



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:03 PM UTC

PDB ID : 6LTH / pdb_00006lth
EMDB ID : EMD-0968
Title : Structure of human BAF Base module
Authors : He, S.; Wu, Z.; Tian, Y.; Yu, Z.; Yu, J.; Wang, X.; Li, J.; Liu, B.; Xu, Y.
Deposited on : 2020-01-22
Resolution : 3.00 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:

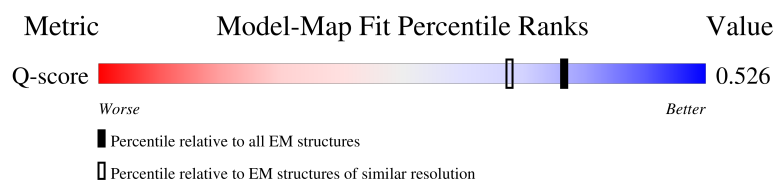
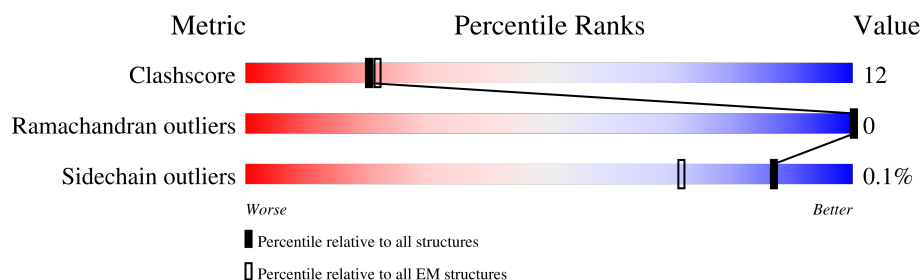
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	I	1647	 5% . 93%
2	L	2285	 15% 6% 80%
3	M	385	 51% 16% 33%
4	N	1214	 14% 8% 79%

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Mol	Chain	Length	Quality of chain
4	O	1214	 5% 19% 8% 73%
5	P	515	 5% 30% 16% 54%
6	Q	411	 10% 17% 9% 74%
7	R	391	 13% 5% 5% 82%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14970 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 Transcription activator BRG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	I	120	Total	C	N	O	S	0	0
			1022	632	208	180	2		

- Molecule 2 is a protein called AT-rich interactive domain-containing protein 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	466	Total	C	N	O	S	0	0
			3670	2341	620	688	21		

- Molecule 3 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	259	Total	C	N	O	S	0	0
			2070	1318	341	401	10		

- Molecule 4 is a protein called SWI/SNF complex subunit SMARCC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	261	Total	C	N	O	S	0	0
			2120	1346	374	388	12		
4	O	325	Total	C	N	O	S	0	0
			2632	1676	458	485	13		

- Molecule 5 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	239	Total	C	N	O	S	0	0
			2015	1281	362	361	11		

- Molecule 6 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	105	Total	C	N	O	S	0	0
			860	530	161	165	4		

- Molecule 7 is a protein called Zinc finger protein ubi-d4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	70	Total	C	N	O	S	0	0
			580	361	112	102	5		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

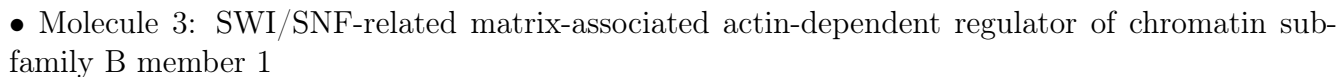
Mol	Chain	Residues	Atoms		AltConf
8	L	1	Total	Zn	0
			1	1	

[illegible]

- Molecule 2: AT-rich interactive domain-containing protein 1A

[illegible]

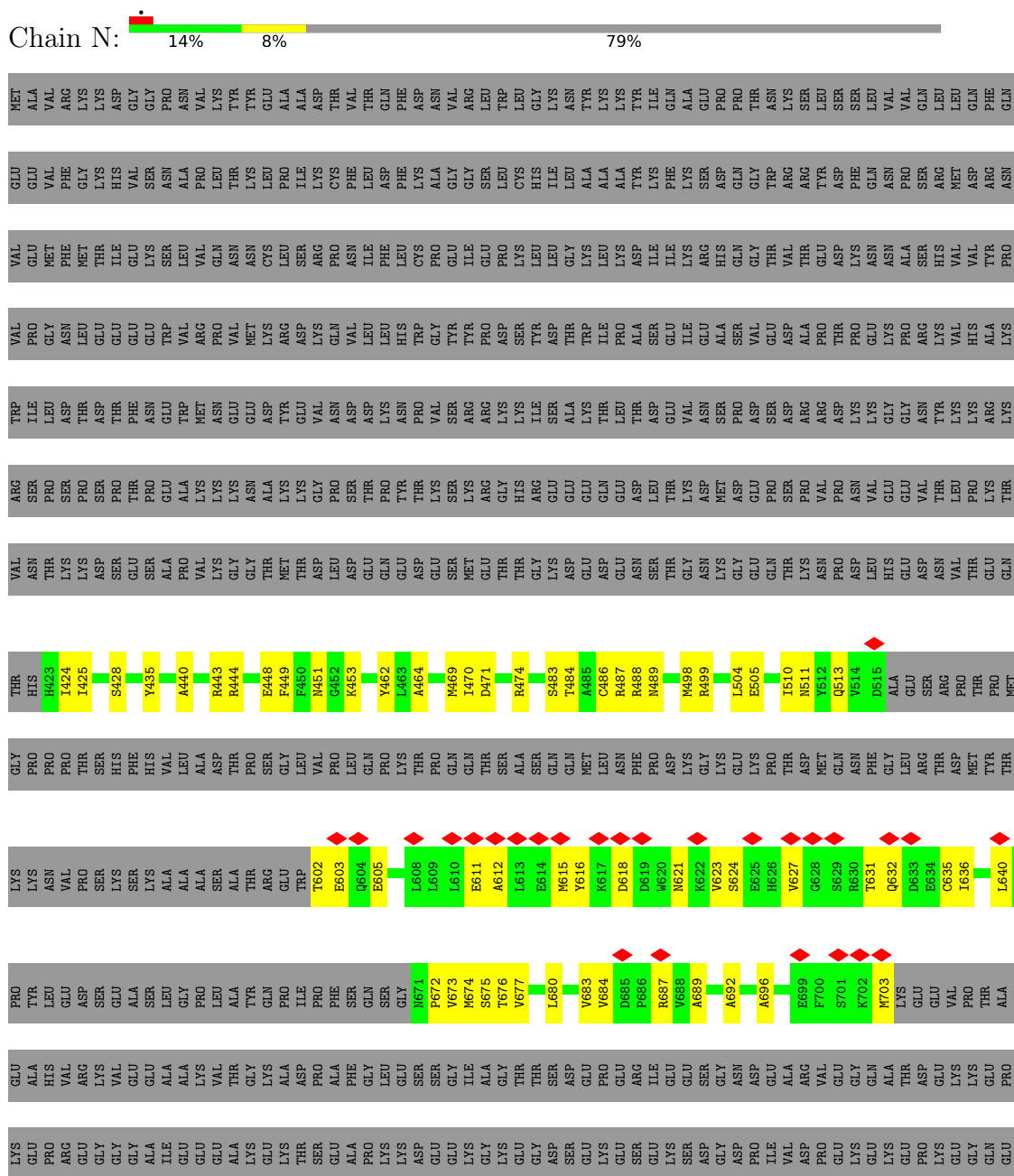




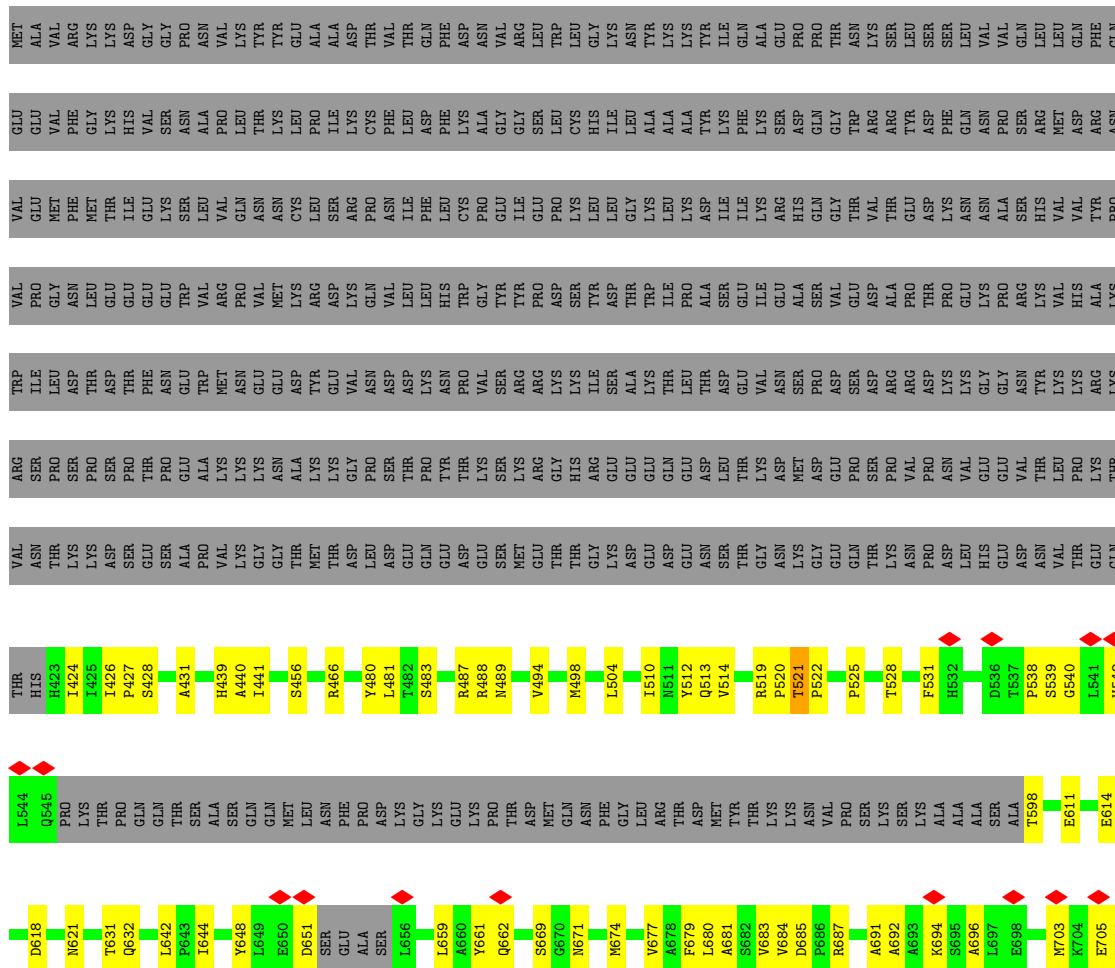
Frequency	Percentage
Daily	51%
Weekly	16%
Monthly	33%

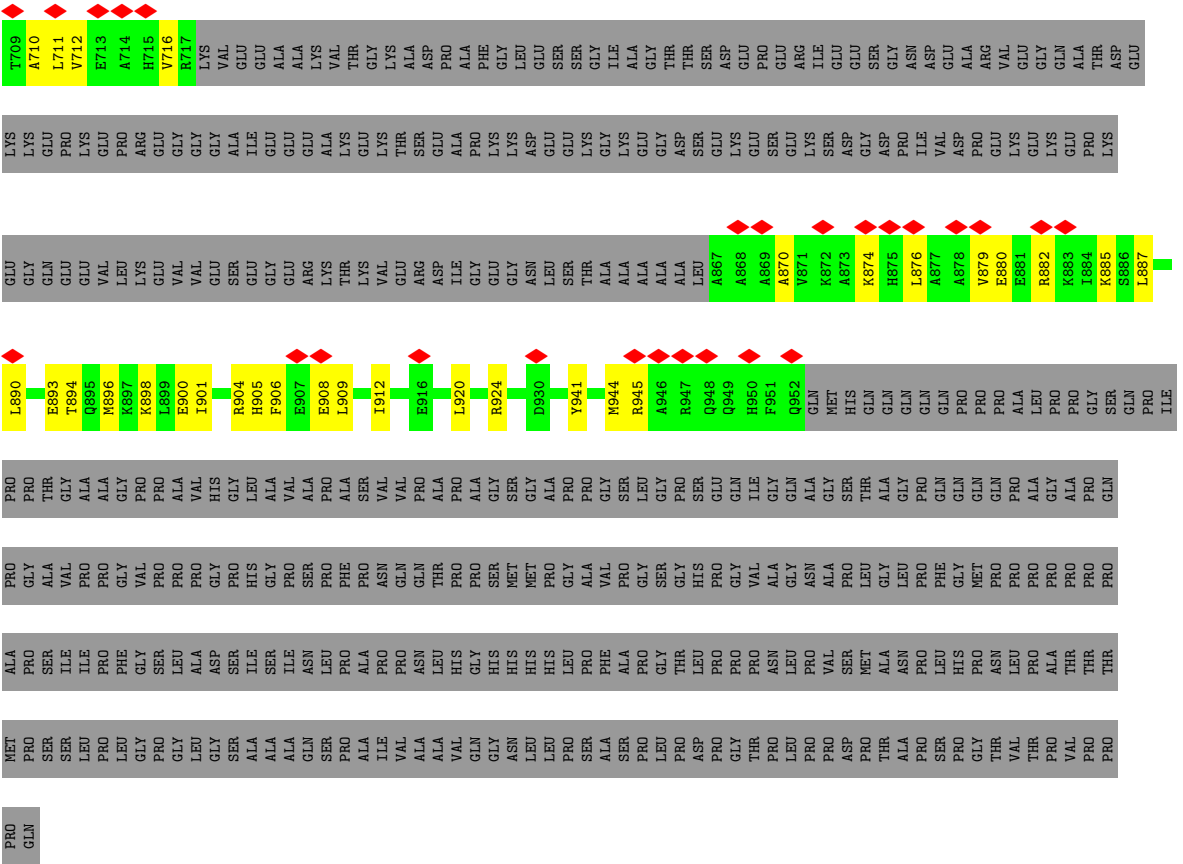


- Molecule 4: SWI/SNF complex subunit SMARCC2

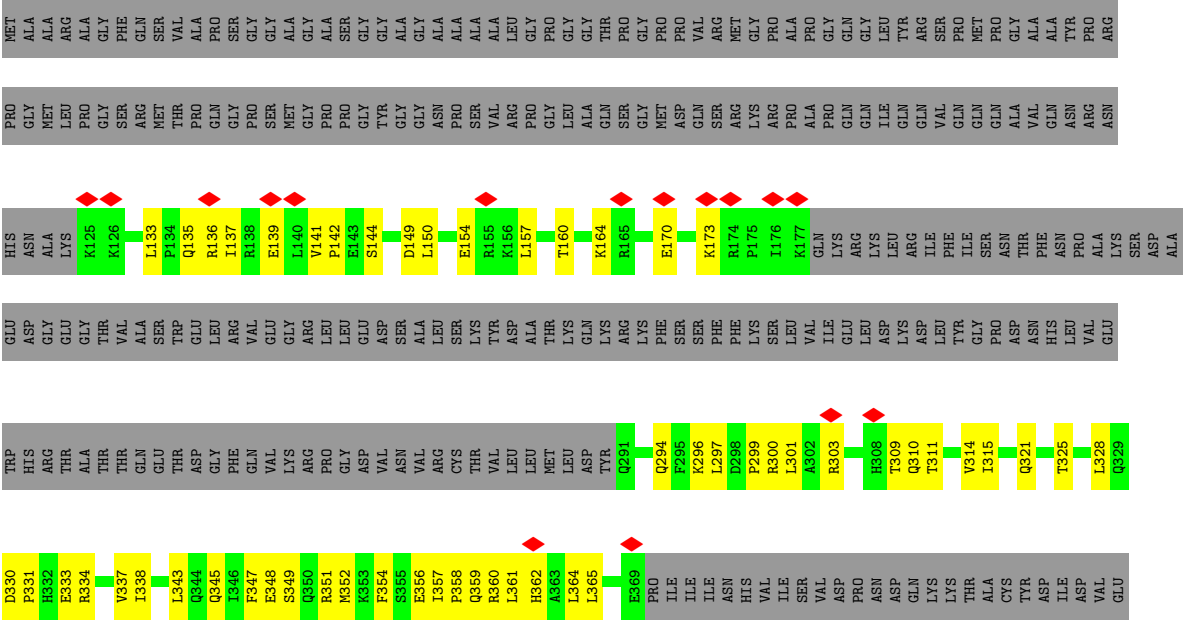
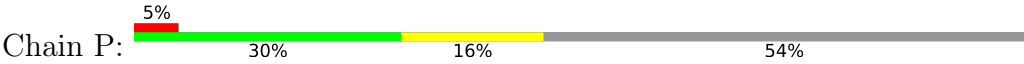


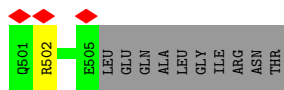
- Molecule 4: SWI/SNF complex subunit SMARCC2

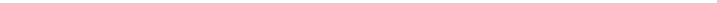


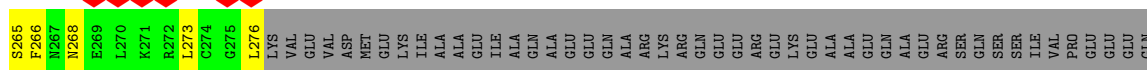


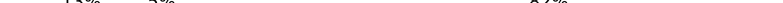
● Molecule 5: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family D member 1

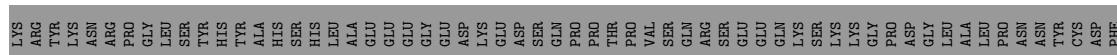




- Chain Q: 



- Chain R:  13% 5% 82%



SER	GLU	ASN	ASP	ASP	GLN	LEU	LEU	PHE	CYS	ASP	ASP	CYS	ASP	ARG	GLY	TYR	HIS	MET	TYR	CYS	THR	PRO	SER	MET	SER	GLU	PRO	PRO	GLU	GLY	SER	TRP	SER	SER	CYS	HIS	LEU	CYS	LEU	ASP	LEU	LEU	LYS	GLU	LYS	ALA	SER	ILE	TYR	GLN	ASN	GLN	ASN	SER	SER
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	197606	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.938	Depositor
Minimum map value	-2.357	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	1	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	I	0.24	0/1029	0.54	0/1370
2	L	0.25	0/3739	0.40	0/5070
3	M	0.26	0/2110	0.45	2/2856 (0.1%)
4	N	0.27	0/2158	0.44	0/2908
4	O	0.25	0/2692	0.46	0/3646
5	P	0.24	0/2055	0.45	0/2764
6	Q	0.24	0/871	0.49	0/1168
7	R	0.25	0/595	0.46	0/799
All	All	0.25	0/15249	0.45	2/20581 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	304	GLY	CA-C-N	-5.01	112.36	121.32
3	M	304	GLY	C-N-CA	-5.01	112.36	121.32

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	I	1022	0	1092	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	3670	0	3724	92	0
3	M	2070	0	2036	43	0
4	N	2120	0	2116	81	0
4	O	2632	0	2606	95	0
5	P	2015	0	2046	71	0
6	Q	860	0	864	31	0
7	R	580	0	557	20	0
8	L	1	0	0	0	0
All	All	14970	0	15041	366	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 12.

All (366) 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)
2:L:1818:GLN:HA	4:O:428:SER:HB3	1.49	0.93
2:L:2263:VAL:HG22	5:P:358:PRO:HD3	1.64	0.79
5:P:352:MET:HE3	5:P:360:ARG:HG2	1.63	0.79
2:L:2157:ASP:OD1	2:L:2158:ARG:N	2.17	0.77
4:N:612:ALA:O	4:N:616:TYR:HB2	1.85	0.77
5:P:296:LYS:HG3	5:P:309:THR:HG22	1.66	0.77
2:L:2140:PRO:HG2	2:L:2143:ARG:HD2	1.67	0.76
5:P:300:ARG:HH22	5:P:345:GLN:HB3	1.50	0.76
3:M:51:TRP:HE1	3:M:92:LYS:HG3	1.49	0.75
3:M:95:GLU:O	3:M:99:ILE:HB	1.87	0.75
2:L:2202:SER:HB3	2:L:2231:MET:HE2	1.70	0.73
2:L:2017:LEU:O	2:L:2057:ARG:NH2	2.21	0.73
4:N:909:LEU:HA	4:N:912:ILE:HD12	1.70	0.73
4:N:683:VAL:HA	6:Q:211:VAL:HG12	1.69	0.73
3:M:347:ASP:OD1	4:O:488:ARG:NH2	2.23	0.72
2:L:1823:PHE:O	7:R:60:ARG:NH1	2.24	0.70
1:I:350:SER:OG	1:I:351:ARG:N	2.23	0.70
3:M:301:LEU:O	7:R:38:ARG:NH1	2.25	0.70
3:M:305:GLY:HA2	4:N:489:ASN:HD22	1.57	0.69
5:P:361:LEU:HG	5:P:365:LEU:HD11	1.74	0.69
2:L:1736:VAL:HG22	2:L:1850:ASP:HA	1.72	0.68
4:N:464:ALA:HA	7:R:55:ILE:HG22	1.75	0.68
5:P:349:SER:H	5:P:360:ARG:HH21	1.43	0.67
4:N:484:THR:HA	4:N:487:ARG:HG2	1.76	0.67
2:L:1718:GLU:OE2	2:L:1721:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:902:LYS:NZ	5:P:154:GLU:OE2	2.29	0.66
4:O:894:THR:HG23	6:Q:241:LEU:HD23	1.79	0.65
6:Q:264:ASP:O	6:Q:268:ASN:ND2	2.29	0.65
1:I:377:ARG:NH1	4:O:651:ASP:OD2	2.30	0.65
4:N:687:ARG:NH1	4:O:703:MET:SD	2.70	0.65
4:O:887:LEU:HD23	6:Q:234:LEU:HB2	1.77	0.64
3:M:274:SER:O	3:M:353:LEU:HA	1.97	0.63
1:I:405:LYS:NZ	4:O:614:GLU:OE1	2.30	0.63
4:N:424:ILE:HD13	4:N:474:ARG:HD3	1.80	0.63
2:L:2178:ASP:OD1	2:L:2179:SER:N	2.30	0.62
4:N:932:GLN:HG2	6:Q:273:LEU:HD21	1.80	0.62
2:L:1805:LEU:HD21	4:O:431:ALA:HA	1.80	0.62
4:O:662:GLN:HG3	5:P:473:PRO:HG2	1.82	0.62
4:N:448:GLU:OE2	4:N:499:ARG:NE	2.29	0.62
4:N:692:ALA:HB2	4:O:696:ALA:HB2	1.82	0.61
1:I:468:ARG:HA	1:I:471:LYS:HD2	1.83	0.61
6:Q:188:MET:HA	6:Q:191:THR:HG22	1.81	0.61
2:L:2158:ARG:NH1	2:L:2201:ASP:OD2	2.34	0.61
4:N:913:MET:HE1	4:O:909:LEU:HD23	1.82	0.61
4:N:901:ILE:HB	5:P:417:ILE:HD11	1.83	0.61
5:P:297:LEU:HD21	5:P:315:ILE:HD13	1.82	0.60
6:Q:223:ARG:HB3	6:Q:224:MET:HE2	1.83	0.60
6:Q:180:ASP:OD1	6:Q:181:ASP:N	2.34	0.60
5:P:300:ARG:NH1	5:P:345:GLN:O	2.23	0.60
4:O:621:ASN:OD1	4:O:632:GLN:NE2	2.34	0.59
4:N:877:ALA:HB2	5:P:441:MET:HB2	1.85	0.59
4:O:684:VAL:O	5:P:449:GLN:NE2	2.36	0.59
4:N:696:ALA:HB2	4:O:692:ALA:HB2	1.85	0.59
2:L:1847:GLY:HA3	2:L:2009:LEU:HD22	1.84	0.58
2:L:2096:SER:OG	2:L:2098:GLU:OE1	2.22	0.58
4:N:489:ASN:ND2	7:R:43:ASP:OD2	2.36	0.58
3:M:185:VAL:HG13	3:M:208:MET:HB3	1.85	0.58
4:N:917:ARG:HH12	4:O:909:LEU:HG	1.68	0.58
7:R:58:GLU:H	7:R:61:HIS:HD2	1.51	0.58
2:L:1828:SER:OG	2:L:1835:GLN:NE2	2.36	0.58
5:P:294:GLN:HB2	5:P:311:THR:HG22	1.86	0.58
2:L:1705:ASN:ND2	2:L:1707:SER:OG	2.37	0.58
2:L:2162:VAL:HG22	2:L:2166:MET:HE3	1.85	0.58
5:P:294:GLN:HA	5:P:311:THR:HA	1.86	0.58
1:I:451:ARG:NH2	2:L:2165:GLU:OE2	2.36	0.58
4:O:890:LEU:O	4:O:893:GLU:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:367:LEU:HD13	4:O:659:LEU:HD12	1.86	0.57
5:P:297:LEU:HD22	5:P:301:LEU:HD23	1.84	0.57
7:R:17:TYR:O	7:R:21:MET:HG2	2.04	0.57
3:M:265:LYS:O	3:M:318:GLN:NE2	2.31	0.57
4:N:923:GLN:OE1	4:O:924:ARG:NH2	2.37	0.57
4:O:908:GLU:OE2	6:Q:252:HIS:NE2	2.33	0.57
4:N:618:ASP:OD1	4:N:618:ASP:N	2.36	0.57
1:I:406:ALA:HB1	4:O:644:ILE:HG12	1.88	0.56
2:L:1686:TRP:CD1	4:O:542:VAL:HG23	2.40	0.56
3:M:277:ASP:HB3	3:M:351:PRO:HA	1.86	0.56
5:P:328:LEU:O	5:P:338:ILE:N	2.39	0.56
2:L:1652:VAL:O	6:Q:189:LYS:NZ	2.35	0.56
4:O:427:PRO:HG3	4:O:512:TYR:CZ	2.41	0.56
5:P:410:SER:O	5:P:413:SER:OG	2.21	0.56
1:I:377:ARG:HD2	4:O:648:TYR:HD2	1.72	0.55
3:M:305:GLY:HA2	4:N:489:ASN:ND2	2.21	0.55
3:M:216:GLU:OE2	3:M:242:ARG:NH1	2.27	0.55
4:N:602:THR:HG23	4:N:605:GLU:H	1.70	0.55
4:O:876:LEU:HA	4:O:879:VAL:HG12	1.89	0.55
4:N:470:ILE:HA	4:N:510:ILE:HD11	1.88	0.55
4:O:941:TYR:HA	4:O:944:MET:HB2	1.88	0.55
4:O:618:ASP:OD2	5:P:498:LYS:NZ	2.30	0.55
2:L:2002:SER:O	2:L:2076:TYR:OH	2.23	0.55
1:I:467:LYS:HG2	1:I:471:LYS:HE3	1.88	0.55
2:L:2203:LEU:HD22	2:L:2266:LEU:HD12	1.89	0.55
4:O:611:GLU:HG3	4:O:615:MET:HE3	1.88	0.55
2:L:2227:SER:OG	2:L:2228:VAL:N	2.38	0.54
4:N:948:GLN:O	4:N:952:GLN:NE2	2.37	0.54
3:M:51:TRP:NE1	3:M:92:LYS:HG3	2.21	0.54
4:N:621:ASN:OD1	4:N:632:GLN:NE2	2.41	0.54
2:L:1676:LEU:HD23	2:L:1687:ALA:HB1	1.89	0.54
4:N:909:LEU:HD11	5:P:164:LYS:HB2	1.88	0.54
4:O:514:VAL:HB	4:O:519:ARG:HH21	1.73	0.54
2:L:1706:LEU:H	2:L:1997:ASN:ND2	2.05	0.54
5:P:425:HIS:O	5:P:429:GLU:HG3	2.08	0.54
4:O:661:TYR:CE1	5:P:457:GLN:HG2	2.43	0.54
4:O:887:LEU:HD21	6:Q:235:MET:HG3	1.90	0.54
5:P:331:PRO:O	5:P:334:ARG:NE	2.32	0.54
5:P:401:LYS:HG2	5:P:405:ASN:HD21	1.72	0.53
7:R:44:SER:C	7:R:46:THR:H	2.16	0.53
2:L:1998:ASP:OD1	2:L:1999:PHE:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:439:HIS:CD2	4:O:441:ILE:H	2.27	0.53
5:P:401:LYS:O	5:P:405:ASN:ND2	2.41	0.53
1:I:424:MET:O	1:I:428:THR:OG1	2.23	0.53
4:N:504:LEU:HB3	4:N:510:ILE:HG12	1.90	0.52
5:P:462:ASP:OD1	6:Q:195:ARG:NH1	2.43	0.52
1:I:361:LEU:HD13	4:N:672:PRO:HG3	1.91	0.52
2:L:1671:ARG:NH2	4:O:539:SER:HB3	2.24	0.52
2:L:2103:PHE:HB2	2:L:2106:LEU:HD23	1.92	0.52
2:L:1959:PRO:HG3	2:L:2019:HIS:CE1	2.45	0.52
3:M:186:LEU:HB3	3:M:205:THR:CG2	2.39	0.52
4:O:879:VAL:O	4:O:882:ARG:HD3	2.10	0.52
5:P:321:GLN:NE2	5:P:325:THR:OG1	2.43	0.52
4:N:449:PHE:CG	4:N:462:TYR:HB2	2.45	0.52
3:M:38:MET:HE3	3:M:46:ARG:HG2	1.90	0.51
4:N:435:TYR:OH	4:N:471:ASP:OD2	2.24	0.51
5:P:354:PHE:O	5:P:357:ILE:HG13	2.10	0.51
4:N:483:SER:OG	4:N:498:MET:HG2	2.11	0.51
4:O:708:PRO:HG2	4:O:711:LEU:HD23	1.92	0.51
4:O:880:GLU:HG2	6:Q:227:LEU:HB3	1.93	0.51
3:M:32:VAL:HG21	3:M:91:LEU:HD22	1.92	0.51
2:L:1971:LEU:HB2	2:L:1974:GLN:HG3	1.93	0.50
3:M:180:ALA:O	4:N:451:ASN:ND2	2.45	0.50
5:P:361:LEU:HD12	5:P:364:LEU:HB2	1.92	0.50
3:M:60:ARG:HH11	3:M:88:VAL:HG12	1.76	0.50
6:Q:178:ASP:OD1	6:Q:178:ASP:N	2.44	0.50
2:L:2165:GLU:HA	2:L:2168:VAL:HG12	1.92	0.50
4:O:674:MET:HA	4:O:677:VAL:HG12	1.94	0.50
1:I:461:LYS:HE3	2:L:2128:GLN:HA	1.93	0.50
2:L:1657:ARG:NH1	2:L:1658:ARG:O	2.43	0.50
4:O:631:THR:HG22	4:O:632:GLN:H	1.76	0.50
3:M:21:ASP:N	3:M:21:ASP:OD1	2.43	0.49
4:N:939:LEU:O	4:N:943:GLU:HG2	2.12	0.49
4:O:598:THR:N	7:R:78:ARG:HA	2.26	0.49
5:P:437:GLN:O	5:P:441:MET:HG2	2.12	0.49
1:I:449:GLU:HG3	1:I:450:ALA:H	1.77	0.49
2:L:1731:LEU:HD21	2:L:2013:LYS:HG3	1.94	0.49
3:M:58:GLU:OE2	3:M:62:LYS:NZ	2.45	0.49
3:M:214:THR:HG23	3:M:217:MET:HE3	1.95	0.49
4:N:948:GLN:HE22	4:O:945:ARG:HH11	1.59	0.49
2:L:2113:SER:OG	2:L:2116:ARG:HG3	2.12	0.49
2:L:2146:LYS:O	2:L:2150:THR:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:137:ILE:HG12	5:P:435:LYS:HD3	1.94	0.49
5:P:321:GLN:NE2	5:P:321:GLN:O	2.45	0.49
2:L:1714:GLU:O	2:L:1718:GLU:HG2	2.13	0.49
4:O:898:LYS:O	4:O:901:ILE:HG22	2.12	0.49
4:O:466:ARG:HB2	4:O:504:LEU:HD11	1.94	0.49
5:P:135:GLN:O	5:P:139:GLU:HG2	2.13	0.49
4:O:525:PRO:HB3	7:R:48:VAL:HG11	1.94	0.49
7:R:30:ARG:O	7:R:34:GLU:HG3	2.12	0.49
2:L:1648:ALA:O	2:L:1650:GLN:NE2	2.46	0.49
4:O:712:VAL:O	4:O:716:VAL:HG23	2.13	0.49
2:L:1673:MET:O	2:L:1677:LYS:HB2	2.13	0.49
4:O:679:PHE:O	4:O:683:VAL:HG23	2.13	0.49
5:P:300:ARG:NH2	5:P:345:GLN:HB3	2.22	0.49
2:L:1686:TRP:HD1	4:O:542:VAL:HG23	1.78	0.48
2:L:1740:GLY:O	2:L:1744:LEU:N	2.46	0.48
2:L:2086:ASP:OD1	2:L:2143:ARG:NH1	2.34	0.48
4:O:882:ARG:HA	4:O:885:LYS:HG2	1.95	0.48
2:L:2275:ILE:HA	2:L:2278:VAL:HG12	1.95	0.48
4:N:935:HIS:ND1	6:Q:276:LEU:O	2.31	0.48
4:N:611:GLU:O	4:N:615:MET:HG2	2.14	0.48
2:L:1706:LEU:H	2:L:1997:ASN:HD21	1.61	0.48
5:P:498:LYS:O	5:P:502:ARG:HG2	2.14	0.48
1:I:441:ARG:NE	6:Q:177:GLU:OE1	2.46	0.48
4:N:602:THR:OG1	4:N:603:GLU:N	2.46	0.48
5:P:488:GLN:O	5:P:491:VAL:HG22	2.14	0.48
7:R:58:GLU:H	7:R:61:HIS:CD2	2.32	0.48
4:N:632:GLN:O	4:N:636:ILE:HG22	2.14	0.48
1:I:463:GLU:O	1:I:466:ARG:HG3	2.13	0.48
4:O:540:GLY:O	4:O:543:PRO:HD2	2.14	0.48
5:P:343:LEU:O	5:P:347:PHE:N	2.47	0.48
4:N:623:VAL:O	4:N:627:VAL:HG23	2.13	0.48
4:N:928:LEU:O	4:N:932:GLN:HG3	2.13	0.48
3:M:293:PHE:HD1	4:O:498:MET:SD	2.36	0.47
4:O:488:ARG:NH1	4:O:489:ASN:OD1	2.47	0.47
2:L:1667:PRO:HG3	2:L:1690:THR:HG21	1.95	0.47
4:N:673:VAL:HG23	4:O:680:LEU:HD21	1.96	0.47
2:L:2156:SER:HB3	2:L:2194:ASN:ND2	2.28	0.47
5:P:337:VAL:HB	5:P:354:PHE:CE1	2.49	0.47
1:I:358:PRO:HB3	4:N:676:THR:OG1	2.15	0.47
1:I:444:ARG:NH2	6:Q:176:ALA:O	2.48	0.47
4:N:898:LYS:HG3	5:P:417:ILE:HD12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:224:MET:O	6:Q:228:LYS:HG3	2.15	0.47
2:L:1971:LEU:HD23	5:P:461:ARG:NH2	2.30	0.47
4:O:481:LEU:HA	7:R:28:ASN:ND2	2.29	0.47
5:P:137:ILE:HD11	5:P:435:LYS:HB2	1.97	0.47
5:P:333:GLU:OE1	5:P:351:ARG:NH2	2.48	0.47
4:N:879:VAL:HG12	4:N:883:LYS:HE3	1.96	0.46
1:I:356:GLN:NE2	4:N:675:SER:HB2	2.30	0.46
2:L:2007:LEU:O	2:L:2011:LEU:HG	2.15	0.46
2:L:1723:CYS:HB3	2:L:1981:CYS:HB2	1.98	0.46
4:O:480:TYR:HB2	4:O:514:VAL:HG11	1.96	0.46
5:P:474:GLU:OE1	5:P:478:ARG:NH1	2.46	0.46
2:L:1741:GLN:HE21	2:L:1843:HIS:CD2	2.33	0.46
4:O:705:GLU:O	4:O:705:GLU:HG2	2.16	0.46
6:Q:265:SER:HA	6:Q:268:ASN:HD21	1.81	0.46
2:L:1828:SER:C	2:L:1830:LYS:H	2.22	0.46
3:M:28:ILE:HB	3:M:31:GLU:HG3	1.98	0.46
3:M:306:GLU:OE1	3:M:306:GLU:N	2.37	0.46
5:P:356:GLU:N	5:P:356:GLU:OE1	2.48	0.46
1:I:398:THR:HA	1:I:401:THR:HG22	1.98	0.46
4:N:631:THR:O	4:N:635:CYS:N	2.37	0.46
4:O:480:TYR:CD2	4:O:520:PRO:HD2	2.49	0.46
4:O:481:LEU:HD23	4:O:510:ILE:HD11	1.98	0.46
5:P:297:LEU:HD23	5:P:297:LEU:HA	1.76	0.46
2:L:1828:SER:O	2:L:1829:ASP:HB2	2.16	0.46
2:L:2229:ASP:O	2:L:2233:ARG:HG3	2.16	0.46
2:L:1673:MET:HE2	2:L:1673:MET:HB3	1.79	0.45
2:L:1847:GLY:H	2:L:2080:ILE:HD11	1.81	0.45
6:Q:229:ARG:O	6:Q:232:GLN:HG3	2.17	0.45
6:Q:254:GLU:O	6:Q:258:LYS:HG2	2.16	0.45
2:L:1653:LEU:HD11	6:Q:190:HIS:HE1	1.80	0.45
2:L:1805:LEU:HD23	4:O:426:ILE:HG21	1.98	0.45
4:N:505:GLU:OE2	4:N:511:ASN:ND2	2.43	0.45
4:O:424:ILE:HA	4:O:513:GLN:HE22	1.81	0.45
4:O:671:ASN:HB3	4:O:674:MET:HB3	1.98	0.45
3:M:350:CYS:HB2	7:R:27:TYR:CZ	2.52	0.45
4:O:424:ILE:HA	4:O:513:GLN:NE2	2.32	0.45
2:L:1980:ARG:O	2:L:1984:VAL:HG23	2.17	0.45
2:L:2011:LEU:O	2:L:2015:ILE:HG13	2.17	0.45
3:M:283:MET:HE3	3:M:323:GLN:OE1	2.17	0.45
4:N:909:LEU:HD22	4:O:906:PHE:CZ	2.52	0.45
5:P:330:ASP:HB3	5:P:333:GLU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:900:GLU:C	4:O:904:ARG:HE	2.22	0.45
2:L:1854:HIS:HB3	4:N:440:ALA:HB3	1.99	0.45
4:N:866:LEU:HD11	4:O:681:ALA:HA	1.99	0.45
4:O:439:HIS:CG	4:O:440:ALA:H	2.35	0.45
1:I:356:GLN:HE22	1:I:358:PRO:HA	1.81	0.44
2:L:1851:THR:OG1	2:L:1853:GLU:HG3	2.17	0.44
1:I:448:ARG:O	1:I:452:ILE:HG12	2.17	0.44
3:M:36:LEU:HD21	3:M:100:LEU:HD23	1.98	0.44
4:N:673:VAL:O	4:N:677:VAL:HG13	2.17	0.44
4:O:896:MET:HE2	4:O:896:MET:HB2	1.70	0.44
4:N:872:LYS:NZ	6:Q:210:SER:O	2.45	0.44
3:M:17:PHE:CE2	3:M:28:ILE:HG13	2.52	0.44
4:N:424:ILE:HD11	4:O:531:PHE:HD2	1.83	0.44
4:N:928:LEU:HG	6:Q:266:PHE:HE1	1.82	0.44
5:P:310:GLN:HB3	5:P:314:VAL:HG21	1.99	0.44
2:L:2232:ARG:HG3	2:L:2236:ARG:NH1	2.33	0.44
3:M:86:THR:OG1	3:M:87:SER:N	2.50	0.44
2:L:2171:LEU:HD23	2:L:2171:LEU:HA	1.81	0.44
4:N:945:ARG:O	4:N:949:GLN:HG2	2.18	0.44
2:L:2156:SER:HB3	2:L:2194:ASN:HD21	1.81	0.44
3:M:350:CYS:HB2	7:R:27:TYR:OH	2.17	0.44
4:N:923:GLN:HB3	4:O:920:LEU:HD21	1.99	0.44
4:O:481:LEU:HA	7:R:28:ASN:HD21	1.83	0.44
2:L:1694:LEU:HB3	2:L:1704:PHE:HE2	1.83	0.44
5:P:297:LEU:HD13	5:P:301:LEU:HG	2.00	0.44
5:P:432:ASN:O	5:P:436:THR:HG23	2.17	0.44
1:I:378:ILE:O	1:I:382:ILE:HG13	2.18	0.43
2:L:1672:VAL:HG11	2:L:1691:ILE:HD11	2.00	0.43
3:M:345:ASP:O	3:M:349:TRP:HD1	2.01	0.43
4:N:471:ASP:OD1	4:O:528:THR:OG1	2.21	0.43
4:N:895:GLN:HG2	5:P:150:LEU:HB3	1.99	0.43
2:L:2015:ILE:HG21	2:L:2087:GLY:HA3	1.99	0.43
3:M:263:ILE:HD11	3:M:278:GLN:NE2	2.33	0.43
5:P:299:PRO:O	5:P:303:ARG:HG2	2.18	0.43
5:P:359:GLN:HA	5:P:362:HIS:HB2	2.00	0.43
1:I:449:GLU:HG3	1:I:450:ALA:N	2.32	0.43
1:I:374:LEU:HD23	1:I:374:LEU:HA	1.86	0.43
2:L:2024:ARG:HH22	5:P:149:ASP:CG	2.25	0.43
4:O:685:ASP:N	4:O:685:ASP:OD1	2.50	0.43
6:Q:214:ASP:HA	6:Q:216:ARG:CZ	2.48	0.43
6:Q:230:GLN:O	6:Q:234:LEU:HG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:79:TRP:HZ3	7:R:81:LYS:HE2	1.82	0.43
2:L:2232:ARG:HE	2:L:2236:ARG:HH22	1.64	0.43
4:N:428:SER:CB	4:O:538:PRO:HA	2.49	0.43
4:N:948:GLN:NE2	4:O:945:ARG:HD3	2.33	0.43
4:O:662:GLN:HE21	5:P:474:GLU:HG2	1.83	0.43
5:P:399:THR:OG1	5:P:400:LEU:N	2.50	0.43
4:N:488:ARG:HH11	7:R:45:GLN:HG2	1.84	0.43
5:P:453:ASN:O	5:P:457:GLN:HG3	2.18	0.43
6:Q:255:LYS:HD3	6:Q:255:LYS:HA	1.78	0.43
3:M:341:ARG:NH1	4:O:488:ARG:O	2.51	0.43
4:N:946:ALA:O	4:N:950:HIS:HB2	2.19	0.43
4:O:540:GLY:HA3	5:P:493:ARG:HH22	1.84	0.43
5:P:401:LYS:HG2	5:P:405:ASN:ND2	2.33	0.43
1:I:417:ARG:HB3	5:P:482:TYR:OH	2.18	0.43
4:N:640:LEU:HD21	4:N:689:ALA:HB1	2.01	0.43
5:P:435:LYS:HE3	5:P:435:LYS:HB3	1.83	0.43
3:M:259:ASP:OD2	4:O:456:SER:OG	2.26	0.43
4:N:948:GLN:HE22	4:O:945:ARG:NH1	2.16	0.43
2:L:1735:GLU:HA	2:L:1849:GLY:O	2.19	0.42
3:M:60:ARG:O	3:M:64:VAL:HG23	2.19	0.42
4:N:703:MET:HE3	4:O:687:ARG:HD2	2.01	0.42
5:P:348:GLU:OE1	5:P:348:GLU:N	2.40	0.42
1:I:350:SER:C	1:I:351:ARG:HD2	2.45	0.42
4:N:674:MET:HA	4:N:677:VAL:HG22	2.01	0.42
2:L:1736:VAL:HG23	4:N:443:ARG:HH22	1.84	0.42
2:L:1702:MET:HE1	2:L:1995:PRO:HG2	2.02	0.42
2:L:1956:GLU:HB2	2:L:2022:PRO:HD2	2.02	0.42
2:L:2133:ASP:HB3	3:M:39:PHE:CG	2.53	0.42
7:R:21:MET:HE2	7:R:21:MET:HB3	1.80	0.42
1:I:456:LEU:O	1:I:460:GLN:HG3	2.19	0.42
2:L:1989:ARG:O	2:L:1992:SER:OG	2.30	0.42
4:N:624:SER:HB2	4:N:635:CYS:SG	2.59	0.42
4:N:680:LEU:O	4:N:683:VAL:HG22	2.19	0.42
4:N:917:ARG:NH1	4:O:909:LEU:HG	2.34	0.42
4:O:691:ALA:O	4:O:694:LYS:HG3	2.19	0.42
5:P:457:GLN:O	5:P:461:ARG:HD3	2.20	0.42
1:I:461:LYS:HE3	2:L:2129:ASP:H	1.84	0.42
3:M:195:ILE:HG21	3:M:232:THR:HG21	2.02	0.42
4:N:903:LEU:O	4:N:906:PHE:HB3	2.20	0.42
4:O:870:ALA:O	4:O:874:LYS:HG2	2.19	0.42
5:P:170:GLU:O	5:P:173:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:43:ASP:OD1	7:R:44:SER:N	2.52	0.42
3:M:344:GLY:O	3:M:345:ASP:C	2.63	0.42
4:O:708:PRO:C	4:O:710:ALA:H	2.27	0.42
5:P:133:LEU:HD12	5:P:144:SER:HB2	2.01	0.42
5:P:474:GLU:O	5:P:478:ARG:NH1	2.52	0.42
1:I:413:GLN:O	1:I:417:ARG:HG3	2.19	0.42
2:L:2007:LEU:HA	2:L:2007:LEU:HD23	1.85	0.42
3:M:266:LEU:O	3:M:276:VAL:HA	2.19	0.42
7:R:14:GLU:CD	7:R:14:GLU:H	2.28	0.42
3:M:306:GLU:HA	4:N:488:ARG:O	2.18	0.41
4:O:439:HIS:CG	4:O:440:ALA:N	2.88	0.41
4:O:521:THR:HG22	4:O:522:PRO:HD2	2.01	0.41
4:O:901:ILE:HD11	6:Q:249:GLU:OE1	2.20	0.41
2:L:2057:ARG:HD3	2:L:2091:TRP:CZ2	2.55	0.41
4:O:659:LEU:O	4:O:662:GLN:NE2	2.54	0.41
4:O:703:MET:O	4:O:706:GLU:HG2	2.20	0.41
2:L:2057:ARG:HA	2:L:2060:THR:HG22	2.02	0.41
2:L:2169:VAL:HG23	2:L:2230:MET:HE1	2.02	0.41
2:L:1645:SER:OG	4:O:669:SER:OG	2.20	0.41
2:L:2024:ARG:NH2	5:P:149:ASP:OD1	2.54	0.41
4:N:919:ALA:HA	4:N:922:TYR:CD2	2.55	0.41
4:O:488:ARG:HD3	4:O:489:ASN:ND2	2.36	0.41
4:O:908:GLU:O	4:O:912:ILE:HG23	2.20	0.41
6:Q:258:LYS:O	6:Q:261:GLU:HG3	2.20	0.41
1:I:358:PRO:HG3	4:N:676:THR:HA	2.03	0.41
2:L:2074:SER:OG	2:L:2130:ASN:HB3	2.21	0.41
3:M:291:GLU:OE2	3:M:316:ARG:NH1	2.54	0.41
4:O:901:ILE:HG12	4:O:905:HIS:NE2	2.35	0.41
1:I:405:LYS:NZ	4:O:611:GLU:OE2	2.53	0.41
2:L:2232:ARG:NE	2:L:2236:ARG:HH22	2.19	0.41
4:O:487:ARG:HD2	4:O:494:VAL:CG2	2.51	0.41
2:L:1730:ILE:HG23	2:L:1731:LEU:HG	2.02	0.41
2:L:1851:THR:O	4:N:444:ARG:HD2	2.21	0.41
4:N:425:ILE:H	4:N:513:GLN:NE2	2.19	0.41
5:P:136:ARG:HB2	5:P:435:LYS:HD2	2.02	0.41
4:N:451:ASN:HB3	4:N:453:LYS:HG2	2.03	0.41
5:P:141:VAL:HG22	5:P:142:PRO:O	2.20	0.41
4:N:684:VAL:HG21	4:N:871:VAL:HG21	2.02	0.40
2:L:2117:LEU:HD23	2:L:2117:LEU:HA	1.95	0.40
4:N:931:ARG:HG2	6:Q:273:LEU:HG	2.01	0.40
5:P:357:ILE:N	5:P:358:PRO:HD2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:1850:ASP:OD1	4:N:444:ARG:NH1	2.54	0.40
2:L:2085:LEU:HD11	2:L:2134:LEU:HB3	2.02	0.40
3:M:300:GLU:OE2	4:O:483:SER:N	2.42	0.40
2:L:1741:GLN:HE21	2:L:1843:HIS:HD2	1.68	0.40
2:L:2025:LYS:HA	2:L:2025:LYS:HD2	1.92	0.40
4:N:469:MET:HG2	4:N:486:CYS:SG	2.61	0.40
6:Q:229:ARG:CZ	6:Q:229:ARG:HB2	2.50	0.40
2:L:2262:SER:HB3	2:L:2275:ILE:HG22	2.04	0.40
3:M:17:PHE:CE1	3:M:63:ILE:HD11	2.56	0.40
3:M:351:PRO:HD3	4:O:487:ARG:NH2	2.36	0.40
4:O:642:LEU:HD23	4:O:642:LEU:HA	1.88	0.40
5:P:142:PRO:C	5:P:144:SER:H	2.29	0.40
5:P:157:LEU:O	5:P:160:THR:HG22	2.22	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	I	116/1647 (7%)	113 (97%)	3 (3%)	0	100	100
2	L	456/2285 (20%)	434 (95%)	22 (5%)	0	100	100
3	M	249/385 (65%)	239 (96%)	10 (4%)	0	100	100
4	N	253/1214 (21%)	247 (98%)	6 (2%)	0	100	100
4	O	317/1214 (26%)	303 (96%)	14 (4%)	0	100	100
5	P	233/515 (45%)	220 (94%)	13 (6%)	0	100	100
6	Q	103/411 (25%)	96 (93%)	7 (7%)	0	100	100
7	R	68/391 (17%)	61 (90%)	7 (10%)	0	100	100
All	All	1795/8062 (22%)	1713 (95%)	82 (5%)	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	I	110/1422 (8%)	110 (100%)	0	100	100
2	L	418/1845 (23%)	417 (100%)	1 (0%)	87	92
3	M	230/346 (66%)	230 (100%)	0	100	100
4	N	222/1030 (22%)	222 (100%)	0	100	100
4	O	282/1030 (27%)	281 (100%)	1 (0%)	84	90
5	P	223/442 (50%)	223 (100%)	0	100	100
6	Q	98/361 (27%)	98 (100%)	0	100	100
7	R	59/344 (17%)	59 (100%)	0	100	100
All	All	1642/6820 (24%)	1640 (100%)	2 (0%)	87	93

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

Mol	Chain	Res	Type
2	L	1692	ASN
4	O	521	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	I	356	GLN
2	L	1650	GLN
2	L	1692	ASN
2	L	1705	ASN
2	L	1835	GLN
2	L	1843	HIS
2	L	1858	HIS
2	L	1986	ASN
2	L	1997	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	L	2268	ASN
3	M	244	GLN
3	M	322	HIS
4	N	489	ASN
4	N	513	GLN
4	N	604	GLN
4	N	621	ASN
4	N	632	GLN
4	N	638	HIS
4	N	925	GLN
4	N	938	GLN
4	N	948	GLN
4	O	439	HIS
4	O	478	GLN
4	O	501	HIS
4	O	513	GLN
4	O	545	GLN
4	O	638	HIS
4	O	662	GLN
5	P	135	GLN
5	P	321	GLN
5	P	326	HIS
5	P	344	GLN
5	P	405	ASN
5	P	432	ASN
5	P	453	ASN
5	P	457	GLN
6	Q	190	HIS
6	Q	238	GLN
6	Q	267	ASN
6	Q	268	ASN
7	R	28	ASN
7	R	61	HIS
7	R	70	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

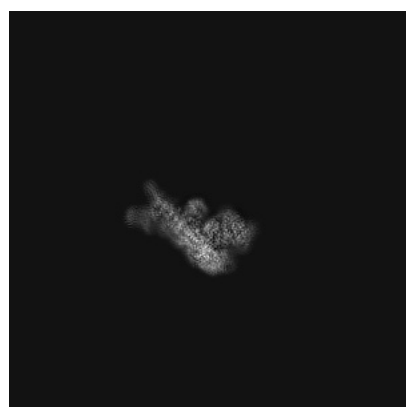
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0968. These allow visual inspection of the internal detail of the map and identification of artifacts.

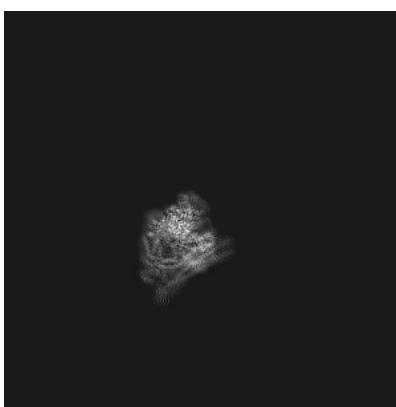
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

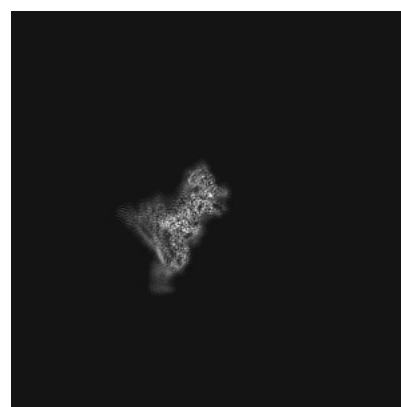
6.1.1 Primary map



X



Y

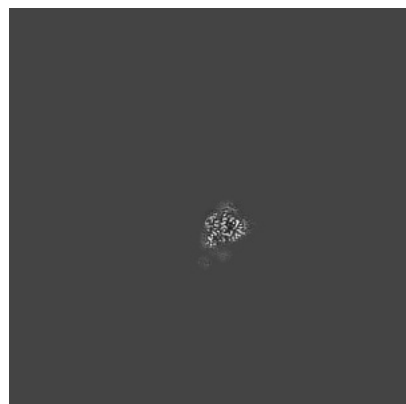


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256



Y Index: 256

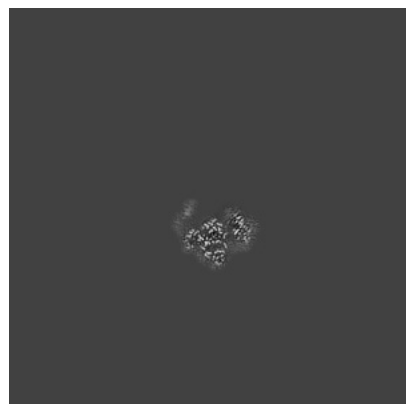


Z Index: 256

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

6.3 Largest variance slices [i](#)

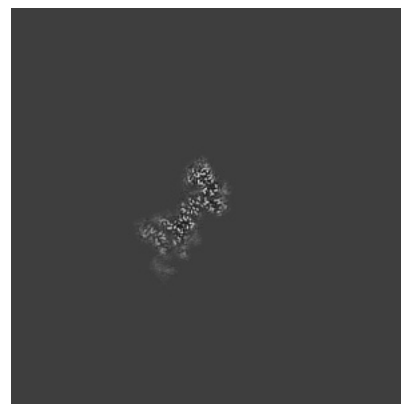
6.3.1 Primary map



X Index: 238



Y Index: 255

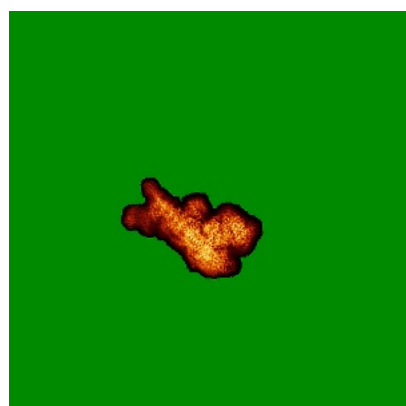


Z Index: 231

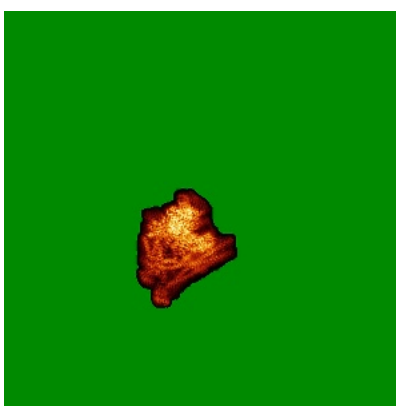
The images above show the largest variance slices of the map in three orthogonal directions.

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

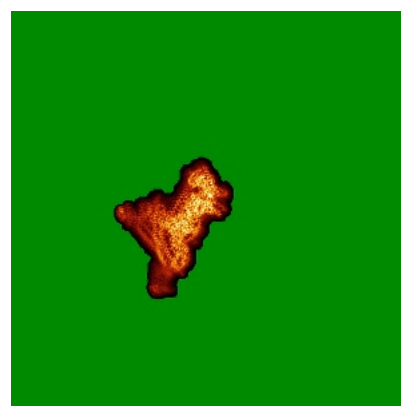
6.4.1 Primary map



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

This section was not generated.

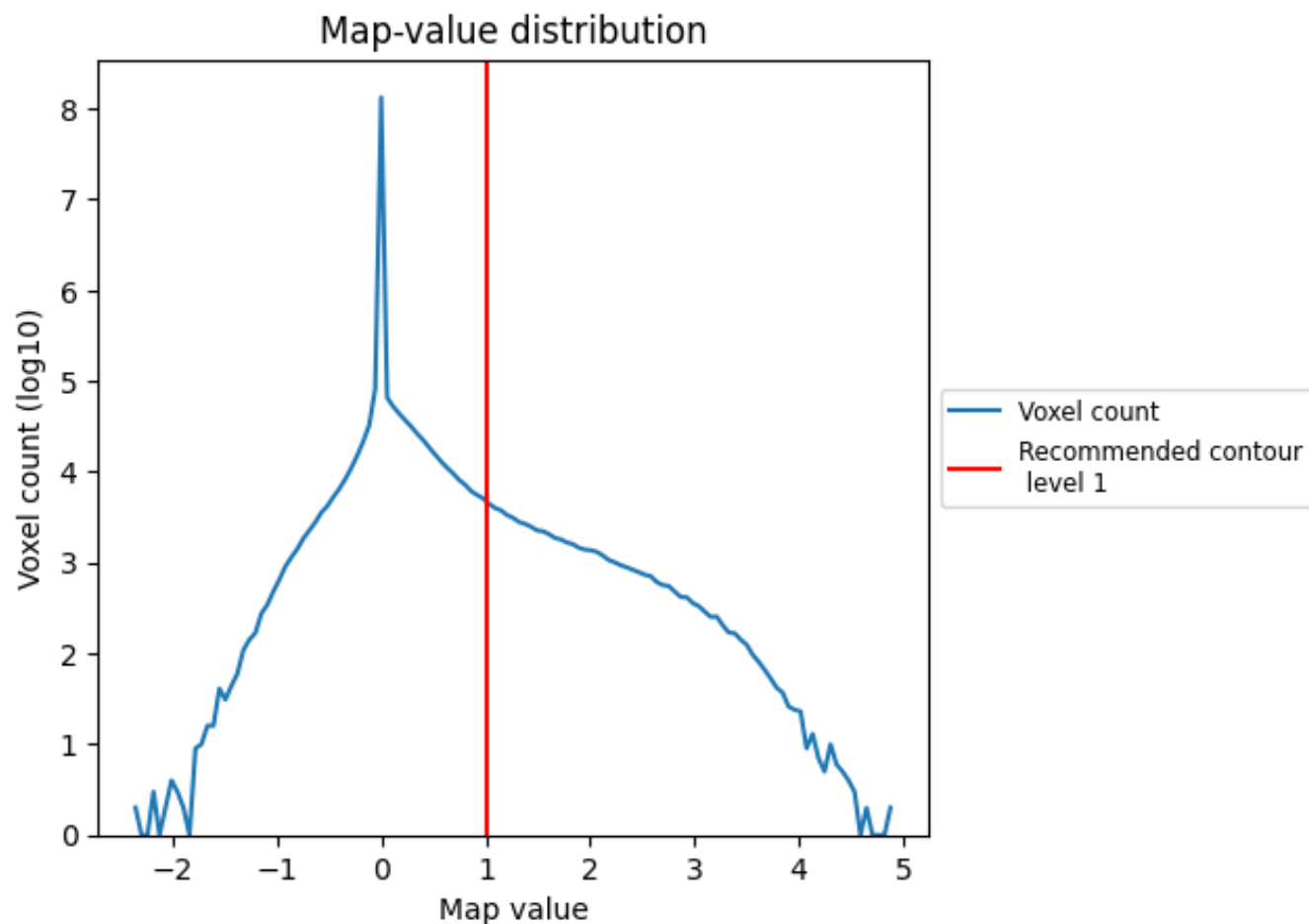
6.6 Mask visualisation

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

7 Map analysis [i](#)

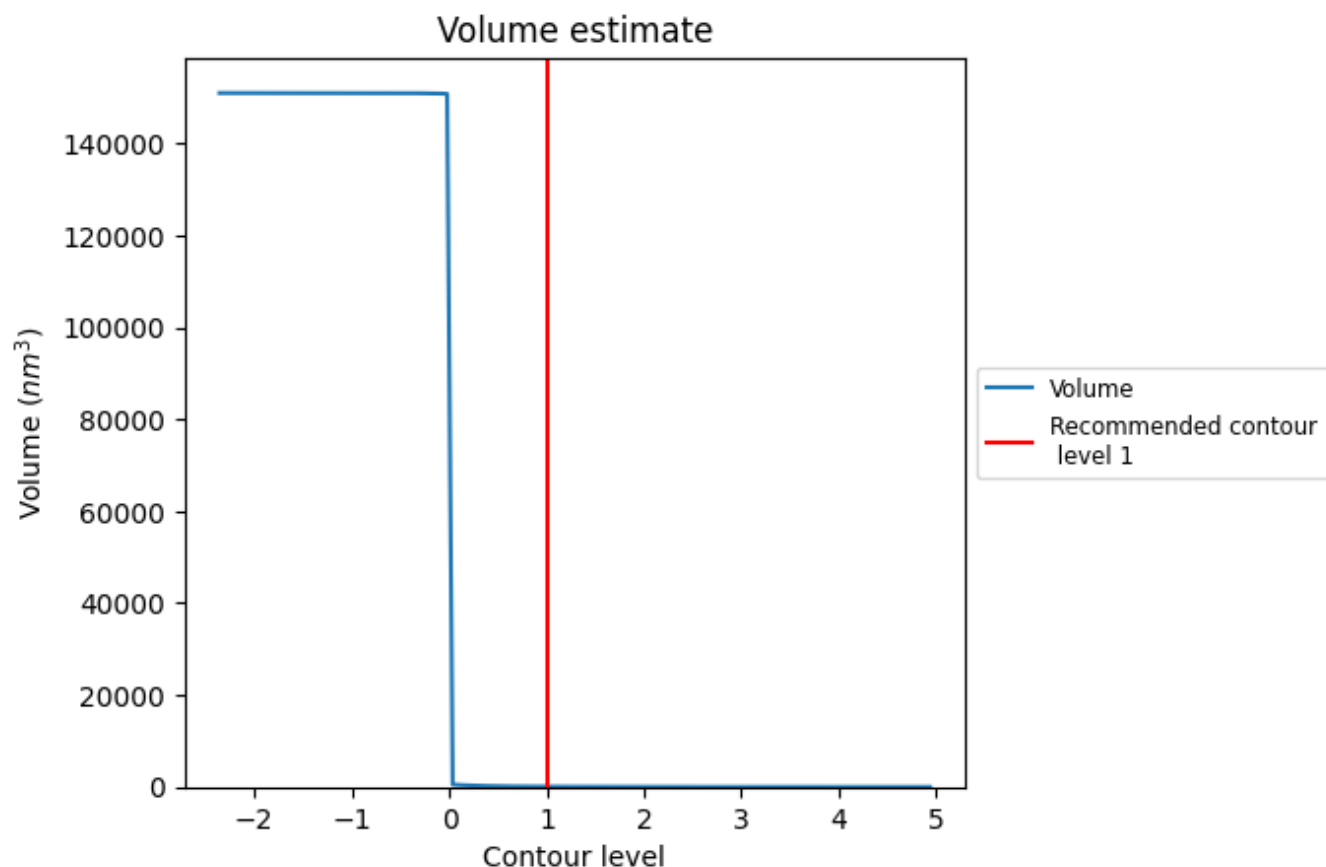
This section contains the results of statistical analysis of the map.

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.

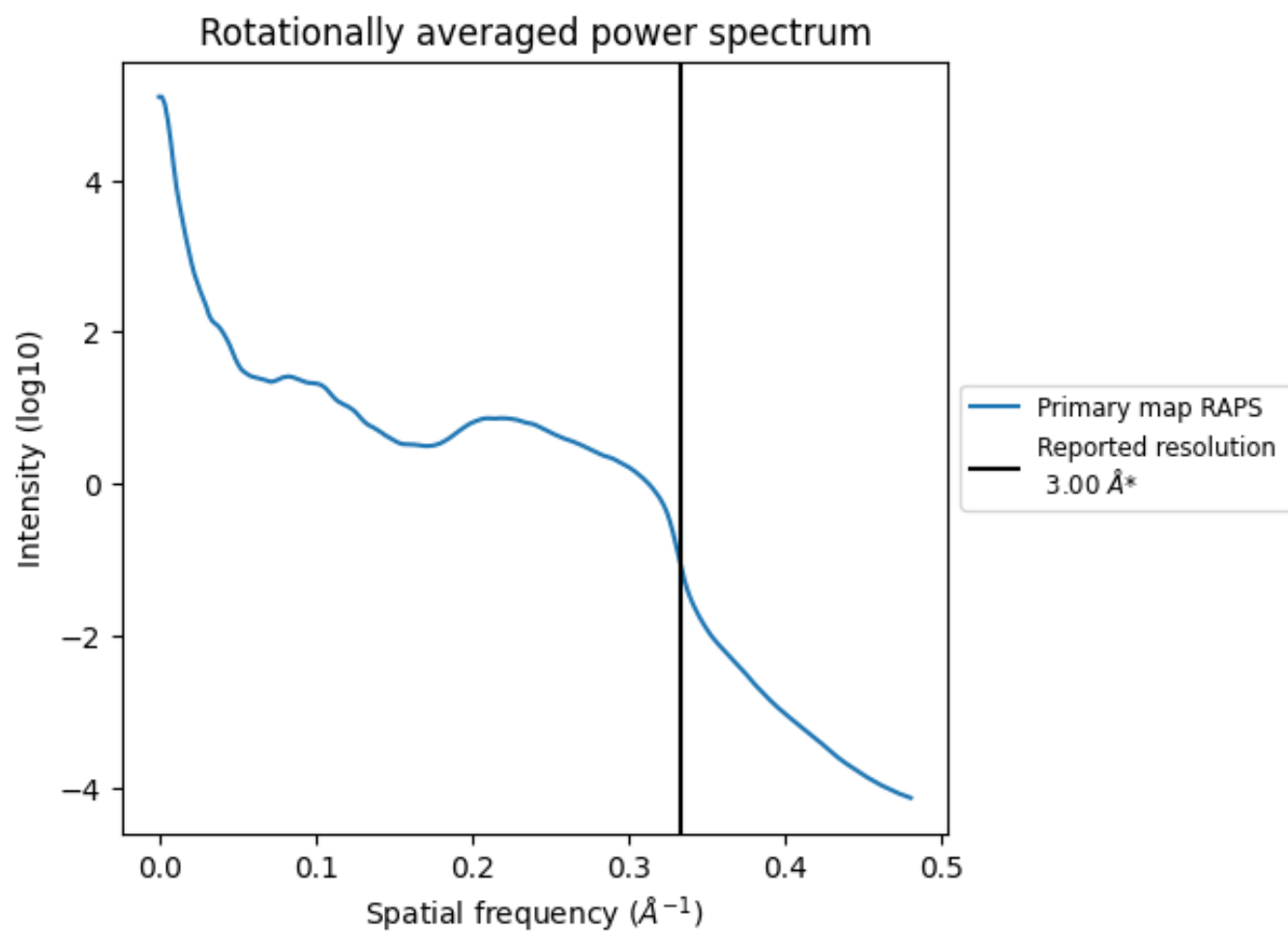
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 63 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 0.333 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

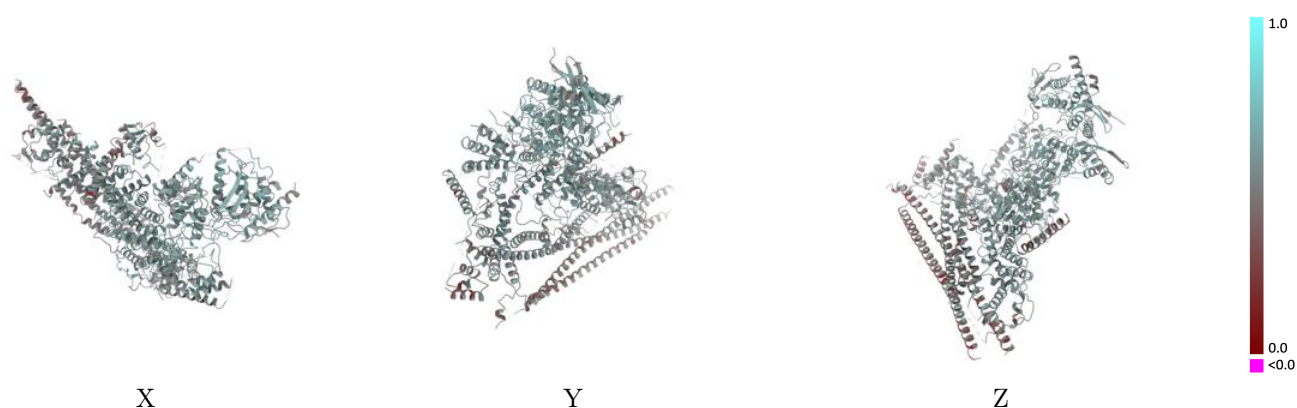
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0968 and PDB model 6LTH. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

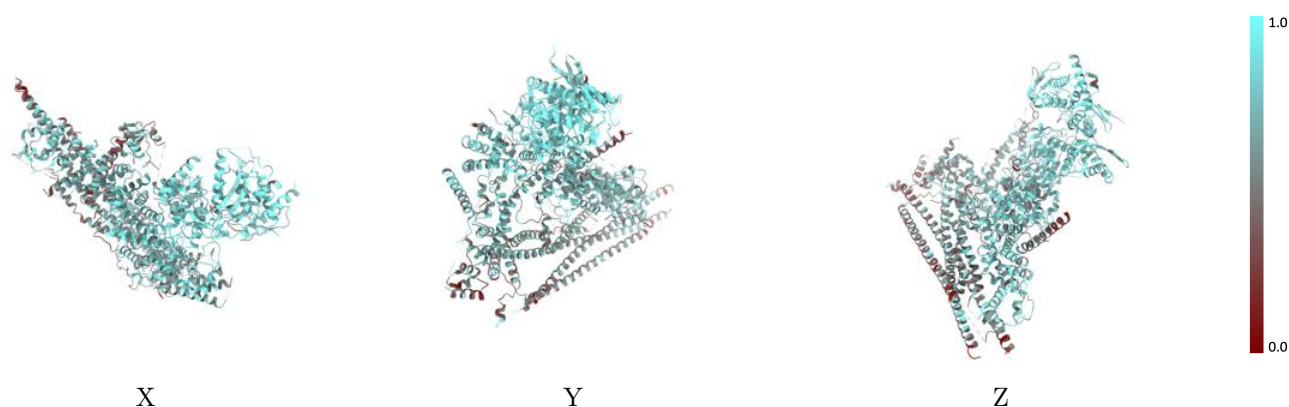
This section was not generated.

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



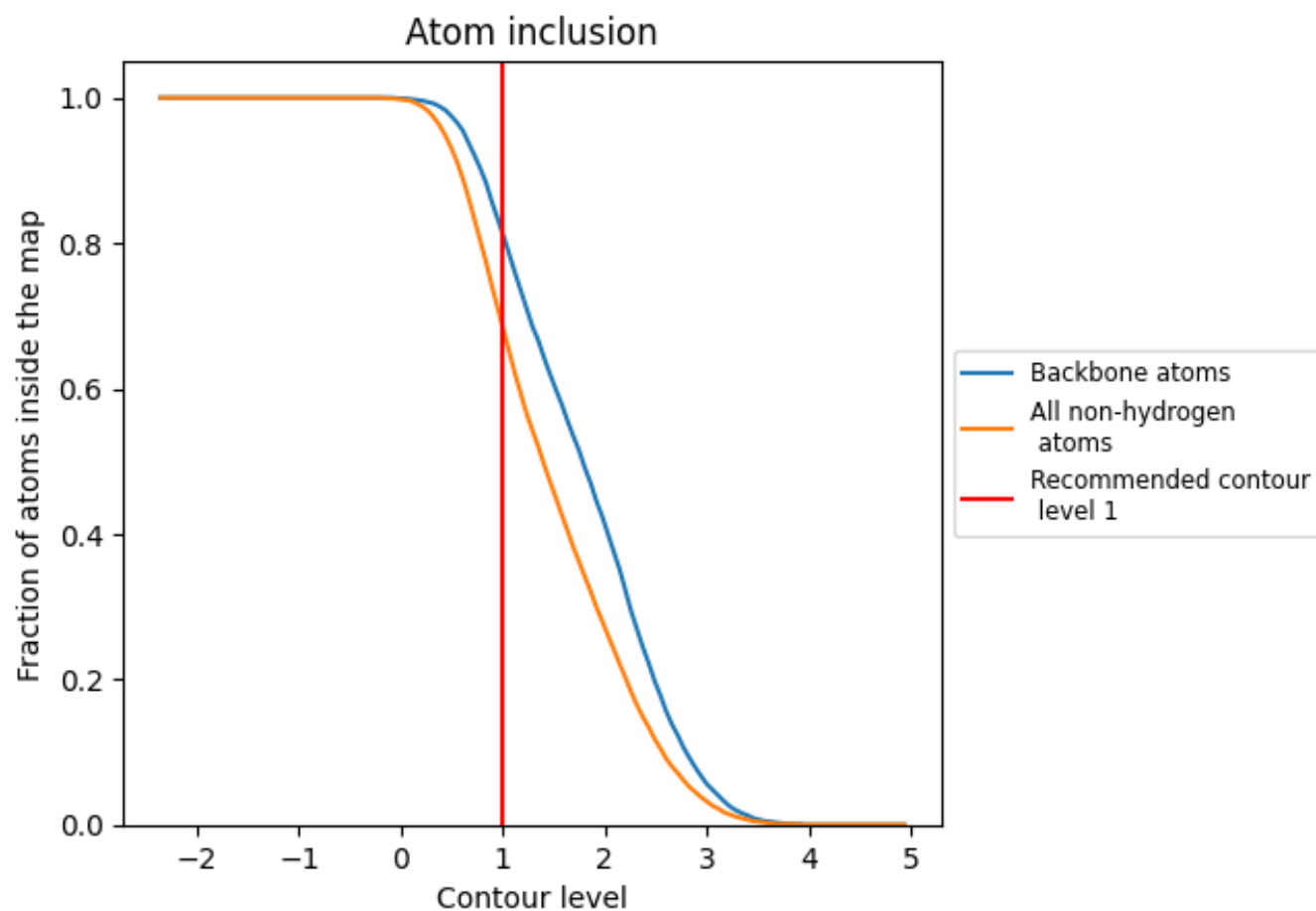
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 81% of all backbone atoms, 68% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6830	0.5260
I	0.6160	0.4980
L	0.7200	0.5540
M	0.7340	0.5400
N	0.6610	0.5130
O	0.6820	0.5150
P	0.6630	0.5170
Q	0.5070	0.4540
R	0.8090	0.5670

1.0

0.0

<0.0