



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 07:05 PM UTC

PDB ID : 7MO9 / pdb_00007mo9
EMDB ID : EMD-23921
Title : Cryo-EM map of the c-MET II/HGF I/HGF II (K4 and SPH) sub-complex
Authors : Uchikawa, E.; Chen, Z.M.; Xiao, G.Y.; Zhang, X.W.; Bai, X.C.
Deposited on : 2021-05-01
Resolution : 4.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

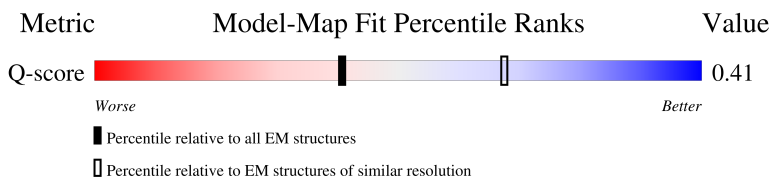
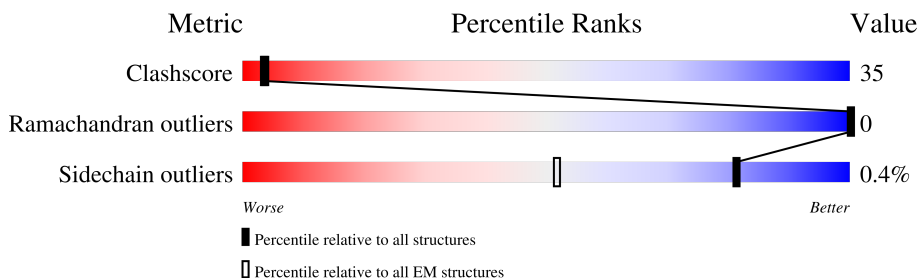
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	728	 13% 22% 65%
1	D	728	 19% 23% 58%
2	E	1390	 24% 25% 51%
3	B	6	 50% 67% 33%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9755 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.

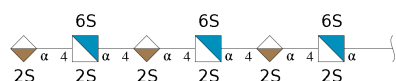
- Molecule 1 is a protein called Hepatocyte growth factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	254	Total	C	N	O	S	0	0
			2047	1283	370	373	21		
1	D	305	Total	C	N	O	S	0	0
			2287	1443	404	418	22		

- Molecule 2 is a protein called Hepatocyte growth factor receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	688	Total	C	N	O	S	0	0
			5324	3373	905	1006	40		

- Molecule 3 is an oligosaccharide called 2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	6	Total	C	N	O	S	0	0
			97	35	3	51	8		

VAL	PRO	GLY	ARG	CYS	ALA	ILE	PRO	ASN	ARG	PRO	GLY	ILE	PHE	ARG	VAL	ALA	TYR	TYR	ALA	LYS	ILE	ILE	LEU	THR	THR	LYS	VAL	PRO	GLN	SER
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● Molecule 1: Hepatocyte growth factor



MET	TRP	VAL	THR	LYS	ASN	THR	LEU	PRO	ALA	GLN	CYS	ALA	LEU	LEU	GLN	HIS	THR	VAL	ARG	LEU	ASN	LYS	HIS	LEU	LEU	LEU	LEU	LEU	LYS
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THR	LYS	VAL	THR	ASN	THR	ASP	ALA	ASP	GLN	CYS	ALA	LEU	LEU	GLN	ASP	THR	ARG	VAL	ASN	LYS	GLY	HIS	LEU	LEU	LEU	LEU	LEU	LEU	GLU
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ASN	LYS	ASP	TYR	THR	ILE	ARG	ASN	CYS	ASN	CYS	THR	GLY	ALA	LEU	GLN	ARG	SER	THR	VAL	ASN	GLY	THR	GLY	LEU	LEU	LEU	LEU	LEU	PRO
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ARG	GLY	GLU	GLU	GLY	GLY	PRO	TRP	TRP	CYS	THR	PHE	GLY	THR	THR	ASP	ASN	PRO	GLU	VAL	ARG	TYR	GLY	THR	GLY	VAL	VAL	CYS	SER	PRO
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HIS	ARG	HIS	HIS	PHE	LEU	PRO	GLU	GLY	GLN	ARG	THR	TYR	ASP	LYS	GLY	PHE	ASP	VAL	ASN	ASN	TYR	GLY	THR	THR	CYS	VAL	CYS	GLN	LEU
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GLU	THR	THR	THR	CYS	ILE	GLN	GLY	GLY	GLN	GLN	TRP	ASN	GLY	ILE	ASP	PRO	CYS	GLN	PRO	GLN	ARG	GLU	TRP	TRP	TRP	TRP	TRP	TRP	SER
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GLU	SER	PRO	TRP	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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ALA	SER	K434	K435	N436	N437	N438	N439	N440	N441	N442	N443	N444	N445	N446	N447	N448	N449	N450	N451	N452	N453	N454	N455	N456	N457	N458	N459	N460
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ARG	V495	V496	N497	N498	N499	N500	N501	N502	N503	N504	N505	N506	N507	N508	N509	N510	N511	N512	N513	N514	N515	N516	N517	N518	N519	N520	N521	N522
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H566	V567	S568	Q569	L570	P574	P575	P576	P577	P578	P579	P580	P581	P582	P583	P584	P585	P586	P587	P588	P589	P590	P591	P592	P593	P594	P595	P596	P597
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S643	Q644	H645	H646	K649	V650	T651	L652	N653	E654	S655	E656	I657	C658	E662	K663	I664	G665	S666	G667	P668	G669	E670	G671	P672	P673	P674	P675	P676
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H717	L720	L721	T722	TYR	LYS	VAL	GLN	SER
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● Molecule 2: Hepatocyte growth factor receptor



MET	LYS	ALA	PRO	PRO	ALA	VAL	LEU	ALA	ALA	PRO	GLY	ILE	LEU	VAL	LEU	LEU	PHE	THR	LEU	VAL	GLN	ARG	CYS	ASN	GLY	CYS	GLU	CYS	GLU
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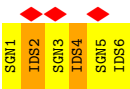


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- Molecule 3: 2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45471	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.077	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	291.6, 291.6, 291.6	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.36	0/2105	0.73	0/2840
1	D	0.37	0/2344	0.64	0/3196
2	E	0.45	1/5444 (0.0%)	0.69	3/7397 (0.0%)
All	All	0.41	1/9893 (0.0%)	0.69	3/13433 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	86	THR	CA-CB	-6.31	1.43	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	561	CYS	CA-C-N	7.47	131.10	120.49
2	E	561	CYS	C-N-CA	7.47	131.10	120.49
2	E	413	ARG	CB-CG-CD	-5.75	98.06	111.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2047	0	1933	179	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2287	0	2128	165	0
2	E	5324	0	5126	326	0
3	B	97	0	34	3	0
All	All	9755	0	9221	659	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 35.

All (659) 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:E:189:LYS:O	2:E:192:PHE:HB2	1.55	1.04
1:A:36:ARG:O	1:A:72:ASN:ND2	2.01	0.93
1:D:415:TRP:HB2	1:D:438:ASN:H	1.35	0.90
2:E:176:VAL:HA	2:E:217:ARG:HH21	1.35	0.90
2:E:232:GLN:NE2	2:E:415:GLU:OE2	2.08	0.86
2:E:374:PHE:O	2:E:404:ARG:NH1	2.09	0.86
1:D:657:ILE:HG12	1:D:708:ARG:HB2	1.57	0.85
2:E:382:ASN:HD22	2:E:422:THR:HG21	1.40	0.84
1:A:163:LEU:HD23	1:A:167:TYR:HE2	1.41	0.84
2:E:118:MET:HE1	2:E:179:ALA:HA	1.60	0.83
1:A:275:ASP:OD1	1:A:277:HIS:ND1	2.10	0.83
2:E:65:GLY:HA3	2:E:117:ASN:HD22	1.41	0.83
2:E:222:THR:OG1	2:E:224:ASP:OD1	1.98	0.82
2:E:424:LEU:HD21	2:E:426:ARG:HH21	1.46	0.80
2:E:428:ASP:OD1	2:E:430:PHE:N	2.13	0.80
1:A:243:HIS:NE2	1:A:245:PHE:O	2.14	0.80
1:D:389:GLN:N	1:D:467:SER:HG	1.80	0.80
1:A:159:GLU:OE2	2:E:426:ARG:NH1	2.15	0.79
2:E:62:ILE:HD13	2:E:503:LEU:HD21	1.64	0.79
1:D:550:ILE:HD11	1:D:555:GLY:HA2	1.63	0.78
1:D:552:ASP:OD1	1:D:556:ARG:NH2	2.15	0.78
2:E:666:TYR:HA	2:E:737:SER:HB3	1.64	0.78
1:D:653:ASN:OD1	1:D:654:GLU:N	2.16	0.77
1:A:165:SER:HA	1:A:168:ARG:HH12	1.49	0.76
1:D:530:LEU:HD11	1:D:579:LEU:HD11	1.67	0.76
1:A:85:LYS:NZ	1:A:100:PRO:O	2.18	0.76
1:A:147:ILE:HG21	1:A:193:ASN:HB2	1.68	0.76
1:D:534:GLN:NE2	2:E:190:ASP:O	2.19	0.76
2:E:378:VAL:O	2:E:404:ARG:NH2	2.20	0.75
2:E:327:ALA:HB3	2:E:449:ASP:HB2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:547:ARG:NH1	2:E:548:SER:H	1.85	0.75
1:A:223:MET:HE1	1:A:260:CYS:HB2	1.68	0.75
1:D:713:ALA:HA	1:D:716:ILE:HD12	1.67	0.75
2:E:269:LEU:HD11	2:E:387:GLN:HB3	1.68	0.74
2:E:412:ARG:NH2	2:E:414:ASP:O	2.21	0.74
1:D:640:GLU:O	1:D:644:GLN:NE2	2.18	0.73
1:A:82:PHE:HZ	1:A:98:TRP:HB2	1.53	0.72
1:A:183:GLU:OE1	1:A:185:GLY:N	2.20	0.72
1:A:96:CYS:SG	1:A:98:TRP:NE1	2.63	0.72
1:A:245:PHE:HA	1:A:250:TYR:HE2	1.54	0.72
2:E:217:ARG:HD3	2:E:228:PHE:HE1	1.54	0.72
1:D:602:TYR:HB2	1:D:714:LYS:HD3	1.72	0.71
2:E:358:ASP:HA	2:E:438:LEU:HB2	1.72	0.71
1:D:392:TYR:H	1:D:469:CYS:HB2	1.55	0.71
1:A:43:LYS:HB3	1:A:120:GLU:HB2	1.73	0.71
2:E:537:GLN:O	2:E:547:ARG:NH1	2.24	0.71
1:A:246:LEU:HG	1:A:249:ARG:HH11	1.56	0.71
1:D:524:ILE:HG22	1:D:525:LYS:HD2	1.71	0.71
1:A:177:CYS:C	1:A:178:ARG:HD3	2.15	0.70
1:D:534:GLN:HE22	2:E:190:ASP:HB3	1.55	0.70
2:E:386:LEU:HD22	2:E:389:PHE:HB3	1.74	0.70
2:E:590:PHE:HB3	2:E:597:ASP:HB2	1.73	0.70
1:D:513:TYR:OH	1:D:514:ARG:NH2	2.25	0.70
1:A:160:HIS:HB2	1:A:197:ARG:HH22	1.57	0.70
1:D:541:LEU:HD23	1:D:567:VAL:HG12	1.74	0.69
1:D:507:TRP:CD1	1:D:597:ILE:HB	2.28	0.69
1:A:227:GLU:HG3	1:A:284:ALA:HB2	1.75	0.69
1:A:88:VAL:HG23	1:A:99:PHE:CE2	2.28	0.69
1:D:460:PRO:HB2	1:D:461:TRP:HD1	1.58	0.69
1:D:680:GLU:HA	1:D:685:ARG:HA	1.75	0.69
2:E:563:PRO:O	2:E:647:THR:OG1	2.11	0.69
1:A:163:LEU:HD12	1:A:163:LEU:H	1.57	0.68
2:E:571:ASN:O	2:E:653:SER:OG	2.08	0.68
2:E:267:GLU:HG2	2:E:275:HIS:CD2	2.28	0.68
2:E:671:GLY:HA3	2:E:713:ALA:HA	1.75	0.68
1:D:540:ASP:OD1	1:D:541:LEU:N	2.26	0.68
1:A:63:LYS:HD2	1:A:95:GLN:HE22	1.59	0.68
1:A:88:VAL:HG23	1:A:99:PHE:HE2	1.57	0.68
1:A:82:PHE:HD2	1:A:100:PRO:HB3	1.59	0.68
1:D:454:THR:OG1	1:D:459:ILE:O	2.11	0.68
1:D:606:ILE:HD12	1:D:607:PRO:HD2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:113:LYS:HG3	2:E:114:ASP:H	1.59	0.67
2:E:91:GLU:O	2:E:110:GLY:N	2.26	0.67
2:E:343:PHE:HE2	2:E:444:THR:HG21	1.59	0.67
1:A:234:ARG:NH2	1:A:236:ASP:OD2	2.27	0.67
1:D:678:VAL:HA	1:D:687:VAL:HA	1.77	0.67
2:E:498:GLN:O	2:E:516:ASN:ND2	2.28	0.67
2:E:27:LYS:H	2:E:27:LYS:HD2	1.60	0.66
2:E:332:GLN:OE1	2:E:469:ARG:N	2.27	0.66
1:A:144:LYS:HG2	1:A:202:ASP:HB3	1.77	0.66
1:D:446:ASP:OD1	1:D:447:ALA:N	2.27	0.66
2:E:697:CYS:HB3	2:E:712:PRO:HD3	1.77	0.66
2:E:231:ASP:OD1	2:E:232:GLN:N	2.29	0.66
1:D:561:CYS:HB3	1:D:593:PHE:CD2	2.31	0.66
2:E:60:HIS:HA	2:E:75:GLU:OE2	1.94	0.66
1:D:524:ILE:HD12	1:D:599:LEU:HD21	1.79	0.65
2:E:211:LEU:O	2:E:212:HIS:ND1	2.29	0.65
2:E:675:LEU:O	2:E:708:GLU:HA	1.96	0.65
2:E:247:ILE:HG22	2:E:265:GLN:HB3	1.78	0.65
1:A:223:MET:HE2	1:A:285:ILE:HD11	1.79	0.65
2:E:26:CYS:N	2:E:584:CYS:SG	2.70	0.65
1:A:70:CYS:HB3	1:A:98:TRP:NE1	2.12	0.64
1:D:657:ILE:CG1	1:D:708:ARG:HB2	2.25	0.64
1:D:670:GLU:OE2	2:E:221:GLU:N	2.29	0.64
2:E:267:GLU:HG2	2:E:275:HIS:HD2	1.59	0.64
2:E:415:GLU:CD	2:E:415:GLU:H	2.05	0.64
1:D:540:ASP:OD1	1:D:542:LYS:N	2.27	0.64
2:E:119:ALA:HB3	2:E:133:CYS:HB2	1.80	0.64
2:E:213:SER:OG	2:E:235:ILE:O	2.13	0.64
2:E:675:LEU:HD11	2:E:711:THR:HB	1.79	0.64
1:A:188:TRP:HA	1:A:200:VAL:HA	1.79	0.64
2:E:129:GLN:OE1	2:E:143:ARG:NH2	2.22	0.64
2:E:299:ILE:HG22	2:E:313:VAL:HG12	1.80	0.64
2:E:74:ASN:OD1	2:E:75:GLU:N	2.31	0.64
1:A:90:ASP:HB3	1:A:93:ARG:HG2	1.79	0.63
1:D:538:SER:O	1:D:544:TYR:OH	2.11	0.63
2:E:562:LEU:HD12	2:E:563:PRO:HD2	1.79	0.63
2:E:49:GLU:N	2:E:49:GLU:OE1	2.31	0.63
1:A:238:GLN:NE2	1:A:243:HIS:O	2.26	0.63
1:D:606:ILE:HG12	1:D:636:ILE:HG13	1.80	0.63
1:A:63:LYS:HD2	1:A:95:GLN:NE2	2.14	0.62
2:E:68:ASN:HB3	2:E:87:GLY:HA2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ILE:HG12	1:A:109:LYS:HZ3	1.64	0.62
2:E:261:PHE:HB2	2:E:279:ILE:HB	1.81	0.62
2:E:494:HIS:CD2	2:E:497:ASN:HA	2.34	0.62
2:E:239:PRO:HA	2:E:242:ARG:NE	2.15	0.62
1:A:85:LYS:HB2	1:A:124:TYR:CE2	2.35	0.62
1:D:496:VAL:O	1:D:666:SER:OG	2.13	0.62
1:A:88:VAL:HG11	1:A:116:PHE:HB3	1.81	0.62
1:D:639:ASN:HB3	1:D:652:LEU:HD22	1.82	0.62
1:A:53:ILE:HG12	1:A:109:LYS:NZ	2.15	0.62
1:D:540:ASP:HA	2:E:413:ARG:HH21	1.64	0.62
1:A:158:HIS:CD2	1:A:197:ARG:HA	2.35	0.61
1:D:497:ASN:ND2	1:D:665:GLY:O	2.33	0.61
2:E:230:THR:O	2:E:233:SER:OG	2.14	0.61
1:D:416:ASP:HA	1:D:419:MET:SD	2.40	0.61
1:D:612:CYS:HB2	1:D:679:CYS:HA	1.81	0.61
2:E:220:LYS:HE3	2:E:227:MET:SD	2.40	0.61
2:E:362:MET:HG2	2:E:430:PHE:CE2	2.35	0.61
2:E:46:PHE:HE2	2:E:80:LYS:HB2	1.65	0.61
2:E:244:SER:HB3	2:E:266:ARG:HH22	1.65	0.61
1:A:231:ILE:O	1:A:274:LEU:HD22	2.00	0.61
1:A:66:THR:HG23	1:A:69:GLN:H	1.65	0.61
1:A:150:GLN:NE2	1:A:154:SER:O	2.33	0.61
1:A:207:SER:OG	1:A:208:GLU:OE2	2.16	0.61
1:A:250:TYR:HB3	1:A:253:LYS:HD3	1.81	0.61
1:A:262:ASN:ND2	1:A:269:PRO:HA	2.16	0.61
1:A:85:LYS:HZ2	1:A:100:PRO:C	2.09	0.61
1:A:188:TRP:HB3	1:A:200:VAL:HG22	1.82	0.61
1:A:99:PHE:HB3	1:A:101:PHE:CE1	2.35	0.61
1:D:508:MET:HA	1:D:508:MET:HE3	1.83	0.61
1:A:72:ASN:HA	1:A:75:THR:HG22	1.83	0.60
1:D:422:LEU:O	1:D:426:ILE:N	2.34	0.60
1:A:220:ARG:HH21	1:A:261:ARG:HG3	1.67	0.60
1:A:241:HIS:HB3	1:A:279:ARG:HH21	1.65	0.60
2:E:503:LEU:HB3	2:E:510:ILE:HD11	1.81	0.60
1:A:87:PHE:HB2	1:A:98:TRP:HD1	1.65	0.60
1:D:697:CYS:HB2	2:E:221:GLU:OE1	2.02	0.60
1:D:656:GLU:O	1:D:657:ILE:HD13	2.02	0.60
2:E:196:PHE:CD1	2:E:216:VAL:HG22	2.37	0.60
1:A:108:VAL:C	1:A:109:LYS:HD3	2.28	0.59
1:A:259:TYR:HB3	1:A:261:ARG:NH1	2.16	0.59
2:E:149:ASN:OD1	2:E:150:HIS:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:220:LYS:HG2	2:E:225:GLY:C	2.26	0.59
1:A:219:TYR:CZ	1:A:221:GLY:HA3	2.37	0.59
1:A:37:ASN:OD1	1:A:38:THR:N	2.36	0.59
2:E:76:GLU:CD	2:E:76:GLU:H	2.10	0.59
1:A:73:ARG:HH22	3:B:2:IDS:H4	1.67	0.59
2:E:590:PHE:CD1	2:E:643:GLY:HA3	2.37	0.59
2:E:403:LEU:HD22	2:E:406:SER:HB2	1.85	0.59
1:A:63:LYS:NZ	1:A:94:LYS:HB2	2.17	0.59
1:D:452:CYS:SG	1:D:453:TYR:N	2.76	0.59
1:D:579:LEU:HD12	1:D:580:VAL:H	1.68	0.59
2:E:238:LEU:HD12	2:E:240:GLU:H	1.68	0.59
1:A:150:GLN:NE2	1:A:156:ILE:O	2.35	0.58
1:D:695:ARG:NH1	2:E:125:TYR:HE1	2.00	0.58
1:D:712:TYR:O	1:D:716:ILE:HG13	2.03	0.58
2:E:46:PHE:CE2	2:E:80:LYS:HB2	2.37	0.58
2:E:341:ILE:HD13	2:E:366:PRO:HA	1.85	0.58
1:D:569:GLN:NE2	1:D:570:LEU:O	2.37	0.58
1:A:164:PRO:HA	1:A:172:LEU:HD21	1.84	0.58
1:D:640:GLU:O	1:D:643:SER:OG	2.18	0.58
2:E:69:TYR:CE1	2:E:85:LYS:HD3	2.38	0.58
2:E:623:LYS:HA	2:E:623:LYS:HE2	1.84	0.58
1:A:73:ARG:HB3	1:A:80:LEU:HD21	1.84	0.58
1:A:215:ASN:HD21	1:A:218:SER:H	1.51	0.58
2:E:595:LYS:NZ	2:E:596:PHE:O	2.29	0.58
1:A:87:PHE:O	1:A:119:TYR:HB2	2.02	0.58
1:A:102:ASN:OD1	1:A:104:MET:N	2.31	0.58
2:E:358:ASP:OD1	2:E:438:LEU:N	2.36	0.58
1:A:183:GLU:CD	1:A:185:GLY:H	2.11	0.57
2:E:220:LYS:HG2	2:E:225:GLY:O	2.04	0.57
2:E:360:SER:OG	2:E:439:LEU:HG	2.04	0.57
1:D:554:HIS:HB2	1:D:556:ARG:HE	1.69	0.57
1:D:717:HIS:O	1:D:720:ILE:HG22	2.05	0.57
2:E:196:PHE:HD1	2:E:216:VAL:HG22	1.68	0.57
2:E:275:HIS:HE1	2:E:277:ARG:NE	2.02	0.57
2:E:588:PHE:HB2	2:E:619:MET:HA	1.87	0.57
1:A:234:ARG:HE	1:A:237:HIS:CE1	2.23	0.57
1:D:547:TRP:HD1	1:D:564:VAL:HA	1.69	0.57
2:E:382:ASN:ND2	2:E:422:THR:HG21	2.18	0.57
2:E:591:ARG:HG3	2:E:596:PHE:HE1	1.69	0.57
2:E:619:MET:SD	2:E:619:MET:N	2.78	0.57
2:E:113:LYS:HG3	2:E:114:ASP:N	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:700:LYS:N	2:E:708:GLU:O	2.38	0.56
2:E:730:ASN:CG	2:E:731:ARG:H	2.12	0.56
1:D:556:ARG:NH2	1:D:626:ASP:O	2.38	0.56
1:D:600:PRO:HG3	1:D:709:VAL:HG23	1.88	0.56
2:E:362:MET:HE2	2:E:429:LEU:HD12	1.88	0.56
2:E:592:ARG:HB3	2:E:595:LYS:O	2.05	0.56
2:E:659:ILE:HD11	2:E:677:LEU:HD12	1.87	0.56
1:D:643:SER:OG	1:D:644:GLN:NE2	2.39	0.56
2:E:274:PHE:CE2	2:E:354:ALA:HB2	2.41	0.56
2:E:400:ARG:NH1	2:E:414:ASP:HB3	2.20	0.56
1:D:591:ASP:OD1	1:D:593:PHE:N	2.35	0.56
2:E:317:LEU:HA	2:E:346:PHE:HD1	1.71	0.56
2:E:460:GLY:HA3	2:E:482:ASP:O	2.05	0.56
2:E:703:SER:HB3	2:E:706:ILE:HG22	1.87	0.56
1:A:70:CYS:HA	1:A:73:ARG:HG2	1.88	0.56
1:A:177:CYS:HB2	1:A:189:CYS:HB3	1.88	0.56
2:E:267:GLU:OE2	2:E:273:THR:HG23	2.06	0.55
2:E:599:LYS:NZ	2:E:600:LYS:HE2	2.21	0.55
2:E:611:THR:OG1	2:E:625:THR:O	2.23	0.55
1:D:511:LEU:HD11	1:D:536:PHE:HE1	1.71	0.55
2:E:101:CYS:HB2	2:E:104:LYS:HG3	1.88	0.55
2:E:123:ASP:OD2	2:E:129:GLN:NE2	2.39	0.55
2:E:294:MET:HE1	2:E:373:PHE:HB3	1.88	0.55
1:D:568:SER:OG	1:D:583:LYS:O	2.18	0.55
1:A:213:THR:O	1:A:216:GLY:N	2.39	0.55
1:D:626:ASP:OD1	1:D:626:ASP:N	2.40	0.55
1:A:215:ASN:OD1	1:A:218:SER:OG	2.24	0.55
2:E:266:ARG:NH1	2:E:269:LEU:O	2.40	0.55
2:E:394:HIS:NE2	2:E:396:HIS:CE1	2.75	0.55
1:A:125:ILE:HD12	1:A:125:ILE:H	1.70	0.54
1:A:190:PHE:CD1	1:A:198:TYR:HB3	2.41	0.54
2:E:544:LYS:NZ	2:E:546:VAL:HG21	2.22	0.54
1:A:259:TYR:HB3	1:A:261:ARG:HH12	1.71	0.54
2:E:726:ILE:C	2:E:728:LEU:H	2.15	0.54
1:D:396:GLY:H	1:D:445:ASP:HA	1.71	0.54
1:D:560:LYS:HD3	1:D:560:LYS:N	2.23	0.54
2:E:35:MET:HA	2:E:524:GLN:OE1	2.08	0.54
1:A:220:ARG:NH2	1:A:261:ARG:HG3	2.23	0.54
1:A:223:MET:SD	1:A:225:HIS:N	2.75	0.54
1:D:396:GLY:N	1:D:445:ASP:OD1	2.40	0.54
2:E:526:CYS:HA	2:E:540:TRP:CE3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:PHE:CE1	1:A:96:CYS:HB3	2.42	0.54
1:A:246:LEU:HB2	1:A:249:ARG:HD2	1.89	0.54
2:E:730:ASN:OD1	2:E:731:ARG:N	2.38	0.54
1:A:80:LEU:HD13	1:A:98:TRP:CE3	2.43	0.54
1:A:34:LYS:HG3	1:A:35:ARG:H	1.72	0.54
1:A:70:CYS:HB3	1:A:98:TRP:HE1	1.71	0.54
1:A:163:LEU:HD23	1:A:167:TYR:CE2	2.33	0.54
2:E:181:GLY:N	2:E:200:THR:OG1	2.41	0.54
2:E:674:LEU:HD12	2:E:709:CYS:O	2.08	0.54
1:A:238:GLN:HG3	1:A:242:ARG:HG2	1.89	0.54
1:D:688:LEU:O	1:D:709:VAL:HG22	2.08	0.54
2:E:540:TRP:CD1	2:E:542:HIS:H	2.27	0.53
2:E:559:GLN:OE1	2:E:559:GLN:N	2.40	0.53
2:E:659:ILE:HD12	2:E:678:THR:O	2.08	0.53
1:A:171:ASP:O	1:A:178:ARG:NH1	2.41	0.53
1:D:497:ASN:HD22	1:D:666:SER:HA	1.73	0.53
1:D:574:PRO:O	1:D:577:SER:OG	2.17	0.53
1:D:539:ARG:HH11	1:D:539:ARG:HG2	1.72	0.53
1:A:246:LEU:O	1:A:249:ARG:HG2	2.08	0.53
1:D:708:ARG:HH21	1:D:711:TYR:HB2	1.73	0.53
1:D:415:TRP:HB2	1:D:438:ASN:N	2.16	0.53
1:D:512:ARG:HG3	1:D:512:ARG:HH11	1.73	0.53
1:D:564:VAL:C	1:D:565:LEU:HD12	2.34	0.53
1:A:273:THR:OG1	1:A:278:THR:O	2.26	0.53
2:E:80:LYS:NZ	2:E:83:GLU:HB2	2.24	0.53
2:E:241:PHE:CE2	2:E:269:LEU:HD13	2.43	0.53
2:E:267:GLU:CG	2:E:275:HIS:CD2	2.92	0.53
2:E:291:TYR:HB3	2:E:417:ARG:HD2	1.91	0.53
1:D:508:MET:HG3	1:D:629:LEU:HD11	1.90	0.53
2:E:245:TYR:H	2:E:266:ARG:NH2	2.07	0.53
1:D:561:CYS:HB3	1:D:593:PHE:HD2	1.74	0.52
1:A:136:TYR:C	1:A:137:LYS:HD3	2.34	0.52
1:D:695:ARG:NH1	2:E:125:TYR:CE1	2.77	0.52
2:E:394:HIS:NE2	2:E:396:HIS:HE1	2.07	0.52
1:A:137:LYS:HD2	1:A:171:ASP:HB2	1.90	0.52
2:E:415:GLU:OE1	2:E:415:GLU:N	2.38	0.52
2:E:716:ILE:HG21	2:E:720:PHE:HZ	1.74	0.52
1:A:160:HIS:HB2	1:A:197:ARG:NH2	2.25	0.52
2:E:96:PHE:HB2	2:E:99:GLN:HG2	1.92	0.52
2:E:261:PHE:O	2:E:262:LEU:HD23	2.10	0.52
1:A:53:ILE:H	1:A:109:LYS:NZ	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ARG:HD2	1:A:95:GLN:HB3	1.92	0.52
1:D:508:MET:HG3	1:D:629:LEU:CD1	2.40	0.52
2:E:673:THR:H	2:E:711:THR:HG22	1.74	0.52
2:E:225:GLY:O	2:E:226:PHE:HD1	1.93	0.52
2:E:417:ARG:HD3	2:E:417:ARG:N	2.24	0.52
1:D:442:ASN:HB2	1:D:451:TRP:CD1	2.45	0.52
1:D:653:ASN:H	1:D:656:GLU:CD	2.18	0.51
2:E:277:ARG:NH1	2:E:293:GLU:OE1	2.43	0.51
2:E:339:ASP:OD2	2:E:368:LYS:HD3	2.10	0.51
2:E:677:LEU:O	2:E:706:ILE:HD12	2.10	0.51
2:E:235:ILE:HD11	2:E:417:ARG:NH1	2.24	0.51
2:E:546:VAL:HG12	2:E:547:ARG:O	2.10	0.51
1:A:42:PHE:HD2	1:A:119:TYR:HB3	1.75	0.51
2:E:117:ASN:HD21	2:E:120:LEU:HB2	1.76	0.51
2:E:247:ILE:HG22	2:E:265:GLN:CB	2.41	0.51
2:E:422:THR:O	2:E:422:THR:OG1	2.28	0.51
1:D:547:TRP:HA	1:D:563:GLN:O	2.10	0.51
1:D:579:LEU:HD12	1:D:580:VAL:N	2.25	0.51
1:D:714:LYS:HE3	1:D:714:LYS:HA	1.91	0.51
2:E:526:CYS:O	2:E:530:LEU:HG	2.11	0.51
1:D:543:ASP:OD1	1:D:543:ASP:N	2.37	0.51
1:A:176:TYR:HB2	1:A:178:ARG:HE	1.76	0.51
1:D:422:LEU:HG	1:D:426:ILE:HB	1.93	0.51
2:E:202:ASN:OD1	2:E:203:SER:N	2.44	0.51
2:E:382:ASN:HD22	2:E:422:THR:CG2	2.18	0.51
2:E:201:ILE:HB	2:E:206:PHE:HE1	1.75	0.51
2:E:253:PHE:CE1	2:E:260:TYR:HB2	2.46	0.51
1:D:717:HIS:O	1:D:721:LEU:HG	2.11	0.50
2:E:69:TYR:HB3	2:E:71:TYR:CE1	2.46	0.50
2:E:77:ASP:HB2	2:E:79:GLN:HG2	1.92	0.50
1:A:40:HIS:HD2	1:A:231:ILE:HG21	1.76	0.50
2:E:218:ARG:HG2	2:E:219:LEU:N	2.22	0.50
2:E:359:ARG:HG2	2:E:359:ARG:HH11	1.75	0.50
2:E:720:PHE:O	2:E:735:ILE:HA	2.11	0.50
2:E:690:ILE:HD13	2:E:724:LEU:HD12	1.92	0.50
2:E:445:PHE:CE1	2:E:452:ILE:HB	2.47	0.50
2:E:494:HIS:NE2	2:E:497:ASN:HA	2.26	0.50
2:E:595:LYS:HD2	2:E:596:PHE:N	2.26	0.50
1:A:142:ILE:HD11	1:A:146:GLY:C	2.37	0.50
2:E:296:LEU:HD22	2:E:365:PHE:CE2	2.46	0.50
1:A:43:LYS:NZ	1:A:45:SER:HB3	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:281:PHE:CE2	2:E:288:LEU:HD23	2.47	0.50
2:E:566:TYR:N	2:E:584:CYS:O	2.42	0.50
1:D:402:ASN:HA	1:D:439:TYR:CD2	2.47	0.50
1:A:80:LEU:HD12	1:A:84:CYS:SG	2.52	0.49
1:A:93:ARG:HH21	1:A:96:CYS:HA	1.77	0.49
2:E:170:SER:HB2	2:E:171:GLN:NE2	2.27	0.49
2:E:174:ASP:O	2:E:176:VAL:HG23	2.12	0.49
1:D:510:SER:OG	1:D:547:TRP:HB2	2.11	0.49
2:E:224:ASP:OD1	2:E:224:ASP:N	2.45	0.49
2:E:395:GLU:HG3	2:E:396:HIS:N	2.26	0.49
2:E:452:ILE:HD13	2:E:466:VAL:HA	1.94	0.49
1:D:568:SER:HB3	1:D:585:ALA:HA	1.93	0.49
2:E:28:GLU:CD	2:E:28:GLU:H	2.20	0.49
2:E:56:ILE:HG23	2:E:63:PHE:HD2	1.77	0.49
1:A:38:THR:H	1:A:39:ILE:HD12	1.78	0.49
2:E:271:ALA:O	2:E:273:THR:HG22	2.12	0.49
2:E:544:LYS:HZ3	2:E:546:VAL:HG21	1.78	0.49
2:E:239:PRO:HA	2:E:242:ARG:CZ	2.41	0.49
2:E:659:ILE:HD11	2:E:677:LEU:HB3	1.95	0.49
2:E:194:ASN:HA	2:E:217:ARG:O	2.13	0.49
2:E:638:ILE:HG22	2:E:649:TYR:HD2	1.78	0.49
1:A:136:TYR:O	1:A:137:LYS:HD3	2.13	0.49
1:D:552:ASP:OD2	1:D:555:GLY:N	2.46	0.49
1:D:552:ASP:HA	1:D:627:GLY:O	2.12	0.49
1:A:88:VAL:HG22	1:A:118:LEU:HA	1.95	0.49
1:D:581:LEU:HD23	1:D:715:TRP:CH2	2.47	0.49
1:D:694:GLY:O	1:D:696:GLY:N	2.45	0.49
1:D:708:ARG:HE	1:D:711:TYR:HB2	1.77	0.49
2:E:127:ASP:O	2:E:129:GLN:HG3	2.12	0.49
2:E:550:GLU:OE1	2:E:550:GLU:N	2.46	0.49
2:E:560:ILE:HA	2:E:644:HIS:CE1	2.48	0.49
2:E:676:THR:HA	2:E:707:LEU:O	2.12	0.49
1:A:49:THR:HG23	1:A:111:GLU:OE1	2.13	0.48
1:A:62:LYS:HG3	1:A:64:VAL:HG23	1.95	0.48
1:D:406:THR:HG22	1:D:410:LEU:O	2.13	0.48
1:D:679:CYS:O	1:D:686:MET:N	2.35	0.48
2:E:284:ILE:HG22	2:E:286:SER:H	1.78	0.48
2:E:524:GLN:O	2:E:540:TRP:HH2	1.96	0.48
1:A:159:GLU:N	1:A:159:GLU:OE1	2.46	0.48
2:E:335:ALA:HA	2:E:368:LYS:NZ	2.27	0.48
1:D:695:ARG:HH12	2:E:125:TYR:HE1	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:218:ARG:CD	2:E:227:MET:HE2	2.43	0.48
1:A:109:LYS:HB2	1:A:111:GLU:OE2	2.13	0.48
1:D:590:LEU:HD13	1:D:594:VAL:HG23	1.95	0.48
1:D:669:CYS:N	1:D:672:ASP:OD2	2.35	0.48
2:E:163:SER:OG	2:E:174:ASP:OD2	2.30	0.48
2:E:590:PHE:HD1	2:E:643:GLY:HA3	1.78	0.48
1:A:39:ILE:HD12	1:A:39:ILE:H	1.79	0.48
1:D:702:ARG:HG3	1:D:702:ARG:HH11	1.78	0.48
2:E:583:ILE:HB	2:E:622:LEU:HB2	1.96	0.48
1:A:227:GLU:CD	1:A:268:ARG:HH21	2.21	0.48
1:D:519:CYS:HB3	1:D:673:TYR:O	2.13	0.48
2:E:443:SER:HB2	2:E:490:VAL:HG21	1.94	0.48
1:A:263:PRO:HD2	1:A:270:TRP:NE1	2.29	0.47
2:E:219:LEU:HD11	2:E:223:LYS:HA	1.96	0.47
2:E:582:THR:O	2:E:583:ILE:HD13	2.14	0.47
1:A:144:LYS:NZ	1:A:200:VAL:O	2.44	0.47
1:D:670:GLU:HA	1:D:673:TYR:CZ	2.50	0.47
2:E:30:LEU:HD23	2:E:584:CYS:HB3	1.94	0.47
2:E:331:ARG:HB2	2:E:331:ARG:CZ	2.44	0.47
2:E:526:CYS:HB3	2:E:587:ASP:OD2	2.14	0.47
2:E:617:SER:HB2	2:E:622:LEU:HD13	1.97	0.47
1:A:144:LYS:HG3	1:A:200:VAL:O	2.15	0.47
1:A:241:HIS:CB	1:A:279:ARG:HH21	2.27	0.47
1:A:243:HIS:CD2	1:A:245:PHE:H	2.32	0.47
1:A:245:PHE:O	1:A:246:LEU:HD23	2.15	0.47
1:D:406:THR:C	1:D:465:PRO:HD3	2.39	0.47
2:E:137:ASN:O	2:E:140:THR:HG23	2.14	0.47
1:A:88:VAL:HB	1:A:97:LEU:HD21	1.97	0.47
2:E:277:ARG:NH1	2:E:419:GLU:OE2	2.41	0.47
2:E:386:LEU:HD23	2:E:389:PHE:H	1.80	0.47
2:E:677:LEU:HB2	2:E:707:LEU:HB2	1.96	0.47
2:E:678:THR:OG1	2:E:705:SER:O	2.23	0.47
1:A:129:ILE:N	1:A:204:PRO:O	2.47	0.47
1:D:615:TYR:HB3	1:D:629:LEU:HD21	1.96	0.47
2:E:136:VAL:O	2:E:138:ARG:N	2.41	0.47
2:E:217:ARG:HD3	2:E:228:PHE:CE1	2.42	0.47
2:E:384:ARG:NH1	2:E:387:GLN:OE1	2.41	0.47
2:E:661:SER:O	2:E:677:LEU:HA	2.15	0.47
1:A:43:LYS:C	1:A:43:LYS:HD3	2.39	0.47
1:A:190:PHE:CE1	1:A:198:TYR:HB3	2.50	0.47
1:D:568:SER:OG	1:D:583:LYS:HG3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:600:PRO:HA	1:D:686:MET:HE1	1.96	0.47
2:E:316:ILE:HG12	2:E:349:SER:HB3	1.97	0.47
2:E:726:ILE:C	2:E:728:LEU:N	2.73	0.47
2:E:46:PHE:HB3	2:E:510:ILE:HG23	1.97	0.47
2:E:218:ARG:HD3	2:E:227:MET:HE2	1.97	0.47
1:A:63:LYS:HZ3	1:A:94:LYS:HB2	1.79	0.47
1:A:65:ASN:OD1	1:A:66:THR:N	2.48	0.47
1:A:122:LYS:O	1:A:126:ARG:HG3	2.15	0.47
2:E:86:THR:O	2:E:86:THR:OG1	2.24	0.47
2:E:394:HIS:CE1	2:E:395:GLU:HG2	2.50	0.47
2:E:575:LEU:HD12	2:E:576:GLU:N	2.30	0.47
2:E:718:THR:O	2:E:738:TYR:HB2	2.15	0.46
1:A:238:GLN:HG3	1:A:238:GLN:O	2.15	0.46
1:D:514:ARG:HB2	1:D:516:LYS:NZ	2.30	0.46
1:A:51:ILE:HD12	1:A:53:ILE:HD11	1.96	0.46
1:A:137:LYS:HA	1:A:178:ARG:NH1	2.30	0.46
1:A:246:LEU:H	1:A:249:ARG:HD3	1.81	0.46
2:E:72:VAL:C	2:E:73:LEU:HD23	2.41	0.46
2:E:547:ARG:CZ	2:E:548:SER:H	2.29	0.46
1:A:109:LYS:HD3	1:A:109:LYS:N	2.31	0.46
1:D:617:TRP:CZ2	1:D:629:LEU:HB2	2.51	0.46
2:E:410:GLU:OE1	2:E:410:GLU:N	2.48	0.46
2:E:530:LEU:HB2	2:E:591:ARG:HE	1.79	0.46
2:E:580:ARG:HA	2:E:625:THR:HG22	1.98	0.46
1:D:536:PHE:CE2	1:D:570:LEU:HD21	2.51	0.46
2:E:463:MET:HA	2:E:477:VAL:O	2.16	0.46
1:D:598:ASP:OD1	1:D:686:MET:HB2	2.16	0.46
2:E:562:LEU:HD12	2:E:563:PRO:CD	2.46	0.46
2:E:478:ASN:OD1	2:E:478:ASN:O	2.33	0.46
2:E:550:GLU:O	2:E:552:LEU:HD22	2.16	0.46
1:A:123:ASP:HA	1:A:126:ARG:HD3	1.97	0.46
2:E:400:ARG:HH12	2:E:414:ASP:HB3	1.81	0.46
1:A:129:ILE:HG23	1:A:205:GLN:OE1	2.15	0.46
1:D:524:ILE:C	1:D:525:LYS:HD2	2.40	0.46
2:E:192:PHE:CZ	2:E:218:ARG:NH1	2.84	0.46
1:A:165:SER:CA	1:A:168:ARG:HH12	2.23	0.45
2:E:211:LEU:HD23	2:E:211:LEU:HA	1.74	0.45
2:E:636:MET:N	2:E:652:PHE:O	2.36	0.45
1:A:222:LEU:HD23	1:A:222:LEU:HA	1.78	0.45
2:E:245:TYR:CE1	2:E:266:ARG:HB2	2.51	0.45
2:E:692:ILE:HD13	2:E:722:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:697:CYS:HB2	2:E:709:CYS:HB3	1.68	0.45
1:D:658:CYS:SG	1:D:703:PRO:HB2	2.56	0.45
2:E:278:ILE:HB	2:E:296:LEU:HD12	1.98	0.45
2:E:323:SER:OG	2:E:324:LYS:N	2.48	0.45
2:E:671:GLY:HA2	2:E:711:THR:HG23	1.97	0.45
1:A:273:THR:HG21	1:A:278:THR:HG23	1.98	0.45
1:D:402:ASN:HA	1:D:439:TYR:CE2	2.51	0.45
1:A:129:ILE:HG22	1:A:204:PRO:O	2.17	0.45
1:D:523:LEU:HG	1:D:596:THR:HG22	1.98	0.45
2:E:260:TYR:HA	2:E:279:ILE:O	2.17	0.45
2:E:343:PHE:CE2	2:E:444:THR:HG21	2.45	0.45
1:A:47:LYS:HA	1:A:114:HIS:HA	1.99	0.45
1:D:598:ASP:C	1:D:599:LEU:HD22	2.41	0.45
2:E:80:LYS:HZ3	2:E:83:GLU:HB2	1.82	0.45
2:E:157:GLU:OE2	2:E:159:HIS:CE1	2.70	0.45
2:E:403:LEU:HD23	2:E:403:LEU:HA	1.75	0.45
1:A:93:ARG:NE	1:A:95:GLN:O	2.50	0.45
1:D:512:ARG:HG2	1:D:515:ASN:HA	1.98	0.45
1:D:529:VAL:HG21	1:D:582:MET:HE3	1.99	0.45
2:E:72:VAL:O	2:E:73:LEU:HD23	2.16	0.45
1:A:260:CYS:O	1:A:261:ARG:NH2	2.49	0.45
1:D:407:ARG:N	1:D:463:TYR:O	2.49	0.45
1:D:533:ARG:HH21	1:D:578:ASP:H	1.65	0.45
2:E:41:TYR:CD2	2:E:518:LEU:HD21	2.51	0.45
2:E:53:GLN:NE2	2:E:116:ILE:HB	2.31	0.45
2:E:67:THR:HG23	2:E:116:ILE:HG22	1.98	0.45
2:E:114:ASP:N	2:E:114:ASP:OD1	2.50	0.45
2:E:279:ILE:CD1	2:E:293:GLU:HG2	2.47	0.45
1:D:547:TRP:HE1	1:D:564:VAL:HG23	1.81	0.45
2:E:53:GLN:HE21	2:E:116:ILE:HB	1.81	0.45
2:E:540:TRP:HD1	2:E:542:HIS:H	1.62	0.45
1:A:266:GLN:HB3	1:A:267:PRO:HD2	1.99	0.44
1:D:456:ASN:OD1	1:D:458:LEU:N	2.50	0.44
2:E:60:HIS:O	2:E:61:HIS:ND1	2.43	0.44
2:E:72:VAL:HG13	2:E:81:VAL:HG13	1.99	0.44
2:E:563:PRO:HG3	2:E:642:ASN:HD22	1.83	0.44
1:A:220:ARG:NH2	1:A:253:LYS:O	2.46	0.44
1:D:542:LYS:O	1:D:542:LYS:HD3	2.18	0.44
1:D:652:LEU:HD12	1:D:652:LEU:H	1.82	0.44
2:E:445:PHE:CZ	2:E:515:LEU:HB2	2.52	0.44
2:E:494:HIS:HE2	2:E:497:ASN:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ASN:HB3	1:A:123:ASP:OD1	2.16	0.44
1:D:598:ASP:OD1	1:D:686:MET:HE3	2.17	0.44
1:A:44:LYS:HD2	1:A:44:LYS:HA	1.74	0.44
1:A:44:LYS:NZ	1:A:117:ASP:HB3	2.33	0.44
1:D:497:ASN:HB2	1:D:666:SER:OG	2.17	0.44
1:A:102:ASN:CG	1:A:103:SER:N	2.76	0.44
1:D:499:ILE:O	1:D:631:VAL:HG12	2.17	0.44
1:D:530:LEU:HA	1:D:581:LEU:HD13	1.98	0.44
1:D:606:ILE:HG21	1:D:636:ILE:HG21	1.99	0.44
2:E:385:CYS:HB3	2:E:397:CYS:HB3	1.38	0.44
1:A:90:ASP:OD2	1:A:92:ALA:HB3	2.17	0.44
2:E:515:LEU:C	2:E:517:GLY:H	2.26	0.44
1:A:42:PHE:CD1	1:A:121:ASN:ND2	2.86	0.44
1:A:270:TRP:CE3	1:A:280:TRP:CE3	3.06	0.44
2:E:92:HIS:HE1	2:E:94:ASP:HB2	1.83	0.44
2:E:184:VAL:HG13	2:E:197:VAL:HG12	2.00	0.44
2:E:582:THR:N	2:E:623:LYS:HZ1	2.15	0.44
1:A:54:ASP:OD1	1:A:54:ASP:N	2.46	0.44
2:E:231:ASP:OD1	2:E:231:ASP:C	2.60	0.44
2:E:315:ASN:ND2	2:E:349:SER:OG	2.49	0.44
2:E:504:VAL:O	2:E:510:ILE:HD12	2.18	0.44
2:E:580:ARG:C	2:E:623:LYS:HZ3	2.25	0.44
1:D:552:ASP:O	1:D:555:GLY:N	2.46	0.43
1:D:651:THR:O	1:D:651:THR:OG1	2.32	0.43
2:E:180:LEU:HB2	2:E:200:THR:OG1	2.18	0.43
1:A:234:ARG:HE	1:A:237:HIS:HE1	1.64	0.43
1:A:251:PRO:O	1:A:253:LYS:HD2	2.18	0.43
1:D:513:TYR:O	1:D:516:LYS:NZ	2.50	0.43
2:E:68:ASN:OD1	2:E:114:ASP:HB2	2.17	0.43
2:E:699:LEU:HD21	2:E:702:VAL:HB	1.99	0.43
1:A:34:LYS:N	3:B:4:IDS:O1S	2.51	0.43
1:A:262:ASN:HD21	1:A:268:ARG:C	2.26	0.43
1:D:403:LEU:HD23	1:D:405:GLN:H	1.82	0.43
2:E:130:LEU:HA	2:E:130:LEU:HD12	1.75	0.43
2:E:275:HIS:CE1	2:E:277:ARG:NE	2.84	0.43
2:E:281:PHE:CD2	2:E:288:LEU:HD23	2.53	0.43
2:E:505:ILE:HG13	2:E:510:ILE:HD13	2.00	0.43
1:A:177:CYS:CB	1:A:189:CYS:HB3	2.47	0.43
2:E:509:LYS:HD3	2:E:509:LYS:HA	1.89	0.43
2:E:724:LEU:HD12	2:E:724:LEU:HA	1.90	0.43
1:A:53:ILE:H	1:A:109:LYS:HZ1	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:ASN:OD1	1:A:216:GLY:N	2.51	0.43
1:A:230:LYS:HE3	1:A:278:THR:HG21	2.00	0.43
2:E:378:VAL:HG21	2:E:420:PHE:CE2	2.54	0.43
2:E:602:ARG:O	2:E:640:ILE:HD12	2.18	0.43
2:E:75:GLU:N	2:E:75:GLU:OE1	2.47	0.43
2:E:126:TYR:OH	2:E:221:GLU:HG2	2.18	0.43
2:E:533:PRO:HB2	2:E:535:PHE:CD1	2.53	0.43
1:A:203:ILE:HD12	1:A:203:ILE:HA	1.92	0.43
1:A:226:THR:HA	1:A:283:CYS:HA	2.01	0.43
1:D:405:GLN:OE1	1:D:406:THR:N	2.52	0.43
1:D:686:MET:HB2	1:D:686:MET:HE3	1.84	0.43
2:E:36:ASN:OD1	2:E:36:ASN:N	2.52	0.43
2:E:592:ARG:O	2:E:593:ASN:C	2.60	0.43
1:A:211:CYS:HB3	1:A:288:CYS:HB3	1.95	0.43
1:A:215:ASN:ND2	1:A:218:SER:H	2.16	0.43
1:D:528:TRP:CH2	1:D:583:LYS:HB3	2.54	0.43
1:D:438:ASN:O	1:D:439:TYR:CD1	2.71	0.43
1:A:53:ILE:O	1:A:55:PRO:HD3	2.19	0.43
1:A:220:ARG:HE	1:A:261:ARG:HD2	1.83	0.43
1:D:406:THR:OG1	1:D:407:ARG:N	2.52	0.43
1:D:547:TRP:CD1	1:D:564:VAL:HA	2.51	0.43
2:E:63:PHE:C	2:E:64:LEU:HD12	2.44	0.43
2:E:384:ARG:HH22	2:E:387:GLN:HG2	1.83	0.43
1:D:512:ARG:NH2	1:D:547:TRP:CE3	2.87	0.42
1:D:570:LEU:HD23	1:D:570:LEU:HA	1.69	0.42
1:D:673:TYR:CE1	1:D:693:PRO:HG3	2.54	0.42
2:E:455:LEU:HA	2:E:455:LEU:HD23	1.68	0.42
2:E:462:PHE:HE2	2:E:513:ILE:HG21	1.84	0.42
2:E:530:LEU:HB2	2:E:591:ARG:HH21	1.84	0.42
1:A:48:THR:O	1:A:116:PHE:HB2	2.19	0.42
1:A:241:HIS:NE2	1:A:276:PRO:O	2.51	0.42
1:D:564:VAL:O	1:D:565:LEU:HD12	2.19	0.42
2:E:76:GLU:CD	2:E:76:GLU:N	2.77	0.42
2:E:200:THR:HG22	2:E:247:ILE:O	2.19	0.42
2:E:227:MET:HE3	2:E:229:LEU:HD21	2.00	0.42
2:E:539:GLY:H	2:E:556:TRP:HE1	1.67	0.42
2:E:591:ARG:HG2	2:E:591:ARG:HH11	1.83	0.42
2:E:599:LYS:HZ2	2:E:600:LYS:HE2	1.84	0.42
1:A:41:GLU:C	1:A:122:LYS:HZ3	2.26	0.42
1:D:412:CYS:HB2	1:D:438:ASN:OD1	2.19	0.42
1:D:708:ARG:NH2	1:D:711:TYR:HB2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:99:GLN:NE2	2:E:101:CYS:HB3	2.35	0.42
1:A:63:LYS:HZ1	1:A:94:LYS:HB2	1.84	0.42
1:A:82:PHE:CD2	1:A:100:PRO:HB3	2.47	0.42
1:A:219:TYR:C	1:A:220:ARG:HD2	2.45	0.42
2:E:690:ILE:HD11	2:E:722:VAL:CG1	2.49	0.42
1:D:451:TRP:HA	1:D:463:TYR:HA	2.01	0.42
1:D:614:VAL:C	1:D:615:TYR:HD1	2.27	0.42
1:D:646:HIS:HE1	1:D:695:ARG:HB3	1.84	0.42
2:E:46:PHE:CD1	2:E:46:PHE:C	2.97	0.42
2:E:537:GLN:O	2:E:547:ARG:HD2	2.19	0.42
2:E:540:TRP:CD1	2:E:542:HIS:N	2.87	0.42
2:E:671:GLY:HA3	2:E:713:ALA:CA	2.48	0.42
1:D:649:LYS:NZ	2:E:124:THR:HB	2.34	0.42
1:A:142:ILE:HD11	1:A:146:GLY:HA2	2.02	0.42
1:D:569:GLN:CD	1:D:570:LEU:H	2.27	0.42
1:D:646:HIS:CE1	1:D:695:ARG:HG3	2.55	0.42
1:D:699:ILE:HD12	1:D:699:ILE:H	1.84	0.42
2:E:192:PHE:CE2	2:E:218:ARG:CZ	3.03	0.42
2:E:250:VAL:HG11	2:E:317:LEU:HD22	2.02	0.42
2:E:279:ILE:HD13	2:E:293:GLU:HG2	2.01	0.42
2:E:690:ILE:HD11	2:E:722:VAL:HG12	2.02	0.42
1:D:528:TRP:CZ3	1:D:583:LYS:HB3	2.54	0.42
2:E:598:LEU:HD13	2:E:617:SER:O	2.19	0.42
1:D:406:THR:HA	1:D:464:CYS:HA	2.02	0.42
1:D:619:TYR:O	1:D:620:THR:OG1	2.35	0.42
2:E:113:LYS:HE2	2:E:113:LYS:HB2	1.95	0.42
2:E:206:PHE:CG	2:E:242:ARG:NH1	2.88	0.42
2:E:714:GLN:HB2	2:E:738:TYR:CE2	2.55	0.42
1:A:39:ILE:HD12	1:A:39:ILE:N	2.35	0.42
1:A:41:GLU:C	1:A:122:LYS:NZ	2.78	0.42
1:D:436:ASN:OD1	1:D:439:TYR:HB2	2.19	0.42
2:E:569:PHE:HA	2:E:570:PRO:HA	1.83	0.42
2:E:640:ILE:CG2	2:E:647:THR:HB	2.50	0.42
1:A:34:LYS:N	3:B:4:IDS:O2S	2.52	0.41
1:D:619:TYR:CZ	1:D:621:GLY:HA2	2.55	0.41
2:E:238:LEU:HD12	2:E:241:PHE:H	1.85	0.41
1:A:238:GLN:HG3	1:A:242:ARG:HA	2.01	0.41
2:E:513:ILE:HD12	2:E:513:ILE:N	2.35	0.41
2:E:523:PHE:CD1	2:E:528:GLN:HB3	2.55	0.41
1:A:257:ASP:HB3	1:A:258:ASN:H	1.74	0.41
1:D:640:GLU:C	1:D:644:GLN:HE21	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ASN:OD1	1:A:103:SER:N	2.53	0.41
2:E:200:THR:HG22	2:E:248:LYS:HA	2.03	0.41
2:E:367:ILE:HA	2:E:370:VAL:HG12	2.02	0.41
2:E:460:GLY:O	2:E:481:LEU:N	2.45	0.41
1:A:63:LYS:HZ1	1:A:94:LYS:C	2.27	0.41
1:D:598:ASP:OD1	1:D:598:ASP:C	2.63	0.41
2:E:84:TYR:HD1	2:E:155:GLN:HG3	1.85	0.41
2:E:329:LEU:O	2:E:333:ILE:HG12	2.20	0.41
1:A:123:ASP:OD1	1:A:124:TYR:N	2.53	0.41
1:A:160:HIS:ND1	1:A:162:PHE:HE1	2.18	0.41
2:E:39:MET:HG2	2:E:40:LYS:N	2.35	0.41
2:E:48:ALA:HB3	2:E:52:ILE:HD11	2.00	0.41
2:E:592:ARG:O	2:E:594:ASN:N	2.54	0.41
1:D:442:ASN:HA	1:D:443:PRO:HD3	1.92	0.41
2:E:533:PRO:HA	2:E:534:PRO:HD3	1.90	0.41
2:E:706:ILE:O	2:E:707:LEU:HD23	2.21	0.41
1:A:142:ILE:HD12	1:A:142:ILE:HA	1.91	0.41
1:D:522:SER:OG	1:D:676:PRO:HB3	2.21	0.41
1:D:539:ARG:C	2:E:413:ARG:NH2	2.78	0.41
2:E:530:LEU:C	2:E:591:ARG:HH21	2.28	0.41
1:A:60:LYS:HD3	1:A:98:TRP:CZ3	2.55	0.41
1:A:159:GLU:C	1:A:161:SER:N	2.79	0.41
1:A:223:MET:SD	1:A:223:MET:C	3.04	0.41
1:D:405:GLN:O	1:D:464:CYS:HB2	2.21	0.41
1:D:442:ASN:HD22	1:D:450:PRO:HA	1.86	0.41
1:D:509:VAL:HG22	1:D:548:LEU:HD11	2.03	0.41
1:D:617:TRP:HZ3	1:D:627:GLY:O	2.04	0.41
1:D:688:LEU:C	1:D:709:VAL:HG22	2.46	0.41
2:E:190:ASP:O	2:E:192:PHE:HD1	2.04	0.41
2:E:688:ARG:HA	2:E:726:ILE:HA	2.03	0.41
1:A:94:LYS:N	1:A:94:LYS:HD2	2.36	0.41
1:A:195:GLU:OE1	1:A:195:GLU:N	2.42	0.40
1:D:606:ILE:HD11	1:D:610:THR:HG21	2.03	0.40
2:E:296:LEU:HD23	2:E:424:LEU:HB3	2.02	0.40
2:E:559:GLN:HG2	2:E:560:ILE:H	1.86	0.40
1:A:84:CYS:HA	1:A:100:PRO:HA	2.02	0.40
1:A:215:ASN:HD21	1:A:218:SER:N	2.16	0.40
1:D:442:ASN:HB3	1:D:450:PRO:HA	2.03	0.40
1:D:713:ALA:HA	1:D:716:ILE:CD1	2.45	0.40
2:E:61:HIS:NE2	2:E:151:THR:OG1	2.53	0.40
2:E:245:TYR:CE2	2:E:388:HIS:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:618:THR:C	2:E:620:ASN:N	2.78	0.40
2:E:661:SER:O	2:E:677:LEU:HD13	2.21	0.40
2:E:229:LEU:HA	2:E:229:LEU:HD23	1.66	0.40
2:E:266:ARG:HA	2:E:274:PHE:HD1	1.86	0.40
2:E:285:ASN:OD1	2:E:286:SER:N	2.54	0.40
2:E:532:ALA:HA	2:E:533:PRO:HD3	1.96	0.40
1:A:219:TYR:CE1	1:A:221:GLY:HA3	2.56	0.40
1:D:495:VAL:HG23	1:D:667:GLY:C	2.47	0.40
1:D:511:LEU:HD23	1:D:512:ARG:N	2.36	0.40
2:E:318:GLN:OE1	2:E:318:GLN:HA	2.21	0.40
2:E:461:ARG:NH2	2:E:478:ASN:O	2.54	0.40
2:E:598:LEU:HD23	2:E:598:LEU:HA	1.86	0.40
2:E:604:LEU:O	2:E:638:ILE:HD12	2.22	0.40
2:E:699:LEU:HD11	2:E:702:VAL:HB	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/728 (34%)	224 (90%)	26 (10%)	0	100	100
1	D	299/728 (41%)	275 (92%)	24 (8%)	0	100	100
2	E	678/1390 (49%)	615 (91%)	63 (9%)	0	100	100
All	All	1227/2846 (43%)	1114 (91%)	113 (9%)	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	A	224/646 (35%)	222 (99%)	2 (1%)	70	76
1	D	235/646 (36%)	235 (100%)	0	100	100
2	E	598/1246 (48%)	596 (100%)	2 (0%)	86	85
All	All	1057/2538 (42%)	1053 (100%)	4 (0%)	81	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	ASN
1	A	258	ASN
2	E	38	ASN
2	E	594	ASN

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

Mol	Chain	Res	Type
1	A	72	ASN
1	D	497	ASN
1	D	504	ASN
1	D	644	GLN
1	D	646	HIS
2	E	275	HIS
2	E	393	ASN
2	E	396	HIS
2	E	607	ASN

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 ⓘ

6 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SGN	B	1	3	15,18,20	1.33	1 (6%)	20,26,31	1.53	3 (15%)
3	IDS	B	2	3	16,16,17	1.12	0	16,24,26	1.00	1 (6%)
3	SGN	B	3	3	19,19,20	3.78	4 (21%)	23,29,31	1.54	3 (13%)
3	IDS	B	4	3	16,16,17	1.28	2 (12%)	16,24,26	1.11	1 (6%)
3	SGN	B	5	3	13,13,20	4.17	4 (30%)	12,19,31	2.23	3 (25%)
3	IDS	B	6	3	15,15,17	1.08	0	14,22,26	2.50	6 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SGN	B	1	3	-	3/8/27/31	0/1/1/1
3	IDS	B	2	3	-	1/9/26/29	0/1/1/1
3	SGN	B	3	3	-	3/11/28/31	0/1/1/1
3	IDS	B	4	3	-	0/9/26/29	1/1/1/1
3	SGN	B	5	3	-	5/5/19/31	0/1/1/1
3	IDS	B	6	3	-	6/9/22/29	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	5	SGN	O2S-S1	9.95	1.53	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	5	SGN	O1S-S1	9.72	1.53	1.42
3	B	3	SGN	O2S-S1	9.72	1.53	1.42
3	B	3	SGN	O1S-S1	9.35	1.52	1.42
3	B	3	SGN	S1-N2	8.33	1.70	1.59
3	B	5	SGN	S1-N2	3.84	1.64	1.59
3	B	5	SGN	O4-C4	2.81	1.49	1.43
3	B	1	SGN	C1-C2	-2.54	1.48	1.52
3	B	4	IDS	O2-C2	-2.45	1.43	1.47
3	B	4	IDS	O4-C4	2.21	1.48	1.43
3	B	3	SGN	C4-C5	2.12	1.57	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	6	IDS	C1-O5-C5	-5.91	104.22	113.81
3	B	5	SGN	O1S-S1-O2S	-5.13	108.94	120.36
3	B	6	IDS	C1-C2-C3	-5.08	102.68	109.84
3	B	3	SGN	O1S-S1-O2S	-4.89	109.48	120.36
3	B	5	SGN	C3-C2-N2	3.80	115.31	110.32
3	B	1	SGN	O5-C1-C2	-3.47	105.93	111.29
3	B	1	SGN	C3-C4-C5	3.17	115.97	110.23
3	B	5	SGN	C5-O5-C1	2.76	115.87	111.42
3	B	6	IDS	O6A-C6-C5	-2.71	117.00	122.85
3	B	3	SGN	O5-C5-C6	2.70	113.43	107.59
3	B	2	IDS	O2-C2-C3	2.69	110.70	106.95
3	B	6	IDS	O5-C1-C2	-2.48	104.49	109.51
3	B	4	IDS	O3S-S-O2	2.35	111.77	106.37
3	B	1	SGN	C2-N2-S1	-2.35	110.92	116.99
3	B	3	SGN	O6-C6-C5	2.16	111.41	107.57
3	B	6	IDS	O3S-S-O2	2.15	111.32	106.37
3	B	6	IDS	C4-C3-C2	-2.05	108.15	110.76

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1	SGN	C4-C5-C6-O6
3	B	1	SGN	O5-C5-C6-O6
3	B	2	IDS	C3-C2-O2-S
3	B	3	SGN	C2-N2-S1-O1S
3	B	3	SGN	C2-N2-S1-O3S
3	B	5	SGN	C2-N2-S1-O1S

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Mol	Chain	Res	Type	Atoms
3	B	5	SGN	C2-N2-S1-O2S
3	B	5	SGN	C2-N2-S1-O3S
3	B	6	IDS	C1-C2-O2-S
3	B	6	IDS	C3-C2-O2-S
3	B	6	IDS	C2-O2-S-O2S
3	B	6	IDS	C2-O2-S-O1S
3	B	6	IDS	C2-O2-S-O3S
3	B	5	SGN	C1-C2-N2-S1
3	B	5	SGN	C3-C2-N2-S1
3	B	3	SGN	C2-N2-S1-O2S
3	B	6	IDS	O5-C5-C6-O6A
3	B	1	SGN	C5-C6-O6-S2

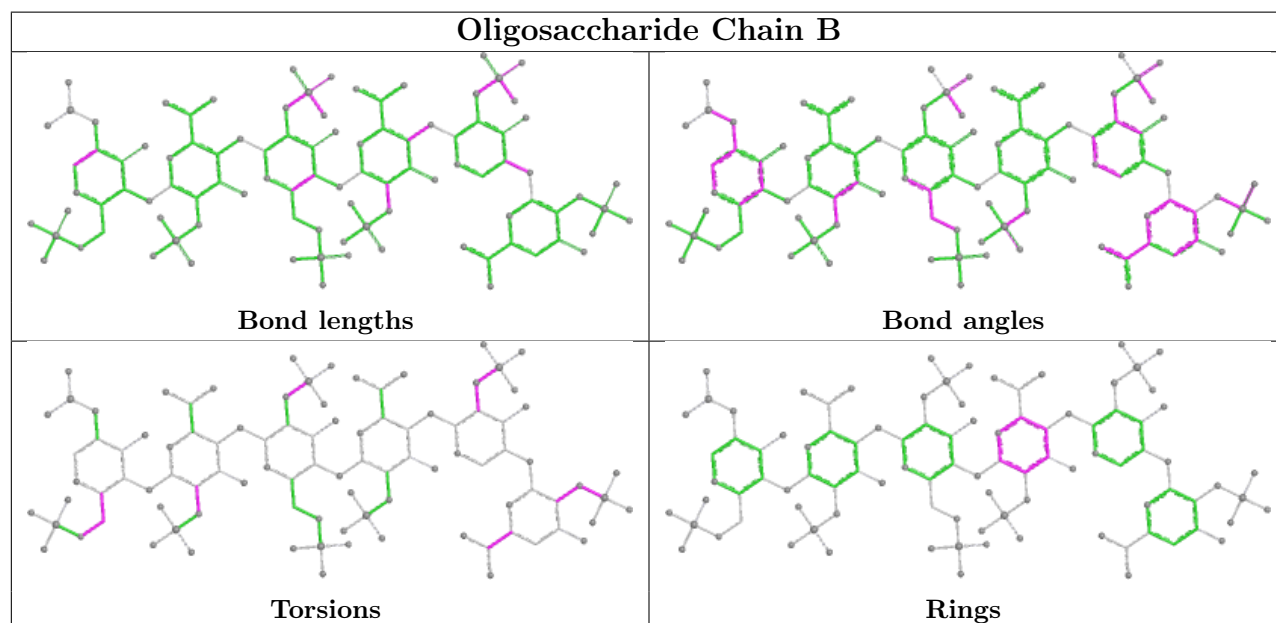
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	4	IDS	C1-C2-C3-C4-C5-O5

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	4	IDS	2	0
3	B	2	IDS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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.

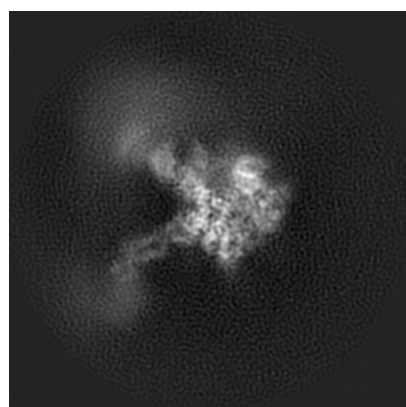
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23921. These allow visual inspection of the internal detail of the map and identification of artifacts.

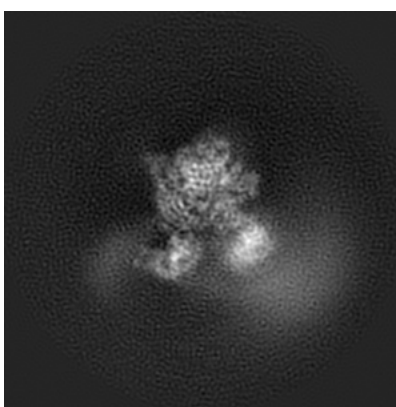
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

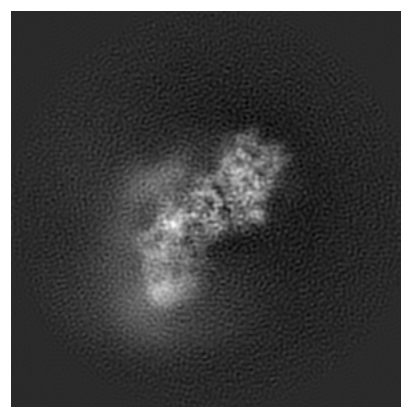
6.1.1 Primary map



X



Y

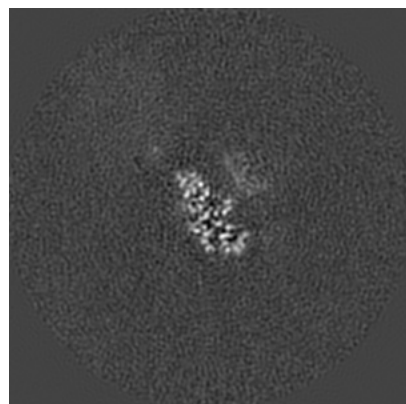


Z

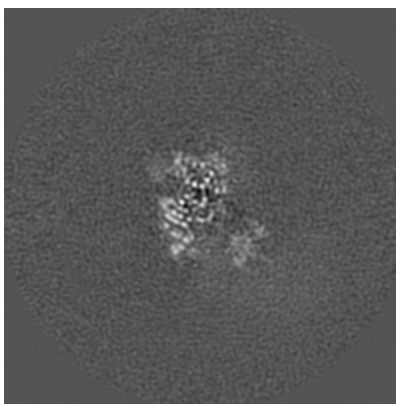
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

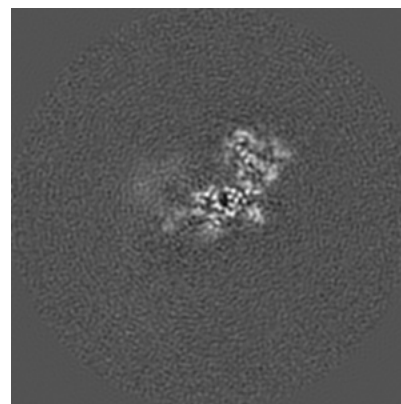
6.2.1 Primary map



X Index: 135



Y Index: 135

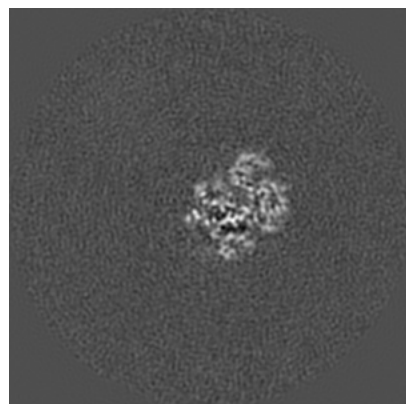


Z Index: 135

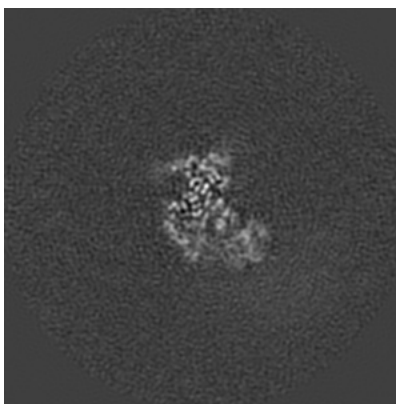
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

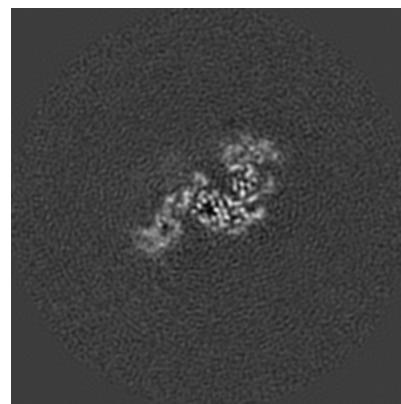
6.3.1 Primary map



X Index: 155



Y Index: 131

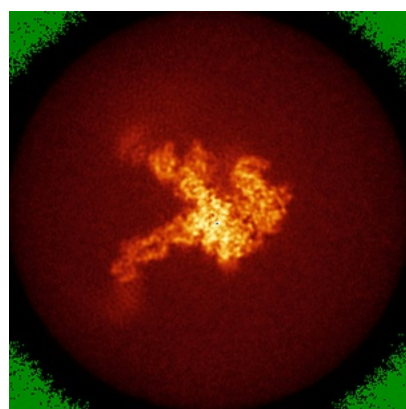


Z Index: 125

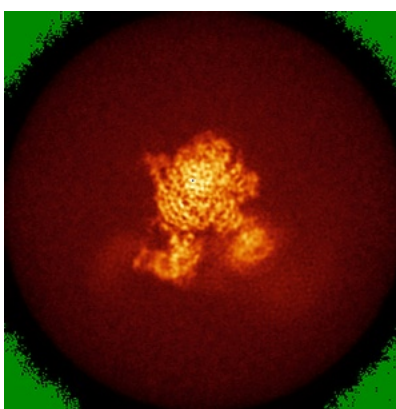
The images above show the largest variance slices of the map in three orthogonal directions.

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

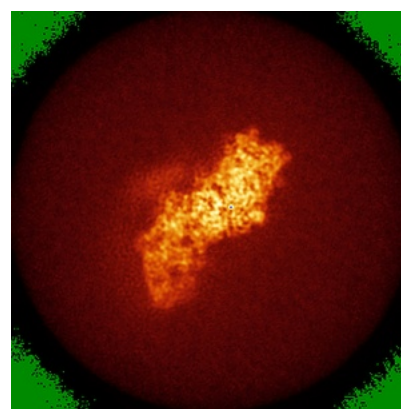
6.4.1 Primary map



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

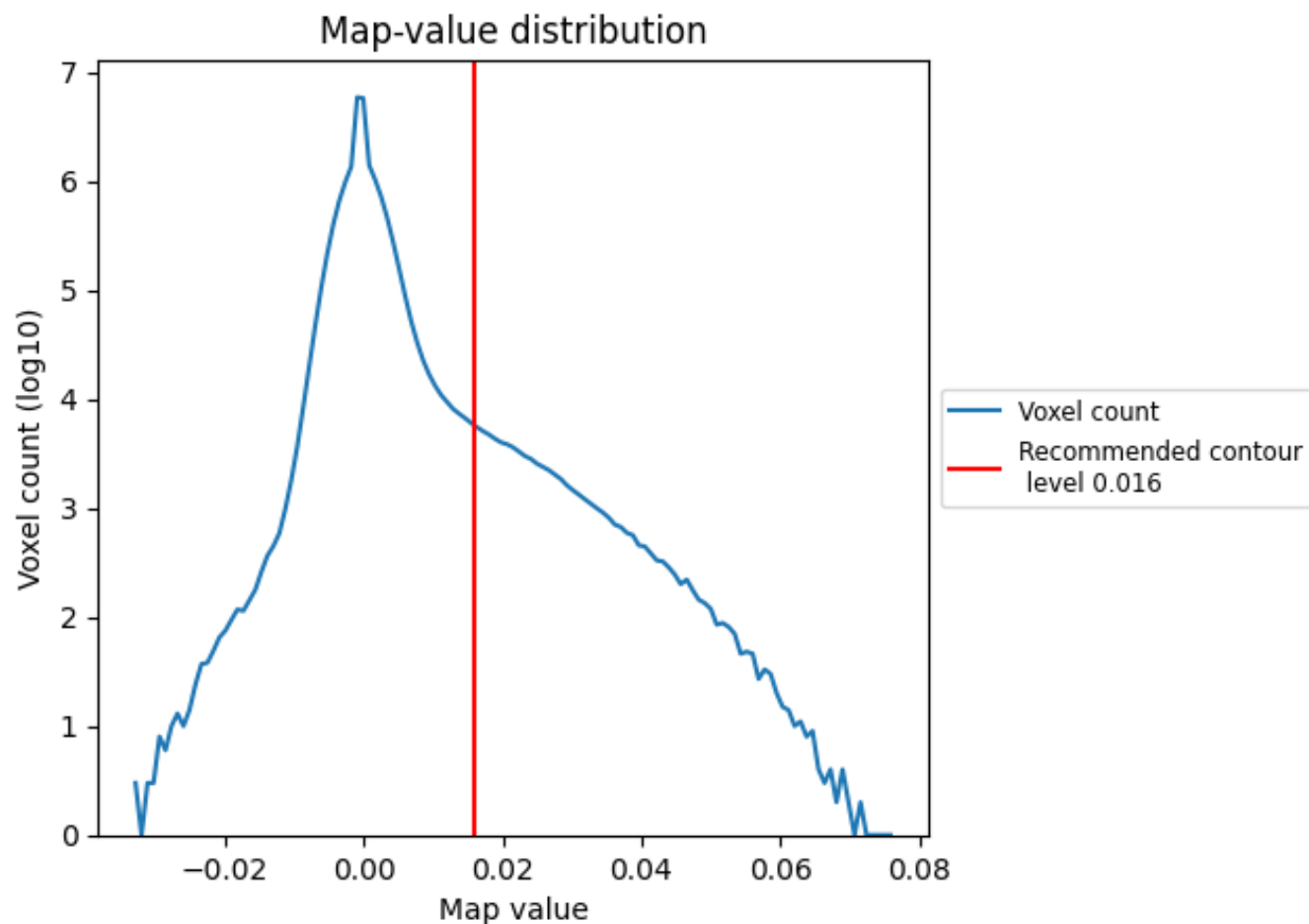
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

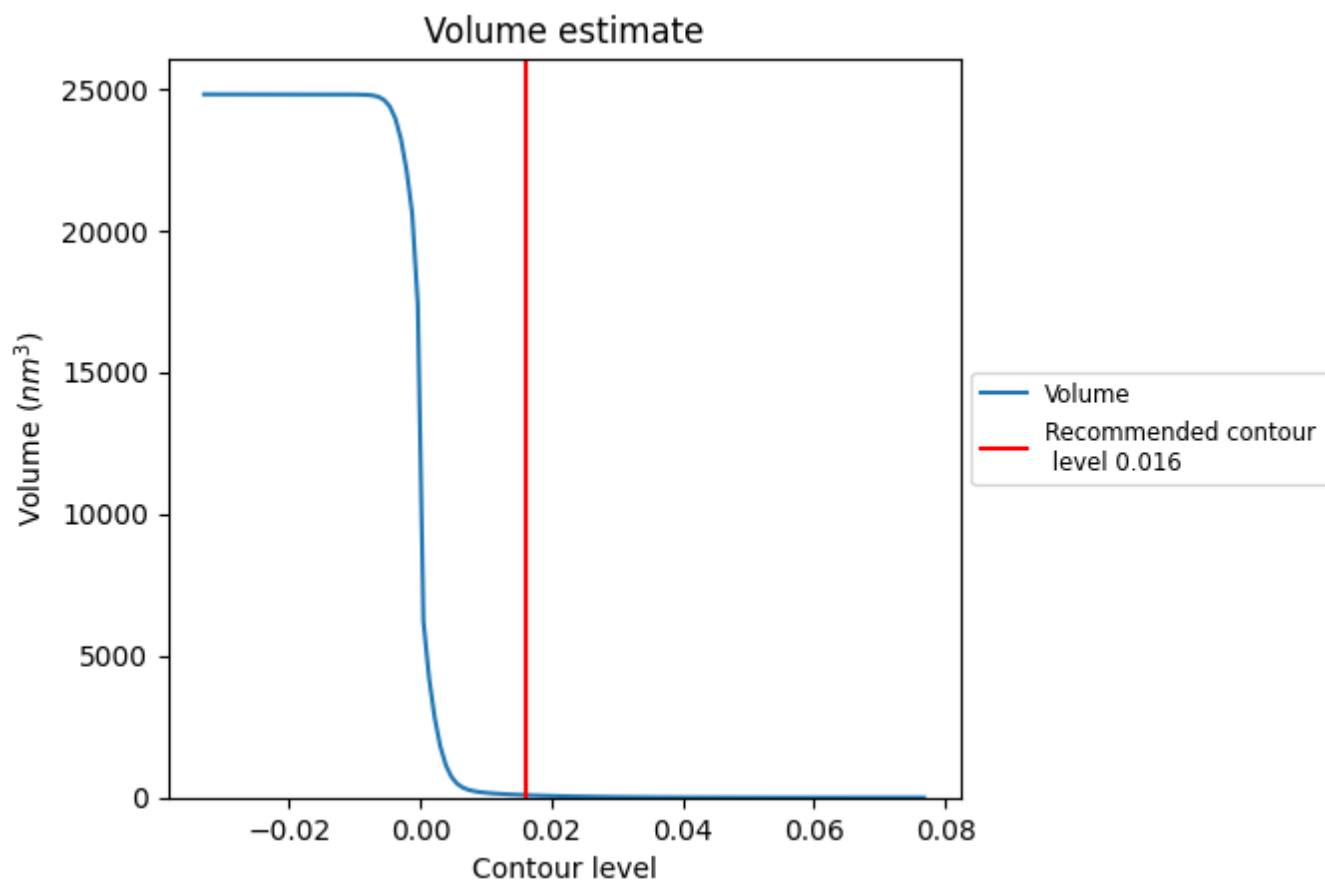
This section contains the results of statistical analysis of the map.

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.

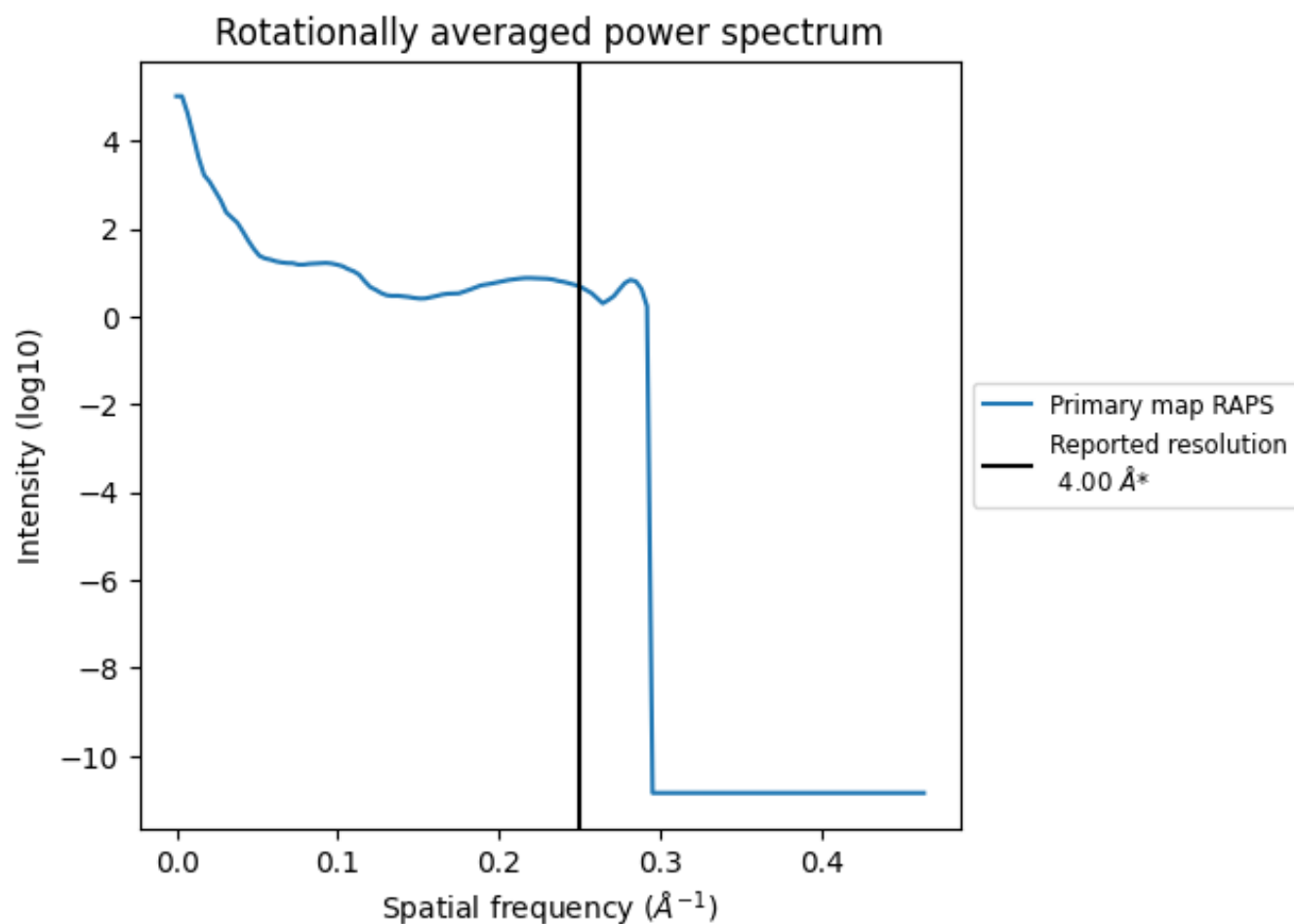
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 87 nm³; this corresponds to an approximate mass of 79 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.250 $\text{\AA}^{-1}$

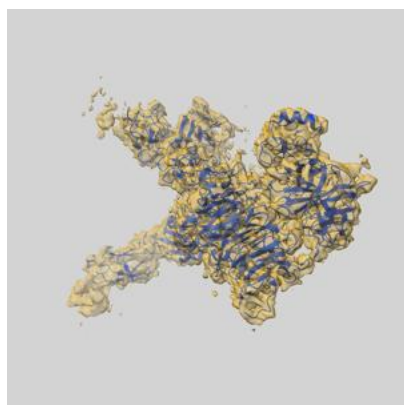
8 Fourier-Shell correlation ⓘ

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

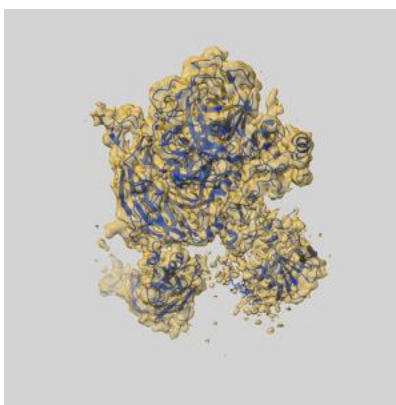
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23921 and PDB model 7MO9. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

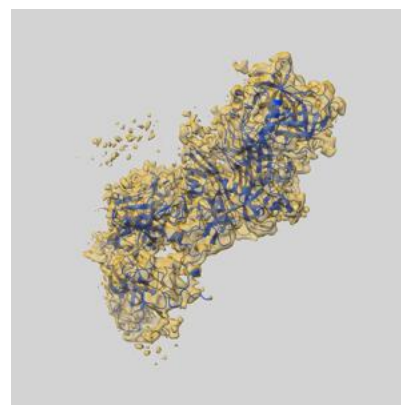
9.1 Map-model overlay [i](#)



X



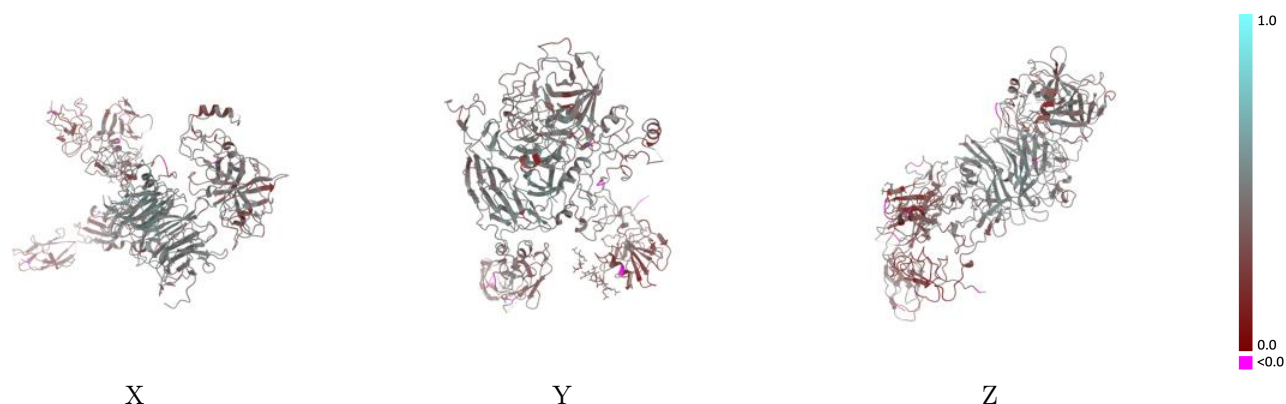
Y



Z

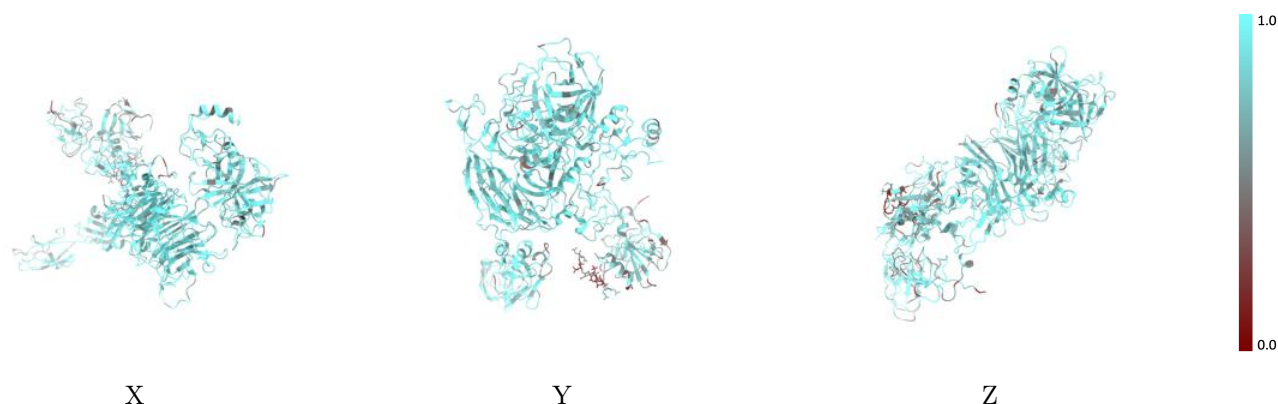
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



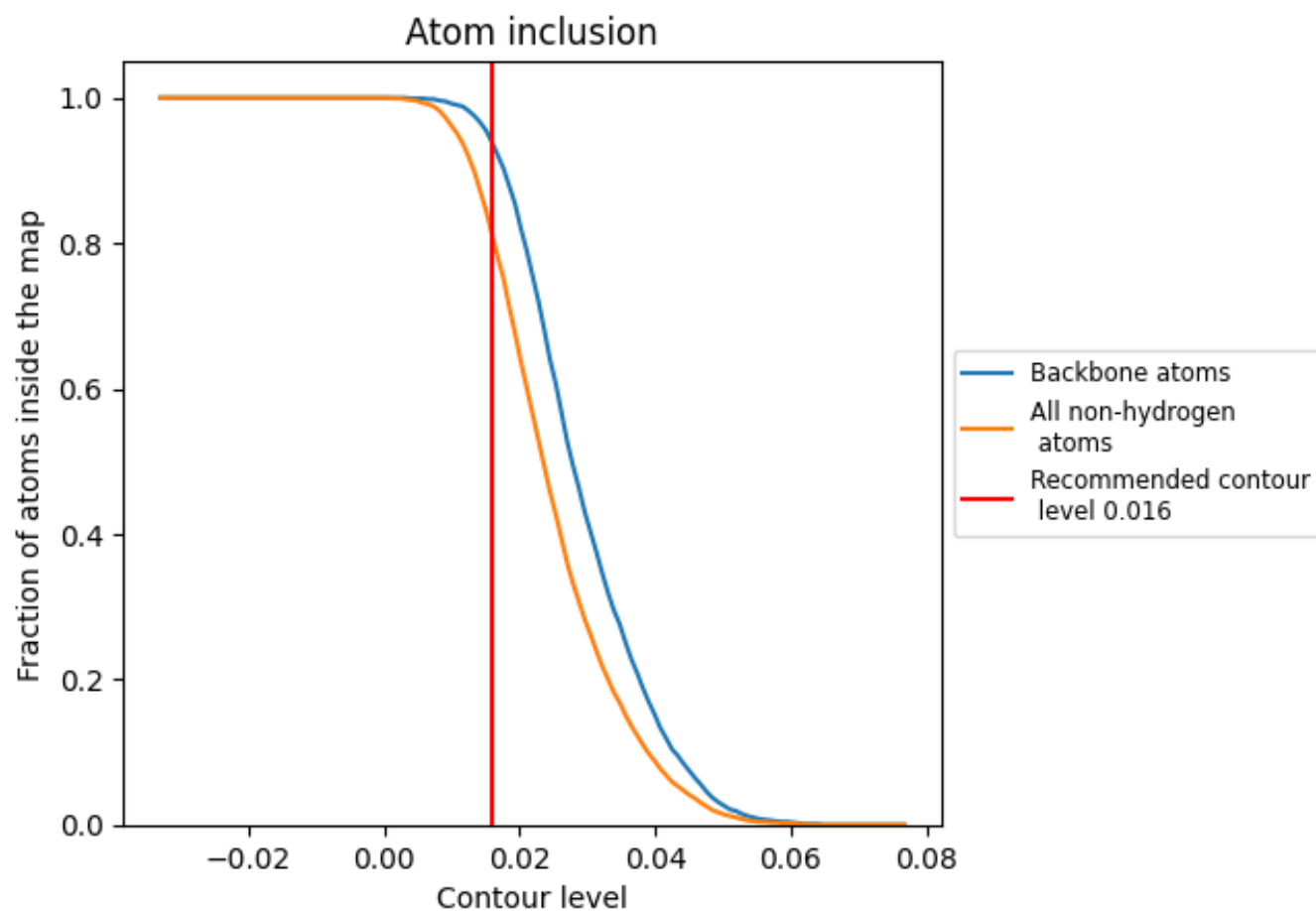
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 81% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8100	0.4100
A	0.7350	0.3300
B	0.3400	0.3710
D	0.8210	0.4140
E	0.8430	0.4400

