



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Apr 13, 2019 – 12:45 PM EDT

PDB ID : 6O7W  
EMDB ID: : EMD-0647  
Title : Saccharomyces cerevisiae V-ATPase Stv1-V1VO State 2  
Authors : Vasanthakumar, T.; Bueler, S.A.; Wu, D.; Beilsten-Edmands, V.; Robinson, C.V.; Rubinstein, J.L.  
Deposited on : 2019-03-08  
Resolution : 7.00 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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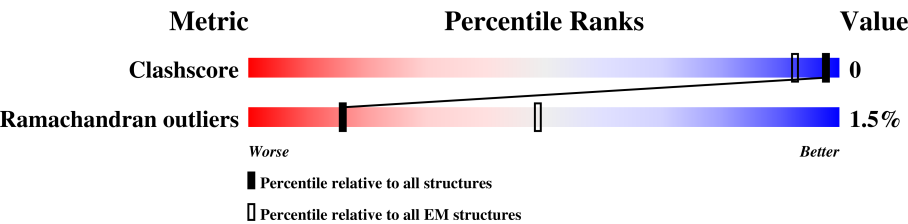
MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 7.00 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.







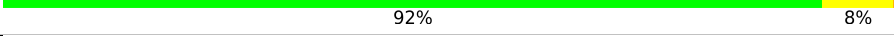


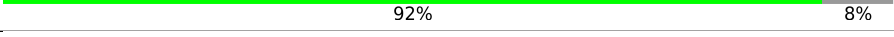
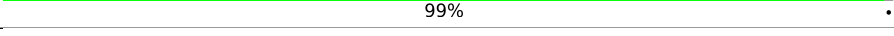
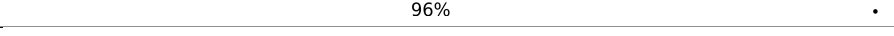
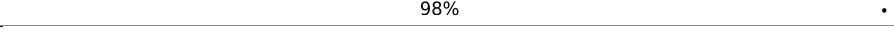
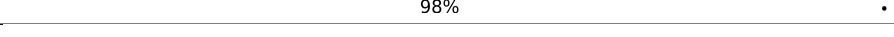
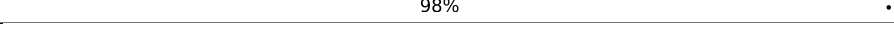
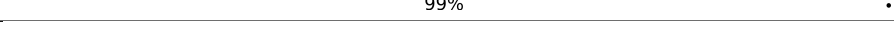
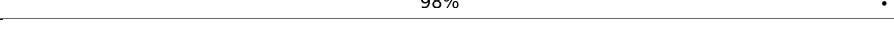
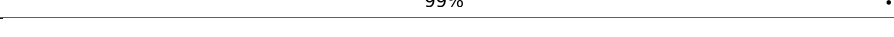
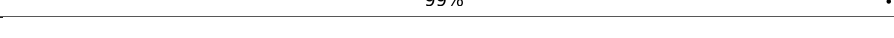
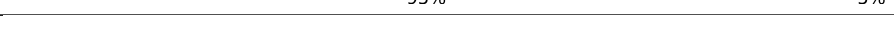
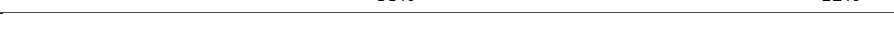

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	M	256	78% 18% .
2	N	118	88% 8% . .
3	A	639	84% 9% 7%
3	C	639	87% 6% 7%
3	E	639	85% 7% . 7%
4	B	517	81% 7% 12%
4	D	517	82% 6% 12%
4	F	517	81% 7% 12%
5	H	114	89% . 8%
5	J	114	89% . 8%
5	L	114	85% 7% 8%

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Mol	Chain	Length	Quality of chain
6	G	233	 90% 5% 7%
6	I	233	 88% 5% 7%
6	K	233	 88% 5% 7%
7	P	478	 91% 5% .
8	O	392	 92% 8% .
9	a	890	 70% 30%
10	b	265	 17% 83%
11	c	213	 92% 8%
12	d	345	 99% .
13	g	160	 96% .
13	h	160	 98% .
13	i	160	 98% .
13	j	160	 98% .
13	k	160	 99% .
13	l	160	 98% .
13	m	160	 99% .
13	n	160	 99% .
14	o	164	 95% 5%
15	e	73	 88% 12%
16	f	85	 72% 28%

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 39578 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 D.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	M	210	Total	C	N	O	0	0
			1039	619	210	210		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	N	115	Total	C	N	O	0	0
			571	341	115	115		

- Molecule 3 is a protein called Vacuolar ATP synthase catalytic subunit A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	593	Total	C	N	O	0	0
			2915	1729	593	593		
3	E	593	Total	C	N	O	0	0
			2915	1729	593	593		
3	A	593	Total	C	N	O	0	0
			2915	1729	593	593		

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	617	ASP	-	SEE REMARK 999	UNP B3LH69
C	618	TYR	-	SEE REMARK 999	UNP B3LH69
C	619	LYS	-	SEE REMARK 999	UNP B3LH69
C	620	ASP	-	SEE REMARK 999	UNP B3LH69
C	621	HIS	-	SEE REMARK 999	UNP B3LH69
C	622	ASP	-	SEE REMARK 999	UNP B3LH69
C	623	GLY	-	SEE REMARK 999	UNP B3LH69
C	624	ASP	-	SEE REMARK 999	UNP B3LH69
C	625	TYR	-	SEE REMARK 999	UNP B3LH69
C	626	LYS	-	SEE REMARK 999	UNP B3LH69
C	627	ASP	-	SEE REMARK 999	UNP B3LH69

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Chain	Residue	Modelled	Actual	Comment	Reference
C	628	HIS	-	SEE REMARK 999	UNP B3LH69
C	629	ASP	-	SEE REMARK 999	UNP B3LH69
C	630	ILE	-	SEE REMARK 999	UNP B3LH69
C	631	ASP	-	SEE REMARK 999	UNP B3LH69
C	632	TYR	-	SEE REMARK 999	UNP B3LH69
C	633	LYS	-	SEE REMARK 999	UNP B3LH69
C	634	ASP	-	SEE REMARK 999	UNP B3LH69
C	635	ASP	-	SEE REMARK 999	UNP B3LH69
C	636	ASP	-	SEE REMARK 999	UNP B3LH69
C	637	ASP	-	SEE REMARK 999	UNP B3LH69
C	638	LYS	-	SEE REMARK 999	UNP B3LH69
E	617	ASP	-	SEE REMARK 999	UNP B3LH69
E	618	TYR	-	SEE REMARK 999	UNP B3LH69
E	619	LYS	-	SEE REMARK 999	UNP B3LH69
E	620	ASP	-	SEE REMARK 999	UNP B3LH69
E	621	HIS	-	SEE REMARK 999	UNP B3LH69
E	622	ASP	-	SEE REMARK 999	UNP B3LH69
E	623	GLY	-	SEE REMARK 999	UNP B3LH69
E	624	ASP	-	SEE REMARK 999	UNP B3LH69
E	625	TYR	-	SEE REMARK 999	UNP B3LH69
E	626	LYS	-	SEE REMARK 999	UNP B3LH69
E	627	ASP	-	SEE REMARK 999	UNP B3LH69
E	628	HIS	-	SEE REMARK 999	UNP B3LH69
E	629	ASP	-	SEE REMARK 999	UNP B3LH69
E	630	ILE	-	SEE REMARK 999	UNP B3LH69
E	631	ASP	-	SEE REMARK 999	UNP B3LH69
E	632	TYR	-	SEE REMARK 999	UNP B3LH69
E	633	LYS	-	SEE REMARK 999	UNP B3LH69
E	634	ASP	-	SEE REMARK 999	UNP B3LH69
E	635	ASP	-	SEE REMARK 999	UNP B3LH69
E	636	ASP	-	SEE REMARK 999	UNP B3LH69
E	637	ASP	-	SEE REMARK 999	UNP B3LH69
E	638	LYS	-	SEE REMARK 999	UNP B3LH69
A	617	ASP	-	SEE REMARK 999	UNP B3LH69
A	618	TYR	-	SEE REMARK 999	UNP B3LH69
A	619	LYS	-	SEE REMARK 999	UNP B3LH69
A	620	ASP	-	SEE REMARK 999	UNP B3LH69
A	621	HIS	-	SEE REMARK 999	UNP B3LH69
A	622	ASP	-	SEE REMARK 999	UNP B3LH69
A	623	GLY	-	SEE REMARK 999	UNP B3LH69
A	624	ASP	-	SEE REMARK 999	UNP B3LH69
A	625	TYR	-	SEE REMARK 999	UNP B3LH69

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Chain	Residue	Modelled	Actual	Comment	Reference
A	626	LYS	-	SEE REMARK 999	UNP B3LH69
A	627	ASP	-	SEE REMARK 999	UNP B3LH69
A	628	HIS	-	SEE REMARK 999	UNP B3LH69
A	629	ASP	-	SEE REMARK 999	UNP B3LH69
A	630	ILE	-	SEE REMARK 999	UNP B3LH69
A	631	ASP	-	SEE REMARK 999	UNP B3LH69
A	632	TYR	-	SEE REMARK 999	UNP B3LH69
A	633	LYS	-	SEE REMARK 999	UNP B3LH69
A	634	ASP	-	SEE REMARK 999	UNP B3LH69
A	635	ASP	-	SEE REMARK 999	UNP B3LH69
A	636	ASP	-	SEE REMARK 999	UNP B3LH69
A	637	ASP	-	SEE REMARK 999	UNP B3LH69
A	638	LYS	-	SEE REMARK 999	UNP B3LH69

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	457	Total	C	N	O	0	0
			2250	1336	457	457		
4	F	457	Total	C	N	O	0	0
			2250	1336	457	457		
4	B	457	Total	C	N	O	0	0
			2250	1336	457	457		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L	105	Total	C	N	O	0	0
			519	309	105	105		
5	H	105	Total	C	N	O	0	0
			519	309	105	105		
5	J	105	Total	C	N	O	0	0
			519	309	105	105		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
6	K	217	Total	C	N	O	0	0
			1078	644	217	217		
6	G	217	Total	C	N	O	0	0
			1078	644	217	217		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	217	Total	C	N	O	0	0
			1078	644	217	217		

- Molecule 7 is a protein called V-type proton ATPase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	461	Total	C	N	O	0	0
			2292	1370	461	461		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	O	392	Total	C	N	O	0	0
			1947	1163	392	392		

- Molecule 9 is a protein called V-type proton ATPase subunit a, Golgi isoform.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	a	625	Total	C	N	O	0	0
			3092	1842	625	625		

- Molecule 10 is a protein called V0 assembly protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	b	44	Total	C	N	O	0	0
			218	130	44	44		

- Molecule 11 is a protein called V-type proton ATPase subunit c”.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	c	197	Total	C	N	O	0	0
			962	568	197	197		

- Molecule 12 is a protein called V-type proton ATPase subunit d.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	d	343	Total	C	N	O	0	0
			1699	1013	343	343		

- Molecule 13 is a protein called V-type proton ATPase subunit c.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	g	153	Total	C	N	O	0	0
			743	437	153	153		
13	h	157	Total	C	N	O	0	0
			763	449	157	157		
13	i	157	Total	C	N	O	0	0
			763	449	157	157		
13	j	156	Total	C	N	O	0	0
			758	446	156	156		
13	k	158	Total	C	N	O	0	0
			768	452	158	158		
13	l	157	Total	C	N	O	0	0
			763	449	157	157		
13	m	158	Total	C	N	O	0	0
			768	452	158	158		
13	n	158	Total	C	N	O	0	0
			768	452	158	158		

- Molecule 14 is a protein called V-type proton ATPase subunit c'.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	156	Total	C	N	O	0	0
			758	446	156	156		

- Molecule 15 is a protein called V-type proton ATPase subunit e.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	e	64	Total	C	N	O	0	0
			319	191	64	64		

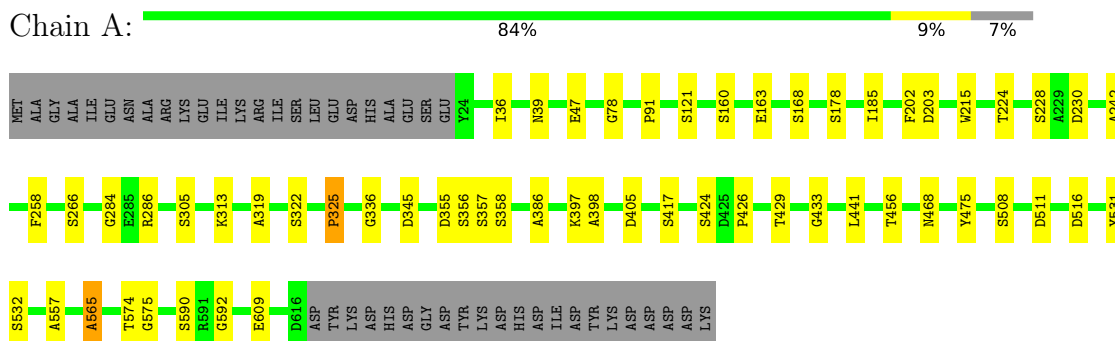
- Molecule 16 is a protein called Putative protein YPR170W-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	f	61	Total	C	N	O	0	0
			301	179	61	61		

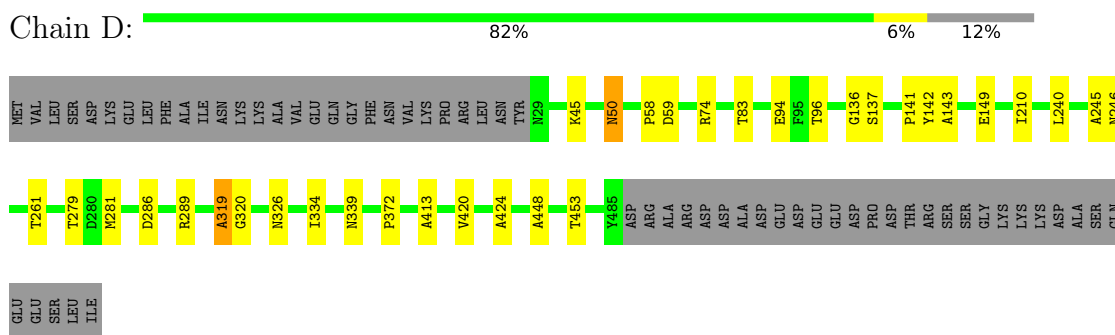




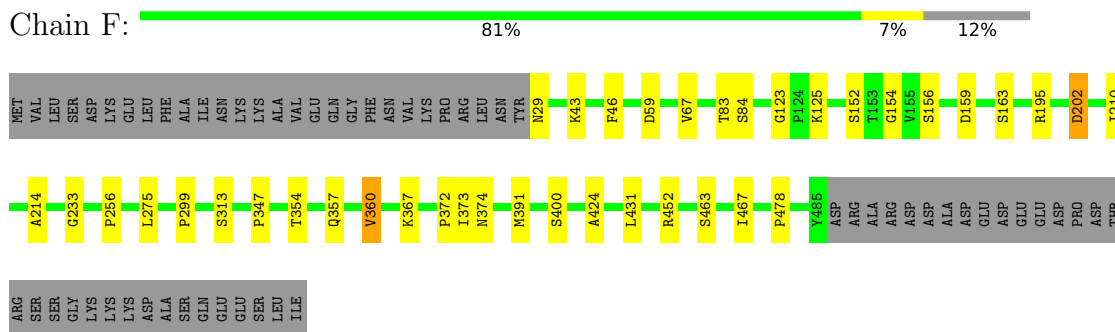
- Molecule 3: Vacuolar ATP synthase catalytic subunit A



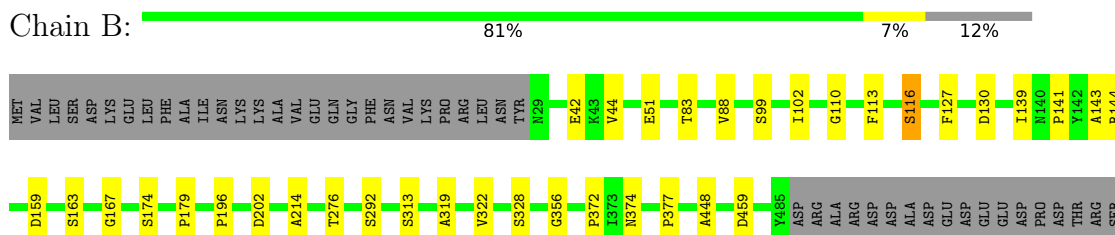
- Molecule 4: V-type proton ATPase subunit B



- Molecule 4: V-type proton ATPase subunit B




- Molecule 4: V-type proton ATPase subunit B




SER  
GLY  
LYS  
LYS  
LYS  
ASP  
ALA  
SER  
GLN  
GLU  
GLU  
SER  
LEU  
ILE

- Molecule 5: V-type proton ATPase subunit G

Chain L:  85% 7% 8%

MET S2 G6 K50 E53 G63 E69 A74 A87 K104 P105 S106  
ALA  
GLU  
VAL  
HIS  
ILE  
ASN  
ALA  
LEU

- Molecule 5: V-type proton ATPase subunit G

Chain H:  89% 1% 8%


MET S2 A8 S22 D51 Q77 S108  
ALA  
GLU  
VAL  
HIS  
ILE  
ASN  
ALA  
LEU

- Molecule 5: V-type proton ATPase subunit G

Chain J:  89% 1% 8%


MET S2 Y27 G66 A72 E73 A74 S108  
ALA  
GLU  
VAL  
HIS  
ILE  
ASN  
ALA  
LEU

- Molecule 6: V-type proton ATPase subunit E

Chain K:  88% 5% 7%


MET SER SER SER ALA THR THR L8 E16 E34 A81 R82 K83 S108 D145 S151 M152 S185 G186 G187 T202 A214 G224  
PRO  
SER  
LYS  
THR  
ARG  
LYS  
PHE  
PHE  
ASP

- Molecule 6: V-type proton ATPase subunit E

Chain G:  90% 1% 7%

MET SER SER SER ALA THR THR L8 N53 E54 T55 P135 Q165 R166 A167 E171 D195 Y223 G224  
PRO  
SER  
LYS  
THR  
ARG  
LYS  
PHE  
PHE  
ASP

- Molecule 6: V-type proton ATPase subunit E

Chain I:  88% 5% 7%

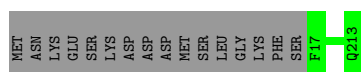
MET SER SER SER ALA THR THR L8 E16 E34 A39 M49 N53 R166 A167 R85 A137 A141 Q165 R166 A167 G187 N192 K208 S211 G224  
PRO  
SER  
LYS  
THR  
ARG  
LYS  
PHE  
PHE  
ASP

- Molecule 7: V-type proton ATPase subunit H

Chain P:  91% 5% 1%

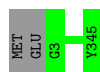
M1 G2 A3 L7 S22 S33 E34 E35 N55 ILE GLY ASP GLY GLY LEU SER SER SER ASN ASN ALA HIS SER GLY PHE LYS VAL N73 G74 K75 S85 S105 D120 P121 D129 V130 S131 S142 Q152 M211 S292 N317 S331 E349 P372





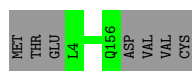
- Molecule 12: V-type proton ATPase subunit d

Chain d: 99%



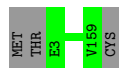
- Molecule 13: V-type proton ATPase subunit c

Chain g: 96%



- Molecule 13: V-type proton ATPase subunit c

Chain h: 98%



- Molecule 13: V-type proton ATPase subunit c

Chain i: 98%



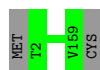
- Molecule 13: V-type proton ATPase subunit c

Chain j: 98%



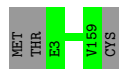
- Molecule 13: V-type proton ATPase subunit c

Chain k: 99%



- Molecule 13: V-type proton ATPase subunit c

Chain l: 98%



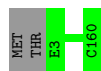
- Molecule 13: V-type proton ATPase subunit c

Chain m:  99%



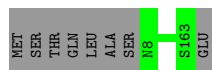
- Molecule 13: V-type proton ATPase subunit c

Chain n:  99%




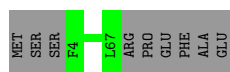
- Molecule 14: V-type proton ATPase subunit c'

Chain o:  95% 5%



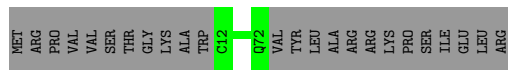
- Molecule 15: V-type proton ATPase subunit e

Chain e:  88% 12%



- Molecule 16: Putative protein YPR170W-B

Chain f:  72% 28%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	19265	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	35	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	M	1.57	3/1038 (0.3%)	1.69	7/1445 (0.5%)
10	b	0.25	0/217	0.45	0/301
11	c	0.27	0/961	0.50	0/1330
12	d	0.25	0/1698	0.48	0/2366
13	g	0.27	0/742	0.49	0/1024
13	h	0.27	0/762	0.48	0/1052
13	i	0.27	0/762	0.52	0/1052
13	j	0.26	0/757	0.48	0/1045
13	k	0.25	0/767	0.49	0/1059
13	l	0.26	0/762	0.49	0/1052
13	m	0.25	0/767	0.49	0/1059
13	n	0.26	0/767	0.49	0/1059
14	o	0.26	0/757	0.50	0/1045
15	e	0.23	0/318	0.45	0/443
16	f	0.24	0/300	0.44	0/416
2	N	1.64	2/570 (0.4%)	1.71	6/794 (0.8%)
3	A	1.62	16/2914 (0.5%)	1.75	25/4048 (0.6%)
3	C	1.55	3/2914 (0.1%)	1.72	22/4048 (0.5%)
3	E	1.57	10/2914 (0.3%)	1.72	26/4048 (0.6%)
4	B	1.53	6/2249 (0.3%)	1.69	15/3126 (0.5%)
4	D	1.57	4/2249 (0.2%)	1.78	18/3126 (0.6%)
4	F	1.62	9/2249 (0.4%)	1.74	16/3126 (0.5%)
5	H	1.47	0/518	1.66	3/720 (0.4%)
5	J	1.51	1/518 (0.2%)	1.57	3/720 (0.4%)
5	L	1.58	2/518 (0.4%)	1.67	5/720 (0.7%)
6	G	1.54	0/1077	1.70	7/1502 (0.5%)
6	I	1.57	2/1077 (0.2%)	1.67	10/1502 (0.7%)
6	K	1.59	3/1077 (0.3%)	1.61	6/1502 (0.4%)
7	P	1.57	6/2290 (0.3%)	1.67	17/3195 (0.5%)
8	O	1.58	6/1946 (0.3%)	1.73	14/2715 (0.5%)
9	a	0.25	0/3085	0.49	0/4288
All	All	1.29	73/39540 (0.2%)	1.42	200/54928 (0.4%)

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
4	B	0	1

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	417	SER	CA-CB	7.86	1.64	1.52
3	A	322	SER	CA-CB	7.46	1.64	1.52
6	K	108	SER	CA-CB	7.46	1.64	1.52
7	P	105	SER	CA-CB	7.12	1.63	1.52
3	A	336	GLY	N-CA	-7.02	1.35	1.46
3	A	574	THR	C-N	6.95	1.45	1.33
8	O	181	PRO	N-CA	-6.70	1.35	1.47
3	E	160	SER	CA-CB	6.67	1.62	1.52
8	O	46	SER	CA-CB	6.62	1.62	1.52
4	F	233	GLY	CA-C	-6.50	1.41	1.51
7	P	85	SER	CA-CB	6.10	1.62	1.52
3	A	178	SER	CA-CB	6.10	1.62	1.52
5	J	66	GLY	CA-C	-6.05	1.42	1.51
7	P	372	PRO	CA-C	-6.03	1.40	1.52
3	A	215	TRP	CA-CB	6.03	1.67	1.53
3	C	436	GLN	N-CA	-6.01	1.34	1.46
7	P	292	SER	CA-CB	5.95	1.61	1.52
8	O	254	LYS	N-CA	-5.94	1.34	1.46
1	M	179	PRO	N-CA	-5.92	1.37	1.47
3	A	417	SER	CA-CB	5.91	1.61	1.52
4	B	313	SER	CA-CB	5.89	1.61	1.52
3	A	325	PRO	N-CA	-5.87	1.37	1.47
1	M	16	GLY	N-CA	5.85	1.54	1.46
3	E	255	PRO	C-N	5.79	1.43	1.33
3	E	72	VAL	CA-CB	-5.76	1.42	1.54
4	F	313	SER	CA-CB	5.75	1.61	1.52
3	E	228	SER	CA-CB	5.74	1.61	1.52
6	I	187	GLY	CA-C	-5.73	1.42	1.51
6	K	151	SER	CA-CB	5.72	1.61	1.52
4	F	400	SER	CA-CB	5.71	1.61	1.52
3	E	356	SER	CA-CB	5.69	1.61	1.52
4	F	84	SER	C-N	5.65	1.43	1.33
3	A	433	GLY	N-CA	-5.63	1.37	1.46
3	A	357	SER	CA-CB	5.58	1.61	1.52
4	B	356	GLY	N-CA	-5.55	1.37	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	320	GLY	CA-C	-5.53	1.43	1.51
7	P	331	SER	CA-CB	5.53	1.61	1.52
2	N	6	THR	N-CA	-5.51	1.35	1.46
4	F	43	LYS	N-CA	-5.51	1.35	1.46
3	C	249	GLY	N-CA	-5.50	1.37	1.46
3	A	358	SER	N-CA	-5.46	1.35	1.46
5	L	74	ALA	C-N	5.44	1.42	1.33
4	D	289	ARG	CA-CB	5.43	1.65	1.53
4	F	152	SER	CA-CB	5.41	1.61	1.52
4	B	328	SER	CA-CB	5.40	1.61	1.52
1	M	124	GLY	CA-C	-5.38	1.43	1.51
4	F	431	LEU	CA-C	-5.35	1.39	1.52
4	F	59	ASP	C-N	5.34	1.42	1.33
8	O	355	ALA	CA-CB	5.34	1.63	1.52
5	L	6	GLY	N-CA	-5.32	1.38	1.46
7	P	349	GLU	N-CA	-5.31	1.35	1.46
8	O	123	LEU	CA-CB	5.30	1.66	1.53
3	E	231	TYR	CA-CB	5.27	1.65	1.53
3	C	305	SER	CA-CB	5.23	1.60	1.52
3	E	473	SER	CA-CB	5.22	1.60	1.52
3	A	424	SER	CA-CB	5.21	1.60	1.52
3	A	397	LYS	C-N	5.20	1.46	1.34
6	I	167	ALA	CA-CB	5.19	1.63	1.52
4	B	102	ILE	C-N	-5.18	1.24	1.34
3	E	57	VAL	C-N	5.18	1.42	1.33
3	A	121	SER	CA-CB	-5.18	1.45	1.52
3	A	319	ALA	CA-CB	5.17	1.63	1.52
6	K	185	SER	CA-CB	5.15	1.60	1.52
4	F	367	LYS	C-N	5.14	1.42	1.33
3	A	266	SER	CA-CB	5.11	1.60	1.52
4	D	96	THR	C-N	5.08	1.42	1.33
4	D	286	ASP	CA-CB	5.08	1.65	1.53
8	O	71	VAL	CA-CB	-5.08	1.44	1.54
2	N	87	ALA	N-CA	-5.07	1.36	1.46
4	B	174	SER	CA-CB	5.05	1.60	1.52
3	A	185	ILE	CA-C	-5.04	1.39	1.52
3	E	599	GLU	CA-CB	5.02	1.65	1.53
4	B	116	SER	CA-CB	5.01	1.60	1.52

All (200) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	508	SER	N-CA-CB	8.67	123.51	110.50
4	D	74	ARG	N-CA-CB	8.57	126.02	110.60
3	C	414	ALA	N-CA-CB	8.10	121.43	110.10
6	G	195	ASP	N-CA-CB	7.92	124.85	110.60
8	O	375	ALA	N-CA-CB	7.88	121.13	110.10
6	G	167	ALA	N-CA-CB	7.79	121.01	110.10
8	O	160	ALA	CB-CA-C	-7.53	98.81	110.10
3	A	386	ALA	N-CA-CB	7.49	120.59	110.10
3	A	345	ASP	N-CA-CB	7.40	123.92	110.60
5	H	22	SER	N-CA-CB	7.34	121.50	110.50
4	D	319	ALA	N-CA-CB	7.28	120.30	110.10
3	E	110	ARG	N-CA-CB	7.27	123.68	110.60
4	B	448	ALA	CB-CA-C	-7.20	99.30	110.10
3	E	207	SER	N-CA-CB	7.17	121.25	110.50
3	E	284	GLY	N-CA-C	-7.17	95.19	113.10
1	M	65	ALA	N-CA-CB	7.11	120.05	110.10
4	F	400	SER	N-CA-CB	-7.09	99.86	110.50
3	E	164	ASN	N-CA-CB	6.95	123.11	110.60
3	C	98	PRO	N-CA-CB	6.85	111.52	103.30
4	B	319	ALA	CB-CA-C	-6.82	99.87	110.10
3	E	266	SER	CB-CA-C	-6.75	97.28	110.10
3	E	46	TYR	CB-CA-C	-6.73	96.94	110.40
3	A	168	SER	N-CA-CB	6.62	120.43	110.50
4	F	256	PRO	N-CA-CB	6.60	111.22	103.30
3	C	186	ALA	N-CA-CB	6.59	119.33	110.10
6	I	211	SER	N-CA-CB	6.52	120.28	110.50
8	O	353	GLY	O-C-N	6.46	133.04	122.70
4	F	354	THR	N-CA-CB	6.45	122.55	110.30
3	C	354	ALA	N-CA-CB	6.44	119.12	110.10
3	A	468	ASN	CB-CA-C	6.44	123.28	110.40
1	M	67	SER	N-CA-CB	6.43	120.14	110.50
3	E	270	SER	CB-CA-C	-6.41	97.92	110.10
3	A	565	ALA	CB-CA-C	-6.40	100.50	110.10
3	E	37	ALA	N-CA-CB	6.39	119.05	110.10
3	C	102	GLU	N-CA-CB	6.38	122.09	110.60
8	O	365	ASN	N-CA-CB	6.38	122.08	110.60
7	P	33	SER	N-CA-CB	6.36	120.03	110.50
7	P	152	GLN	N-CA-CB	6.33	122.00	110.60
6	I	165	GLN	C-N-CA	6.32	137.50	121.70
3	C	377	ASP	C-N-CA	6.30	137.46	121.70
4	D	448	ALA	CB-CA-C	6.27	119.51	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	452	PRO	N-CA-CB	6.22	110.76	103.30
6	G	53	ASN	C-N-CA	6.21	137.23	121.70
4	F	463	SER	N-CA-CB	6.20	119.80	110.50
4	B	374	ASN	N-CA-CB	6.20	121.76	110.60
6	G	165	GLN	C-N-CA	6.19	137.17	121.70
7	P	22	SER	N-CA-CB	6.14	119.71	110.50
6	K	83	LYS	CB-CA-C	-6.10	98.20	110.40
5	L	87	ALA	O-C-N	-6.09	112.95	122.70
4	D	261	THR	O-C-N	-6.08	112.97	122.70
4	B	196	PRO	N-CA-CB	6.06	110.57	103.30
3	C	305	SER	N-CA-CB	6.02	119.52	110.50
1	M	122	LEU	CB-CA-C	-6.01	98.78	110.20
4	F	357	GLN	N-CA-CB	6.01	121.41	110.60
4	D	339	ASN	N-CA-CB	6.00	121.41	110.60
6	K	214	ALA	CB-CA-C	-5.98	101.13	110.10
7	P	211	MET	CA-C-O	-5.98	107.54	120.10
3	A	511	ASP	O-C-N	-5.98	113.14	122.70
3	A	305	SER	N-CA-CB	5.97	119.45	110.50
2	N	74	ALA	CB-CA-C	-5.95	101.17	110.10
8	O	197	ALA	N-CA-CB	5.92	118.39	110.10
3	C	141	PHE	O-C-N	5.92	132.17	122.70
3	E	278	ILE	CB-CA-C	5.92	123.43	111.60
3	A	557	ALA	CB-CA-C	-5.89	101.26	110.10
7	P	7	LEU	N-CA-CB	5.87	122.15	110.40
2	N	98	ASP	N-CA-CB	5.87	121.17	110.60
3	C	448	ARG	N-CA-CB	5.85	121.12	110.60
4	D	240	LEU	CB-CA-C	-5.83	99.13	110.20
3	E	475	TYR	N-CA-CB	5.83	121.08	110.60
6	I	137	ALA	CB-CA-C	-5.82	101.37	110.10
3	E	273	SER	N-CA-CB	5.79	119.19	110.50
6	K	16	GLU	CB-CA-C	-5.79	98.82	110.40
4	B	113	PHE	O-C-N	-5.79	113.44	122.70
1	M	20	THR	N-CA-CB	-5.79	99.31	110.30
7	P	120	ASP	CB-CA-C	-5.78	98.83	110.40
5	J	74	ALA	N-CA-CB	5.77	118.18	110.10
7	P	413	ALA	N-CA-CB	5.76	118.16	110.10
6	I	141	ALA	N-CA-CB	5.75	118.15	110.10
4	B	144	ARG	N-CA-CB	5.74	120.94	110.60
4	D	246	ASN	N-CA-CB	5.72	120.89	110.60
6	I	16	GLU	N-CA-CB	5.71	120.88	110.60
4	F	347	PRO	N-CA-CB	5.66	110.10	103.30
3	C	181	THR	N-CA-C	-5.66	95.73	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	212	TYR	N-CA-CB	5.65	120.77	110.60
3	A	592	GLY	N-CA-C	-5.64	98.99	113.10
7	P	129	ASP	N-CA-CB	5.64	120.76	110.60
6	I	39	ALA	CB-CA-C	-5.63	101.65	110.10
3	A	508	SER	CB-CA-C	-5.62	99.42	110.10
7	P	411	VAL	CB-CA-C	5.61	122.06	111.40
3	C	110	ARG	N-CA-CB	5.61	120.70	110.60
6	K	34	GLU	N-CA-CB	5.59	120.66	110.60
5	L	50	LYS	N-CA-CB	5.58	120.65	110.60
3	A	160	SER	N-CA-CB	5.58	118.87	110.50
7	P	317	ASN	N-CA-CB	5.58	120.64	110.60
4	F	214	ALA	N-CA-CB	5.58	117.91	110.10
5	J	72	ALA	N-CA-CB	5.56	117.89	110.10
4	D	413	ALA	N-CA-CB	5.56	117.88	110.10
4	B	130	ASP	N-CA-C	-5.55	96.02	111.00
4	D	326	ASN	N-CA-CB	5.53	120.56	110.60
3	E	228	SER	CB-CA-C	-5.53	99.60	110.10
3	A	36	ILE	N-CA-C	-5.52	96.09	111.00
5	J	27	TYR	N-CA-CB	5.52	120.54	110.60
3	E	328	ALA	CB-CA-C	-5.52	101.82	110.10
7	P	142	SER	N-CA-CB	5.51	118.76	110.50
1	M	112	TYR	N-CA-CB	5.50	120.50	110.60
4	D	94	GLU	N-CA-C	-5.50	96.14	111.00
3	A	242	ALA	N-CA-CB	5.49	117.78	110.10
5	H	8	ALA	CB-CA-C	-5.49	101.87	110.10
3	E	461	SER	N-CA-CB	5.48	118.72	110.50
4	F	163	SER	N-CA-CB	5.47	118.71	110.50
7	P	390	ASP	N-CA-C	-5.47	96.22	111.00
4	D	334	ILE	N-CA-C	-5.47	96.23	111.00
3	A	398	ALA	CB-CA-C	-5.47	101.90	110.10
8	O	373	GLN	N-CA-CB	5.46	120.43	110.60
6	I	53	ASN	CB-CA-C	-5.46	99.48	110.40
3	A	286	ARG	CB-CA-C	-5.46	99.49	110.40
4	B	110	GLY	C-N-CA	5.46	135.34	121.70
3	C	601	GLU	CB-CA-C	-5.45	99.49	110.40
3	A	398	ALA	N-CA-CB	5.45	117.73	110.10
1	M	118	ASN	N-CA-CB	5.42	120.36	110.60
3	E	475	TYR	CA-C-N	5.42	132.28	117.10
3	C	100	LEU	CB-CA-C	-5.42	99.91	110.20
6	G	223	TYR	C-N-CA	-5.41	110.94	122.30
6	G	55	THR	O-C-N	-5.41	114.05	122.70
3	C	246	CYS	N-CA-C	-5.41	96.41	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	276	THR	N-CA-CB	5.40	120.55	110.30
3	C	580	ALA	N-CA-CB	5.39	117.65	110.10
3	E	44	ALA	N-CA-CB	5.39	117.65	110.10
4	B	214	ALA	CB-CA-C	-5.39	102.01	110.10
4	F	202	ASP	N-CA-CB	5.38	120.28	110.60
5	L	104	LYS	N-CA-CB	5.38	120.27	110.60
4	D	210	ILE	CB-CA-C	-5.37	100.85	111.60
3	E	562	ALA	N-CA-CB	5.37	117.62	110.10
8	O	116	TRP	N-CA-CB	5.37	120.26	110.60
4	D	142	TYR	C-N-CA	5.35	135.08	121.70
4	D	453	THR	N-CA-C	-5.35	96.55	111.00
4	B	42	GLU	N-CA-C	-5.35	96.56	111.00
4	B	322	VAL	N-CA-C	-5.35	96.56	111.00
3	E	545	ASP	CB-CA-C	-5.34	99.72	110.40
6	G	171	GLU	N-CA-CB	-5.34	100.99	110.60
4	F	478	PRO	N-CA-CB	5.34	109.70	103.30
4	F	374	ASN	N-CA-CB	5.33	120.19	110.60
8	O	57	SER	CB-CA-C	-5.33	99.97	110.10
3	C	399	VAL	N-CA-C	-5.33	96.62	111.00
6	K	81	ALA	CB-CA-C	-5.32	102.12	110.10
3	A	313	LYS	CB-CA-C	-5.32	99.77	110.40
5	L	53	GLU	O-C-N	-5.30	114.22	122.70
8	O	196	VAL	N-CA-C	-5.29	96.71	111.00
7	P	75	LYS	C-N-CA	5.29	134.93	121.70
3	E	305	SER	N-CA-CB	5.28	118.41	110.50
5	H	51	ASP	N-CA-CB	5.25	120.05	110.60
1	M	15	LEU	CA-C-N	5.25	126.70	116.20
3	E	468	ASN	N-CA-CB	5.25	120.04	110.60
2	N	28	ILE	N-CA-C	-5.24	96.85	111.00
7	P	121	PRO	N-CA-CB	5.24	109.59	103.30
4	D	50	ASN	N-CA-CB	5.24	120.02	110.60
4	D	281	MET	N-CA-CB	5.23	120.02	110.60
6	K	145	ASP	O-C-N	-5.22	114.34	122.70
7	P	413	ALA	N-CA-C	-5.22	96.89	111.00
2	N	37	PHE	N-CA-CB	5.22	120.00	110.60
8	O	351	LEU	CB-CA-C	-5.21	100.30	110.20
3	A	609	GLU	O-C-N	-5.20	114.39	122.70
4	F	156	SER	C-N-CA	5.19	134.68	121.70
3	C	434	ILE	C-N-CA	5.19	134.68	121.70
6	I	208	LYS	N-CA-CB	5.19	119.94	110.60
4	F	29	ASN	N-CA-C	-5.19	96.99	111.00
8	O	219	PRO	N-CA-CB	5.19	109.52	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	159	ASP	CB-CA-C	-5.19	100.03	110.40
7	P	390	ASP	N-CA-CB	5.18	119.93	110.60
4	D	279	THR	N-CA-C	-5.17	97.05	111.00
8	O	10	ASP	N-CA-C	-5.16	97.06	111.00
7	P	131	SER	N-CA-CB	5.16	118.24	110.50
3	C	176	PRO	N-CA-CB	5.15	109.48	103.30
2	N	41	GLN	O-C-N	5.15	130.93	122.70
6	I	49	ASN	CB-CA-C	-5.14	100.12	110.40
3	C	51	VAL	N-CA-CB	5.14	122.80	111.50
8	O	9	ASN	N-CA-CB	5.14	119.85	110.60
4	F	67	VAL	O-C-N	-5.13	114.48	122.70
4	D	420	VAL	C-N-CA	5.13	133.07	122.30
3	A	426	PRO	N-CA-CB	5.13	109.45	103.30
5	L	69	GLU	CB-CA-C	-5.12	100.15	110.40
3	E	294	LEU	O-C-N	-5.12	114.51	122.70
3	A	516	ASP	CB-CA-C	-5.11	100.19	110.40
3	C	616	ASP	N-CA-CB	5.09	119.77	110.60
3	E	308	LYS	N-CA-CB	5.09	119.77	110.60
8	O	316	VAL	O-C-N	-5.09	114.55	122.70
3	A	429	THR	N-CA-CB	5.08	119.95	110.30
3	E	453	SER	C-N-CA	5.08	134.39	121.70
6	I	85	ARG	N-CA-CB	5.08	119.73	110.60
3	C	494	GLU	CB-CA-C	-5.07	100.25	110.40
2	N	61	ARG	N-CA-CB	5.07	119.73	110.60
3	A	228	SER	N-CA-CB	5.07	118.10	110.50
3	A	163	GLU	N-CA-CB	-5.06	101.48	110.60
4	F	159	ASP	N-CA-CB	5.06	119.71	110.60
4	B	319	ALA	N-CA-CB	5.04	117.16	110.10
3	C	279	ILE	N-CA-C	-5.04	97.39	111.00
4	B	459	ASP	N-CA-CB	5.02	119.63	110.60
3	E	161	VAL	N-CA-C	-5.01	97.48	111.00
4	F	195	ARG	CA-C-N	5.01	131.12	117.10
3	A	224	THR	N-CA-CB	5.01	119.81	110.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	44	VAL	Peptide



## 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	M	1039	0	475	0	0
2	N	571	0	255	0	0
3	A	2915	0	1343	2	0
3	C	2915	0	1342	0	0
3	E	2915	0	1343	3	0
4	B	2250	0	1016	1	0
4	D	2250	0	1016	1	0
4	F	2250	0	1016	4	0
5	H	519	0	250	0	0
5	J	519	0	250	0	0
5	L	519	0	250	0	0
6	G	1078	0	483	0	0
6	I	1078	0	483	0	0
6	K	1078	0	483	1	0
7	P	2292	0	993	0	0
8	O	1947	0	876	0	0
9	a	3092	0	1352	0	0
10	b	218	0	98	0	0
11	c	962	0	477	0	0
12	d	1699	0	752	0	0
13	g	743	0	379	0	0
13	h	763	0	387	0	0
13	i	763	0	387	0	0
13	j	758	0	385	0	0
13	k	768	0	389	0	0
13	l	763	0	387	0	0
13	m	768	0	389	0	0
13	n	768	0	389	0	0
14	o	758	0	375	0	0
15	e	319	0	143	0	0
16	f	301	0	141	0	0
All	All	39578	0	18304	10	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 0.

All (10) 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)
3:E:503:GLY:HA2	4:F:424:ALA:HB2	1.87	0.55
3:A:47:GLU:HA	3:A:91:PRO:HA	1.95	0.47
3:E:93:SER:HA	3:E:216:PRO:HA	1.99	0.45
4:B:51:GLU:HA	4:B:99:SER:HA	1.99	0.44
4:D:245:ALA:HB1	3:E:389:ALA:HB1	1.99	0.43
4:F:154:GLY:HA2	4:F:452:ARG:H	1.83	0.43
6:K:187:GLY:HA3	6:K:202:THR:HA	2.03	0.41
4:F:360:VAL:HA	4:F:373:ILE:HA	2.01	0.41
4:F:210:ILE:HA	4:F:275:LEU:O	2.21	0.41
3:A:355:ASP:HA	3:A:356:SER:HA	1.92	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	M	208/256 (81%)	202 (97%)	5 (2%)	1 (0%)	31	74
2	N	113/118 (96%)	102 (90%)	7 (6%)	4 (4%)	4	32
3	A	591/639 (92%)	551 (93%)	23 (4%)	17 (3%)	5	36
3	C	591/639 (92%)	545 (92%)	31 (5%)	15 (2%)	6	39
3	E	591/639 (92%)	544 (92%)	31 (5%)	16 (3%)	5	38
4	B	455/517 (88%)	415 (91%)	26 (6%)	14 (3%)	4	35
4	D	455/517 (88%)	410 (90%)	32 (7%)	13 (3%)	5	36
4	F	455/517 (88%)	425 (93%)	20 (4%)	10 (2%)	7	42
5	H	103/114 (90%)	102 (99%)	0	1 (1%)	17	60
5	J	103/114 (90%)	100 (97%)	3 (3%)	0	100	100
5	L	103/114 (90%)	98 (95%)	4 (4%)	1 (1%)	17	60
6	G	215/233 (92%)	206 (96%)	7 (3%)	2 (1%)	19	61
6	I	215/233 (92%)	207 (96%)	6 (3%)	2 (1%)	19	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	K	215/233 (92%)	206 (96%)	8 (4%)	1 (0%)	31	74
7	P	457/478 (96%)	434 (95%)	18 (4%)	5 (1%)	16	58
8	O	390/392 (100%)	350 (90%)	26 (7%)	14 (4%)	4	32
9	a	611/890 (69%)	588 (96%)	23 (4%)	0	100	100
10	b	42/265 (16%)	42 (100%)	0	0	100	100
11	c	195/213 (92%)	189 (97%)	6 (3%)	0	100	100
12	d	341/345 (99%)	327 (96%)	14 (4%)	0	100	100
13	g	151/160 (94%)	149 (99%)	2 (1%)	0	100	100
13	h	155/160 (97%)	154 (99%)	1 (1%)	0	100	100
13	i	155/160 (97%)	153 (99%)	2 (1%)	0	100	100
13	j	154/160 (96%)	152 (99%)	2 (1%)	0	100	100
13	k	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
13	l	155/160 (97%)	153 (99%)	2 (1%)	0	100	100
13	m	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
13	n	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
14	o	154/164 (94%)	152 (99%)	2 (1%)	0	100	100
15	e	62/73 (85%)	62 (100%)	0	0	100	100
16	f	59/85 (69%)	59 (100%)	0	0	100	100
All	All	7962/9068 (88%)	7539 (95%)	307 (4%)	116 (2%)	16	51

All (116) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	475	TYR
4	D	45	LYS
4	D	59	ASP
4	D	143	ALA
3	E	475	TYR
3	E	565	ALA
3	E	575	GLY
4	F	46	PHE
3	A	202	PHE
3	A	475	TYR
4	B	141	PRO
4	B	372	PRO
8	O	120	LYS

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Mol	Chain	Res	Type
8	O	186	LEU
5	H	77	GLN
6	I	167	ALA
6	I	192	ASN
2	N	115	LEU
3	C	230	ASP
3	C	575	GLY
4	D	319	ALA
4	D	372	PRO
3	E	164	ASN
4	F	467	ILE
3	A	230	ASP
3	A	258	PHE
3	A	532	SER
3	A	575	GLY
4	B	139	ILE
4	B	377	PRO
7	P	3	ALA
8	O	39	ILE
8	O	172	VAL
8	O	375	ALA
1	M	124	GLY
2	N	98	ASP
3	C	261	GLY
3	C	310	PRO
4	D	58	PRO
4	D	141	PRO
4	D	149	GLU
3	E	405	ASP
3	E	449	LYS
3	E	536	ALA
4	F	299	PRO
3	A	39	ASN
3	A	203	ASP
3	A	284	GLY
3	A	441	LEU
3	A	565	ALA
5	L	63	GLY
7	P	35	GLU
8	O	90	ASN
8	O	167	THR
8	O	176	HIS

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Mol	Chain	Res	Type
3	C	257	ALA
3	C	305	SER
3	C	591	ARG
4	D	136	GLY
4	D	424	ALA
3	E	207	SER
3	E	257	ALA
4	F	83	THR
4	F	202	ASP
4	F	372	PRO
4	F	391	MET
3	A	325	PRO
3	A	405	ASP
3	A	531	TYR
3	A	590	SER
4	B	83	THR
4	B	116	SER
4	B	127	PHE
4	B	163	SER
4	B	167	GLY
4	B	292	SER
8	O	171	SER
6	G	195	ASP
3	C	207	SER
3	C	420	GLY
4	D	83	THR
3	E	230	ASP
3	E	305	SER
3	E	590	SER
4	F	123	GLY
4	F	125	LYS
4	F	360	VAL
4	B	143	ALA
4	B	202	ASP
6	K	152	MET
7	P	458	ASP
8	O	7	THR
8	O	95	ASN
8	O	100	LEU
8	O	116	TRP
6	G	135	PRO
2	N	4	LYS

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Mol	Chain	Res	Type
3	C	109	GLN
3	C	405	ASP
4	D	50	ASN
4	D	137	SER
3	E	259	GLY
3	A	456	THR
7	P	390	ASP
7	P	412	ASN
3	E	310	PRO
3	A	78	GLY
4	B	88	VAL
3	E	284	GLY
2	N	25	ILE
3	C	284	GLY
8	O	106	PRO
3	C	381	PRO
3	C	539	PRO
3	E	197	ILE
4	B	179	PRO

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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 carbohydrates 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.