



Full wwPDB EM Validation Report ⓘ

Nov 21, 2022 – 09:26 PM EST

PDB ID : 3J41
EMDB ID : EMD-5679
Title : Pseudo-atomic model of the Aquaporin-0/Calmodulin complex derived from electron microscopy
Authors : Reichow, S.L.; Clemens, D.M.; Freites, J.A.; Nemeth-Cahalan, K.L.; Heyden, M.; Tobias, D.J.; Hall, J.E.; Gonen, T.
Deposited on : 2013-05-31
Resolution : 25.00 Å (reported)
Based on initial models : 1NWD, 2B6P

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

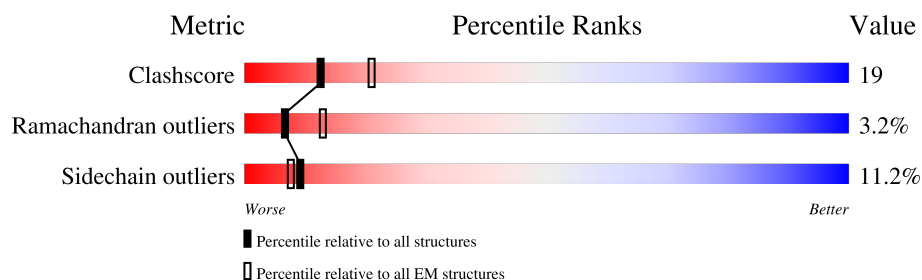
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 25.00 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)
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	A	263	
1	B	263	
1	C	263	
1	D	263	
2	E	149	
2	F	149	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9338 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 Lens fiber major intrinsic protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	233	Total	C	N	O	S	0	0
			1768	1169	300	292	7		
1	B	233	Total	C	N	O	S	0	0
			1768	1169	300	292	7		
1	C	233	Total	C	N	O	S	0	0
			1768	1169	300	292	7		
1	D	233	Total	C	N	O	S	0	0
			1768	1169	300	292	7		

- Molecule 2 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	143	Total	C	N	O	S	0	0
			1129	692	182	246	9		
2	F	143	Total	C	N	O	S	0	0
			1129	692	182	246	9		

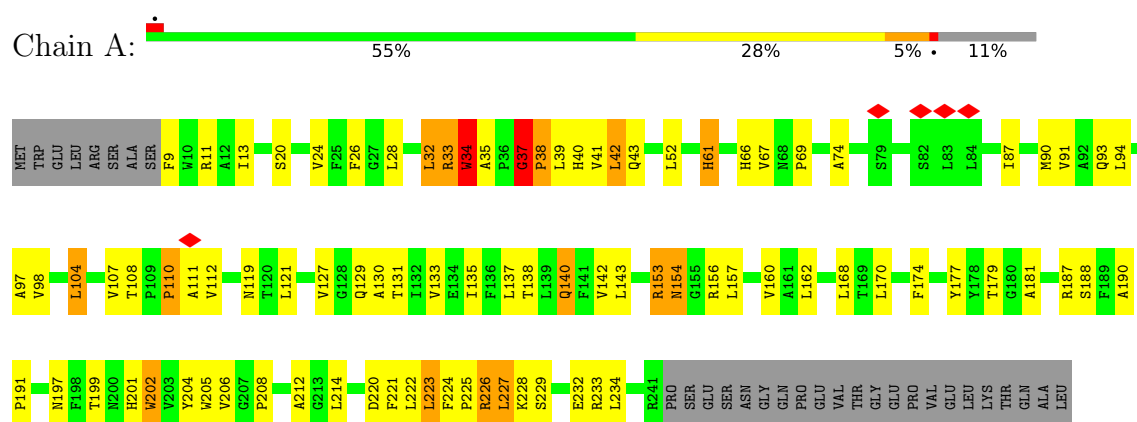
- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
3	E	4	Total	Ca	0
			4	4	
3	F	4	Total	Ca	0
			4	4	

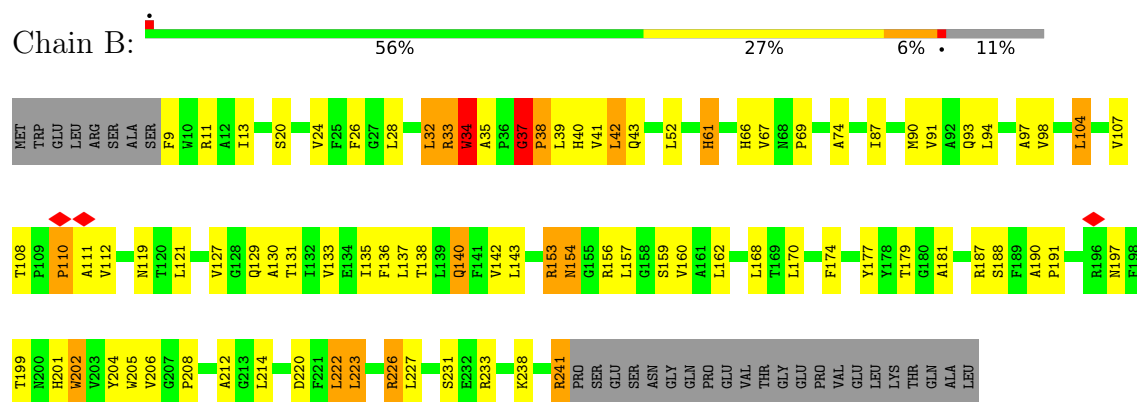
3 Residue-property plots

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.

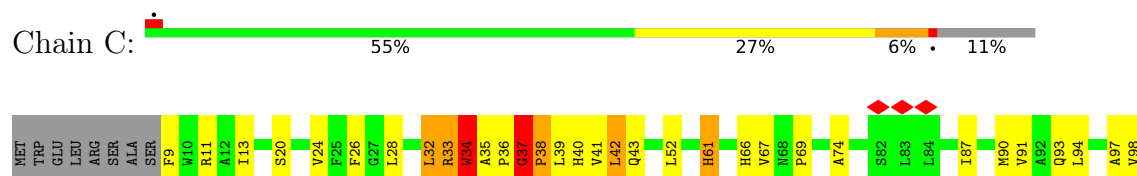
• Molecule 1: Lens fiber major intrinsic protein

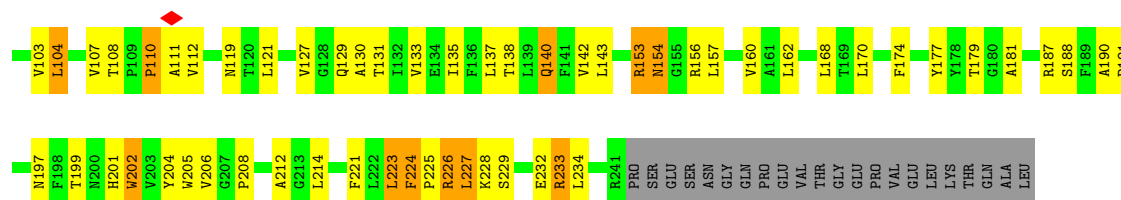


• Molecule 1: Lens fiber major intrinsic protein

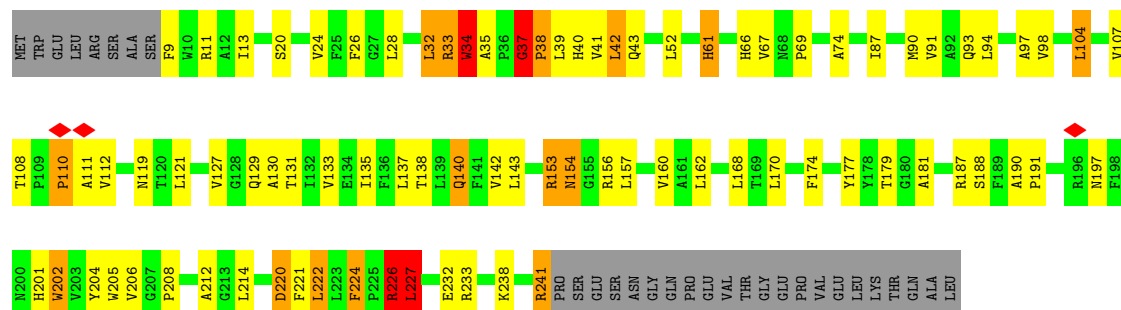


• Molecule 1: Lens fiber major intrinsic protein

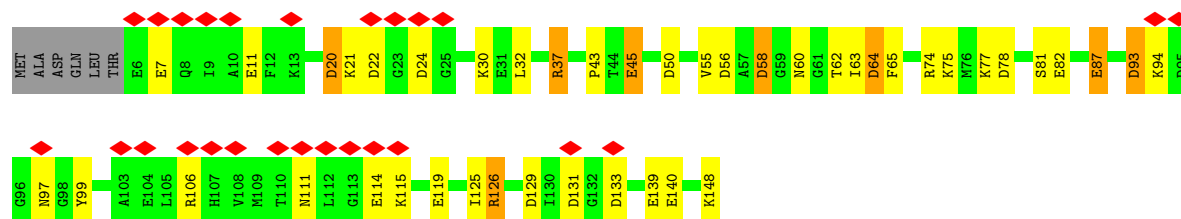




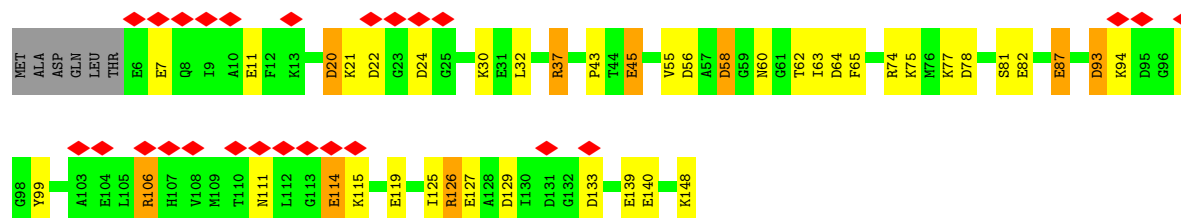
• Molecule 1: Lens fiber major intrinsic protein



• Molecule 2: Calmodulin



• Molecule 2: Calmodulin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	11720	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	CTF-TILT, each micrograph	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	52000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	8.374	Depositor
Minimum map value	-3.114	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4.96	Depositor
Map size (\AA)	262.68, 262.68, 262.68	wwPDB
Map dimensions	66, 66, 66	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3.9799998, 3.9799998, 3.9799998	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	0/1817	0.79	5/2478 (0.2%)
1	B	0.46	0/1817	0.79	4/2478 (0.2%)
1	C	0.46	0/1817	0.79	4/2478 (0.2%)
1	D	0.46	0/1817	0.78	3/2478 (0.1%)
2	E	0.74	0/1141	1.21	9/1529 (0.6%)
2	F	0.73	0/1141	1.21	9/1529 (0.6%)
All	All	0.54	0/9550	0.90	34/12970 (0.3%)

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	A	0	7
1	B	0	6
1	C	0	8
1	D	0	9
2	E	0	25
2	F	0	25
All	All	0	80

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	74	ARG	NE-CZ-NH1	9.93	125.27	120.30
2	E	74	ARG	NE-CZ-NH1	9.84	125.22	120.30
1	B	37	GLY	N-CA-C	8.27	133.77	113.10
1	C	37	GLY	N-CA-C	8.21	133.64	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	GLY	N-CA-C	8.20	133.60	113.10
1	D	37	GLY	N-CA-C	8.20	133.60	113.10
2	E	93	ASP	CB-CG-OD2	-7.30	111.73	118.30
2	F	93	ASP	CB-CG-OD2	-7.29	111.74	118.30
2	E	58	ASP	OD1-CG-OD2	-6.10	111.72	123.30
2	E	106	ARG	NE-CZ-NH1	6.08	123.34	120.30
2	F	106	ARG	NE-CZ-NH1	6.00	123.30	120.30
2	E	20	ASP	OD1-CG-OD2	-5.99	111.92	123.30
2	E	140	GLU	OE1-CD-OE2	-5.97	116.14	123.30
2	F	20	ASP	OD1-CG-OD2	-5.96	111.98	123.30
2	F	140	GLU	OE1-CD-OE2	-5.94	116.17	123.30
2	F	58	ASP	OD1-CG-OD2	-5.90	112.09	123.30
1	C	233	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	233	ARG	NE-CZ-NH1	5.61	123.10	120.30
1	C	223	LEU	CB-CA-C	5.59	120.82	110.20
2	F	37	ARG	NE-CZ-NH1	5.58	123.09	120.30
2	E	87	GLU	OE1-CD-OE2	-5.54	116.65	123.30
2	F	87	GLU	OE1-CD-OE2	-5.52	116.67	123.30
1	D	233	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	B	223	LEU	C-N-CA	5.28	134.91	121.70
2	E	126	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	A	223	LEU	CB-CA-C	5.22	120.13	110.20
2	E	37	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	B	233	ARG	NE-CZ-NH1	5.18	122.89	120.30
2	F	126	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	226	ARG	C-N-CA	5.07	134.36	121.70
1	B	37	GLY	O-C-N	-5.07	111.47	121.10
1	D	37	GLY	O-C-N	-5.05	111.51	121.10
1	C	37	GLY	O-C-N	-5.03	111.54	121.10
1	A	37	GLY	O-C-N	-5.01	111.57	121.10

There are no chirality outliers.

All (80) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	220	ASP	Sidechain
1	A	221	PHE	Peptide,Mainchain
1	A	232	GLU	Sidechain
1	A	34	TRP	Peptide,Mainchain
1	A	37	GLY	Mainchain
1	B	220	ASP	Sidechain
1	B	222	LEU	Mainchain

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Mol	Chain	Res	Type	Group
1	B	241	ARG	Sidechain
1	B	34	TRP	Peptide,Mainchain
1	B	37	GLY	Mainchain
1	C	221	PHE	Peptide,Mainchain
1	C	224	PHE	Mainchain
1	C	232	GLU	Sidechain
1	C	233	ARG	Mainchain
1	C	34	TRP	Peptide,Mainchain
1	C	37	GLY	Mainchain
1	D	220	ASP	Sidechain
1	D	222	LEU	Mainchain
1	D	226	ARG	Peptide
1	D	227	LEU	Mainchain
1	D	232	GLU	Sidechain
1	D	241	ARG	Sidechain
1	D	34	TRP	Peptide,Mainchain
1	D	37	GLY	Mainchain
2	E	114	GLU	Sidechain
2	E	119	GLU	Sidechain
2	E	125	ILE	Mainchain
2	E	126	ARG	Peptide
2	E	129	ASP	Sidechain
2	E	133	ASP	Sidechain
2	E	20	ASP	Sidechain
2	E	24	ASP	Sidechain
2	E	37	ARG	Sidechain
2	E	43	PRO	Peptide
2	E	45	GLU	Mainchain
2	E	50	ASP	Sidechain
2	E	55	VAL	Mainchain
2	E	56	ASP	Sidechain
2	E	58	ASP	Sidechain
2	E	63	ILE	Mainchain
2	E	64	ASP	Sidechain
2	E	7	GLU	Sidechain
2	E	78	ASP	Peptide,Mainchain
2	E	82	GLU	Sidechain
2	E	87	GLU	Sidechain,Mainchain
2	E	93	ASP	Sidechain
2	E	99	TYR	Sidechain
2	F	106	ARG	Sidechain
2	F	114	GLU	Sidechain

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Mol	Chain	Res	Type	Group
2	F	119	GLU	Sidechain
2	F	125	ILE	Mainchain
2	F	126	ARG	Peptide
2	F	127	GLU	Sidechain
2	F	129	ASP	Sidechain
2	F	133	ASP	Sidechain
2	F	20	ASP	Sidechain
2	F	24	ASP	Sidechain
2	F	37	ARG	Sidechain
2	F	43	PRO	Peptide
2	F	45	GLU	Mainchain
2	F	55	VAL	Mainchain
2	F	56	ASP	Sidechain
2	F	58	ASP	Sidechain
2	F	63	ILE	Mainchain
2	F	7	GLU	Sidechain
2	F	78	ASP	Peptide,Mainchain
2	F	82	GLU	Sidechain
2	F	87	GLU	Sidechain,Mainchain
2	F	93	ASP	Sidechain
2	F	99	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1768	0	1805	97	0
1	B	1768	0	1805	97	0
1	C	1768	0	1805	101	0
1	D	1768	0	1805	94	0
2	E	1129	0	1058	2	0
2	F	1129	0	1058	2	0
3	E	4	0	0	0	0
3	F	4	0	0	0	0
All	All	9338	0	9336	351	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 19.

All (351) 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:133:VAL:HG23	1:C:107:VAL:HG11	1.56	0.88
1:A:133:VAL:HG23	1:B:107:VAL:HG11	1.56	0.86
1:C:133:VAL:HG23	1:D:107:VAL:HG11	1.57	0.86
1:A:107:VAL:HG11	1:D:133:VAL:HG23	1.56	0.86
1:C:154:ASN:HB2	1:C:157:LEU:HG	1.58	0.85
1:A:154:ASN:HB2	1:A:157:LEU:HG	1.58	0.85
1:B:154:ASN:HB2	1:B:157:LEU:HG	1.58	0.84
1:D:154:ASN:HB2	1:D:157:LEU:HG	1.58	0.82
1:D:197:ASN:OD1	1:D:199:THR:HG22	1.81	0.80
1:B:197:ASN:OD1	1:B:199:THR:HG22	1.81	0.80
1:A:197:ASN:OD1	1:A:199:THR:HG22	1.81	0.80
1:C:197:ASN:OD1	1:C:199:THR:HG22	1.81	0.80
1:A:37:GLY:HA3	1:A:177:TYR:HE1	1.48	0.79
1:D:37:GLY:HA3	1:D:177:TYR:HE1	1.48	0.78
1:B:37:GLY:HA3	1:B:177:TYR:HE1	1.48	0.78
1:C:37:GLY:HA3	1:C:177:TYR:HE1	1.48	0.77
1:C:33:ARG:HG3	1:C:34:TRP:N	2.04	0.72
1:D:33:ARG:HG3	1:D:34:TRP:N	2.04	0.72
1:B:33:ARG:HG3	1:B:34:TRP:N	2.04	0.71
1:C:153:ARG:HE	1:C:154:ASN:CG	1.94	0.71
1:D:153:ARG:HE	1:D:154:ASN:CG	1.94	0.71
1:A:153:ARG:HE	1:A:154:ASN:CG	1.94	0.70
1:B:153:ARG:HE	1:B:154:ASN:CG	1.94	0.70
1:B:104:LEU:O	1:B:108:THR:HG22	1.92	0.70
1:A:38:PRO:O	1:B:43:GLN:NE2	2.25	0.70
1:C:104:LEU:O	1:C:108:THR:HG22	1.92	0.70
1:C:38:PRO:O	1:D:43:GLN:NE2	2.26	0.69
1:A:104:LEU:O	1:A:108:THR:HG22	1.92	0.69
1:D:104:LEU:O	1:D:108:THR:HG22	1.92	0.69
1:A:33:ARG:HG3	1:A:34:TRP:N	2.04	0.69
1:A:43:GLN:NE2	1:D:38:PRO:O	2.26	0.69
1:D:67:VAL:O	1:D:67:VAL:HG12	1.93	0.68
1:B:38:PRO:O	1:C:43:GLN:NE2	2.27	0.68
1:C:67:VAL:HG12	1:C:67:VAL:O	1.93	0.68
1:A:67:VAL:HG12	1:A:67:VAL:O	1.93	0.68
1:B:67:VAL:HG12	1:B:67:VAL:O	1.93	0.68
1:D:61:HIS:H	1:D:61:HIS:CD2	2.13	0.66
1:D:190:ALA:HB3	1:D:191:PRO:HD3	1.78	0.66
1:B:190:ALA:HB3	1:B:191:PRO:HD3	1.78	0.65
1:C:190:ALA:HB3	1:C:191:PRO:HD3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:HIS:H	1:B:61:HIS:CD2	2.13	0.64
1:A:190:ALA:HB3	1:A:191:PRO:HD3	1.78	0.64
1:B:154:ASN:CB	1:B:157:LEU:HG	2.28	0.64
1:C:61:HIS:CD2	1:C:61:HIS:H	2.13	0.64
1:C:33:ARG:HH21	1:C:40:HIS:HA	1.62	0.64
1:D:154:ASN:CB	1:D:157:LEU:HG	2.28	0.64
1:A:61:HIS:CD2	1:A:61:HIS:H	2.13	0.64
1:D:33:ARG:HH21	1:D:40:HIS:HA	1.62	0.64
1:A:129:GLN:HB3	1:B:107:VAL:HG13	1.80	0.64
1:C:154:ASN:CB	1:C:157:LEU:HG	2.28	0.63
1:A:33:ARG:HH21	1:A:40:HIS:HA	1.62	0.63
1:C:133:VAL:O	1:C:137:LEU:HG	1.99	0.63
1:B:133:VAL:O	1:B:137:LEU:HG	1.98	0.63
1:A:107:VAL:HG13	1:D:129:GLN:HB3	1.80	0.63
1:B:33:ARG:HH21	1:B:40:HIS:HA	1.62	0.63
1:D:133:VAL:O	1:D:137:LEU:HG	1.98	0.63
1:A:154:ASN:CB	1:A:157:LEU:HG	2.28	0.62
1:A:133:VAL:O	1:A:137:LEU:HG	1.99	0.62
1:B:9:PHE:CE1	1:B:13:ILE:HD11	2.35	0.62
1:A:9:PHE:CE1	1:A:13:ILE:HD11	2.35	0.62
1:A:121:LEU:CD1	1:A:179:THR:HG22	2.30	0.61
1:A:202:TRP:CZ2	1:A:206:VAL:HG21	2.35	0.61
1:A:202:TRP:CE2	1:A:206:VAL:HG21	2.35	0.61
1:B:121:LEU:CD1	1:B:179:THR:HG22	2.31	0.61
1:D:188:SER:O	1:D:191:PRO:HD2	2.01	0.61
1:D:202:TRP:CE2	1:D:206:VAL:HG21	2.36	0.61
1:B:129:GLN:HB3	1:C:107:VAL:HG13	1.81	0.61
1:C:9:PHE:CE1	1:C:13:ILE:HD11	2.35	0.61
1:D:9:PHE:CE1	1:D:13:ILE:HD11	2.35	0.61
1:B:24:VAL:CG1	1:B:28:LEU:HD22	2.31	0.61
1:B:202:TRP:CZ2	1:B:206:VAL:HG21	2.35	0.61
1:D:24:VAL:CG1	1:D:28:LEU:HD22	2.31	0.61
1:A:24:VAL:CG1	1:A:28:LEU:HD22	2.31	0.61
1:D:202:TRP:CZ2	1:D:206:VAL:HG21	2.35	0.61
1:C:202:TRP:CZ2	1:C:206:VAL:HG21	2.35	0.61
1:D:121:LEU:CD1	1:D:179:THR:HG22	2.30	0.61
1:C:188:SER:O	1:C:191:PRO:HD2	2.01	0.61
1:A:133:VAL:HG23	1:B:107:VAL:CG1	2.31	0.60
1:C:129:GLN:HB3	1:D:107:VAL:HG13	1.81	0.60
1:A:188:SER:O	1:A:191:PRO:HD2	2.00	0.60
1:B:188:SER:O	1:B:191:PRO:HD2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:LEU:CD1	1:C:179:THR:HG22	2.31	0.60
1:C:24:VAL:CG1	1:C:28:LEU:HD22	2.31	0.60
1:B:133:VAL:HG23	1:C:107:VAL:CG1	2.31	0.60
1:B:202:TRP:CE2	1:B:206:VAL:HG21	2.36	0.60
1:C:202:TRP:CE2	1:C:206:VAL:HG21	2.35	0.60
1:C:201:HIS:CE1	1:C:205:TRP:HE1	2.21	0.59
1:B:201:HIS:CE1	1:B:205:TRP:HE1	2.21	0.59
1:C:133:VAL:HG23	1:D:107:VAL:CG1	2.32	0.59
1:D:201:HIS:CE1	1:D:205:TRP:HE1	2.21	0.59
1:A:201:HIS:CE1	1:A:205:TRP:HE1	2.21	0.58
1:B:131:THR:O	1:B:135:ILE:HG13	2.04	0.58
1:D:131:THR:O	1:D:135:ILE:HG13	2.04	0.58
1:A:38:PRO:HB3	1:B:39:LEU:HD11	1.86	0.58
1:C:142:VAL:HG21	1:C:212:ALA:HA	1.86	0.57
1:B:142:VAL:HG21	1:B:212:ALA:HA	1.86	0.57
1:C:28:LEU:O	1:C:32:LEU:HD13	2.04	0.57
1:D:142:VAL:HG21	1:D:212:ALA:HA	1.86	0.57
1:D:69:PRO:HB3	1:D:90:MET:HE2	1.84	0.57
1:A:28:LEU:O	1:A:32:LEU:HD13	2.04	0.57
1:C:24:VAL:HG12	1:C:28:LEU:HD22	1.87	0.57
1:A:142:VAL:HG21	1:A:212:ALA:HA	1.86	0.57
1:B:20:SER:HA	1:B:67:VAL:HG13	1.87	0.57
1:A:32:LEU:O	1:A:33:ARG:HB3	2.05	0.57
1:C:32:LEU:O	1:C:33:ARG:CB	2.53	0.57
1:D:28:LEU:O	1:D:32:LEU:HD13	2.04	0.57
1:D:32:LEU:O	1:D:33:ARG:CB	2.53	0.57
1:D:32:LEU:O	1:D:33:ARG:HB3	2.05	0.57
1:A:131:THR:O	1:A:135:ILE:HG13	2.04	0.57
1:C:32:LEU:O	1:C:33:ARG:HB3	2.05	0.57
1:C:20:SER:HA	1:C:67:VAL:HG13	1.86	0.57
1:C:69:PRO:HB3	1:C:90:MET:HE2	1.86	0.57
1:D:20:SER:HA	1:D:67:VAL:HG13	1.87	0.57
1:B:24:VAL:HG12	1:B:28:LEU:HD22	1.87	0.56
1:B:32:LEU:O	1:B:33:ARG:HB3	2.05	0.56
1:B:28:LEU:O	1:B:32:LEU:HD13	2.04	0.56
1:B:32:LEU:O	1:B:33:ARG:CB	2.53	0.56
1:C:131:THR:O	1:C:135:ILE:HG13	2.04	0.56
1:A:140:GLN:HG2	1:B:26:PHE:CZ	2.40	0.56
1:B:38:PRO:HB3	1:C:39:LEU:HD11	1.87	0.56
1:B:140:GLN:HG2	1:C:26:PHE:CZ	2.40	0.56
1:C:38:PRO:HB3	1:D:39:LEU:HD11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:GLN:HG2	1:D:26:PHE:CZ	2.40	0.56
1:A:20:SER:HA	1:A:67:VAL:HG13	1.87	0.56
1:A:32:LEU:O	1:A:33:ARG:CB	2.53	0.56
1:A:121:LEU:CD1	1:A:130:ALA:HB1	2.36	0.56
1:C:107:VAL:HG12	1:C:107:VAL:O	2.06	0.56
1:A:26:PHE:CZ	1:D:140:GLN:HG2	2.41	0.56
1:D:24:VAL:HG12	1:D:28:LEU:HD22	1.87	0.56
1:A:37:GLY:HA3	1:A:177:TYR:CE1	2.36	0.56
1:A:24:VAL:HG12	1:A:28:LEU:HD22	1.87	0.56
1:A:107:VAL:O	1:A:107:VAL:HG12	2.06	0.56
1:B:121:LEU:CD1	1:B:130:ALA:HB1	2.36	0.56
1:C:121:LEU:CD1	1:C:130:ALA:HB1	2.36	0.56
1:B:37:GLY:HA3	1:B:177:TYR:CE1	2.36	0.55
1:D:121:LEU:CD1	1:D:130:ALA:HB1	2.36	0.55
1:D:107:VAL:HG12	1:D:107:VAL:O	2.06	0.55
1:B:61:HIS:H	1:B:61:HIS:HD2	1.54	0.55
1:A:110:PRO:C	1:A:112:VAL:H	2.10	0.55
1:C:52:LEU:HD22	1:C:168:LEU:HD22	1.89	0.55
1:B:107:VAL:HG12	1:B:107:VAL:O	2.06	0.55
1:A:52:LEU:HD22	1:A:168:LEU:HD22	1.89	0.55
1:A:107:VAL:CG1	1:D:133:VAL:HG23	2.31	0.55
1:D:110:PRO:C	1:D:112:VAL:H	2.10	0.55
1:A:37:GLY:N	1:A:38:PRO:HD3	2.22	0.54
1:A:39:LEU:HD11	1:D:38:PRO:HB3	1.88	0.54
1:C:61:HIS:H	1:C:61:HIS:HD2	1.53	0.54
1:D:37:GLY:N	1:D:38:PRO:HD3	2.22	0.54
1:B:110:PRO:C	1:B:112:VAL:H	2.10	0.54
1:C:37:GLY:HA3	1:C:177:TYR:CE1	2.36	0.54
1:C:110:PRO:C	1:C:112:VAL:H	2.09	0.54
1:B:52:LEU:HD22	1:B:168:LEU:HD22	1.89	0.54
1:B:110:PRO:O	1:B:112:VAL:N	2.38	0.54
1:D:37:GLY:HA3	1:D:177:TYR:CE1	2.36	0.54
1:B:69:PRO:HB3	1:B:90:MET:HE2	1.88	0.54
1:B:37:GLY:N	1:B:38:PRO:HD3	2.23	0.54
1:D:52:LEU:HD22	1:D:168:LEU:HD22	1.89	0.54
1:C:37:GLY:N	1:C:38:PRO:HD3	2.22	0.54
1:D:121:LEU:HD12	1:D:179:THR:HG22	1.91	0.53
1:A:61:HIS:H	1:A:61:HIS:HD2	1.54	0.53
1:A:121:LEU:HD12	1:A:179:THR:HG22	1.91	0.53
1:C:121:LEU:HD12	1:C:179:THR:HG22	1.91	0.53
1:B:121:LEU:HD12	1:B:179:THR:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:33:ARG:HG3	1:D:34:TRP:H	1.75	0.52
1:B:33:ARG:HG3	1:B:34:TRP:H	1.75	0.52
1:D:61:HIS:H	1:D:61:HIS:HD2	1.54	0.52
1:D:110:PRO:O	1:D:111:ALA:HB3	2.11	0.51
1:A:110:PRO:O	1:A:112:VAL:N	2.38	0.51
1:A:121:LEU:HD11	1:A:130:ALA:HB1	1.93	0.51
1:D:32:LEU:O	1:D:33:ARG:HG2	2.11	0.51
1:A:110:PRO:O	1:A:111:ALA:HB3	2.11	0.51
1:C:24:VAL:HG21	1:C:97:ALA:CB	2.40	0.51
1:C:121:LEU:HD11	1:C:130:ALA:HB1	1.93	0.51
1:D:121:LEU:HD11	1:D:130:ALA:HB1	1.93	0.51
1:B:121:LEU:HD11	1:B:130:ALA:HB1	1.93	0.51
1:D:24:VAL:HG21	1:D:97:ALA:CB	2.40	0.51
1:C:32:LEU:O	1:C:33:ARG:HG2	2.11	0.51
1:B:24:VAL:HG21	1:B:97:ALA:CB	2.40	0.50
1:C:33:ARG:HG3	1:C:34:TRP:H	1.74	0.50
1:C:110:PRO:O	1:C:111:ALA:HB3	2.10	0.50
1:A:24:VAL:HG21	1:A:97:ALA:CB	2.40	0.50
1:A:223:LEU:HD23	1:A:224:PHE:H	1.76	0.50
1:A:32:LEU:O	1:A:33:ARG:HG2	2.11	0.50
1:B:32:LEU:O	1:B:33:ARG:HG2	2.11	0.50
1:B:110:PRO:O	1:B:111:ALA:HB3	2.11	0.50
1:A:33:ARG:HG3	1:A:34:TRP:H	1.74	0.50
1:C:143:LEU:HD12	1:C:143:LEU:O	2.12	0.49
1:D:137:LEU:HD21	1:D:174:PHE:HD2	1.77	0.49
1:A:143:LEU:O	1:A:143:LEU:HD12	2.12	0.49
1:B:143:LEU:HD12	1:B:143:LEU:O	2.12	0.49
1:A:153:ARG:HH21	1:A:154:ASN:ND2	2.10	0.49
1:C:110:PRO:O	1:C:112:VAL:N	2.38	0.49
1:D:143:LEU:HD12	1:D:143:LEU:O	2.12	0.49
2:F:139:GLU:H	2:F:139:GLU:CD	2.16	0.49
1:B:153:ARG:HH21	1:B:154:ASN:ND2	2.10	0.49
1:C:137:LEU:HD21	1:C:174:PHE:HD2	1.77	0.49
1:D:153:ARG:HH21	1:D:154:ASN:ND2	2.10	0.49
2:E:139:GLU:CD	2:E:139:GLU:H	2.16	0.49
1:A:153:ARG:HE	1:A:154:ASN:CB	2.26	0.49
1:D:153:ARG:HE	1:D:154:ASN:CB	2.26	0.48
1:B:87:ILE:O	1:B:91:VAL:HG23	2.13	0.48
1:C:87:ILE:O	1:C:91:VAL:HG23	2.13	0.48
1:D:11:ARG:HH11	1:D:11:ARG:HG2	1.79	0.48
1:D:110:PRO:O	1:D:112:VAL:N	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ILE:O	1:A:91:VAL:HG23	2.13	0.48
1:B:28:LEU:HD21	1:B:191:PRO:HG3	1.95	0.48
1:C:153:ARG:HH21	1:C:154:ASN:ND2	2.10	0.48
1:C:28:LEU:HD21	1:C:191:PRO:HG3	1.95	0.48
1:C:11:ARG:HG2	1:C:11:ARG:HH11	1.78	0.48
1:A:11:ARG:HG2	1:A:11:ARG:HH11	1.79	0.48
1:A:137:LEU:HD21	1:A:174:PHE:HD2	1.77	0.48
1:B:153:ARG:HE	1:B:154:ASN:CB	2.26	0.48
1:B:11:ARG:HG2	1:B:11:ARG:HH11	1.79	0.48
1:C:153:ARG:HE	1:C:154:ASN:CB	2.26	0.48
1:B:137:LEU:HD21	1:B:174:PHE:HD2	1.77	0.47
1:D:87:ILE:O	1:D:91:VAL:HG23	2.13	0.47
1:A:28:LEU:HD21	1:A:191:PRO:HG3	1.95	0.47
1:A:69:PRO:HB3	1:A:90:MET:HE2	1.95	0.47
1:B:37:GLY:HA2	1:B:41:VAL:HG23	1.97	0.47
1:D:39:LEU:HD12	1:D:40:HIS:N	2.30	0.47
1:A:153:ARG:HH21	1:A:154:ASN:CG	2.18	0.47
1:C:37:GLY:HA2	1:C:41:VAL:HG23	1.97	0.47
1:C:74:ALA:HB2	1:C:212:ALA:HB1	1.96	0.47
1:D:28:LEU:HD21	1:D:191:PRO:HG3	1.95	0.47
1:A:37:GLY:HA2	1:A:41:VAL:HG23	1.97	0.47
1:B:153:ARG:HH21	1:B:154:ASN:CG	2.18	0.47
1:B:39:LEU:HD12	1:B:40:HIS:N	2.30	0.46
1:B:74:ALA:HB2	1:B:212:ALA:HB1	1.96	0.46
1:A:133:VAL:CG2	1:B:107:VAL:HG11	2.39	0.46
1:D:121:LEU:N	1:D:121:LEU:HD22	2.31	0.46
1:D:153:ARG:HH21	1:D:154:ASN:CG	2.18	0.46
1:C:153:ARG:HH21	1:C:154:ASN:CG	2.18	0.46
1:A:138:THR:OG1	1:A:208:PRO:HA	2.16	0.46
1:D:33:ARG:CG	1:D:34:TRP:H	2.29	0.46
1:D:121:LEU:HD12	1:D:130:ALA:CB	2.46	0.46
1:A:39:LEU:HD12	1:A:40:HIS:N	2.30	0.46
1:B:121:LEU:HD22	1:B:121:LEU:N	2.31	0.46
1:C:39:LEU:HD12	1:C:40:HIS:N	2.30	0.46
1:A:121:LEU:HD12	1:A:130:ALA:CB	2.46	0.46
1:D:37:GLY:HA2	1:D:41:VAL:HG23	1.97	0.46
1:D:138:THR:OG1	1:D:208:PRO:HA	2.16	0.46
1:A:121:LEU:N	1:A:121:LEU:HD22	2.31	0.46
1:C:61:HIS:CD2	1:C:61:HIS:N	2.84	0.46
1:D:74:ALA:HB2	1:D:212:ALA:HB1	1.96	0.46
1:A:74:ALA:HB2	1:A:212:ALA:HB1	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:202:TRP:CH2	1:C:206:VAL:HG21	2.52	0.45
1:D:202:TRP:CH2	1:D:206:VAL:HG21	2.52	0.45
1:A:37:GLY:O	1:A:41:VAL:HG23	2.16	0.45
1:B:119:ASN:ND2	1:B:188:SER:OG	2.50	0.45
1:B:119:ASN:HB3	1:B:204:TYR:CZ	2.52	0.45
1:B:121:LEU:HD12	1:B:130:ALA:CB	2.46	0.45
1:C:37:GLY:O	1:C:41:VAL:HG23	2.16	0.45
1:C:119:ASN:HB3	1:C:204:TYR:CZ	2.52	0.45
1:C:33:ARG:CG	1:C:34:TRP:H	2.28	0.45
1:C:133:VAL:HG13	1:C:174:PHE:HE2	1.82	0.45
1:D:37:GLY:O	1:D:41:VAL:HG23	2.16	0.45
1:B:37:GLY:O	1:B:41:VAL:HG23	2.16	0.45
1:D:133:VAL:HG13	1:D:174:PHE:HE2	1.82	0.45
1:A:119:ASN:ND2	1:A:188:SER:OG	2.50	0.45
1:B:202:TRP:CH2	1:B:206:VAL:HG21	2.52	0.45
1:C:121:LEU:HD12	1:C:130:ALA:CB	2.46	0.45
1:D:119:ASN:HB3	1:D:204:TYR:CZ	2.52	0.45
1:A:33:ARG:CG	1:A:34:TRP:H	2.28	0.45
1:C:121:LEU:N	1:C:121:LEU:HD22	2.31	0.45
1:D:119:ASN:ND2	1:D:188:SER:OG	2.50	0.45
1:B:33:ARG:CG	1:B:34:TRP:H	2.29	0.45
1:B:138:THR:OG1	1:B:208:PRO:HA	2.16	0.45
1:C:138:THR:OG1	1:C:208:PRO:HA	2.16	0.45
1:A:94:LEU:O	1:A:98:VAL:HG23	2.17	0.44
1:A:133:VAL:HG13	1:A:174:PHE:HE2	1.82	0.44
1:C:24:VAL:HG21	1:C:97:ALA:HB1	2.00	0.44
1:C:119:ASN:ND2	1:C:188:SER:OG	2.50	0.44
2:E:94:LYS:HE2	2:E:94:LYS:HA	1.99	0.44
2:F:94:LYS:HE2	2:F:94:LYS:HA	1.99	0.44
1:A:156:ARG:HB3	1:B:160:VAL:HG13	1.99	0.44
1:A:202:TRP:CH2	1:A:206:VAL:HG21	2.52	0.44
1:B:24:VAL:HG21	1:B:97:ALA:HB1	2.00	0.44
1:C:24:VAL:O	1:C:28:LEU:HB2	2.17	0.44
1:A:24:VAL:O	1:A:28:LEU:HB2	2.17	0.44
1:A:119:ASN:HB3	1:A:204:TYR:CZ	2.52	0.44
1:C:94:LEU:O	1:C:98:VAL:HG23	2.17	0.44
1:D:24:VAL:HG21	1:D:97:ALA:HB1	1.99	0.44
1:B:24:VAL:O	1:B:28:LEU:HB2	2.17	0.44
1:A:24:VAL:HG21	1:A:97:ALA:HB1	1.99	0.44
1:B:61:HIS:CD2	1:B:61:HIS:N	2.84	0.44
1:B:94:LEU:O	1:B:98:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:VAL:CG2	1:C:107:VAL:HG11	2.39	0.44
1:B:156:ARG:HB3	1:C:160:VAL:HG13	1.99	0.44
1:D:110:PRO:C	1:D:112:VAL:N	2.72	0.44
1:A:33:ARG:HG2	1:A:33:ARG:HH11	1.83	0.44
1:B:133:VAL:HG13	1:B:174:PHE:HE2	1.82	0.44
1:C:110:PRO:C	1:C:112:VAL:N	2.71	0.43
1:D:94:LEU:O	1:D:98:VAL:HG23	2.17	0.43
1:D:33:ARG:HG2	1:D:33:ARG:HH11	1.83	0.43
1:C:33:ARG:HG2	1:C:33:ARG:HH11	1.84	0.43
1:D:90:MET:HA	1:D:93:GLN:NE2	2.34	0.43
1:D:24:VAL:O	1:D:28:LEU:HB2	2.17	0.43
1:B:119:ASN:HB3	1:B:204:TYR:CE1	2.54	0.43
1:D:137:LEU:HD21	1:D:174:PHE:CD2	2.54	0.43
1:B:33:ARG:HG2	1:B:33:ARG:HH11	1.83	0.43
1:B:121:LEU:HD12	1:B:130:ALA:HB1	2.00	0.43
1:C:156:ARG:HB3	1:D:160:VAL:HG13	1.99	0.43
1:A:110:PRO:C	1:A:112:VAL:N	2.72	0.43
1:A:119:ASN:HB3	1:A:204:TYR:CE1	2.54	0.43
1:A:121:LEU:HD12	1:A:130:ALA:HB1	2.01	0.43
1:C:90:MET:HA	1:C:93:GLN:NE2	2.34	0.43
1:B:37:GLY:O	1:B:41:VAL:CG2	2.67	0.43
1:C:223:LEU:HD23	1:C:224:PHE:H	1.83	0.43
1:D:121:LEU:HD12	1:D:130:ALA:HB1	2.00	0.43
1:A:37:GLY:O	1:A:41:VAL:CG2	2.67	0.43
1:A:160:VAL:HG13	1:D:156:ARG:HB3	1.99	0.43
1:B:90:MET:HA	1:B:93:GLN:NE2	2.34	0.43
1:C:69:PRO:HB3	1:C:90:MET:CE	2.49	0.42
1:C:119:ASN:HB3	1:C:204:TYR:CE1	2.54	0.42
1:A:90:MET:HA	1:A:93:GLN:NE2	2.34	0.42
1:A:137:LEU:HD21	1:A:174:PHE:CD2	2.54	0.42
1:D:37:GLY:O	1:D:41:VAL:CG2	2.67	0.42
1:D:119:ASN:HB3	1:D:204:TYR:CE1	2.54	0.42
1:A:129:GLN:CB	1:B:107:VAL:HG13	2.49	0.42
1:B:137:LEU:HD21	1:B:174:PHE:CD2	2.54	0.42
1:C:37:GLY:O	1:C:41:VAL:CG2	2.67	0.42
1:A:225:PRO:HA	1:A:226:ARG:HB3	2.01	0.42
1:B:129:GLN:CB	1:C:107:VAL:HG13	2.49	0.42
1:C:42:LEU:HD11	1:D:42:LEU:HD13	2.02	0.42
1:A:69:PRO:HB3	1:A:90:MET:CE	2.49	0.42
1:B:110:PRO:C	1:B:112:VAL:N	2.72	0.42
1:C:223:LEU:HB3	1:D:11:ARG:HH22	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:PRO:HA	1:C:226:ARG:HB3	2.01	0.42
1:C:121:LEU:HD12	1:C:130:ALA:HB1	2.01	0.41
1:A:107:VAL:HG13	1:D:129:GLN:CB	2.49	0.41
1:A:121:LEU:CD1	1:A:130:ALA:CB	2.99	0.41
1:B:69:PRO:HB3	1:B:90:MET:CE	2.49	0.41
1:C:137:LEU:HD21	1:C:174:PHE:CD2	2.54	0.41
1:D:121:LEU:CD1	1:D:130:ALA:CB	2.98	0.41
1:B:32:LEU:O	1:B:33:ARG:CG	2.69	0.41
1:C:32:LEU:O	1:C:33:ARG:CG	2.69	0.41
1:A:32:LEU:O	1:A:33:ARG:CG	2.69	0.41
1:A:42:LEU:HD11	1:B:42:LEU:HD13	2.02	0.41
1:C:38:PRO:HB3	1:D:39:LEU:CD1	2.51	0.41
1:C:121:LEU:CD1	1:C:130:ALA:CB	2.99	0.41
1:D:32:LEU:O	1:D:33:ARG:CG	2.69	0.41
1:B:42:LEU:HD11	1:C:42:LEU:HD13	2.02	0.41
1:B:129:GLN:HB3	1:C:107:VAL:CG1	2.50	0.41
1:A:107:VAL:CG1	1:D:129:GLN:HB3	2.50	0.40
1:C:38:PRO:HB2	1:C:39:LEU:H	1.68	0.40
1:D:201:HIS:HE1	1:D:205:TRP:HE1	1.69	0.40
1:D:220:ASP:CB	1:D:221:PHE:HA	2.51	0.40
1:A:38:PRO:HB2	1:A:39:LEU:H	1.68	0.40
1:A:157:LEU:O	1:B:159:SER:HB2	2.22	0.40
1:B:136:PHE:CZ	1:C:103:VAL:HG11	2.56	0.40
1:C:37:GLY:N	1:C:38:PRO:CD	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	231/263 (88%)	209 (90%)	15 (6%)	7 (3%)	4 28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	231/263 (88%)	205 (89%)	17 (7%)	9 (4%)	3	23
1	C	231/263 (88%)	209 (90%)	14 (6%)	8 (4%)	3	25
1	D	231/263 (88%)	203 (88%)	18 (8%)	10 (4%)	2	22
2	E	141/149 (95%)	119 (84%)	20 (14%)	2 (1%)	11	46
2	F	141/149 (95%)	121 (86%)	18 (13%)	2 (1%)	11	46
All	All	1206/1350 (89%)	1066 (88%)	102 (8%)	38 (3%)	7	26

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	ARG
1	A	38	PRO
1	A	154	ASN
1	A	227	LEU
1	B	33	ARG
1	B	38	PRO
1	B	154	ASN
1	B	226	ARG
1	B	227	LEU
1	C	33	ARG
1	C	38	PRO
1	C	154	ASN
1	C	227	LEU
1	D	33	ARG
1	D	38	PRO
1	D	154	ASN
1	D	227	LEU
1	D	226	ARG
2	E	81	SER
2	E	97	ASN
2	F	81	SER
2	F	97	ASN
1	A	181	ALA
1	B	181	ALA
1	C	181	ALA
1	C	226	ARG
1	D	181	ALA
1	B	222	LEU
1	D	222	LEU
1	C	35	ALA

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Mol	Chain	Res	Type
1	D	35	ALA
1	D	224	PHE
1	A	35	ALA
1	A	110	PRO
1	B	35	ALA
1	B	110	PRO
1	C	110	PRO
1	D	110	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/205 (87%)	160 (89%)	19 (11%)	6	24
1	B	179/205 (87%)	160 (89%)	19 (11%)	6	24
1	C	179/205 (87%)	160 (89%)	19 (11%)	6	24
1	D	179/205 (87%)	160 (89%)	19 (11%)	6	24
2	E	122/127 (96%)	106 (87%)	16 (13%)	4	18
2	F	122/127 (96%)	106 (87%)	16 (13%)	4	18
All	All	960/1074 (89%)	852 (89%)	108 (11%)	9	21

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LEU
1	A	34	TRP
1	A	42	LEU
1	A	61	HIS
1	A	66	HIS
1	A	104	LEU
1	A	127	VAL
1	A	140	GLN
1	A	153	ARG
1	A	162	LEU

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Mol	Chain	Res	Type
1	A	170	LEU
1	A	187	ARG
1	A	202	TRP
1	A	214	LEU
1	A	222	LEU
1	A	227	LEU
1	A	228	LYS
1	A	229	SER
1	A	234	LEU
1	B	32	LEU
1	B	34	TRP
1	B	42	LEU
1	B	61	HIS
1	B	66	HIS
1	B	104	LEU
1	B	127	VAL
1	B	140	GLN
1	B	153	ARG
1	B	162	LEU
1	B	170	LEU
1	B	187	ARG
1	B	202	TRP
1	B	214	LEU
1	B	223	LEU
1	B	226	ARG
1	B	231	SER
1	B	238	LYS
1	B	241	ARG
1	C	32	LEU
1	C	34	TRP
1	C	36	PRO
1	C	42	LEU
1	C	61	HIS
1	C	66	HIS
1	C	104	LEU
1	C	127	VAL
1	C	140	GLN
1	C	153	ARG
1	C	162	LEU
1	C	170	LEU
1	C	187	ARG
1	C	202	TRP

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Mol	Chain	Res	Type
1	C	214	LEU
1	C	227	LEU
1	C	228	LYS
1	C	229	SER
1	C	234	LEU
1	D	32	LEU
1	D	34	TRP
1	D	42	LEU
1	D	61	HIS
1	D	66	HIS
1	D	104	LEU
1	D	127	VAL
1	D	140	GLN
1	D	153	ARG
1	D	162	LEU
1	D	170	LEU
1	D	187	ARG
1	D	202	TRP
1	D	214	LEU
1	D	224	PHE
1	D	226	ARG
1	D	227	LEU
1	D	238	LYS
1	D	241	ARG
2	E	11	GLU
2	E	21	LYS
2	E	22	ASP
2	E	30	LYS
2	E	32	LEU
2	E	45	GLU
2	E	60	ASN
2	E	62	THR
2	E	64	ASP
2	E	65	PHE
2	E	75	LYS
2	E	77	LYS
2	E	111	ASN
2	E	115	LYS
2	E	131	ASP
2	E	148	LYS
2	F	11	GLU
2	F	21	LYS

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Mol	Chain	Res	Type
2	F	22	ASP
2	F	30	LYS
2	F	32	LEU
2	F	45	GLU
2	F	60	ASN
2	F	62	THR
2	F	64	ASP
2	F	65	PHE
2	F	75	LYS
2	F	77	LYS
2	F	111	ASN
2	F	114	GLU
2	F	115	LYS
2	F	148	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	HIS
1	A	66	HIS
1	A	80	GLN
1	A	93	GLN
1	A	119	ASN
1	A	140	GLN
1	A	201	HIS
1	B	61	HIS
1	B	66	HIS
1	B	80	GLN
1	B	93	GLN
1	B	119	ASN
1	B	140	GLN
1	B	201	HIS
1	C	61	HIS
1	C	66	HIS
1	C	80	GLN
1	C	93	GLN
1	C	119	ASN
1	C	140	GLN
1	C	201	HIS
1	D	61	HIS
1	D	66	HIS
1	D	80	GLN

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Mol	Chain	Res	Type
1	D	93	GLN
1	D	119	ASN
1	D	140	GLN
1	D	201	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are 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.

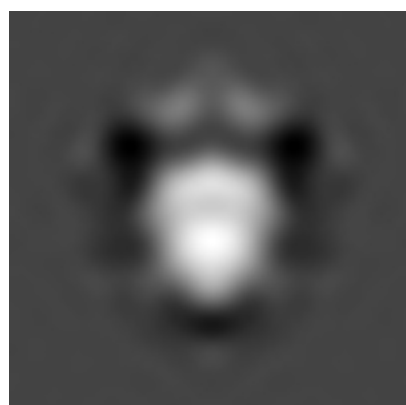
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5679. These allow visual inspection of the internal detail of the map and identification of artifacts.

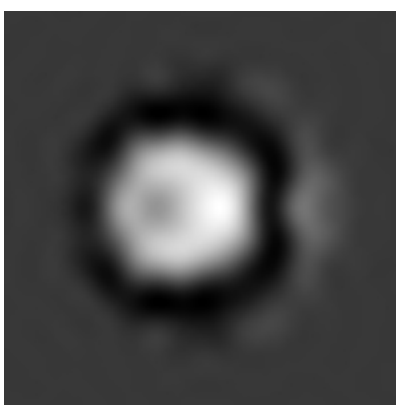
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

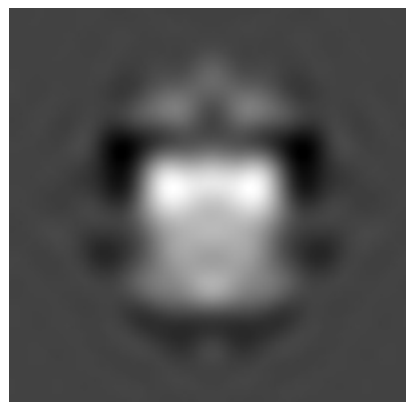


Z

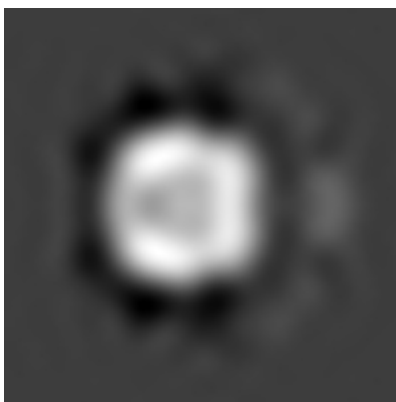
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

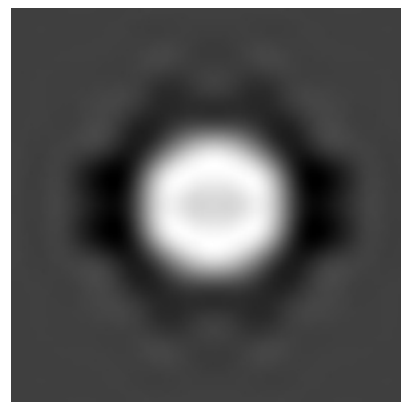
6.2.1 Primary map



X Index: 33



Y Index: 33

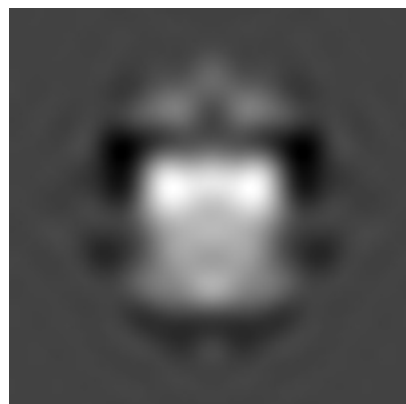


Z Index: 33

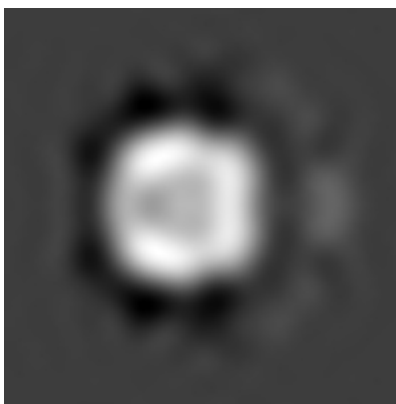
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

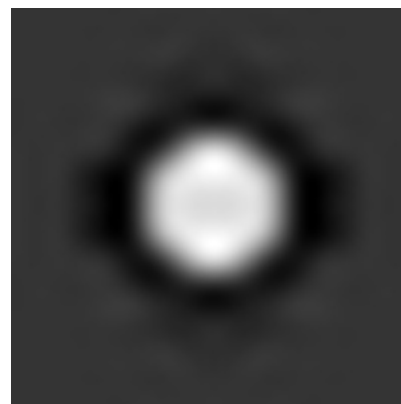
6.3.1 Primary map



X Index: 33



Y Index: 33



Z Index: 35

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

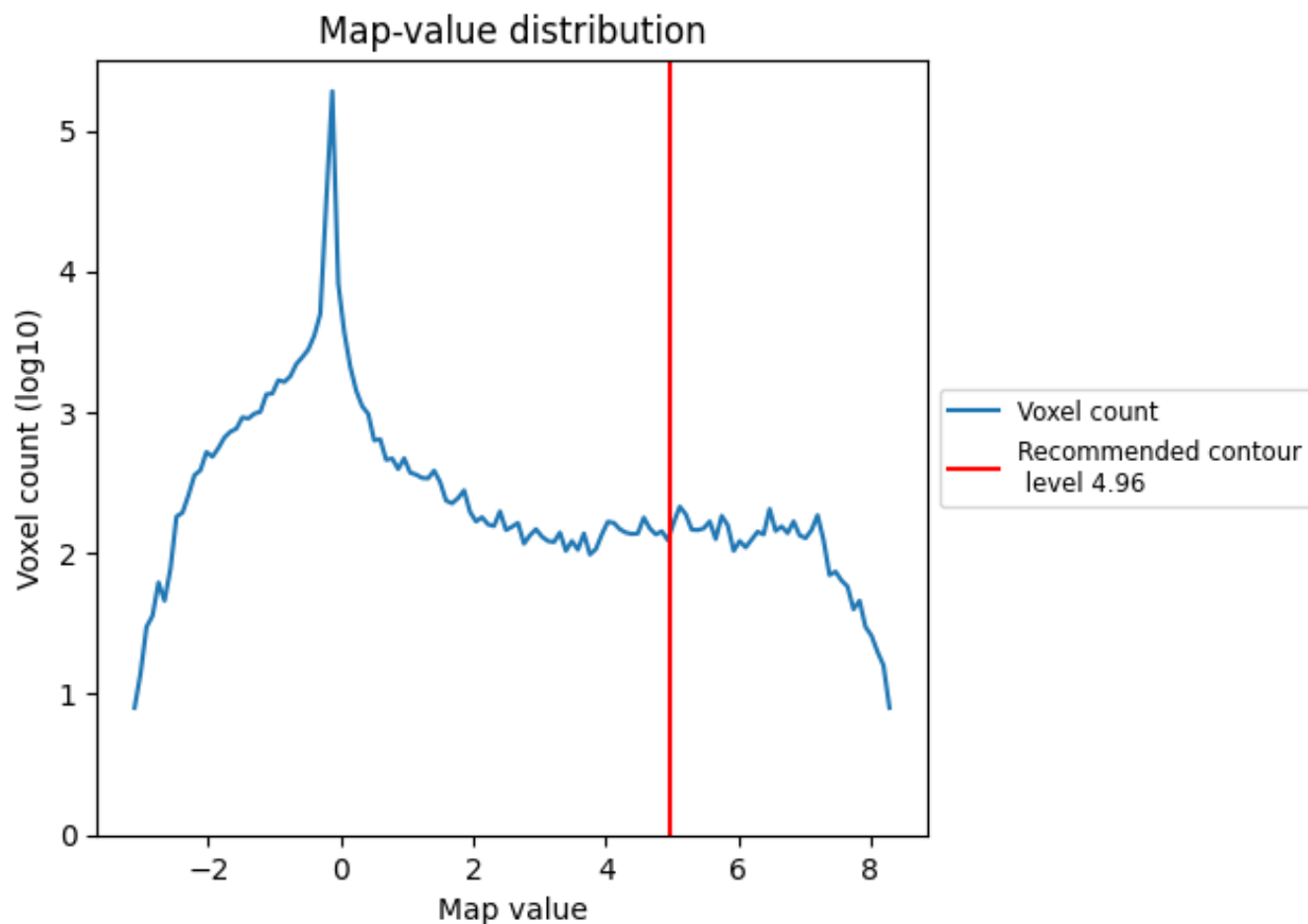
6.5 Mask visualisation

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

7 Map analysis [i](#)

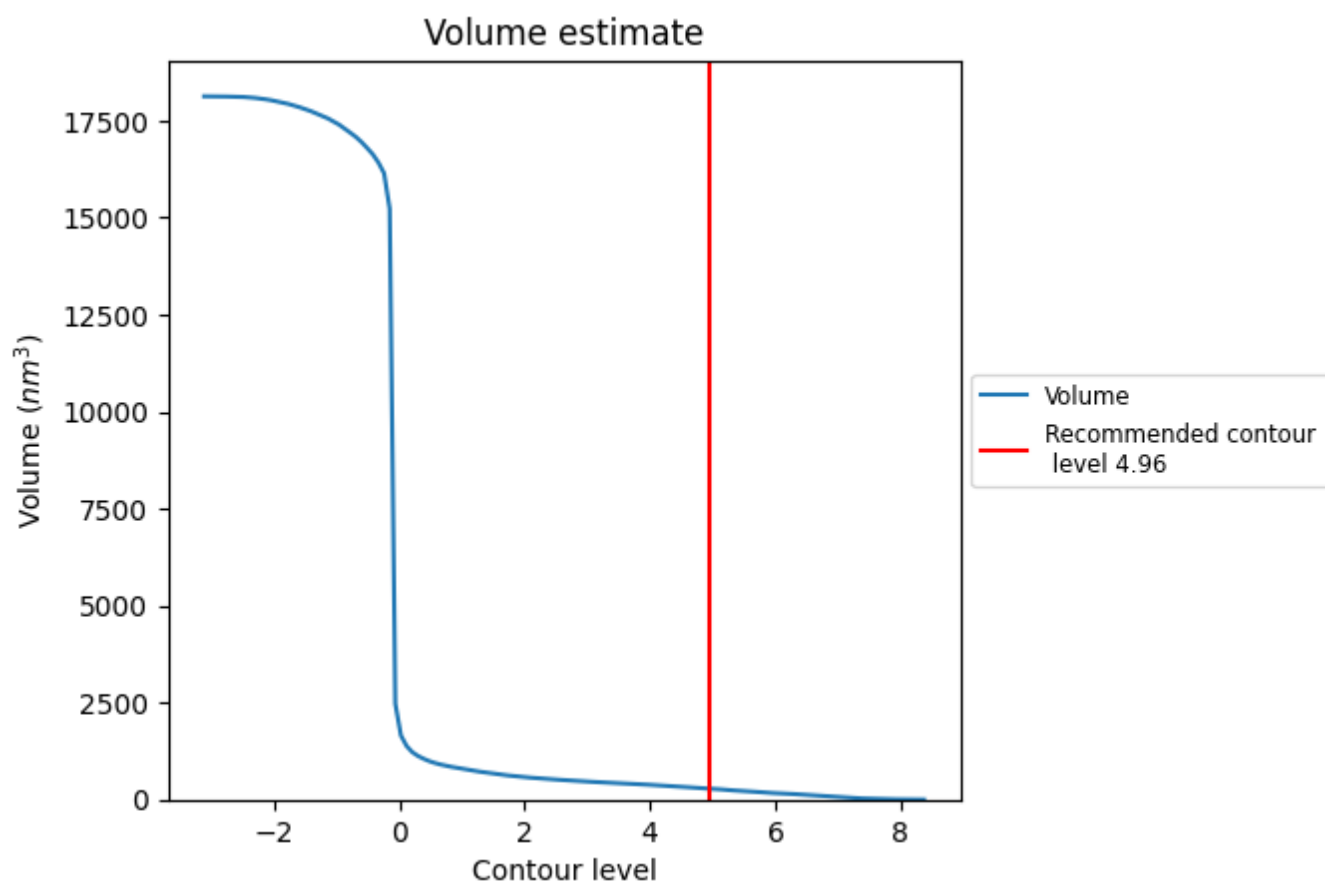
This section contains the results of statistical analysis of the map.

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.

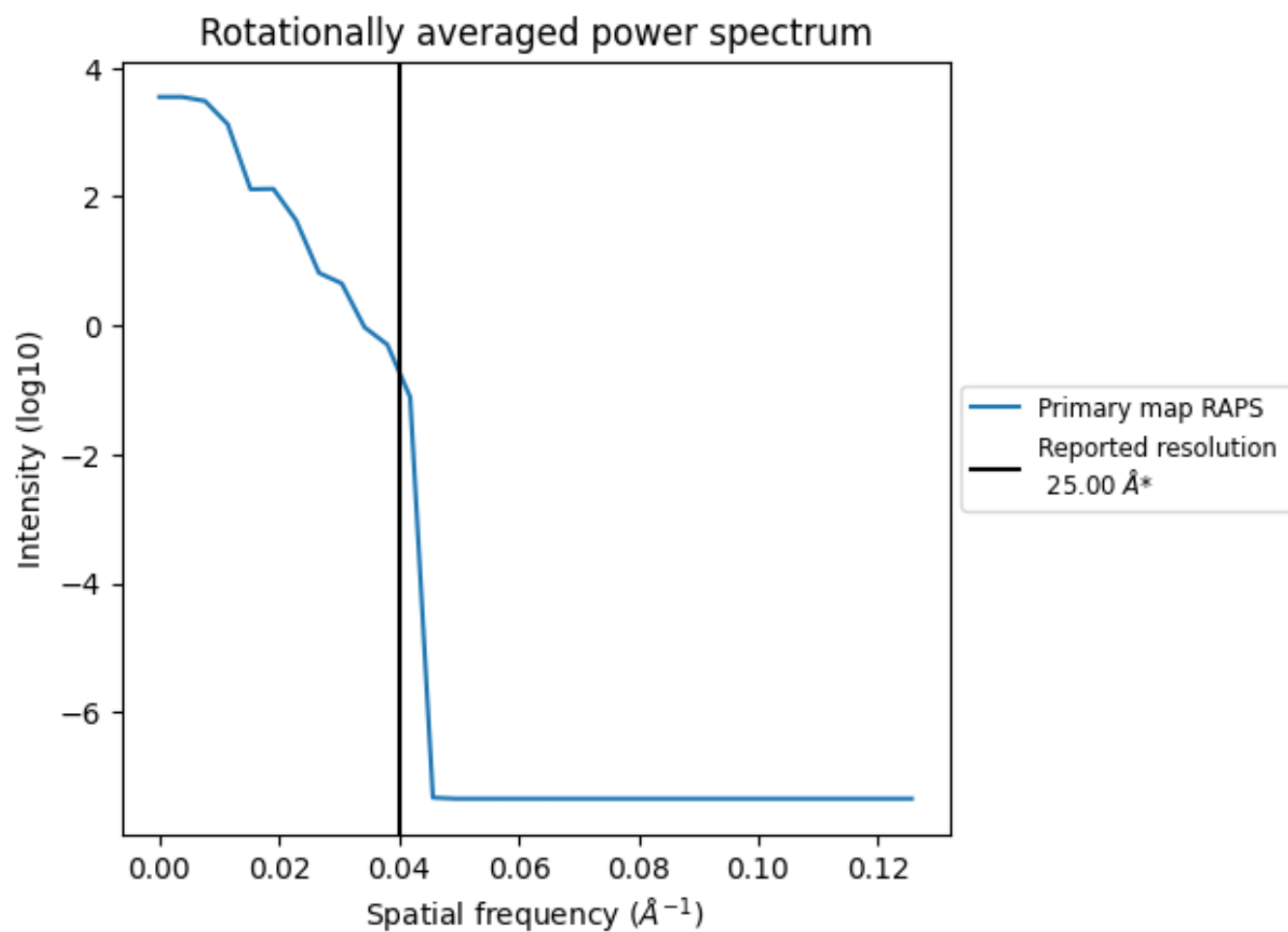
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 281 nm³; this corresponds to an approximate mass of 254 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 0.040 Å⁻¹

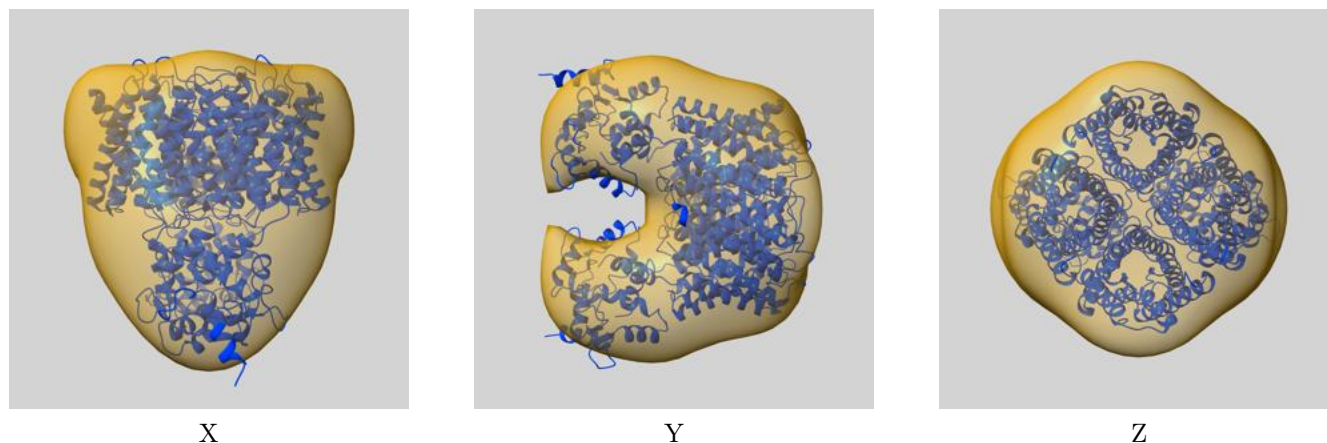
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

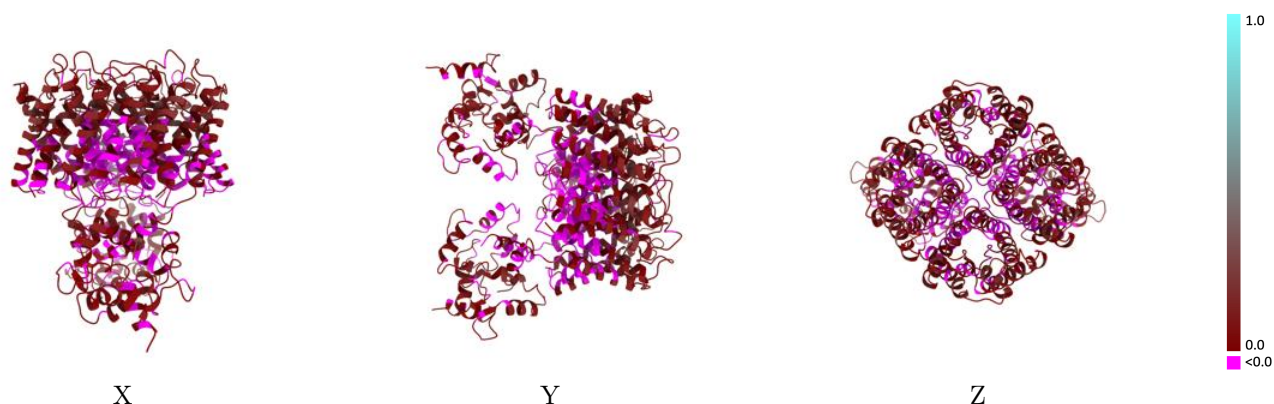
This section contains information regarding the fit between EMDB map EMD-5679 and PDB model 3J41. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



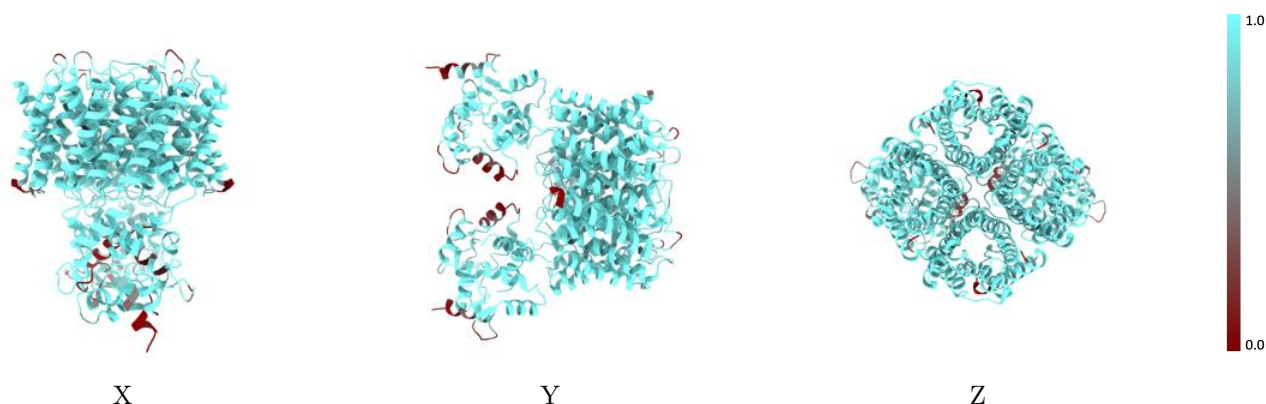
The images above show the 3D surface view of the map at the recommended contour level 4.96 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



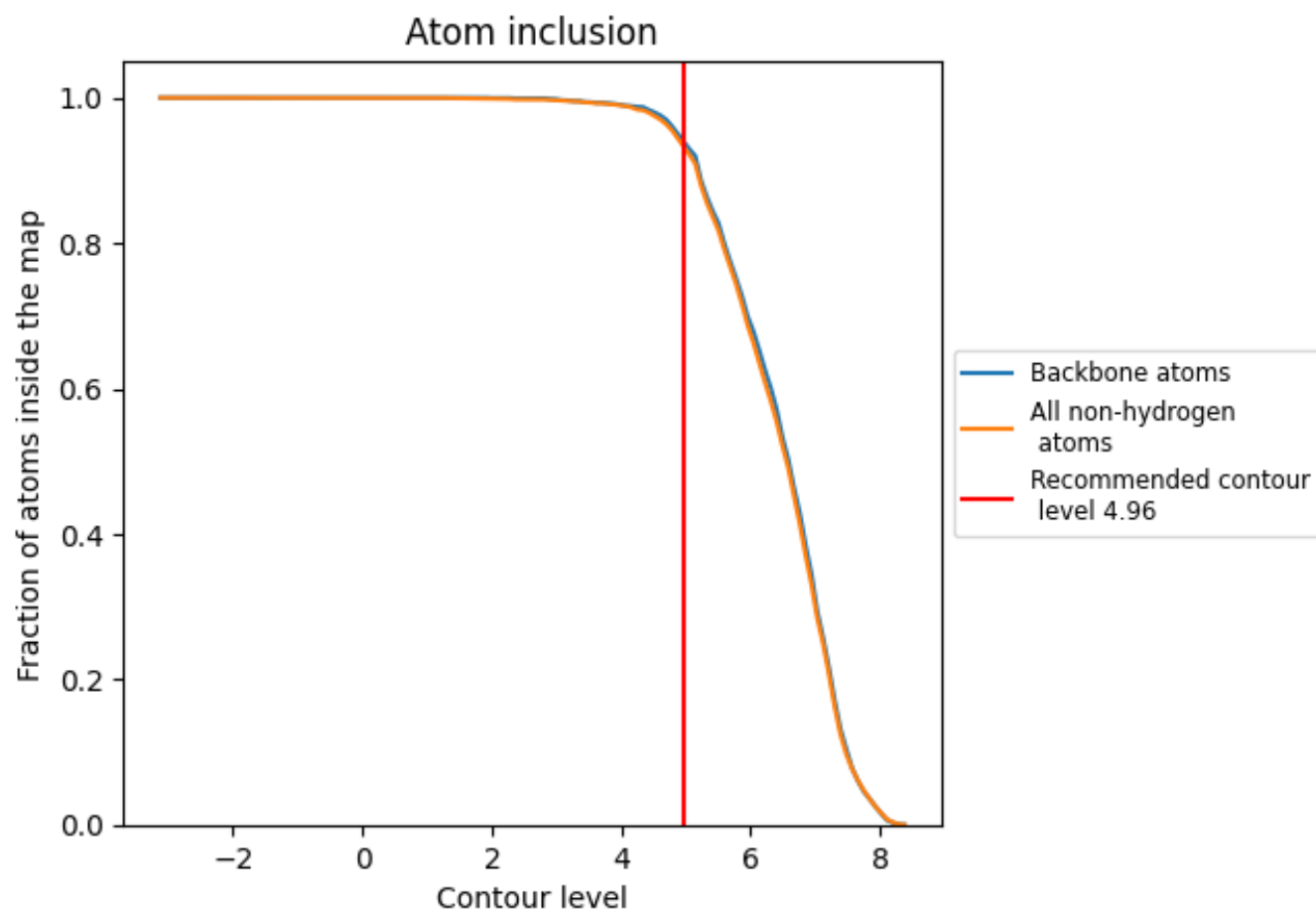
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.96).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (4.96) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.9336</div>	<div><div></div>0.0420</div>
A	<div><div></div>0.9665</div>	<div><div></div>0.0390</div>
B	<div><div></div>0.9861</div>	<div><div></div>0.0340</div>
C	<div><div></div>0.9671</div>	<div><div></div>0.0430</div>
D	<div><div></div>0.9861</div>	<div><div></div>0.0400</div>
E	<div><div></div>0.8007</div>	<div><div></div>0.0520</div>
F	<div><div></div>0.8007</div>	<div><div></div>0.0540</div>

1.0

0.0

<0.0