



Full wwPDB EM Validation Report ⓘ

Nov 7, 2022 – 01:33 AM EST

PDB ID : 6C6L
EMDB ID : EMD-7348
Title : Yeast Vacuolar ATPase Vo in lipid nanodisc
Authors : Roh, S.; Stam, N.J.; Hryc, C.; Couoh-Cardel, S.; Pintilie, G.; Chiu, W.;
Wilkens, S.
Deposited on : 2018-01-19
Resolution : 3.50 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

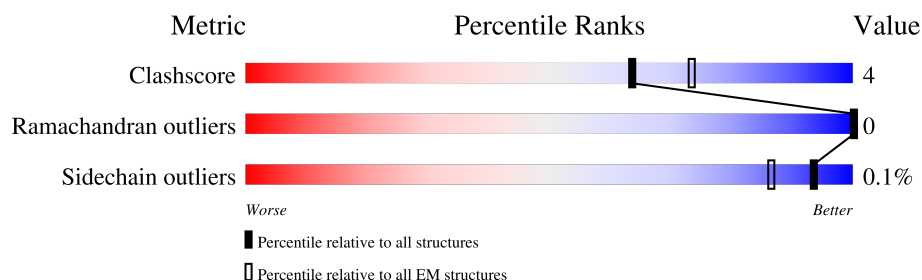
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	D	164	83% 13% .
2	C	213	79% 15% 6%
3	N	265	16% . 80%
4	M	73	84% 10% . 5%
5	E	160	89% 11% .
5	F	160	88% 11% .
5	G	160	88% 12% .
5	H	160	92% 8%
5	I	160	94% 6% .

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Mol	Chain	Length	Quality of chain
5	J	160	 88% 12%
5	K	160	 88% 12%
5	L	160	 86% 14%
6	B	345	 89% 11%
7	A	840	 76% 12% 11%
8	O	85	 82% 7% 11%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 22110 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 V-type proton ATPase subunit c'.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	157	Total	C	N	O	S	0	0
			1139	753	179	195	12		

- Molecule 2 is a protein called V-type proton ATPase subunit c''.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	200	Total	C	N	O	S	0	0
			1488	992	230	259	7		

- Molecule 3 is a protein called V0 assembly protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	52	Total	C	N	O	S	0	0
			395	262	57	74	2		

- Molecule 4 is a protein called V-type proton ATPase subunit e.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	69	Total	C	N	O	S	0	0
			550	367	91	86	6		

- Molecule 5 is a protein called V-type proton ATPase subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	159	Total	C	N	O	S	0	0
			1137	749	182	199	7		
5	F	159	Total	C	N	O	S	0	0
			1137	749	182	199	7		
5	G	159	Total	C	N	O	S	0	0
			1137	749	182	199	7		
5	H	160	Total	C	N	O	S	0	0
			1143	752	183	200	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	159	Total	C	N	O	S	0	0
			1137	749	182	199	7		
5	J	159	Total	C	N	O	S	0	0
			1137	749	182	199	7		
5	K	160	Total	C	N	O	S	0	0
			1143	752	183	200	8		
5	L	159	Total	C	N	O	S	0	0
			1137	749	182	199	7		

- Molecule 6 is a protein called V-type proton ATPase subunit d.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	344	Total	C	N	O	S	0	0
			2793	1774	453	553	13		

- Molecule 7 is a protein called V-type proton ATPase subunit a, vacuolar isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	746	Total	C	N	O	S	0	0
			6054	3951	985	1083	35		


- Molecule 8 is a protein called V-type proton ATPase subunit f.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	76	Total	C	N	O	S	0	0
			583	386	94	100	3		

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. 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. 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.

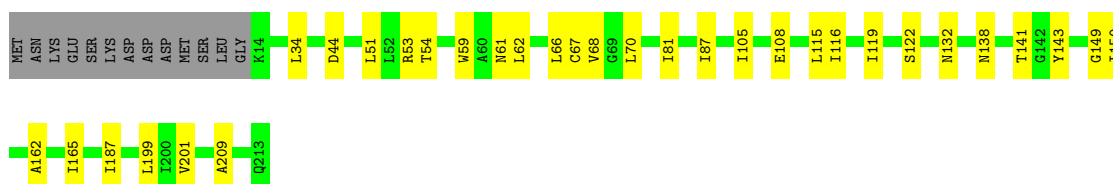
- Molecule 1: V-type proton ATPase subunit c'

Chain D: 



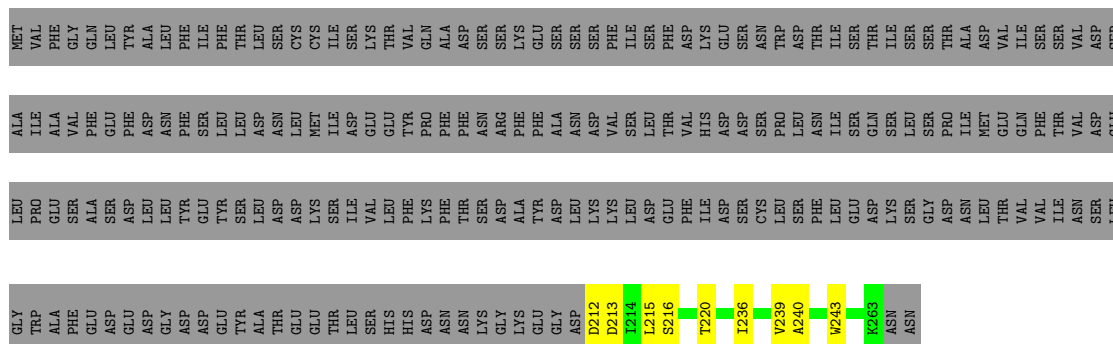
- Molecule 2: V-type proton ATPase subunit c''

Chain C: 




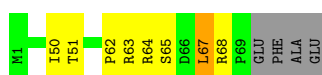
- Molecule 3: V0 assembly protein 1

Chain N: 




- Molecule 4: V-type proton ATPase subunit e

Chain M: 




- Molecule 5: V-type proton ATPase subunit c

Chain E:  89% 11%




- Molecule 5: V-type proton ATPase subunit c

Chain F:  88% 11%



- Molecule 5: V-type proton ATPase subunit c

Chain G:  88% 12%



- Molecule 5: V-type proton ATPase subunit c

Chain H:  92% 8%




- Molecule 5: V-type proton ATPase subunit c

Chain I:  94% 6%



- Molecule 5: V-type proton ATPase subunit c

Chain J:  88% 12%



- Molecule 5: V-type proton ATPase subunit c

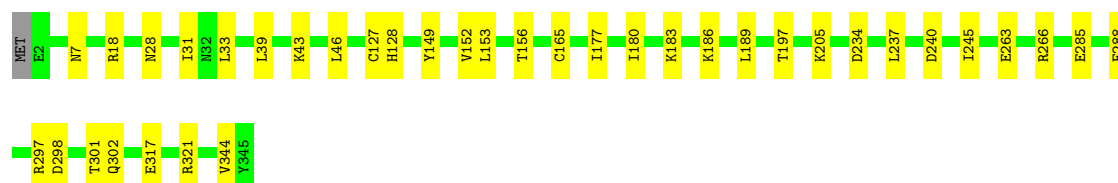
Chain K:  88% 12%

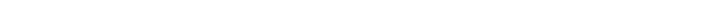


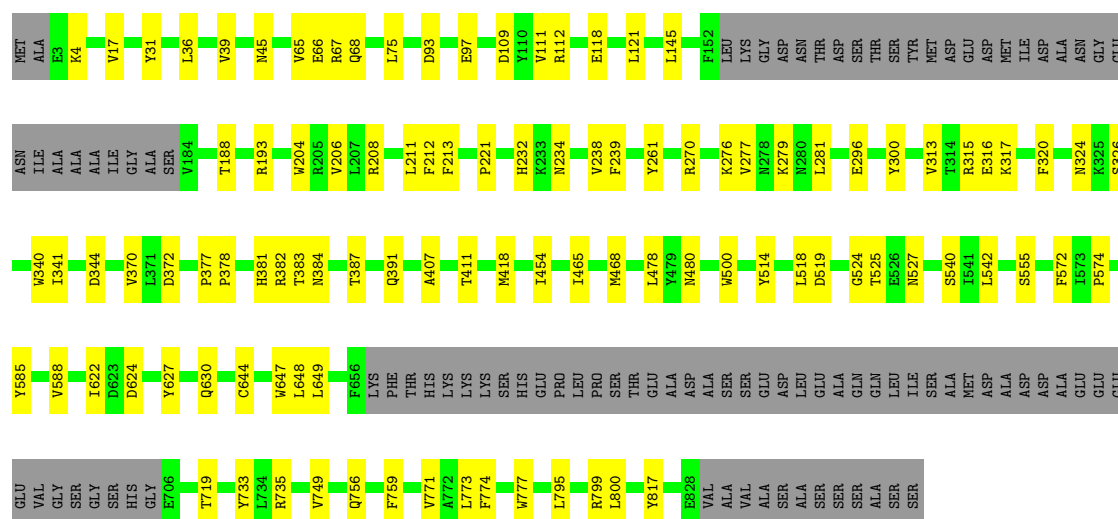
- Molecule 5: V-type proton ATPase subunit c

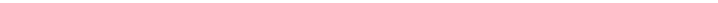
M1	T22	F23	T24	G27	R46	P47	N53	V69	V70	F88	G92	V97	G101	L102	V116	S120	L125	I134	F135	I145	V146	R153	V159	C159
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- Chain B:  89% 11%



- Chain A:  76% 12% 11%



- Chain O:  82% 7% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	180528	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 3200FSC	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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	D	0.38	0/1162	0.55	0/1575
2	C	0.37	0/1519	0.58	2/2064 (0.1%)
3	N	0.33	0/401	0.67	0/549
4	M	0.35	0/566	0.65	1/773 (0.1%)
5	E	0.34	0/1155	0.56	0/1571
5	F	0.36	0/1155	0.58	0/1571
5	G	0.33	0/1155	0.61	1/1571 (0.1%)
5	H	0.33	0/1161	0.55	0/1579
5	I	0.33	0/1155	0.63	1/1571 (0.1%)
5	J	0.33	0/1155	0.57	0/1571
5	K	0.34	0/1161	0.56	0/1579
5	L	0.37	0/1155	0.63	0/1571
6	B	0.35	0/2852	0.58	0/3870
7	A	0.34	0/6206	0.56	0/8401
8	O	0.35	0/600	0.59	0/822
All	All	0.35	0/22558	0.58	5/30638 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	157	ASP	CB-CG-OD1	6.08	123.77	118.30
4	M	67	LEU	CA-CB-CG	5.65	128.29	115.30
2	C	34	LEU	CA-CB-CG	5.10	127.02	115.30
5	G	54	ILE	CG1-CB-CG2	-5.07	100.25	111.40
2	C	70	LEU	CA-CB-CG	5.03	126.86	115.30

There are no chirality outliers.

There are no planarity outliers.

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	D	1139	0	1194	16	0
2	C	1488	0	1551	23	0
3	N	395	0	410	6	0
4	M	550	0	574	7	0
5	E	1137	0	1207	11	0
5	F	1137	0	1207	13	0
5	G	1137	0	1207	11	0
5	H	1143	0	1212	7	0
5	I	1137	0	1207	5	0
5	J	1137	0	1207	12	0
5	K	1143	0	1212	12	0
5	L	1137	0	1207	17	0
6	B	2793	0	2677	22	0
7	A	6054	0	6024	62	0
8	O	583	0	576	5	0
All	All	22110	0	22672	193	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 4.

All (193) 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)
4:M:62:PRO:HB2	4:M:64:ARG:HH22	1.51	0.73
5:F:70:VAL:HG11	5:F:97:VAL:HG11	1.73	0.70
5:G:70:VAL:HG11	5:G:97:VAL:HG11	1.74	0.69
6:B:127:CYS:SG	6:B:128:HIS:N	2.66	0.69
5:K:70:VAL:HG11	5:K:97:VAL:HG11	1.74	0.68
7:A:525:THR:HG22	7:A:527:ASN:H	1.61	0.66
7:A:480:ASN:ND2	7:A:518:LEU:O	2.29	0.65
7:A:39:VAL:HG22	7:A:341:ILE:HD11	1.78	0.65
5:I:70:VAL:HG11	5:I:97:VAL:HG11	1.80	0.63
5:E:70:VAL:HG11	5:E:97:VAL:HG11	1.80	0.63
5:F:24:THR:HG21	5:F:67:GLY:HA3	1.82	0.62
5:J:24:THR:HG21	5:J:67:GLY:HA3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:649:LEU:HB3	7:A:719:THR:HG21	1.82	0.61
7:A:4:LYS:HB3	7:A:382:ARG:HH12	1.66	0.61
6:B:183:LYS:NZ	6:B:240:ASP:OD2	2.34	0.60
2:C:67:CYS:SG	2:C:68:VAL:N	2.75	0.60
7:A:212:PHE:HB2	7:A:239:PHE:HB2	1.83	0.60
5:E:89:ILE:HD11	5:E:154:ALA:HA	1.83	0.60
7:A:68:GLN:NE2	7:A:118:GLU:OE1	2.35	0.59
5:J:70:VAL:HG11	5:J:97:VAL:HG11	1.84	0.59
2:C:53:ARG:NH2	3:N:213:ASP:O	2.36	0.58
5:L:46:ARG:NH1	5:L:120:SER:O	2.37	0.58
1:D:132:ARG:HH21	5:E:48:ASP:HB2	1.68	0.58
2:C:81:ILE:HG23	6:B:7:ASN:HD22	1.68	0.58
6:B:33:LEU:HD21	6:B:46:LEU:HD23	1.87	0.57
1:D:27:MET:HG2	2:C:201:VAL:HG11	1.86	0.57
4:M:68:ARG:NH2	7:A:500:TRP:O	2.37	0.57
7:A:344:ASP:OD2	7:A:382:ARG:NH2	2.37	0.57
7:A:36:LEU:HD13	7:A:97:GLU:HA	1.87	0.57
5:H:24:THR:HG21	5:H:67:GLY:HA3	1.88	0.56
5:K:39:ILE:HD13	5:K:116:VAL:HG21	1.87	0.56
7:A:45:ASN:ND2	7:A:326:SER:O	2.39	0.56
7:A:276:LYS:HA	7:A:279:LYS:HE2	1.88	0.56
5:I:99:LEU:HD12	5:J:22:ILE:HD13	1.88	0.55
6:B:297:ARG:HD3	6:B:344:VAL:HG11	1.86	0.55
6:B:186:LYS:NZ	6:B:240:ASP:O	2.36	0.55
2:C:116:ILE:HA	2:C:119:ILE:HG12	1.89	0.55
7:A:627:TYR:HB3	7:A:630:GLN:HB2	1.89	0.55
2:C:108:GLU:OE1	7:A:735:ARG:NH2	2.40	0.55
5:K:46:ARG:NH1	5:K:120:SER:O	2.40	0.54
1:D:125:ARG:NH2	6:B:302:GLN:OE1	2.41	0.54
6:B:317:GLU:OE1	6:B:321:ARG:NH2	2.35	0.54
2:C:132:ASN:O	2:C:138:ASN:ND2	2.38	0.54
5:F:146:VAL:HG11	5:G:21:ILE:HG13	1.90	0.54
2:C:66:LEU:HD23	2:C:150:ILE:HG22	1.90	0.54
7:A:193:ARG:HE	7:A:232:HIS:HB3	1.71	0.53
7:A:622:ILE:HG22	7:A:624:ASP:H	1.73	0.53
5:F:2:THR:OG1	5:F:5:CYS:SG	2.66	0.53
6:B:152:VAL:O	6:B:156:THR:OG1	2.22	0.53
5:I:80:GLN:HG2	5:I:81:LYS:HG3	1.91	0.53
5:G:49:LEU:O	5:G:53:ASN:ND2	2.42	0.53
7:A:31:TYR:OH	7:A:316:GLU:OE1	2.24	0.53
7:A:320:PHE:O	7:A:324:ASN:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:26:ALA:HB2	1:D:102:GLY:HA2	1.92	0.52
5:E:87:GLY:HA2	5:E:90:GLN:HE21	1.73	0.52
5:J:124:ARG:NH1	5:K:48:ASP:OD1	2.42	0.52
2:C:44:ASP:OD1	3:N:216:SER:OG	2.27	0.52
6:B:234:ASP:HB2	6:B:237:LEU:HD23	1.92	0.51
7:A:66:GLU:OE1	7:A:317:LYS:NZ	2.43	0.51
7:A:75:LEU:HD22	7:A:121:LEU:HD21	1.91	0.51
7:A:756:GLN:HA	7:A:759:PHE:HB3	1.92	0.51
5:K:55:VAL:HA	5:K:58:ILE:HG22	1.92	0.51
6:B:165:CYS:HA	6:B:183:LYS:HE2	1.93	0.51
7:A:17:VAL:HA	7:A:370:VAL:HA	1.91	0.51
4:M:50:ILE:HD13	7:A:542:LEU:HD22	1.93	0.51
6:B:189:LEU:HB3	6:B:245:ILE:HD11	1.92	0.51
5:H:88:PHE:O	5:H:92:GLY:N	2.41	0.50
5:K:23:PHE:HB3	5:K:102:LEU:HD23	1.93	0.50
2:C:122:SER:O	5:L:153:ARG:NH2	2.44	0.50
6:B:285:GLU:HA	6:B:288:PHE:HD2	1.75	0.50
7:A:67:ARG:NH1	7:A:118:GLU:OE2	2.41	0.50
5:F:39:ILE:HD13	5:F:116:VAL:HG21	1.94	0.50
7:A:540:SER:OG	7:A:733:TYR:O	2.29	0.50
7:A:372:ASP:OD1	7:A:372:ASP:N	2.43	0.50
5:I:24:THR:HG21	5:I:67:GLY:HA3	1.94	0.49
2:C:68:VAL:HG11	5:L:146:VAL:HG21	1.94	0.49
7:A:418:MET:HG2	7:A:800:LEU:HD22	1.95	0.49
1:D:100:SER:HB2	5:E:14:ALA:HB1	1.93	0.49
6:B:186:LYS:NZ	6:B:240:ASP:OD1	2.45	0.49
5:K:125:LEU:O	5:K:129:MET:N	2.46	0.49
5:L:27:GLY:HA3	5:L:102:LEU:HA	1.94	0.49
7:A:465:ILE:HG23	7:A:468:MET:HE3	1.95	0.49
5:F:42:THR:HG21	5:F:116:VAL:HG22	1.95	0.49
5:L:24:THR:HG22	5:L:101:GLY:HA3	1.94	0.48
6:B:18:ARG:NH2	6:B:302:GLN:O	2.46	0.48
5:L:135:PHE:HZ	7:A:799:ARG:HG3	1.77	0.48
7:A:109:ASP:HA	7:A:112:ARG:HG2	1.94	0.48
7:A:771:VAL:HG13	8:O:62:TYR:HE1	1.77	0.48
2:C:87:ILE:HD11	5:L:125:LEU:HD13	1.96	0.48
6:B:28:ASN:HA	6:B:31:ILE:HD12	1.95	0.48
5:L:70:VAL:HG11	5:L:97:VAL:HG11	1.96	0.48
6:B:298:ASP:O	6:B:301:THR:OG1	2.29	0.48
2:C:141:THR:HG22	2:C:209:ALA:HB1	1.96	0.48
1:D:23:CYS:HB2	1:D:80:ILE:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:46:ARG:HD3	5:G:49:LEU:HD13	1.96	0.48
7:A:378:PRO:HB2	7:A:817:TYR:HA	1.95	0.48
4:M:63:ARG:HH22	7:A:524:GLY:H	1.62	0.47
5:E:6:PRO:HD2	5:E:84:LEU:HB2	1.96	0.47
3:N:215:LEU:HD13	3:N:220:THR:HG22	1.96	0.47
7:A:407:ALA:O	7:A:411:THR:OG1	2.31	0.47
5:J:91:LEU:HB2	5:J:95:LEU:HD23	1.95	0.47
5:L:23:PHE:HB3	5:L:102:LEU:HD23	1.96	0.47
7:A:277:VAL:HG13	7:A:281:LEU:HD13	1.96	0.47
5:G:55:VAL:HA	5:G:58:ILE:HG12	1.97	0.47
5:J:6:PRO:HD2	5:J:84:LEU:HB2	1.96	0.47
2:C:54:THR:HG21	2:C:59:TRP:HE1	1.80	0.47
5:L:88:PHE:O	5:L:92:GLY:N	2.39	0.47
7:A:574:PRO:HB2	7:A:648:LEU:HD13	1.97	0.47
5:G:146:VAL:HG11	5:H:21:ILE:HG13	1.96	0.47
5:I:96:SER:HB2	5:J:21:ILE:HD11	1.97	0.46
3:N:212:ASP:N	3:N:212:ASP:OD1	2.48	0.46
5:J:71:SER:HA	5:J:74:VAL:HG12	1.97	0.46
3:N:240:ALA:HA	3:N:243:TRP:HD1	1.81	0.46
5:G:6:PRO:HD2	5:G:84:LEU:HB2	1.98	0.46
7:A:206:VAL:O	7:A:208:ARG:NH1	2.49	0.46
7:A:381:HIS:HB2	7:A:391:GLN:HE22	1.81	0.46
7:A:145:LEU:HD12	7:A:270:ARG:HG3	1.97	0.46
1:D:63:VAL:HG21	2:C:187:ILE:HG22	1.98	0.45
5:G:108:ILE:HA	5:G:111:VAL:HG12	1.97	0.45
8:O:3:PRO:HG3	8:O:75:LEU:HD12	1.98	0.45
5:E:19:SER:HA	5:E:22:ILE:HG12	1.98	0.45
8:O:4:VAL:HG12	8:O:5:VAL:H	1.81	0.45
5:E:24:THR:HG21	5:E:67:GLY:HA3	1.99	0.45
5:H:80:GLN:HG2	5:H:81:LYS:HG3	1.97	0.45
6:B:39:LEU:O	6:B:43:LYS:N	2.49	0.45
5:G:71:SER:HA	5:G:74:VAL:HG12	1.97	0.45
7:A:93:ASP:OD2	7:A:315:ARG:NH2	2.47	0.45
1:D:127:TYR:HE1	1:D:134:PHE:HB2	1.82	0.44
2:C:51:LEU:O	2:C:143:TYR:OH	2.35	0.44
4:M:51:THR:HG21	7:A:478:LEU:HD21	1.99	0.44
7:A:644:CYS:HA	7:A:647:TRP:HB3	1.99	0.44
2:C:67:CYS:HB3	2:C:149:GLY:HA2	1.98	0.44
5:F:113:ASP:HA	5:F:116:VAL:HG12	1.99	0.44
5:E:146:VAL:HG11	5:F:21:ILE:HG13	1.99	0.44
5:J:12:PHE:HB3	5:J:91:LEU:HD23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:177:ILE:HA	6:B:180:ILE:HG12	1.99	0.44
1:D:35:ALA:HB1	2:C:162:ALA:HB2	2.00	0.44
2:C:105:ILE:HD12	7:A:799:ARG:HE	1.83	0.44
5:L:134:ILE:HG21	7:A:795:LEU:HD12	2.00	0.44
4:M:63:ARG:HG2	4:M:65:SER:H	1.81	0.44
6:B:149:TYR:CE1	6:B:153:LEU:HD13	2.53	0.44
4:M:67:LEU:HD13	8:O:42:ILE:HG22	2.01	0.43
5:K:46:ARG:HG2	5:K:49:LEU:HD23	2.00	0.43
5:F:89:ILE:HD11	5:F:154:ALA:HA	1.99	0.43
7:A:585:TYR:HA	7:A:588:VAL:HG12	2.00	0.43
7:A:773:LEU:O	7:A:777:TRP:N	2.51	0.43
2:C:115:LEU:HD11	5:L:145:ILE:HD11	2.01	0.43
1:D:48:ILE:H	1:D:48:ILE:HG13	1.63	0.43
2:C:81:ILE:HG21	2:C:165:ILE:HG22	2.01	0.43
1:D:112:SER:OG	1:D:148:GLY:N	2.52	0.42
1:D:122:VAL:HG11	5:E:37:VAL:HG22	2.01	0.42
5:L:70:VAL:HG11	5:L:97:VAL:HG21	2.00	0.42
7:A:555:SER:HB3	7:A:572:PHE:HE1	1.84	0.42
5:E:107:ALA:HB2	5:F:29:ALA:HB1	2.01	0.42
7:A:221:PRO:HG3	7:A:232:HIS:HA	2.02	0.42
5:J:46:ARG:NH1	5:J:120:SER:O	2.52	0.42
5:J:108:ILE:HA	5:J:111:VAL:HG12	2.01	0.42
7:A:514:TYR:CG	7:A:519:ASP:HB3	2.55	0.42
2:C:62:LEU:O	2:C:66:LEU:N	2.40	0.42
7:A:383:THR:O	7:A:387:THR:OG1	2.33	0.42
1:D:40:LYS:HA	1:D:43:ILE:HD12	2.01	0.42
3:N:236:ILE:HA	3:N:239:VAL:HG12	2.02	0.42
7:A:313:VAL:O	7:A:317:LYS:N	2.48	0.42
1:D:89:ASP:OD1	1:D:89:ASP:N	2.47	0.41
6:B:197:THR:O	6:B:205:LYS:NZ	2.51	0.41
7:A:213:PHE:HD1	7:A:238:VAL:HG12	1.85	0.41
5:L:69:VAL:HB	7:A:749:VAL:HG11	2.02	0.41
7:A:340:TRP:CZ3	7:A:377:PRO:HB3	2.56	0.41
1:D:80:ILE:HB	1:D:98:HIS:HD2	1.86	0.41
5:F:24:THR:OG1	5:F:63:ILE:O	2.38	0.41
2:C:116:ILE:HD11	2:C:199:LEU:HD11	2.03	0.41
5:K:122:GLN:HE21	5:K:124:ARG:HB2	1.85	0.41
7:A:204:TRP:HD1	7:A:211:LEU:HD22	1.86	0.41
5:K:6:PRO:HD2	5:K:84:LEU:HB2	2.03	0.41
5:H:6:PRO:HD2	5:H:84:LEU:HB2	2.02	0.41
6:B:263:GLU:HA	6:B:266:ARG:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:131:LEU:HA	5:G:134:ILE:HD12	2.03	0.41
5:G:136:ALA:HB2	5:H:32:THR:HG21	2.02	0.41
5:H:10:PRO:HA	5:H:82:GLN:HE22	1.86	0.41
7:A:65:VAL:HG21	7:A:111:VAL:HG22	2.03	0.41
7:A:774:PHE:HD2	8:O:62:TYR:HH	1.67	0.41
1:D:119:VAL:HA	1:D:122:VAL:HG12	2.02	0.41
5:F:71:SER:HA	5:F:74:VAL:HG12	2.03	0.41
5:K:99:LEU:HD22	5:L:22:ILE:HD12	2.03	0.40
5:K:122:GLN:HE22	5:L:47:PRO:HB3	1.86	0.40
5:F:2:THR:HG1	5:F:5:CYS:HG	1.58	0.40
5:J:54:ILE:H	5:J:54:ILE:HG13	1.67	0.40
5:L:53:ASN:HD22	5:L:116:VAL:HG12	1.87	0.40
7:A:188:THR:OG1	7:A:261:TYR:O	2.37	0.40
7:A:193:ARG:HG3	7:A:234:ASN:HD21	1.87	0.40
7:A:296:GLU:O	7:A:300:TYR:N	2.51	0.40
7:A:454:ILE:H	7:A:454:ILE:HG13	1.79	0.40
7:A:795:LEU:HD23	7:A:795:LEU:HA	1.93	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	D	155/164 (94%)	153 (99%)	2 (1%)	0	100	100
2	C	198/213 (93%)	195 (98%)	3 (2%)	0	100	100
3	N	50/265 (19%)	47 (94%)	3 (6%)	0	100	100
4	M	67/73 (92%)	65 (97%)	2 (3%)	0	100	100
5	E	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
5	F	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
5	G	157/160 (98%)	154 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	H	158/160 (99%)	154 (98%)	4 (2%)	0	100	100
5	I	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
5	J	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
5	K	158/160 (99%)	156 (99%)	2 (1%)	0	100	100
5	L	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
6	B	342/345 (99%)	335 (98%)	7 (2%)	0	100	100
7	A	740/840 (88%)	716 (97%)	24 (3%)	0	100	100
8	O	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
All	All	2884/3265 (88%)	2813 (98%)	71 (2%)	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	D	119/125 (95%)	119 (100%)	0	100	100
2	C	155/168 (92%)	154 (99%)	1 (1%)	86	94
3	N	45/244 (18%)	45 (100%)	0	100	100
4	M	61/65 (94%)	61 (100%)	0	100	100
5	E	117/119 (98%)	117 (100%)	0	100	100
5	F	117/119 (98%)	117 (100%)	0	100	100
5	G	117/119 (98%)	117 (100%)	0	100	100
5	H	118/119 (99%)	118 (100%)	0	100	100
5	I	117/119 (98%)	117 (100%)	0	100	100
5	J	117/119 (98%)	117 (100%)	0	100	100
5	K	118/119 (99%)	117 (99%)	1 (1%)	81	91
5	L	117/119 (98%)	117 (100%)	0	100	100
6	B	308/309 (100%)	308 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	A	654/728 (90%)	653 (100%)	1 (0%)	93	98
8	O	63/72 (88%)	63 (100%)	0	100	100
All	All	2343/2663 (88%)	2340 (100%)	3 (0%)	93	98

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	61	ASN
5	K	131	LEU
7	A	384	ASN

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

Mol	Chain	Res	Type
5	E	90	GLN
6	B	128	HIS
5	G	90	GLN
5	G	156	GLN
5	J	80	GLN
5	J	90	GLN
5	K	122	GLN
7	A	311	GLN
7	A	391	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 ⓘ

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](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-7348. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit

This section was not generated.