



Full wwPDB EM Validation Report ⓘ

Apr 22, 2024 – 08:44 pm BST

PDB ID : 7B9S
EMDB ID : EMD-12105
Title : Structure of the mycobacterial ESX-5 Type VII Secretion System hexameric pore complex
Authors : Chojnowski, G.; Ritter, C.; Beckham, K.S.H.; Mullapudi, E.; Rettel, M.; Savitski, M.M.; Mortensen, S.A.; Ziemianowicz, D.; Kosinski, J.; Wilmanns, M.
Deposited on : 2020-12-14
Resolution : 3.40 Å (reported)
Based on initial model : 7B9F

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

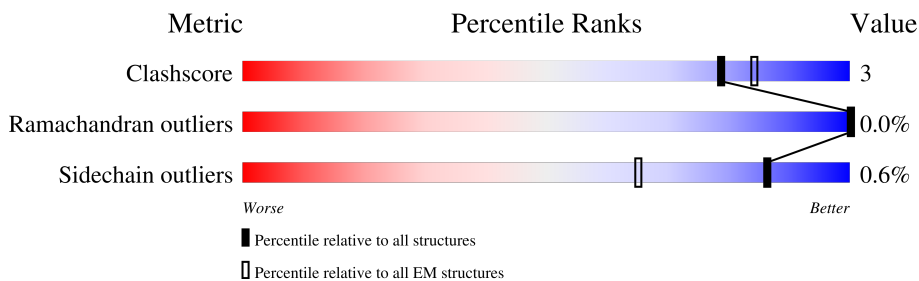
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.




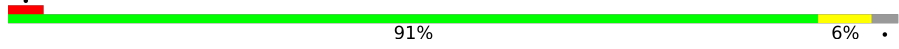

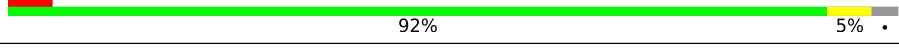

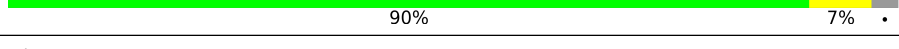
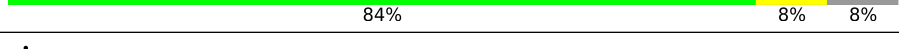
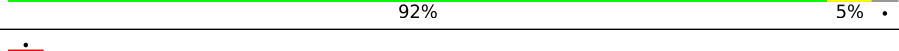
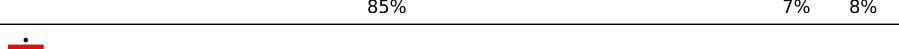
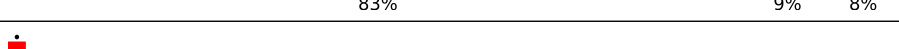












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	4	400	
1	E	400	
1	H	400	
1	M	400	
1	R	400	
1	Y	400	
2	3	502	
2	5	502	

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Mol	Chain	Length	Quality of chain
2	D	502	 90% 7%
2	G	502	 91% 6%
2	I	502	 86% 6% 8%
2	L	502	 5% 92% 5%
2	N	502	 87% 5% 8%
2	Q	502	 90% 7%
2	S	502	 84% 8% 8%
2	W	502	 92% 5%
2	X	502	 85% 7% 8%
2	Z	502	 83% 9% 8%
3	2	1392	 25% 72%
3	C	1392	 25% 72%
3	F	1392	 25% 72%
3	K	1392	 25% 72%
3	P	1392	 25% 72%
3	V	1392	 25% 72%
4	1	506	 11% 88%
4	A	506	 12% 88%
4	B	506	 11% 88%
4	J	506	 12% 88%
4	O	506	 12% 88%
4	T	506	 12% 88%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 72030 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 EccE5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	E	165	1305	814	249	240	2	0	0
1	H	165	1305	814	249	240	2	0	0
1	M	165	1305	814	249	240	2	0	0
1	R	165	1305	814	249	240	2	0	0
1	Y	165	1305	814	249	240	2	0	0
1	4	165	1305	814	249	240	2	0	0

- Molecule 2 is a protein called EccD5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	X	462	3469	2272	598	581	18	0	0
2	D	485	3644	2382	628	616	18	0	0
2	I	462	3469	2272	598	581	18	0	0
2	G	485	3644	2382	628	616	18	0	0
2	N	462	3469	2272	598	581	18	0	0
2	L	485	3644	2382	628	616	18	0	0
2	S	462	3469	2272	598	581	18	0	0
2	Q	485	3644	2382	628	616	18	0	0
2	Z	462	3469	2272	598	581	18	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	W	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		
2	5	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		
2	3	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		

- Molecule 3 is a protein called EccC5.

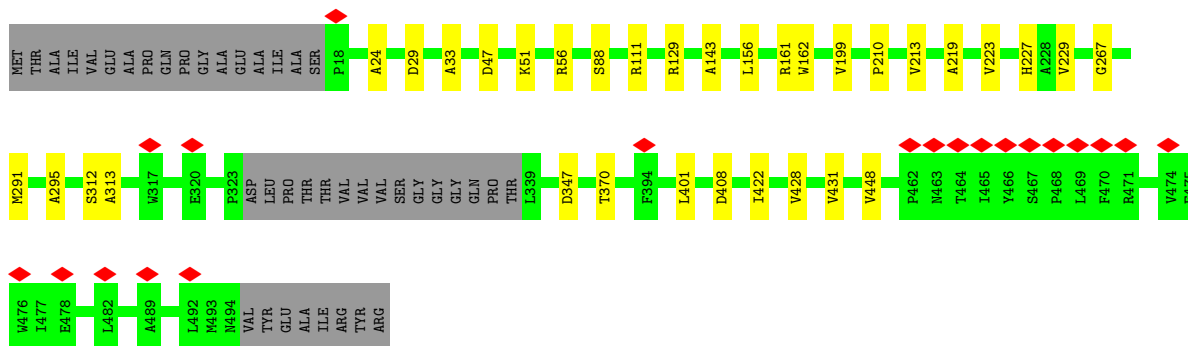
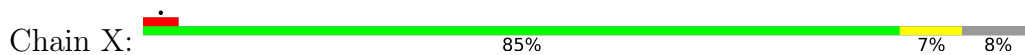
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	F	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	K	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	P	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	V	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	2	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		

- Molecule 4 is a protein called EccB5.

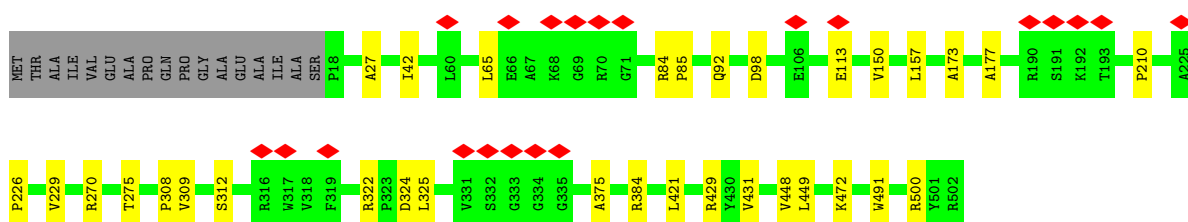
Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	A	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	J	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	O	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	T	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	1	63	Total	C	N	O	S	0	0
			480	304	92	81	3		

ALA
ARG
GLU
LEU
ILE
VAL
HIS
ASP
GLY
GLU
GLN
LEU
VAL
ALA
LEU
VAL
GLY
GLN
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PRO
PRO
SER
SER
SER
PRO
PRO
ALA
ALA
ARG

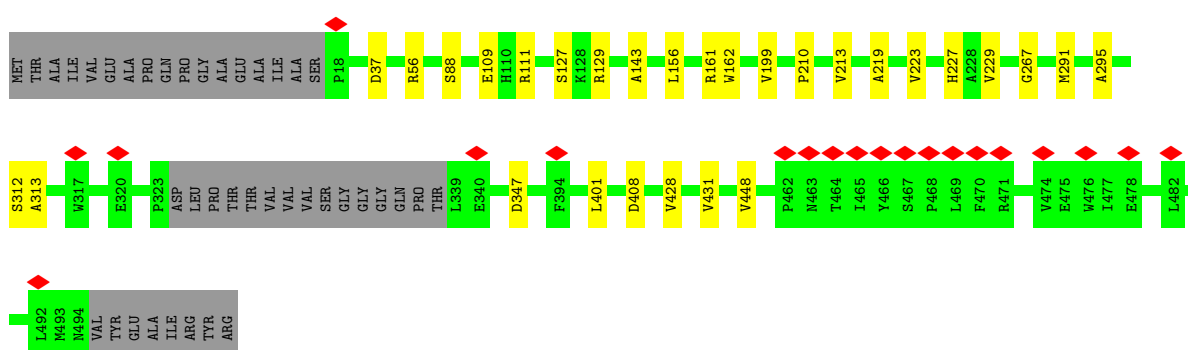
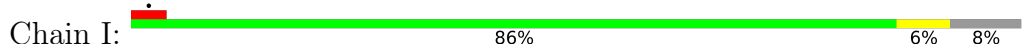
• Molecule 2: EccD5



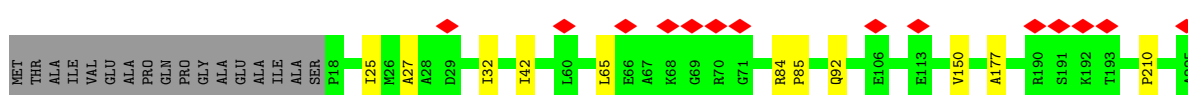
• Molecule 2: EccD5

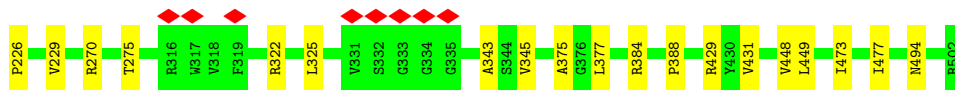


• Molecule 2: EccD5

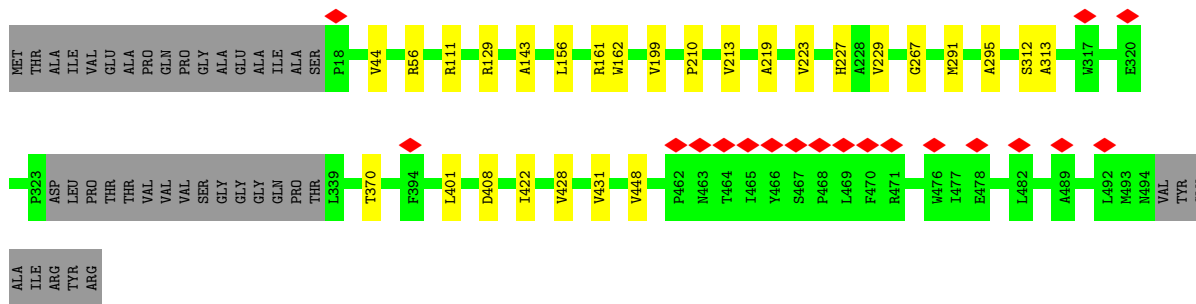
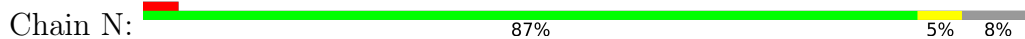


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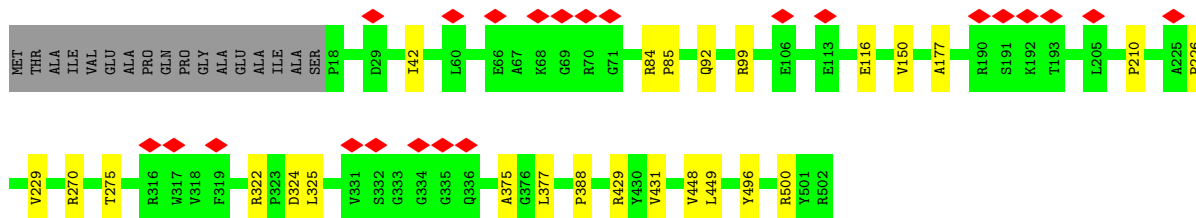
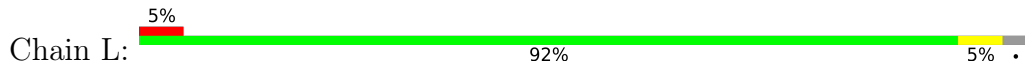




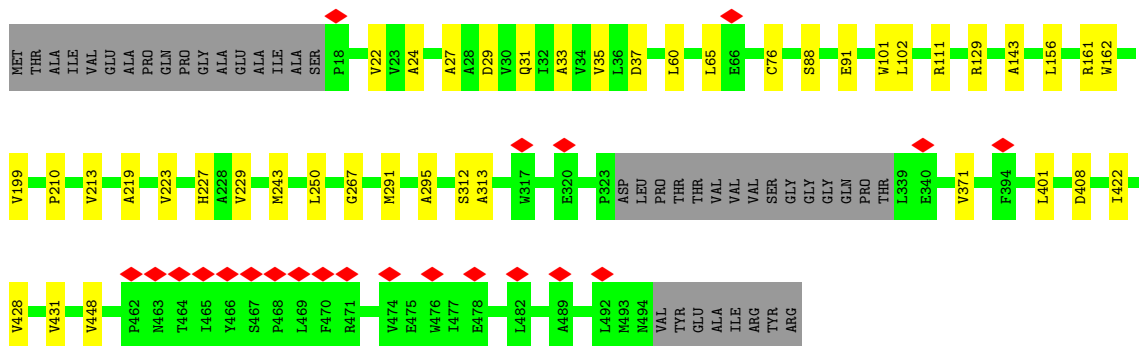
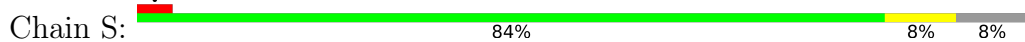
• Molecule 2: EccD5



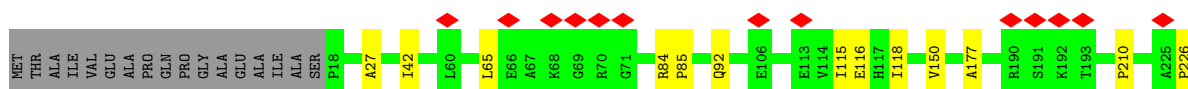
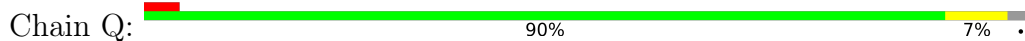
• Molecule 2: EccD5

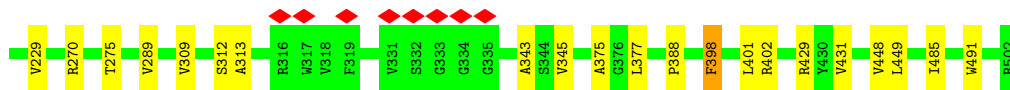


• Molecule 2: EccD5

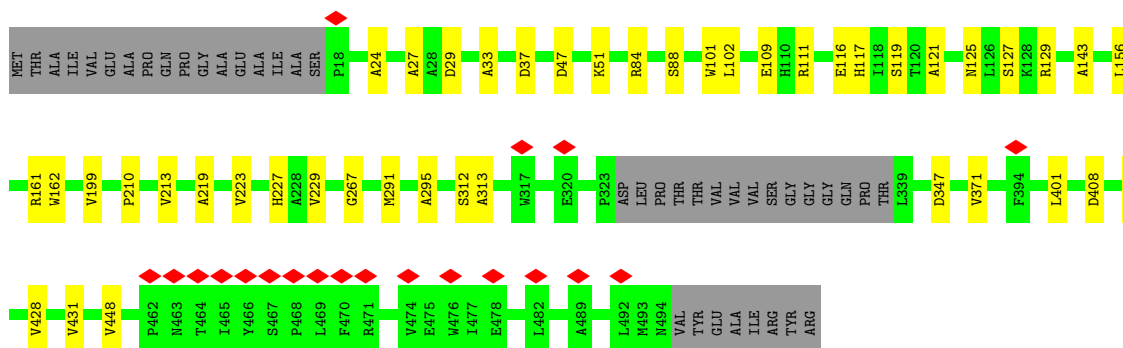
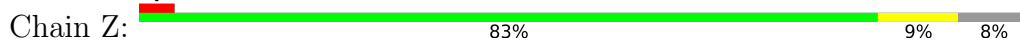


• Molecule 2: EccD5

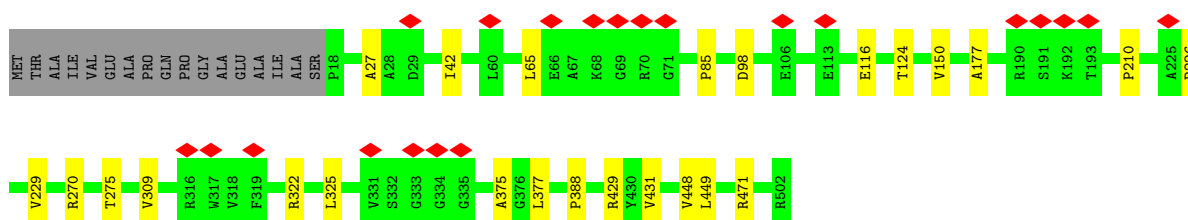




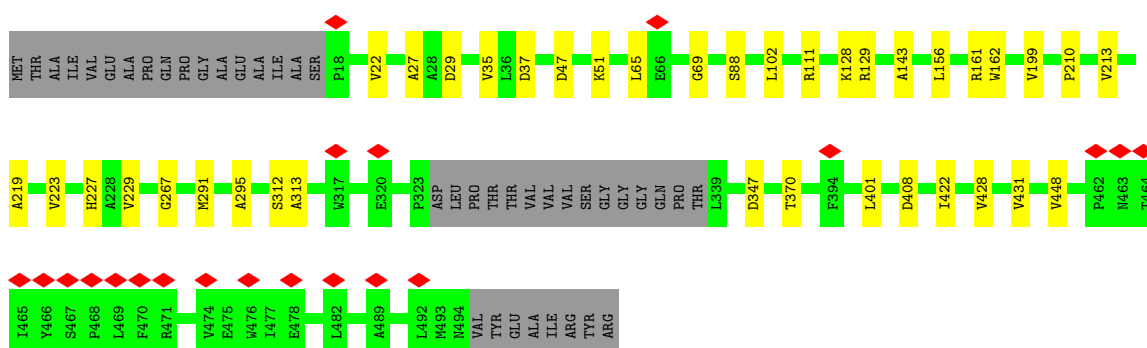
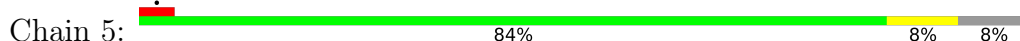
• Molecule 2: EccD5



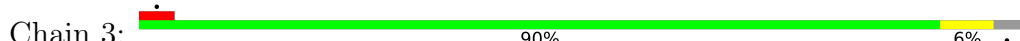
• Molecule 2: EccD5



• Molecule 2: EccD5



• Molecule 2: EccD5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121974	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.34	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.687	Depositor
Minimum map value	-0.260	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	580.5, 580.5, 580.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.29, 1.29, 1.29	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	4	0.26	0/1330	0.58	0/1814
1	E	0.26	0/1330	0.58	0/1814
1	H	0.26	0/1330	0.58	0/1814
1	M	0.26	0/1330	0.58	0/1814
1	R	0.26	0/1330	0.58	0/1814
1	Y	0.26	0/1330	0.58	0/1814
2	3	0.38	0/3727	0.58	1/5110 (0.0%)
2	5	0.34	0/3547	0.61	5/4862 (0.1%)
2	D	0.37	0/3727	0.58	1/5110 (0.0%)
2	G	0.38	0/3727	0.60	1/5110 (0.0%)
2	I	0.33	0/3547	0.61	4/4862 (0.1%)
2	L	0.39	0/3727	0.61	1/5110 (0.0%)
2	N	0.33	0/3547	0.60	2/4862 (0.0%)
2	Q	0.38	0/3727	0.59	0/5110
2	S	0.33	0/3547	0.60	4/4862 (0.1%)
2	W	0.39	0/3727	0.60	1/5110 (0.0%)
2	X	0.33	0/3547	0.61	4/4862 (0.1%)
2	Z	0.34	0/3547	0.62	5/4862 (0.1%)
3	2	0.33	0/3196	0.56	0/4355
3	C	0.33	0/3196	0.56	0/4355
3	F	0.33	0/3196	0.56	0/4355
3	K	0.33	0/3196	0.56	0/4355
3	P	0.33	0/3196	0.56	0/4355
3	V	0.33	0/3196	0.56	0/4355
4	1	0.45	0/487	0.63	0/659
4	A	0.45	0/487	0.63	0/659
4	B	0.45	0/487	0.63	0/659
4	J	0.45	0/487	0.63	0/659
4	O	0.45	0/487	0.63	0/659
4	T	0.45	0/487	0.63	0/659
All	All	0.35	0/73722	0.59	29/100800 (0.0%)

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Z	347	ASP	CB-CG-OD1	7.29	124.86	118.30
2	5	347	ASP	CB-CG-OD1	7.25	124.82	118.30
2	I	347	ASP	CB-CG-OD1	7.22	124.80	118.30
2	X	347	ASP	CB-CG-OD1	7.22	124.80	118.30
2	Z	29	ASP	CB-CG-OD1	6.38	124.04	118.30
2	G	325	LEU	CA-CB-CG	6.35	129.91	115.30
2	X	29	ASP	CB-CG-OD1	6.34	124.00	118.30
2	Z	37	ASP	CB-CG-OD1	6.32	123.98	118.30
2	S	29	ASP	CB-CG-OD1	6.30	123.97	118.30
2	5	29	ASP	CB-CG-OD1	6.29	123.97	118.30
2	W	325	LEU	CA-CB-CG	6.20	129.55	115.30
2	3	325	LEU	CA-CB-CG	6.18	129.51	115.30
2	I	37	ASP	CB-CG-OD1	6.02	123.72	118.30
2	L	325	LEU	CA-CB-CG	5.73	128.47	115.30
2	D	325	LEU	CA-CB-CG	5.71	128.43	115.30
2	Z	401	LEU	CA-CB-CG	5.70	128.42	115.30
2	N	401	LEU	CA-CB-CG	5.69	128.40	115.30
2	X	401	LEU	CA-CB-CG	5.69	128.39	115.30
2	S	401	LEU	CA-CB-CG	5.69	128.39	115.30
2	5	401	LEU	CA-CB-CG	5.68	128.36	115.30
2	I	401	LEU	CA-CB-CG	5.67	128.33	115.30
2	S	37	ASP	CB-CG-OD1	5.45	123.21	118.30
2	N	408	ASP	CB-CG-OD1	5.33	123.09	118.30
2	5	408	ASP	CB-CG-OD1	5.28	123.05	118.30
2	Z	408	ASP	CB-CG-OD1	5.25	123.02	118.30
2	I	408	ASP	CB-CG-OD1	5.23	123.01	118.30
2	S	408	ASP	CB-CG-OD1	5.21	122.99	118.30
2	X	408	ASP	CB-CG-OD1	5.21	122.98	118.30
2	5	37	ASP	CB-CG-OD1	5.01	122.81	118.30

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	4	1305	0	1283	5	0
1	E	1305	0	1283	8	0
1	H	1305	0	1283	8	0
1	M	1305	0	1283	8	0
1	R	1305	0	1283	9	0
1	Y	1305	0	1283	8	0
2	3	3644	0	3854	18	0
2	5	3469	0	3679	18	0
2	D	3644	0	3854	20	0
2	G	3644	0	3854	15	0
2	I	3469	0	3679	13	0
2	L	3644	0	3854	14	0
2	N	3469	0	3679	14	0
2	Q	3644	0	3854	22	0
2	S	3469	0	3679	22	0
2	W	3644	0	3854	15	0
2	X	3469	0	3679	17	0
2	Z	3469	0	3679	22	0
3	2	3107	0	3031	30	0
3	C	3107	0	3031	36	0
3	F	3107	0	3031	34	0
3	K	3107	0	3031	31	0
3	P	3107	0	3031	32	0
3	V	3107	0	3031	33	0
4	1	480	0	503	4	0
4	A	480	0	503	3	0
4	B	480	0	503	6	0
4	J	480	0	503	2	0
4	O	480	0	503	3	0
4	T	480	0	503	3	0
All	All	72030	0	74100	415	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 3.

All (415) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:375:ALA:O	2:Q:429:ARG:NH1	2.27	0.68
2:W:375:ALA:O	2:W:429:ARG:NH1	2.29	0.66
2:G:375:ALA:O	2:G:429:ARG:NH1	2.28	0.66
4:J:43:ARG:NH1	2:Q:313:ALA:O	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:375:ALA:O	2:L:429:ARG:NH1	2.28	0.66
2:3:375:ALA:O	2:3:429:ARG:NH1	2.28	0.65
2:D:375:ALA:O	2:D:429:ARG:NH1	2.28	0.64
3:P:194:LYS:NZ	2:Q:309:VAL:O	2.27	0.64
2:Q:312:SER:HB3	4:O:22:GLN:HE22	1.63	0.63
1:E:151:ARG:NH2	1:E:320:HIS:O	2.32	0.63
1:4:151:ARG:NH2	1:4:320:HIS:O	2.32	0.62
1:M:151:ARG:NH2	1:M:320:HIS:O	2.32	0.62
1:R:151:ARG:NH2	1:R:320:HIS:O	2.32	0.62
2:D:177:ALA:HB2	2:D:210:PRO:HB2	1.81	0.62
1:Y:151:ARG:NH2	1:Y:320:HIS:O	2.32	0.62
1:H:151:ARG:NH2	1:H:320:HIS:O	2.32	0.62
2:W:177:ALA:HB2	2:W:210:PRO:HB2	1.82	0.62
3:F:215:LEU:O	3:F:304:ARG:NH2	2.29	0.62
2:3:177:ALA:HB2	2:3:210:PRO:HB2	1.82	0.61
2:Q:177:ALA:HB2	2:Q:210:PRO:HB2	1.81	0.61
3:K:215:LEU:O	3:K:304:ARG:NH2	2.29	0.61
2:Q:42:ILE:HB	2:Q:85:PRO:HA	1.83	0.61
3:C:19:GLU:HB2	3:C:174:VAL:HG12	1.83	0.60
2:G:177:ALA:HB2	2:G:210:PRO:HB2	1.82	0.60
3:P:152:GLN:NE2	3:P:154:ASP:O	2.34	0.60
3:C:215:LEU:O	3:C:304:ARG:NH2	2.29	0.60
3:2:152:GLN:NE2	3:2:154:ASP:O	2.34	0.60
3:C:152:GLN:NE2	3:C:154:ASP:O	2.34	0.60
3:K:19:GLU:HB2	3:K:174:VAL:HG12	1.83	0.60
3:K:152:GLN:NE2	3:K:154:ASP:O	2.34	0.60
3:F:19:GLU:HB2	3:F:174:VAL:HG12	1.83	0.60
3:V:152:GLN:NE2	3:V:154:ASP:O	2.34	0.60
2:D:42:ILE:HB	2:D:85:PRO:HA	1.83	0.60
3:2:19:GLU:HB2	3:2:174:VAL:HG12	1.83	0.60
2:3:270:ARG:NH1	2:3:275:THR:O	2.35	0.60
2:L:177:ALA:HB2	2:L:210:PRO:HB2	1.82	0.60
3:F:152:GLN:NE2	3:F:154:ASP:O	2.34	0.59
2:L:42:ILE:HB	2:L:85:PRO:HA	1.84	0.59
2:L:270:ARG:NH1	2:L:275:THR:O	2.35	0.59
2:G:270:ARG:NH1	2:G:275:THR:O	2.35	0.59
2:W:42:ILE:HB	2:W:85:PRO:HA	1.83	0.59
2:X:111:ARG:NH1	3:C:123:ASP:OD1	2.34	0.59
3:P:19:GLU:HB2	3:P:174:VAL:HG12	1.83	0.59
3:V:19:GLU:HB2	3:V:174:VAL:HG12	1.83	0.59
2:G:42:ILE:HB	2:G:85:PRO:HA	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:42:ILE:HB	2:3:85:PRO:HA	1.83	0.59
2:D:270:ARG:NH1	2:D:275:THR:O	2.36	0.59
2:Q:270:ARG:NH1	2:Q:275:THR:O	2.36	0.58
1:M:166:GLY:HA2	1:M:195:GLU:HG3	1.85	0.58
3:P:215:LEU:O	3:P:304:ARG:NH2	2.29	0.58
3:C:126:ASP:OD1	3:C:130:ARG:NH1	2.32	0.58
1:4:166:GLY:HA2	1:4:195:GLU:HG3	1.85	0.58
1:H:166:GLY:HA2	1:H:195:GLU:HG3	1.85	0.58
3:2:380:ASP:HB2	3:2:387:ILE:HD11	1.86	0.58
1:Y:216:ARG:NE	2:W:116:GLU:OE1	2.34	0.58
3:2:215:LEU:O	3:2:304:ARG:NH2	2.29	0.57
1:R:166:GLY:HA2	1:R:195:GLU:HG3	1.85	0.57
3:P:126:ASP:OD1	3:P:130:ARG:NH1	2.32	0.57
2:X:156:LEU:HD21	2:D:431:VAL:HG21	1.86	0.57
1:Y:166:GLY:HA2	1:Y:195:GLU:HG3	1.85	0.57
3:V:380:ASP:HB2	3:V:387:ILE:HD11	1.86	0.57
3:K:380:ASP:HB2	3:K:387:ILE:HD11	1.86	0.57
2:S:156:LEU:HD21	2:Q:431:VAL:HG21	1.86	0.57
2:5:156:LEU:HD21	2:3:431:VAL:HG21	1.87	0.57
3:K:126:ASP:OD1	3:K:130:ARG:NH1	2.32	0.57
3:F:126:ASP:OD1	3:F:130:ARG:NH1	2.32	0.57
2:W:270:ARG:NH1	2:W:275:THR:O	2.35	0.57
3:P:380:ASP:HB2	3:P:387:ILE:HD11	1.86	0.57
3:V:215:LEU:O	3:V:304:ARG:NH2	2.29	0.57
2:Z:156:LEU:HD21	2:W:431:VAL:HG21	1.87	0.56
2:N:111:ARG:NH1	3:K:123:ASP:OD1	2.35	0.56
3:C:380:ASP:HB2	3:C:387:ILE:HD11	1.86	0.56
3:F:380:ASP:HB2	3:F:387:ILE:HD11	1.86	0.56
2:N:156:LEU:HD21	2:L:431:VAL:HG21	1.87	0.56
2:I:156:LEU:HD21	2:G:431:VAL:HG21	1.87	0.56
3:C:267:TRP:HB2	3:C:409:ALA:HB1	1.88	0.56
1:E:166:GLY:HA2	1:E:195:GLU:HG3	1.85	0.56
3:F:267:TRP:HB2	3:F:409:ALA:HB1	1.88	0.56
3:V:126:ASP:OD1	3:V:130:ARG:NH1	2.32	0.56
2:D:312:SER:HB3	4:B:22:GLN:HE22	1.71	0.55
2:Z:229:VAL:HB	2:Z:267:GLY:HA3	1.88	0.55
2:S:229:VAL:HB	2:S:267:GLY:HA3	1.88	0.55
3:2:126:ASP:OD1	3:2:130:ARG:NH1	2.32	0.55
3:2:267:TRP:HB2	3:2:409:ALA:HB1	1.88	0.55
3:V:267:TRP:HB2	3:V:409:ALA:HB1	1.88	0.55
2:I:229:VAL:HB	2:I:267:GLY:HA3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:64:LEU:HD13	3:2:65:PHE:HE1	1.72	0.55
3:P:267:TRP:HB2	3:P:409:ALA:HB1	1.88	0.55
3:V:18:PRO:HA	3:V:173:GLU:HB3	1.89	0.54
3:K:267:TRP:HB2	3:K:409:ALA:HB1	1.88	0.54
3:P:18:PRO:HA	3:P:173:GLU:HB3	1.89	0.54
2:5:229:VAL:HB	2:5:267:GLY:HA3	1.88	0.54
2:S:27:ALA:HB2	2:S:102:LEU:HB3	1.89	0.54
2:X:229:VAL:HB	2:X:267:GLY:HA3	1.88	0.54
3:K:18:PRO:HA	3:K:173:GLU:HB3	1.89	0.54
3:P:248:ASP:OD1	3:P:248:ASP:N	2.40	0.54
3:2:18:PRO:HA	3:2:173:GLU:HB3	1.89	0.54
3:C:326:ILE:HG23	3:C:351:LEU:HD13	1.91	0.53
2:N:229:VAL:HB	2:N:267:GLY:HA3	1.89	0.53
3:V:326:ILE:HG23	3:V:351:LEU:HD13	1.91	0.53
3:C:18:PRO:HA	3:C:173:GLU:HB3	1.89	0.53
3:F:18:PRO:HA	3:F:173:GLU:HB3	1.89	0.53
3:F:326:ILE:HG23	3:F:351:LEU:HD13	1.91	0.53
1:R:216:ARG:NE	2:Q:116:GLU:OE1	2.32	0.53
3:2:326:ILE:HG23	3:2:351:LEU:HD13	1.91	0.53
3:K:339:SER:OG	3:K:340:SER:N	2.42	0.53
2:Z:219:ALA:O	2:Z:227:HIS:NE2	2.42	0.53
3:V:339:SER:OG	3:V:340:SER:N	2.42	0.53
3:C:248:ASP:OD1	3:C:248:ASP:N	2.40	0.53
3:F:339:SER:OG	3:F:340:SER:N	2.42	0.53
3:K:326:ILE:HG23	3:K:351:LEU:HD13	1.91	0.53
3:P:326:ILE:HG23	3:P:351:LEU:HD13	1.91	0.53
3:2:339:SER:OG	3:2:340:SER:N	2.42	0.53
3:V:194:LYS:NZ	2:W:309:VAL:O	2.42	0.53
3:P:64:LEU:HD13	3:V:65:PHE:HE1	1.74	0.52
3:2:248:ASP:OD1	3:2:248:ASP:N	2.40	0.52
2:5:219:ALA:O	2:5:227:HIS:NE2	2.43	0.52
2:L:496:TYR:O	2:L:500:ARG:HB2	2.10	0.52
3:P:339:SER:OG	3:P:340:SER:N	2.42	0.52
2:Z:47:ASP:OD2	3:V:411:GLN:NE2	2.37	0.52
3:C:339:SER:OG	3:C:340:SER:N	2.42	0.52
2:N:312:SER:OG	2:N:313:ALA:N	2.43	0.51
2:S:210:PRO:HA	2:S:213:VAL:HG12	1.93	0.51
2:X:24:ALA:HA	2:X:33:ALA:HA	1.92	0.51
4:B:65:VAL:HG11	3:F:48:GLY:HA3	1.93	0.51
2:I:219:ALA:O	2:I:227:HIS:NE2	2.42	0.51
1:R:216:ARG:HG2	2:Q:118:ILE:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:219:ALA:O	2:S:227:HIS:NE2	2.43	0.51
2:X:312:SER:OG	2:X:313:ALA:N	2.44	0.51
2:N:219:ALA:O	2:N:227:HIS:NE2	2.43	0.51
2:Z:210:PRO:HA	2:Z:213:VAL:HG12	1.93	0.51
2:I:312:SER:OG	2:I:313:ALA:N	2.44	0.51
2:Z:127:SER:HB3	4:T:40:TRP:HB3	1.92	0.51
3:K:248:ASP:OD1	3:K:248:ASP:N	2.40	0.51
3:K:160:PHE:O	3:K:245:HIS:NE2	2.44	0.50
3:P:160:PHE:O	3:P:245:HIS:NE2	2.44	0.50
3:V:160:PHE:O	3:V:245:HIS:NE2	2.44	0.50
2:S:111:ARG:NH1	3:P:123:ASP:OD1	2.39	0.50
2:5:111:ARG:NH1	3:2:123:ASP:OD1	2.41	0.50
2:X:219:ALA:O	2:X:227:HIS:NE2	2.43	0.50
2:N:210:PRO:HA	2:N:213:VAL:HG12	1.93	0.50
2:5:312:SER:OG	2:5:313:ALA:N	2.44	0.50
2:5:210:PRO:HA	2:5:213:VAL:HG12	1.93	0.50
3:F:160:PHE:O	3:F:245:HIS:NE2	2.44	0.50
2:X:143:ALA:HB2	2:X:199:VAL:HG13	1.94	0.50
3:F:64:LEU:HD13	3:K:65:PHE:HE1	1.77	0.50
2:5:143:ALA:HB2	2:5:199:VAL:HG13	1.93	0.50
2:X:210:PRO:HA	2:X:213:VAL:HG12	1.93	0.50
1:E:232:HIS:ND1	2:D:113:GLU:OE1	2.35	0.50
3:C:160:PHE:O	3:C:245:HIS:NE2	2.44	0.49
2:I:210:PRO:HA	2:I:213:VAL:HG12	1.93	0.49
3:2:160:PHE:O	3:2:245:HIS:NE2	2.44	0.49
3:P:245:HIS:O	3:P:270:HIS:NE2	2.41	0.49
2:3:483:MET:HA	4:1:59:SER:OG	2.13	0.49
2:Z:51:LYS:NZ	2:W:98:ASP:OD1	2.44	0.49
3:C:64:LEU:HD13	3:F:65:PHE:HE1	1.78	0.49
3:C:414:HIS:O	3:C:414:HIS:ND1	2.46	0.49
2:S:143:ALA:HB2	2:S:199:VAL:HG13	1.94	0.49
2:Z:27:ALA:HB2	2:Z:102:LEU:HB3	1.94	0.49
2:N:143:ALA:HB2	2:N:199:VAL:HG13	1.93	0.49
2:5:47:ASP:OD2	3:2:411:GLN:NE2	2.39	0.49
3:P:323:HIS:HB2	3:P:346:VAL:HG22	1.95	0.49
3:2:414:HIS:O	3:2:414:HIS:ND1	2.46	0.49
2:X:47:ASP:OD2	3:C:411:GLN:NE2	2.38	0.49
2:Z:312:SER:OG	2:Z:313:ALA:N	2.44	0.49
3:F:323:HIS:HB2	3:F:346:VAL:HG22	1.95	0.49
3:K:323:HIS:HB2	3:K:346:VAL:HG22	1.95	0.49
2:5:51:LYS:NZ	2:3:98:ASP:OD1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:60:LEU:HD11	2:Q:115:ILE:HG21	1.94	0.48
3:V:323:HIS:HB2	3:V:346:VAL:HG22	1.95	0.48
1:E:256:VAL:O	1:E:330:ARG:NH2	2.42	0.48
2:Z:143:ALA:HB2	2:Z:199:VAL:HG13	1.94	0.48
3:C:65:PHE:HE1	3:2:64:LEU:HD13	1.79	0.48
2:N:448:VAL:HG23	2:L:150:VAL:HG12	1.95	0.48
3:P:217:VAL:HA	3:P:306:SER:HB3	1.96	0.48
3:V:414:HIS:ND1	3:V:414:HIS:O	2.46	0.48
3:C:323:HIS:HB2	3:C:346:VAL:HG22	1.95	0.48
2:I:143:ALA:HB2	2:I:199:VAL:HG13	1.94	0.48
3:K:217:VAL:HA	3:K:306:SER:HB3	1.96	0.48
3:K:245:HIS:O	3:K:270:HIS:NE2	2.41	0.48
3:V:217:VAL:HA	3:V:306:SER:HB3	1.96	0.48
2:5:219:ALA:HB3	2:5:227:HIS:CD2	2.49	0.48
2:N:219:ALA:HB3	2:N:227:HIS:CD2	2.49	0.48
2:S:448:VAL:HG23	2:Q:150:VAL:HG12	1.96	0.48
2:I:219:ALA:HB3	2:I:227:HIS:CD2	2.49	0.47
3:2:323:HIS:HB2	3:2:346:VAL:HG22	1.95	0.47
2:S:31:GLN:HB2	2:Q:118:ILE:HG12	1.95	0.47
2:X:219:ALA:HB3	2:X:227:HIS:CD2	2.49	0.47
3:F:248:ASP:OD1	3:F:248:ASP:N	2.40	0.47
2:Z:219:ALA:HB3	2:Z:227:HIS:CD2	2.49	0.47
2:X:448:VAL:HG23	2:D:150:VAL:HG12	1.96	0.47
2:S:219:ALA:HB3	2:S:227:HIS:CD2	2.49	0.47
2:5:448:VAL:HG23	2:3:150:VAL:HG12	1.95	0.47
2:D:324:ASP:N	2:D:324:ASP:OD1	2.47	0.47
3:F:217:VAL:HA	3:F:306:SER:HB3	1.96	0.47
3:K:133:HIS:O	3:K:164:ARG:NH1	2.44	0.47
1:4:256:VAL:O	1:4:330:ARG:NH2	2.42	0.47
2:I:448:VAL:HG23	2:G:150:VAL:HG12	1.95	0.47
2:S:88:SER:OG	2:S:91:GLU:OE1	2.29	0.47
2:Q:27:ALA:HB1	2:Q:65:LEU:HD11	1.97	0.47
3:2:133:HIS:O	3:2:164:ARG:NH1	2.44	0.47
1:H:163:VAL:O	1:H:199:TRP:N	2.42	0.47
3:C:217:VAL:HA	3:C:306:SER:HB3	1.96	0.47
2:Q:343:ALA:HB3	2:Q:345:VAL:HG22	1.97	0.47
3:2:217:VAL:HA	3:2:306:SER:HB3	1.96	0.47
3:F:414:HIS:O	3:F:414:HIS:ND1	2.46	0.46
3:K:414:HIS:O	3:K:414:HIS:ND1	2.46	0.46
2:Z:448:VAL:HG23	2:W:150:VAL:HG12	1.95	0.46
3:P:414:HIS:O	3:P:414:HIS:ND1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:245:HIS:O	3:2:270:HIS:NE2	2.41	0.46
2:3:320:GLU:O	2:3:322:ARG:NH1	2.41	0.46
2:G:27:ALA:HB1	2:G:65:LEU:HD11	1.96	0.46
3:V:133:HIS:O	3:V:164:ARG:NH1	2.44	0.46
2:G:84:ARG:N	2:G:92:GLN:OE1	2.45	0.46
2:Z:111:ARG:NH1	3:V:123:ASP:OD1	2.39	0.46
3:F:133:HIS:O	3:F:164:ARG:NH1	2.44	0.46
3:C:194:LYS:NZ	2:D:309:VAL:O	2.49	0.46
3:F:245:HIS:O	3:F:270:HIS:NE2	2.41	0.46
2:D:472:LYS:HE2	4:A:20:ARG:HG3	1.98	0.46
3:K:257:SER:HB3	3:K:329:ILE:HD12	1.99	0.46
3:V:257:SER:HB3	3:V:329:ILE:HD12	1.99	0.46
3:C:245:HIS:O	3:C:270:HIS:NE2	2.41	0.45
3:P:257:SER:HB3	3:P:329:ILE:HD12	1.99	0.45
3:V:245:HIS:O	3:V:270:HIS:NE2	2.41	0.45
2:W:27:ALA:HB1	2:W:65:LEU:HD11	1.98	0.45
3:C:133:HIS:O	3:C:164:ARG:NH1	2.44	0.45
2:D:27:ALA:HB1	2:D:65:LEU:HD11	1.98	0.45
2:Q:401:LEU:HD12	2:Q:401:LEU:HA	1.77	0.45
3:F:257:SER:HB3	3:F:329:ILE:HD12	1.99	0.45
2:5:27:ALA:HB2	2:5:102:LEU:HB3	1.97	0.45
2:X:51:LYS:NZ	2:D:98:ASP:OD1	2.45	0.45
3:C:257:SER:HB3	3:C:329:ILE:HD12	1.99	0.45
3:C:301:PHE:HB2	3:C:343:VAL:HG13	1.99	0.45
2:5:27:ALA:HB1	2:5:65:LEU:HD11	1.98	0.45
3:2:257:SER:HB3	3:2:329:ILE:HD12	1.98	0.45
3:C:109:LEU:HD21	4:B:43:ARG:HA	1.98	0.45
3:P:301:PHE:HB2	3:P:343:VAL:HG13	1.99	0.45
2:X:162:TRP:HA	2:X:223:VAL:HG11	1.99	0.45
2:I:127:SER:HB3	4:A:40:TRP:HB3	1.97	0.45
3:F:301:PHE:HB2	3:F:343:VAL:HG13	1.99	0.45
1:M:163:VAL:O	1:M:199:TRP:N	2.42	0.45
1:M:256:VAL:O	1:M:330:ARG:NH2	2.42	0.45
3:K:231:LEU:O	3:K:235:ARG:HG3	2.17	0.45
3:K:301:PHE:HB2	3:K:343:VAL:HG13	1.99	0.45
2:L:377:LEU:HG	2:L:388:PRO:HB2	1.99	0.45
2:S:312:SER:OG	2:S:313:ALA:N	2.47	0.45
3:2:301:PHE:HB2	3:2:343:VAL:HG13	1.99	0.45
2:S:291:MET:O	2:S:295:ALA:N	2.50	0.45
3:P:231:LEU:O	3:P:235:ARG:HG3	2.17	0.45
2:W:471:ARG:NE	4:1:16:GLY:O	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:149:ARG:HH22	1:R:229:ARG:HB3	1.82	0.44
1:4:149:ARG:HH22	1:4:229:ARG:HB3	1.82	0.44
3:2:231:LEU:O	3:2:235:ARG:HG3	2.17	0.44
2:I:428:VAL:HA	2:I:431:VAL:HG22	1.99	0.44
2:N:291:MET:O	2:N:295:ALA:N	2.51	0.44
3:P:133:HIS:O	3:P:164:ARG:NH1	2.44	0.44
2:Q:289:VAL:HG11	2:Q:485:ILE:HD11	1.99	0.44
2:Z:24:ALA:HA	2:Z:33:ALA:HA	2.00	0.44
3:V:301:PHE:HB2	3:V:343:VAL:HG13	1.99	0.44
2:3:27:ALA:HB1	2:3:65:LEU:HD11	1.98	0.44
1:E:149:ARG:HH22	1:E:229:ARG:HB3	1.82	0.44
1:M:149:ARG:HH22	1:M:229:ARG:HB3	1.82	0.44
2:3:84:ARG:N	2:3:92:GLN:OE1	2.46	0.44
4:B:23:VAL:HG21	2:3:472:LYS:HG3	1.99	0.44
2:N:428:VAL:HA	2:N:431:VAL:HG22	1.99	0.44
2:S:24:ALA:HA	2:S:33:ALA:HA	1.99	0.44
2:S:162:TRP:HA	2:S:223:VAL:HG11	1.99	0.44
2:3:226:PRO:HG2	2:3:229:VAL:H	1.83	0.44
3:C:231:LEU:O	3:C:235:ARG:HG3	2.17	0.44
1:H:149:ARG:HH22	1:H:229:ARG:HB3	1.82	0.44
3:F:133:HIS:HB3	3:F:164:ARG:HB2	1.99	0.44
3:F:231:LEU:O	3:F:235:ARG:HG3	2.17	0.44
1:R:163:VAL:O	1:R:199:TRP:N	2.42	0.44
2:D:226:PRO:HG2	2:D:229:VAL:H	1.83	0.44
2:Q:448:VAL:HG13	2:Q:449:LEU:HD22	2.00	0.44
1:Y:149:ARG:HH22	1:Y:229:ARG:HB3	1.82	0.44
2:Z:428:VAL:HA	2:Z:431:VAL:HG22	1.99	0.44
3:V:133:HIS:HB3	3:V:164:ARG:HB2	1.99	0.44
3:C:133:HIS:HB3	3:C:164:ARG:HB2	1.99	0.44
2:S:27:ALA:HB1	2:S:65:LEU:HD11	1.99	0.44
3:P:133:HIS:HB3	3:P:164:ARG:HB2	1.99	0.44
2:5:162:TRP:HA	2:5:223:VAL:HG11	2.00	0.44
2:I:162:TRP:HA	2:I:223:VAL:HG11	2.00	0.44
2:N:44:VAL:O	2:L:99:ARG:NH1	2.50	0.44
3:K:133:HIS:HB3	3:K:164:ARG:HB2	1.99	0.44
2:W:377:LEU:HG	2:W:388:PRO:HB2	2.00	0.44
3:2:133:HIS:HB3	3:2:164:ARG:HB2	1.99	0.44
3:K:254:VAL:HG23	3:K:271:PHE:HE2	1.83	0.43
2:L:226:PRO:HG2	2:L:229:VAL:H	1.82	0.43
2:Q:377:LEU:HG	2:Q:388:PRO:HB2	2.00	0.43
3:C:254:VAL:HG23	3:C:271:PHE:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:53:MET:O	3:V:57:THR:HG23	2.18	0.43
2:L:448:VAL:HG13	2:L:449:LEU:HD22	2.00	0.43
2:5:428:VAL:HA	2:5:431:VAL:HG22	2.00	0.43
3:F:254:VAL:HG23	3:F:271:PHE:HE2	1.84	0.43
3:V:231:LEU:O	3:V:235:ARG:HG3	2.17	0.43
2:X:428:VAL:HA	2:X:431:VAL:HG22	2.00	0.43
2:I:291:MET:O	2:I:295:ALA:N	2.52	0.43
2:G:377:LEU:HG	2:G:388:PRO:HB2	2.00	0.43
3:P:254:VAL:HG23	3:P:271:PHE:HE2	1.83	0.43
1:Y:163:VAL:HB	1:Y:199:TRP:HB2	2.01	0.43
3:2:254:VAL:HG23	3:2:271:PHE:HE2	1.83	0.43
3:2:328:ASP:OD1	3:2:328:ASP:N	2.52	0.43
1:R:163:VAL:HB	1:R:199:TRP:HB2	2.00	0.43
2:S:428:VAL:HA	2:S:431:VAL:HG22	2.00	0.43
2:Z:101:TRP:CD2	2:W:124:THR:HG21	2.54	0.43
3:V:254:VAL:HG23	3:V:271:PHE:HE2	1.83	0.43
3:P:53:MET:O	3:P:57:THR:HG23	2.18	0.43
2:X:291:MET:O	2:X:295:ALA:N	2.52	0.43
4:B:51:ARG:NH1	3:F:34:GLY:HA2	2.34	0.43
1:H:256:VAL:O	1:H:330:ARG:NH2	2.42	0.43
2:G:343:ALA:HB3	2:G:345:VAL:HG22	2.01	0.43
3:K:53:MET:O	3:K:57:THR:HG23	2.18	0.43
2:Z:162:TRP:HA	2:Z:223:VAL:HG11	1.99	0.43
2:W:448:VAL:HG13	2:W:449:LEU:HD22	2.00	0.43
2:Q:226:PRO:HG2	2:Q:229:VAL:H	1.83	0.43
2:3:448:VAL:HG13	2:3:449:LEU:HD22	2.00	0.43
2:D:384:ARG:NH2	2:D:491:TRP:O	2.50	0.43
2:G:226:PRO:HG2	2:G:229:VAL:H	1.83	0.43
3:2:53:MET:O	3:2:57:THR:HG23	2.18	0.43
3:C:53:MET:O	3:C:57:THR:HG23	2.18	0.42
2:D:448:VAL:HG13	2:D:449:LEU:HD22	2.00	0.42
1:H:163:VAL:HB	1:H:199:TRP:HB2	2.00	0.42
2:Z:291:MET:O	2:Z:295:ALA:N	2.52	0.42
1:4:163:VAL:HB	1:4:199:TRP:HB2	2.00	0.42
3:K:35:LYS:HB2	3:K:39:LEU:HD13	2.01	0.42
3:P:35:LYS:HB2	3:P:39:LEU:HD13	2.01	0.42
2:Q:84:ARG:N	2:Q:92:GLN:OE1	2.46	0.42
4:O:50:ARG:O	4:O:54:LEU:HG	2.19	0.42
1:E:163:VAL:O	1:E:199:TRP:N	2.42	0.42
3:C:35:LYS:HB2	3:C:39:LEU:HD13	2.01	0.42
3:F:53:MET:O	3:F:57:THR:HG23	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:50:ARG:O	4:A:54:LEU:HG	2.20	0.42
3:K:64:LEU:HD13	3:P:65:PHE:HE1	1.84	0.42
4:T:50:ARG:O	4:T:54:LEU:HG	2.19	0.42
2:3:377:LEU:HG	2:3:388:PRO:HB2	2.00	0.42
1:E:163:VAL:HB	1:E:199:TRP:HB2	2.01	0.42
3:C:194:LYS:HZ3	2:D:308:PRO:HB3	1.84	0.42
2:S:76:CYS:N	2:S:101:TRP:O	2.48	0.42
3:C:328:ASP:OD1	3:C:328:ASP:N	2.52	0.42
2:I:111:ARG:NH1	3:F:123:ASP:OD1	2.40	0.42
2:G:384:ARG:NH1	2:G:494:ASN:OD1	2.52	0.42
2:N:162:TRP:HA	2:N:223:VAL:HG11	2.00	0.42
2:Z:121:ALA:O	2:Z:125:ASN:ND2	2.52	0.42
3:V:35:LYS:HB2	3:V:39:LEU:HD13	2.01	0.42
3:2:35:LYS:HB2	3:2:39:LEU:HD13	2.01	0.42
3:F:35:LYS:HB2	3:F:39:LEU:HD13	2.01	0.42
2:5:291:MET:O	2:5:295:ALA:N	2.52	0.42
1:M:229:ARG:NH2	2:L:116:GLU:OE2	2.41	0.42
2:W:226:PRO:HG2	2:W:229:VAL:H	1.83	0.42
3:C:48:GLY:HA3	4:1:65:VAL:HG11	2.02	0.42
4:O:65:VAL:HG11	3:V:48:GLY:HA3	2.01	0.42
3:V:248:ASP:OD1	3:V:248:ASP:N	2.40	0.42
4:B:50:ARG:O	4:B:54:LEU:HG	2.19	0.42
3:F:62:SER:HB3	3:F:65:PHE:CD2	2.55	0.42
3:F:328:ASP:N	3:F:328:ASP:OD1	2.52	0.42
1:R:256:VAL:O	1:R:330:ARG:NH2	2.42	0.42
3:P:152:GLN:HA	3:P:153:PRO:HD3	1.86	0.42
3:C:62:SER:HB3	3:C:65:PHE:CD2	2.55	0.42
1:M:163:VAL:HB	1:M:199:TRP:HB2	2.00	0.42
2:S:22:VAL:HG22	2:S:35:VAL:HG22	2.02	0.42
4:1:50:ARG:O	4:1:54:LEU:HG	2.20	0.42
1:H:238:ARG:O	1:H:238:ARG:NE	2.53	0.41
3:2:71:ILE:O	3:2:74:ILE:HG22	2.20	0.41
3:C:71:ILE:O	3:C:74:ILE:HG22	2.20	0.41
3:K:328:ASP:OD1	3:K:328:ASP:N	2.52	0.41
3:V:62:SER:HB3	3:V:65:PHE:CD2	2.55	0.41
3:F:152:GLN:HA	3:F:153:PRO:HD3	1.86	0.41
2:G:448:VAL:HG13	2:G:449:LEU:HD22	2.00	0.41
4:J:50:ARG:O	4:J:54:LEU:HG	2.20	0.41
3:P:71:ILE:O	3:P:74:ILE:HG22	2.21	0.41
2:Z:127:SER:HA	4:T:40:TRP:CE3	2.55	0.41
3:V:71:ILE:O	3:V:74:ILE:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:328:ASP:OD1	3:V:328:ASP:N	2.52	0.41
3:2:62:SER:HB3	3:2:65:PHE:CD2	2.55	0.41
3:K:62:SER:HB3	3:K:65:PHE:CD2	2.55	0.41
3:V:216:LEU:HB3	3:V:307:PHE:HB3	2.02	0.41
1:E:238:ARG:O	1:E:238:ARG:NE	2.53	0.41
1:R:150:LEU:HD12	1:R:160:ILE:HG12	2.03	0.41
2:S:243:MET:HE1	2:S:250:LEU:HA	2.03	0.41
2:Z:371:VAL:HA	2:Z:422:ILE:HD13	2.03	0.41
2:3:56:ARG:NH1	2:3:59:GLU:OE1	2.51	0.41
3:F:71:ILE:O	3:F:74:ILE:HG22	2.20	0.41
2:L:84:ARG:N	2:L:92:GLN:OE1	2.46	0.41
1:Y:163:VAL:O	1:Y:199:TRP:N	2.42	0.41
2:D:421:LEU:HD23	2:D:421:LEU:HA	1.92	0.41
2:G:473:ILE:O	2:G:477:ILE:HG12	2.20	0.41
1:M:150:LEU:HD12	1:M:160:ILE:HG12	2.03	0.41
3:K:152:GLN:HA	3:K:153:PRO:HD3	1.85	0.41
3:P:62:SER:HB3	3:P:65:PHE:CD2	2.55	0.41
3:P:216:LEU:HB3	3:P:307:PHE:HB3	2.03	0.41
2:Q:398:PHE:CE1	2:Q:402:ARG:HD3	2.56	0.41
2:3:157:LEU:HD13	2:3:173:ALA:HB2	2.03	0.41
1:H:150:LEU:HD12	1:H:160:ILE:HG12	2.03	0.41
2:G:25:ILE:N	2:G:32:ILE:O	2.43	0.41
3:K:216:LEU:HB3	3:K:307:PHE:HB3	2.03	0.40
3:P:328:ASP:OD1	3:P:328:ASP:N	2.52	0.40
1:Y:238:ARG:O	1:Y:238:ARG:NE	2.53	0.40
2:5:370:THR:HG22	2:5:422:ILE:HD11	2.03	0.40
3:C:152:GLN:HA	3:C:153:PRO:HD3	1.86	0.40
3:C:328:ASP:HB3	3:C:351:LEU:HB2	2.04	0.40
2:S:371:VAL:HA	2:S:422:ILE:HD13	2.03	0.40
1:Y:150:LEU:HD12	1:Y:160:ILE:HG12	2.03	0.40
2:Z:117:HIS:CE1	2:Z:119:SER:HB3	2.56	0.40
2:X:56:ARG:HD3	2:X:56:ARG:HA	1.98	0.40
2:D:157:LEU:HD13	2:D:173:ALA:HB2	2.03	0.40
3:F:216:LEU:HB3	3:F:307:PHE:HB3	2.02	0.40
3:F:328:ASP:HB3	3:F:351:LEU:HB2	2.04	0.40
2:N:370:THR:HG22	2:N:422:ILE:HD11	2.03	0.40
3:K:71:ILE:O	3:K:74:ILE:HG22	2.20	0.40
2:L:324:ASP:OD1	2:L:324:ASP:N	2.52	0.40
2:X:370:THR:HG22	2:X:422:ILE:HD11	2.03	0.40
2:D:84:ARG:N	2:D:92:GLN:OE1	2.45	0.40
2:3:286:LEU:HD23	2:3:286:LEU:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:22:VAL:HG22	2:5:35:VAL:HG22	2.04	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	4	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
1	E	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
1	H	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
1	M	157/400 (39%)	146 (93%)	11 (7%)	0	100	100
1	R	157/400 (39%)	146 (93%)	11 (7%)	0	100	100
1	Y	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
2	3	483/502 (96%)	466 (96%)	17 (4%)	0	100	100
2	5	458/502 (91%)	447 (98%)	10 (2%)	1 (0%)	47	78
2	D	483/502 (96%)	466 (96%)	17 (4%)	0	100	100
2	G	483/502 (96%)	465 (96%)	18 (4%)	0	100	100
2	I	458/502 (91%)	448 (98%)	10 (2%)	0	100	100
2	L	483/502 (96%)	468 (97%)	15 (3%)	0	100	100
2	N	458/502 (91%)	449 (98%)	9 (2%)	0	100	100
2	Q	483/502 (96%)	463 (96%)	20 (4%)	0	100	100
2	S	458/502 (91%)	447 (98%)	11 (2%)	0	100	100
2	W	483/502 (96%)	464 (96%)	19 (4%)	0	100	100
2	X	458/502 (91%)	447 (98%)	11 (2%)	0	100	100
2	Z	458/502 (91%)	448 (98%)	10 (2%)	0	100	100
3	2	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	F	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	K	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	P	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	V	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
4	1	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	A	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	B	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	J	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	O	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	T	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
All	All	9306/19812 (47%)	8954 (96%)	351 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	5	69	GLY

5.3.2 Protein sidechains [i](#)

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	4	136/328 (42%)	135 (99%)	1 (1%)	84	92
1	E	136/328 (42%)	135 (99%)	1 (1%)	84	92
1	H	136/328 (42%)	135 (99%)	1 (1%)	84	92
1	M	136/328 (42%)	135 (99%)	1 (1%)	84	92
1	R	136/328 (42%)	135 (99%)	1 (1%)	84	92
1	Y	136/328 (42%)	135 (99%)	1 (1%)	84	92
2	3	381/392 (97%)	379 (100%)	2 (0%)	88	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	5	362/392 (92%)	358 (99%)	4 (1%)	73	86
2	D	381/392 (97%)	379 (100%)	2 (0%)	88	94
2	G	381/392 (97%)	380 (100%)	1 (0%)	92	97
2	I	362/392 (92%)	357 (99%)	5 (1%)	67	83
2	L	381/392 (97%)	380 (100%)	1 (0%)	92	97
2	N	362/392 (92%)	359 (99%)	3 (1%)	81	91
2	Q	381/392 (97%)	379 (100%)	2 (0%)	88	94
2	S	362/392 (92%)	360 (99%)	2 (1%)	86	94
2	W	381/392 (97%)	380 (100%)	1 (0%)	92	97
2	X	362/392 (92%)	359 (99%)	3 (1%)	81	91
2	Z	362/392 (92%)	356 (98%)	6 (2%)	60	80
3	2	330/1127 (29%)	329 (100%)	1 (0%)	92	97
3	C	330/1127 (29%)	329 (100%)	1 (0%)	92	97
3	F	330/1127 (29%)	329 (100%)	1 (0%)	92	97
3	K	330/1127 (29%)	329 (100%)	1 (0%)	92	97
3	P	330/1127 (29%)	329 (100%)	1 (0%)	92	97
3	V	330/1127 (29%)	329 (100%)	1 (0%)	92	97
4	1	48/402 (12%)	48 (100%)	0	100	100
4	A	48/402 (12%)	48 (100%)	0	100	100
4	B	48/402 (12%)	48 (100%)	0	100	100
4	J	48/402 (12%)	48 (100%)	0	100	100
4	O	48/402 (12%)	48 (100%)	0	100	100
4	T	48/402 (12%)	48 (100%)	0	100	100
All	All	7542/15846 (48%)	7498 (99%)	44 (1%)	86	94

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	96	HIS
2	X	88	SER
2	X	129	ARG
2	X	161	ARG
3	C	89	PHE
2	D	322	ARG

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Mol	Chain	Res	Type
2	D	500	ARG
1	H	96	HIS
2	I	56	ARG
2	I	88	SER
2	I	109	GLU
2	I	129	ARG
2	I	161	ARG
3	F	89	PHE
2	G	322	ARG
1	M	96	HIS
2	N	56	ARG
2	N	129	ARG
2	N	161	ARG
3	K	89	PHE
2	L	322	ARG
1	R	96	HIS
2	S	129	ARG
2	S	161	ARG
3	P	89	PHE
2	Q	398	PHE
2	Q	491	TRP
1	Y	96	HIS
2	Z	84	ARG
2	Z	88	SER
2	Z	109	GLU
2	Z	116	GLU
2	Z	129	ARG
2	Z	161	ARG
3	V	89	PHE
2	W	322	ARG
1	4	96	HIS
2	5	88	SER
2	5	128	LYS
2	5	129	ARG
2	5	161	ARG
3	2	89	PHE
2	3	322	ARG
2	3	398	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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.

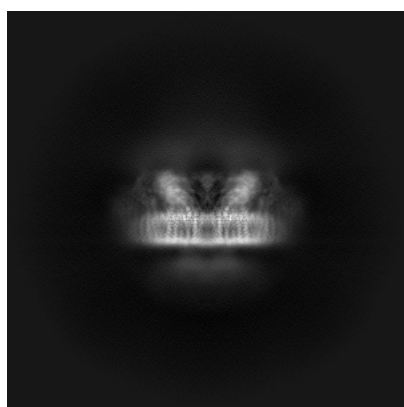
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12105. These allow visual inspection of the internal detail of the map and identification of artifacts.

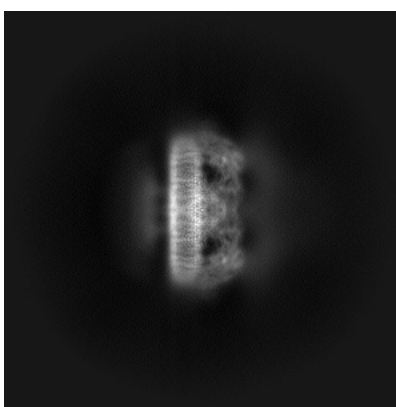
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

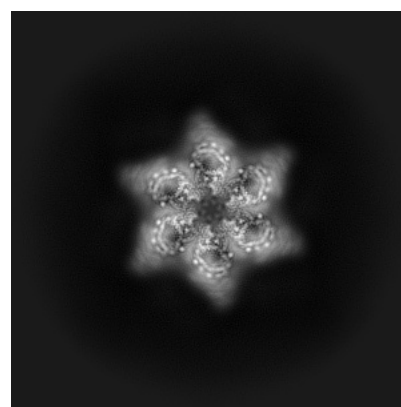
6.1.1 Primary map



X



Y

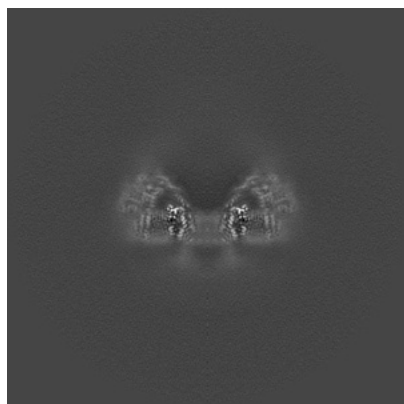


Z

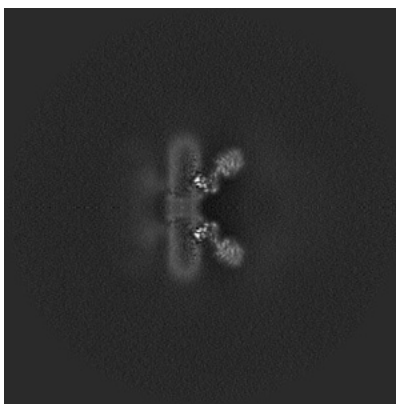
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

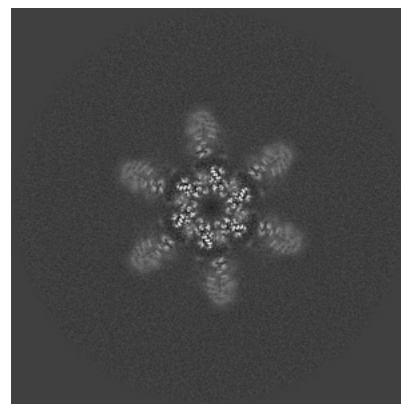
6.2.1 Primary map



X Index: 225



Y Index: 225

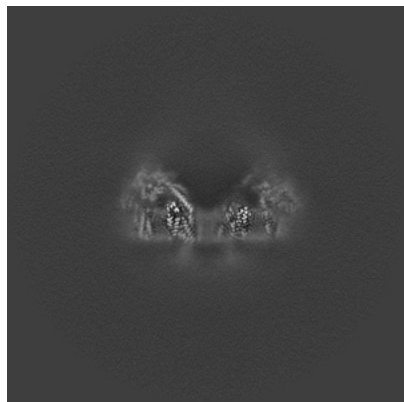


Z Index: 225

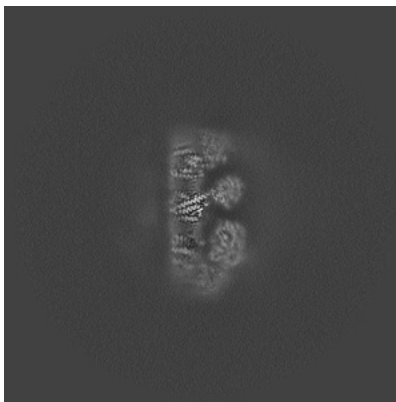
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

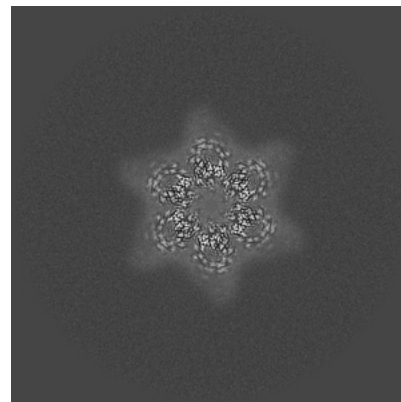
6.3.1 Primary map



X Index: 222



Y Index: 267

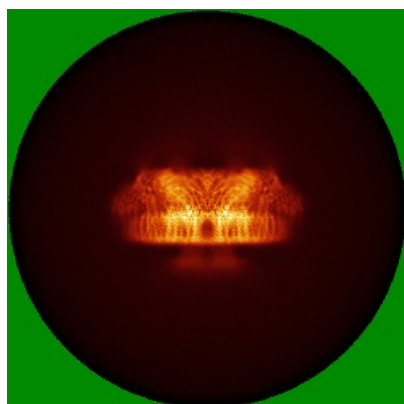


Z Index: 215

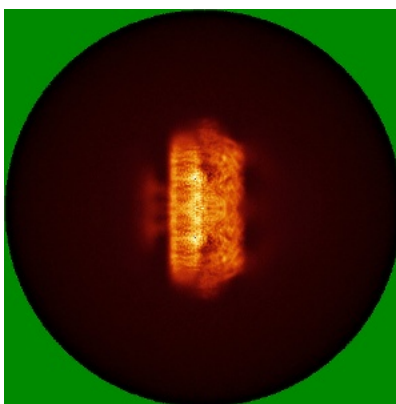
The images above show the largest variance slices of the map in three orthogonal directions.

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

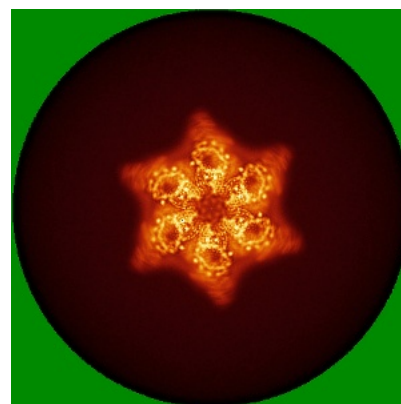
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

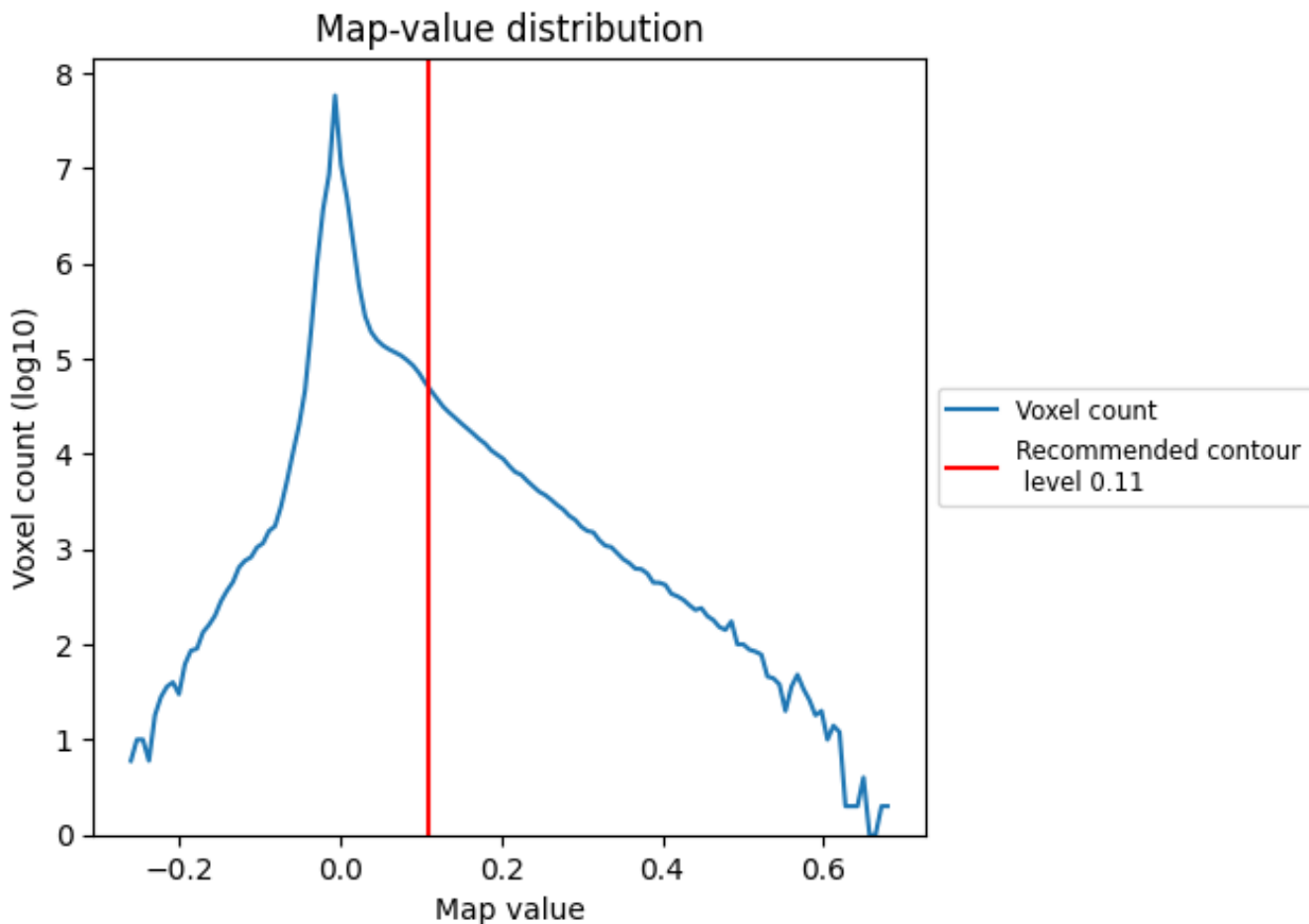
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

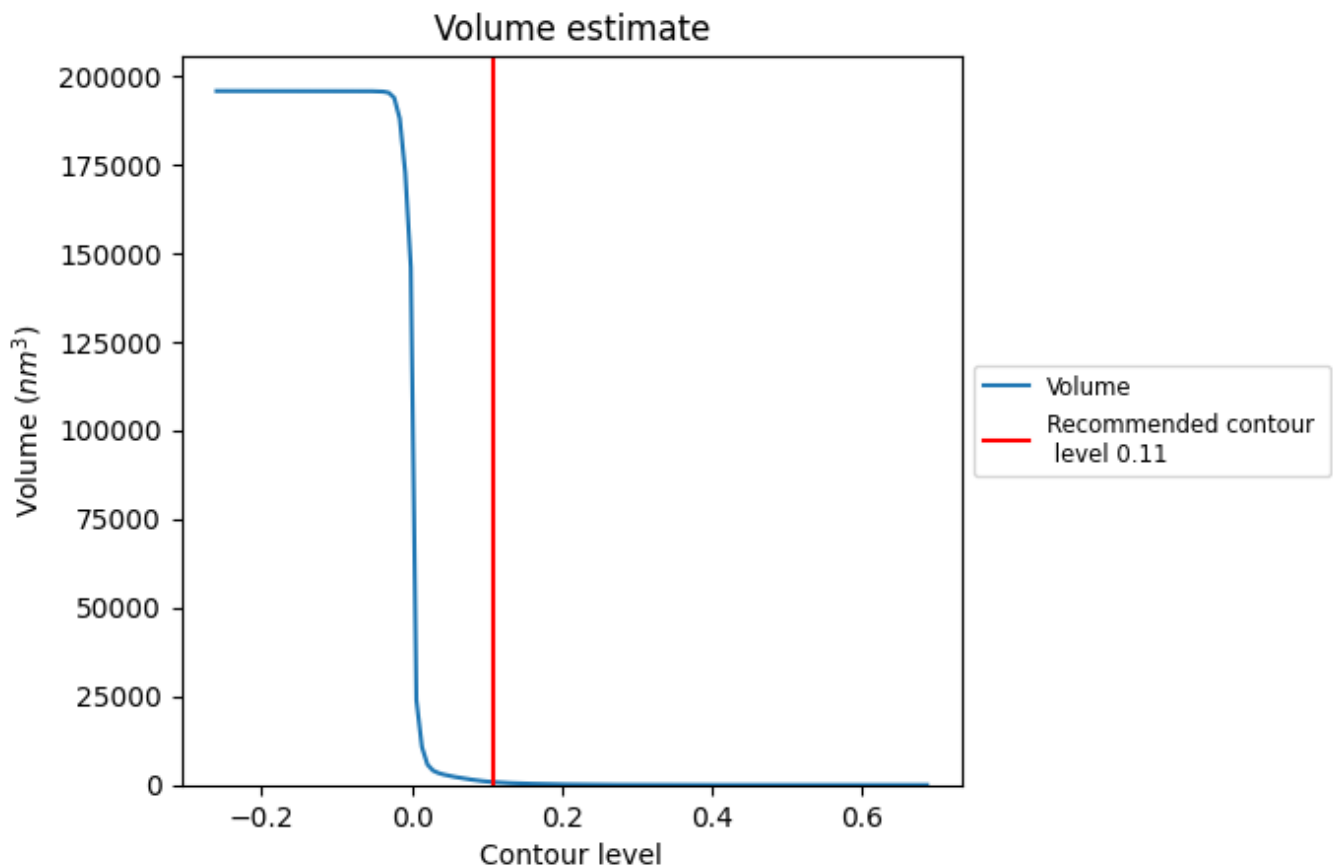
This section contains the results of statistical analysis of the map.

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.

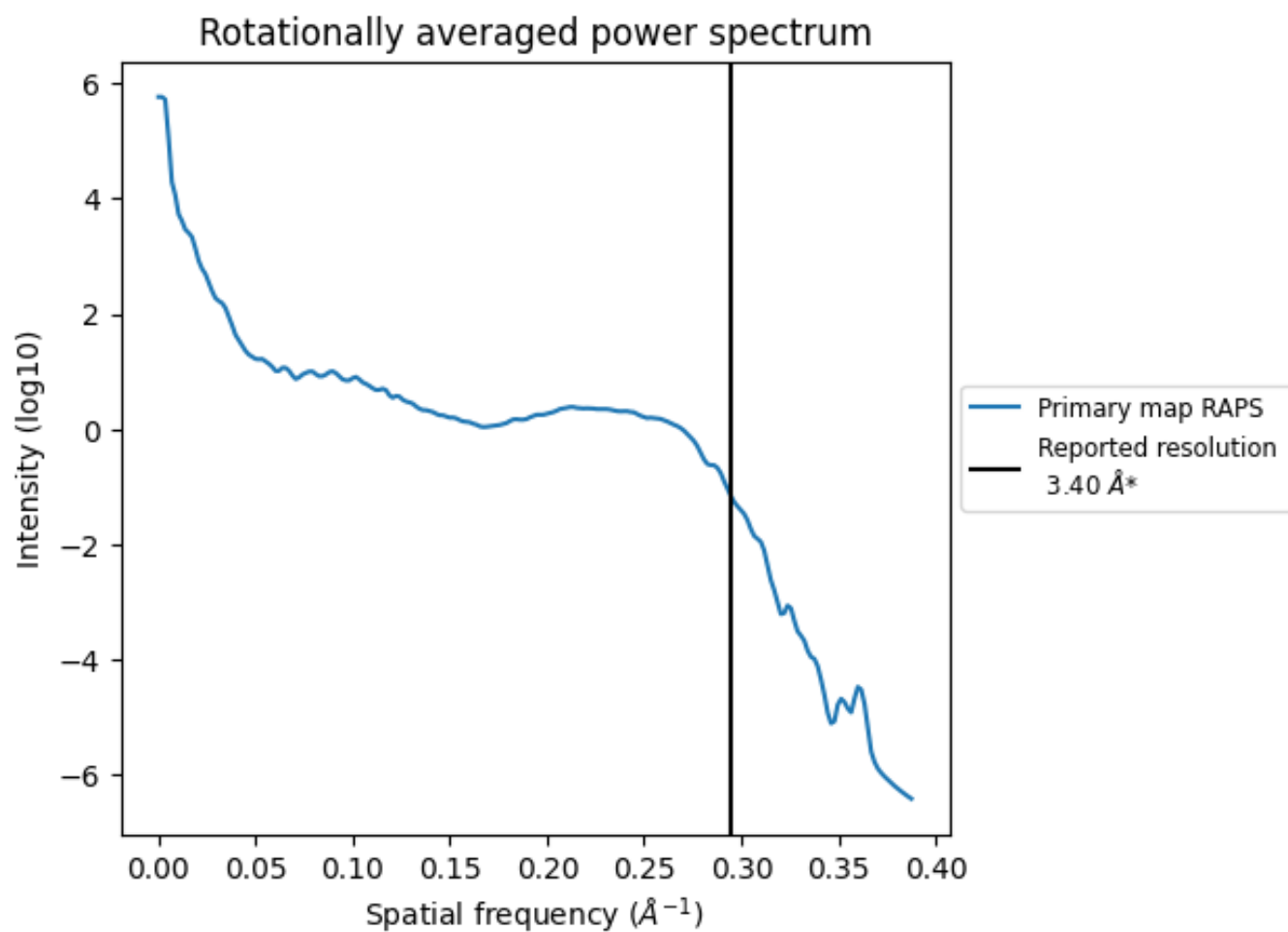
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 786 nm^3 ; this corresponds to an approximate mass of 710 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 i



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

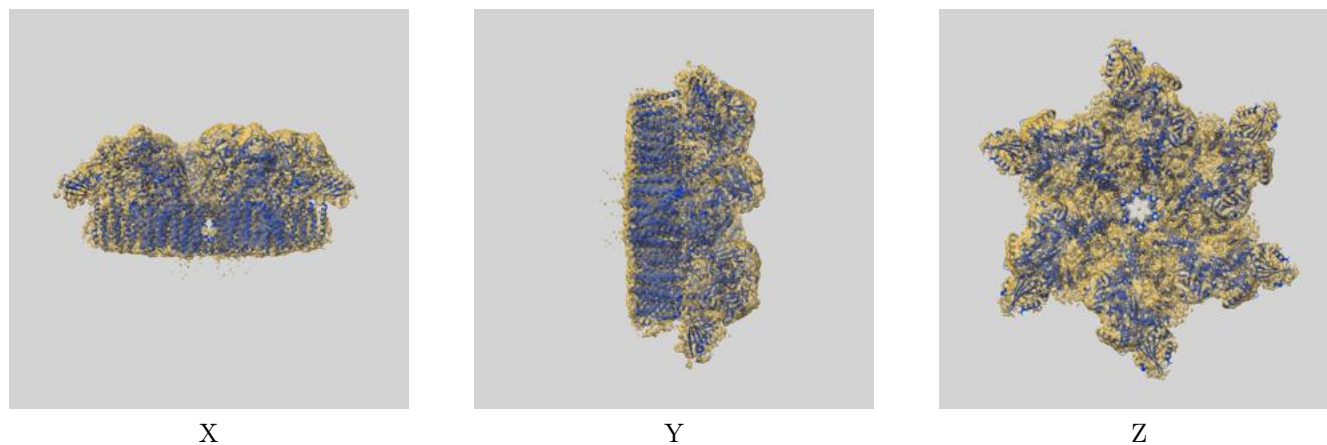
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

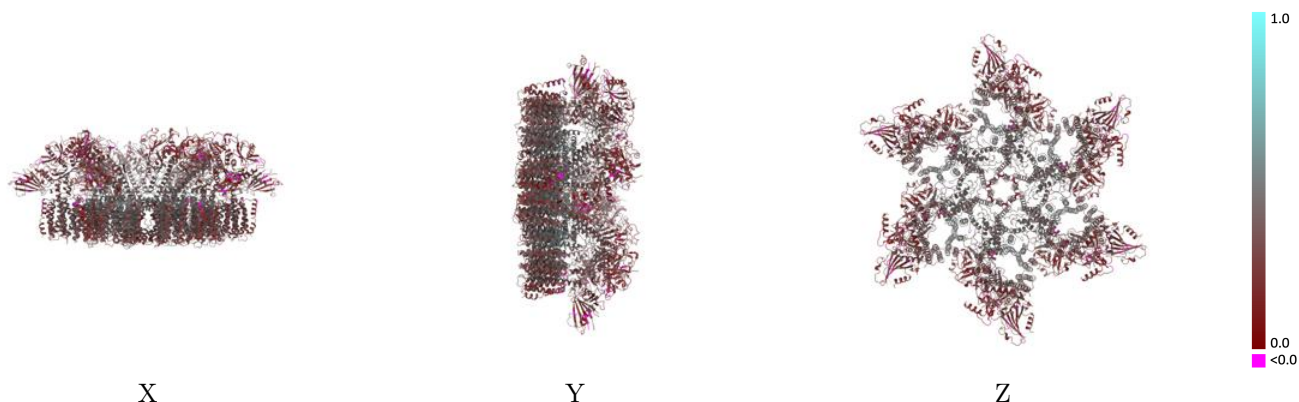
This section contains information regarding the fit between EMDB map EMD-12105 and PDB model 7B9S. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



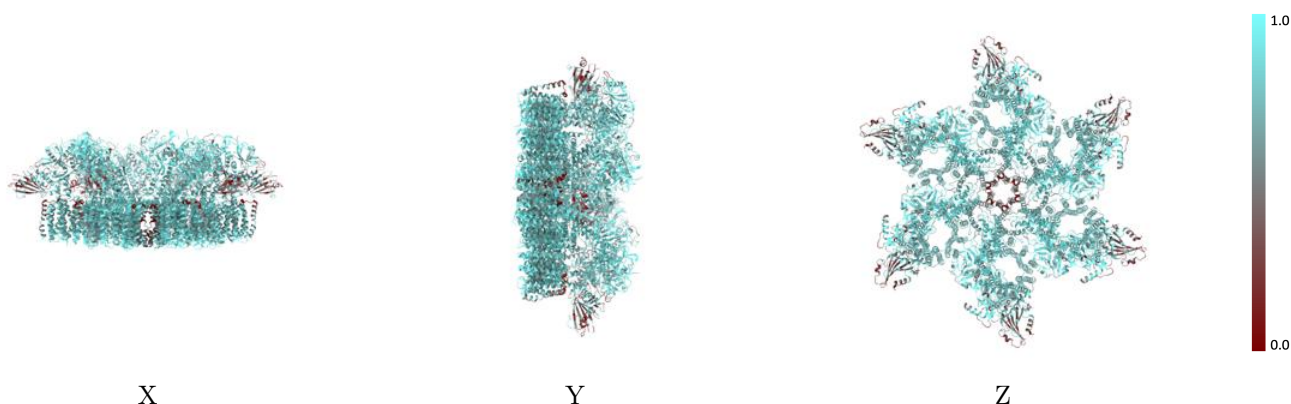
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



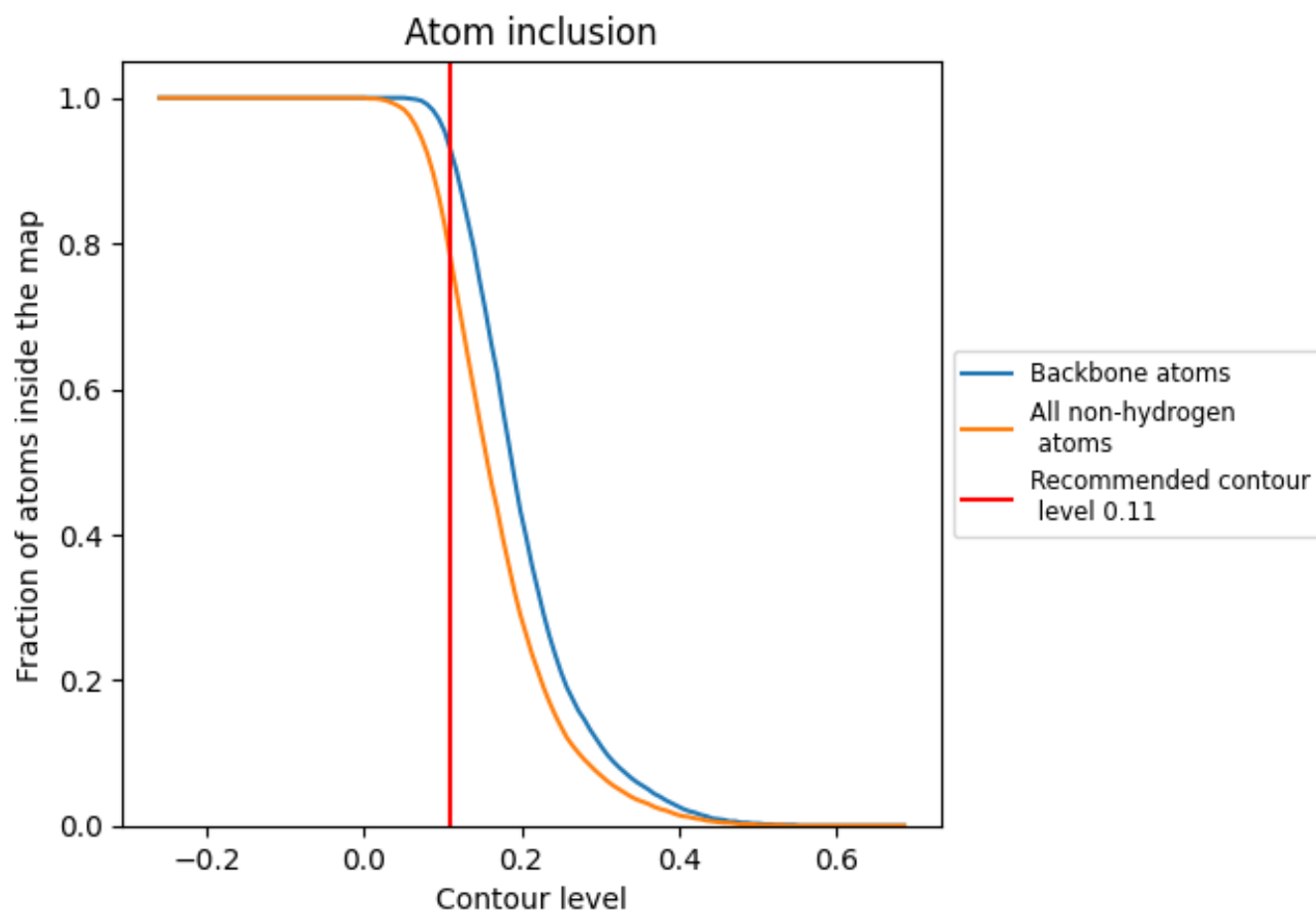
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 78% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.3320
1	 0.8850	 0.4460
2	 0.8080	 0.3130
3	 0.8250	 0.3550
4	 0.5700	 0.2620
5	 0.7750	 0.3340
A	 0.9000	 0.4490
B	 0.8700	 0.4440
C	 0.8070	 0.3130
D	 0.8240	 0.3570
E	 0.5660	 0.2660
F	 0.8060	 0.3140
G	 0.8250	 0.3550
H	 0.5660	 0.2630
I	 0.7780	 0.3340
J	 0.8780	 0.4300
K	 0.8070	 0.3140
L	 0.8220	 0.3540
M	 0.5620	 0.2630
N	 0.7770	 0.3350
O	 0.8870	 0.4410
P	 0.8070	 0.3150
Q	 0.8240	 0.3590
R	 0.5660	 0.2640
S	 0.7730	 0.3350
T	 0.8740	 0.4340
V	 0.8040	 0.3140
W	 0.8230	 0.3550
X	 0.7730	 0.3350
Y	 0.5670	 0.2630
Z	 0.7790	 0.3350

