:R:264:VAL:HG12	4:R:323:ILE:CG2	2.51	0.41
1:B:222:PHE:HE2	1:B:241:PHE:HZ	1.38	0.41
4:R:278:PHE:O	4:R:281:VAL:HG12	2.21	0.41
1:B:40:VAL:CG2	1:B:298:ASP:OD1	2.68	0.41
1:B:320:VAL:HG12	1:B:321:THR:N	2.36	0.41
4:R:150:TRP:CG	4:R:181:ILE:HD11	2.56	0.41
1:B:89:LYS:N	3:A:19:ILE:HG21	2.35	0.41
3:A:167:PHE:CD1	3:A:167:PHE:O	2.73	0.41
5:S:207:LEU:C	5:S:207:LEU:HD23	2.46	0.41
1:B:54:HIS:CD2	1:B:58:ILE:HD11	2.56	0.41
3:A:210:ILE:HD11	4:R:251:ARG:CZ	2.51	0.41
5:S:36:TRP:O	5:S:48:VAL:HB	2.20	0.41
4:R:307:HIS:O	4:R:311:LEU:HG	2.20	0.40
1:B:311:HIS:CD2	1:B:315:VAL:HG12	2.57	0.40
5:S:24:ALA:HB1	5:S:27:PHE:CZ	2.56	0.40
5:S:101:TYR:OH	5:S:220:HIS:NE2	2.52	0.40
3:A:243:TYR:CE1	4:R:94:PRO:HG3	2.56	0.40

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	B	335/374 (90%)	321 (96%)	14 (4%)	0	100	100
2	G	49/68 (72%)	49 (100%)	0	0	100	100
3	A	212/258 (82%)	209 (99%)	3 (1%)	0	100	100
4	R	265/850 (31%)	248 (94%)	17 (6%)	0	100	100
5	S	227/260 (87%)	221 (97%)	6 (3%)	0	100	100
All	All	1088/1810 (60%)	1048 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	B	247/304 (81%)	246 (100%)	1 (0%)	84	84
2	G	30/56 (54%)	30 (100%)	0	100	100
3	A	176/218 (81%)	176 (100%)	0	100	100
4	R	242/724 (33%)	241 (100%)	1 (0%)	84	84
5	S	181/209 (87%)	181 (100%)	0	100	100
All	All	876/1511 (58%)	874 (100%)	2 (0%)	85	87

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

Mol	Chain	Res	Type
1	B	234	PHE
4	R	168	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	239	ASN
3	A	98	GLN
3	A	214	HIS
4	R	53	GLN
4	R	140	ASN
4	R	172	HIS
4	R	245	HIS
4	R	316	ASN
5	S	171	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

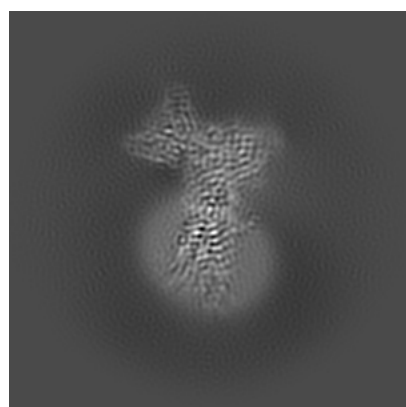
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66632. These allow visual inspection of the internal detail of the map and identification of artifacts.

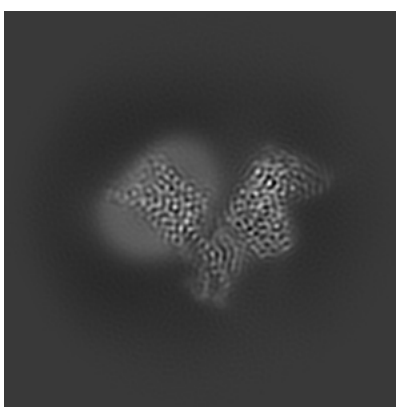
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

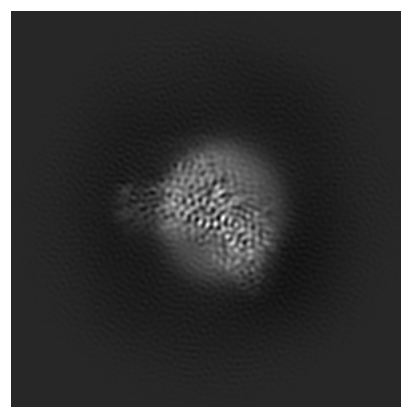
6.1.1 Primary map



X



Y

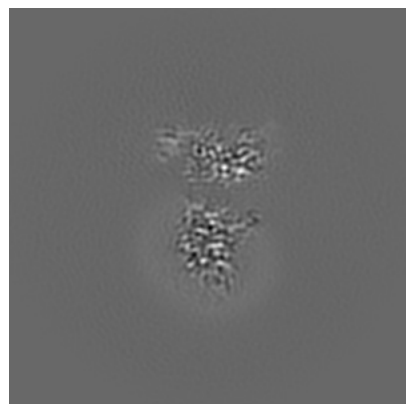


Z

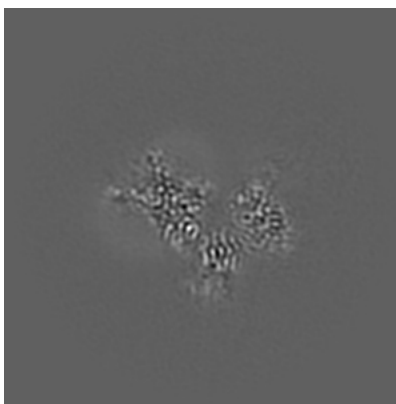
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

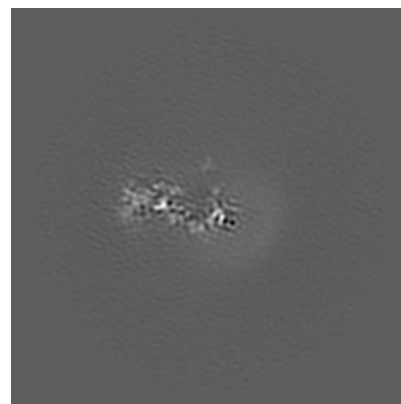
6.2.1 Primary map



X Index: 100



Y Index: 100

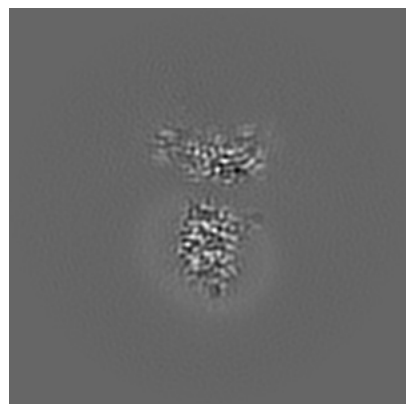


Z Index: 100

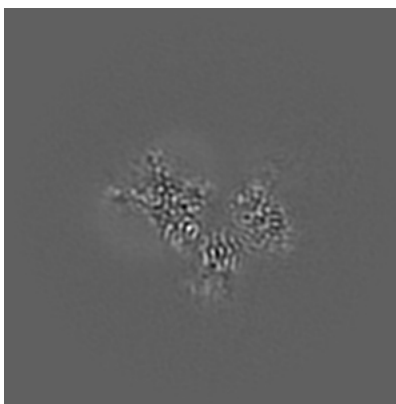
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

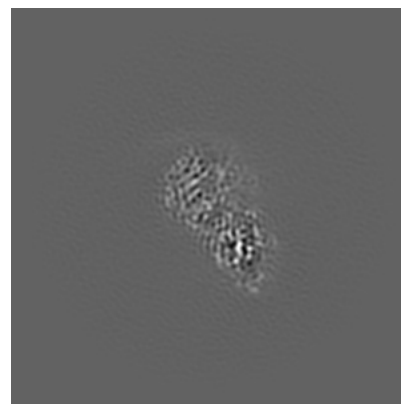
6.3.1 Primary map



X Index: 102



Y Index: 100

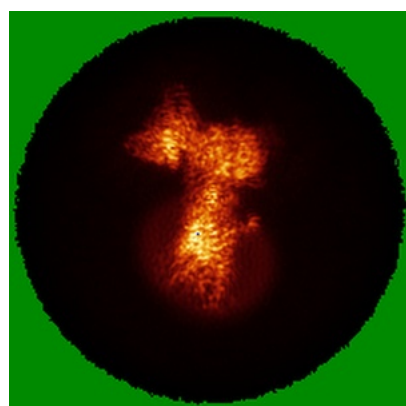


Z Index: 132

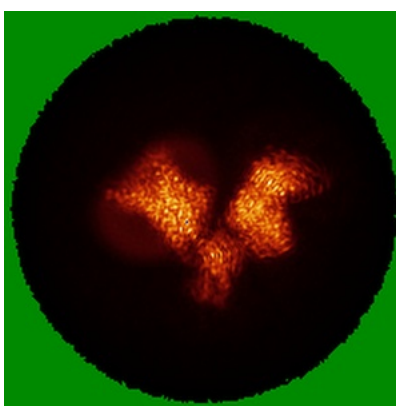
The images above show the largest variance slices of the map in three orthogonal directions.

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

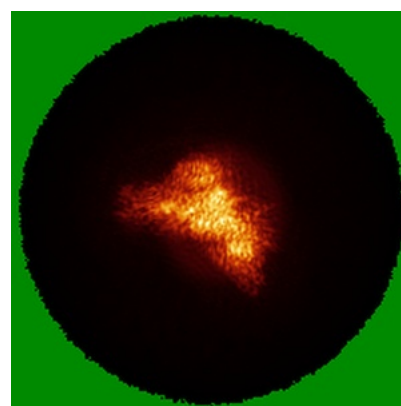
6.4.1 Primary map



X



Y

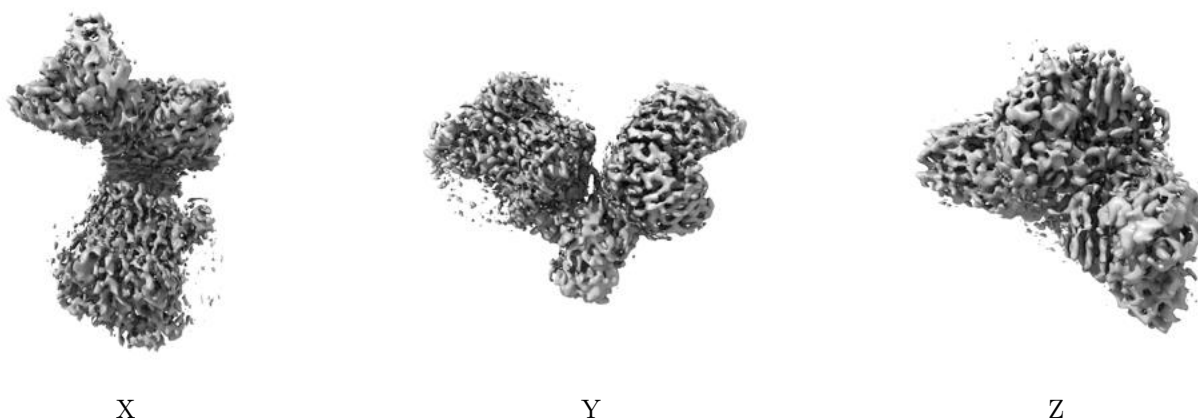


Z

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

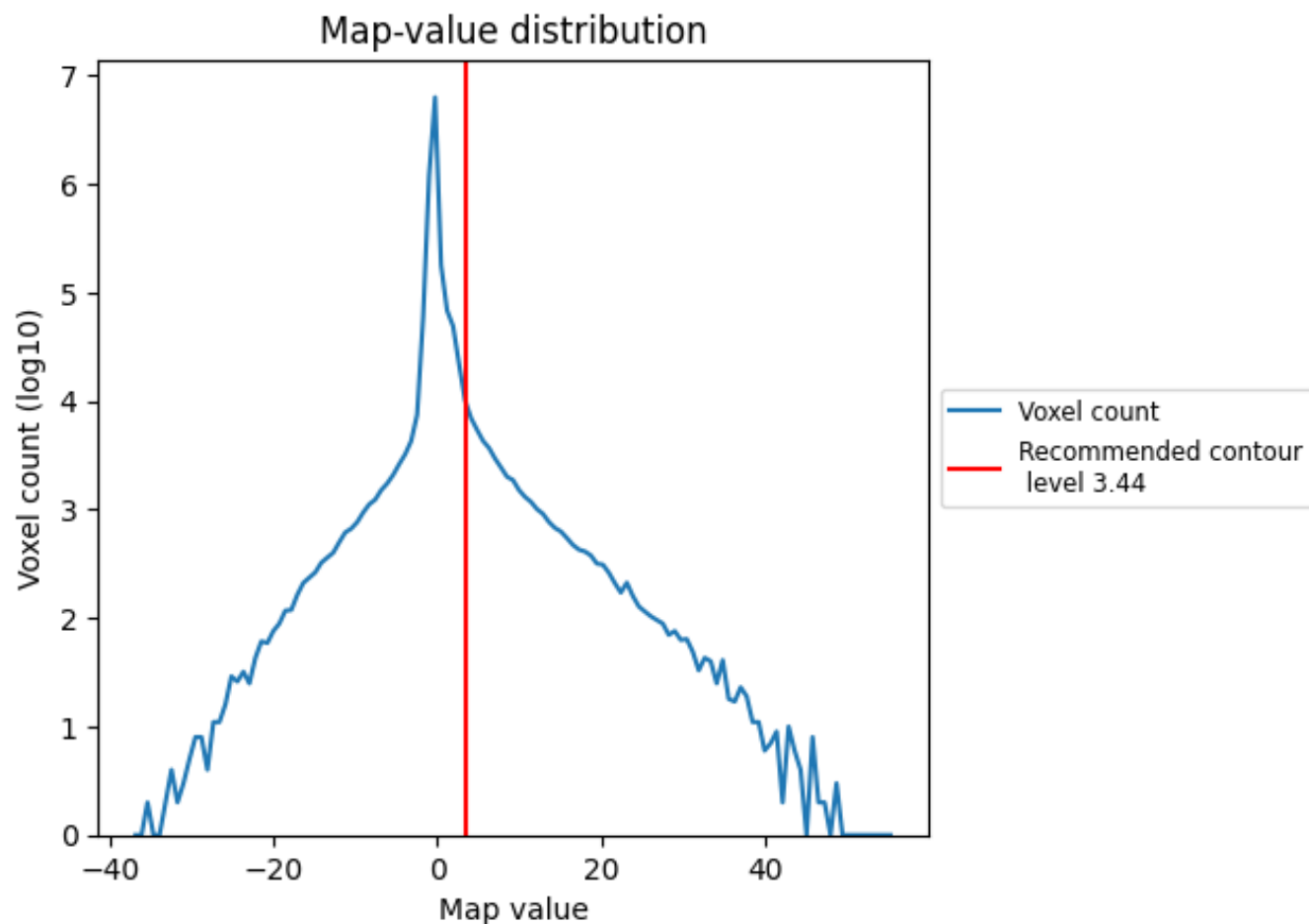
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

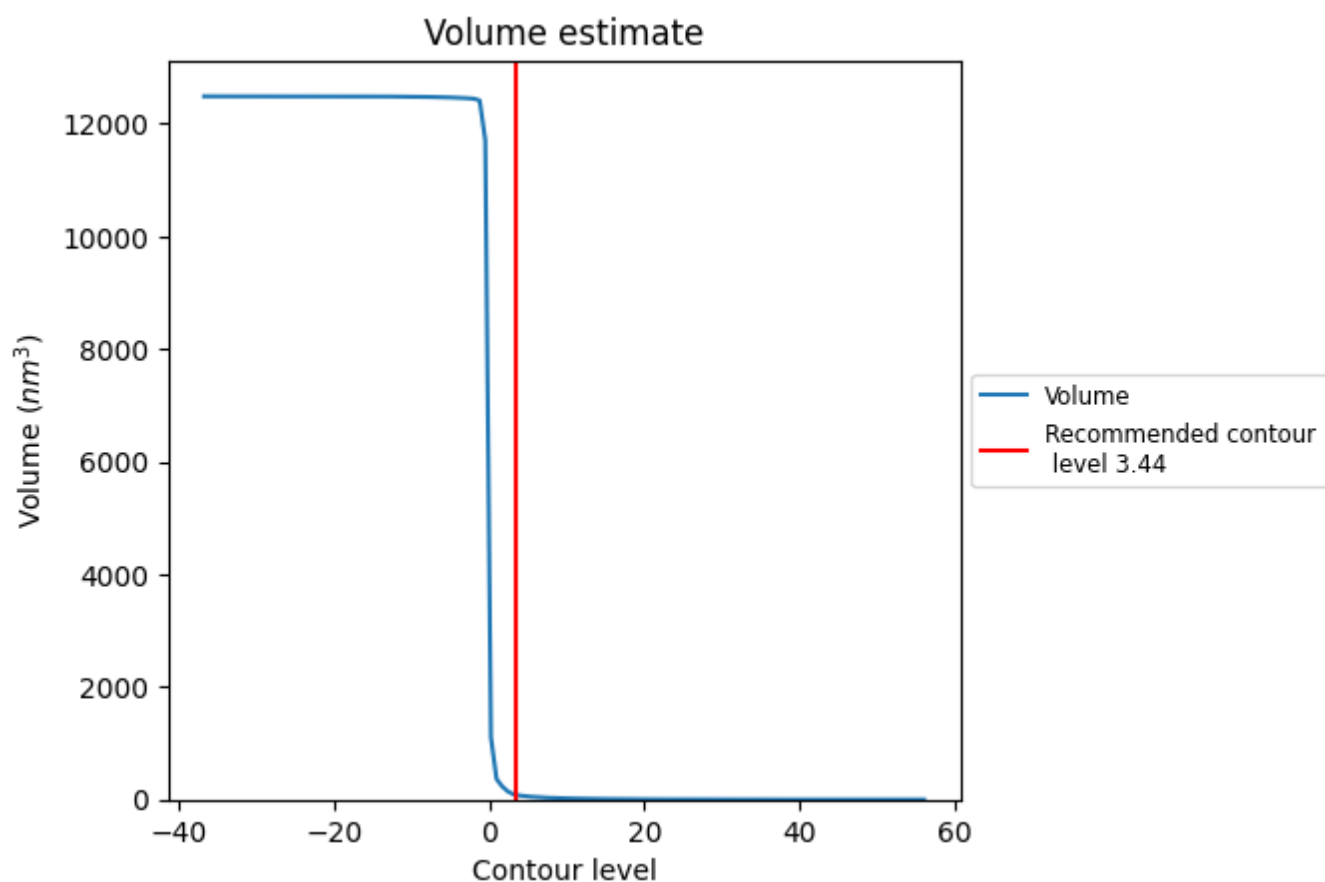
This section contains the results of statistical analysis of the map.

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.

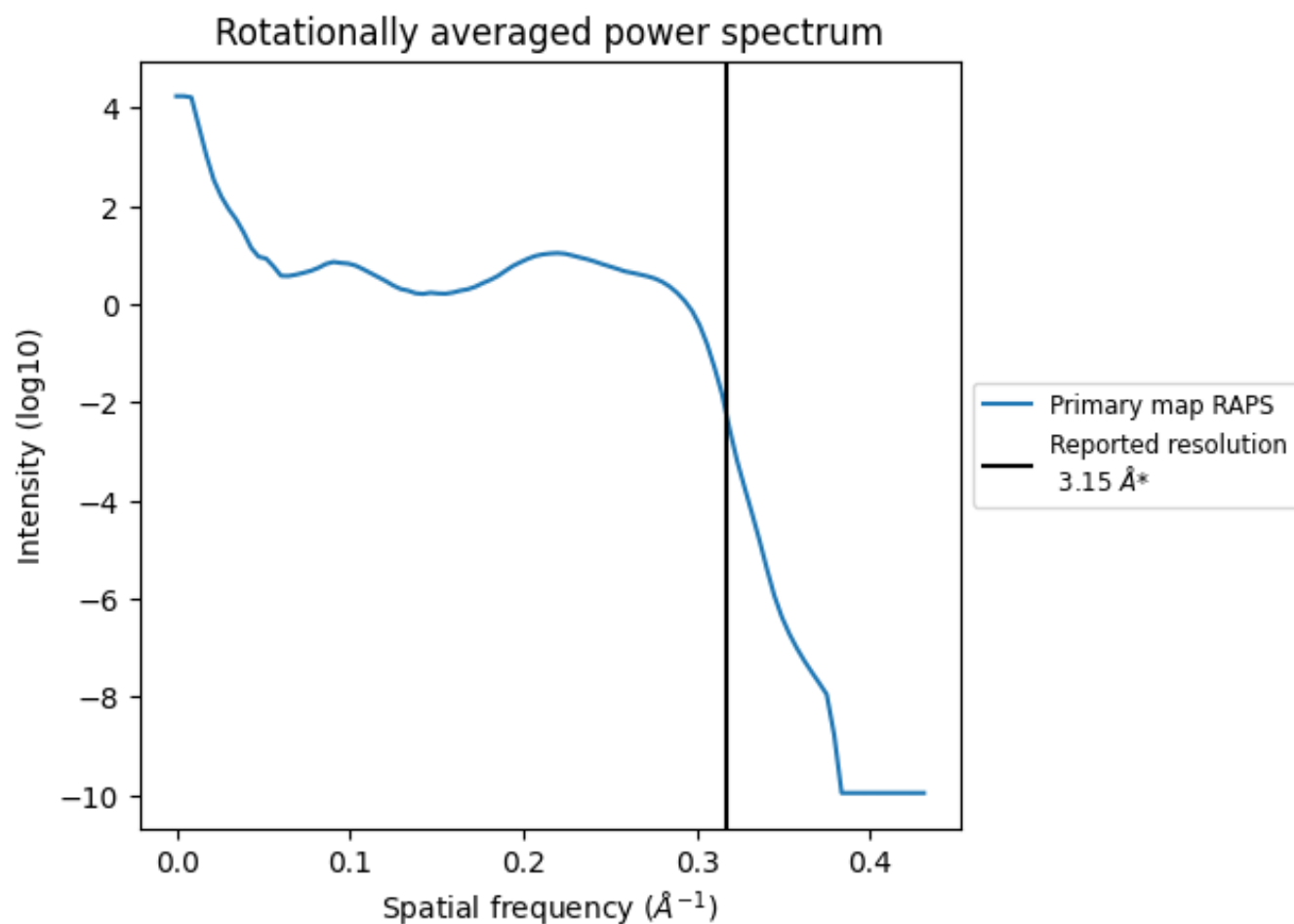
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm³; this corresponds to an approximate mass of 76 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 0.317 Å⁻¹

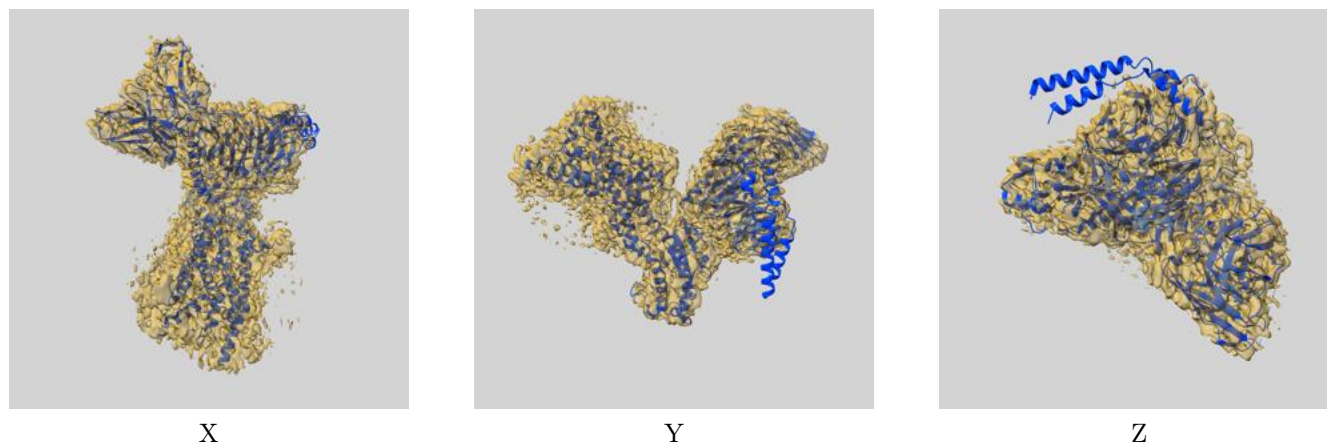
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

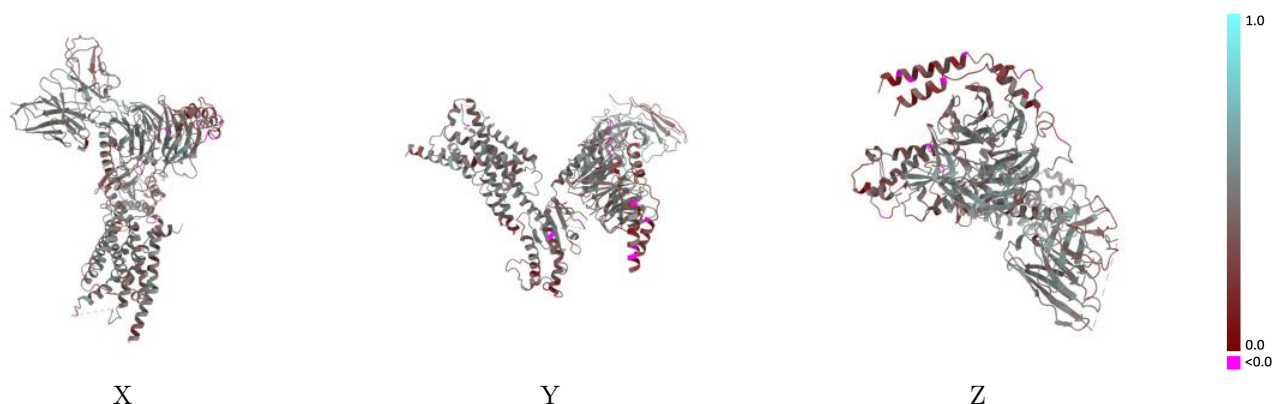
This section contains information regarding the fit between EMDB map EMD-66632 and PDB model 9X74. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



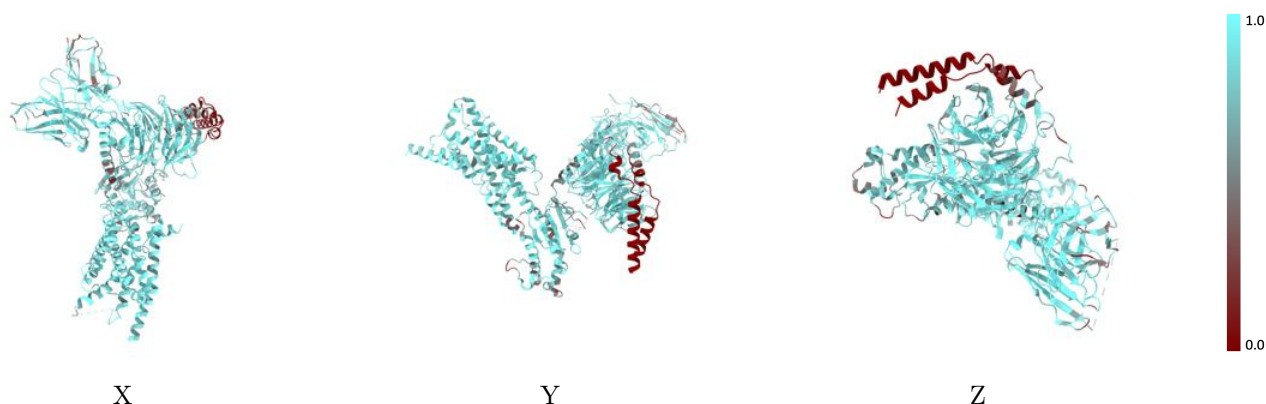
The images above show the 3D surface view of the map at the recommended contour level 3.44 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



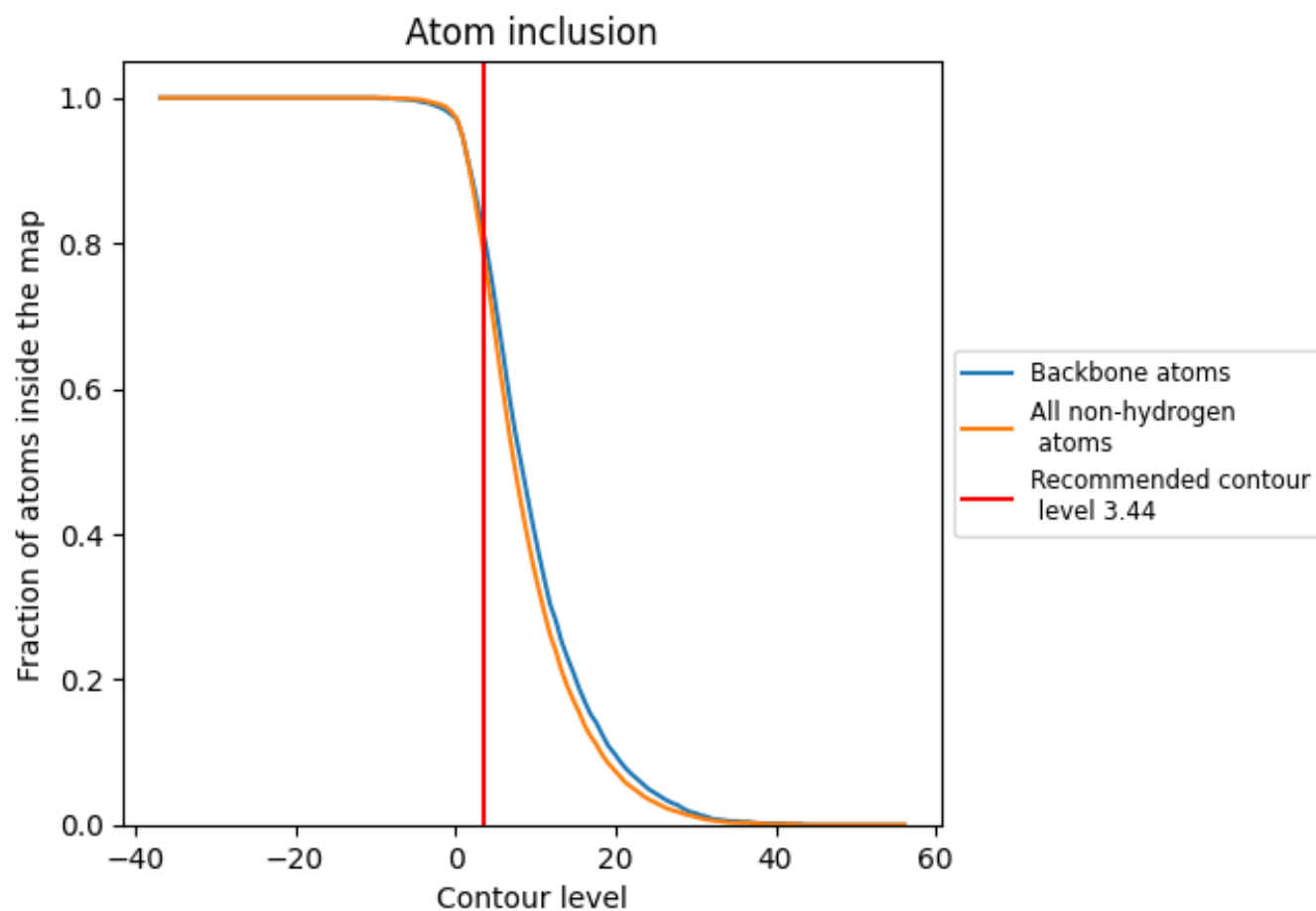
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.44).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 79% 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 (3.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7940	0.4270
A	0.7500	0.3890
B	0.7890	0.4370
G	0.3830	0.2850
R	0.8670	0.4430
S	0.8340	0.4560

