



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:55 AM UTC

PDB ID : 7RLO / pdb_00007rlo
EMDB ID : EMD-24535
Title : Structure of the human eukaryotic translation initiation factor 2B (eIF2B) in complex with a viral protein NSs
Authors : Wang, L.; Schoof, M.; Cogan, J.; Lawrence, R.; Boone, M.; Wuerth, J.; Frost, M.; Walter, P.
Deposited on : 2021-07-26
Resolution : 2.60 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
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

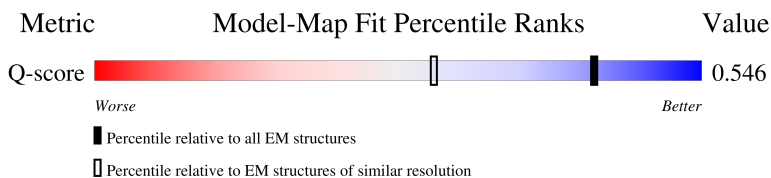
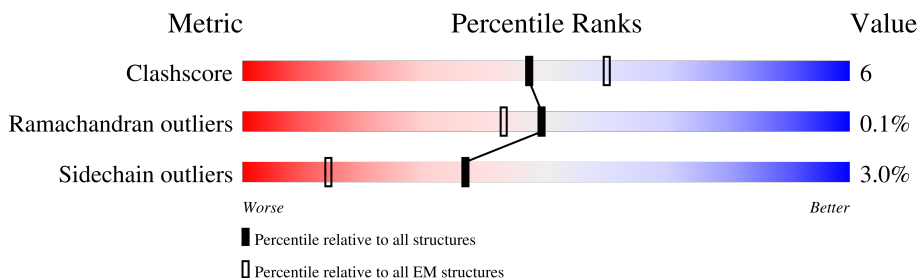
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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	721	 48% 9% 43%
1	B	721	 47% 10% 43%
2	C	351	 75% 17% • 5%
2	D	351	 75% 17% • 5%

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Mol	Chain	Length	Quality of chain
3	E	523	
3	F	523	
4	G	305	
4	H	305	
5	I	452	
5	J	452	
6	K	269	
6	L	269	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 28707 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 Translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	414	Total	C	N	O	S	0	0
			3210	2030	570	595	15		
1	B	414	Total	C	N	O	S	0	0
			3202	2026	569	592	15		

- Molecule 2 is a protein called Translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	333	Total	C	N	O	S	0	0
			2604	1648	457	484	15		
2	D	333	Total	C	N	O	S	0	0
			2604	1648	457	484	15		

- Molecule 3 is a protein called Translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	353	Total	C	N	O	S	2	0
			2772	1753	498	507	14		
3	F	353	Total	C	N	O	S	2	0
			2772	1753	498	507	14		

- Molecule 4 is a protein called Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	284	Total	C	N	O	S	1	0
			2205	1419	366	409	11		
4	H	284	Total	C	N	O	S	1	0
			2205	1419	366	409	11		

- Molecule 5 is a protein called Translation initiation factor eIF-2B subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	238	Total	C	N	O	S	0	0
			1867	1214	314	323	16		
5	J	228	Total	C	N	O	S	0	0
			1789	1160	304	309	16		

- Molecule 6 is a protein called Non-structural protein NS-S.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	218	Total	C	N	O	S	0	0
			1741	1108	299	320	14		
6	L	218	Total	C	N	O	S	0	0
			1736	1103	299	320	14		

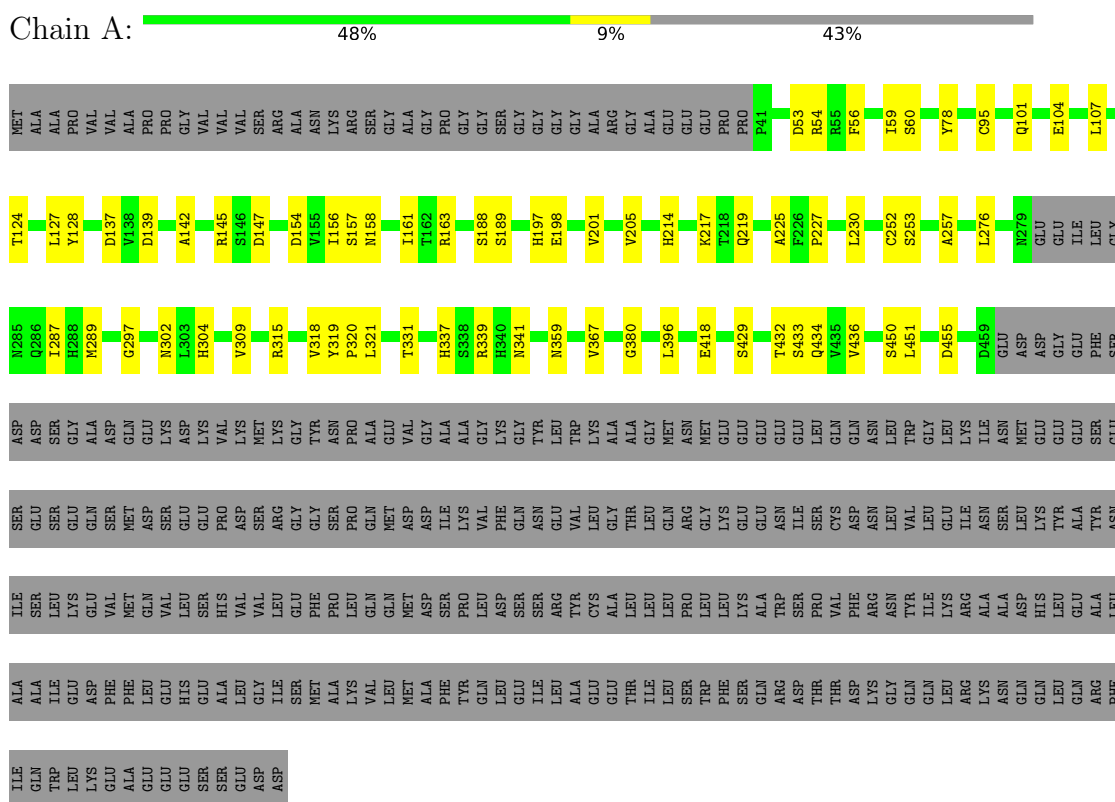
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	262	GLY	-	expression tag	UNP P12792
K	263	SER	-	expression tag	UNP P12792
K	264	HIS	-	expression tag	UNP P12792
K	265	HIS	-	expression tag	UNP P12792
K	266	HIS	-	expression tag	UNP P12792
K	267	HIS	-	expression tag	UNP P12792
K	268	HIS	-	expression tag	UNP P12792
K	269	HIS	-	expression tag	UNP P12792
L	262	GLY	-	expression tag	UNP P12792
L	263	SER	-	expression tag	UNP P12792
L	264	HIS	-	expression tag	UNP P12792
L	265	HIS	-	expression tag	UNP P12792
L	266	HIS	-	expression tag	UNP P12792
L	267	HIS	-	expression tag	UNP P12792
L	268	HIS	-	expression tag	UNP P12792
L	269	HIS	-	expression tag	UNP P12792

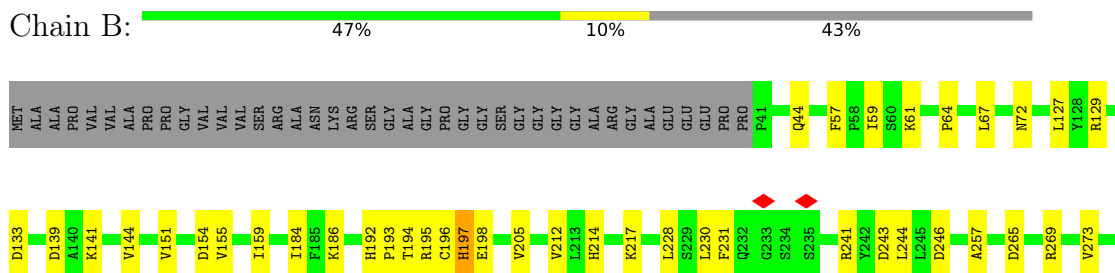
3 Residue-property plots

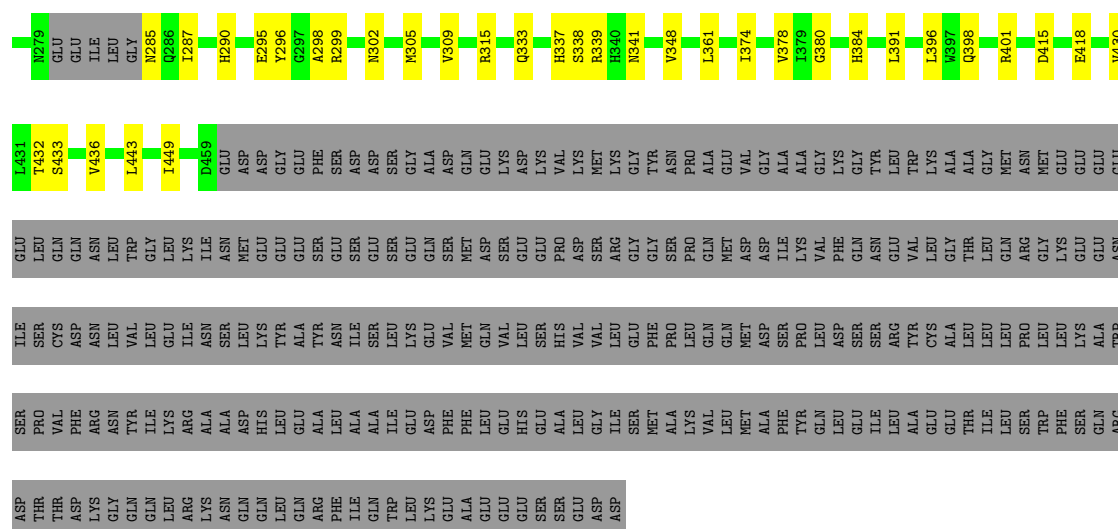
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Translation initiation factor eIF-2B subunit epsilon



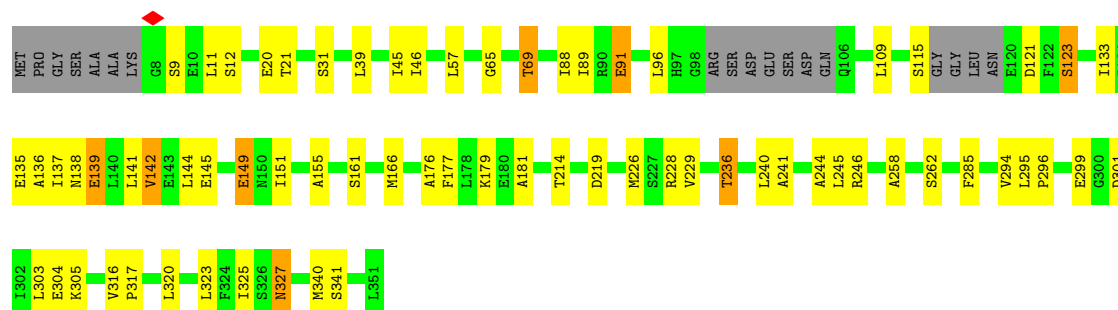
- Molecule 1: Translation initiation factor eIF-2B subunit epsilon





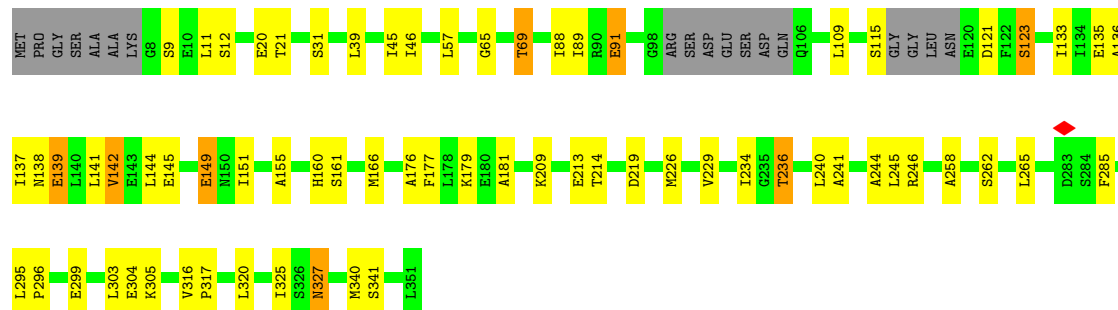
• Molecule 2: Translation initiation factor eIF-2B subunit beta

Chain C: 75% 17% 5%



• Molecule 2: Translation initiation factor eIF-2B subunit beta

Chain D: 75% 17% 5%

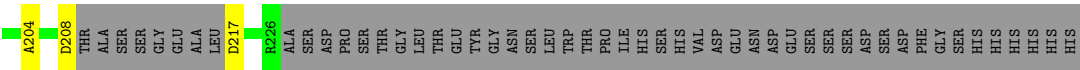


• Molecule 3: Translation initiation factor eIF-2B subunit delta

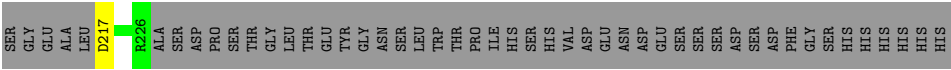
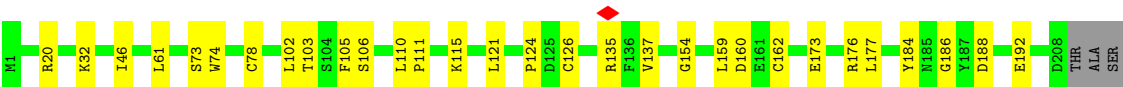
Chain E: 58% 10% 33%







• Molecule 6: Non-structural protein NS-S



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	137093	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 ($e^-/\text{\AA}^2$)	67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.294	Depositor
Minimum map value	-1.117	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	334.0, 334.0, 334.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.835, 0.835, 0.835	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	A	0.09	0/3277	0.27	0/4465
1	B	0.09	0/3269	0.29	0/4455
2	C	0.11	0/2653	0.29	0/3586
2	D	0.11	0/2653	0.29	0/3586
3	E	0.09	0/2824	0.26	0/3836
3	F	0.10	0/2824	0.26	0/3836
4	G	0.08	0/2241	0.24	0/3030
4	H	0.09	0/2241	0.25	0/3030
5	I	0.12	0/1895	0.32	0/2553
5	J	0.14	0/1815	0.43	0/2445
6	K	0.10	0/1782	0.30	1/2408 (0.0%)
6	L	0.11	0/1777	0.32	0/2401
All	All	0.10	0/29251	0.29	1/39631 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	K	17	ARG	N-CA-C	-5.35	106.06	113.18

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	3210	0	3160	34	0
1	B	3202	0	3150	48	0
2	C	2604	0	2610	37	0
2	D	2604	0	2610	36	0
3	E	2772	0	2840	29	0
3	F	2772	0	2840	29	0
4	G	2205	0	2270	23	0
4	H	2205	0	2270	25	0
5	I	1867	0	1931	29	0
5	J	1789	0	1864	40	0
6	K	1741	0	1688	20	0
6	L	1736	0	1672	18	0
All	All	28707	0	28905	343	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 6.

All (343) 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)
5:J:91:ARG:HB2	5:J:216:MET:HG3	1.63	0.79
3:F:418:VAL:HA	3:F:490:ASP:HB2	1.72	0.70
6:K:21:LEU:HD11	6:K:123:ILE:HG21	1.73	0.70
5:J:75:ILE:H	5:J:75:ILE:HD12	1.56	0.69
1:B:432:THR:HG22	1:B:433:SER:H	1.57	0.68
3:F:198:ILE:O	5:J:122:ARG:NH2	2.27	0.68
1:A:198:GLU:OE2	1:A:219:GLN:NE2	2.27	0.67
3:E:307:TYR:O	3:E:311:LYS:HB2	1.96	0.66
3:E:244:PRO:O	3:E:245:ASN:ND2	2.29	0.65
4:G:85:ASP:OD2	4:G:87:SER:OG	2.13	0.65
1:B:193:PRO:HD3	2:C:301:ASP:HA	1.79	0.65
5:J:88:ASP:HA	5:J:91:ARG:HG2	1.78	0.64
1:A:339:ARG:NH2	3:E:393:TYR:O	2.31	0.64
2:C:155:ALA:HB1	2:C:181:ALA:HB2	1.80	0.64
6:K:108:LYS:NZ	6:K:208:ASP:OD1	2.30	0.64
5:I:88:ASP:HA	5:I:91:ARG:HG2	1.80	0.63
5:I:115:HIS:HA	5:I:118:VAL:HG22	1.80	0.63
2:C:236:THR:HG21	2:C:245:LEU:HD22	1.80	0.63
1:A:432:THR:HG22	1:A:433:SER:H	1.62	0.63
2:D:155:ALA:HB1	2:D:181:ALA:HB2	1.80	0.63
2:D:236:THR:HG21	2:D:245:LEU:HD22	1.80	0.63
5:J:133:ARG:NE	5:J:308:GLY:O	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:409:LEU:HD12	3:F:413:SER:HB2	1.82	0.62
1:B:246:ASP:OD2	1:B:269:ARG:NH2	2.33	0.62
3:E:198:ILE:O	5:I:122:ARG:NH2	2.33	0.62
2:D:241:ALA:HA	2:D:340:MET:HE3	1.83	0.61
1:A:214:HIS:HB2	1:A:230:LEU:HD21	1.81	0.61
2:D:245:LEU:HB2	2:D:316:VAL:HB	1.81	0.61
2:C:241:ALA:HA	2:C:340:MET:HE3	1.83	0.61
2:C:245:LEU:HB2	2:C:316:VAL:HB	1.81	0.61
1:A:205:VAL:HG21	1:A:289:MET:HE2	1.81	0.61
1:B:196:CYS:O	1:B:197:HIS:ND1	2.29	0.60
1:A:139:ASP:HB2	1:A:257:ALA:HB1	1.83	0.60
2:D:121:ASP:OD2	2:D:123:SER:OG	2.20	0.60
4:G:128:HIS:HB2	4:G:215:MET:HE1	1.83	0.60
5:J:74:ASP:O	5:J:76:VAL:HG13	2.02	0.60
2:C:121:ASP:OD2	2:C:123:SER:OG	2.20	0.59
1:B:195:ARG:HH22	1:B:243:ASP:HA	1.66	0.59
5:J:128:LEU:HD11	5:J:229:ILE:HD12	1.85	0.59
1:A:56:PHE:O	1:A:60:SER:N	2.36	0.58
4:G:287:ASP:OD1	4:G:287:ASP:N	2.34	0.58
4:H:33:PHE:HA	4:H:36:ARG:HG2	1.85	0.58
5:J:88:ASP:OD1	5:J:88:ASP:N	2.34	0.58
5:J:39:PRO:HG2	5:J:106:CYS:HA	1.84	0.58
4:G:27:ILE:HG21	4:G:100:PHE:HE2	1.67	0.58
1:A:53:ASP:O	1:A:54:ARG:NH2	2.36	0.58
6:L:73:SER:OG	6:L:78:CYS:SG	2.62	0.58
1:A:163:ARG:NH1	3:E:469:GLU:OE2	2.35	0.58
2:D:135:GLU:O	2:D:138:ASN:HB2	2.04	0.57
2:C:304:GLU:HG3	2:C:305:LYS:HG3	1.86	0.57
2:D:304:GLU:HG3	2:D:305:LYS:HG3	1.87	0.57
4:H:206:ILE:HG21	4:H:228:VAL:HG11	1.86	0.57
3:E:319:ILE:HG22	3:E:345:ILE:HD11	1.87	0.57
3:F:307:TYR:O	3:F:311:LYS:HB2	2.04	0.57
2:C:135:GLU:O	2:C:138:ASN:HB2	2.04	0.57
2:C:166:MET:HE3	2:C:229:VAL:HG21	1.86	0.57
3:F:319:ILE:HG22	3:F:345:ILE:HD11	1.86	0.57
2:D:166:MET:HE3	2:D:229:VAL:HG21	1.86	0.56
1:B:339:ARG:NH2	3:F:393:TYR:O	2.39	0.56
3:F:320:SER:HA	3:F:345:ILE:HG12	1.88	0.56
5:J:134:LYS:HG3	5:J:136:GLN:HE22	1.69	0.56
6:K:86:MET:HE1	6:K:183:HIS:HA	1.87	0.56
4:G:112:ALA:HA	4:G:137:VAL:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:229:VAL:HG12	4:G:285:PHE:HB2	1.87	0.56
5:J:130:MET:HG3	5:J:302:VAL:HG13	1.88	0.55
4:H:228:VAL:HB	4:H:284:LEU:HD23	1.87	0.55
5:I:315:THR:OG1	5:I:316:LEU:N	2.40	0.55
5:J:217:GLU:OE2	5:J:218:ASN:ND2	2.40	0.55
3:E:320:SER:HA	3:E:345:ILE:HG12	1.88	0.55
3:F:170:ARG:NH1	3:F:187:SER:O	2.40	0.54
1:B:198:GLU:O	1:B:217:LYS:NZ	2.40	0.54
4:G:206:ILE:HG21	4:G:228:VAL:HG11	1.89	0.54
1:B:230:LEU:H	1:B:230:LEU:HD12	1.73	0.54
4:H:229:VAL:HG12	4:H:285:PHE:HB2	1.89	0.54
3:F:319:ILE:HG21	3:F:341:LEU:HD21	1.90	0.54
3:F:428:ARG:NH2	3:F:495:GLU:O	2.41	0.54
3:F:388:ILE:HG23	3:F:389:PRO:HD3	1.89	0.54
5:J:316:LEU:HA	5:J:319:TYR:HB3	1.88	0.53
3:E:499:LEU:HD11	3:E:506:MET:HB3	1.91	0.53
6:K:46:ILE:HG23	6:K:159:LEU:HB3	1.89	0.53
2:D:109:LEU:HD11	4:H:235:PHE:HD2	1.72	0.53
3:E:431:ASN:ND2	4:H:222:GLN:O	2.40	0.53
4:H:237:ARG:HD2	4:H:305:LEU:HB3	1.91	0.53
2:C:109:LEU:HD11	4:G:235:PHE:HD2	1.74	0.53
3:F:275:ASN:ND2	3:F:441:TYR:O	2.42	0.53
4:G:80:SER:O	4:G:80:SER:OG	2.25	0.53
1:A:276:LEU:HD22	1:A:287:ILE:HG13	1.90	0.52
3:F:332:VAL:H	3:F:399:SER:HB2	1.75	0.52
6:K:173:GLU:HB3	6:K:196:LEU:HD13	1.92	0.52
1:B:59:ILE:HD11	1:B:430:VAL:HG11	1.92	0.52
5:J:87:ALA:HB3	5:J:222:THR:HA	1.92	0.52
5:J:163:THR:HG23	5:J:165:LYS:H	1.75	0.52
6:K:160:ASP:OD1	6:K:160:ASP:N	2.41	0.52
6:L:173:GLU:OE1	6:L:176:ARG:NH1	2.41	0.52
1:B:273:VAL:HG12	1:B:287:ILE:HD13	1.92	0.52
3:E:171:LYS:H	3:E:171:LYS:HD2	1.75	0.52
2:D:46:ILE:HG12	2:D:57:LEU:HD11	1.92	0.51
5:I:125:ASP:OD1	5:I:208:LYS:NZ	2.38	0.51
5:J:101:VAL:HG21	5:J:212:VAL:HG21	1.92	0.51
6:K:51:LEU:HD12	6:K:160:ASP:HB2	1.91	0.51
1:A:188:SER:OG	1:A:189:SER:N	2.43	0.51
1:B:205:VAL:HG12	1:B:212:VAL:HA	1.93	0.51
3:F:431:ASN:ND2	4:G:222:GLN:O	2.43	0.51
2:C:246:ARG:NH1	2:C:285:PHE:O	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:ASP:HA	1:A:252:CYS:O	2.11	0.51
2:C:89:ILE:HG12	2:C:133:ILE:HD13	1.93	0.51
3:E:332:VAL:H	3:E:399:SER:HB3	1.75	0.51
3:F:238:GLN:HB2	3:F:301:ARG:HH12	1.76	0.51
5:I:133:ARG:HD2	5:I:310:CYS:HB3	1.93	0.51
5:J:322:ALA:O	5:J:326:VAL:HG13	2.11	0.51
2:D:246:ARG:NH1	2:D:285:PHE:O	2.43	0.50
2:D:327:ASN:OD1	2:D:327:ASN:N	2.42	0.50
4:G:74:ARG:HB2	4:G:305:LEU:HD13	1.92	0.50
1:B:265:ASP:OD1	1:B:265:ASP:N	2.44	0.50
6:K:19:HIS:HD2	6:K:20:ARG:HH21	1.59	0.50
1:B:195:ARG:HH12	1:B:244:LEU:H	1.59	0.50
2:C:46:ILE:HG12	2:C:57:LEU:HD11	1.92	0.50
4:G:237:ARG:HD2	4:G:305:LEU:HB3	1.94	0.50
1:A:225:ALA:HB1	5:I:179:GLU:HG3	1.94	0.50
1:B:129:ARG:N	1:B:133:ASP:OD2	2.39	0.50
1:B:72:ASN:O	1:B:333:GLN:NE2	2.44	0.50
1:B:214:HIS:HB2	1:B:230:LEU:HD21	1.93	0.50
2:D:89:ILE:HG12	2:D:133:ILE:HD13	1.93	0.50
2:D:176:ALA:HA	2:D:179:LYS:HG2	1.93	0.50
3:E:275:ASN:ND2	3:E:441:TYR:O	2.45	0.50
4:G:128:HIS:CD2	4:G:209:LYS:HB3	2.47	0.50
5:I:25:LYS:HA	5:I:28:LEU:HD13	1.94	0.50
5:I:131:LEU:HB3	5:I:204:LEU:HB3	1.93	0.50
5:I:30:VAL:HA	5:I:323:ASN:HD21	1.76	0.49
4:G:83:TYR:CZ	4:G:92:ILE:HG13	2.47	0.49
5:J:189:LYS:HG3	5:J:190:HIS:CD2	2.46	0.49
6:K:116:ALA:O	6:K:200:ARG:NH2	2.45	0.49
6:L:154:GLY:HA3	6:L:162:CYS:HB3	1.93	0.49
1:A:156:ILE:HG13	1:A:309:VAL:HG11	1.95	0.49
2:C:176:ALA:HA	2:C:179:LYS:HG2	1.93	0.49
3:E:409:LEU:HD12	3:E:413:SER:HB2	1.94	0.49
2:C:138:ASN:O	2:C:141:LEU:HB2	2.13	0.49
2:D:138:ASN:O	2:D:141:LEU:HB2	2.13	0.49
5:J:58:ASP:OD1	5:J:58:ASP:N	2.44	0.49
4:G:157:PRO:HG3	4:H:179:LEU:HD13	1.93	0.49
1:A:157:SER:HB2	1:A:297:GLY:HA2	1.95	0.48
1:B:139:ASP:HB3	1:B:257:ALA:HB1	1.95	0.48
1:A:418:GLU:HB3	1:A:436:VAL:HG22	1.95	0.48
6:K:173:GLU:OE1	6:K:176:ARG:NH1	2.45	0.48
6:K:102:LEU:HA	6:K:105:PHE:HD2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:K:117:LEU:HD11	6:K:201:LEU:HD12	1.94	0.48
5:I:26:PRO:HA	5:I:35:LEU:HB3	1.96	0.48
5:I:99:THR:HG22	5:I:100:ASP:H	1.79	0.48
5:I:110:THR:HB	5:I:310:CYS:HA	1.95	0.48
2:C:141:LEU:O	2:C:144:LEU:HB2	2.14	0.48
2:D:141:LEU:O	2:D:144:LEU:HB2	2.14	0.48
4:H:109:ASN:HD22	4:H:136:ARG:HH21	1.61	0.48
5:J:26:PRO:HB2	5:J:36:ILE:HB	1.95	0.48
1:B:186:LYS:HE2	1:B:296:TYR:HA	1.95	0.47
2:D:240:LEU:HD12	2:D:244:ALA:HB3	1.96	0.47
3:E:416:SER:OG	3:E:417:ARG:N	2.47	0.47
1:A:154:ASP:OD1	1:A:154:ASP:N	2.46	0.47
4:H:114:LEU:HD22	4:H:289:GLY:HA2	1.96	0.47
3:E:405:ALA:HB3	3:E:438:CYS:HB2	1.95	0.47
2:C:142:VAL:O	2:C:145:GLU:HG2	2.15	0.47
4:G:228:VAL:HB	4:G:284:LEU:HD23	1.95	0.47
6:K:180:SER:HB2	6:K:182:GLU:HG3	1.96	0.47
6:L:61:LEU:HB2	6:L:186:GLY:HA3	1.97	0.47
6:L:160:ASP:OD1	6:L:160:ASP:N	2.47	0.47
2:C:240:LEU:HD12	2:C:244:ALA:HB3	1.97	0.47
3:F:416:SER:OG	3:F:417:ARG:N	2.46	0.47
4:H:112:ALA:HA	4:H:137:VAL:HG22	1.96	0.47
4:H:128:HIS:CD2	4:H:209:LYS:HB3	2.50	0.47
5:I:163:THR:HG23	5:I:165:LYS:H	1.80	0.46
5:I:305:MET:HE2	5:I:308:GLY:HA3	1.98	0.46
5:J:305:MET:HG3	5:J:310:CYS:SG	2.55	0.46
6:L:102:LEU:HA	6:L:105:PHE:HD2	1.78	0.46
1:B:384:HIS:HB2	1:B:401:ARG:HG2	1.96	0.46
2:D:142:VAL:O	2:D:145:GLU:HG2	2.15	0.46
1:B:338:SER:OG	1:B:339:ARG:N	2.47	0.46
4:H:203:ASN:OD1	4:H:203:ASN:N	2.44	0.46
2:C:65:GLY:O	2:C:69:THR:OG1	2.33	0.46
5:J:44:GLU:C	5:J:46:VAL:H	2.22	0.46
1:A:227:PRO:HG2	1:A:230:LEU:HD13	1.97	0.46
1:A:201:VAL:HG12	1:A:217:LYS:HD2	1.97	0.46
3:E:319:ILE:HG21	3:E:341:LEU:HD21	1.97	0.46
1:B:374:ILE:HG23	1:B:391:LEU:HB2	1.97	0.46
3:E:170:ARG:NH2	3:E:266:CYS:O	2.49	0.46
5:I:87:ALA:HB2	5:I:224:ILE:HG23	1.97	0.46
1:B:64:PRO:HD2	1:B:67:LEU:HD12	1.97	0.46
5:J:26:PRO:HG2	5:J:27:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:K:110:LEU:HD12	6:K:113:VAL:HG22	1.98	0.46
5:I:9:ALA:HB1	5:I:26:PRO:HG3	1.98	0.45
5:I:158:ILE:HD12	5:I:199:LEU:HD12	1.99	0.45
3:E:413:SER:HB3	3:E:491:VAL:HG13	1.97	0.45
2:D:155:ALA:HA	2:D:177:PHE:CZ	2.51	0.45
5:I:321:GLU:OE2	5:I:325:GLN:NE2	2.49	0.45
1:A:197:HIS:NE2	1:A:304:HIS:HB3	2.32	0.45
1:B:155:VAL:HG22	1:B:299:ARG:HB2	1.98	0.45
2:C:155:ALA:HA	2:C:177:PHE:CZ	2.51	0.45
2:D:88:ILE:HA	2:D:91:GLU:OE2	2.16	0.45
4:G:34:LEU:HD12	4:G:49:LEU:HD11	1.98	0.45
4:G:88:LYS:HE3	4:G:88:LYS:HB3	1.66	0.45
5:I:44:GLU:C	5:I:46:VAL:H	2.25	0.45
3:E:480:ALA:O	3:E:483:ARG:NH1	2.38	0.45
5:J:5:ALA:HB1	5:J:43:LEU:HD23	1.98	0.45
5:J:99:THR:HG22	5:J:100:ASP:H	1.82	0.45
2:C:295:LEU:HG	2:C:299:GLU:HG3	1.99	0.45
3:F:473:LEU:HD13	3:F:484:LEU:HD21	1.99	0.45
5:J:224:ILE:O	5:J:229:ILE:HG12	2.16	0.45
2:D:136:ALA:O	2:D:139:GLU:HG3	2.16	0.45
3:F:409:LEU:HD13	3:F:448:GLN:HB3	1.98	0.45
1:A:337:HIS:HE1	1:A:341:ASN:HA	1.81	0.44
1:B:337:HIS:HE1	1:B:341:ASN:HA	1.82	0.44
2:D:295:LEU:HG	2:D:299:GLU:HG3	1.99	0.44
3:E:187:SER:HB3	3:E:190:ASN:HD22	1.83	0.44
4:G:104:ILE:HD12	4:G:233:PHE:HD2	1.82	0.44
6:L:102:LEU:HD21	6:L:124:PRO:HB2	1.99	0.44
1:A:128:TYR:OH	1:A:137:ASP:OD1	2.33	0.44
2:C:136:ALA:O	2:C:139:GLU:HG3	2.16	0.44
6:L:217:ASP:OD1	6:L:217:ASP:N	2.49	0.44
1:A:158:ASN:ND2	1:A:319:TYR:O	2.50	0.44
4:H:227:TYR:HB3	4:H:285:PHE:HE2	1.81	0.44
1:B:192:HIS:ND1	1:B:194:THR:HG22	2.32	0.44
2:C:88:ILE:HA	2:C:91:GLU:OE2	2.16	0.44
2:D:65:GLY:O	2:D:69:THR:OG1	2.33	0.44
5:J:115:HIS:HA	5:J:118:VAL:HG22	1.98	0.44
2:C:226:MET:HE2	2:C:258:ALA:HA	1.99	0.44
6:K:46:ILE:HG12	6:K:159:LEU:HD23	1.99	0.44
2:D:11:LEU:HD21	2:D:45:ILE:HG12	1.98	0.44
5:I:87:ALA:HB3	5:I:222:THR:HA	1.99	0.44
1:B:57:PHE:O	1:B:61:LYS:NZ	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:276:LEU:HD23	1:B:287:ILE:HD11	1.99	0.44
1:B:380:GLY:N	1:B:396:LEU:O	2.49	0.44
6:L:46:ILE:HG23	6:L:159:LEU:HB3	1.99	0.44
2:C:11:LEU:HD21	2:C:45:ILE:HG12	1.98	0.44
2:C:96:LEU:HD23	2:C:96:LEU:HA	1.84	0.44
2:D:317:PRO:HD2	2:D:320:LEU:HD12	1.99	0.44
2:D:226:MET:HE2	2:D:258:ALA:HA	1.99	0.44
2:D:295:LEU:HD12	2:D:296:PRO:HD2	2.00	0.44
4:H:251:LYS:HA	4:H:273:VAL:HG12	1.98	0.44
1:B:159:ILE:HG12	1:B:295:GLU:HB3	1.99	0.43
3:F:479:HIS:HB2	3:F:482:LEU:HB3	1.99	0.43
1:B:315:ARG:NH1	2:C:303:LEU:O	2.51	0.43
3:E:310:GLU:HA	3:E:314:LEU:HB2	1.99	0.43
5:J:225:ARG:HD3	5:J:312:ARG:HH12	1.83	0.43
6:K:65:TYR:OH	6:K:167:HIS:ND1	2.36	0.43
6:L:188:ASP:O	6:L:192:GLU:HG3	2.17	0.43
1:A:380:GLY:N	1:A:396:LEU:O	2.48	0.43
1:A:127:LEU:H	1:A:127:LEU:HD23	1.83	0.43
2:C:295:LEU:HD12	2:C:296:PRO:HD2	2.00	0.43
2:D:151:ILE:HG23	2:D:325:ILE:HG22	2.00	0.43
4:G:227:TYR:HB3	4:G:285:PHE:HE2	1.84	0.43
1:B:305:MET:O	1:B:309:VAL:HG23	2.19	0.43
5:J:185:SER:HA	5:J:188:GLN:HB2	2.01	0.43
1:B:198:GLU:OE2	1:B:302:ASN:ND2	2.51	0.43
2:C:317:PRO:HD2	2:C:320:LEU:HD12	1.99	0.43
1:A:302:ASN:OD1	1:A:302:ASN:N	2.52	0.43
2:C:323:LEU:HD21	3:E:447:VAL:HG21	2.01	0.43
6:L:74:TRP:NE1	6:L:186:GLY:O	2.51	0.43
1:A:78:TYR:HD1	1:A:321:LEU:HD23	1.84	0.42
5:I:25:LYS:N	5:I:26:PRO:HD2	2.34	0.42
6:L:135:ARG:HD2	6:L:135:ARG:O	2.18	0.42
1:B:228:LEU:HD21	5:J:176:LEU:HD13	2.01	0.42
2:C:151:ILE:HG23	2:C:325:ILE:HG22	2.00	0.42
3:E:394:VAL:O	3:E:397:GLU:HG2	2.19	0.42
1:B:241:ARG:HD3	1:B:244:LEU:HD11	2.00	0.42
1:B:418:GLU:HB3	1:B:436:VAL:HG13	2.02	0.42
3:F:199:PRO:HG2	5:J:47:GLY:HA3	2.02	0.42
4:H:126:LEU:HB3	4:H:193:VAL:HG22	2.00	0.42
3:F:326:LYS:NZ	4:H:239:PHE:O	2.42	0.42
1:B:44:GLN:HE22	1:B:144:VAL:HA	1.85	0.42
3:E:435:LEU:HD23	3:E:501:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:193:THR:HG22	5:J:115:HIS:HB2	2.01	0.42
3:E:257:LYS:HB3	3:E:258:PRO:HD3	2.02	0.42
3:F:400:LYS:HG2	3:F:433:PRO:HG2	2.02	0.42
4:H:5:GLU:N	4:H:8:GLU:OE2	2.53	0.42
5:I:8:MET:HE1	5:I:90:LEU:HB2	2.01	0.42
1:B:127:LEU:HD23	1:B:127:LEU:H	1.85	0.42
6:L:110:LEU:HA	6:L:111:PRO:HD3	1.91	0.42
6:L:103:THR:HA	6:L:106:SER:OG	2.20	0.42
5:J:35:LEU:HA	5:J:38:TYR:HD1	1.85	0.42
6:K:112:ASN:HD22	6:K:204:ALA:HB1	1.84	0.42
1:A:315:ARG:NH1	2:D:303:LEU:O	2.52	0.42
1:B:269:ARG:O	1:B:273:VAL:HG22	2.19	0.42
1:A:337:HIS:CE1	1:A:341:ASN:HA	2.55	0.41
1:A:142:ALA:O	1:A:145:ARG:NH2	2.53	0.41
1:A:434:GLN:HB2	1:A:451:LEU:HD11	2.00	0.41
5:J:235:LYS:NZ	5:J:298:VAL:O	2.47	0.41
5:J:158:ILE:HG22	5:J:160:VAL:HG23	2.01	0.41
1:B:154:ASP:OD1	1:B:154:ASP:N	2.54	0.41
5:I:98:LYS:HE3	5:I:98:LYS:HB2	1.90	0.41
5:I:158:ILE:HG22	5:I:160:VAL:HG23	2.03	0.41
6:K:19:HIS:CD2	6:K:20:ARG:HH21	2.37	0.41
1:B:184:ILE:HD13	1:B:290:HIS:HB3	2.02	0.41
2:D:149:GLU:O	2:D:149:GLU:HG3	2.20	0.41
3:E:388:ILE:HG22	3:E:389:PRO:HD3	2.01	0.41
4:H:27:ILE:HG21	4:H:100:PHE:HE2	1.85	0.41
5:J:26:PRO:HB3	5:J:106:CYS:SG	2.60	0.41
5:J:229:ILE:HB	5:J:230:PRO:HD3	2.03	0.41
3:F:194:GLN:HB3	5:J:115:HIS:CE1	2.56	0.41
5:J:41:ASN:HA	5:J:44:GLU:HG3	2.02	0.41
6:L:46:ILE:HG12	6:L:159:LEU:HD23	2.02	0.41
1:A:101:GLN:O	1:A:104:GLU:HG3	2.21	0.41
1:B:276:LEU:HD11	1:B:285:ASN:HB2	2.03	0.41
1:B:398:GLN:HE21	1:B:398:GLN:HB2	1.71	0.41
2:D:209:LYS:HE3	2:D:209:LYS:HB2	1.91	0.41
2:D:213:GLU:HA	3:E:481:SER:HB2	2.02	0.41
3:F:341:LEU:HD23	3:F:437:CYS:HB3	2.02	0.41
4:G:179:LEU:HD13	4:H:157:PRO:HG3	2.03	0.41
4:G:243:GLN:HE22	4:G:274:ASP:HB2	1.86	0.41
4:H:125:ILE:HG12	4:H:192:LEU:HD21	2.03	0.41
6:L:20:ARG:HG3	6:L:121:LEU:HB3	2.01	0.41
1:B:228:LEU:HA	1:B:231:PHE:HD2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:454:SER:O	3:F:455:ASN:ND2	2.54	0.41
5:I:133:ARG:NE	5:I:308:GLY:O	2.49	0.41
1:B:141:LYS:HE3	1:B:141:LYS:HB2	1.88	0.41
1:B:298:ALA:HB1	1:B:305:MET:HE3	2.02	0.41
3:E:200:SER:HB3	3:E:203:ILE:O	2.20	0.41
4:G:251:LYS:HA	4:G:273:VAL:HG12	2.02	0.41
4:H:158:ASP:O	4:H:160:SER:N	2.53	0.41
1:A:319:TYR:CG	1:A:320:PRO:HA	2.56	0.41
5:I:58:ASP:OD1	5:I:58:ASP:N	2.42	0.41
1:B:192:HIS:HE2	2:C:303:LEU:HD12	1.85	0.40
1:B:443:LEU:HD13	1:B:449:ILE:HD11	2.03	0.40
2:C:149:GLU:O	2:C:149:GLU:HG3	2.20	0.40
2:C:228:ARG:HH21	2:D:160:HIS:HE1	1.69	0.40
4:H:83:TYR:CZ	4:H:92:ILE:HG13	2.56	0.40
2:D:39:LEU:HG	2:D:137:ILE:HG23	2.03	0.40
3:E:220:SER:O	3:E:220:SER:OG	2.32	0.40
6:K:217:ASP:N	6:K:217:ASP:OD1	2.53	0.40
2:C:327:ASN:OD1	2:C:327:ASN:N	2.42	0.40
2:D:234:ILE:HD11	2:D:265:LEU:HD21	2.03	0.40
4:H:197:ALA:HB3	4:H:230:ALA:HB2	2.03	0.40
5:I:215:LEU:HD21	5:I:228:LEU:HD22	2.03	0.40
6:K:101:ASP:OD1	6:K:103:THR:OG1	2.30	0.40
6:L:102:LEU:HB2	6:L:126:CYS:SG	2.61	0.40
6:L:184:TYR:HD2	6:L:192:GLU:HB3	1.87	0.40
1:B:361:LEU:HD23	1:B:378:VAL:HG13	2.03	0.40
2:C:294:VAL:HG13	3:F:387:LEU:HG	2.03	0.40
3:F:499:LEU:HD13	3:F:506:MET:HB3	2.03	0.40
4:H:11:LYS:HG3	4:H:56:LEU:HD22	2.03	0.40
5:J:320:MET:HE3	5:J:321:GLU:HB2	2.03	0.40
1:A:450:SER:OG	1:A:455:ASP:OD2	2.39	0.40
2:C:39:LEU:HG	2:C:137:ILE:HG23	2.04	0.40
2:D:295:LEU:HD12	2:D:295:LEU:HA	1.96	0.40
3:F:394:VAL:O	3:F:397:GLU:HG2	2.21	0.40
5:I:263:ILE:H	5:I:263:ILE:HG12	1.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	410/721 (57%)	394 (96%)	16 (4%)	0	100	100
1	B	410/721 (57%)	380 (93%)	30 (7%)	0	100	100
2	C	327/351 (93%)	315 (96%)	12 (4%)	0	100	100
2	D	327/351 (93%)	315 (96%)	12 (4%)	0	100	100
3	E	353/523 (68%)	348 (99%)	5 (1%)	0	100	100
3	F	353/523 (68%)	349 (99%)	4 (1%)	0	100	100
4	G	281/305 (92%)	275 (98%)	6 (2%)	0	100	100
4	H	281/305 (92%)	272 (97%)	9 (3%)	0	100	100
5	I	224/452 (50%)	206 (92%)	18 (8%)	0	100	100
5	J	216/452 (48%)	193 (89%)	23 (11%)	0	100	100
6	K	214/269 (80%)	205 (96%)	8 (4%)	1 (0%)	24	46
6	L	214/269 (80%)	199 (93%)	14 (6%)	1 (0%)	24	46
All	All	3610/5242 (69%)	3451 (96%)	157 (4%)	2 (0%)	49	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	K	32	LYS
6	L	32	LYS

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	355/626 (57%)	344 (97%)	11 (3%)	35	63
1	B	353/626 (56%)	349 (99%)	4 (1%)	65	84
2	C	283/298 (95%)	264 (93%)	19 (7%)	15	33
2	D	283/298 (95%)	264 (93%)	19 (7%)	15	33
3	E	311/444 (70%)	308 (99%)	3 (1%)	68	86
3	F	311/444 (70%)	307 (99%)	4 (1%)	61	82
4	G	241/260 (93%)	236 (98%)	5 (2%)	47	73
4	H	241/260 (93%)	235 (98%)	6 (2%)	42	69
5	I	203/398 (51%)	196 (97%)	7 (3%)	32	60
5	J	196/398 (49%)	188 (96%)	8 (4%)	27	54
6	K	191/240 (80%)	184 (96%)	7 (4%)	30	57
6	L	189/240 (79%)	186 (98%)	3 (2%)	55	79
All	All	3157/4532 (70%)	3061 (97%)	96 (3%)	37	64

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	ILE
1	A	95	CYS
1	A	107	LEU
1	A	124	THR
1	A	161	ILE
1	A	253	SER
1	A	318	VAL
1	A	331	THR
1	A	359	ASN
1	A	367	VAL
1	A	429	SER
1	B	151	VAL
1	B	197	HIS
1	B	348	VAL
1	B	415	ASP
2	C	9	SER
2	C	12	SER
2	C	20	GLU
2	C	21	THR
2	C	31	SER
2	C	69	THR
2	C	91	GLU

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Mol	Chain	Res	Type
2	C	115	SER
2	C	123	SER
2	C	139	GLU
2	C	142	VAL
2	C	149	GLU
2	C	161	SER
2	C	214	THR
2	C	219	ASP
2	C	236	THR
2	C	262	SER
2	C	327	ASN
2	C	341	SER
2	D	9	SER
2	D	12	SER
2	D	20	GLU
2	D	21	THR
2	D	31	SER
2	D	69	THR
2	D	91	GLU
2	D	115	SER
2	D	123	SER
2	D	139	GLU
2	D	142	VAL
2	D	149	GLU
2	D	161	SER
2	D	214	THR
2	D	219	ASP
2	D	236	THR
2	D	262	SER
2	D	327	ASN
2	D	341	SER
3	E	172	ASP
3	E	241	THR
3	E	340	SER
3	F	194	GLN
3	F	286	SER
3	F	340	SER
3	F	386	LEU
4	G	80	SER
4	G	113	ASP
4	G	153	THR
4	G	186	ILE

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Mol	Chain	Res	Type
4	G	273	VAL
4	H	132[A]	ARG
4	H	132[B]	ARG
4	H	203	ASN
4	H	229	VAL
4	H	273	VAL
4	H	294	SER
5	I	25	LYS
5	I	46	VAL
5	I	88	ASP
5	I	89	SER
5	I	99	THR
5	I	263	ILE
5	I	326	VAL
5	J	35	LEU
5	J	43	LEU
5	J	59	VAL
5	J	77	CYS
5	J	88	ASP
5	J	97	LEU
5	J	99	THR
5	J	197	THR
6	K	14	ILE
6	K	15	ASP
6	K	16	VAL
6	K	81	SER
6	K	102	LEU
6	K	110	LEU
6	K	118	SER
6	L	115	LYS
6	L	137	VAL
6	L	177	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	89	GLN
1	A	160	ASN
1	A	263	ASN
1	A	337	HIS
1	A	359	ASN

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Mol	Chain	Res	Type
1	A	371	ASN
1	A	376	ASN
1	A	393	GLN
1	A	409	HIS
1	B	44	GLN
1	B	72	ASN
1	B	89	GLN
1	B	219	GLN
1	B	263	ASN
1	B	290	HIS
1	B	337	HIS
1	B	393	GLN
1	B	398	GLN
1	B	416	ASN
2	C	72	GLN
2	C	80	ASN
2	C	110	HIS
2	C	130	GLN
2	C	280	ASN
2	C	345	HIS
2	D	72	GLN
2	D	80	ASN
2	D	110	HIS
2	D	130	GLN
2	D	158	HIS
2	D	280	ASN
2	D	345	HIS
3	E	189	GLN
3	E	190	ASN
3	E	194	GLN
3	E	213	GLN
3	E	235	GLN
3	E	254	ASN
3	E	281	ASN
3	E	411	ASN
3	E	430	HIS
3	E	448	GLN
3	E	464	GLN
3	E	470	HIS
3	F	194	GLN
3	F	213	GLN
3	F	238	GLN

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Mol	Chain	Res	Type
3	F	274	HIS
3	F	281	ASN
3	F	371	HIS
3	F	411	ASN
3	F	430	HIS
3	F	431	ASN
3	F	448	GLN
3	F	455	ASN
3	F	464	GLN
3	F	477	GLN
4	G	109	ASN
4	G	128	HIS
4	G	214	GLN
4	G	243	GLN
4	G	244	GLN
4	H	109	ASN
4	H	170	HIS
4	H	214	GLN
4	H	222	GLN
4	H	243	GLN
5	I	218	ASN
5	I	323	ASN
5	I	325	GLN
5	J	32	ASN
5	J	136	GLN
5	J	190	HIS
5	J	218	ASN
5	J	325	GLN
6	K	19	HIS
6	K	34	HIS
6	K	59	ASN
6	K	112	ASN
6	K	145	GLN
6	K	172	GLN
6	L	91	GLN
6	L	145	GLN
6	L	172	GLN
6	L	203	ASN

5.3.3 RNA ⓘ

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 oligosaccharides 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.

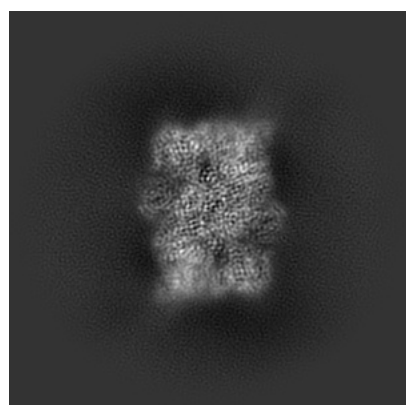
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24535. These allow visual inspection of the internal detail of the map and identification of artifacts.

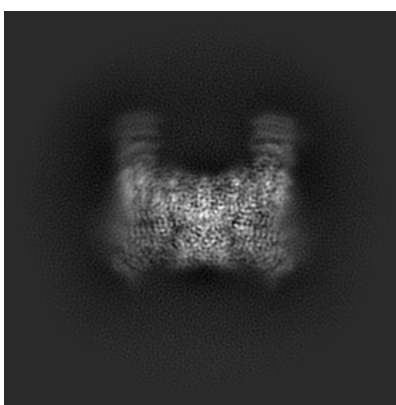
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

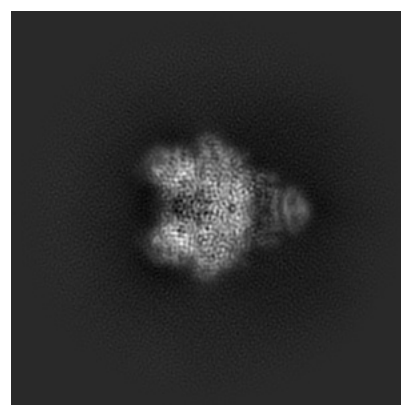
6.1.1 Primary map



X



Y

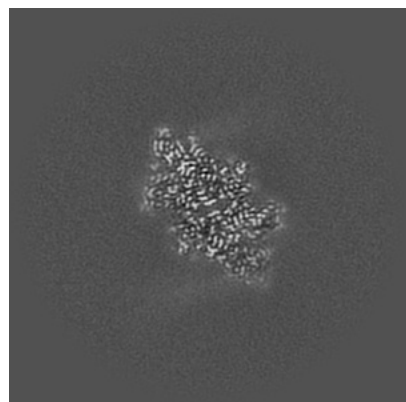


Z

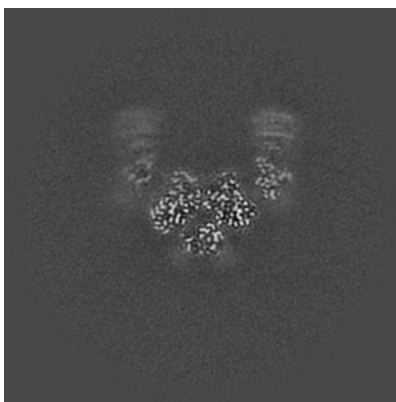
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

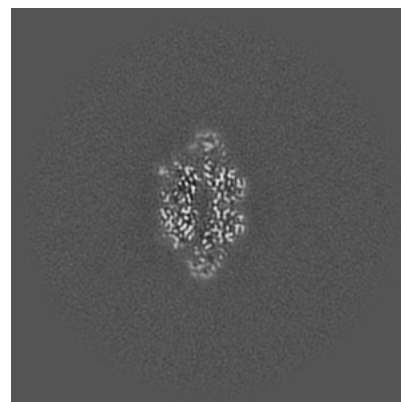
6.2.1 Primary map



X Index: 200



Y Index: 200

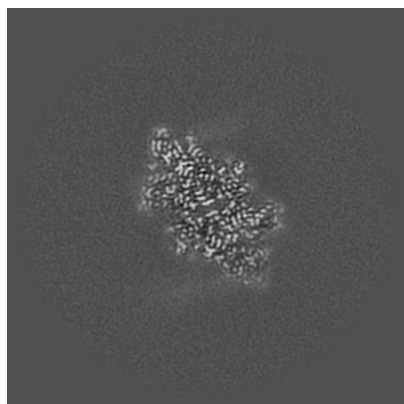


Z Index: 200

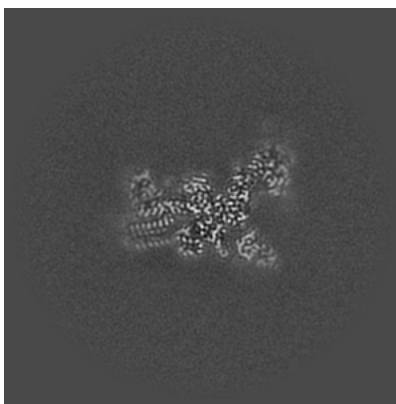
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

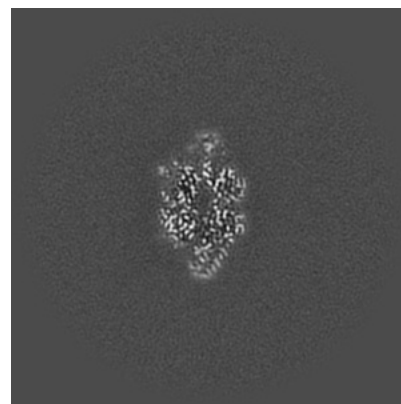
6.3.1 Primary map



X Index: 200



Y Index: 226

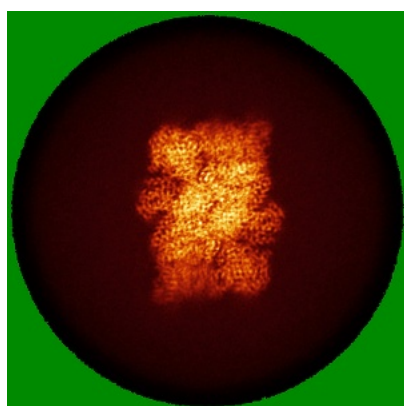


Z Index: 201

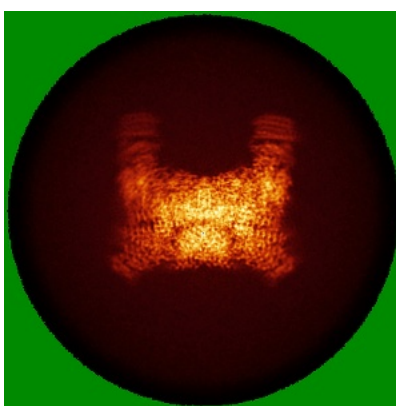
The images above show the largest variance slices of the map in three orthogonal directions.

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

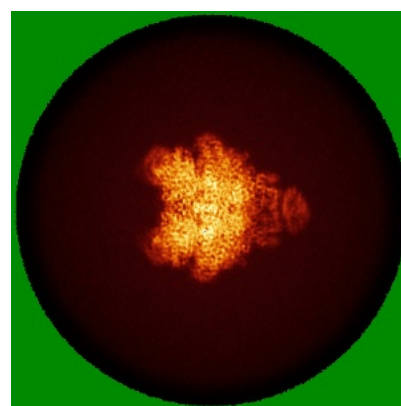
6.4.1 Primary map



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

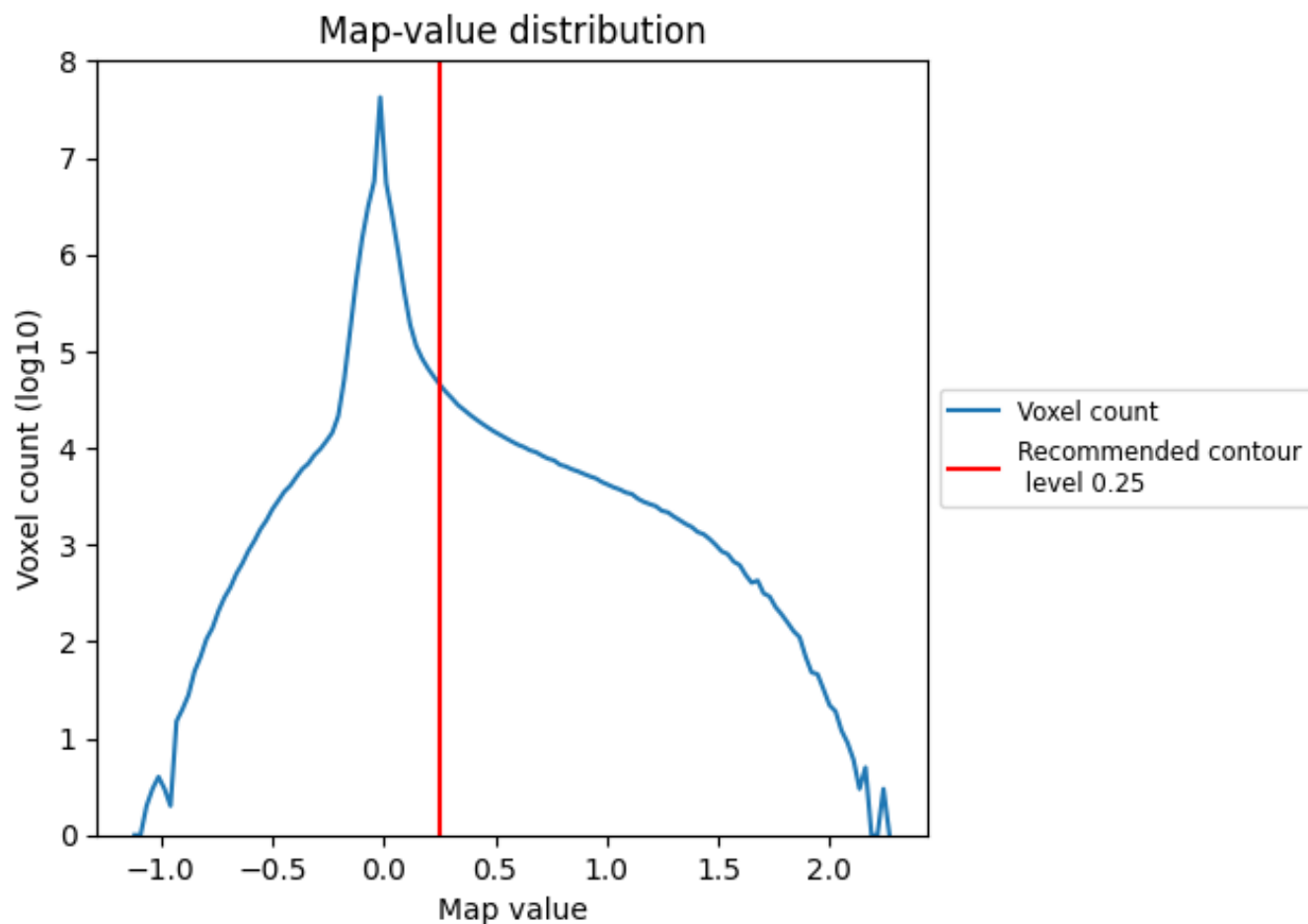
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

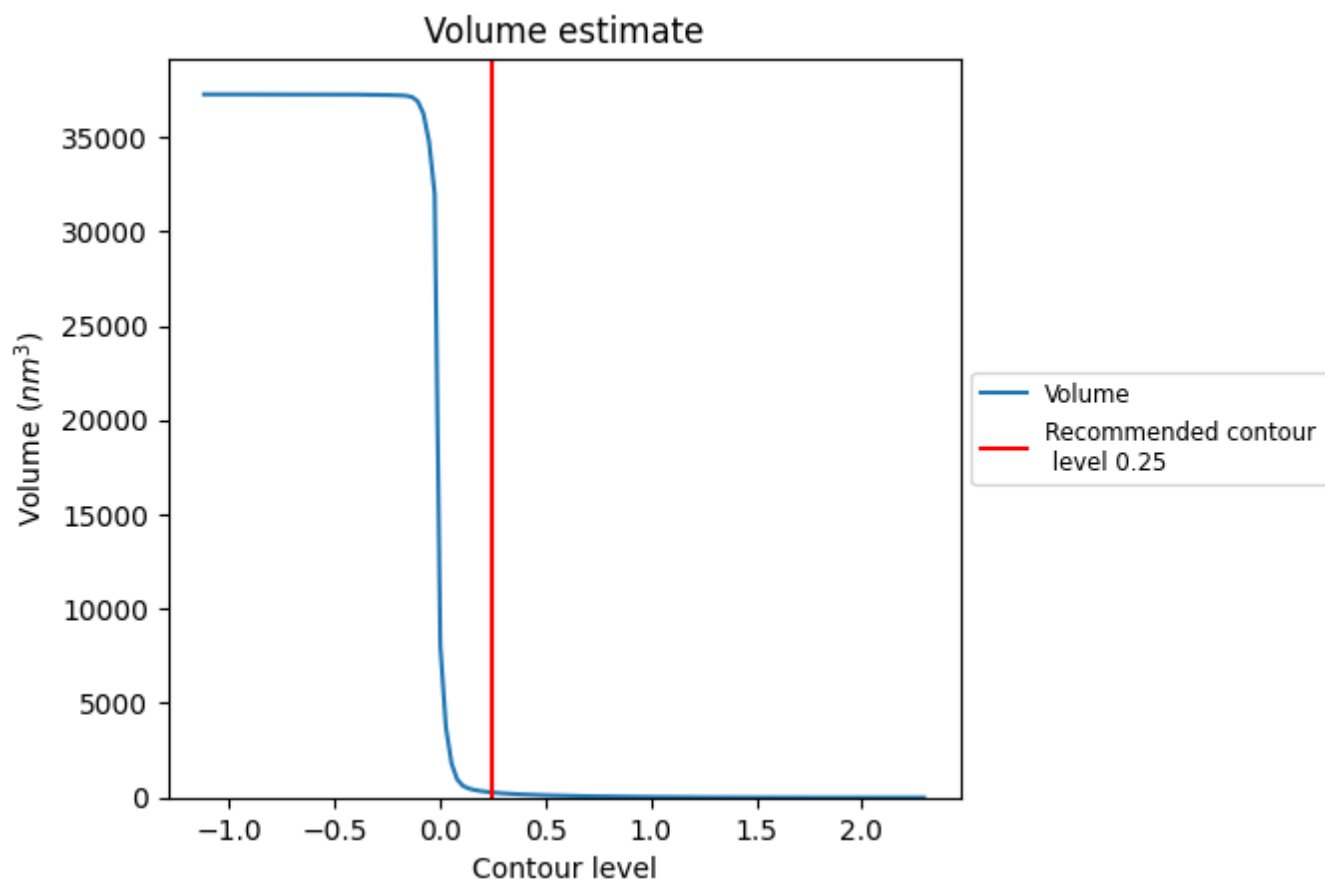
This section contains the results of statistical analysis of the map.

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.

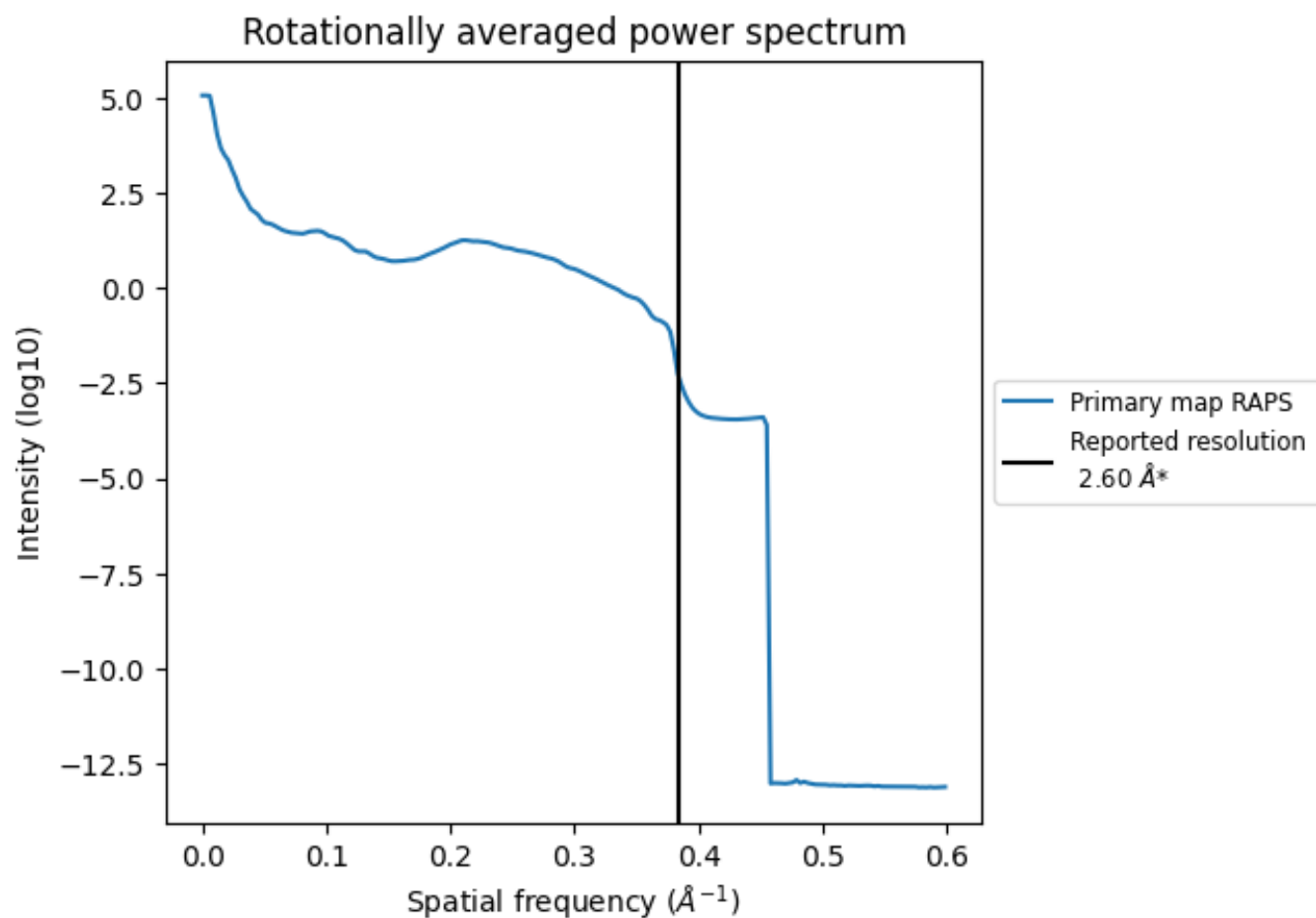
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 269 nm^3 ; this corresponds to an approximate mass of 243 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 0.385 Å⁻¹

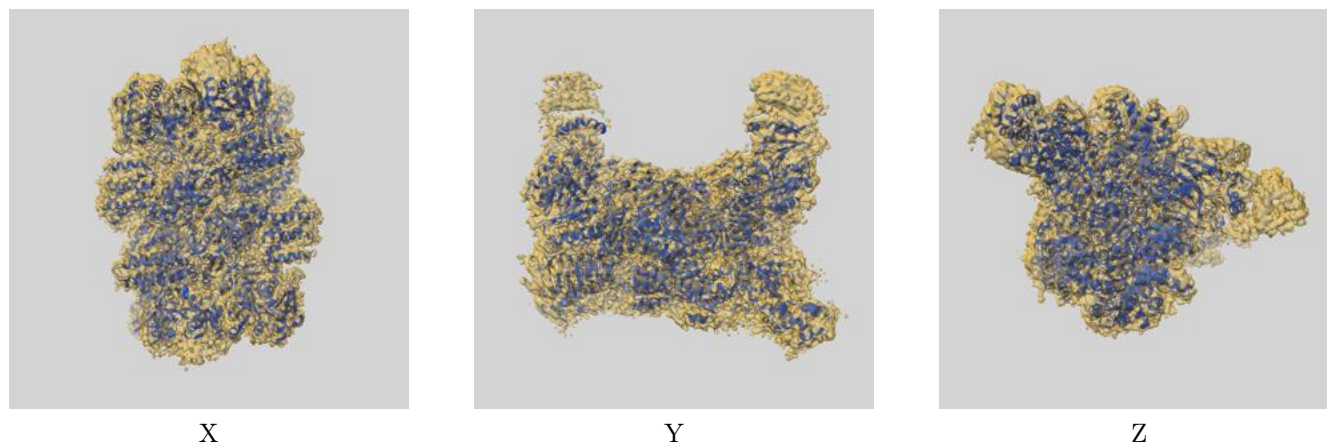
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

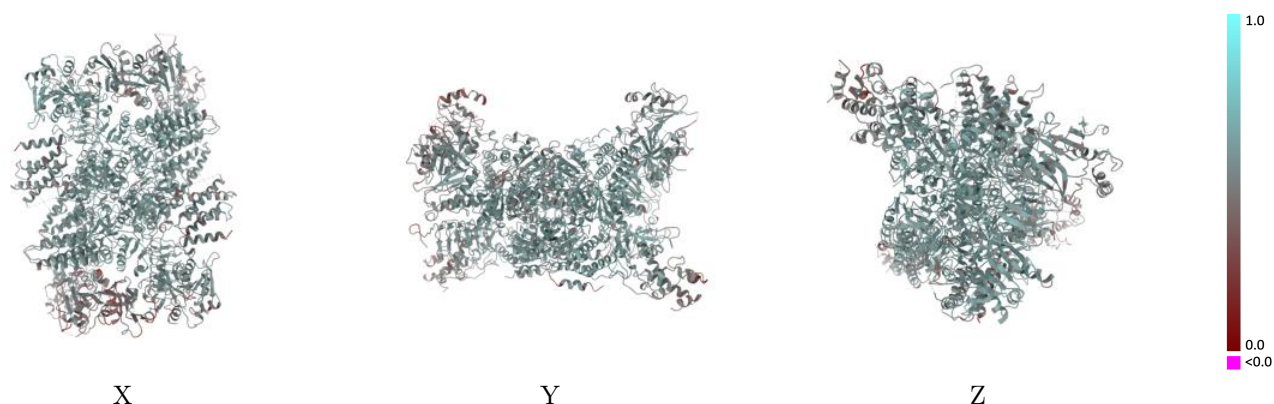
This section contains information regarding the fit between EMDB map EMD-24535 and PDB model 7RLO. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



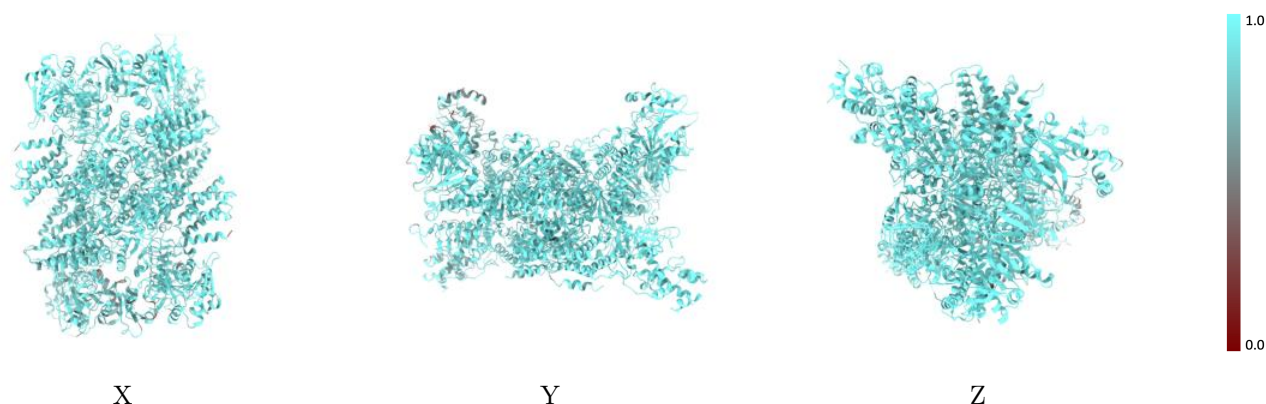
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



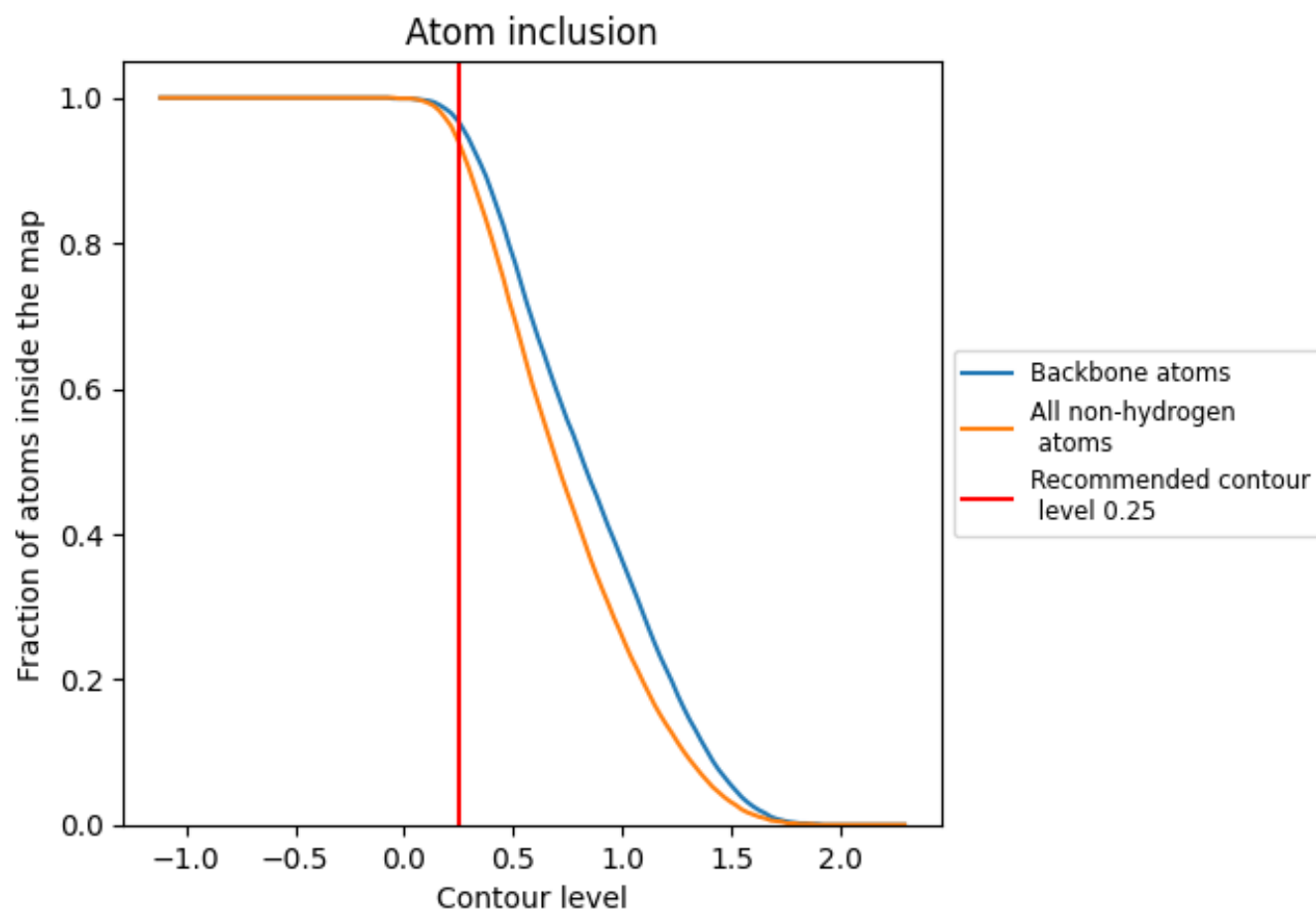
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9390	0.5460
A	0.9720	0.5680
B	0.9120	0.5210
C	0.9460	0.5450
D	0.9550	0.5570
E	0.9760	0.5950
F	0.9380	0.5750
G	0.9640	0.5760
H	0.9640	0.5780
I	0.9370	0.5230
J	0.8070	0.4440
K	0.9460	0.5080
L	0.9000	0.4940

1.0

0.0

<0.0