



Full wwPDB EM Validation Report ⓘ

Jun 15, 2022 – 07:04 PM JST

PDB ID : 7Y35
EMDB ID : EMD-33588
Title : Cryo-EM structure of the Abaloparatide-bound human PTH1R-Gs complex
Deposited on : 2022-06-09
Resolution : 2.90 Å(reported)

This wwPDB validation report is for manuscript review

This is a Full wwPDB EM Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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

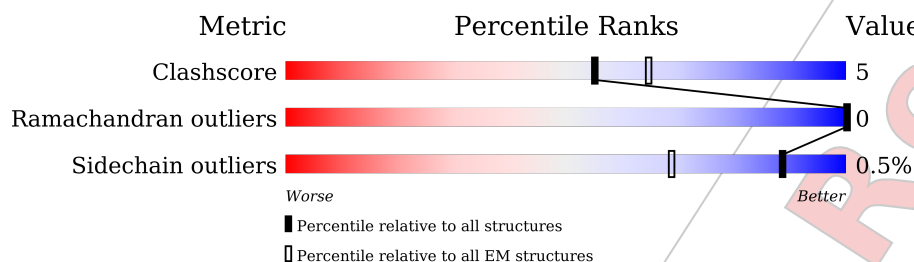
EMDB validation analysis : 0.0.1.dev8
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.28.1

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 2.90 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	R	727	
2	P	34	
3	A	380	
4	B	380	
5	G	70	
6	N	126	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9204 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 Parathyroid hormone/parathyroid hormone-related peptide receptor, PTH1R.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	R	373	3065	2024	514	507	20	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	188	ALA	GLY	conflict	UNP Q03431

- Molecule 2 is a protein called Abaloparatide.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	P	33	273	171	54	48	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A	224	1860	1174	337	343	6	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	ASN	SER	engineered mutation	UNP P63092-2
A	226	ALA	GLY	engineered mutation	UNP P63092-2
A	268	ALA	GLU	engineered mutation	UNP P63092-2
A	271	LYS	ASN	engineered mutation	UNP P63092-2
A	274	ASP	LYS	engineered mutation	UNP P63092-2
A	280	LYS	ARG	engineered mutation	UNP P63092-2
A	284	ASP	THR	engineered mutation	UNP P63092-2
A	285	THR	ILE	engineered mutation	UNP P63092-2

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	338	Total	C	N	O	S	0	0
			2600	1604	467	508	21		

There are 41 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	MET	-	initiating methionine	UNP P54311
B	-12	HIS	-	expression tag	UNP P54311
B	-11	HIS	-	expression tag	UNP P54311
B	-10	HIS	-	expression tag	UNP P54311
B	-9	HIS	-	expression tag	UNP P54311
B	-8	HIS	-	expression tag	UNP P54311
B	-7	HIS	-	expression tag	UNP P54311
B	-6	LEU	-	expression tag	UNP P54311
B	-5	GLU	-	expression tag	UNP P54311
B	-4	VAL	-	expression tag	UNP P54311
B	-3	LEU	-	expression tag	UNP P54311
B	-2	PHE	-	expression tag	UNP P54311
B	-1	GLN	-	expression tag	UNP P54311
B	0	GLY	-	expression tag	UNP P54311
B	1	PRO	-	expression tag	UNP P54311
B	341	GLY	-	expression tag	UNP P54311
B	342	SER	-	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	GLY	-	expression tag	UNP P54311
B	348	SER	-	expression tag	UNP P54311
B	349	GLY	-	expression tag	UNP P54311
B	350	GLY	-	expression tag	UNP P54311
B	351	GLY	-	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	VAL	-	expression tag	UNP P54311
B	357	SER	-	expression tag	UNP P54311
B	358	GLY	-	expression tag	UNP P54311
B	359	TRP	-	expression tag	UNP P54311
B	360	ARG	-	expression tag	UNP P54311

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Chain	Residue	Modelled	Actual	Comment	Reference
B	361	LEU	-	expression tag	UNP P54311
B	362	PHE	-	expression tag	UNP P54311
B	363	LYS	-	expression tag	UNP P54311
B	364	LYS	-	expression tag	UNP P54311
B	365	ILE	-	expression tag	UNP P54311
B	366	SER	-	expression tag	UNP P54311

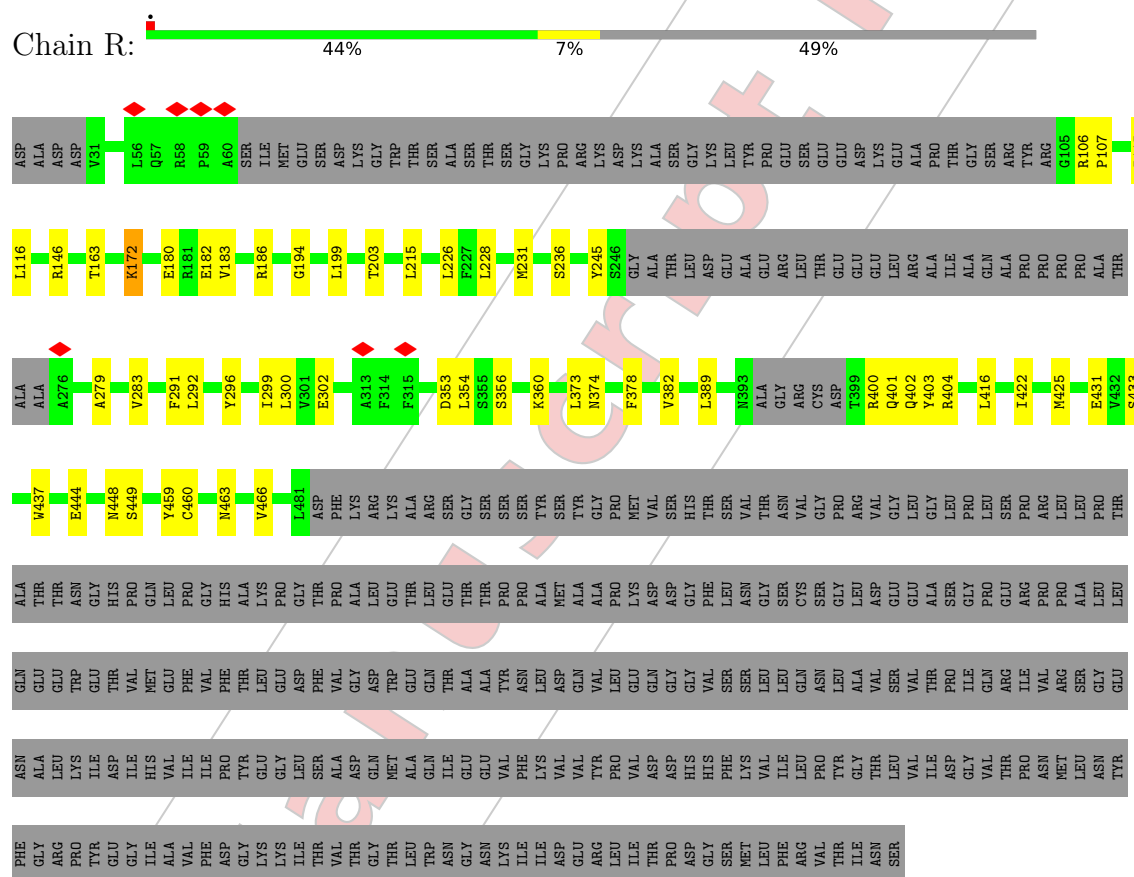
- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	58	Total	C	N	O	S	0	0
			445	278	78	86	3		

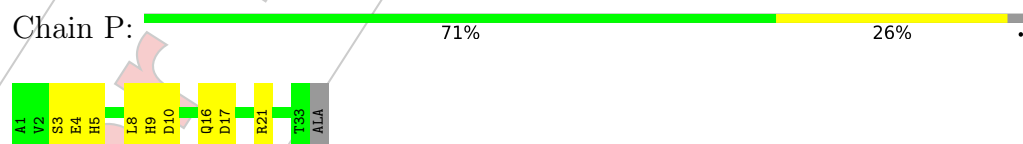
- Molecule 6 is a protein called NanoBody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	126	Total	C	N	O	S	0	0
			961	599	168	188	6		

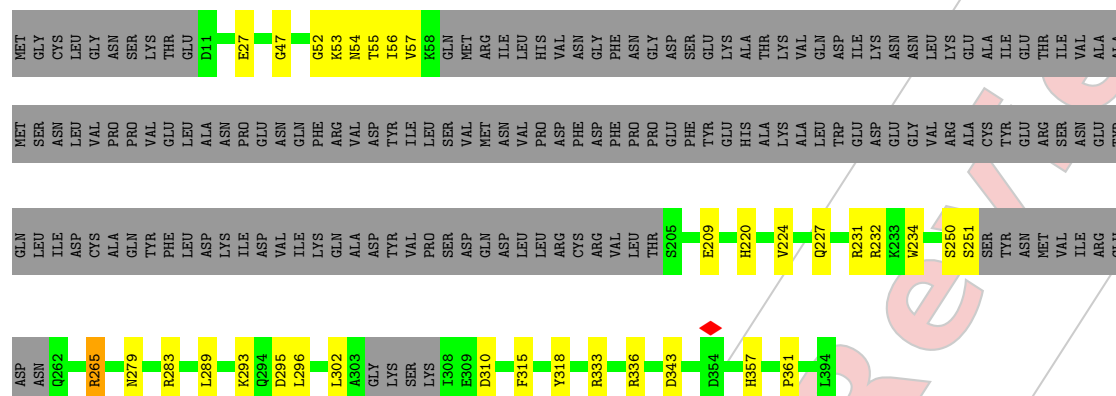
- Molecule 1: Parathyroid hormone/parathyroid hormone-related peptide receptor, PTH1R



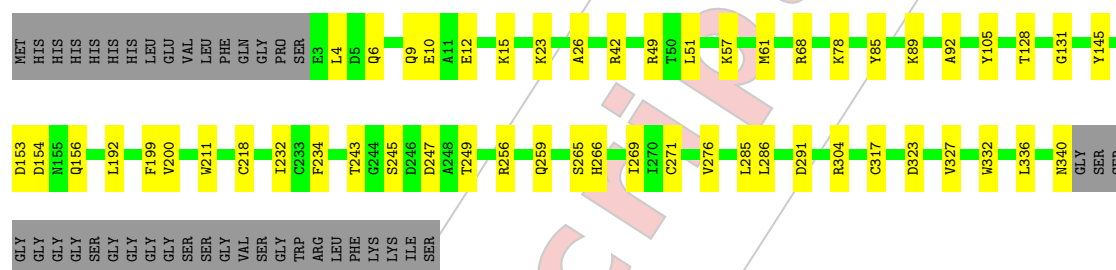
- Molecule 2: Abaloparatide



- Molecule 3: Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

Chain A: 

- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B: 

- Molecule 5: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

Chain G: 

- Molecule 6: NanoBody 35

Chain N: 

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	456840	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	49310	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.772	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	227.13602, 227.13602, 227.13602	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.014, 1.014, 1.014	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	R	0.62	1/3157 (0.0%)	0.53	3/4291 (0.1%)
2	P	0.71	0/269	0.40	0/357
3	A	0.45	0/1894	0.48	0/2546
4	B	0.47	0/2647	0.56	0/3589
5	G	0.34	0/451	0.45	0/609
6	N	0.55	0/981	0.52	0/1329
All	All	0.53	1/9399 (0.0%)	0.52	3/12721 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	R	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	R	182	GLU	C-N	-14.47	1.00	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	172	LYS	CA-C-N	-7.64	100.39	117.20
1	R	172	LYS	O-C-N	6.54	133.17	122.70
1	R	172	LYS	C-N-CA	5.84	136.29	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	R	172	LYS	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	3065	0	3058	34	0
2	P	273	0	296	8	0
3	A	1860	0	1836	24	0
4	B	2600	0	2505	30	0
5	G	445	0	454	5	0
6	N	961	0	928	10	0
All	All	9204	0	9077	97	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 5.

All (97) 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:R:444:GLU:OE1	2:P:3:SER:HB2	1.73	0.86
1:R:448:ASN:ND2	2:P:4:GLU:OE2	2.22	0.70
4:B:49:ARG:NH1	5:G:61:PHE:O	2.23	0.69
1:R:422:ILE:HA	1:R:425:MET:HG2	1.75	0.67
3:A:27:GLU:OE2	4:B:89:LYS:NZ	2.31	0.64
4:B:232:ILE:HG12	4:B:243:THR:HG22	1.80	0.63
6:N:100:PRO:HD2	6:N:107:CYS:HB2	1.79	0.63
4:B:61:MET:HG3	4:B:317:CYS:HB3	1.82	0.62
1:R:180:GLU:O	1:R:183:VAL:HG22	2.00	0.61
1:R:354:LEU:HD11	2:P:16:GLN:HG3	1.81	0.61
6:N:62:GLY:HA2	6:N:65:LYS:HE2	1.84	0.60
1:R:401:GLN:OE1	1:R:404:ARG:NH1	2.35	0.59
6:N:51:ILE:HD13	6:N:72:ARG:HG3	1.82	0.59
1:R:437:TRP:NE1	2:P:10:ASP:OD2	2.34	0.59
3:A:251:SER:O	3:A:265:ARG:NH2	2.35	0.59
4:B:192:LEU:HD23	4:B:199:PHE:HB3	1.86	0.58
3:A:315:PHE:O	3:A:336:ARG:NH2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:146:ARG:NH2	1:R:163:THR:OG1	2.37	0.57
3:A:227:GLN:HE22	4:B:145:TYR:H	1.52	0.57
4:B:42:ARG:NH1	4:B:304:ARG:O	2.37	0.57
3:A:232:ARG:HH12	6:N:115:TYR:HE1	1.53	0.57
1:R:463:ASN:HB3	1:R:466:VAL:HG22	1.87	0.56
4:B:154:ASP:N	4:B:154:ASP:OD1	2.40	0.55
3:A:289:LEU:HB3	3:A:361:PRO:HA	1.89	0.55
6:N:91:THR:HG23	6:N:125:THR:HA	1.90	0.53
4:B:340:ASN:ND2	5:G:59:ASN:OD1	2.40	0.53
3:A:52:GLY:O	3:A:55:THR:HG22	2.09	0.53
3:A:231:ARG:HG2	3:A:234:TRP:CZ2	2.44	0.52
6:N:51:ILE:HD12	6:N:70:ILE:HG23	1.91	0.52
4:B:26:ALA:HB2	4:B:259:GLN:HE22	1.75	0.51
4:B:51:LEU:HB2	4:B:336:LEU:HB2	1.92	0.51
4:B:128:THR:HG23	4:B:131:GLY:H	1.74	0.51
4:B:323:ASP:OD1	4:B:323:ASP:N	2.39	0.51
1:R:194:GLY:HA3	1:R:449:SER:HB2	1.92	0.50
4:B:256:ARG:NH2	5:G:36:ASP:OD2	2.42	0.50
1:R:431:GLU:HG3	1:R:433:SER:H	1.77	0.50
4:B:276:VAL:HG13	4:B:285:LEU:HD11	1.94	0.49
1:R:228:LEU:HA	1:R:231:MET:HE2	1.94	0.49
3:A:302:LEU:HA	3:A:333:ARG:HH22	1.77	0.49
3:A:293:LYS:HD3	3:A:296:LEU:HD12	1.93	0.49
4:B:249:THR:HG22	4:B:265:SER:HB3	1.94	0.49
3:A:279:ASN:O	3:A:283:ARG:HG2	2.13	0.49
3:A:209:GLU:OE2	3:A:220:HIS:NE2	2.36	0.48
4:B:286:LEU:HD22	4:B:327:VAL:HG21	1.96	0.48
3:A:265:ARG:HD3	3:A:265:ARG:H	1.79	0.48
4:B:4:LEU:HD13	5:G:9:ILE:HD13	1.95	0.48
2:P:17:ASP:O	2:P:21:ARG:HG3	2.14	0.48
4:B:200:VAL:HG13	4:B:232:ILE:HG21	1.95	0.47
1:R:106:ARG:N	1:R:107:PRO:CD	2.78	0.47
1:R:226:LEU:HD22	1:R:302:GLU:OE1	2.15	0.47
3:A:52:GLY:O	3:A:56:ILE:HG13	2.14	0.47
1:R:389:LEU:C	1:R:402:GLN:HE22	2.19	0.47
1:R:183:VAL:HG12	1:R:186:ARG:HH21	1.80	0.46
4:B:211:TRP:CZ3	4:B:218:CYS:HB2	2.51	0.46
6:N:60:TYR:HB2	6:N:65:LYS:HG2	1.98	0.46
1:R:215:LEU:HD13	1:R:466:VAL:HG12	1.97	0.46
3:A:310:ASP:N	3:A:310:ASP:OD1	2.47	0.46
4:B:153:ASP:OD1	4:B:156:GLN:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:6:GLN:O	4:B:9:GLN:NE2	2.50	0.45
3:A:47:GLY:HA3	3:A:53:LYS:HE2	1.98	0.45
3:A:54:ASN:C	3:A:56:ILE:H	2.19	0.45
4:B:68:ARG:HG2	4:B:85:TYR:CZ	2.51	0.45
4:B:78:LYS:HE2	4:B:92:ALA:HB1	1.98	0.44
1:R:400:ARG:HE	1:R:403:TYR:HD2	1.64	0.44
3:A:54:ASN:O	3:A:57:VAL:N	2.48	0.44
1:R:292:LEU:HD22	1:R:296:TYR:HE2	1.83	0.44
1:R:353:ASP:O	2:P:9:HIS:CD2	2.71	0.44
3:A:224:VAL:HG21	3:A:234:TRP:CH2	2.53	0.43
1:R:115:ILE:HG13	1:R:116:LEU:N	2.34	0.43
3:A:251:SER:HB2	3:A:265:ARG:HH21	1.83	0.43
3:A:318:TYR:OH	3:A:343:ASP:OD2	2.26	0.43
4:B:266:HIS:HB3	4:B:269:ILE:HG13	2.01	0.43
1:R:236:SER:HB3	1:R:291:PHE:HD2	1.85	0.42
1:R:180:GLU:HA	1:R:183:VAL:HG22	2.01	0.42
1:R:354:LEU:HD23	1:R:354:LEU:HA	1.91	0.42
6:N:37:VAL:HG23	6:N:95:TYR:HB2	2.01	0.42
4:B:245:SER:HB3	4:B:247:ASP:OD1	2.20	0.42
1:R:300:LEU:HD11	1:R:373:LEU:HD23	2.01	0.41
4:B:9:GLN:NE2	4:B:10:GLU:HG2	2.35	0.41
1:R:356:SER:O	1:R:356:SER:OG	2.36	0.41
4:B:271:CYS:SG	4:B:291:ASP:HB3	2.60	0.41
5:G:54:VAL:HG22	5:G:58:GLU:HB2	2.03	0.41
1:R:360:LYS:HB2	2:P:5:HIS:HE1	1.84	0.41
1:R:416:LEU:HD13	1:R:459:TYR:CE2	2.56	0.41
4:B:12:GLU:HA	4:B:15:LYS:HG2	2.01	0.41
6:N:29:PHE:O	6:N:72:ARG:NH2	2.54	0.41
1:R:299:ILE:HG22	1:R:374:ASN:ND2	2.36	0.41
1:R:378:PHE:O	1:R:382:VAL:HG23	2.21	0.41
1:R:199:LEU:O	1:R:203:THR:HG23	2.21	0.40
3:A:53:LYS:HE2	3:A:53:LYS:HB2	1.95	0.40
1:R:245:TYR:OH	2:P:8:LEU:HD12	2.21	0.40
1:R:279:ALA:O	1:R:283:VAL:HG23	2.21	0.40
3:A:295:ASP:OD1	3:A:296:LEU:N	2.54	0.40
1:R:460:CYS:O	1:R:466:VAL:HG21	2.21	0.40
3:A:250:SER:O	3:A:250:SER:OG	2.38	0.40
4:B:57:LYS:HD2	4:B:332:TRP:CD2	2.56	0.40
6:N:99:CYS:HB3	6:N:107:CYS:HB3	1.82	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	R	367/727 (50%)	352 (96%)	15 (4%)	0	100	100
2	P	30/34 (88%)	30 (100%)	0	0	100	100
3	A	216/380 (57%)	206 (95%)	10 (5%)	0	100	100
4	B	336/380 (88%)	321 (96%)	15 (4%)	0	100	100
5	G	56/70 (80%)	56 (100%)	0	0	100	100
6	N	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
All	All	1129/1717 (66%)	1083 (96%)	46 (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	R	326/620 (53%)	326 (100%)	0	100	100
2	P	30/30 (100%)	30 (100%)	0	100	100
3	A	200/340 (59%)	198 (99%)	2 (1%)	76	92
4	B	281/311 (90%)	278 (99%)	3 (1%)	73	92
5	G	47/57 (82%)	47 (100%)	0	100	100
6	N	104/104 (100%)	104 (100%)	0	100	100
All	All	988/1462 (68%)	983 (100%)	5 (0%)	89	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	265	ARG
3	A	357	HIS
4	B	23	LYS
4	B	105	TYR
4	B	234	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	307	HIS
1	R	402	GLN
1	R	420	HIS
2	P	9	HIS
3	A	54	ASN
3	A	227	GLN
4	B	6	GLN
4	B	36	ASN
4	B	75	GLN
4	B	259	GLN
5	G	24	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	AIB	P	29	2	1,5,6	1.20	0	2,7,9	0.87	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AIB	P	29	2	-	0/2/3/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	182:GLU	C	183:VAL	N	1.00

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-33588. These allow visual inspection of the internal detail of the map and identification of artifacts.

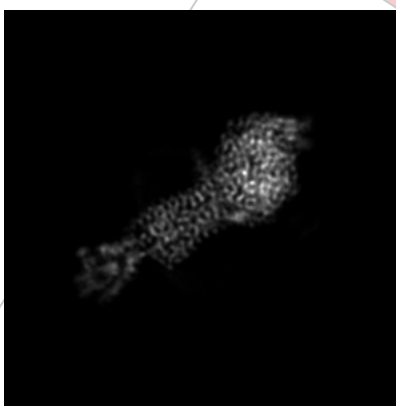
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections ⓘ

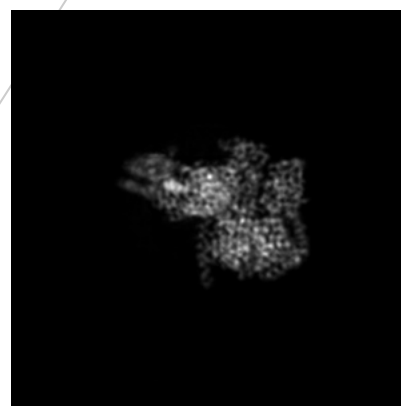
6.1.1 Primary map



X



Y

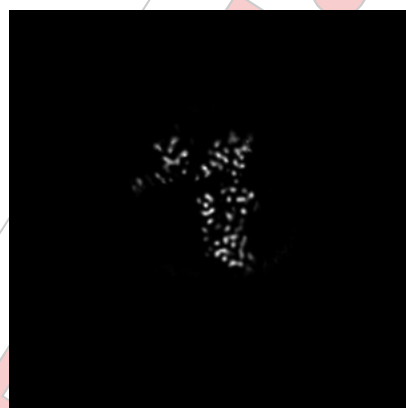


Z

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

6.2 Central slices ⓘ

6.2.1 Primary map



X Index: 112



Y Index: 112



Z Index: 112

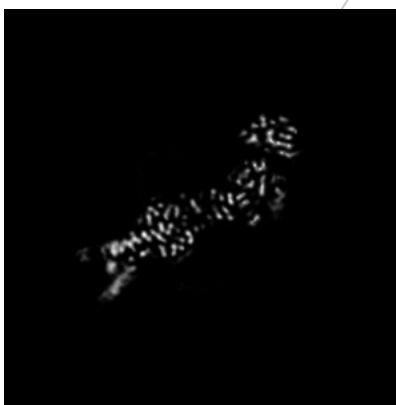
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 122



Y Index: 124



Z Index: 148

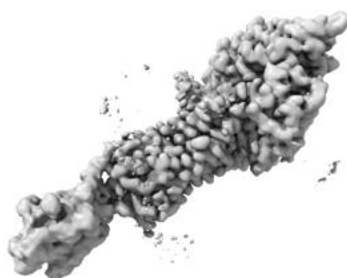
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

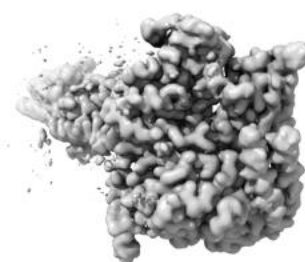
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5 Mask visualisation

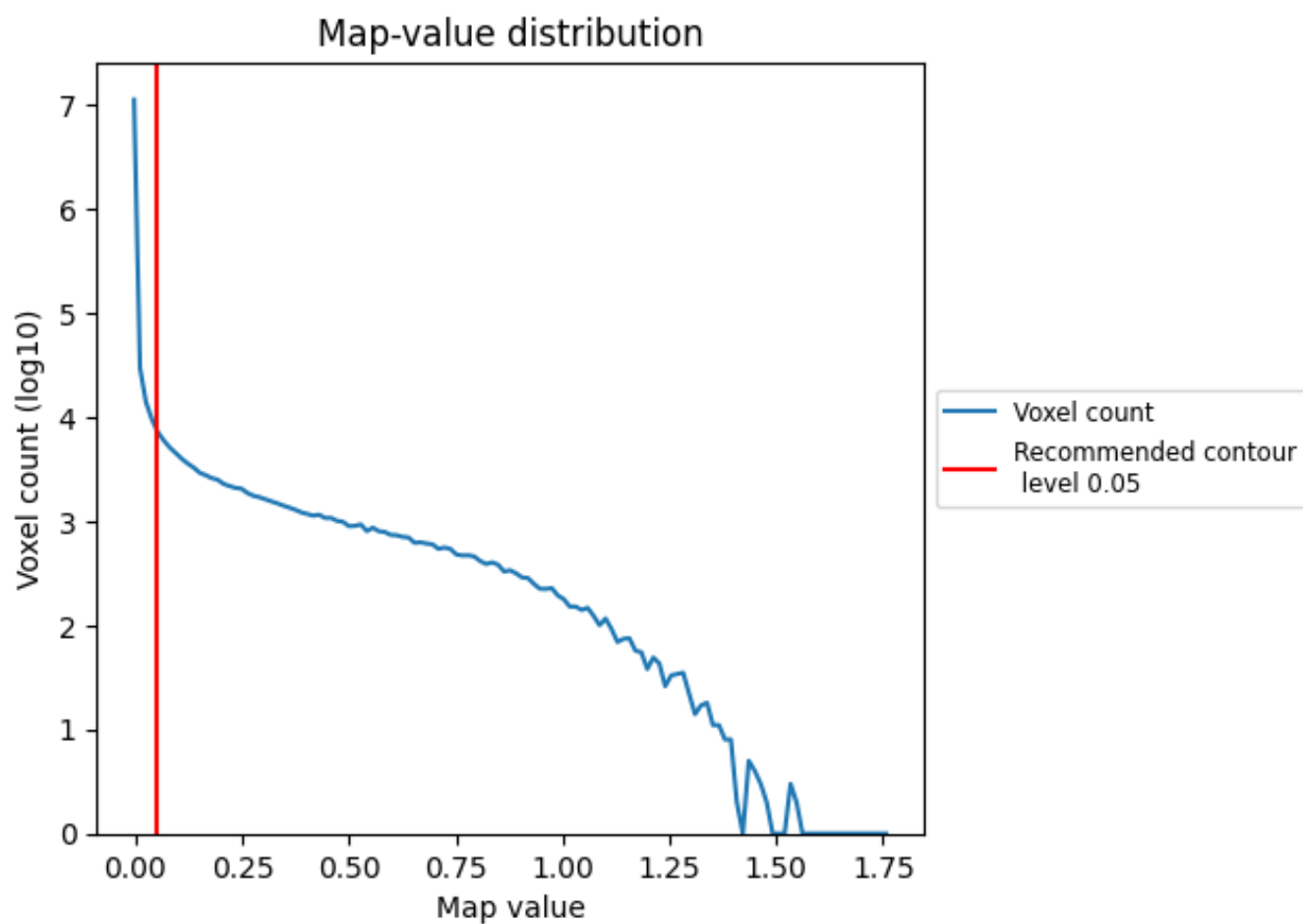
This section was not generated. No masks/segmentation were deposited.

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7 Map analysis [i](#)

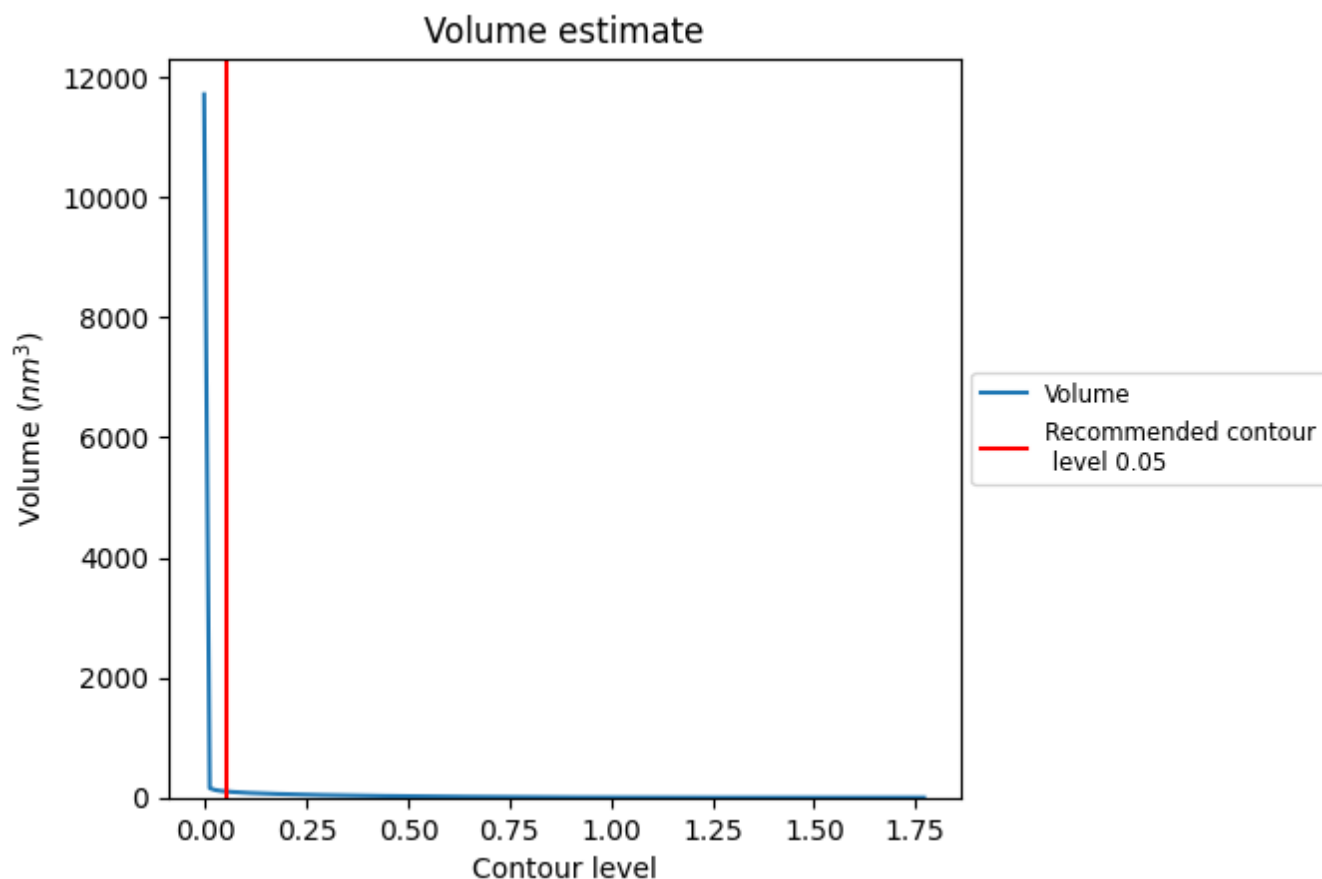
This section contains the results of statistical analysis of the map.

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.

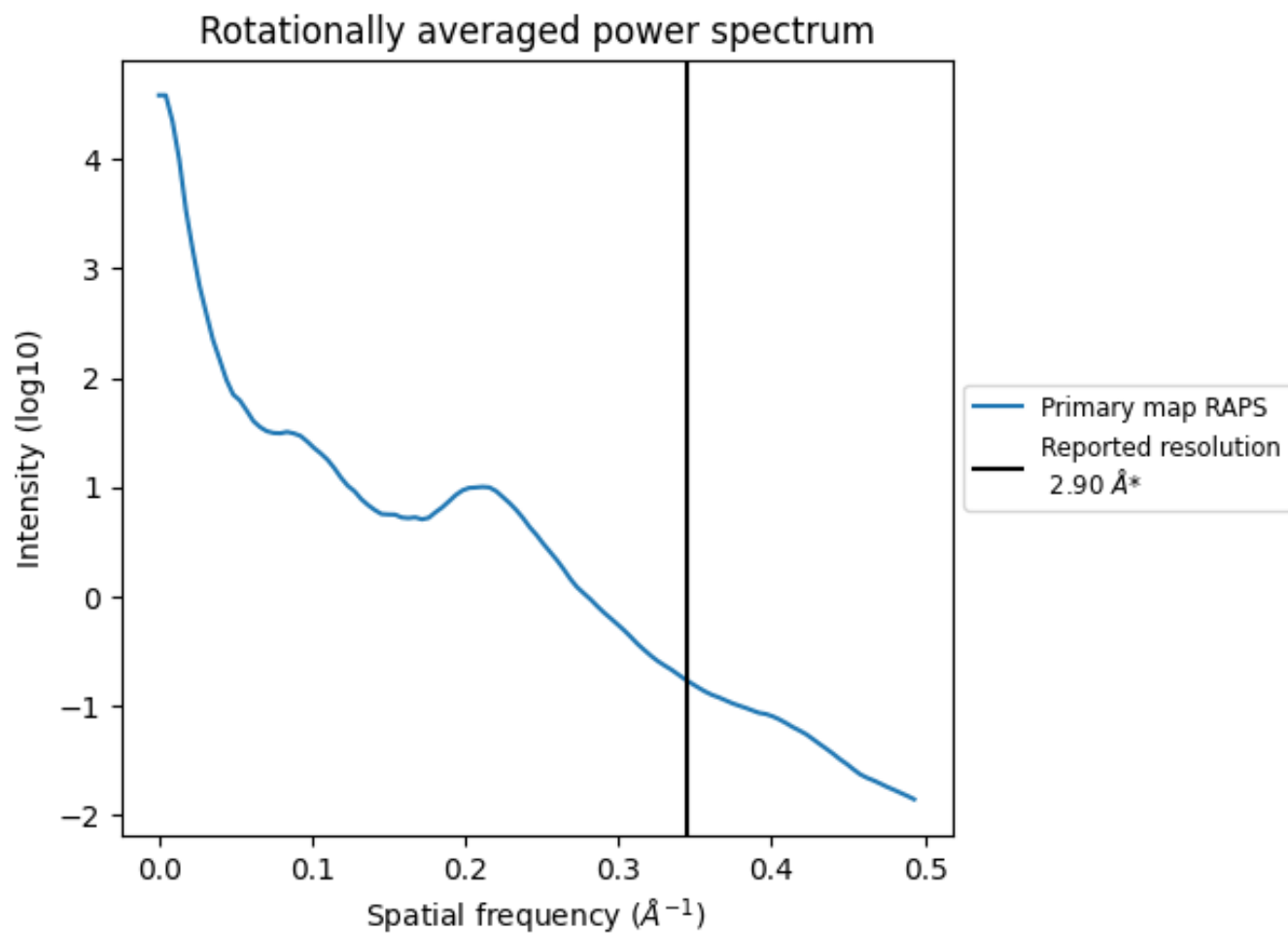
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 102 nm³; this corresponds to an approximate mass of 92 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 0.345 Å⁻¹

8 Fourier-Shell correlation ⓘ

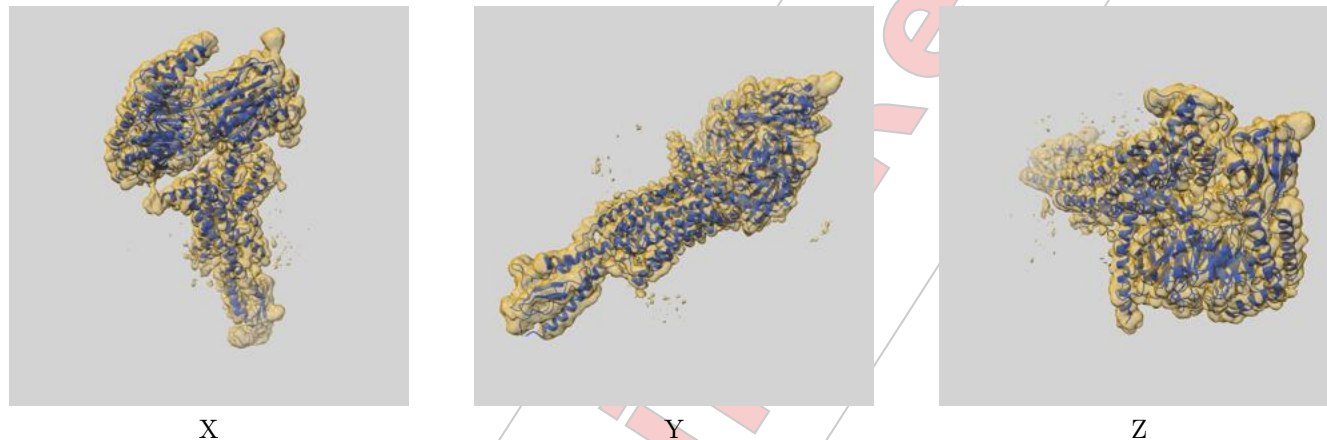
This section was not generated. No FSC curve or half-maps provided.

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9 Map-model fit ⓘ

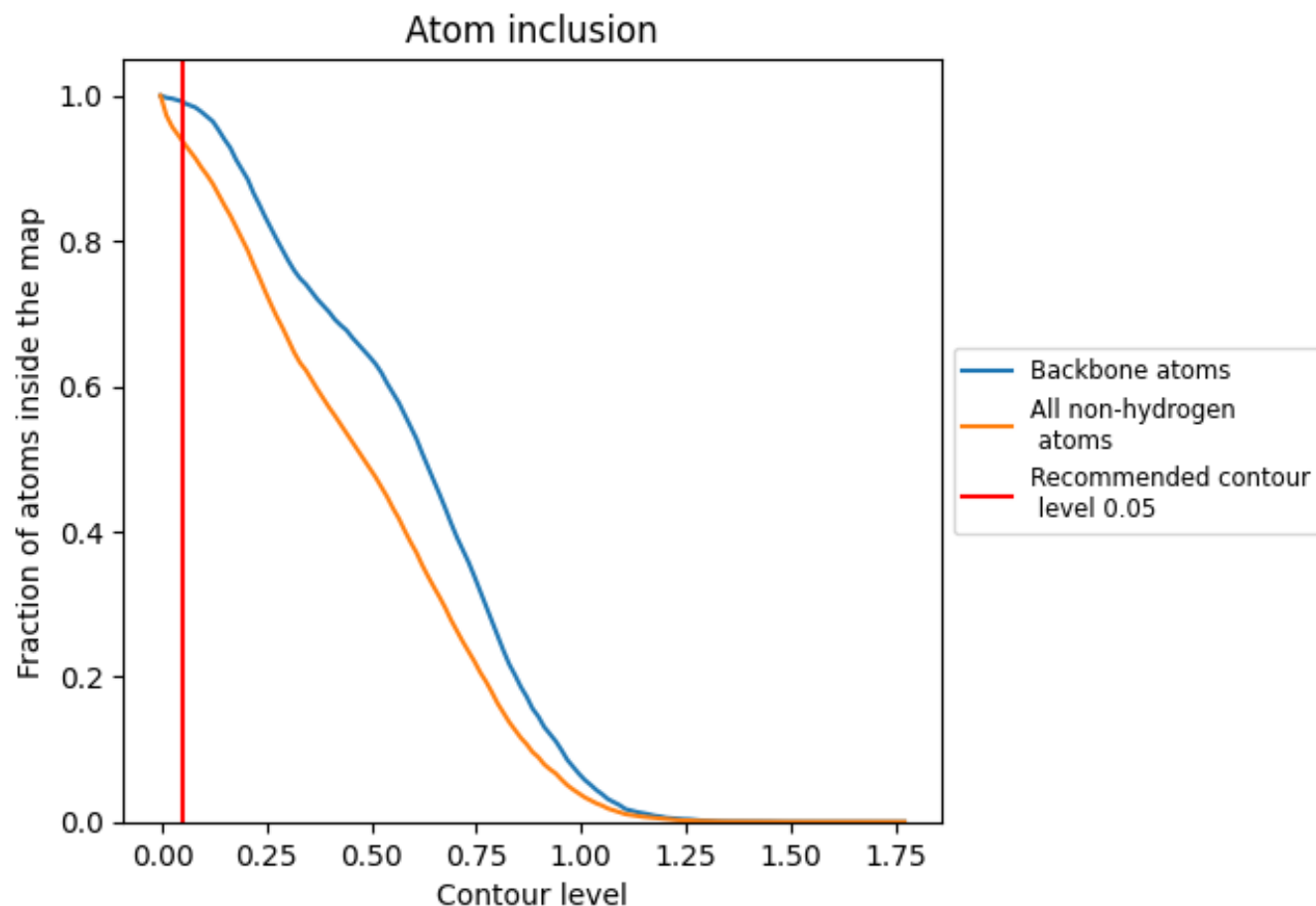
This section contains information regarding the fit between EMDB map EMD-33588 and PDB model 7Y35. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay ⓘ



The images above show the 3D surface view of the map at the recommended contour level 0.05 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 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.