



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:04 AM UTC

PDB ID : 8D4X / pdb_00008d4x
EMDB ID : EMD-27201
Title : Structure of the human UBR5 HECT-type E3 ubiquitin ligase in a dimeric form
Authors : Wang, F.; He, Q.; Lin, G.; Li, H.
Deposited on : 2022-06-02
Resolution : 2.80 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

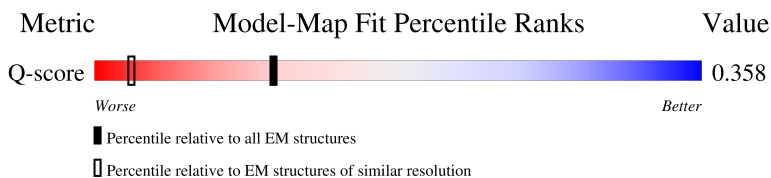
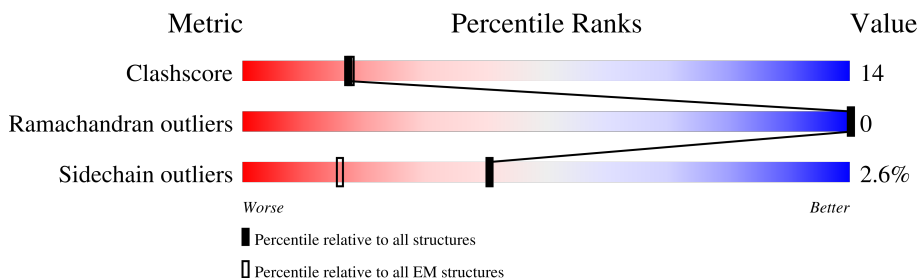
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	2806	 5% 43% 17% 40%
1	B	2806	 5% 41% 17% 41%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 26409 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 E3 ubiquitin-protein ligase UBR5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1684	Total	C	N	O	S	0	0
			13260	8374	2321	2465	100		
1	B	1669	Total	C	N	O	S	0	0
			13143	8305	2300	2439	99		

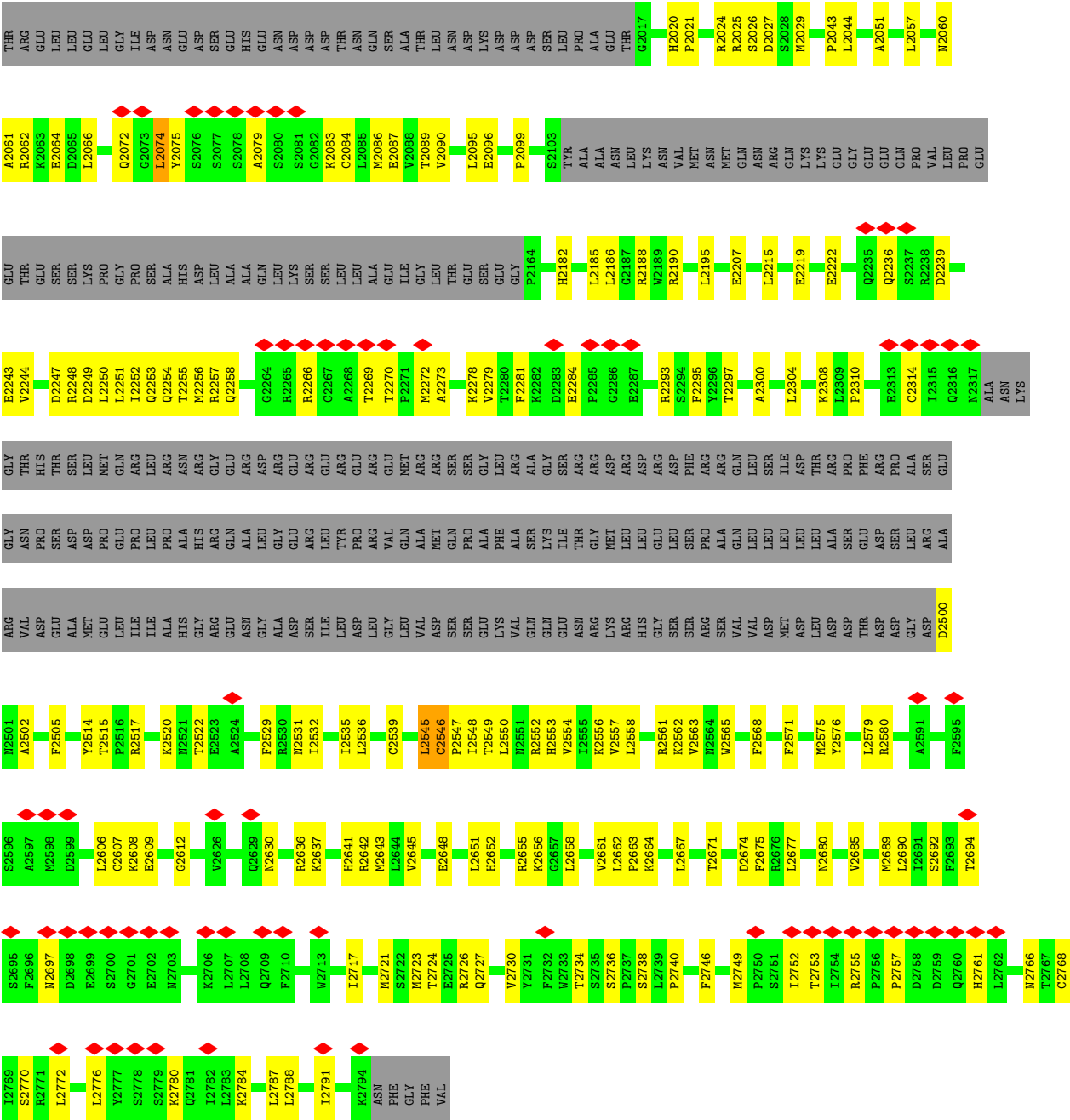
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ASP	-	expression tag	UNP O95071
A	-5	TYR	-	expression tag	UNP O95071
A	-4	LYS	-	expression tag	UNP O95071
A	-3	ASP	-	expression tag	UNP O95071
A	-2	ASP	-	expression tag	UNP O95071
A	-1	ASP	-	expression tag	UNP O95071
A	0	LYS	-	expression tag	UNP O95071
B	-6	ASP	-	expression tag	UNP O95071
B	-5	TYR	-	expression tag	UNP O95071
B	-4	LYS	-	expression tag	UNP O95071
B	-3	ASP	-	expression tag	UNP O95071
B	-2	ASP	-	expression tag	UNP O95071
B	-1	ASP	-	expression tag	UNP O95071
B	0	LYS	-	expression tag	UNP O95071

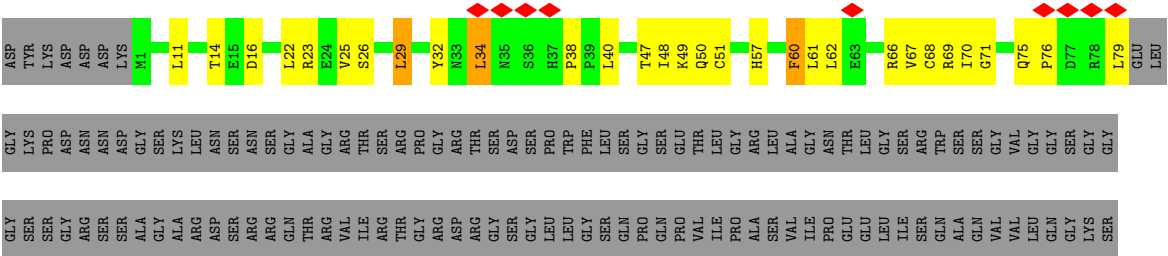
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	3	Total	Zn	0
			3	3	
2	B	3	Total	Zn	0
			3	3	





● Molecule 1: E3 ubiquitin-protein ligase UBR5









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	844403	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	65	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.744	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	331.2, 331.2, 331.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.828, 0.828, 0.828	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: ZN

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	0.18	0/13536	0.37	0/18339
1	B	0.15	0/13417	0.36	1/18177 (0.0%)
All	All	0.16	0/26953	0.37	1/36516 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1203	GLU	CB-CA-C	-5.55	110.16	116.54

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	13260	0	13247	387	0
1	B	13143	0	13138	365	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
All	All	26409	0	26385	717	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 14.

All (717) 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)
1:A:2505:PHE:CE2	1:A:2548:ILE:HD11	1.45	1.48
1:A:2505:PHE:HE2	1:A:2548:ILE:CD1	1.53	1.22
1:A:2300:ALA:CB	1:A:2547:PRO:HG2	1.74	1.17
1:A:2304:LEU:HD21	1:A:2548:ILE:HG13	1.29	1.06
1:A:2300:ALA:HB3	1:A:2547:PRO:HG2	1.27	1.06
1:A:2300:ALA:HB2	1:A:2547:PRO:HD2	1.50	0.93
1:A:1442:GLU:OE2	1:A:1509:GLY:HA3	1.75	0.87
1:B:907:MET:HE3	1:B:907:MET:H	1.39	0.85
1:A:2553:HIS:ND1	1:A:2643:MET:SD	2.49	0.85
1:A:2606:LEU:O	1:A:2612:GLY:HA2	1.77	0.85
1:B:2606:LEU:O	1:B:2612:GLY:HA2	1.77	0.84
1:A:2300:ALA:CB	1:A:2547:PRO:CG	2.55	0.84
1:B:29:LEU:O	1:B:29:LEU:HD22	1.79	0.83
1:A:568:MET:HE3	1:A:568:MET:H	1.45	0.81
1:B:818:THR:HG21	1:B:917:ASP:HA	1.64	0.80
1:B:2579:LEU:HD22	1:B:2635:VAL:HG22	1.60	0.80
1:A:2505:PHE:CE2	1:A:2548:ILE:CD1	2.40	0.80
1:B:1839:TRP:HE1	1:B:2176:MET:HE3	1.49	0.78
1:B:799:VAL:HA	1:B:813:ARG:O	1.85	0.77
1:A:2721:MET:HE1	1:A:2726:ARG:HA	1.66	0.76
1:A:2545:LEU:HD23	1:A:2545:LEU:N	2.01	0.75
1:B:2097:VAL:HG13	1:B:2101:LYS:HD2	1.68	0.74
1:A:2532:ILE:HD11	1:A:2548:ILE:HD12	1.69	0.74
1:B:904:ASN:HA	1:B:907:MET:HE1	1.69	0.74
1:B:2186:LEU:HD13	1:B:2215:LEU:HD11	1.70	0.74
1:A:478:CYS:SG	1:A:479:CYS:N	2.61	0.74
1:A:2539:CYS:SG	1:A:2546:CYS:HB3	2.28	0.74
1:A:747:LEU:HD21	1:A:761:LYS:HB3	1.68	0.74
1:A:2545:LEU:HD11	1:A:2740:PRO:HD3	1.71	0.73
1:B:463:GLN:HG3	1:B:465:TYR:HE1	1.51	0.72
1:B:922:ILE:HD11	1:B:1105:LEU:HD21	1.71	0.72
1:B:827:MET:SD	1:B:828:GLY:N	2.63	0.72
1:A:1343:ILE:HD13	1:A:1428:PHE:HB2	1.71	0.72
1:A:2545:LEU:HD12	1:A:2738:SER:O	1.89	0.72
1:A:2253:GLN:HA	1:A:2256:MET:HE3	1.72	0.71
1:B:1386:CYS:HA	1:B:1390:LYS:HB2	1.72	0.71
1:A:2300:ALA:HB2	1:A:2547:PRO:CD	2.21	0.71
1:A:503:LYS:HE2	1:A:506:LEU:HD23	1.73	0.70
1:A:463:GLN:HG3	1:A:465:TYR:HE1	1.54	0.70
1:A:2304:LEU:CD2	1:A:2548:ILE:HG13	2.16	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1256:TYR:HE1	1:A:1331:ARG:HG3	1.56	0.70
1:A:2557:VAL:HB	1:A:2651:LEU:HD12	1.73	0.69
1:B:22:LEU:HB3	1:B:836:LEU:HD11	1.74	0.68
1:B:2044:LEU:HD11	1:B:2051:ALA:HB3	1.75	0.68
1:B:76:PRO:HG3	1:B:854:LEU:HD11	1.74	0.68
1:B:433:ARG:NH1	1:B:481:LEU:O	2.27	0.68
1:A:1269:ASN:HD21	1:A:1273:GLU:HG3	1.58	0.68
1:A:479:CYS:SG	1:A:480:ALA:N	2.67	0.67
1:B:377:LEU:HG	1:B:379:SER:H	1.58	0.67
1:B:813:ARG:NH2	1:B:841:ILE:O	2.27	0.67
1:B:2607:CYS:SG	1:B:2608:LYS:N	2.67	0.67
1:A:2637:LYS:HE2	1:A:2637:LYS:HA	1.75	0.67
1:A:23:ARG:NH2	1:A:834:ASP:OD1	2.27	0.67
1:A:760:LEU:HD12	1:A:767:ARG:HH12	1.59	0.67
1:A:1697:ARG:HH12	1:B:2695:SER:HB3	1.59	0.67
1:B:1408:GLU:OE1	1:B:1417:ARG:NH1	2.26	0.67
1:A:908:LEU:HD13	1:A:911:PHE:HE1	1.59	0.67
1:A:2505:PHE:HB3	1:A:2514:TYR:HB3	1.76	0.67
1:A:1852:GLN:HG2	1:A:2090:VAL:HG13	1.77	0.66
1:B:747:LEU:HB2	1:B:759:VAL:HG13	1.78	0.66
1:B:2050:LEU:HD13	1:B:2066:LEU:HD22	1.76	0.66
1:B:2505:PHE:HB3	1:B:2514:TYR:HB3	1.78	0.66
1:B:1810:TYR:OH	1:B:1818:LYS:NZ	2.29	0.65
1:B:837:ASP:N	1:B:917:ASP:OD2	2.24	0.65
1:B:1088:ILE:HD12	1:B:1089:LEU:N	2.12	0.65
1:A:1265:VAL:O	1:A:1274:HIS:NE2	2.28	0.65
1:A:2062:ARG:NH1	1:B:1713:SER:OG	2.28	0.65
1:A:413:ARG:HH22	1:A:459:GLU:HG3	1.61	0.65
1:A:2087:GLU:OE1	1:A:2087:GLU:N	2.19	0.65
1:A:1434:ARG:NH2	1:B:1931:GLU:OE1	2.29	0.65
1:B:1331:ARG:O	1:B:1331:ARG:NH1	2.30	0.65
1:B:1850:GLU:HG3	1:B:2189:TRP:HA	1.78	0.64
1:A:361:GLN:N	1:A:361:GLN:OE1	2.31	0.64
1:A:2074:LEU:HB3	1:A:2086:MET:HB2	1.78	0.64
1:B:547:VAL:HG13	1:B:659:VAL:HB	1.80	0.64
1:A:1490:ILE:HD13	1:B:1845:ILE:HD12	1.80	0.64
1:B:2688:GLN:OE1	1:B:2688:GLN:N	2.25	0.64
1:B:502:ARG:HA	1:B:505:MET:HE2	1.80	0.64
1:A:2248:ARG:NH2	1:A:2308:LYS:O	2.30	0.64
1:A:1407:LYS:NZ	1:A:1408:GLU:OE2	2.31	0.63
1:A:2243:GLU:O	1:A:2258:GLN:NE2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2057:LEU:HG	1:A:2677:LEU:HD13	1.81	0.63
1:A:569:ASN:OD1	1:A:654:ARG:NH2	2.32	0.63
1:B:66:ARG:HH22	1:B:68:CYS:HB2	1.64	0.63
1:A:818:THR:HG21	1:A:917:ASP:HA	1.81	0.62
1:A:2061:ALA:HB1	1:A:2066:LEU:HD11	1.81	0.62
1:B:2637:LYS:HA	1:B:2637:LYS:HE2	1.81	0.62
1:A:2025:ARG:HD3	1:A:2029:MET:HB3	1.81	0.62
1:B:1088:ILE:O	1:B:1092:LEU:HD12	2.00	0.62
1:B:916:CYS:SG	1:B:917:ASP:N	2.70	0.62
1:A:2552:ARG:NH1	1:A:2556:LYS:HE3	2.15	0.62
1:A:1444:ALA:HB2	1:A:1499:LEU:HB3	1.82	0.62
1:A:747:LEU:HB2	1:A:759:VAL:HG13	1.82	0.61
1:B:812:LEU:HD12	1:B:822:MET:HE3	1.81	0.61
1:B:2218:PHE:CE1	1:B:2222:GLU:HB3	2.35	0.61
1:A:414:ALA:O	1:A:418:GLY:N	2.33	0.61
1:B:501:GLN:O	1:B:505:MET:HG3	2.00	0.61
1:A:1799:MET:HE2	1:A:1799:MET:HA	1.83	0.61
1:A:2548:ILE:HG23	1:A:2550:LEU:CD1	2.30	0.60
1:A:799:VAL:HA	1:A:813:ARG:O	2.00	0.60
1:B:1461:LYS:NZ	1:B:1794:GLN:OE1	2.32	0.60
1:A:18:LEU:HD22	1:A:809:PRO:HG2	1.84	0.60
1:A:2300:ALA:HB3	1:A:2547:PRO:CG	2.16	0.60
1:B:2218:PHE:CE2	1:B:2677:LEU:HD21	2.36	0.60
1:A:2607:CYS:SG	1:A:2608:LYS:N	2.68	0.60
1:B:1343:ILE:HD13	1:B:1428:PHE:HB2	1.84	0.60
1:B:66:ARG:HG3	1:B:66:ARG:HH11	1.65	0.59
1:B:1373:GLN:O	1:B:1373:GLN:NE2	2.32	0.59
1:A:372:ILE:HG22	1:A:373:CYS:SG	2.42	0.59
1:A:2249:ASP:O	1:A:2253:GLN:HG2	2.03	0.59
1:A:2552:ARG:HH12	1:A:2556:LYS:HE3	1.67	0.59
1:A:2766:ASN:O	1:A:2770:SER:N	2.35	0.59
1:A:505:MET:HE3	1:A:728:PRO:HB2	1.83	0.59
1:A:1149:LYS:HE2	1:A:1149:LYS:H	1.68	0.59
1:A:2186:LEU:HD13	1:A:2215:LEU:HD11	1.85	0.59
1:B:838:LEU:HD23	1:B:839:PRO:HD2	1.85	0.59
1:A:761:LYS:HB2	1:A:766:VAL:HG22	1.84	0.59
1:B:2650:PRO:O	1:B:2654:MET:HG2	2.03	0.59
1:B:428:SER:OG	1:B:478:CYS:SG	2.61	0.58
1:A:11:LEU:HD11	1:A:848:VAL:HG13	1.85	0.58
1:A:2641:HIS:HA	1:A:2645:VAL:HG12	1.85	0.58
1:B:1109:LYS:HB3	1:B:1113:GLY:HA2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2228:GLU:OE1	1:B:2229:MET:HE2	2.04	0.58
1:A:2662:LEU:HD12	1:A:2663:PRO:HD2	1.85	0.58
1:B:1144:ILE:HG23	1:B:1146:SER:H	1.68	0.58
1:B:2545:LEU:HD11	1:B:2740:PRO:HA	1.86	0.58
1:A:844:LEU:HD23	1:A:869:MET:HE3	1.85	0.58
1:B:1799:MET:HE1	1:B:1828:GLN:HA	1.84	0.57
1:A:2293:ARG:NH1	1:A:2734:THR:OG1	2.37	0.57
1:A:2247:ASP:O	1:A:2251:LEU:N	2.32	0.57
1:B:1199:CYS:C	1:B:1237:LYS:HZ1	2.12	0.57
1:A:1197:ARG:HG3	1:A:1197:ARG:HH11	1.69	0.57
1:A:2539:CYS:SG	1:A:2546:CYS:CB	2.92	0.57
1:B:498:PRO:HD2	1:B:501:GLN:HE22	1.69	0.57
1:B:2558:LEU:HD23	1:B:2658:LEU:HD13	1.85	0.57
1:B:2780:LYS:O	1:B:2784:LYS:HD2	2.03	0.57
1:A:503:LYS:HZ3	1:A:568:MET:HB2	1.70	0.57
1:A:2044:LEU:HB2	1:A:2576:TYR:HE2	1.66	0.57
1:A:742:GLU:HB2	1:A:743:LYS:NZ	2.20	0.57
1:A:1480:GLU:OE1	1:B:1928:HIS:NE2	2.37	0.57
1:A:1513:LEU:HD22	1:B:1918:LEU:HB3	1.86	0.57
1:A:1962:ASN:O	1:A:1965:THR:OG1	2.20	0.57
1:B:2233:ARG:HB3	1:B:2541:LEU:HD11	1.87	0.57
1:A:2064:GLU:OE2	1:A:2190:ARG:NH1	2.38	0.57
1:A:2182:HIS:HA	1:A:2185:LEU:HD12	1.87	0.57
1:A:2548:ILE:HG23	1:A:2550:LEU:HD11	1.86	0.57
1:B:841:ILE:HD12	1:B:869:MET:HE1	1.87	0.57
1:A:52:VAL:HB	1:A:376:ALA:HB2	1.87	0.56
1:A:2257:ARG:NH2	1:A:2314:CYS:SG	2.78	0.56
1:B:890:GLN:HA	1:B:893:MET:HE2	1.85	0.56
1:B:1962:ASN:O	1:B:1965:THR:OG1	2.20	0.56
1:B:2020:HIS:ND1	1:B:2021:PRO:HD2	2.20	0.56
1:A:61:LEU:HD22	1:A:374:ILE:HG23	1.87	0.56
1:A:1845:ILE:HD12	1:B:1490:ILE:HD13	1.86	0.56
1:B:1854:ARG:HG2	1:B:2191:LEU:HD12	1.87	0.56
1:B:2610:GLU:OE2	1:B:2612:GLY:N	2.38	0.56
1:A:562:MET:HE2	1:A:575:GLN:HB2	1.87	0.56
1:B:2044:LEU:HD21	1:B:2569:ALA:HB1	1.88	0.56
1:A:877:MET:HE3	1:A:916:CYS:HB2	1.88	0.56
1:A:2249:ASP:HA	1:A:2310:PRO:HG3	1.87	0.56
1:A:796:GLU:N	1:A:796:GLU:OE1	2.39	0.56
1:B:48:ILE:HD12	1:B:48:ILE:H	1.69	0.56
1:B:2216:GLY:HA3	1:B:2220:VAL:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2083:LYS:O	1:A:2188:ARG:NH1	2.39	0.56
1:A:2548:ILE:HG23	1:A:2548:ILE:O	2.05	0.56
1:B:2679:VAL:HG12	1:B:2680:ASN:OD1	2.06	0.56
1:A:461:THR:O	1:A:463:GLN:NE2	2.36	0.56
1:A:567:ASN:HB3	1:A:570:ASP:HB2	1.87	0.56
1:A:2652:HIS:CE1	1:A:2656:LYS:HE3	2.39	0.56
1:A:1512:GLU:HA	1:A:1512:GLU:OE2	2.05	0.56
1:A:2236:GLN:HG3	1:A:2273:ALA:HB3	1.88	0.56
1:A:2502:ALA:HB1	1:A:2517:ARG:HH11	1.70	0.56
1:B:1334:GLN:HA	1:B:1404:THR:HG21	1.87	0.56
1:B:2735:SER:O	1:B:2735:SER:OG	2.24	0.56
1:A:2749:MET:O	1:A:2749:MET:HG2	2.06	0.55
1:A:752:ASP:HA	1:A:805:GLY:HA2	1.87	0.55
1:A:2690:LEU:O	1:A:2694:THR:OG1	2.21	0.55
1:B:2044:LEU:HD23	1:B:2576:TYR:CE1	2.41	0.55
1:A:1224:LYS:NZ	1:A:1226:THR:O	2.39	0.55
1:B:2248:ARG:NE	1:B:2307:GLU:OE2	2.40	0.55
1:B:2636:ARG:HD2	1:B:2640:GLU:OE1	2.05	0.55
1:B:461:THR:O	1:B:463:GLN:NE2	2.39	0.55
1:B:752:ASP:HA	1:B:805:GLY:HA2	1.88	0.55
1:B:2300:ALA:CB	1:B:2547:PRO:HD2	2.37	0.55
1:B:2504:LEU:HD11	1:B:2528:CYS:SG	2.46	0.55
1:B:1155:MET:HE1	1:B:1262:THR:HG22	1.88	0.55
1:B:76:PRO:HA	1:B:79:LEU:HD12	1.88	0.55
1:B:1103:ARG:HH21	1:B:1153:VAL:HG23	1.72	0.55
1:B:1177:ASP:HB2	1:B:1210:GLU:HG2	1.88	0.55
1:B:2763:PRO:HB3	1:B:2774:VAL:HA	1.89	0.55
1:A:387:LYS:HA	1:A:423:LYS:HE3	1.88	0.54
1:A:2300:ALA:CB	1:A:2547:PRO:CD	2.85	0.54
1:A:68:CYS:SG	1:A:69:ARG:N	2.81	0.54
1:B:2583:ILE:HD11	1:B:2635:VAL:HG21	1.88	0.54
1:A:1848:SER:O	1:A:1852:GLN:HG3	2.08	0.54
1:B:746:ILE:HD11	1:B:760:LEU:HD23	1.89	0.54
1:B:876:LEU:HD11	1:B:911:PHE:CE1	2.42	0.54
1:B:1381:ASP:OD1	1:B:1434:ARG:NH1	2.41	0.54
1:A:2247:ASP:HB3	1:A:2250:LEU:HB2	1.88	0.54
1:A:12:PRO:HG2	1:A:861:LYS:HD3	1.90	0.54
1:A:2074:LEU:HD23	1:A:2086:MET:HA	1.89	0.54
1:A:2664:LYS:HA	1:A:2667:LEU:HD23	1.89	0.54
1:B:1951:PHE:CZ	1:B:2193:LEU:HD11	2.42	0.54
1:A:2553:HIS:CD2	1:A:2563:VAL:HB	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1295:PRO:HD2	1:B:1297:ARG:HH21	1.72	0.54
1:A:1468:LEU:HD11	1:A:1798:LEU:HB3	1.90	0.54
1:A:1522:ARG:HH21	1:B:1865:PRO:HG3	1.71	0.54
1:A:2717:ILE:HG21	1:A:2787:LEU:HD23	1.90	0.54
1:B:2641:HIS:HA	1:B:2645:VAL:HB	1.90	0.54
1:A:1841:TRP:O	1:A:1845:ILE:HG12	2.07	0.54
1:B:14:THR:HG23	1:B:16:ASP:H	1.71	0.54
1:A:438:THR:HG23	1:A:440:ASN:H	1.73	0.54
1:B:2684:GLU:N	1:B:2684:GLU:OE1	2.40	0.54
1:A:803:THR:HB	1:A:810:ILE:HD13	1.90	0.53
1:A:1164:ASN:OD1	1:A:1164:ASN:N	2.40	0.53
1:A:816:ASN:ND2	1:A:919:ASN:OD1	2.39	0.53
1:A:1865:PRO:HG3	1:B:1522:ARG:HH21	1.72	0.53
1:B:2713:TRP:CD1	1:B:2780:LYS:HZ3	2.27	0.53
1:A:2752:ILE:HG12	1:A:2772:LEU:HB3	1.90	0.53
1:B:1464:PHE:HB3	1:B:1798:LEU:HD11	1.89	0.53
1:B:2546:CYS:SG	1:B:2548:ILE:HG22	2.48	0.53
1:A:473:ILE:HA	1:A:487:LEU:HD13	1.90	0.53
1:A:1464:PHE:HB3	1:A:1798:LEU:HD11	1.91	0.53
1:A:1472:VAL:HG11	1:A:1827:LEU:HD21	1.91	0.53
1:A:11:LEU:HD22	1:A:807:GLU:HB3	1.89	0.53
1:A:546:ALA:HB3	1:A:561:LEU:HB3	1.90	0.53
1:A:885:TYR:HE1	1:A:1091:LEU:HD12	1.74	0.53
1:A:479:CYS:HB2	1:A:751:VAL:HG12	1.91	0.53
1:A:2079:ALA:HB1	1:A:2084:CYS:HB2	1.91	0.53
1:A:2300:ALA:CB	1:A:2547:PRO:HD2	2.33	0.53
1:B:1156:GLY:HA2	1:B:1160:PRO:HA	1.91	0.53
1:B:2529:PHE:CE2	1:B:2650:PRO:HB3	2.44	0.53
1:A:1114:MET:HG2	1:A:1118:MET:HE2	1.91	0.53
1:A:2087:GLU:H	1:A:2087:GLU:CD	2.13	0.53
1:A:2689:MET:O	1:A:2692:SER:OG	2.26	0.53
1:B:874:GLN:OE1	1:B:914:HIS:ND1	2.40	0.53
1:A:765:TRP:CH2	1:A:767:ARG:HD3	2.44	0.53
1:A:493:TRP:CE2	1:A:773:LEU:HD13	2.44	0.53
1:A:1405:LEU:HD23	1:A:1425:THR:HG23	1.91	0.52
1:A:40:LEU:HD21	1:A:356:LEU:HD13	1.90	0.52
1:B:1180:SER:O	1:B:1184:THR:HG23	2.09	0.52
1:B:2543:ASN:ND2	1:B:2543:ASN:O	2.42	0.52
1:A:568:MET:SD	1:A:569:ASN:N	2.82	0.52
1:A:1114:MET:HE3	1:A:1119:SER:HA	1.90	0.52
1:A:399:GLU:HG2	1:A:400:PRO:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:ALA:HA	1:A:417:LEU:HB2	1.89	0.52
1:B:803:THR:N	1:B:846:MET:HE1	2.24	0.52
1:A:917:ASP:OD1	1:A:917:ASP:N	2.40	0.52
1:A:2664:LYS:HE2	1:A:2664:LYS:H	1.73	0.52
1:B:1962:ASN:ND2	1:B:2180:ILE:O	2.32	0.52
1:B:2178:MET:HE3	1:B:2178:MET:N	2.23	0.52
1:A:661:ASP:N	1:A:661:ASP:OD1	2.43	0.52
1:A:756:VAL:HG13	1:A:771:PHE:HB2	1.91	0.52
1:A:837:ASP:OD1	1:A:920:ARG:NH2	2.38	0.52
1:B:66:ARG:HH21	1:B:362:TRP:HB3	1.74	0.52
1:A:1280:VAL:HG22	1:A:1329:LEU:HD21	1.92	0.52
1:A:1475:LEU:HD22	1:A:1791:VAL:HG13	1.91	0.52
1:A:2554:VAL:HG13	1:A:2651:LEU:HD11	1.92	0.52
1:B:2542:GLN:HA	1:B:2542:GLN:OE1	2.10	0.52
1:B:2183:ASP:N	1:B:2183:ASP:OD1	2.42	0.52
1:B:2594:VAL:O	1:B:2598:MET:HG3	2.09	0.52
1:A:1343:ILE:HD12	1:A:1424:VAL:HG13	1.91	0.51
1:A:2297:THR:HA	1:A:2547:PRO:HG3	1.92	0.51
1:B:68:CYS:SG	1:B:69:ARG:N	2.83	0.51
1:A:850:SER:HA	1:A:863:LYS:HA	1.92	0.51
1:B:1493:PRO:O	1:B:1719:ARG:NH2	2.42	0.51
1:A:825:ASP:HB3	1:A:831:ARG:HG3	1.93	0.51
1:A:2697:ASN:HB2	1:A:2753:THR:HG23	1.92	0.51
1:B:1095:SER:O	1:B:1099:GLN:NE2	2.29	0.51
1:A:893:MET:O	1:A:896:GLU:HG3	2.11	0.51
1:A:2545:LEU:CD1	1:A:2738:SER:O	2.58	0.51
1:B:494:TRP:HB3	1:B:735:PRO:HB3	1.92	0.51
1:B:1515:SER:O	1:B:1515:SER:OG	2.26	0.51
1:A:1490:ILE:HD12	1:B:2092:ARG:HD3	1.93	0.51
1:B:501:GLN:HA	1:B:504:LYS:HB2	1.93	0.51
1:A:2207:GLU:H	1:A:2207:GLU:CD	2.14	0.51
1:A:1713:SER:OG	1:B:2062:ARG:NH1	2.42	0.51
1:B:413:ARG:O	1:B:417:LEU:N	2.40	0.51
1:B:875:THR:OG1	1:B:876:LEU:N	2.44	0.51
1:B:29:LEU:HD22	1:B:29:LEU:C	2.36	0.51
1:B:1171:TYR:OH	1:B:1271:ARG:NH2	2.38	0.51
1:A:406:ASN:HB3	1:A:409:LEU:HB2	1.92	0.51
1:A:1084:ASN:O	1:A:1088:ILE:HG13	2.12	0.51
1:A:433:ARG:NH2	1:A:481:LEU:O	2.44	0.50
1:B:23:ARG:NH2	1:B:834:ASP:OD1	2.44	0.50
1:B:50:GLN:N	1:B:50:GLN:OE1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2690:LEU:HD11	1:B:2733:TRP:CZ3	2.46	0.50
1:A:427:LEU:HD23	1:A:436:VAL:HG22	1.92	0.50
1:A:744:THR:HG22	1:A:762:THR:HB	1.92	0.50
1:A:1192:ASP:OD1	1:A:1209:THR:OG1	2.29	0.50
1:B:757:HIS:HD2	1:B:810:ILE:HD11	1.75	0.50
1:A:1174:CYS:HA	1:A:1324:PHE:HE2	1.77	0.50
1:A:1363:LEU:HD11	1:B:1862:ALA:HB2	1.93	0.50
1:A:2026:SER:OG	1:A:2027:ASP:N	2.42	0.50
1:A:2724:THR:O	1:A:2727:GLN:HG2	2.12	0.50
1:A:1508:GLN:HA	1:A:1508:GLN:HE21	1.77	0.50
1:B:756:VAL:HG13	1:B:771:PHE:HB2	1.93	0.50
1:B:823:ALA:HB1	1:B:831:ARG:HH21	1.76	0.50
1:B:886:GLU:O	1:B:890:GLN:HG2	2.12	0.50
1:B:1096:VAL:HA	1:B:1099:GLN:HG2	1.92	0.50
1:A:1412:LYS:HE2	1:A:1412:LYS:HA	1.92	0.50
1:A:2757:PRO:HG3	1:A:2776:LEU:HD23	1.93	0.50
1:B:1961:MET:O	1:B:1965:THR:HG23	2.11	0.50
1:A:1441:VAL:HG11	1:B:1917:PHE:HE2	1.76	0.50
1:B:22:LEU:O	1:B:25:VAL:HG12	2.12	0.50
1:A:1274:HIS:HB3	1:A:1342:MET:CE	2.42	0.49
1:A:1941:VAL:HG21	1:A:2195:LEU:HD23	1.94	0.49
1:A:1153:VAL:O	1:A:1157:MET:HG3	2.11	0.49
1:B:1342:MET:O	1:B:1342:MET:HE3	2.12	0.49
1:B:1955:ILE:HG21	1:B:2211:ILE:HD13	1.94	0.49
1:A:746:ILE:HG13	1:A:760:LEU:HD22	1.93	0.49
1:B:836:LEU:HD22	1:B:838:LEU:HD12	1.94	0.49
1:B:1233:ASP:HB2	1:B:1236:GLU:HG2	1.95	0.49
1:B:2186:LEU:HD22	1:B:2193:LEU:HD21	1.94	0.49
1:A:802:PHE:CG	1:A:844:LEU:HD12	2.47	0.49
1:A:2062:ARG:HH11	1:B:1713:SER:HG	1.54	0.49
1:B:1871:PRO:HG3	1:B:1936:LEU:HD11	1.94	0.49
1:A:741:PRO:HB2	1:A:744:THR:HG21	1.94	0.49
1:A:392:GLN:OE1	1:A:411:HIS:ND1	2.45	0.49
1:A:1256:TYR:CE1	1:A:1331:ARG:HG3	2.43	0.49
1:B:2181:SER:HB3	1:B:2184:MET:HE3	1.94	0.49
1:B:2568:PHE:HE2	1:B:2639:ALA:HA	1.77	0.49
1:A:2500:ASP:OD2	1:A:2522:THR:OG1	2.21	0.49
1:B:757:HIS:ND1	1:B:770:ILE:HG12	2.27	0.49
1:B:922:ILE:HG13	1:B:923:LEU:HD22	1.93	0.49
1:A:886:GLU:O	1:A:890:GLN:NE2	2.44	0.49
1:B:414:ALA:O	1:B:418:GLY:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2176:MET:HB2	1:B:2180:ILE:HD11	1.95	0.49
1:A:1918:LEU:HD22	1:B:1438:ILE:HD12	1.95	0.49
1:A:2630:ASN:OD1	1:A:2630:ASN:N	2.45	0.49
1:B:493:TRP:CE2	1:B:773:LEU:HD13	2.48	0.49
1:B:2721:MET:SD	1:B:2721:MET:N	2.86	0.49
1:A:839:PRO:HG3	1:A:878:GLN:HE21	1.77	0.49
1:B:32:TYR:HB3	1:B:34:LEU:HD23	1.94	0.49
1:B:2281:PHE:HB3	1:B:2284:GLU:HB2	1.93	0.49
1:B:832:ASP:OD1	1:B:1112:ARG:NH2	2.40	0.48
1:B:1828:GLN:HE22	1:B:2171:PRO:HB3	1.78	0.48
1:B:1852:GLN:HG2	1:B:2090:VAL:CG1	2.43	0.48
1:A:1381:ASP:OD1	1:A:1434:ARG:NH1	2.47	0.48
1:A:1925:MET:HE1	1:B:1437:VAL:HB	1.95	0.48
1:A:1274:HIS:HB3	1:A:1342:MET:HE2	1.96	0.48
1:A:2565:TRP:O	1:A:2568:PHE:HB3	2.13	0.48
1:B:1269:ASN:HD21	1:B:1273:GLU:HG3	1.78	0.48
1:B:1712:ARG:HA	1:B:1715:GLN:HG2	1.96	0.48
1:A:895:LEU:HD11	1:A:907:MET:HG2	1.94	0.48
1:A:1199:CYS:SG	1:A:1216:HIS:HE1	2.35	0.48
1:A:1442:GLU:OE2	1:A:1509:GLY:CA	2.56	0.48
1:B:836:LEU:N	1:B:917:ASP:OD2	2.47	0.48
1:B:1259:LEU:HD11	1:B:1332:VAL:HG22	1.95	0.48
1:A:72:PHE:C	1:A:72:PHE:CD1	2.90	0.48
1:A:75:GLN:OE1	1:A:78:ARG:N	2.46	0.48
1:A:438:THR:OG1	1:A:439:GLU:OE1	2.32	0.48
1:A:2549:THR:HA	1:A:2680:ASN:ND2	2.28	0.48
1:B:437:ALA:HB2	1:B:476:LEU:HD11	1.96	0.48
1:B:433:ARG:NE	1:B:483:THR:OG1	2.46	0.48
1:A:818:THR:OG1	1:A:819:ILE:N	2.47	0.48
1:A:2269:THR:OG1	1:A:2270:THR:N	2.47	0.48
1:B:1848:SER:O	1:B:1852:GLN:HG3	2.14	0.48
1:B:2689:MET:O	1:B:2692:SER:OG	2.32	0.48
1:A:38:PRO:N	1:A:39:PRO:HD2	2.29	0.48
1:A:378:TYR:CD2	1:A:556:PRO:HD2	2.48	0.48
1:A:908:LEU:HD12	1:A:1101:TYR:CE2	2.49	0.48
1:A:413:ARG:O	1:A:417:LEU:N	2.42	0.48
1:B:2279:VAL:HB	1:B:2291:VAL:HG13	1.96	0.48
1:B:2530:ARG:HD2	1:B:2656:LYS:HE3	1.96	0.48
1:B:1240:CYS:SG	1:B:1242:THR:OG1	2.72	0.47
1:B:1854:ARG:NH1	1:B:2087:GLU:OE2	2.47	0.47
1:B:2099:PRO:HA	1:B:2102:MET:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2218:PHE:HE1	1:B:2222:GLU:HB3	1.79	0.47
1:A:503:LYS:HE3	1:A:503:LYS:HA	1.95	0.47
1:A:2500:ASP:OD1	1:A:2520:LYS:N	2.41	0.47
1:B:2749:MET:HE3	1:B:2750:PRO:HD2	1.97	0.47
1:A:742:GLU:HB2	1:A:743:LYS:HZ3	1.77	0.47
1:B:66:ARG:HH12	1:B:68:CYS:HB2	1.79	0.47
1:B:482:TYR:CE2	1:B:773:LEU:HD11	2.49	0.47
1:A:2571:PHE:HE2	1:A:2642:ARG:HE	1.62	0.47
1:B:2532:ILE:HA	1:B:2535:ILE:HD12	1.96	0.47
1:B:2762:LEU:HD23	1:B:2786:LYS:HD3	1.96	0.47
1:A:427:LEU:HD22	1:A:428:SER:N	2.29	0.47
1:A:2637:LYS:O	1:A:2641:HIS:HB2	2.14	0.47
1:B:1117:PHE:CD2	1:B:1158:VAL:HG23	2.50	0.47
1:B:1256:TYR:CE1	1:B:1331:ARG:HG3	2.50	0.47
1:B:1928:HIS:HA	1:B:2091:ASP:HB3	1.96	0.47
1:A:43:LEU:HD11	1:A:48:ILE:HD11	1.97	0.47
1:A:846:MET:HB3	1:A:867:ILE:HD13	1.96	0.47
1:A:1256:TYR:O	1:A:1260:THR:HG23	2.15	0.47
1:A:1351:LYS:HE3	1:A:1357:SER:HB2	1.97	0.47
1:A:2044:LEU:HD11	1:A:2051:ALA:HB3	1.97	0.47
1:A:2529:PHE:O	1:A:2532:ILE:HG22	2.15	0.47
1:A:2740:PRO:HD2	1:A:2746:PHE:CE2	2.50	0.47
1:A:1871:PRO:HB3	1:B:1716:TRP:CD1	2.49	0.47
1:A:2253:GLN:CA	1:A:2256:MET:HE3	2.42	0.47
1:B:498:PRO:HD2	1:B:501:GLN:NE2	2.29	0.47
1:B:1443:MET:HE1	1:B:1454:PRO:HG2	1.97	0.47
1:B:2031:PHE:CD2	1:B:2070:PRO:HG3	2.49	0.47
1:A:2685:VAL:H	1:A:2723:MET:HE1	1.80	0.47
1:A:2766:ASN:O	1:A:2770:SER:CA	2.63	0.47
1:B:1314:MET:HE1	1:B:1317:HIS:CD2	2.49	0.47
1:B:2269:THR:OG1	1:B:2270:THR:N	2.45	0.47
1:B:2653:ALA:HA	1:B:2656:LYS:HE2	1.96	0.47
1:A:417:LEU:O	1:A:461:THR:OG1	2.33	0.46
1:A:908:LEU:HD12	1:A:1101:TYR:HE2	1.80	0.46
1:B:57:HIS:NE2	1:B:69:ARG:HB2	2.30	0.46
1:B:501:GLN:HB3	1:B:774:ALA:HB2	1.96	0.46
1:B:1164:ASN:N	1:B:1164:ASN:OD1	2.41	0.46
1:B:1868:PRO:HA	1:B:1873:HIS:ND1	2.30	0.46
1:B:2700:SER:OG	1:B:2755:ARG:O	2.33	0.46
1:B:48:ILE:HD12	1:B:48:ILE:N	2.31	0.46
1:B:417:LEU:HD21	1:B:446:TRP:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:931:PHE:CE1	1:B:1123:GLY:HA3	2.50	0.46
1:B:2035:ILE:HD12	1:B:2035:ILE:O	2.14	0.46
1:B:2575:MET:HE2	1:B:2638:TYR:CZ	2.50	0.46
1:B:2583:ILE:O	1:B:2586:SER:OG	2.30	0.46
1:A:2281:PHE:HB3	1:A:2284:GLU:HB2	1.96	0.46
1:A:2558:LEU:O	1:A:2655:ARG:NH1	2.49	0.46
1:B:57:HIS:CE1	1:B:69:ARG:HB2	2.50	0.46
1:B:550:SER:O	1:B:556:PRO:HA	2.14	0.46
1:A:837:ASP:N	1:A:917:ASP:OD2	2.43	0.46
1:A:2553:HIS:O	1:A:2557:VAL:HG23	2.15	0.46
1:A:1370:TYR:HE1	1:B:2088:VAL:HA	1.80	0.46
1:A:1695:LEU:HD12	1:A:1696:GLU:HG2	1.97	0.46
1:A:2239:ASP:OD2	1:A:2278:LYS:NZ	2.48	0.46
1:B:438:THR:HG22	1:B:442:LYS:HB2	1.97	0.46
1:A:573:ARG:HA	1:A:650:GLN:HA	1.98	0.46
1:A:753:SER:N	1:A:805:GLY:O	2.49	0.46
1:A:2545:LEU:HD11	1:A:2740:PRO:CD	2.44	0.46
1:A:2656:LYS:H	1:A:2656:LYS:HD2	1.80	0.46
1:B:1855:TYR:OH	1:B:1933:SER:HA	2.15	0.46
1:B:1962:ASN:ND2	1:B:2181:SER:HA	2.31	0.46
1:B:2315:ILE:HG23	1:B:2316:GLN:HG3	1.96	0.46
1:A:841:ILE:HD13	1:A:869:MET:HE1	1.98	0.46
1:A:1329:LEU:HD23	1:A:1397:LEU:HD13	1.97	0.46
1:A:1714:MET:HE3	1:B:2195:LEU:HD13	1.98	0.46
1:B:66:ARG:HG3	1:B:66:ARG:NH1	2.29	0.46
1:B:393:TRP:CZ2	1:B:400:PRO:HG3	2.51	0.46
1:B:2300:ALA:HB3	1:B:2547:PRO:HD2	1.96	0.46
1:A:1513:LEU:CD2	1:B:1918:LEU:HB3	2.46	0.46
1:A:2244:VAL:HG13	1:A:2251:LEU:HD23	1.98	0.46
1:A:2532:ILE:CD1	1:A:2548:ILE:HD12	2.41	0.46
1:B:1313:ASP:OD1	1:B:1313:ASP:N	2.38	0.46
1:B:2057:LEU:HG	1:B:2677:LEU:HD12	1.97	0.46
1:B:882:ARG:C	1:B:1081:ARG:HH22	2.24	0.46
1:A:767:ARG:NH1	1:A:781:GLU:OE2	2.48	0.45
1:B:70:ILE:HD13	1:B:360:LEU:HB3	1.98	0.45
1:B:2648:GLU:OE2	1:B:2649:GLN:NE2	2.49	0.45
1:A:76:PRO:HG3	1:A:854:LEU:HD11	1.98	0.45
1:A:920:ARG:HG2	1:A:924:HIS:HB3	1.98	0.45
1:A:1508:GLN:HA	1:A:1508:GLN:NE2	2.31	0.45
1:A:2652:HIS:O	1:A:2656:LYS:HD2	2.16	0.45
1:A:378:TYR:HE2	1:A:555:ILE:HG23	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1932:HIS:ND1	1:A:1935:VAL:HG23	2.31	0.45
1:A:2266:ARG:HB2	1:A:2272:MET:HE2	1.98	0.45
1:A:2730:VAL:HG12	1:A:2736:SER:O	2.17	0.45
1:B:1847:ASP:OD2	1:B:2188:ARG:NH2	2.34	0.45
1:B:1852:GLN:HG2	1:B:2090:VAL:HG12	1.98	0.45
1:B:1860:ALA:HB2	1:B:1871:PRO:HG2	1.98	0.45
1:A:752:ASP:OD1	1:A:757:HIS:NE2	2.50	0.45
1:A:2568:PHE:CZ	1:A:2575:MET:HE1	2.50	0.45
1:B:579:PRO:HA	1:B:582:LEU:HD12	1.98	0.45
1:B:1350:ASN:N	1:B:1350:ASN:OD1	2.49	0.45
1:B:1437:VAL:HG11	1:B:1482:LEU:HD11	1.97	0.45
1:B:2218:PHE:HB3	1:B:2219:GLU:OE1	2.17	0.45
1:B:2288:GLY:O	1:B:2291:VAL:HG12	2.16	0.45
1:A:1408:GLU:OE1	1:A:1417:ARG:HD3	2.16	0.45
1:A:2021:PRO:HA	1:A:2024:ARG:HG3	1.99	0.45
1:B:2083:LYS:HB2	1:B:2083:LYS:NZ	2.31	0.45
1:A:1406:VAL:O	1:A:1410:GLN:HG2	2.16	0.45
1:A:2244:VAL:HG21	1:A:2295:PHE:CD1	2.51	0.45
1:B:2717:ILE:HD11	1:B:2784:LYS:HZ2	1.81	0.45
1:A:392:GLN:HE22	1:A:411:HIS:HB2	1.82	0.45
1:A:2546:CYS:SG	1:A:2547:PRO:N	2.88	0.45
1:A:2780:LYS:O	1:A:2784:LYS:HG2	2.16	0.45
1:B:491:LEU:HB2	1:B:738:LEU:HD12	1.99	0.45
1:B:542:TYR:HB2	1:B:565:VAL:HB	1.98	0.45
1:A:2086:MET:HE1	1:B:1369:VAL:HG11	1.98	0.45
1:A:2089:THR:O	1:A:2095:LEU:HD21	2.16	0.45
1:A:2182:HIS:O	1:A:2186:LEU:HG	2.17	0.45
1:B:911:PHE:HA	1:B:914:HIS:CD2	2.52	0.45
1:B:1517:GLU:OE1	1:B:1517:GLU:N	2.44	0.45
1:B:1787:ALA:O	1:B:1791:VAL:HG23	2.16	0.45
1:B:2091:ASP:O	1:B:2095:LEU:HD23	2.17	0.45
1:B:2633:GLU:O	1:B:2637:LYS:HG2	2.17	0.45
1:A:904:ASN:HB3	1:A:907:MET:HB3	1.98	0.45
1:B:1289:GLU:O	1:B:1292:GLN:NE2	2.47	0.45
1:B:2087:GLU:HG2	1:B:2087:GLU:O	2.17	0.45
1:A:380:GLU:HB2	1:A:394:LYS:HA	1.98	0.44
1:A:493:TRP:CZ3	1:A:736:LYS:HD3	2.51	0.44
1:A:1118:MET:HE3	1:A:1167:ASP:O	2.17	0.44
1:B:75:GLN:NE2	1:B:353:PRO:O	2.51	0.44
1:B:855:PRO:O	1:B:858:SER:OG	2.35	0.44
1:B:1327:LEU:HD12	1:B:1327:LEU:H	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2579:LEU:CD2	1:B:2635:VAL:HG22	2.39	0.44
1:B:2688:GLN:H	1:B:2688:GLN:CD	2.21	0.44
1:A:1094:ASP:OD1	1:A:1094:ASP:C	2.60	0.44
1:A:1121:VAL:HG22	1:A:1254:LEU:HD21	1.99	0.44
1:A:1276:LEU:HD12	1:A:1342:MET:HB2	1.99	0.44
1:A:2072:GLN:HG2	1:A:2074:LEU:HD13	1.99	0.44
1:A:2755:ARG:HH12	1:A:2761:HIS:CG	2.34	0.44
1:B:1443:MET:O	1:B:1786:ARG:NH2	2.39	0.44
1:B:2087:GLU:CD	1:B:2087:GLU:H	2.25	0.44
1:A:1320:GLU:OE2	1:A:1320:GLU:HA	2.17	0.44
1:A:1917:PHE:HE2	1:B:1441:VAL:HG11	1.83	0.44
1:B:1842:MET:HG3	1:B:1951:PHE:HB2	1.99	0.44
1:B:2647:ALA:C	1:B:2650:PRO:HD2	2.42	0.44
1:A:1:MET:HE2	1:A:1:MET:HB2	1.87	0.44
1:A:2:THR:OG1	1:A:3:SER:N	2.50	0.44
1:A:1204:SER:OG	1:A:1205:LEU:N	2.51	0.44
1:A:2252:ILE:O	1:A:2256:MET:HG3	2.18	0.44
1:A:2568:PHE:HZ	1:A:2575:MET:HE1	1.82	0.44
1:A:2671:THR:OG1	1:A:2674:ASP:OD2	2.33	0.44
1:A:2675:PHE:CD1	1:A:2675:PHE:C	2.95	0.44
1:B:762:THR:HG23	1:B:767:ARG:NH2	2.32	0.44
1:B:814:ASP:OD1	1:B:814:ASP:N	2.35	0.44
1:B:2182:HIS:O	1:B:2186:LEU:HG	2.17	0.44
1:B:2203:ASP:OD1	1:B:2203:ASP:N	2.50	0.44
1:A:1845:ILE:HD12	1:B:1490:ILE:HG21	2.00	0.44
1:B:1248:LYS:H	1:B:1248:LYS:HG2	1.58	0.44
1:B:2295:PHE:CD1	1:B:2295:PHE:C	2.95	0.44
1:A:1193:ILE:HG23	1:A:1206:CYS:HB3	1.99	0.44
1:A:1959:LYS:HB2	1:A:1959:LYS:HZ3	1.82	0.44
1:B:29:LEU:O	1:B:878:GLN:NE2	2.51	0.44
1:B:2518:PRO:HG3	1:B:2647:ALA:HB2	1.99	0.44
1:A:2219:GLU:O	1:A:2222:GLU:HG3	2.18	0.44
1:A:2556:LYS:HD2	1:A:2561:ARG:HB2	1.99	0.44
1:B:361:GLN:HE22	1:B:393:TRP:HZ3	1.66	0.44
1:B:2201:MET:O	1:B:2201:MET:HG3	2.18	0.44
1:A:886:GLU:H	1:A:886:GLU:CD	2.25	0.44
1:A:1934:ASP:HB3	1:B:1519:LEU:H	1.82	0.44
1:A:1935:VAL:HG13	1:B:1378:ILE:HD11	2.00	0.44
1:A:2075:TYR:HA	1:A:2086:MET:H	1.82	0.44
1:A:2248:ARG:HG3	1:A:2249:ASP:N	2.32	0.44
1:B:438:THR:CG2	1:B:442:LYS:HB2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:741:PRO:HB2	1:B:744:THR:HG21	1.98	0.44
1:B:1454:PRO:HD2	1:B:1457:ILE:HB	2.00	0.44
1:B:2027:ASP:HA	1:B:2030:THR:HG22	1.99	0.44
1:B:2164:PRO:HA	1:B:2165:PRO:HD3	1.92	0.44
1:B:2229:MET:O	1:B:2233:ARG:HD3	2.17	0.44
1:B:2559:LEU:HD22	1:B:2667:LEU:HG	1.98	0.44
1:A:378:TYR:HD2	1:A:556:PRO:HD2	1.83	0.44
1:A:1860:ALA:HB2	1:A:1871:PRO:HG2	2.00	0.44
1:A:1959:LYS:HB2	1:A:1959:LYS:NZ	2.33	0.44
1:A:2609:GLU:CD	1:A:2609:GLU:H	2.25	0.44
1:B:26:SER:HB3	1:B:838:LEU:HG	2.00	0.44
1:B:802:PHE:CD2	1:B:844:LEU:HD22	2.52	0.44
1:B:1201:LEU:HG	1:B:1237:LYS:HZ2	1.83	0.44
1:B:2707:LEU:O	1:B:2711:LYS:HG3	2.18	0.44
1:B:2716:SER:O	1:B:2719:GLU:HG2	2.17	0.44
1:A:438:THR:HG22	1:A:442:LYS:HB2	2.00	0.43
1:A:2020:HIS:CD2	1:A:2636:ARG:HD2	2.53	0.43
1:B:49:LYS:HB3	1:B:50:GLN:OE1	2.17	0.43
1:B:1874:ALA:O	1:B:1877:ASN:HB2	2.18	0.43
1:B:2181:SER:HB3	1:B:2184:MET:CE	2.48	0.43
1:A:2788:LEU:HA	1:A:2791:ILE:HG12	2.00	0.43
1:B:923:LEU:HD22	1:B:923:LEU:H	1.83	0.43
1:B:2097:VAL:HG22	1:B:2101:LYS:NZ	2.33	0.43
1:A:1690:MET:HB3	1:A:1691:LEU:H	1.55	0.43
1:A:2549:THR:HA	1:A:2680:ASN:HD21	1.83	0.43
1:A:2648:GLU:O	1:A:2652:HIS:HB3	2.18	0.43
1:B:1511:GLU:OE2	1:B:1515:SER:OG	2.30	0.43
1:A:550:SER:HB2	1:A:656:VAL:HG12	2.00	0.43
1:B:1314:MET:HE2	1:B:1315:PRO:O	2.19	0.43
1:A:1102:LEU:HD23	1:A:1102:LEU:HA	1.78	0.43
1:B:1336:TRP:CE3	1:B:1408:GLU:HG3	2.52	0.43
1:B:1474:GLU:OE2	1:B:1474:GLU:HA	2.18	0.43
1:A:1351:LYS:HD3	1:A:1351:LYS:HA	1.82	0.43
1:A:2029:MET:HE1	1:A:2552:ARG:NH2	2.33	0.43
1:A:2766:ASN:O	1:A:2770:SER:HA	2.18	0.43
1:B:1256:TYR:O	1:B:1260:THR:HG23	2.18	0.43
1:B:1412:LYS:HD3	1:B:1412:LYS:HA	1.92	0.43
1:B:2255:THR:HG21	1:B:2299:ILE:CD1	2.49	0.43
1:B:2601:ALA:HA	1:B:2625:PRO:HA	2.00	0.43
1:A:28:LYS:HB2	1:A:28:LYS:HE2	1.84	0.43
1:A:426:LEU:HB2	1:A:437:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1916:ASP:CG	1:B:1492:ARG:HH12	2.26	0.43
1:A:2020:HIS:HE2	1:A:2636:ARG:CZ	2.31	0.43
1:A:2250:LEU:O	1:A:2254:GLN:HG2	2.19	0.43
1:B:1841:TRP:O	1:B:1845:ILE:HG12	2.18	0.43
1:A:1925:MET:HE3	1:B:1478:VAL:HG13	2.01	0.43
1:A:2279:VAL:HG11	1:A:2295:PHE:HB2	2.00	0.43
1:A:2558:LEU:HG	1:A:2658:LEU:HD13	2.00	0.43
1:B:62:LEU:HD23	1:B:62:LEU:HA	1.71	0.43
1:B:487:LEU:HD23	1:B:492:TYR:HD1	1.84	0.43
1:B:1339:LEU:HD21	1:B:1401:LEU:HG	2.01	0.43
1:B:2575:MET:HE3	1:B:2579:LEU:HD11	2.01	0.43
1:A:2726:ARG:O	1:A:2730:VAL:HG23	2.19	0.43
1:B:819:ILE:HG21	1:B:836:LEU:HD13	2.01	0.43
1:B:2304:LEU:HD23	1:B:2304:LEU:HA	1.84	0.43
1:B:2550:LEU:O	1:B:2676:ARG:NH2	2.42	0.43
1:A:7:VAL:CG2	1:A:867:ILE:HB	2.49	0.43
1:A:10:PRO:HB3	1:A:861:LYS:HD2	2.00	0.43
1:A:457:LYS:NZ	1:A:662:VAL:O	2.52	0.43
1:A:1294:ARG:H	1:A:1294:ARG:HG2	1.62	0.43
1:A:2207:GLU:OE2	1:A:2207:GLU:N	2.32	0.43
1:B:1422:ILE:O	1:B:1426:MET:HG2	2.19	0.43
1:A:838:LEU:HD23	1:A:839:PRO:HD2	2.01	0.42
1:A:1862:ALA:HB2	1:B:1363:LEU:HD11	2.01	0.42
1:A:1918:LEU:HD11	1:B:1442:GLU:HG3	2.00	0.42
1:A:2645:VAL:HA	1:A:2648:GLU:OE2	2.19	0.42
1:B:1846:MET:HA	1:B:1849:THR:HG22	2.01	0.42
1:B:2059:PRO:HB3	1:B:2218:PHE:HE2	1.84	0.42
1:A:52:VAL:HG23	1:A:59:ALA:HB3	2.01	0.42
1:A:886:GLU:HA	1:A:889:ARG:HH12	1.84	0.42
1:A:2096:GLU:C	1:A:2099:PRO:HD2	2.44	0.42
1:B:1106:LEU:HD23	1:B:1106:LEU:HA	1.92	0.42
1:B:1114:MET:HA	1:B:1118:MET:HE3	2.01	0.42
1:A:378:TYR:CE2	1:A:555:ILE:HG23	2.55	0.42
1:A:1170:LEU:HD12	1:A:1170:LEU:HA	1.83	0.42
1:A:1468:LEU:HD13	1:A:1798:LEU:HD22	2.00	0.42
1:A:2546:CYS:SG	1:A:2548:ILE:HG22	2.59	0.42
1:B:57:HIS:HD1	1:B:71:GLY:HA2	1.84	0.42
1:A:1352:ASP:OD1	1:A:1352:ASP:N	2.35	0.42
1:A:1519:LEU:HA	1:A:1520:PRO:HD3	1.93	0.42
1:A:2579:LEU:HD12	1:A:2579:LEU:HA	1.84	0.42
1:B:1486:VAL:HG22	1:B:1781:ALA:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2236:GLN:HG3	1:B:2273:ALA:HB3	2.01	0.42
1:B:2243:GLU:O	1:B:2258:GLN:NE2	2.52	0.42
1:A:739:CYS:HB2	1:A:777:LYS:HD2	2.01	0.42
1:A:1472:VAL:HG13	1:A:1827:LEU:HD11	2.02	0.42
1:A:2060:ASN:OD1	1:A:2060:ASN:N	2.49	0.42
1:A:2256:MET:SD	1:A:2257:ARG:N	2.93	0.42
1:A:378:TYR:HD1	1:A:378:TYR:O	2.03	0.42
1:A:1931:GLU:OE1	1:B:1375:SER:OG	2.35	0.42
1:A:1961:MET:O	1:A:1965:THR:HG23	2.19	0.42
1:A:2535:ILE:HD12	1:A:2536:LEU:N	2.34	0.42
1:A:2766:ASN:ND2	1:A:2768:CYS:SG	2.93	0.42
1:B:11:LEU:HD12	1:B:863:LYS:HD2	2.02	0.42
1:B:765:TRP:CD1	1:B:765:TRP:C	2.97	0.42
1:B:2652:HIS:C	1:B:2652:HIS:HD1	2.26	0.42
1:A:868:ILE:O	1:A:868:ILE:HD12	2.20	0.42
1:A:1189:ILE:HD11	1:A:1292:GLN:HB2	2.00	0.42
1:A:1336:TRP:CD2	1:A:1408:GLU:HG3	2.55	0.42
1:A:1437:VAL:HG11	1:B:1925:MET:HE1	2.02	0.42
1:B:2552:ARG:N	1:B:2676:ARG:HH22	2.17	0.42
1:B:753:SER:N	1:B:805:GLY:O	2.52	0.42
1:B:756:VAL:CG1	1:B:771:PHE:HB2	2.50	0.42
1:B:1954:LEU:HD23	1:B:1954:LEU:HA	1.85	0.42
1:A:1110:ASP:OD1	1:A:1111:ALA:N	2.49	0.42
1:B:1342:MET:O	1:B:1345:PHE:HB2	2.20	0.42
1:B:2540:LEU:HD23	1:B:2540:LEU:HA	1.83	0.42
1:A:370:LYS:HB2	1:A:386:SER:OG	2.19	0.41
1:A:761:LYS:NZ	1:A:763:GLY:O	2.53	0.41
1:A:1350:ASN:OD1	1:A:1350:ASN:N	2.53	0.41
1:A:2043:PRO:HA	1:A:2580:ARG:CZ	2.50	0.41
1:B:2746:PHE:HB3	1:B:2748:PRO:O	2.20	0.41
1:A:1084:ASN:HA	1:A:1087:PHE:HD2	1.84	0.41
1:B:38:PRO:O	1:B:40:LEU:N	2.53	0.41
1:B:2667:LEU:HD12	1:B:2667:LEU:HA	1.92	0.41
1:A:484:CYS:SG	1:A:485:ALA:N	2.93	0.41
1:A:1203:GLU:O	1:A:1204:SER:HB3	2.21	0.41
1:A:1497:PHE:CD2	1:B:1914:ARG:HG3	2.56	0.41
1:B:51:CYS:SG	1:B:60:PHE:HB3	2.60	0.41
1:B:1256:TYR:HE1	1:B:1331:ARG:HG3	1.84	0.41
1:B:2248:ARG:NH2	1:B:2302:ALA:HA	2.35	0.41
1:B:803:THR:HB	1:B:810:ILE:HD13	2.02	0.41
1:A:844:LEU:CD2	1:A:869:MET:HE3	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:ARG:NH2	1:B:68:CYS:HB2	2.34	0.41
1:B:892:LEU:HD13	1:B:892:LEU:HA	1.86	0.41
1:B:1150:GLU:OE1	1:B:1150:GLU:HA	2.20	0.41
1:B:2089:THR:O	1:B:2095:LEU:HD21	2.19	0.41
1:A:401:TYR:CZ	1:A:412:PRO:HD3	2.55	0.41
1:A:401:TYR:CE2	1:A:412:PRO:HD3	2.55	0.41
1:A:2548:ILE:O	1:A:2550:LEU:CD1	2.69	0.41
1:B:438:THR:OG1	1:B:439:GLU:N	2.52	0.41
1:A:480:ALA:HB1	1:A:551:ILE:HD12	2.03	0.41
1:A:493:TRP:O	1:A:735:PRO:HA	2.21	0.41
1:A:1695:LEU:HB2	1:B:2715:TRP:HE1	1.84	0.41
1:A:1855:TYR:OH	1:A:1933:SER:HA	2.19	0.41
1:A:2532:ILE:O	1:A:2535:ILE:HD12	2.21	0.41
1:B:2241:SER:HB2	1:B:2278:LYS:H	1.85	0.41
1:B:802:PHE:HB3	1:B:846:MET:CE	2.51	0.41
1:B:1426:MET:HB3	1:B:1430:ARG:HH12	1.86	0.41
1:A:424:ILE:HG23	1:A:436:VAL:HG13	2.02	0.41
1:A:439:GLU:HG2	1:A:440:ASN:N	2.35	0.41
1:A:1182:THR:HG22	1:A:1319:LEU:HB3	2.03	0.41
1:A:1716:TRP:CZ2	1:B:1856:GLY:HA3	2.55	0.41
1:B:874:GLN:O	1:B:878:GLN:HB2	2.21	0.41
1:B:1233:ASP:HA	1:B:1235:TRP:CZ3	2.56	0.41
1:B:1277:LEU:O	1:B:1281:GLN:HG3	2.20	0.41
1:B:1951:PHE:CE1	1:B:1955:ILE:HG13	2.56	0.41
1:B:2661:VAL:HG13	1:B:2662:LEU:HD13	2.03	0.41
1:A:893:MET:HE3	1:A:893:MET:HB2	1.76	0.41
1:A:1187:GLU:H	1:A:1187:GLU:HG2	1.73	0.41
1:B:1115:THR:HG23	1:B:1118:MET:HE2	2.02	0.41
1:B:2238:ARG:NH1	1:B:2272:MET:HE2	2.35	0.41
1:B:2602:PHE:CE1	1:B:2634:TYR:HB2	2.56	0.41
1:A:1483:ILE:HB	1:A:1788:TYR:CD1	2.56	0.40
1:A:1856:GLY:HA3	1:B:1716:TRP:CZ2	2.56	0.40
1:A:2062:ARG:HE	1:A:2062:ARG:HB3	1.69	0.40
1:A:2562:LYS:HD3	1:A:2563:VAL:N	2.36	0.40
1:B:792:LEU:O	1:B:815:GLY:HA3	2.20	0.40
1:B:2529:PHE:O	1:B:2532:ILE:HG22	2.21	0.40
1:A:794:GLN:H	1:A:794:GLN:HG2	1.61	0.40
1:A:2531:ASN:O	1:A:2535:ILE:HG13	2.21	0.40
1:B:1154:PHE:O	1:B:1158:VAL:HG12	2.21	0.40
1:B:1517:GLU:H	1:B:1517:GLU:CD	2.28	0.40
1:B:1828:GLN:O	1:B:1832:GLU:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2241:SER:OG	1:B:2242:LEU:N	2.54	0.40
1:A:1468:LEU:O	1:A:1472:VAL:HG12	2.21	0.40
1:A:2780:LYS:HE2	1:A:2784:LYS:HZ1	1.86	0.40
1:B:414:ALA:HA	1:B:417:LEU:HB2	2.03	0.40
1:B:883:CYS:HB2	1:B:1081:ARG:NH2	2.36	0.40
1:B:1102:LEU:HD23	1:B:1102:LEU:HA	1.86	0.40
1:B:1252:LEU:HD11	1:B:1327:LEU:HD22	2.03	0.40
1:B:1839:TRP:HE1	1:B:2176:MET:CE	2.27	0.40
1:B:2784:LYS:HD2	1:B:2784:LYS:H	1.87	0.40
1:A:757:HIS:N	1:A:757:HIS:CD2	2.87	0.40
1:A:777:LYS:HE2	1:A:777:LYS:HB3	1.89	0.40
1:B:482:TYR:CZ	1:B:773:LEU:HD11	2.57	0.40
1:B:1388:ILE:HG22	1:B:1389:VAL:HG12	2.03	0.40
1:B:2239:ASP:OD1	1:B:2276:ARG:N	2.54	0.40
1:A:1080:ASP:O	1:A:1084:ASN:ND2	2.36	0.40
1:A:1149:LYS:HE2	1:A:1149:LYS:N	2.34	0.40
1:B:876:LEU:O	1:B:880:ILE:HG23	2.20	0.40
1:B:1194:PHE:HE2	1:B:1209:THR:HG23	1.85	0.40
1:B:1247:GLN:O	1:B:1251:ARG:HG3	2.22	0.40
1:B:2176:MET:HB3	1:B:2178:MET:HE1	2.04	0.40
1:B:2677:LEU:C	1:B:2677:LEU:HD23	2.47	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	1658/2806 (59%)	1589 (96%)	69 (4%)	0	100	100
1	B	1643/2806 (59%)	1568 (95%)	75 (5%)	0	100	100
All	All	3301/5612 (59%)	3157 (96%)	144 (4%)	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	1482/2426 (61%)	1453 (98%)	29 (2%)	48	80
1	B	1468/2426 (60%)	1419 (97%)	49 (3%)	33	69
All	All	2950/4852 (61%)	2872 (97%)	78 (3%)	41	75

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	VAL
1	A	29	LEU
1	A	34	LEU
1	A	427	LEU
1	A	551	ILE
1	A	562	MET
1	A	819	ILE
1	A	849	HIS
1	A	860	ILE
1	A	1095	SER
1	A	1164	ASN
1	A	1238	CYS
1	A	1298	ILE
1	A	1382	CYS
1	A	1389	VAL
1	A	1405	LEU
1	A	1467	LEU
1	A	1507	MET
1	A	1801	LEU
1	A	1836	ILE
1	A	1844	SER
1	A	1939	LEU
1	A	1952	GLN
1	A	2074	LEU
1	A	2255	THR

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Mol	Chain	Res	Type
1	A	2515	THR
1	A	2545	LEU
1	A	2546	CYS
1	A	2661	VAL
1	B	29	LEU
1	B	34	LEU
1	B	47	THR
1	B	60	PHE
1	B	61	LEU
1	B	67	VAL
1	B	373	CYS
1	B	382	LEU
1	B	491	LEU
1	B	551	ILE
1	B	732	GLN
1	B	744	THR
1	B	760	LEU
1	B	799	VAL
1	B	808	SER
1	B	860	ILE
1	B	892	LEU
1	B	922	ILE
1	B	1097	VAL
1	B	1153	VAL
1	B	1182	THR
1	B	1193	ILE
1	B	1244	ILE
1	B	1298	ILE
1	B	1341	SER
1	B	1350	ASN
1	B	1354	LEU
1	B	1377	THR
1	B	1389	VAL
1	B	1719	ARG
1	B	1775	SER
1	B	1801	LEU
1	B	1811	SER
1	B	1935	VAL
1	B	1955	ILE
1	B	1957	TRP
1	B	2020	HIS
1	B	2057	LEU

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Mol	Chain	Res	Type
1	B	2101	LYS
1	B	2167	THR
1	B	2183	ASP
1	B	2219	GLU
1	B	2220	VAL
1	B	2244	VAL
1	B	2543	ASN
1	B	2667	LEU
1	B	2690	LEU
1	B	2742	SER
1	B	2776	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	469	GLN
1	A	501	GLN
1	A	798	ASN
1	A	924	HIS
1	A	1290	HIS
1	A	1348	GLN
1	A	1508	GLN
1	A	1703	HIS
1	A	1877	ASN
1	A	1919	ASN
1	A	2507	GLN
1	A	2531	ASN
1	A	2620	ASN
1	A	2623	ASN
1	A	2629	GLN
1	A	2766	ASN
1	B	392	GLN
1	B	780	GLN
1	B	782	ASN
1	B	919	ASN
1	B	1281	GLN
1	B	1348	GLN
1	B	1715	GLN
1	B	1964	GLN
1	B	2507	GLN
1	B	2527	ASN

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Mol	Chain	Res	Type
1	B	2629	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

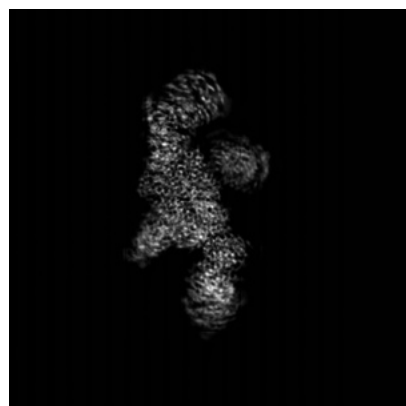
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27201. These allow visual inspection of the internal detail of the map and identification of artifacts.

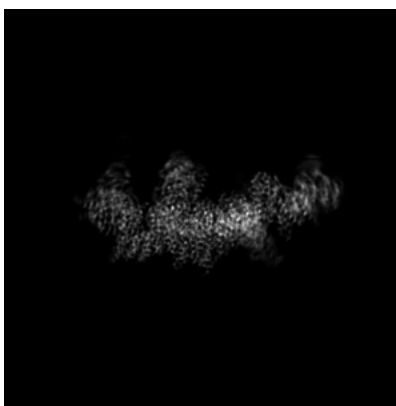
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

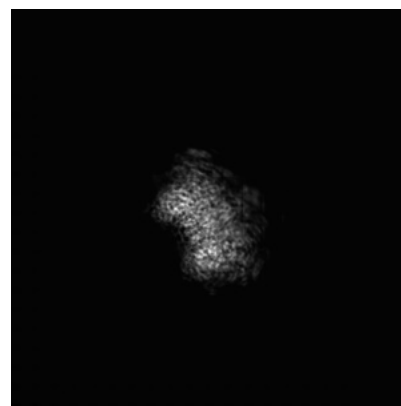
6.1.1 Primary map



X

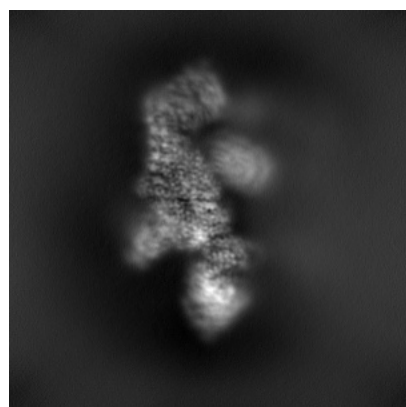


Y

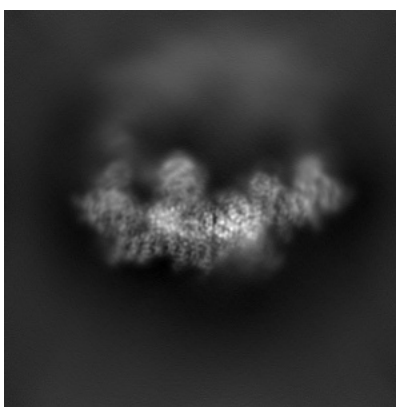


Z

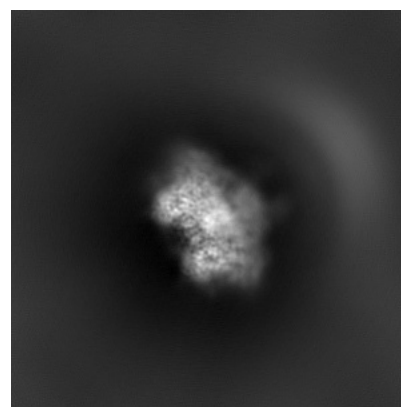
6.1.2 Raw map



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

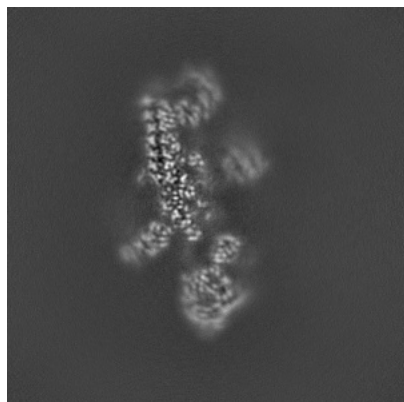


Y Index: 200

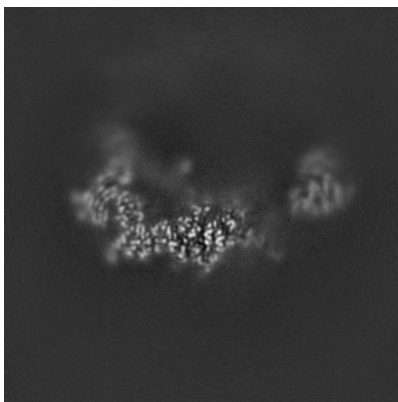


Z Index: 200

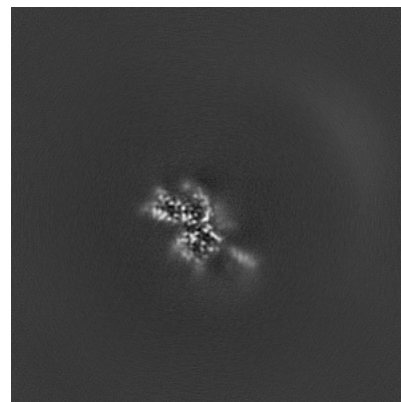
6.2.2 Raw map



X Index: 200



Y Index: 200



Z Index: 200

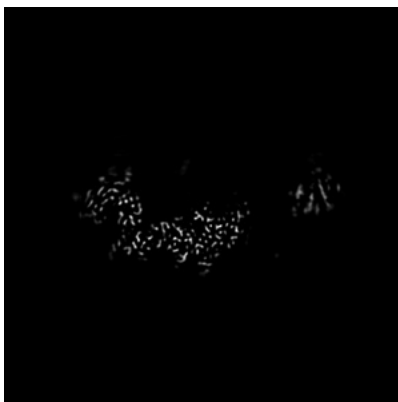
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 187

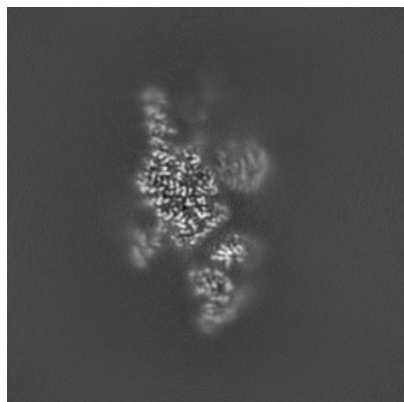


Y Index: 197

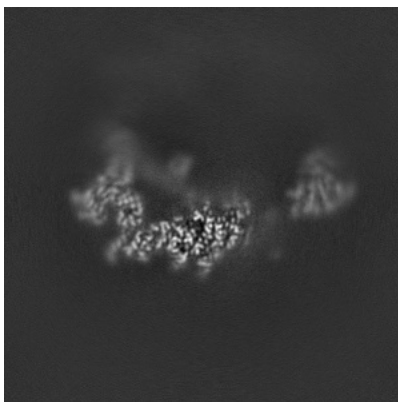


Z Index: 168

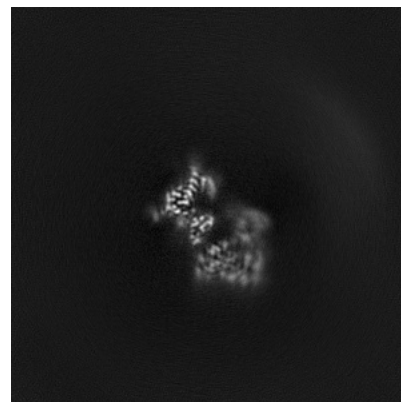
6.3.2 Raw map



X Index: 188



Y Index: 197

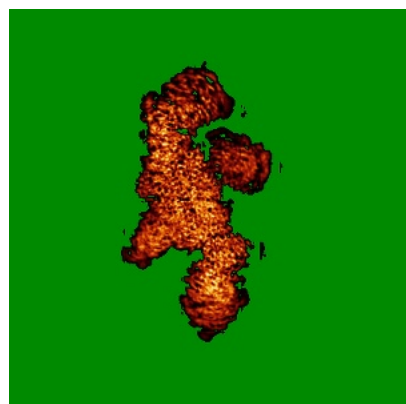


Z Index: 168

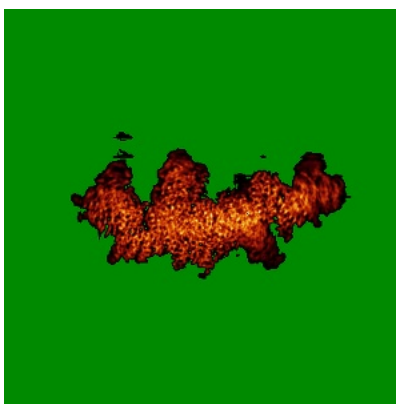
The images above show the largest variance slices of the map in three orthogonal directions.

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

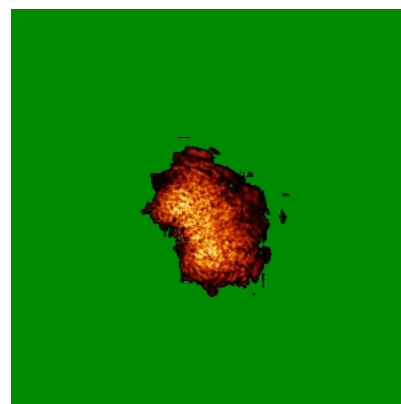
6.4.1 Primary map



X

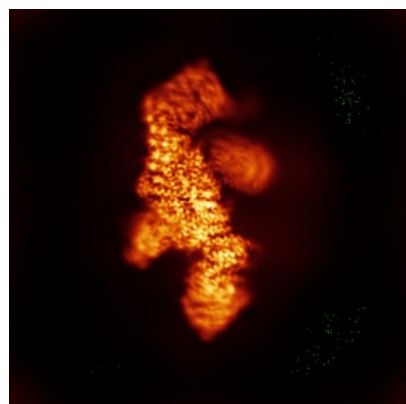


Y

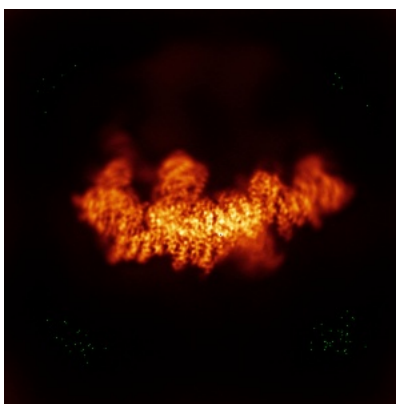


Z

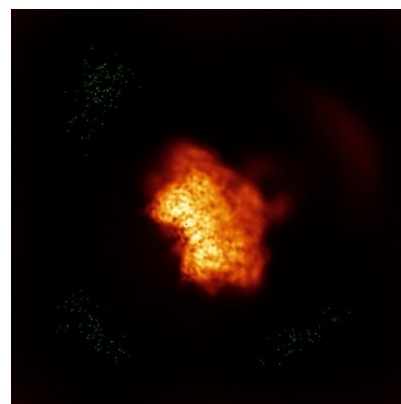
6.4.2 Raw map



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](#)

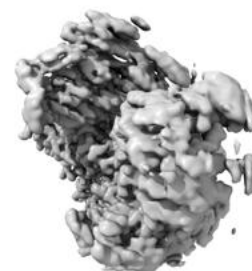
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

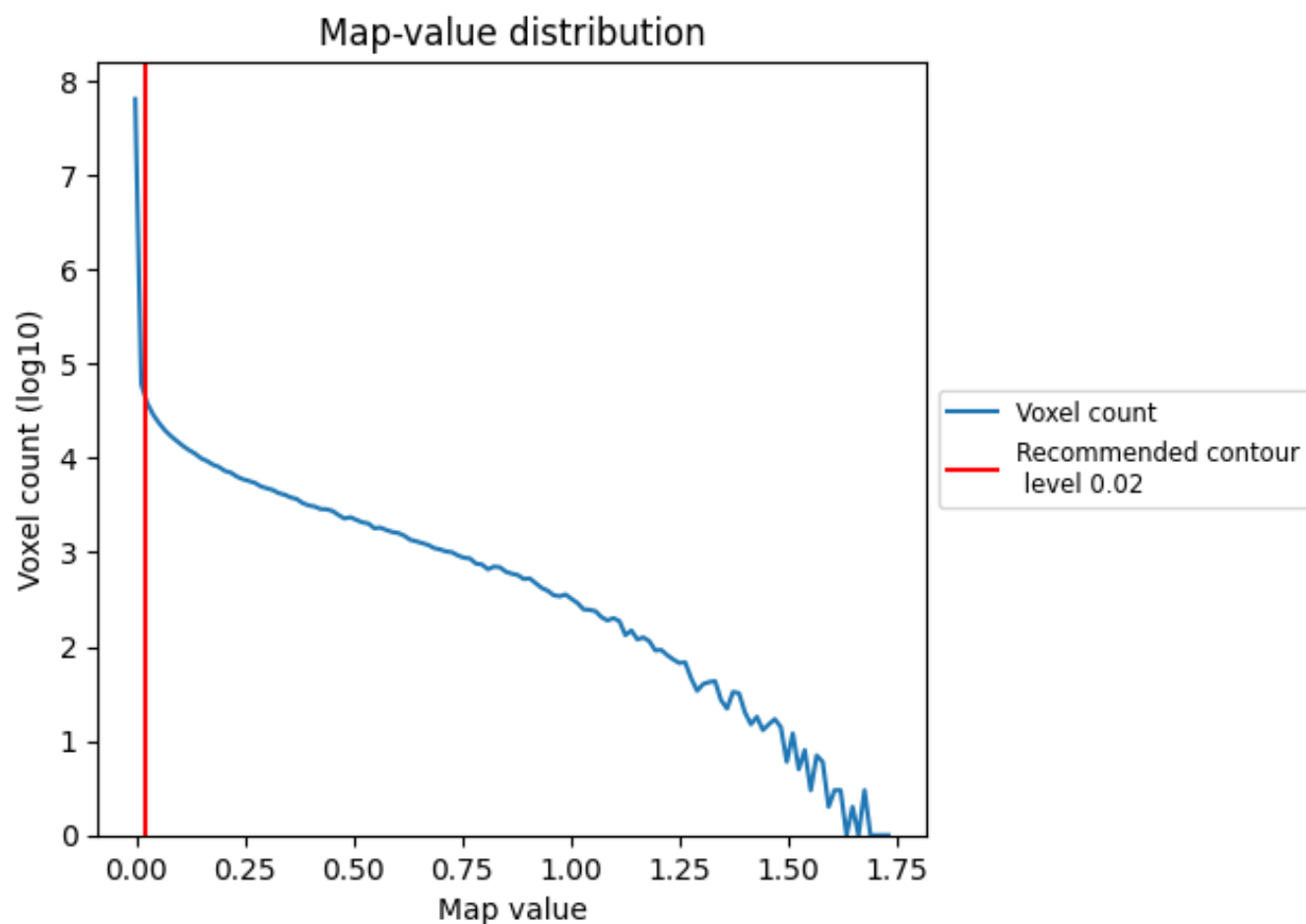
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

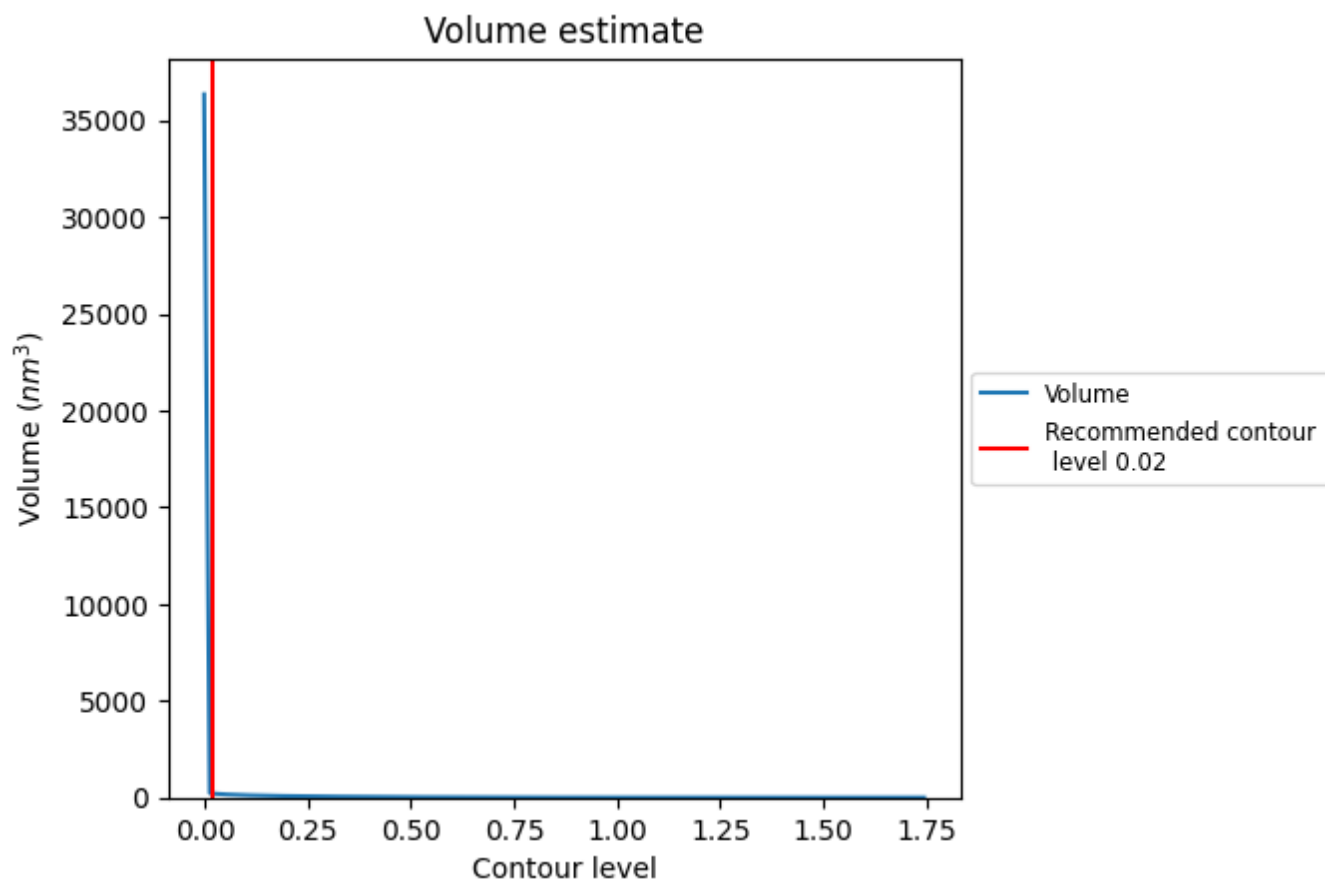
This section contains the results of statistical analysis of the map.

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.

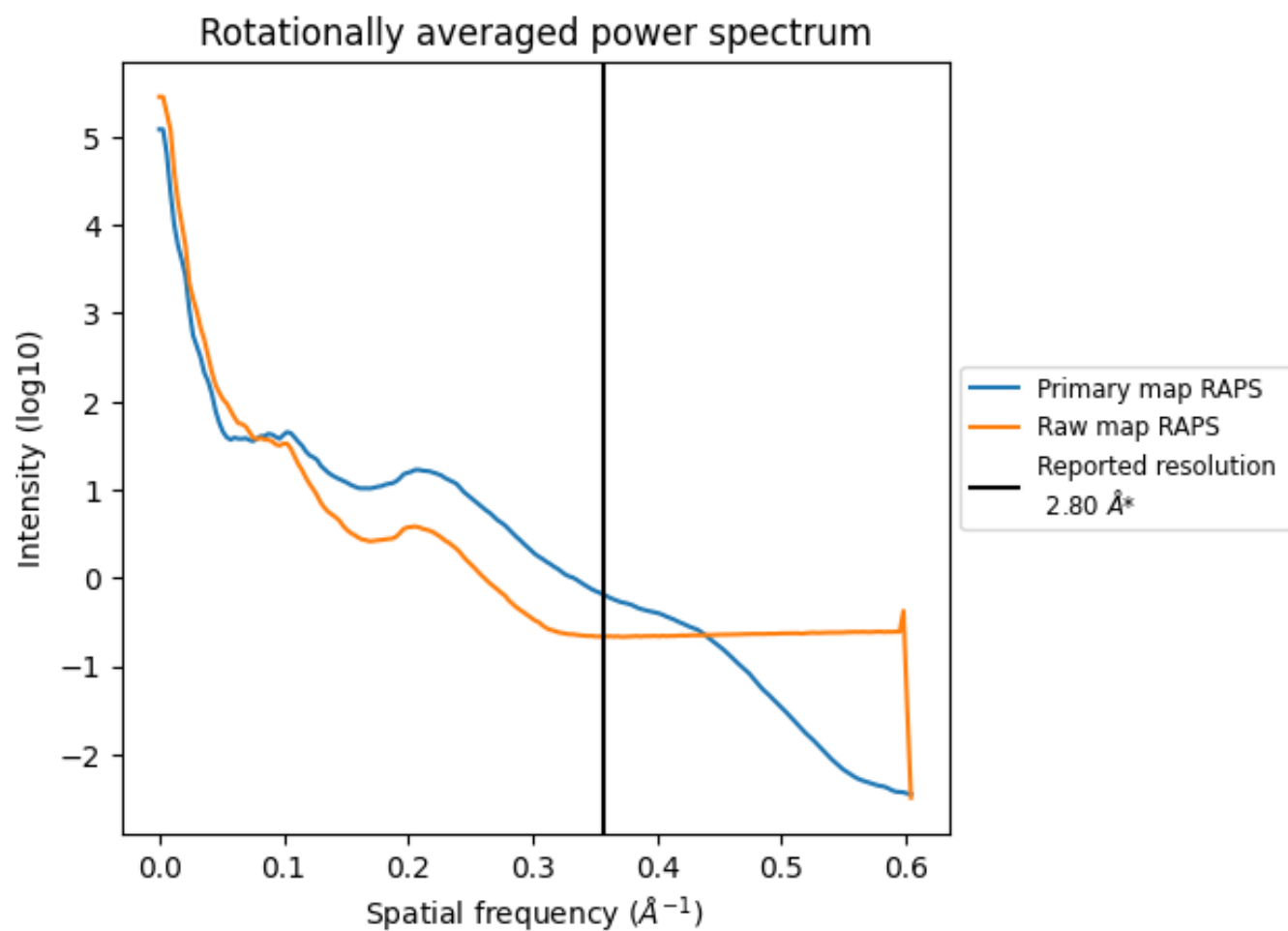
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 211 nm^3 ; this corresponds to an approximate mass of 191 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 ⓘ

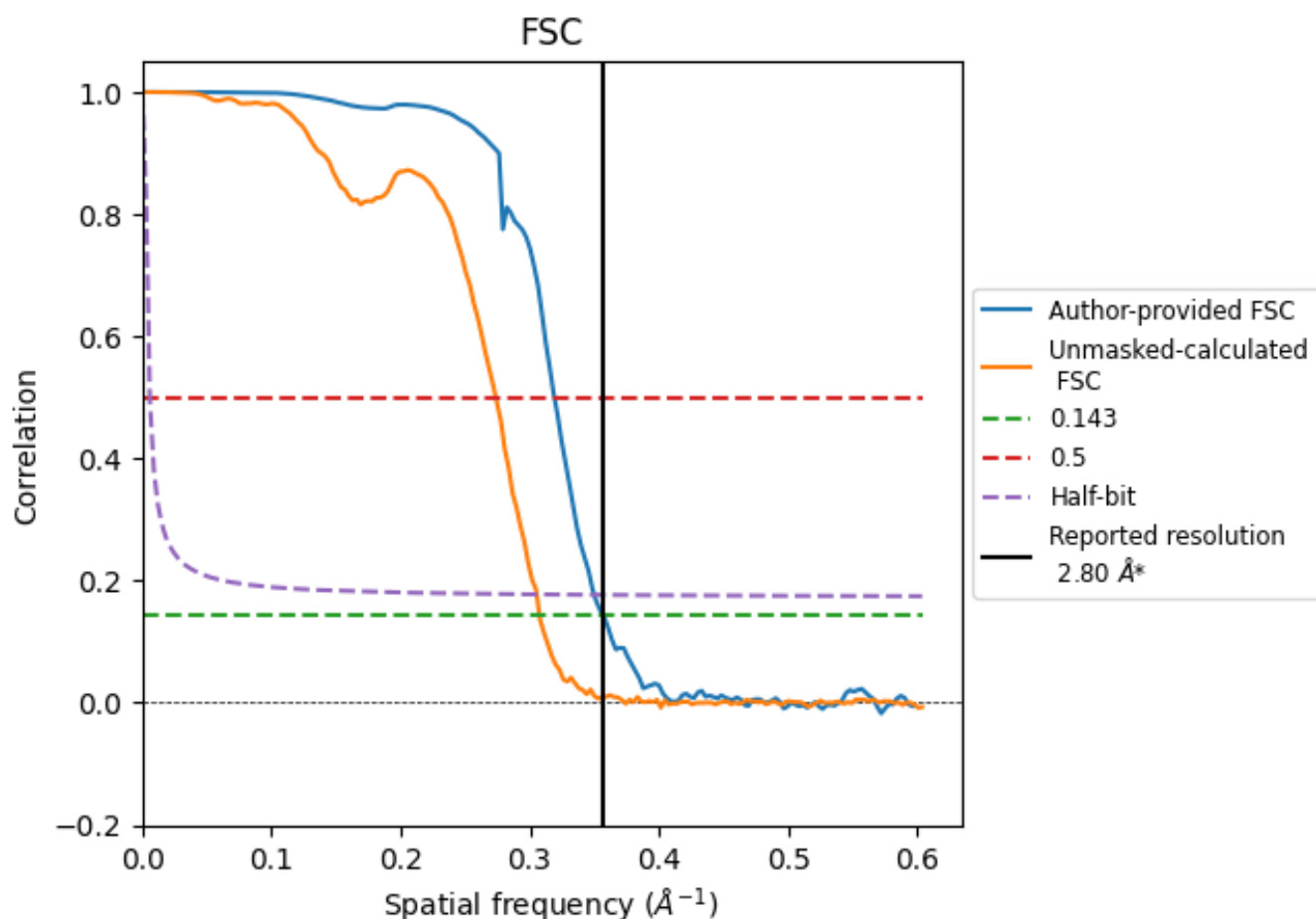


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.80	3.13	2.86
Unmasked-calculated*	3.25	3.65	3.27

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.25 differs from the reported value 2.8 by more than 10 %

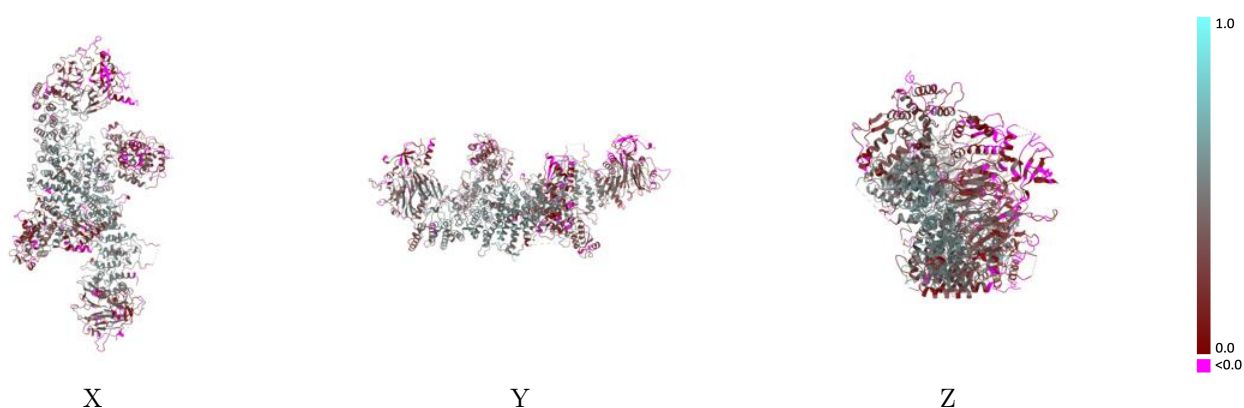
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27201 and PDB model 8D4X. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

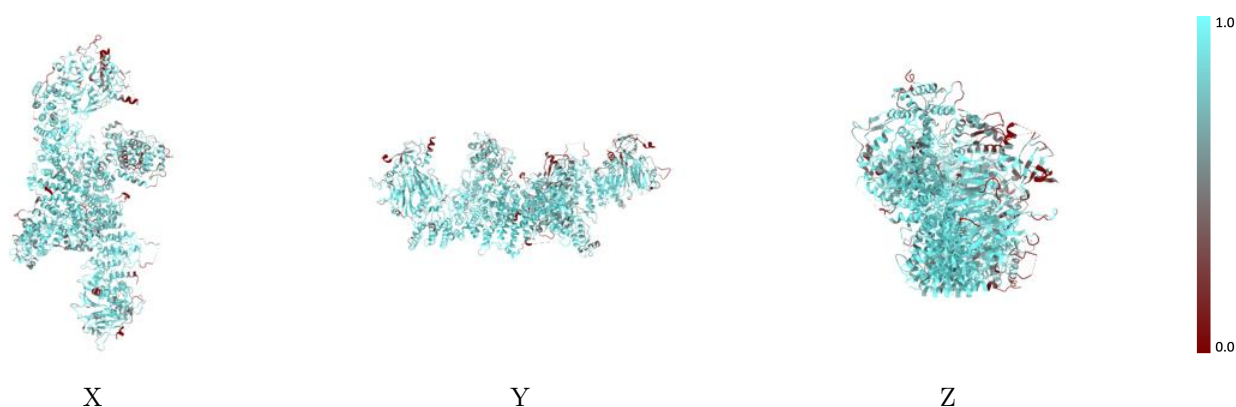
This section was not generated.

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



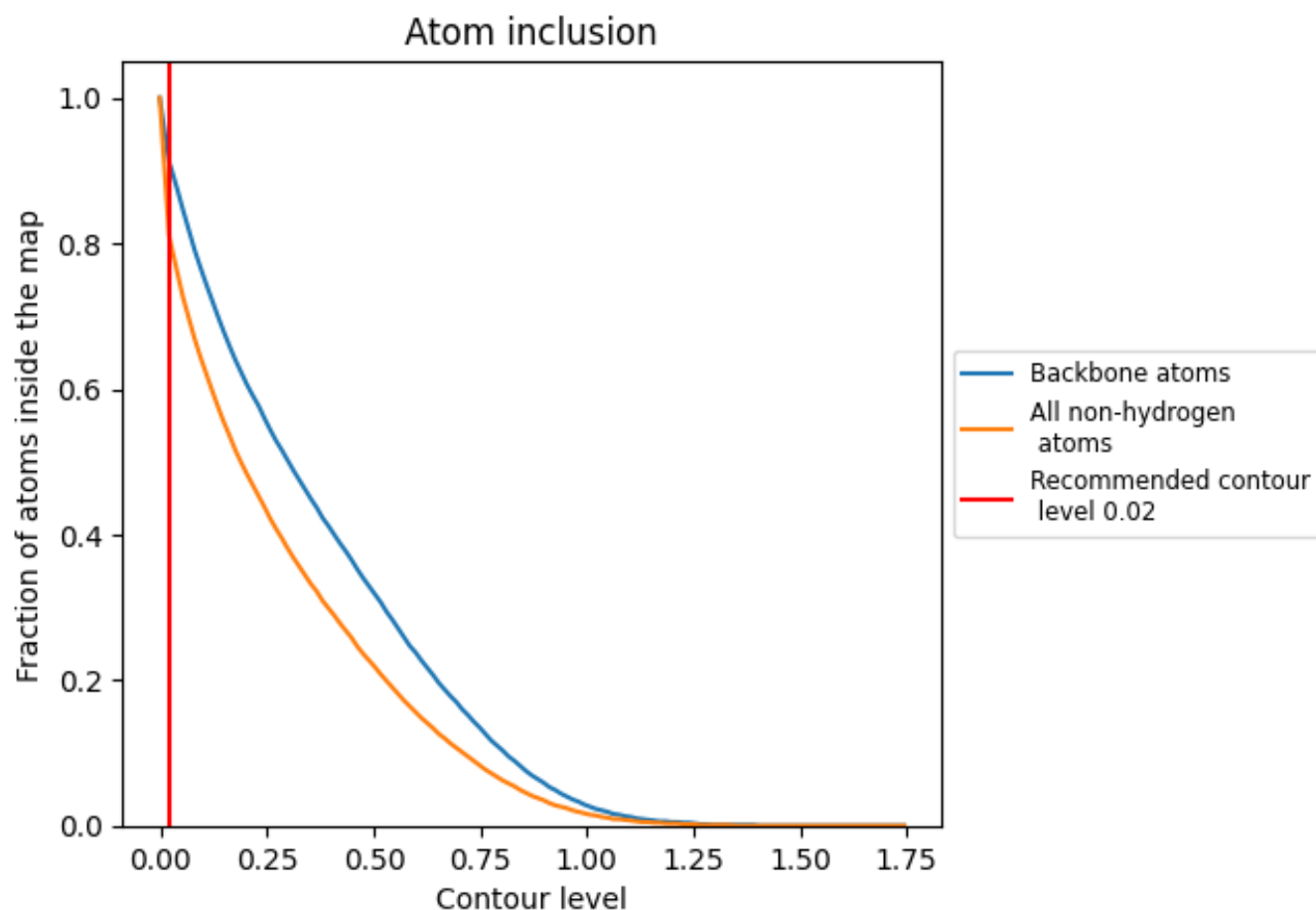
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8110	0.3580
A	0.8090	0.3680
B	0.8130	0.3490

