



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 01:05 AM UTC

PDB ID : 7TDI / pdb_00007tdi
EMDB ID : EMD-25830
Title : Rabbit RyR1 with AMP-PCP and high Ca²⁺ embedded in nanodisc in closed-inactivated conformation class 2 (Dataset-A)
Authors : Nayak, A.R.; Samso, M.
Deposited on : 2021-12-31
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

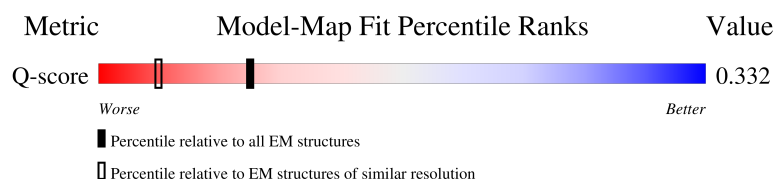
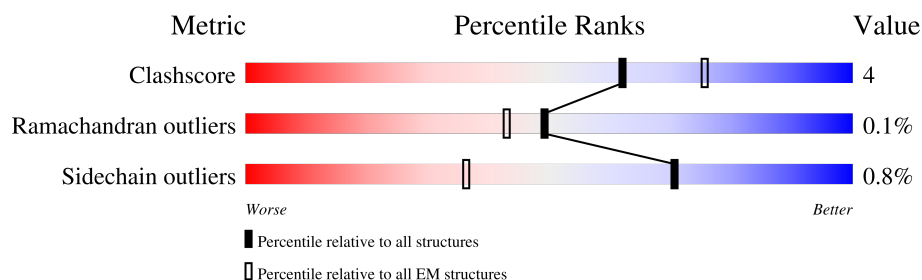
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

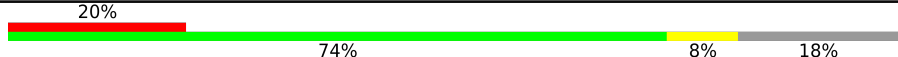
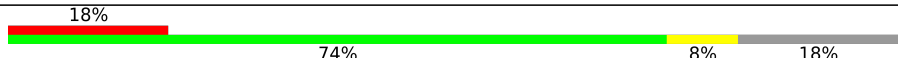
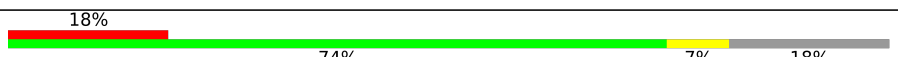
The reported resolution of this entry is 3.30 Å.

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	15087 (2.80 - 3.80)

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	5037	
1	B	5037	
1	C	5037	
1	D	5037	

2 Entry composition [i](#)

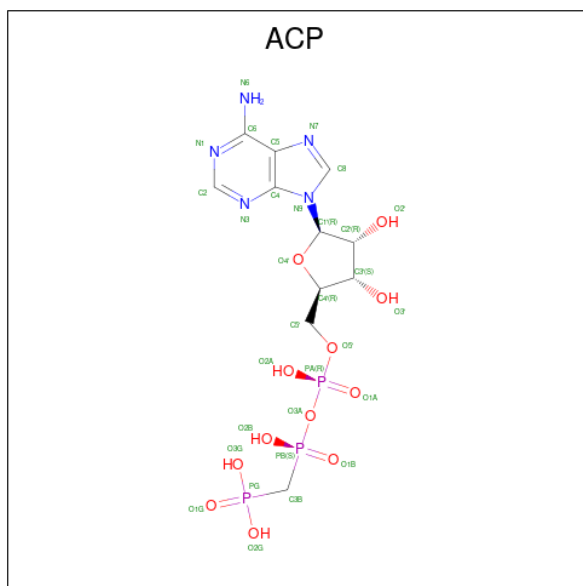
There are 4 unique types of molecules in this entry. The entry contains 117132 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ryanodine receptor 1,Ryanodine receptor 1,RyR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	4134	Total	C	N	O	S	0	0
			29249	18516	5181	5395	157		
1	C	4134	Total	C	N	O	S	0	0
			29249	18516	5181	5395	157		
1	D	4134	Total	C	N	O	S	0	0
			29249	18516	5181	5395	157		
1	A	4134	Total	C	N	O	S	0	0
			29249	18516	5181	5395	157		

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total	C	N	O	P	0
			31	11	5	12	3	
2	C	1	Total	C	N	O	P	0
			31	11	5	12	3	

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Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C	N	O	P	0
			31	11	5	12	3	
2	A	1	Total	C	N	O	P	0
			31	11	5	12	3	

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	
3	A	1	Total	Zn	0
			1	1	

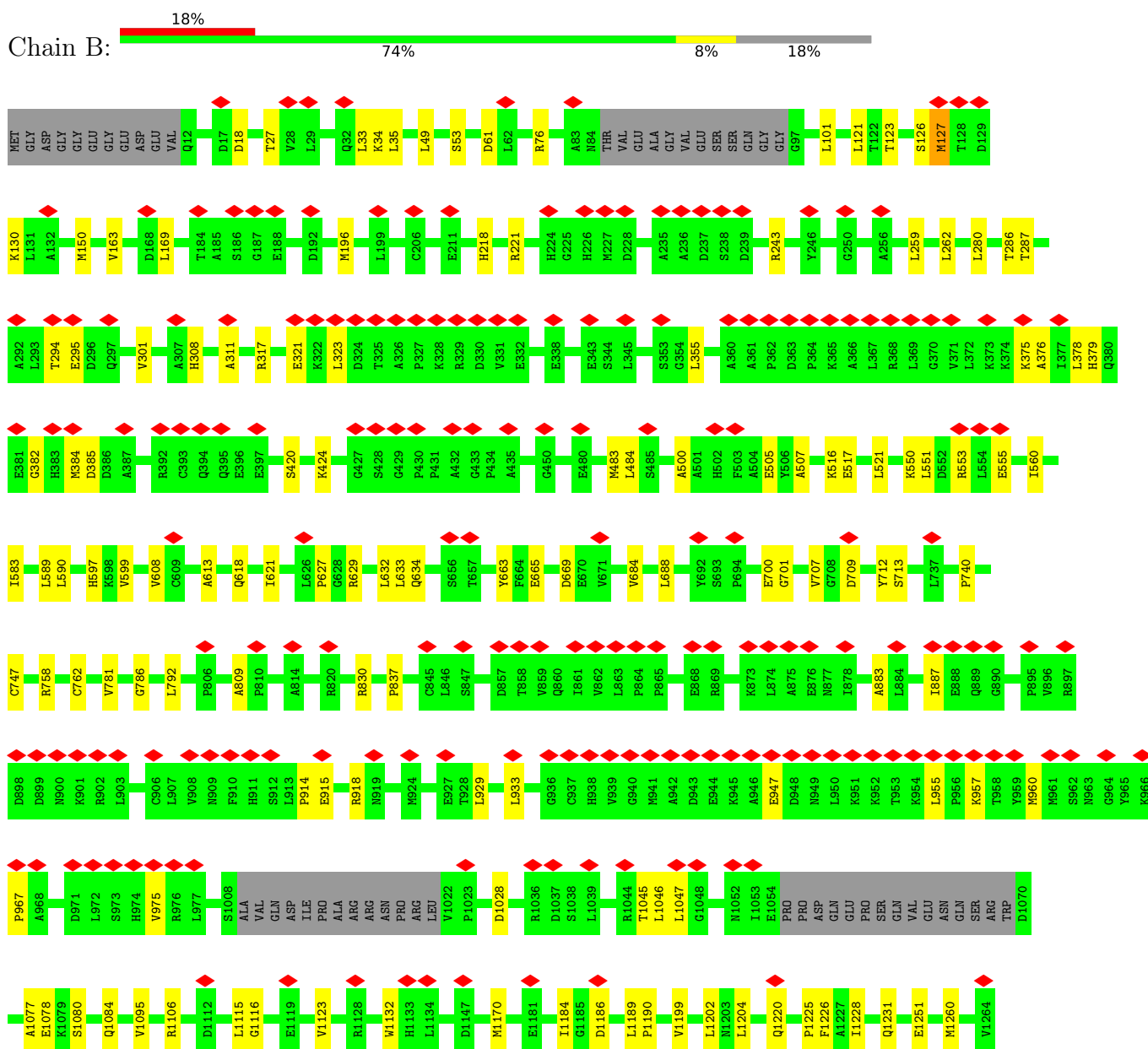
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	B	2	Total	Ca	0
			2	2	
4	C	2	Total	Ca	0
			2	2	
4	D	2	Total	Ca	0
			2	2	
4	A	2	Total	Ca	0
			2	2	

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.

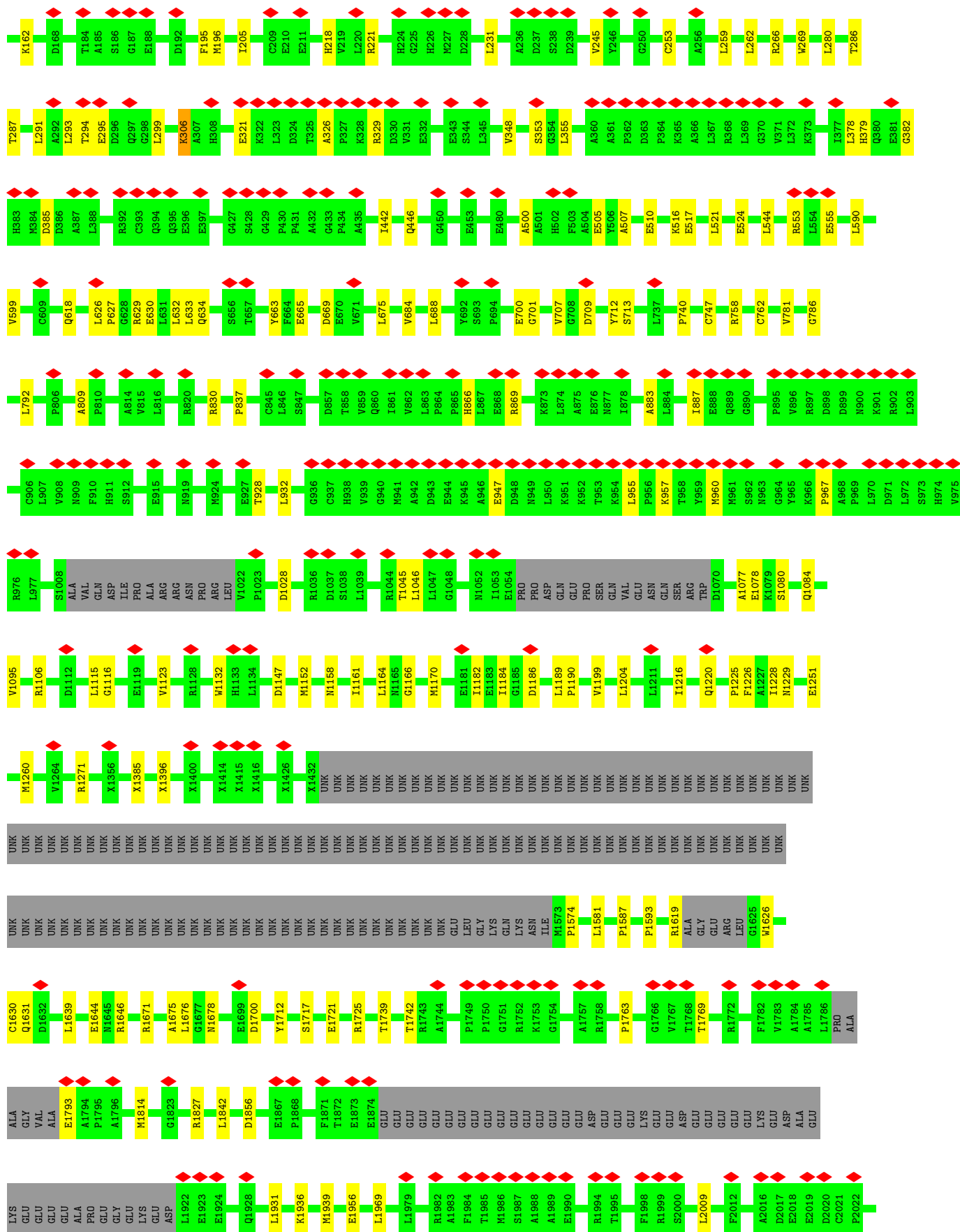
- Molecule 1: Ryanodine receptor 1,Ryanodine receptor 1,RyR1





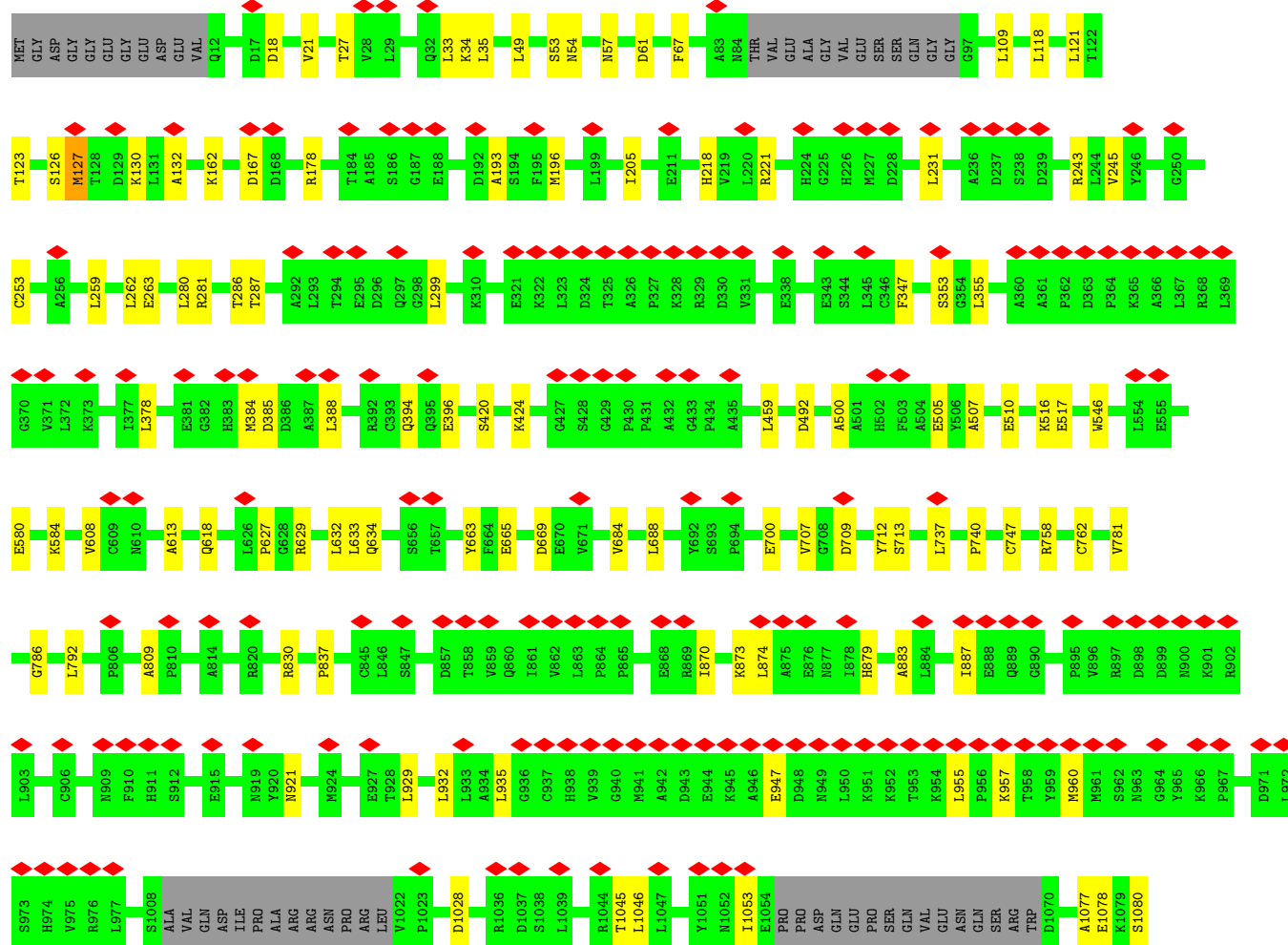


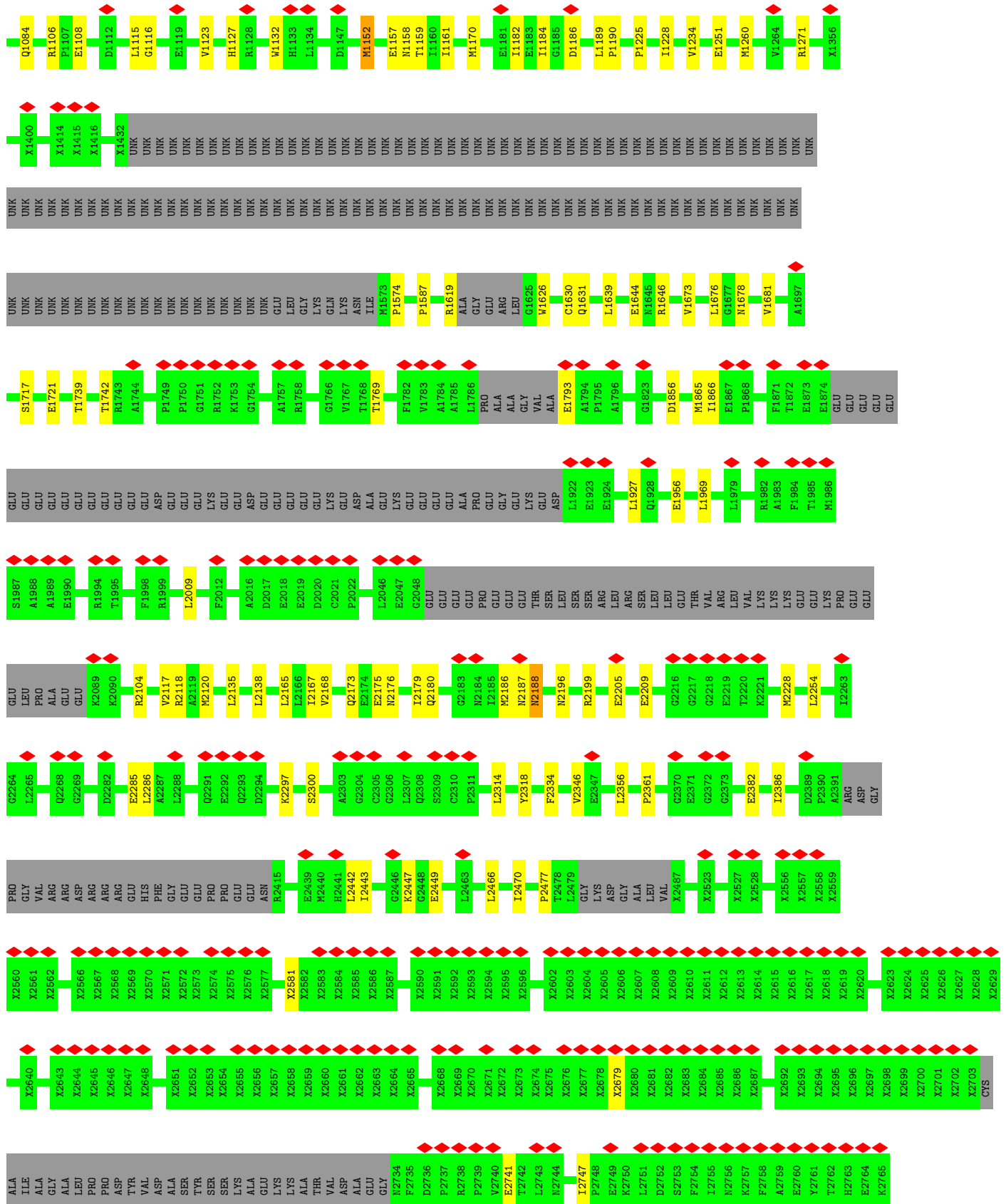




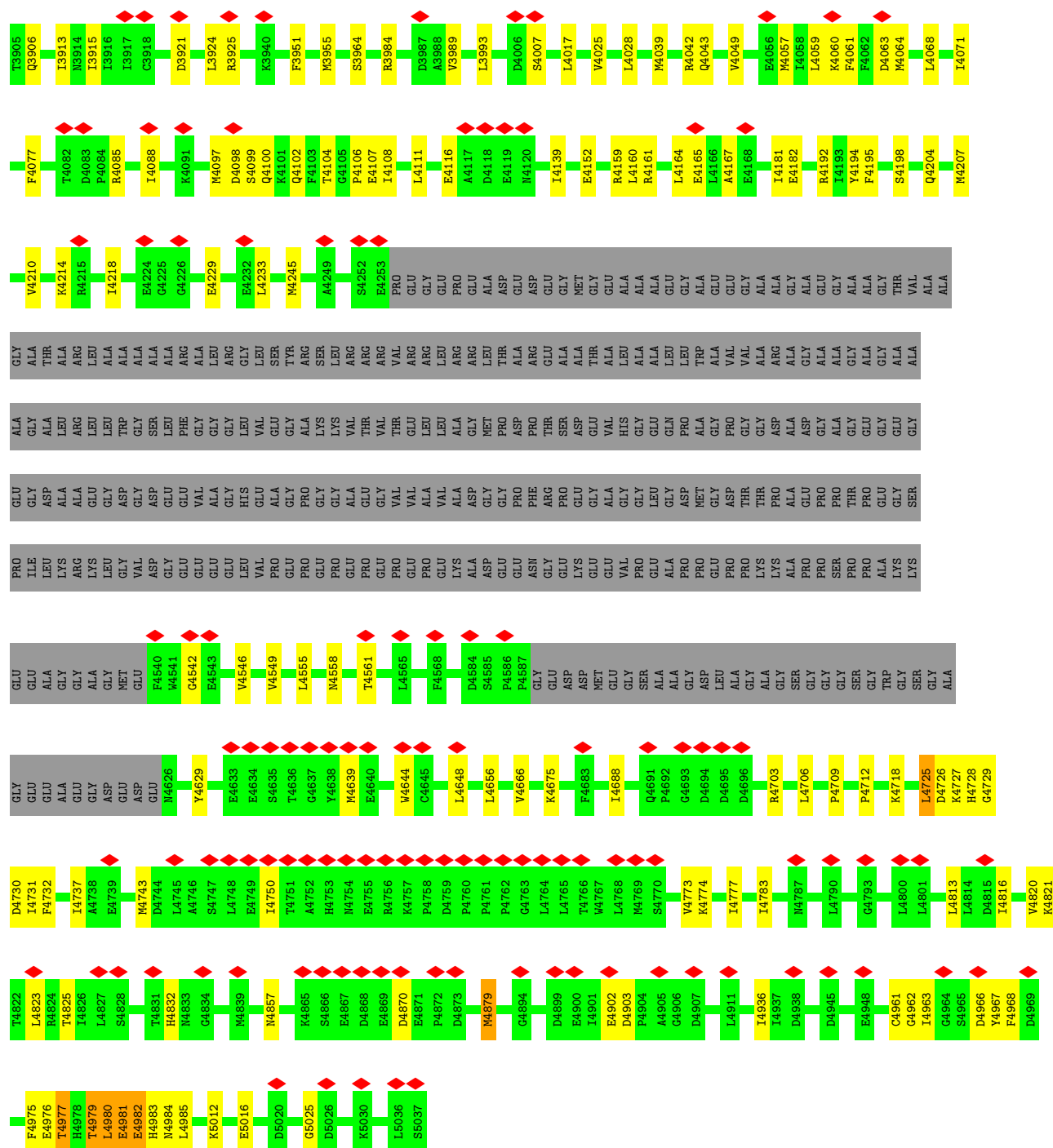


[illegible]

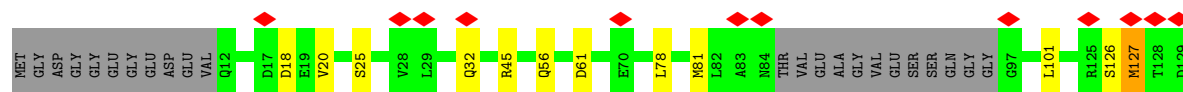








• Molecule 1: Ryanodine receptor 1, Ryanodine receptor 1, RyR1











4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	159444	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 ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	477.36002, 477.36002, 477.36002	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.105, 1.105, 1.105	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: CA, ACP, 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	0.19	0/25301	0.47	9/34345 (0.0%)
1	B	0.20	0/25301	0.47	6/34345 (0.0%)
1	C	0.19	0/25301	0.46	8/34345 (0.0%)
1	D	0.22	2/25301 (0.0%)	0.48	10/34345 (0.0%)
All	All	0.20	2/101204 (0.0%)	0.47	33/137380 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	4709	PRO	CG-CD	-15.66	0.97	1.50
1	D	4709	PRO	N-CD	7.58	1.58	1.47

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	4709	PRO	N-CD-CG	-15.58	79.83	103.20
1	D	4709	PRO	CA-N-CD	-10.97	96.65	112.00
1	A	2462	PRO	CA-N-CD	-10.36	97.50	112.00
1	B	967	PRO	CA-N-CD	-10.14	97.80	112.00
1	C	967	PRO	CA-N-CD	-9.85	98.20	112.00
1	B	1587	PRO	CA-N-CD	-9.17	99.16	112.00
1	D	4709	PRO	CA-CB-CG	-8.86	87.67	104.50
1	A	2477	PRO	CA-N-CD	-8.75	99.75	112.00
1	B	3972	PRO	CA-N-CD	-8.08	100.69	112.00
1	D	1587	PRO	CA-N-CD	-8.00	100.80	112.00
1	C	1587	PRO	CA-N-CD	-7.97	100.85	112.00
1	D	2477	PRO	CA-N-CD	-7.74	101.17	112.00
1	C	2477	PRO	CA-N-CD	-7.65	101.29	112.00
1	B	2477	PRO	CA-N-CD	-7.62	101.33	112.00
1	D	510	GLU	CA-CB-CG	7.22	128.54	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	4709	PRO	N-CA-CB	-6.85	96.97	103.41
1	C	510	GLU	CA-CB-CG	6.28	126.65	114.10
1	C	4745	LEU	CA-CB-CG	5.79	136.58	116.30
1	A	241	GLN	CA-CB-CG	5.47	125.03	114.10
1	A	4639	MET	CB-CG-SD	5.42	128.95	112.70
1	A	1111	PRO	CA-N-CD	-5.37	104.48	112.00
1	B	127	MET	CB-CG-SD	5.35	128.74	112.70
1	D	4639	MET	CB-CG-SD	5.29	128.58	112.70
1	A	4001	MET	CB-CG-SD	5.23	128.38	112.70
1	D	127	MET	CB-CG-SD	5.19	128.27	112.70
1	D	1574	PRO	CA-N-CD	-5.19	104.73	112.00
1	C	127	MET	CB-CG-SD	5.16	128.18	112.70
1	C	1574	PRO	CA-N-CD	-5.16	104.78	112.00
1	A	4639	MET	CA-CB-CG	5.15	124.40	114.10
1	C	2186	MET	CB-CG-SD	5.12	128.06	112.70
1	A	2146	PRO	CA-N-CD	-5.05	104.93	112.00
1	B	2186	MET	CB-CG-SD	5.05	127.84	112.70
1	A	127	MET	CB-CG-SD	5.04	127.81	112.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	29249	0	24792	248	0
1	B	29249	0	24790	236	0
1	C	29249	0	24795	224	0
1	D	29249	0	24791	230	0
2	A	31	0	13	0	0
2	B	31	0	13	4	0
2	C	31	0	13	0	0
2	D	31	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
All	All	117132	0	99220	923	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 4.

All (923) 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:4961:CYS:SG	1:A:4963:ILE:HG22	1.54	1.48
1:A:4961:CYS:SG	1:A:4963:ILE:CG2	2.16	1.33
1:D:4980:LEU:HA	1:D:4984:ASN:HD21	1.34	0.92
1:A:5029:ARG:O	1:A:5033:GLU:HB3	1.73	0.88
1:B:4960:ILE:HG13	1:B:4983:HIS:HB3	1.60	0.83
1:D:4975:PHE:O	1:D:4979:THR:HG22	1.80	0.81
1:C:5029:ARG:O	1:C:5033:GLU:HB3	1.85	0.77
1:A:4975:PHE:O	1:A:4979:THR:HG22	1.85	0.77
1:A:4961:CYS:SG	1:A:4963:ILE:HG21	2.26	0.72
1:B:4104:THR:HB	1:B:4107:GLU:OE2	1.90	0.72
1:A:2117:VAL:HG23	1:A:2120:MET:HE2	1.74	0.69
1:B:384:MET:N	1:B:384:MET:SD	2.66	0.69
1:D:384:MET:SD	1:D:384:MET:N	2.66	0.68
1:A:384:MET:SD	1:A:384:MET:N	2.67	0.68
1:C:4977:THR:HA	1:C:4980:LEU:HD23	1.76	0.68
1:D:4104:THR:HB	1:D:4107:GLU:OE2	1.94	0.67
1:D:4182:GLU:HG2	1:D:4192:ARG:HG3	1.76	0.67
1:B:786:GLY:H	1:B:1631:GLN:HA	1.59	0.67
1:C:786:GLY:H	1:C:1631:GLN:HA	1.59	0.67
1:A:20:VAL:HG22	1:A:204:PRO:HA	1.77	0.67
1:D:786:GLY:H	1:D:1631:GLN:HA	1.61	0.66
1:A:4975:PHE:O	1:A:4979:THR:CG2	2.43	0.66
1:A:533:ASN:HB3	1:A:536:ASN:HB2	1.79	0.65
1:D:3921:ASP:HA	1:D:3924:LEU:HD12	1.78	0.65
1:A:644:ILE:HG13	1:A:1628:VAL:HG21	1.78	0.65
1:B:4104:THR:HG22	1:B:4106:PRO:HD2	1.78	0.64
1:A:4017:LEU:HD22	1:A:4139:ILE:HG21	1.79	0.64
1:C:1936:LYS:HB2	1:C:2116:LEU:HD11	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2885:THR:OG1	1:C:2888:ARG:NH2	2.29	0.64
1:A:786:GLY:H	1:A:1631:GLN:HA	1.62	0.64
1:D:4976:GLU:O	1:D:4979:THR:HG23	1.98	0.64
1:C:4960:ILE:HD11	1:C:4985:LEU:HD21	1.78	0.64
1:B:1078:GLU:HG3	1:B:1080:SER:H	1.64	0.63
1:C:1078:GLU:HG3	1:C:1080:SER:H	1.63	0.63
1:A:1100:MET:HE2	1:A:1198:GLN:HB3	1.81	0.63
1:B:1936:LYS:HB2	1:B:2116:LEU:HD11	1.82	0.62
1:B:3713:LYS:NZ	1:B:3715:LYS:O	2.33	0.62
1:A:181:HIS:HD1	1:A:194:SER:HG	1.42	0.62
1:C:517:GLU:OE1	1:C:517:GLU:N	2.32	0.62
1:A:1078:GLU:HG3	1:A:1080:SER:H	1.64	0.61
1:B:3814:GLN:NE2	1:B:3818:ASP:OD2	2.33	0.61
1:A:4902:GLU:N	1:A:4902:GLU:OE1	2.33	0.61
1:A:4980:LEU:HG	1:A:4981:GLU:N	2.15	0.61
1:D:1078:GLU:HG3	1:D:1080:SER:H	1.64	0.61
1:A:1576:SER:HA	1:A:1579:MET:HE3	1.83	0.61
1:D:1225:PRO:HG2	1:D:1228:ILE:HB	1.82	0.60
1:A:4966:ASP:C	1:A:4968:PHE:H	2.09	0.60
1:D:3696:ASP:OD2	1:D:3773:ARG:NH2	2.34	0.60
1:A:840:VAL:HG12	1:A:1199:VAL:HG22	1.83	0.60
1:B:4960:ILE:HD12	1:B:4988:TYR:HE2	1.67	0.60
1:D:4061:PHE:HA	1:D:4064:MET:HE3	1.84	0.60
1:A:1077:ALA:HB3	1:A:1189:LEU:HB2	1.83	0.60
1:C:2766:TRP:HD1	1:C:2790:MET:HB3	1.65	0.60
1:C:4059:LEU:HD13	1:C:4167:ALA:HB2	1.83	0.60
1:D:2117:VAL:HA	1:D:2120:MET:HG2	1.83	0.59
1:D:2766:TRP:HD1	1:D:2790:MET:HB3	1.67	0.59
1:A:2107:GLN:NE2	1:A:3680:ALA:O	2.35	0.59
1:B:4680:LYS:HD2	1:B:4686:LEU:HD22	1.84	0.59
1:B:2766:TRP:HD1	1:B:2790:MET:HB3	1.68	0.59
1:D:4181:ILE:HG12	1:D:4195:PHE:HE1	1.67	0.59
1:A:4235:VAL:HG11	1:A:5017:ARG:HH12	1.67	0.59
1:C:3772:THR:HG22	1:C:3773:ARG:HG3	1.84	0.59
1:D:4059:LEU:HD13	1:D:4167:ALA:HB2	1.83	0.59
1:B:663:TYR:HD1	1:B:747:CYS:HB3	1.68	0.59
1:A:1671:ARG:NH1	1:A:1713:ASP:OD2	2.36	0.59
1:C:4061:PHE:HA	1:C:4064:MET:HE3	1.84	0.59
1:B:2868:SER:O	1:B:2872:GLN:NE2	2.35	0.58
1:C:4104:THR:HB	1:C:4107:GLU:OE2	2.03	0.58
1:D:2118:ARG:NH2	1:D:3719:ASP:OD1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4059:LEU:HD13	1:A:4167:ALA:HB2	1.84	0.58
1:D:34:LYS:H	1:D:53:SER:HB3	1.67	0.58
1:B:4960:ILE:HD11	2:B:5101:ACP:HN62	1.68	0.58
1:D:3719:ASP:HB3	1:D:3722:TYR:HB3	1.86	0.58
1:D:4068:LEU:HD22	1:D:4111:LEU:HD11	1.86	0.58
1:C:663:TYR:HD1	1:C:747:CYS:HB3	1.68	0.58
1:C:1115:LEU:HB3	1:C:1123:VAL:HG11	1.86	0.58
1:D:663:TYR:HD1	1:D:747:CYS:HB3	1.69	0.58
1:A:4844:LEU:HD13	1:A:4928:LEU:HG	1.84	0.57
1:B:955:LEU:HD22	1:B:960:MET:HG2	1.84	0.57
1:A:4039:MET:SD	1:A:4039:MET:N	2.70	0.57
1:B:4039:MET:SD	1:B:4039:MET:N	2.71	0.57
1:B:4976:GLU:O	1:B:4980:LEU:HB2	2.04	0.57
1:C:4685:GLY:HA3	1:C:4689:THR:HB	1.85	0.57
1:D:221:ARG:NH1	1:D:253:CYS:O	2.38	0.57
1:B:5027:CYS:C	1:B:5029:ARG:H	2.13	0.57
1:C:2314:LEU:HA	1:C:2318:TYR:HB2	1.86	0.57
1:D:3768:SER:O	1:D:3772:THR:OG1	2.21	0.57
1:C:262:LEU:HB2	1:C:280:LEU:HD13	1.86	0.57
1:D:4688:ILE:HD11	1:D:4732:PHE:HD2	1.70	0.57
1:A:2766:TRP:HD1	1:A:2790:MET:HB3	1.69	0.57
1:A:5007:GLU:N	1:A:5007:GLU:OE1	2.38	0.57
1:B:627:PRO:O	1:B:629:ARG:NH1	2.38	0.57
1:A:663:TYR:HD1	1:A:747:CYS:HB3	1.70	0.57
1:B:3799:LYS:NZ	1:B:3883:ASP:OD2	2.37	0.57
1:A:2247:GLN:NE2	1:A:2282:ASP:O	2.37	0.57
1:B:4936:ILE:HG21	1:A:4931:ILE:HG22	1.86	0.57
1:C:3719:ASP:HB3	1:C:3722:TYR:HB3	1.86	0.57
1:A:618:GLN:OE1	1:A:1678:ASN:ND2	2.38	0.57
1:B:34:LYS:H	1:B:53:SER:HB3	1.70	0.56
1:C:4039:MET:SD	1:C:4039:MET:N	2.70	0.56
1:B:2314:LEU:HA	1:B:2318:TYR:HB2	1.86	0.56
1:D:262:LEU:HB2	1:D:280:LEU:HD13	1.87	0.56
1:D:627:PRO:O	1:D:629:ARG:NH1	2.38	0.56
1:D:2188:ASN:C	1:D:2188:ASN:HD22	2.07	0.56
1:A:505:GLU:HG3	1:A:507:ALA:H	1.70	0.56
1:A:665:GLU:HB2	1:A:792:LEU:HD12	1.88	0.56
1:D:2314:LEU:HA	1:D:2318:TYR:HB2	1.87	0.56
1:D:2447:LYS:HG3	1:D:2449:GLU:H	1.71	0.56
1:A:3719:ASP:HB3	1:A:3722:TYR:HB3	1.87	0.56
1:A:1137:GLU:OE1	1:A:1137:GLU:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1854:PHE:HB3	1:A:1858:ASP:HB2	1.86	0.56
1:A:4068:LEU:HD22	1:A:4111:LEU:HD11	1.88	0.56
1:B:5004:THR:OG1	1:B:5005:GLY:N	2.39	0.56
1:D:3733:CYS:HG	1:D:3803:SER:HG	1.51	0.56
1:B:4983:HIS:HA	1:B:4988:TYR:OH	2.06	0.56
1:A:495:ASN:ND2	1:A:555:GLU:OE1	2.39	0.56
1:B:2267:MET:HE2	1:B:2267:MET:H	1.70	0.55
1:D:1045:THR:HG23	1:D:1046:LEU:HD23	1.87	0.55
1:A:2868:SER:O	1:A:2872:GLN:NE2	2.39	0.55
1:A:4184:MET:HG2	1:A:5023:PRO:HA	1.88	0.55
1:B:1115:LEU:HB3	1:B:1123:VAL:HG11	1.88	0.55
1:B:3759:GLU:OE1	1:B:3762:ARG:NH2	2.39	0.55
1:D:505:GLU:HG3	1:D:507:ALA:H	1.72	0.55
1:A:669:ASP:OD1	1:A:669:ASP:N	2.40	0.55
1:B:4180:ARG:HB2	1:B:4192:ARG:HD2	1.89	0.55
1:C:126:SER:HB3	1:C:132:ALA:HB2	1.88	0.55
1:A:882:TRP:HD1	1:A:886:ARG:HD3	1.71	0.55
1:B:1739:THR:HG23	1:B:1742:THR:H	1.72	0.55
1:C:2447:LYS:HG3	1:C:2449:GLU:H	1.72	0.55
1:D:1619:ARG:HA	1:D:1626:TRP:H	1.71	0.55
1:D:4071:ILE:HD12	1:D:4100:GLN:HG3	1.89	0.55
1:B:2466:LEU:O	1:B:2470:ILE:HD12	2.07	0.55
1:D:167:ASP:N	1:D:167:ASP:OD1	2.35	0.55
1:A:4239:GLU:OE2	1:A:4679:ARG:NH2	2.39	0.55
1:D:4983:HIS:C	1:D:4985:LEU:H	2.15	0.55
1:A:1739:THR:HG23	1:A:1742:THR:H	1.71	0.55
1:C:2581:UNK:N	1:C:2899:GLY:O	2.40	0.55
1:A:3877:ASP:HB2	1:A:3880:PHE:HB3	1.89	0.55
1:D:4962:GLY:H	1:D:5025:GLY:HA2	1.72	0.55
1:B:4985:LEU:HA	1:B:4988:TYR:HD2	1.72	0.55
1:C:830:ARG:HH21	1:C:837:PRO:HB3	1.71	0.55
1:C:2331:TYR:HD1	1:C:2332:LEU:H	1.53	0.55
1:D:633:LEU:HD23	1:D:1639:LEU:HD11	1.89	0.55
1:B:308:HIS:CE1	1:B:311:ALA:H	2.23	0.54
1:C:1251:GLU:OE1	1:C:1251:GLU:N	2.39	0.54
1:D:54:ASN:OD1	1:D:57:ASN:ND2	2.40	0.54
1:D:830:ARG:HH21	1:D:837:PRO:HB3	1.72	0.54
1:C:4860:ARG:NH2	1:D:4629:TYR:OH	2.40	0.54
1:D:517:GLU:OE2	1:D:517:GLU:N	2.39	0.54
1:A:420:SER:O	1:A:424:LYS:NZ	2.41	0.54
1:A:2581:UNK:N	1:A:2899:GLY:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1251:GLU:OE1	1:D:1251:GLU:N	2.40	0.54
1:D:4097:MET:HB3	1:D:4108:ILE:HD13	1.89	0.54
1:A:830:ARG:HH21	1:A:837:PRO:HB3	1.72	0.54
1:A:1712:TYR:OH	1:A:1814:MET:SD	2.66	0.54
1:C:1225:PRO:HG2	1:C:1228:ILE:HB	1.89	0.54
1:A:4874:MET:HE3	1:A:4875:LYS:H	1.72	0.54
1:B:3719:ASP:HB3	1:B:3722:TYR:HB3	1.89	0.54
1:B:4229:GLU:OE1	1:B:4229:GLU:N	2.41	0.54
1:C:1229:ASN:H	1:C:1827:ARG:HH21	1.55	0.54
1:D:669:ASP:N	1:D:669:ASP:OD1	2.40	0.54
1:A:221:ARG:HH21	1:A:259:LEU:HD21	1.73	0.54
1:A:291:LEU:HD12	1:A:299:LEU:HD11	1.90	0.54
1:A:4584:ASP:N	1:A:4584:ASP:OD1	2.41	0.54
1:B:2581:UNK:N	1:B:2899:GLY:O	2.41	0.54
1:D:1739:THR:HG23	1:D:1742:THR:H	1.72	0.54
1:B:669:ASP:N	1:B:669:ASP:OD1	2.40	0.54
1:A:1703:LEU:HD23	1:A:1708:ARG:HB2	1.90	0.54
1:B:1251:GLU:OE1	1:B:1251:GLU:N	2.41	0.54
1:C:1739:THR:HG23	1:C:1742:THR:H	1.72	0.54
1:D:2135:LEU:HD13	1:D:3662:ILE:HD13	1.89	0.54
1:B:505:GLU:HG3	1:B:507:ALA:H	1.73	0.53
1:B:4959:PHE:HD2	1:B:4960:ILE:HD13	1.74	0.53
1:D:4060:LYS:HA	1:D:4063:ASP:HB3	1.90	0.53
1:B:196:MET:SD	1:B:196:MET:N	2.82	0.53
1:D:61:ASP:OD1	1:D:61:ASP:N	2.41	0.53
1:A:3768:SER:O	1:A:3772:THR:OG1	2.25	0.53
1:C:669:ASP:OD1	1:C:669:ASP:N	2.40	0.53
1:A:317:ARG:NH1	1:A:349:GLN:OE1	2.41	0.53
1:C:4727:LYS:HD2	1:C:4728:HIS:CD2	2.44	0.53
1:B:1644:GLU:OE1	1:B:1646:ARG:NH1	2.42	0.53
1:C:1045:THR:HG23	1:C:1046:LEU:HD23	1.90	0.53
1:A:2447:LYS:HG3	1:A:2449:GLU:H	1.73	0.53
1:A:4966:ASP:C	1:A:4968:PHE:N	2.65	0.53
1:B:2135:LEU:HD13	1:B:3662:ILE:HD13	1.90	0.53
1:A:3670:GLU:HB3	1:A:3728:ILE:HG23	1.90	0.53
1:A:4963:ILE:HD11	1:A:4967:TYR:HD2	1.73	0.53
1:B:2447:LYS:HG3	1:B:2449:GLU:H	1.73	0.53
1:C:627:PRO:O	1:C:629:ARG:NH1	2.42	0.53
1:D:4039:MET:SD	1:D:4039:MET:N	2.69	0.53
1:B:4978:HIS:CE1	1:B:5027:CYS:SG	3.01	0.53
1:A:2885:THR:HA	1:A:2888:ARG:HE	1.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:420:SER:O	1:B:424:LYS:NZ	2.42	0.53
1:C:505:GLU:HG3	1:C:507:ALA:H	1.73	0.53
1:D:947:GLU:N	1:D:947:GLU:OE1	2.42	0.53
1:B:375:LYS:NZ	1:B:376:ALA:O	2.41	0.52
1:C:4068:LEU:HD22	1:C:4111:LEU:HD11	1.91	0.52
1:D:4773:VAL:O	1:D:4777:ILE:HG12	2.09	0.52
1:A:426:ARG:HH22	1:A:503:PHE:HA	1.74	0.52
1:A:4976:GLU:H	1:A:4976:GLU:CD	2.16	0.52
1:C:955:LEU:HD22	1:C:960:MET:HG2	1.91	0.52
1:D:420:SER:O	1:D:424:LYS:NZ	2.41	0.52
1:D:4204:GLN:HB2	1:D:4245:MET:HE1	1.91	0.52
1:C:955:LEU:HD13	1:C:960:MET:HE3	1.92	0.52
1:D:3902:TYR:O	1:D:3906:GLN:NE2	2.42	0.52
1:C:1619:ARG:HA	1:C:1626:TRP:H	1.73	0.52
1:D:2466:LEU:O	1:D:2470:ILE:HD12	2.10	0.52
1:D:2932:MET:HE3	1:D:2933:ASN:N	2.24	0.52
1:B:955:LEU:HD13	1:B:960:MET:HE3	1.92	0.52
1:D:353:SER:HB3	1:D:355:LEU:HD22	1.91	0.52
1:D:221:ARG:HH21	1:D:259:LEU:HD21	1.75	0.52
1:D:3768:SER:HA	1:D:3771:HIS:CE1	2.44	0.52
1:B:1619:ARG:HA	1:B:1626:TRP:H	1.74	0.52
1:D:2581:UNK:N	1:D:2899:GLY:O	2.42	0.52
1:D:3889:GLN:HB2	1:D:3964:SER:HA	1.91	0.52
1:B:4985:LEU:HA	1:B:4988:TYR:CD2	2.45	0.52
1:C:34:LYS:H	1:C:53:SER:HB3	1.75	0.52
1:C:5004:THR:OG1	1:C:5005:GLY:N	2.43	0.52
1:D:347:PHE:HA	1:D:388:LEU:HD12	1.92	0.52
1:D:4879:MET:HE1	1:A:4577:LEU:HD23	1.91	0.52
1:A:1225:PRO:HG2	1:A:1228:ILE:HB	1.92	0.52
1:D:4983:HIS:C	1:D:4985:LEU:N	2.68	0.52
1:B:4068:LEU:HD22	1:B:4111:LEU:HD11	1.91	0.52
1:C:3777:GLU:O	1:C:3781:GLN:HG3	2.09	0.52
1:D:4902:GLU:OE1	1:D:4902:GLU:N	2.38	0.52
1:A:331:VAL:HG22	1:A:333:GLY:H	1.74	0.52
1:A:4097:MET:HB3	1:A:4108:ILE:HD13	1.92	0.52
1:B:4182:GLU:OE1	1:B:4983:HIS:CD2	2.64	0.51
1:C:1077:ALA:HB3	1:C:1189:LEU:HB3	1.92	0.51
1:A:45:ARG:NH1	1:A:447:ASP:OD2	2.42	0.51
1:C:326:ALA:O	1:C:329:ARG:NH1	2.43	0.51
1:C:4978:HIS:HE1	1:C:4983:HIS:CE1	2.28	0.51
1:D:1115:LEU:HB3	1:D:1123:VAL:HG11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:584:LYS:NZ	1:A:624:ASN:OD1	2.42	0.51
1:B:1077:ALA:HB3	1:B:1189:LEU:HB3	1.92	0.51
1:B:4007:SER:OG	1:B:4116:GLU:OE2	2.27	0.51
1:A:4104:THR:HB	1:A:4107:GLU:OE2	2.11	0.51
1:B:4241:THR:O	1:B:4245:MET:HG2	2.10	0.51
1:D:1077:ALA:HB3	1:D:1189:LEU:HB3	1.92	0.51
1:C:4241:THR:O	1:C:4245:MET:HG2	2.10	0.51
1:B:4844:LEU:HD11	1:B:4924:VAL:HG13	1.91	0.51
1:B:4963:ILE:H	1:B:4963:ILE:HD12	1.76	0.51
1:C:1793:GLU:N	1:C:2173:GLN:O	2.44	0.51
1:D:1260:MET:SD	1:D:1271:ARG:NH2	2.84	0.51
1:A:346:CYS:SG	1:A:347:PHE:N	2.83	0.51
1:A:584:LYS:HG2	1:A:624:ASN:HD21	1.75	0.51
1:D:1644:GLU:OE1	1:D:1646:ARG:NH1	2.43	0.51
1:A:3976:ASN:O	1:A:3980:LEU:HD12	2.11	0.51
1:B:516:LYS:NZ	1:B:555:GLU:O	2.44	0.51
1:B:1028:ASP:N	1:B:1028:ASP:OD1	2.44	0.51
1:B:1793:GLU:N	1:B:2173:GLN:O	2.43	0.51
1:B:2349:ASN:O	1:B:2353:VAL:HG23	2.11	0.51
1:C:2117:VAL:HG23	1:C:2120:MET:HE2	1.92	0.51
1:C:4773:VAL:O	1:C:4777:ILE:HG12	2.11	0.51
1:A:4160:LEU:HA	1:A:4163:PHE:HD2	1.76	0.51
1:D:4104:THR:HG22	1:D:4106:PRO:HD2	1.93	0.51
1:D:4976:GLU:O	1:D:4980:LEU:HG	2.11	0.51
1:B:1260:MET:SD	1:B:1271:ARG:NH2	2.85	0.50
1:A:688:LEU:HB3	1:A:712:TYR:HB3	1.92	0.50
1:B:4860:ARG:NH2	1:B:4876:CYS:O	2.43	0.50
1:C:516:LYS:NZ	1:C:555:GLU:O	2.43	0.50
1:A:196:MET:SD	1:A:196:MET:N	2.84	0.50
1:A:960:MET:SD	1:A:960:MET:N	2.84	0.50
1:B:2331:TYR:HD1	1:B:2332:LEU:H	1.59	0.50
1:A:4053:SER:O	1:A:4056:GLU:HG3	2.10	0.50
1:B:4736:ARG:NH1	1:C:4079:ASP:OD2	2.43	0.50
1:C:1644:GLU:OE1	1:C:1646:ARG:NH1	2.42	0.50
1:C:2102:VAL:HG11	1:C:2124:LEU:HD13	1.92	0.50
1:C:2644:UNK:N	1:C:2871:LEU:O	2.44	0.50
1:C:5000:GLU:OE1	1:C:5000:GLU:N	2.37	0.50
1:A:243:ARG:HD3	1:A:301:VAL:HG23	1.93	0.50
1:B:688:LEU:HB3	1:B:712:TYR:HB3	1.93	0.50
1:C:162:LYS:HG3	1:D:3984:ARG:HH21	1.77	0.50
1:C:2297:LYS:O	1:C:2300:SER:OG	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4728:HIS:HB3	1:D:4732:PHE:CD2	2.46	0.50
1:D:4977:THR:O	1:D:4981:GLU:HB2	2.11	0.50
1:A:144:GLU:OE1	1:A:144:GLU:N	2.40	0.50
1:B:4968:PHE:HB3	1:B:4975:PHE:N	2.27	0.50
1:A:3904:ARG:HG2	1:A:3905:THR:HG23	1.94	0.50
1:B:1045:THR:HG23	1:B:1046:LEU:HD23	1.92	0.50
1:B:1116:GLY:HA3	1:B:1132:TRP:HB3	1.93	0.50
1:C:633:LEU:HD23	1:C:1639:LEU:HD11	1.93	0.50
1:A:221:ARG:NH1	1:A:253:CYS:O	2.44	0.50
1:A:1108:GLU:N	1:A:1108:GLU:OE2	2.45	0.50
1:B:127:MET:HE3	1:B:127:MET:HA	1.93	0.50
1:B:830:ARG:HH21	1:B:837:PRO:HB3	1.76	0.50
1:B:3768:SER:HA	1:B:3771:HIS:CE1	2.47	0.50
1:D:1084:GLN:NE2	1:D:1186:ASP:O	2.45	0.50
1:D:1152:MET:HG3	1:D:1161:ILE:HB	1.93	0.50
1:D:2165:LEU:HD12	1:D:2168:VAL:HB	1.94	0.50
1:A:3969:ILE:HD12	1:A:4030:LEU:HD13	1.93	0.50
1:B:61:ASP:OD1	1:B:61:ASP:N	2.41	0.49
1:B:4980:LEU:HB3	1:B:4981:GLU:CD	2.37	0.49
1:C:4017:LEU:HD22	1:C:4139:ILE:HG21	1.93	0.49
1:D:955:LEU:HD22	1:D:960:MET:HG2	1.93	0.49
1:B:101:LEU:HD23	1:B:163:VAL:HG21	1.94	0.49
1:B:3777:GLU:O	1:B:3781:GLN:HG3	2.12	0.49
1:C:947:GLU:N	1:C:947:GLU:OE1	2.45	0.49
1:D:126:SER:HB3	1:D:132:ALA:HB2	1.95	0.49
1:D:4057:MET:HA	1:D:4060:LYS:HG2	1.93	0.49
1:D:4963:ILE:HD12	1:D:4963:ILE:H	1.77	0.49
1:A:4161:ARG:O	1:A:4165:GLU:HG2	2.12	0.49
1:D:4017:LEU:HD22	1:D:4139:ILE:HG21	1.94	0.49
1:D:4546:VAL:HA	1:D:4549:VAL:HG22	1.94	0.49
1:D:4821:LYS:O	1:D:4825:THR:OG1	2.27	0.49
1:A:684:VAL:HG12	1:A:781:VAL:HG22	1.94	0.49
1:A:1028:ASP:OD1	1:A:1028:ASP:N	2.44	0.49
1:C:3916:ILE:HG21	1:C:3980:LEU:HD11	1.95	0.49
1:D:4820:VAL:HB	1:D:4823:LEU:HB2	1.94	0.49
1:A:4837:LEU:O	1:A:4840:THR:OG1	2.23	0.49
1:C:1700:ASP:OD1	1:C:1700:ASP:N	2.46	0.49
1:C:4152:GLU:OE1	1:C:4194:TYR:OH	2.31	0.49
1:A:669:ASP:HA	1:A:740:PRO:HA	1.94	0.49
1:A:1172:ASP:OD1	1:A:1172:ASP:N	2.37	0.49
1:A:1204:LEU:HD12	1:A:1226:PHE:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2208:MET:O	1:A:2212:VAL:HG23	2.12	0.49
1:A:3780:LEU:HD11	1:A:3816:MET:HG3	1.94	0.49
1:B:3889:GLN:HB2	1:B:3964:SER:HA	1.95	0.49
1:D:4049:VAL:HG21	1:D:4159:ARG:HD2	1.94	0.49
1:B:2897:LYS:O	1:B:2897:LYS:NZ	2.45	0.49
1:D:3829:PHE:HB2	1:D:3913:ILE:HD13	1.95	0.49
1:A:126:SER:HB3	1:A:132:ALA:HB2	1.95	0.49
1:C:2187:ASN:OD1	1:C:2187:ASN:N	2.46	0.49
1:D:632:LEU:O	1:D:634:GLN:NE2	2.45	0.49
1:B:1220:GLN:HG3	1:C:3524:UNK:HA	1.95	0.49
1:B:4773:VAL:O	1:B:4777:ILE:HG12	2.13	0.49
1:C:1095:VAL:HB	1:C:1199:VAL:HB	1.95	0.49
1:C:1260:MET:SD	1:C:1271:ARG:NH2	2.86	0.49
1:C:4089:SER:OG	1:C:4092:ASP:OD1	2.31	0.49
1:D:355:LEU:HD11	1:D:378:LEU:HB3	1.94	0.49
1:D:4982:GLU:O	1:D:4983:HIS:HB2	2.12	0.49
1:B:2186:MET:HA	1:B:2186:MET:HE2	1.95	0.48
1:B:4055:VAL:O	1:B:4059:LEU:HD12	2.13	0.48
1:C:1147:ASP:HB3	1:C:1164:LEU:HD11	1.95	0.48
1:C:2267:MET:SD	1:C:2267:MET:N	2.86	0.48
1:C:4984:ASN:OD1	1:C:4987:ASN:HB2	2.13	0.48
1:A:4230:LYS:HB3	1:A:4231:MET:HE2	1.94	0.48
1:B:1865:MET:HG3	1:B:1866:ILE:HG12	1.94	0.48
1:C:1220:GLN:HG3	1:D:3524:UNK:HA	1.94	0.48
1:A:633:LEU:HD23	1:A:1639:LEU:HD11	1.95	0.48
1:A:1208:VAL:HA	1:A:1211:LEU:HD12	1.95	0.48
1:A:3717:ASP:OD1	1:A:3717:ASP:N	2.41	0.48
1:D:669:ASP:HA	1:D:740:PRO:HA	1.95	0.48
1:D:2228:MET:HE2	1:D:2228:MET:HA	1.96	0.48
1:B:4960:ILE:HD12	1:B:4988:TYR:CE2	2.48	0.48
1:D:4097:MET:HG3	1:D:4108:ILE:HG23	1.95	0.48
1:B:1700:ASP:N	1:B:1700:ASP:OD1	2.46	0.48
1:B:2649:UNK:H	1:B:2869:ARG:HE	1.61	0.48
1:B:4057:MET:HA	1:B:4060:LYS:HG2	1.96	0.48
1:B:4546:VAL:HA	1:B:4549:VAL:HG22	1.94	0.48
1:C:928:THR:O	1:C:932:LEU:HD12	2.14	0.48
1:C:3733:CYS:SG	1:C:3803:SER:OG	2.68	0.48
1:D:955:LEU:HD13	1:D:960:MET:HE3	1.95	0.48
1:B:5028:PHE:CE1	1:B:5032:TYR:HB2	2.48	0.48
1:D:2188:ASN:C	1:D:2188:ASN:ND2	2.71	0.48
1:A:572:PRO:HA	1:A:575:LEU:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:618:GLN:OE1	1:C:1678:ASN:ND2	2.43	0.48
1:C:1028:ASP:OD1	1:C:1028:ASP:N	2.44	0.48
1:D:1028:ASP:OD1	1:D:1028:ASP:N	2.44	0.48
1:A:2314:LEU:HA	1:A:2318:TYR:HB2	1.95	0.48
1:B:3524:UNK:HA	1:A:1220:GLN:HG3	1.96	0.48
1:C:669:ASP:HA	1:C:740:PRO:HA	1.96	0.48
1:C:2186:MET:HE2	1:C:2186:MET:HA	1.96	0.48
1:C:4546:VAL:HA	1:C:4549:VAL:HG22	1.95	0.48
1:D:162:LYS:HG3	1:A:3984:ARG:HH12	1.78	0.48
1:B:2118:ARG:NH2	1:B:3719:ASP:OD1	2.43	0.48
1:D:127:MET:HA	1:D:127:MET:HE3	1.96	0.48
1:D:2196:ASN:OD1	1:D:2199:ARG:NH2	2.46	0.48
1:A:1695:LEU:HD22	1:A:1810:LYS:HE2	1.94	0.48
1:A:2187:ASN:OD1	1:A:2187:ASN:N	2.46	0.48
1:B:4985:LEU:H	1:B:4985:LEU:HG	1.40	0.48
1:C:221:ARG:NH1	1:C:253:CYS:O	2.47	0.48
1:C:1084:GLN:NE2	1:C:1186:ASP:O	2.47	0.48
1:B:669:ASP:HA	1:B:740:PRO:HA	1.95	0.47
1:B:1084:GLN:NE2	1:B:1186:ASP:O	2.47	0.47
1:B:4978:HIS:C	1:B:4980:LEU:H	2.21	0.47
1:C:35:LEU:HB3	1:C:49:LEU:HB3	1.95	0.47
1:A:4124:ASN:HB3	1:A:4127:GLU:HG3	1.96	0.47
1:B:18:ASP:N	1:B:18:ASP:OD1	2.47	0.47
1:B:2922:LYS:HB3	1:B:2922:LYS:HE3	1.65	0.47
1:A:101:LEU:HD23	1:A:163:VAL:HG21	1.96	0.47
1:A:330:ASP:OD1	1:A:330:ASP:N	2.46	0.47
1:B:2581:UNK:HA	1:B:2895:GLU:HG3	1.96	0.47
1:C:4222:VAL:HG21	1:C:4950:VAL:HG23	1.95	0.47
1:D:18:ASP:N	1:D:18:ASP:OD1	2.47	0.47
1:D:4558:ASN:O	1:D:4561:THR:OG1	2.32	0.47
1:B:633:LEU:HD23	1:B:1639:LEU:HD11	1.96	0.47
1:B:4813:LEU:HA	1:B:4816:ILE:HG22	1.97	0.47
1:A:1700:ASP:OD1	1:A:1700:ASP:N	2.45	0.47
1:A:5004:THR:OG1	1:A:5005:GLY:N	2.45	0.47
1:B:1927:LEU:HD13	1:B:2101:MET:HG3	1.96	0.47
1:C:1717:SER:HA	1:C:1721:GLU:HB2	1.97	0.47
1:C:4931:ILE:HG22	1:D:4936:ILE:HG21	1.96	0.47
1:D:1116:GLY:HA3	1:D:1132:TRP:HB3	1.95	0.47
1:D:4152:GLU:OE2	1:D:4194:TYR:OH	2.32	0.47
1:A:78:LEU:HA	1:A:81:MET:HG2	1.96	0.47
1:A:1619:ARG:HA	1:A:1626:TRP:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:700:GLU:HG2	1:C:709:ASP:HB3	1.96	0.47
1:D:665:GLU:HB2	1:D:792:LEU:HD12	1.97	0.47
1:D:935:LEU:HD11	1:D:1053:ILE:HG13	1.96	0.47
1:D:2187:ASN:OD1	1:D:2187:ASN:N	2.46	0.47
1:D:4813:LEU:HA	1:D:4816:ILE:HG22	1.94	0.47
1:A:4985:LEU:O	1:A:4988:TYR:HB2	2.15	0.47
1:B:35:LEU:HB3	1:B:49:LEU:HB3	1.95	0.47
1:B:700:GLU:HG2	1:B:709:ASP:HB3	1.97	0.47
1:B:2644:UNK:N	1:B:2871:LEU:O	2.39	0.47
1:C:21:VAL:HB	1:C:205:ILE:HD11	1.96	0.47
1:C:1158:ASN:HB3	1:C:1182:ILE:HG22	1.96	0.47
1:D:874:LEU:HD21	1:D:929:LEU:HD11	1.96	0.47
1:D:2442:LEU:HD23	1:D:2443:ILE:H	1.79	0.47
1:D:4728:HIS:HB2	1:D:4737:ILE:HD11	1.95	0.47
1:A:578:ILE:HD12	1:A:578:ILE:H	1.78	0.47
1:A:4675:LYS:HB3	1:A:4675:LYS:HE3	1.78	0.47
1:C:517:GLU:O	1:C:521:LEU:HG	2.15	0.47
1:C:3751:VAL:HG13	1:C:3755:GLU:HB2	1.95	0.47
1:C:4984:ASN:O	1:C:4985:LEU:HB2	2.15	0.47
1:D:35:LEU:HB3	1:D:49:LEU:HB3	1.97	0.47
1:D:688:LEU:HB3	1:D:712:TYR:HB3	1.96	0.47
1:D:1793:GLU:N	1:D:2173:GLN:O	2.47	0.47
1:D:4555:LEU:HD11	1:D:4656:LEU:HD22	1.96	0.47
1:A:700:GLU:HG2	1:A:709:ASP:HB3	1.96	0.47
1:B:2332:LEU:HD11	1:B:2428:ALA:HB1	1.97	0.47
1:B:3713:LYS:HZ3	1:B:3715:LYS:H	1.63	0.47
1:B:3751:VAL:HG13	1:B:3755:GLU:HB2	1.96	0.47
1:C:127:MET:HE3	1:C:127:MET:HA	1.97	0.47
1:B:2196:ASN:OD1	1:B:2199:ARG:NH2	2.48	0.46
1:B:2288:LEU:HD23	1:B:3849:ARG:HB3	1.97	0.46
1:C:701:GLY:HA2	1:C:1646:ARG:HA	1.97	0.46
1:C:4828:SER:O	1:C:4832:HIS:HB2	2.15	0.46
1:C:4963:ILE:HD12	1:C:4963:ILE:H	1.79	0.46
1:B:4778:TRP:O	1:B:4782:VAL:HG23	2.15	0.46
1:C:355:LEU:HD11	1:C:378:LEU:HB3	1.96	0.46
1:C:684:VAL:HG12	1:C:781:VAL:HG22	1.97	0.46
1:A:18:ASP:OD1	1:A:18:ASP:N	2.48	0.46
1:A:2145:SER:O	1:A:2148:SER:OG	2.31	0.46
1:A:4692:PRO:HD2	1:A:4703:ARG:HH22	1.79	0.46
1:B:665:GLU:HB2	1:B:792:LEU:HD12	1.97	0.46
1:B:701:GLY:HA2	1:B:1646:ARG:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4774:LYS:HE2	1:B:4774:LYS:HB3	1.74	0.46
1:B:4902:GLU:OE1	1:B:4902:GLU:N	2.42	0.46
1:C:18:ASP:OD1	1:C:18:ASP:N	2.47	0.46
1:C:2442:LEU:HD23	1:C:2443:ILE:H	1.80	0.46
1:C:4727:LYS:HE2	1:C:4727:LYS:HB3	1.43	0.46
1:C:1116:GLY:HA3	1:C:1132:TRP:HB3	1.97	0.46
1:C:4704:LEU:HD11	1:C:4778:TRP:HB2	1.98	0.46
1:D:4712:PRO:HB2	1:D:4718:LYS:HD2	1.96	0.46
1:A:1110:ARG:HG2	1:A:1110:ARG:HH11	1.80	0.46
1:A:3661:TRP:CG	1:A:3662:ILE:H	2.33	0.46
1:B:632:LEU:O	1:B:634:GLN:NE2	2.48	0.46
1:C:663:TYR:HB3	1:C:809:ALA:HB2	1.98	0.46
1:C:4976:GLU:HG3	1:C:4977:THR:N	2.31	0.46
1:A:2114:PRO:HA	1:A:2117:VAL:HG12	1.98	0.46
1:A:4001:MET:HE3	1:A:4001:MET:HA	1.96	0.46
1:A:4055:VAL:O	1:A:4059:LEU:HG	2.16	0.46
1:B:1939:MET:HE3	1:B:1939:MET:HB3	1.83	0.46
1:B:2442:LEU:HD23	1:B:2443:ILE:H	1.81	0.46
1:C:2679:UNK:HA	1:C:2741:GLU:HA	1.98	0.46
1:C:4007:SER:OG	1:C:4116:GLU:OE2	2.33	0.46
1:D:126:SER:OG	1:D:130:LYS:O	2.33	0.46
1:D:3989:VAL:O	1:D:3993:LEU:HG	2.15	0.46
1:B:618:GLN:OE1	1:B:1678:ASN:ND2	2.44	0.46
1:B:1106:ARG:NH1	1:B:1184:ILE:O	2.48	0.46
1:B:1717:SER:HA	1:B:1721:GLU:HB2	1.98	0.46
1:D:618:GLN:OE1	1:D:1678:ASN:ND2	2.46	0.46
1:A:1147:ASP:OD1	1:A:1165:ASN:ND2	2.42	0.46
1:A:3775:ALA:HA	1:A:3778:MET:HG3	1.97	0.46
1:A:3844:LEU:O	1:A:3848:GLU:HG2	2.15	0.46
1:B:517:GLU:O	1:B:521:LEU:HG	2.16	0.46
1:B:4629:TYR:OH	1:A:4860:ARG:NH2	2.44	0.46
1:B:4856:PHE:HA	1:B:4860:ARG:HB2	1.98	0.46
1:D:1157:GLU:OE1	1:D:1159:THR:OG1	2.29	0.46
1:D:2581:UNK:HA	1:D:2895:GLU:HG3	1.96	0.46
1:A:701:GLY:HA2	1:A:1646:ARG:HA	1.97	0.46
1:A:3811:GLU:HA	1:A:3814:GLN:HG3	1.98	0.46
1:A:4733:GLY:H	1:A:4736:ARG:HD3	1.81	0.46
1:C:665:GLU:HB2	1:C:792:LEU:HD12	1.98	0.46
1:D:4961:CYS:HB2	1:D:4963:ILE:HD12	1.98	0.46
1:A:4976:GLU:HB2	1:A:4980:LEU:HD23	1.98	0.46
1:B:4961:CYS:HB2	1:B:4963:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5029:ARG:O	1:B:5033:GLU:HB3	2.16	0.46
1:D:608:VAL:HG22	1:D:613:ALA:HB2	1.98	0.46
1:D:1865:MET:HG3	1:D:1866:ILE:HG12	1.97	0.46
1:A:61:ASP:OD1	1:A:61:ASP:N	2.43	0.46
1:B:4067:LYS:HD2	1:B:4102:GLN:HB3	1.98	0.45
1:C:4056:GLU:HA	1:C:4059:LEU:HG	1.97	0.45
1:C:4658:ILE:HD12	1:C:4792:LEU:HD12	1.97	0.45
1:C:4774:LYS:HE2	1:C:4774:LYS:HB3	1.74	0.45
1:D:1856:ASP:OD1	1:D:1856:ASP:N	2.49	0.45
1:B:4060:LYS:HE2	1:B:4060:LYS:HB2	1.86	0.45
1:B:4712:PRO:HB2	1:B:4718:LYS:HD2	1.98	0.45
1:C:4813:LEU:HA	1:C:4816:ILE:HG22	1.98	0.45
1:D:700:GLU:HG2	1:D:709:ASP:HB3	1.97	0.45
1:B:27:THR:HB	1:B:33:LEU:HB2	1.98	0.45
1:B:3951:PHE:O	1:B:3955:MET:HG3	2.16	0.45
1:C:3877:ASP:HB2	1:C:3880:PHE:HB3	1.98	0.45
1:C:4191:GLU:OE2	1:C:4191:GLU:N	2.49	0.45
1:D:4980:LEU:HG	1:D:4980:LEU:H	1.59	0.45
1:A:4053:SER:O	1:A:4057:MET:HG2	2.15	0.45
1:B:221:ARG:HH21	1:B:259:LEU:HD21	1.81	0.45
1:C:3823:LYS:HA	1:C:3823:LYS:HD3	1.63	0.45
1:A:5013:MET:HG3	1:A:5018:CYS:HB3	1.98	0.45
1:B:4903:ASP:OD1	1:B:4903:ASP:N	2.47	0.45
1:C:286:THR:HG23	1:C:287:THR:HG23	1.98	0.45
1:D:2285:GLU:HG2	1:D:2286:LEU:HG	1.98	0.45
1:A:472:ARG:NH1	1:A:475:GLN:OE1	2.47	0.45
1:A:3716:LEU:HD12	1:A:3716:LEU:H	1.81	0.45
1:B:286:THR:HG23	1:B:287:THR:HG23	1.99	0.45
1:C:707:VAL:HG13	1:C:713:SER:HB3	1.99	0.45
1:C:1385:UNK:HA	1:C:1396:UNK:HA	1.99	0.45
1:C:1769:THR:HG23	1:C:1956:GLU:HG2	1.99	0.45
1:C:4989:MET:HE2	1:C:4989:MET:HB3	1.83	0.45
1:D:286:THR:HG23	1:D:287:THR:HG23	1.97	0.45
1:D:957:LYS:HA	1:D:960:MET:HB2	1.98	0.45
1:D:4007:SER:OG	1:D:4116:GLU:OE2	2.34	0.45
1:A:2581:UNK:HA	1:A:2895:GLU:HG3	1.97	0.45
1:C:61:ASP:OD1	1:C:61:ASP:N	2.41	0.45
1:C:4214:LYS:O	1:C:4218:ILE:HG13	2.16	0.45
1:C:4239:GLU:OE1	1:C:5014:TYR:OH	2.35	0.45
1:C:4903:ASP:OD1	1:C:4903:ASP:N	2.48	0.45
1:D:3719:ASP:O	1:D:3723:MET:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2228:MET:HA	1:B:2228:MET:HE2	1.99	0.45
1:B:2285:GLU:HG2	1:B:2286:LEU:HG	1.97	0.45
1:B:3823:LYS:HA	1:B:3823:LYS:HD3	1.63	0.45
1:C:442:ILE:O	1:C:446:GLN:HG2	2.17	0.45
1:C:866:HIS:O	1:C:869:ARG:NH1	2.46	0.45
1:C:1170:MET:HE2	1:C:1170:MET:HA	1.99	0.45
1:C:2753:SER:HB2	1:C:2932:MET:HE2	1.98	0.45
1:D:663:TYR:HB3	1:D:809:ALA:HB2	1.99	0.45
1:D:4730:ASP:OD1	1:A:4101:LYS:HD3	2.17	0.45
1:A:1952:GLN:O	1:A:1956:GLU:HG2	2.16	0.45
1:A:2297:LYS:O	1:A:2300:SER:OG	2.31	0.45
1:C:3696:ASP:O	1:C:3700:GLN:HG3	2.17	0.45
1:D:2868:SER:O	1:D:2872:GLN:NE2	2.49	0.45
1:D:4774:LYS:HE2	1:D:4774:LYS:HB3	1.73	0.45
1:D:4963:ILE:HB	1:D:4968:PHE:HE1	1.81	0.45
1:A:127:MET:HE3	1:A:127:MET:HA	1.99	0.45
1:C:306:LYS:HE2	1:C:306:LYS:HB3	1.86	0.45
1:C:632:LEU:O	1:C:634:GLN:NE2	2.50	0.45
1:C:1166:GLY:HA2	1:C:1216:ILE:HD13	1.99	0.45
1:D:2897:LYS:O	1:D:2897:LYS:NZ	2.48	0.45
1:D:3921:ASP:O	1:D:3925:ARG:HG3	2.16	0.45
1:B:500:ALA:HB1	1:B:505:GLU:HB2	1.98	0.44
1:B:4844:LEU:HD22	1:B:4928:LEU:HG	1.98	0.44
1:B:4960:ILE:H	1:B:4960:ILE:HG12	1.62	0.44
1:C:266:ARG:NH2	1:C:269:TRP:O	2.50	0.44
1:C:4067:LYS:HB2	1:C:4103:PHE:CE1	2.52	0.44
1:C:4182:GLU:HG2	1:C:4192:ARG:HG3	1.98	0.44
1:A:1094:ALA:HB3	1:A:1143:TRP:HE1	1.83	0.44
1:A:2465:ASP:O	1:A:2469:ILE:HG12	2.17	0.44
1:A:4774:LYS:HE2	1:A:4774:LYS:HB3	1.73	0.44
1:B:663:TYR:HB3	1:B:809:ALA:HB2	2.00	0.44
1:B:914:PRO:O	1:B:918:ARG:HG3	2.17	0.44
1:B:4820:VAL:HB	1:B:4823:LEU:HB2	1.98	0.44
1:C:1106:ARG:NH1	1:C:1184:ILE:O	2.51	0.44
1:C:4791:TYR:OH	1:C:4815:ASP:O	2.35	0.44
1:D:231:LEU:HD12	1:D:245:VAL:HG11	1.99	0.44
1:A:1170:MET:HE2	1:A:1170:MET:HA	1.99	0.44
1:A:2922:LYS:HB3	1:A:2922:LYS:HE3	1.67	0.44
1:A:3719:ASP:O	1:A:3723:MET:HG2	2.17	0.44
1:A:4207:MET:HB2	1:A:4210:VAL:HG23	1.99	0.44
1:B:583:ILE:HD12	1:B:621:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1385:UNK:HA	1:B:1396:UNK:HA	1.99	0.44
1:B:1856:ASP:OD1	1:B:1856:ASP:N	2.49	0.44
1:C:553:ARG:HH21	1:C:1593:PRO:HG3	1.82	0.44
1:B:551:LEU:HG	1:B:589:LEU:HD22	1.99	0.44
1:C:2254:LEU:HD11	1:C:2334:PHE:HZ	1.82	0.44
1:D:4161:ARG:O	1:D:4165:GLU:HG2	2.17	0.44
1:A:2099:SER:O	1:A:2103:VAL:HG22	2.17	0.44
1:A:2261:SER:HA	1:A:2272:PRO:HG2	1.99	0.44
1:A:2466:LEU:O	1:A:2470:ILE:HD12	2.18	0.44
1:B:4105:GLY:O	1:B:4109:GLN:NE2	2.50	0.44
1:C:1856:ASP:N	1:C:1856:ASP:OD1	2.49	0.44
1:C:2145:SER:O	1:C:2148:SER:OG	2.35	0.44
1:C:4207:MET:HB2	1:C:4210:VAL:HG23	2.00	0.44
1:D:684:VAL:HG12	1:D:781:VAL:HG22	1.98	0.44
1:D:2254:LEU:HD11	1:D:2334:PHE:HZ	1.82	0.44
1:D:3877:ASP:HB2	1:D:3880:PHE:HB3	1.99	0.44
1:A:553:ARG:HH21	1:A:1593:PRO:HG3	1.83	0.44
1:A:4976:GLU:O	1:A:4980:LEU:N	2.44	0.44
1:B:4235:VAL:O	1:B:4239:GLU:HG2	2.16	0.44
1:C:27:THR:HB	1:C:33:LEU:HB2	2.00	0.44
1:C:1671:ARG:O	1:C:1675:ALA:HB2	2.17	0.44
1:D:516:LYS:HE2	1:D:516:LYS:HB3	1.66	0.44
1:D:580:GLU:O	1:D:584:LYS:HG2	2.18	0.44
1:D:879:HIS:CE1	1:D:921:ASN:HD22	2.35	0.44
1:B:975:VAL:HB	1:B:1047:LEU:HD21	2.00	0.44
1:B:1225:PRO:HG2	1:B:1228:ILE:HB	2.00	0.44
1:B:2000:SER:O	1:B:2005:GLN:NE2	2.42	0.44
1:B:4675:LYS:HB3	1:B:4675:LYS:HE3	1.81	0.44
1:D:786:GLY:N	1:D:1630:CYS:O	2.51	0.44
1:A:56:GLN:O	1:A:309:THR:OG1	2.30	0.44
1:A:4704:LEU:HD11	1:A:4778:TRP:HB2	2.00	0.44
1:B:3696:ASP:O	1:B:3700:GLN:HG3	2.17	0.44
1:C:521:LEU:HA	1:C:524:GLU:HG3	2.00	0.44
1:D:263:GLU:HG3	1:D:281:ARG:HG3	2.00	0.44
1:D:737:LEU:HD12	1:D:737:LEU:HA	1.86	0.44
1:B:2382:GLU:O	1:B:2386:ILE:HG23	2.17	0.44
1:B:3877:ASP:HB2	1:B:3880:PHE:HB3	2.00	0.44
1:D:883:ALA:O	1:D:887:ILE:HG13	2.18	0.44
1:C:126:SER:OG	1:C:130:LYS:O	2.30	0.43
1:C:500:ALA:HB1	1:C:505:GLU:HB2	2.00	0.43
1:C:2285:GLU:HG2	1:C:2286:LEU:HG	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4207:MET:HB2	1:D:4210:VAL:HG23	2.00	0.43
1:A:957:LYS:HA	1:A:960:MET:HG2	1.99	0.43
1:D:1170:MET:HE2	1:D:1170:MET:HA	2.00	0.43
1:D:1769:THR:HG23	1:D:1956:GLU:HG2	1.99	0.43
1:D:2297:LYS:O	1:D:2300:SER:OG	2.29	0.43
1:A:178:ARG:HE	1:A:195:PHE:HE1	1.65	0.43
1:A:2159:LEU:HD12	1:A:2159:LEU:HA	1.84	0.43
1:A:2897:LYS:O	1:A:2897:LYS:NZ	2.47	0.43
1:B:317:ARG:HH22	1:B:323:LEU:H	1.65	0.43
1:B:1077:ALA:HB2	1:B:1190:PRO:HG2	1.99	0.43
1:B:4207:MET:HB2	1:B:4210:VAL:HG23	2.00	0.43
1:C:5036:LEU:H	1:C:5036:LEU:HD23	1.83	0.43
1:D:3811:GLU:HA	1:D:3814:GLN:HG3	2.00	0.43
1:B:4101:LYS:HG3	1:A:4730:ASP:OD2	2.19	0.43
1:B:4821:LYS:O	1:B:4825:THR:OG1	2.33	0.43
1:C:1581:LEU:HD12	1:C:1581:LEU:HA	1.91	0.43
1:C:1842:LEU:HD23	1:C:1842:LEU:HA	1.90	0.43
1:C:1931:LEU:HB2	1:C:1936:LYS:HE3	2.00	0.43
1:D:1676:LEU:HD22	1:D:2167:ILE:HD12	2.00	0.43
1:D:2205:GLU:O	1:D:2209:GLU:HG3	2.18	0.43
1:D:3834:ALA:O	1:D:3838:THR:HG22	2.19	0.43
1:A:353:SER:HB3	1:A:355:LEU:HD23	1.99	0.43
1:A:3823:LYS:HA	1:A:3823:LYS:HD3	1.62	0.43
1:A:4654:ALA:HB1	1:A:4796:MET:HE1	2.00	0.43
1:B:4156:HIS:HB3	1:B:5036:LEU:HD11	2.00	0.43
1:C:4865:LYS:HA	1:C:4865:LYS:HD2	1.79	0.43
1:D:459:LEU:HD23	1:D:459:LEU:H	1.83	0.43
1:D:870:ILE:HG13	1:D:873:LYS:HD3	2.00	0.43
1:A:707:VAL:HG13	1:A:713:SER:HB2	1.99	0.43
1:A:781:VAL:HG12	1:A:783:PHE:HD2	1.84	0.43
1:A:3820:LEU:HD23	1:A:3820:LEU:HA	1.90	0.43
1:B:355:LEU:HD11	1:B:378:LEU:HB3	2.00	0.43
1:C:2176:ASN:O	1:C:2180:GLN:HG2	2.18	0.43
1:D:5012:LYS:O	1:D:5016:GLU:HG2	2.19	0.43
1:A:1717:SER:HA	1:A:1721:GLU:HB2	2.01	0.43
1:C:3768:SER:HA	1:C:3771:HIS:CE1	2.53	0.43
1:D:27:THR:HB	1:D:33:LEU:HB2	2.01	0.43
1:D:4025:VAL:HA	1:D:4028:LEU:HG	2.01	0.43
1:D:4903:ASP:OD1	1:D:4903:ASP:N	2.47	0.43
1:A:545:ASP:OD1	1:A:582:HIS:NE2	2.52	0.43
1:A:786:GLY:N	1:A:1630:CYS:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1613:LEU:HD23	1:A:1634:LEU:HD12	2.00	0.43
1:B:1204:LEU:HD12	1:B:1226:PHE:HB3	2.00	0.43
1:B:1925:GLY:N	1:B:1928:GLN:OE1	2.49	0.43
1:C:4149:ASN:HD22	1:C:4194:TYR:HE2	1.67	0.43
1:A:265:LEU:HD12	1:A:265:LEU:H	1.84	0.43
1:A:2335:LEU:O	1:A:2339:VAL:HG22	2.19	0.43
1:A:4686:LEU:HD23	1:A:4686:LEU:HA	1.86	0.43
1:B:385:ASP:OD1	1:B:385:ASP:N	2.52	0.43
1:C:231:LEU:HD12	1:C:245:VAL:HG11	2.01	0.43
1:C:4973:HIS:NE2	1:C:4976:GLU:HG2	2.34	0.43
1:D:196:MET:SD	1:D:196:MET:N	2.92	0.43
1:D:394:GLN:NE2	1:D:396:GLU:H	2.16	0.43
1:D:1106:ARG:NH1	1:D:1184:ILE:O	2.48	0.43
1:A:4874:MET:HE3	1:A:4875:LYS:N	2.34	0.43
1:A:4966:ASP:O	1:A:4968:PHE:N	2.52	0.43
1:B:483:MET:HA	1:B:483:MET:HE2	2.01	0.43
1:B:4017:LEU:HD22	1:B:4139:ILE:HG21	2.00	0.43
1:B:4182:GLU:OE1	1:B:4983:HIS:HD2	2.02	0.43
1:A:2442:LEU:HD23	1:A:2443:ILE:H	1.83	0.43
1:A:3921:ASP:OD1	1:A:3922:TYR:N	2.52	0.43
1:B:243:ARG:HA	1:B:243:ARG:HD3	1.78	0.42
1:B:707:VAL:HG13	1:B:713:SER:HB2	1.99	0.42
1:B:2205:GLU:O	1:B:2209:GLU:HG3	2.19	0.42
1:C:196:MET:SD	1:C:196:MET:N	2.91	0.42
1:C:688:LEU:HB3	1:C:712:TYR:HB3	1.99	0.42
1:D:4214:LYS:O	1:D:4218:ILE:HG13	2.19	0.42
1:A:320:LYS:HD2	1:A:320:LYS:H	1.84	0.42
1:A:1619:ARG:O	1:A:1625:GLY:N	2.52	0.42
1:D:4542:GLY:O	1:D:4546:VAL:HG13	2.19	0.42
1:A:692:TYR:HD1	1:A:826:ILE:HD12	1.83	0.42
1:A:2189:LYS:HE2	1:A:2189:LYS:HB2	1.87	0.42
1:A:3963:ASN:O	1:A:3966:THR:OG1	2.37	0.42
1:B:608:VAL:HG22	1:B:613:ALA:HB2	2.01	0.42
1:C:957:LYS:HA	1:C:960:MET:HB2	2.01	0.42
1:C:1077:ALA:HB2	1:C:1190:PRO:HG2	2.00	0.42
1:C:2335:LEU:O	1:C:2339:VAL:HG13	2.19	0.42
1:C:4555:LEU:HD12	1:C:4555:LEU:HA	1.88	0.42
1:C:4675:LYS:HB3	1:C:4675:LYS:HE3	1.82	0.42
1:D:109:LEU:HD12	1:D:118:LEU:HD22	2.01	0.42
1:D:1077:ALA:HB2	1:D:1190:PRO:HG2	2.00	0.42
1:A:774:ASP:N	1:A:774:ASP:OD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4844:LEU:O	1:A:4848:VAL:HG23	2.19	0.42
1:B:126:SER:OG	1:B:130:LYS:O	2.35	0.42
1:B:4870:ASP:OD1	1:B:4870:ASP:N	2.53	0.42
1:C:4985:LEU:O	1:C:4988:TYR:HB2	2.19	0.42
1:D:178:ARG:HB3	1:D:193:ALA:HB1	2.02	0.42
1:A:4813:LEU:HA	1:A:4816:ILE:HG22	2.01	0.42
1:A:4961:CYS:SG	1:A:4963:ILE:HG23	2.41	0.42
1:B:1712:TYR:OH	1:B:1814:MET:SD	2.77	0.42
1:C:758:ARG:HG2	1:C:762:CYS:HA	2.02	0.42
1:C:2581:UNK:HA	1:C:2895:GLU:HG3	2.01	0.42
1:C:4680:LYS:HD2	1:C:4686:LEU:HD11	2.01	0.42
1:C:4712:PRO:HB2	1:C:4718:LYS:HD2	2.01	0.42
1:D:1676:LEU:HD23	1:D:1676:LEU:HA	1.87	0.42
1:A:530:ILE:HD13	1:A:530:ILE:HA	1.91	0.42
1:A:1072:VAL:HG12	1:A:1195:GLY:HA2	2.01	0.42
1:A:1712:TYR:O	1:A:1716:ILE:HG23	2.19	0.42
1:C:3755:GLU:O	1:C:3759:GLU:HG2	2.20	0.42
1:C:5033:GLU:OE1	1:C:5033:GLU:N	2.44	0.42
1:D:500:ALA:HB1	1:D:505:GLU:HB2	2.01	0.42
1:A:385:ASP:OD1	1:A:385:ASP:N	2.52	0.42
1:A:866:HIS:O	1:A:869:ARG:NH1	2.52	0.42
1:A:2694:UNK:HA	1:A:2929:PHE:HE1	1.84	0.42
1:B:2189:LYS:HB2	1:B:2189:LYS:HE2	1.87	0.42
1:C:3889:GLN:HB2	1:C:3964:SER:HA	2.00	0.42
1:D:707:VAL:HG13	1:D:713:SER:HB2	2.00	0.42
1:D:4966:ASP:OD1	1:D:4967:TYR:N	2.52	0.42
1:B:550:LYS:HB3	1:B:560:ILE:HG12	2.01	0.42
1:B:4832:HIS:HD1	1:B:4832:HIS:C	2.28	0.42
1:C:4555:LEU:HD11	1:C:4656:LEU:HB3	2.01	0.42
1:D:4703:ARG:HA	1:D:4706:LEU:HD12	2.02	0.42
1:D:4750:ILE:HD13	1:D:4750:ILE:HA	1.96	0.42
1:A:294:THR:HG23	1:A:295:GLU:H	1.84	0.42
1:A:580:GLU:O	1:A:584:LYS:HG3	2.19	0.42
1:B:2145:SER:O	1:B:2148:SER:OG	2.38	0.42
1:B:3670:GLU:HG2	1:B:3728:ILE:HA	2.01	0.42
1:C:1712:TYR:OH	1:C:1814:MET:SD	2.77	0.42
1:C:4962:GLY:H	1:C:5025:GLY:HA2	1.85	0.42
1:D:4160:LEU:O	1:D:4164:LEU:HD23	2.20	0.42
1:D:4857:ASN:HD21	1:A:4807:PHE:HB2	1.85	0.42
1:B:121:LEU:HB3	1:B:123:THR:HG22	2.02	0.42
1:B:4542:GLY:O	1:B:4546:VAL:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:ARG:HH21	1:C:259:LEU:HD21	1.85	0.42
1:C:1676:LEU:HA	1:C:1725:ARG:HH22	1.85	0.42
1:C:1763:PRO:HG3	1:C:2094:LEU:HD22	2.01	0.42
1:C:4816:ILE:HD12	1:C:4816:ILE:HA	1.90	0.42
1:D:1927:LEU:HB3	1:D:2104:ARG:HH22	1.85	0.42
1:D:1969:LEU:HD21	1:D:2009:LEU:HD11	2.01	0.42
1:D:3696:ASP:O	1:D:3700:GLN:HG3	2.20	0.42
1:D:4555:LEU:HD23	1:D:4555:LEU:HA	1.89	0.42
1:A:3768:SER:HA	1:A:3771:HIS:ND1	2.35	0.42
1:B:553:ARG:HH21	1:B:1593:PRO:HG3	1.84	0.41
1:B:883:ALA:O	1:B:887:ILE:HG13	2.20	0.41
1:B:915:GLU:HA	1:B:918:ARG:HD3	2.02	0.41
1:C:626:LEU:HD11	1:C:630:GLU:H	1.85	0.41
1:D:1158:ASN:HB3	1:D:1182:ILE:HG22	2.02	0.41
1:D:2906:VAL:HG11	1:D:2914:LYS:HG3	2.01	0.41
1:D:3823:LYS:HD3	1:D:3823:LYS:HA	1.62	0.41
1:A:2153:MET:HE3	1:A:2153:MET:HA	2.02	0.41
1:A:4072:VAL:HG13	1:A:4125:PHE:HD2	1.85	0.41
1:A:4232:GLU:OE2	1:A:4232:GLU:N	2.50	0.41
1:B:929:LEU:O	1:B:933:LEU:HG	2.21	0.41
1:B:3984:ARG:H	1:B:3984:ARG:HG2	1.69	0.41
1:B:4192:ARG:HD3	1:B:4193:ILE:N	2.34	0.41
1:B:4214:LYS:O	1:B:4218:ILE:HG13	2.19	0.41
1:D:4085:ARG:HE	1:D:4085:ARG:HB2	1.71	0.41
1:D:4783:ILE:HD13	1:D:4783:ILE:HA	1.85	0.41
1:B:1658:ASP:OD1	1:B:1659:LEU:N	2.54	0.41
1:B:2254:LEU:HD11	1:B:2334:PHE:HZ	1.85	0.41
1:B:4229:GLU:O	1:B:4233:LEU:HG	2.20	0.41
1:C:2189:LYS:HB2	1:C:2189:LYS:HE2	1.87	0.41
1:C:3834:ALA:O	1:C:3838:THR:HG22	2.20	0.41
1:C:4677:LEU:HD12	1:C:4677:LEU:HA	1.88	0.41
1:D:1108:GLU:N	1:D:1108:GLU:OE1	2.53	0.41
1:D:3901:ASN:OD1	1:D:3904:ARG:NH1	2.44	0.41
1:D:4728:HIS:O	1:D:4732:PHE:N	2.53	0.41
1:A:286:THR:HG22	1:A:401:ALA:HB1	2.01	0.41
1:A:608:VAL:HG22	1:A:613:ALA:HB2	2.01	0.41
1:A:3696:ASP:OD1	1:A:3696:ASP:N	2.50	0.41
1:A:4773:VAL:O	1:A:4777:ILE:HG22	2.19	0.41
1:A:4969:ASP:HB2	1:A:4975:PHE:CZ	2.55	0.41
1:B:947:GLU:OE2	1:B:947:GLU:N	2.51	0.41
1:B:2175:GLU:O	1:B:2179:ILE:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2261:SER:HA	1:B:2272:PRO:HG2	2.02	0.41
1:B:3713:LYS:NZ	1:B:3715:LYS:H	2.18	0.41
1:B:3834:ALA:O	1:B:3838:THR:HG22	2.20	0.41
1:C:321:GLU:H	1:C:321:GLU:CD	2.28	0.41
1:C:3775:ALA:O	1:C:3778:MET:HG3	2.21	0.41
1:D:243:ARG:HA	1:D:243:ARG:HD3	1.79	0.41
1:D:2138:LEU:HD23	1:D:2138:LEU:HA	1.93	0.41
1:D:4039:MET:HA	1:D:4042:ARG:HD2	2.02	0.41
1:D:4725:LEU:O	1:D:4729:GLY:N	2.51	0.41
1:A:25:SER:OG	1:A:32:GLN:OE1	2.39	0.41
1:A:287:THR:HB	1:A:289:ARG:HD2	2.03	0.41
1:A:291:LEU:HD23	1:A:291:LEU:H	1.86	0.41
1:A:1155:LEU:HD13	1:A:1184:ILE:HD12	2.02	0.41
1:A:1251:GLU:OE2	1:A:1251:GLU:N	2.53	0.41
1:A:4931:ILE:O	1:A:4935:LEU:HG	2.20	0.41
1:B:957:LYS:HA	1:B:960:MET:HB2	2.02	0.41
1:B:4644:TRP:O	1:B:4648:LEU:HG	2.20	0.41
1:C:294:THR:HG23	1:C:295:GLU:H	1.86	0.41
1:C:2175:GLU:O	1:C:2179:ILE:HG12	2.20	0.41
1:C:4024:VAL:HA	1:C:4027:LEU:HD12	2.02	0.41
1:C:4973:HIS:CE1	1:C:4976:GLU:HG2	2.55	0.41
1:D:2814:LYS:HB2	1:D:2814:LYS:HE2	1.86	0.41
1:D:4229:GLU:O	1:D:4233:LEU:HG	2.21	0.41
1:A:1116:GLY:HA3	1:A:1132:TRP:HB3	2.02	0.41
1:A:3654:LEU:HD23	1:A:3654:LEU:HA	1.94	0.41
1:A:4020:GLN:HG2	1:A:4139:ILE:HD11	2.02	0.41
1:A:4834:GLY:O	1:A:4838:VAL:HG13	2.21	0.41
1:B:321:GLU:H	1:B:321:GLU:CD	2.29	0.41
1:B:2906:VAL:HG11	1:B:2914:LYS:HG3	2.03	0.41
1:B:3824:LYS:HE2	1:B:3824:LYS:HB3	1.93	0.41
1:B:4991:PHE:O	1:B:4995:LEU:HG	2.20	0.41
1:C:2205:GLU:O	1:C:2209:GLU:HG2	2.21	0.41
1:C:4639:MET:O	1:C:4639:MET:HG2	2.21	0.41
1:D:758:ARG:HG2	1:D:762:CYS:HA	2.01	0.41
1:A:1095:VAL:HB	1:A:1199:VAL:HB	2.03	0.41
1:A:2433:LEU:HD23	1:A:2433:LEU:HA	1.90	0.41
1:A:4850:LEU:O	1:A:4854:VAL:HG12	2.19	0.41
1:C:291:LEU:HD23	1:C:299:LEU:HD11	2.01	0.41
1:C:2814:LYS:HE2	1:C:2814:LYS:HB2	1.86	0.41
1:C:4229:GLU:O	1:C:4233:LEU:HG	2.20	0.41
1:D:2175:GLU:O	1:D:2179:ILE:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2176:ASN:O	1:D:2180:GLN:HG2	2.21	0.41
1:D:2679:UNK:HA	1:D:2741:GLU:HA	2.03	0.41
1:A:139:GLU:OE1	1:A:139:GLU:N	2.51	0.41
1:A:805:PRO:HA	1:A:806:PRO:HD3	1.98	0.41
1:A:2331:TYR:HD1	1:A:2331:TYR:HA	1.78	0.41
1:A:4978:HIS:HA	1:A:4982:GLU:CD	2.46	0.41
1:B:1673:VAL:HG12	1:B:1681:VAL:HG21	2.03	0.41
1:B:3719:ASP:O	1:B:3723:MET:HG2	2.21	0.41
1:B:4698:LYS:HB3	1:B:4698:LYS:HE2	1.92	0.41
1:C:786:GLY:N	1:C:1630:CYS:O	2.54	0.41
1:C:2196:ASN:OD1	1:C:2199:ARG:NH2	2.51	0.41
1:D:299:LEU:HD12	1:D:299:LEU:HA	1.93	0.41
1:D:2382:GLU:O	1:D:2386:ILE:HG23	2.20	0.41
1:D:4039:MET:O	1:D:4043:GLN:HG3	2.21	0.41
1:A:758:ARG:HG2	1:A:762:CYS:HA	2.03	0.41
1:A:1863:LEU:HD23	1:A:1863:LEU:HA	1.88	0.41
1:A:1969:LEU:HD21	1:A:2009:LEU:HD11	2.03	0.41
1:A:4184:MET:HE1	1:A:4188:ARG:HE	1.85	0.41
1:B:684:VAL:HG12	1:B:781:VAL:HG22	2.02	0.41
1:B:1742:THR:OG1	1:B:1769:THR:OG1	2.36	0.41
1:B:1968:LYS:NZ	1:B:2030:ASP:OD2	2.54	0.41
1:B:2128:TYR:OH	1:B:3672:ARG:NH1	2.54	0.41
1:B:2176:ASN:O	1:B:2180:GLN:HG2	2.20	0.41
1:B:2187:ASN:OD1	1:B:2187:ASN:N	2.48	0.41
1:B:2679:UNK:HA	1:B:2741:GLU:HA	2.02	0.41
1:B:3971:GLY:HA2	1:B:3972:PRO:HD2	1.91	0.41
1:C:385:ASP:OD1	1:C:385:ASP:N	2.52	0.41
1:C:4743:MET:H	1:C:4743:MET:HG2	1.66	0.41
1:C:4844:LEU:HD22	1:C:4928:LEU:HG	2.03	0.41
1:C:4968:PHE:HE2	1:C:4978:HIS:CG	2.39	0.41
1:C:4982:GLU:H	1:C:4982:GLU:CD	2.28	0.41
1:D:67:PHE:HD1	1:D:67:PHE:HA	1.81	0.41
1:D:492:ASP:OD1	1:D:546:TRP:NE1	2.52	0.41
1:D:1673:VAL:HG12	1:D:1681:VAL:HG21	2.03	0.41
1:D:1717:SER:HA	1:D:1721:GLU:HB2	2.01	0.41
1:D:4077:PHE:HZ	1:D:4088:ILE:HG12	1.86	0.41
1:D:4644:TRP:O	1:D:4648:LEU:HG	2.21	0.41
1:D:4743:MET:H	1:D:4743:MET:HG2	1.57	0.41
1:A:360:ALA:HB2	1:A:377:ILE:HG22	2.03	0.41
1:A:457:GLU:HG2	1:A:464:LYS:HE2	2.03	0.41
1:A:4104:THR:HG22	1:A:4106:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4157:ASP:HB3	1:A:4160:LEU:HD12	2.03	0.41
1:A:4160:LEU:O	1:A:4164:LEU:HD23	2.20	0.41
1:A:4677:LEU:HD12	1:A:4677:LEU:HA	1.88	0.41
1:A:4865:LYS:HA	1:A:4865:LYS:HD3	1.78	0.41
1:B:590:LEU:HB2	1:B:599:VAL:HG11	2.02	0.41
1:B:4960:ILE:HD11	2:B:5101:ACP:N6	2.35	0.41
1:C:195:PHE:HB3	1:D:2361:PRO:HG3	2.02	0.41
1:C:353:SER:HB3	1:C:355:LEU:HD22	2.02	0.41
1:C:883:ALA:O	1:C:887:ILE:HG13	2.20	0.41
1:C:1969:LEU:HD11	1:C:2009:LEU:HD11	2.02	0.41
1:C:4013:LEU:HD12	1:C:4013:LEU:HA	1.93	0.41
1:D:3951:PHE:O	1:D:3955:MET:HG3	2.19	0.41
1:D:4666:VAL:HG13	1:D:4783:ILE:HD11	2.03	0.41
1:A:1131:ARG:HE	1:A:1137:GLU:HB2	1.86	0.41
1:A:2198:MET:HE2	1:A:2198:MET:HA	2.03	0.41
1:A:4041:ALA:O	1:A:4045:VAL:HG22	2.21	0.41
1:A:4150:LEU:HD12	1:A:4150:LEU:HA	1.90	0.41
1:A:4966:ASP:HA	1:A:4969:ASP:HB3	2.02	0.41
1:B:1842:LEU:HD23	1:B:1842:LEU:HA	1.91	0.40
1:B:2902:HIS:HA	1:B:2903:PRO:HD3	1.98	0.40
1:B:4555:LEU:HD11	1:B:4656:LEU:HD22	2.02	0.40
1:C:379:HIS:CD2	1:C:382:GLY:H	2.39	0.40
1:C:3699:HIS:O	1:C:3703:LEU:HG	2.21	0.40
1:A:539:LEU:H	1:A:539:LEU:HD12	1.86	0.40
1:A:544:LEU:HD21	1:A:578:ILE:HG13	2.03	0.40
1:B:294:THR:HG23	1:B:295:GLU:H	1.86	0.40
1:B:1095:VAL:HB	1:B:1199:VAL:HB	2.04	0.40
1:B:1170:MET:HA	1:B:1170:MET:HE2	2.03	0.40
1:B:4215:ARG:NH2	2:B:5101:ACP:O1B	2.55	0.40
1:B:4865:LYS:HA	1:B:4865:LYS:HD2	1.78	0.40
1:B:4983:HIS:O	2:B:5101:ACP:N6	2.54	0.40
1:C:590:LEU:HB2	1:C:599:VAL:HG11	2.04	0.40
1:C:1152:MET:HG3	1:C:1161:ILE:HB	2.02	0.40
1:C:1939:MET:HE3	1:C:1939:MET:HB3	1.83	0.40
1:C:2228:MET:HE2	1:C:2228:MET:HA	2.03	0.40
1:C:4184:MET:HE3	1:C:4184:MET:HB2	1.87	0.40
1:C:4646:LEU:HD23	1:C:4646:LEU:HA	1.91	0.40
1:D:21:VAL:HB	1:D:205:ILE:HD11	2.03	0.40
1:D:385:ASP:OD1	1:D:385:ASP:N	2.52	0.40
1:D:3775:ALA:O	1:D:3778:MET:HG3	2.22	0.40
1:D:4071:ILE:HD13	1:D:4071:ILE:HA	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4100:GLN:HB3	1:D:4102:GLN:OE1	2.21	0.40
1:D:4870:ASP:OD1	1:D:4870:ASP:N	2.53	0.40
1:A:4097:MET:HG3	1:A:4108:ILE:HG23	2.02	0.40
1:B:76:ARG:HD3	1:B:76:ARG:HA	1.95	0.40
1:B:758:ARG:HG2	1:B:762:CYS:HA	2.02	0.40
1:B:4677:LEU:HD21	1:B:4702:ASP:HB3	2.03	0.40
1:C:544:LEU:HD23	1:C:544:LEU:HA	1.96	0.40
1:D:2188:ASN:ND2	1:D:2188:ASN:O	2.41	0.40
1:D:3670:GLU:HG2	1:D:3728:ILE:HA	2.03	0.40
1:A:4984:ASN:O	1:A:4985:LEU:HB3	2.20	0.40
1:B:379:HIS:CD2	1:B:382:GLY:H	2.40	0.40
1:B:2469:ILE:HD13	1:B:2469:ILE:HA	1.86	0.40
1:C:121:LEU:HB3	1:C:123:THR:HG22	2.04	0.40
1:C:1204:LEU:HD12	1:C:1226:PHE:HB3	2.02	0.40
1:C:2182:ILE:HD13	1:C:2182:ILE:HA	2.00	0.40
1:C:3814:GLN:NE2	1:C:3818:ASP:OD2	2.55	0.40
1:C:4177:TYR:HA	1:C:4197:ILE:HB	2.04	0.40
1:D:3699:HIS:O	1:D:3703:LEU:HG	2.21	0.40
1:D:3812:VAL:O	1:D:3816:MET:HG3	2.21	0.40
1:D:4675:LYS:HB3	1:D:4675:LYS:HE3	1.83	0.40
1:A:1842:LEU:HD23	1:A:1842:LEU:HA	1.90	0.40
1:A:2656:UNK:O	1:A:2924:GLN:NE2	2.52	0.40
1:A:3917:ILE:HA	1:A:3920:VAL:HG22	2.02	0.40
1:B:150:MET:HB3	1:B:169:LEU:HD13	2.03	0.40
1:B:1231:GLN:HE22	1:B:1826:ALA:HB2	1.86	0.40
1:B:3696:ASP:OD2	1:B:3773:ARG:NH2	2.54	0.40
1:B:4850:LEU:O	1:B:4854:VAL:HG12	2.21	0.40
1:B:4966:ASP:OD1	1:B:4967:TYR:N	2.55	0.40
1:C:2323:TRP:H	1:C:2323:TRP:CD1	2.40	0.40
1:C:2332:LEU:HD11	1:C:2428:ALA:HB1	2.02	0.40
1:C:4085:ARG:HE	1:C:4085:ARG:HB2	1.72	0.40
1:C:4999:ASP:HB3	1:C:5002:GLU:HG2	2.03	0.40
1:D:121:LEU:HB3	1:D:123:THR:HG22	2.03	0.40
1:A:2030:ASP:N	1:A:2030:ASP:OD1	2.55	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	3203/5037 (64%)	3060 (96%)	140 (4%)	3 (0%)	48	75
1	B	3203/5037 (64%)	3055 (95%)	143 (4%)	5 (0%)	43	71
1	C	3203/5037 (64%)	3056 (95%)	145 (4%)	2 (0%)	48	75
1	D	3203/5037 (64%)	3059 (96%)	141 (4%)	3 (0%)	48	75
All	All	12812/20148 (64%)	12230 (96%)	569 (4%)	13 (0%)	49	75

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	3915	ILE
1	D	3915	ILE
1	B	3788	GLY
1	B	4198	SER
1	C	3788	GLY
1	D	4198	SER
1	A	4967	TYR
1	B	4956	THR
1	C	4198	SER
1	D	3788	GLY
1	A	3788	GLY
1	A	4198	SER
1	B	4972	PRO

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	2513/3264 (77%)	2495 (99%)	18 (1%)	76	80
1	B	2513/3264 (77%)	2483 (99%)	30 (1%)	63	75
1	C	2513/3264 (77%)	2500 (100%)	13 (0%)	81	83
1	D	2513/3264 (77%)	2489 (99%)	24 (1%)	68	76
All	All	10052/13056 (77%)	9967 (99%)	85 (1%)	70	79

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	218	HIS
1	B	262	LEU
1	B	280	LEU
1	B	301	VAL
1	B	484	LEU
1	B	597	HIS
1	B	1202	LEU
1	B	1651	LEU
1	B	1713	ASP
1	B	1863	LEU
1	B	2006	ILE
1	B	2203	MET
1	B	4022	ASP
1	B	4099	SER
1	B	4101	LYS
1	B	4224	GLU
1	B	4832	HIS
1	B	4957	LYS
1	B	4960	ILE
1	B	4969	ASP
1	B	4973	HIS
1	B	4975	PHE
1	B	4976	GLU
1	B	4980	LEU
1	B	4981	GLU
1	B	4982	GLU
1	B	4984	ASN
1	B	4985	LEU
1	B	4987	ASN
1	B	5028	PHE
1	C	218	HIS
1	C	293	LEU
1	C	306	LYS

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Mol	Chain	Res	Type
1	C	348	VAL
1	C	675	LEU
1	C	2331	TYR
1	C	4100	GLN
1	C	4101	LYS
1	C	4584	ASP
1	C	4727	LYS
1	C	4976	GLU
1	C	4977	THR
1	C	4980	LEU
1	D	218	HIS
1	D	932	LEU
1	D	1127	HIS
1	D	1152	MET
1	D	1234	VAL
1	D	2186	MET
1	D	2188	ASN
1	D	2346	VAL
1	D	2356	LEU
1	D	2747	ILE
1	D	2874	MET
1	D	4098	ASP
1	D	4099	SER
1	D	4725	LEU
1	D	4726	ASP
1	D	4727	LYS
1	D	4731	ILE
1	D	4832	HIS
1	D	4879	MET
1	D	4977	THR
1	D	4979	THR
1	D	4980	LEU
1	D	4981	GLU
1	D	4982	GLU
1	A	418	LEU
1	A	597	HIS
1	A	1248	VAL
1	A	3675	ASP
1	A	3826	VAL
1	A	4097	MET
1	A	4098	ASP
1	A	4100	GLN

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Mol	Chain	Res	Type
1	A	4101	LYS
1	A	4153	HIS
1	A	4564	PHE
1	A	4832	HIS
1	A	4965	SER
1	A	4967	TYR
1	A	4976	GLU
1	A	4979	THR
1	A	4980	LEU
1	A	4985	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	113	HIS
1	B	201	ASN
1	B	203	ASN
1	B	308	HIS
1	B	379	HIS
1	B	380	GLN
1	B	383	HIS
1	B	475	GLN
1	B	502	HIS
1	B	617	ASN
1	B	1198	GLN
1	B	1206	GLN
1	B	1231	GLN
1	B	1611	HIS
1	B	1775	HIS
1	B	1938	GLN
1	B	2007	ASN
1	B	2011	HIS
1	B	2734	ASN
1	B	2744	ASN
1	B	2756	ASN
1	B	2872	GLN
1	B	3814	GLN
1	B	3900	GLN
1	B	3960	GLN
1	B	3976	ASN
1	B	4020	GLN
1	B	4100	GLN

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Mol	Chain	Res	Type
1	B	4700	GLN
1	B	4812	HIS
1	B	4864	ASN
1	B	4933	GLN
1	B	4983	HIS
1	B	4997	ASN
1	B	5035	GLN
1	C	201	ASN
1	C	203	ASN
1	C	349	GLN
1	C	380	GLN
1	C	383	HIS
1	C	475	GLN
1	C	1206	GLN
1	C	1775	HIS
1	C	1938	GLN
1	C	2005	GLN
1	C	2011	HIS
1	C	2253	HIS
1	C	2260	ASN
1	C	2734	ASN
1	C	2744	ASN
1	C	2756	ASN
1	C	2933	ASN
1	C	4020	GLN
1	C	4700	GLN
1	C	4714	ASN
1	C	4864	ASN
1	C	4983	HIS
1	C	4997	ASN
1	C	5031	GLN
1	C	5035	GLN
1	D	201	ASN
1	D	203	ASN
1	D	273	HIS
1	D	380	GLN
1	D	383	HIS
1	D	395	GLN
1	D	502	HIS
1	D	597	HIS
1	D	879	HIS
1	D	921	ASN

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Mol	Chain	Res	Type
1	D	1206	GLN
1	D	1775	HIS
1	D	1938	GLN
1	D	2005	GLN
1	D	2011	HIS
1	D	2095	GLN
1	D	2127	GLN
1	D	2260	ASN
1	D	2744	ASN
1	D	2756	ASN
1	D	3833	GLN
1	D	3896	ASN
1	D	3960	GLN
1	D	3963	ASN
1	D	3976	ASN
1	D	4020	GLN
1	D	4043	GLN
1	D	4100	GLN
1	D	4700	GLN
1	D	4714	ASN
1	D	4812	HIS
1	D	4864	ASN
1	D	4947	GLN
1	D	4984	ASN
1	D	4997	ASN
1	D	5006	GLN
1	D	5035	GLN
1	A	201	ASN
1	A	203	ASN
1	A	218	HIS
1	A	495	ASN
1	A	1206	GLN
1	A	1938	GLN
1	A	1949	GLN
1	A	1953	HIS
1	A	2005	GLN
1	A	2011	HIS
1	A	2107	GLN
1	A	2194	HIS
1	A	2260	ASN
1	A	2734	ASN
1	A	2744	ASN

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Mol	Chain	Res	Type
1	A	2756	ASN
1	A	2881	ASN
1	A	3700	GLN
1	A	3895	HIS
1	A	3897	ASN
1	A	3970	GLN
1	A	4209	GLN
1	A	4812	HIS
1	A	4978	HIS
1	A	4983	HIS
1	A	4984	ASN
1	A	4997	ASN
1	A	5006	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 16 ligands modelled in this entry, 12 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACP	C	5101	-	31,33,33	3.18	12 (38%)	47,52,52	1.96	11 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACP	A	5101	-	31,33,33	3.18	12 (38%)	47,52,52	1.96	11 (23%)
2	ACP	D	5101	-	31,33,33	3.18	12 (38%)	47,52,52	1.96	11 (23%)
2	ACP	B	5101	-	31,33,33	3.18	11 (35%)	47,52,52	1.96	11 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACP	C	5101	-	-	6/19/38/38	0/3/3/3
2	ACP	A	5101	-	-	6/19/38/38	0/3/3/3
2	ACP	D	5101	-	-	6/19/38/38	0/3/3/3
2	ACP	B	5101	-	-	6/19/38/38	0/3/3/3

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	5101	ACP	O4'-C1'	8.67	1.62	1.42
2	D	5101	ACP	O4'-C1'	8.66	1.62	1.42
2	C	5101	ACP	O4'-C1'	8.66	1.62	1.42
2	A	5101	ACP	O4'-C1'	8.66	1.62	1.42
2	D	5101	ACP	C2'-C1'	-7.22	1.30	1.53
2	A	5101	ACP	C2'-C1'	-7.19	1.30	1.53
2	C	5101	ACP	C2'-C1'	-7.19	1.30	1.53
2	B	5101	ACP	C2'-C1'	-7.16	1.31	1.53
2	B	5101	ACP	O4'-C4'	-6.30	1.31	1.45
2	A	5101	ACP	PB-O3A	6.29	1.65	1.58
2	C	5101	ACP	PB-O3A	6.28	1.65	1.58
2	C	5101	ACP	O4'-C4'	-6.26	1.31	1.45
2	D	5101	ACP	O4'-C4'	-6.25	1.31	1.45
2	B	5101	ACP	PB-O3A	6.25	1.65	1.58
2	D	5101	ACP	PB-O3A	6.25	1.65	1.58
2	A	5101	ACP	O4'-C4'	-6.23	1.31	1.45
2	A	5101	ACP	PA-O3A	5.40	1.65	1.59
2	D	5101	ACP	PA-O3A	5.38	1.65	1.59
2	C	5101	ACP	PA-O3A	5.35	1.65	1.59
2	B	5101	ACP	PA-O3A	5.32	1.65	1.59
2	C	5101	ACP	C6-N6	4.48	1.45	1.34
2	B	5101	ACP	C6-N6	4.46	1.45	1.34
2	D	5101	ACP	C6-N6	4.45	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5101	ACP	C6-N6	4.45	1.45	1.34
2	C	5101	ACP	O2'-C2'	2.82	1.49	1.43
2	D	5101	ACP	C5-C4	-2.82	1.34	1.39
2	B	5101	ACP	O2'-C2'	2.82	1.49	1.43
2	D	5101	ACP	O2'-C2'	2.82	1.49	1.43
2	C	5101	ACP	C5-C4	-2.81	1.34	1.39
2	A	5101	ACP	O2'-C2'	2.81	1.49	1.43
2	B	5101	ACP	C5-C4	-2.79	1.34	1.39
2	A	5101	ACP	O3'-C3'	-2.77	1.36	1.43
2	B	5101	ACP	O3'-C3'	-2.76	1.36	1.43
2	A	5101	ACP	C5-C4	-2.75	1.34	1.39
2	D	5101	ACP	O3'-C3'	-2.74	1.36	1.43
2	C	5101	ACP	O3'-C3'	-2.71	1.36	1.43
2	B	5101	ACP	C5-N7	-2.57	1.34	1.39
2	D	5101	ACP	C5-N7	-2.56	1.34	1.39
2	C	5101	ACP	C5-N7	-2.55	1.34	1.39
2	A	5101	ACP	C5-N7	-2.55	1.34	1.39
2	B	5101	ACP	PB-O2B	-2.08	1.51	1.56
2	A	5101	ACP	C8-N9	-2.05	1.34	1.37
2	C	5101	ACP	C8-N9	-2.05	1.34	1.37
2	C	5101	ACP	PB-O2B	-2.03	1.51	1.56
2	D	5101	ACP	C8-N9	-2.03	1.34	1.37
2	D	5101	ACP	PB-O2B	-2.02	1.51	1.56
2	A	5101	ACP	PB-O2B	-2.02	1.51	1.56

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	5101	ACP	N3-C2-N1	-5.74	119.89	128.58
2	A	5101	ACP	N3-C2-N1	-5.73	119.90	128.58
2	C	5101	ACP	N3-C2-N1	-5.73	119.91	128.58
2	B	5101	ACP	N3-C2-N1	-5.71	119.94	128.58
2	C	5101	ACP	C5-C4-N3	-4.92	119.94	126.72
2	A	5101	ACP	C5-C4-N3	-4.92	119.94	126.72
2	D	5101	ACP	C5-C4-N3	-4.91	119.95	126.72
2	B	5101	ACP	C5-C4-N3	-4.88	120.00	126.72
2	D	5101	ACP	N6-C6-N1	-4.21	109.00	118.38
2	C	5101	ACP	N6-C6-N1	-4.20	109.01	118.38
2	B	5101	ACP	N6-C6-N1	-4.20	109.03	118.38
2	B	5101	ACP	N9-C8-N7	-4.19	107.99	113.94
2	A	5101	ACP	N9-C8-N7	-4.17	108.03	113.94
2	A	5101	ACP	N6-C6-N1	-4.16	109.11	118.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	5101	ACP	N9-C8-N7	-4.16	108.03	113.94
2	C	5101	ACP	N9-C8-N7	-4.15	108.05	113.94
2	A	5101	ACP	C2-N3-C4	3.42	120.18	111.83
2	C	5101	ACP	C2-N3-C4	3.42	120.18	111.83
2	D	5101	ACP	C2-N3-C4	3.40	120.14	111.83
2	B	5101	ACP	C2-N3-C4	3.39	120.10	111.83
2	C	5101	ACP	C5-C6-N6	3.12	131.00	123.29
2	D	5101	ACP	C5-C6-N6	3.11	130.98	123.29
2	B	5101	ACP	C5-C6-N6	3.09	130.93	123.29
2	A	5101	ACP	C5-C6-N6	3.08	130.91	123.29
2	A	5101	ACP	N3-C4-N9	2.97	132.22	127.17
2	B	5101	ACP	C5-N7-C8	2.95	108.09	103.45
2	C	5101	ACP	N3-C4-N9	2.95	132.18	127.17
2	D	5101	ACP	C5-N7-C8	2.91	108.03	103.45
2	D	5101	ACP	N3-C4-N9	2.91	132.12	127.17
2	A	5101	ACP	C5-N7-C8	2.89	108.00	103.45
2	B	5101	ACP	N3-C4-N9	2.89	132.08	127.17
2	C	5101	ACP	C5-N7-C8	2.88	107.98	103.45
2	D	5101	ACP	PB-O3A-PA	-2.69	123.58	132.37
2	A	5101	ACP	PB-O3A-PA	-2.68	123.63	132.37
2	B	5101	ACP	PB-O3A-PA	-2.67	123.66	132.37
2	C	5101	ACP	PB-O3A-PA	-2.66	123.68	132.37
2	B	5101	ACP	C4-C5-N7	-2.29	107.97	110.58
2	D	5101	ACP	C4-C5-N7	-2.27	107.99	110.58
2	A	5101	ACP	C4-N9-C8	2.26	108.11	105.74
2	A	5101	ACP	C4-C5-N7	-2.23	108.03	110.58
2	C	5101	ACP	C4-C5-N7	-2.22	108.04	110.58
2	C	5101	ACP	C4-N9-C8	2.20	108.05	105.74
2	B	5101	ACP	C4-N9-C8	2.18	108.03	105.74
2	D	5101	ACP	C4-N9-C8	2.17	108.02	105.74

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	5101	ACP	C5'-O5'-PA-O2A
2	B	5101	ACP	C5'-O5'-PA-O3A
2	B	5101	ACP	C4'-C5'-O5'-PA
2	C	5101	ACP	C5'-O5'-PA-O2A
2	C	5101	ACP	C5'-O5'-PA-O3A
2	C	5101	ACP	C4'-C5'-O5'-PA
2	D	5101	ACP	C5'-O5'-PA-O2A

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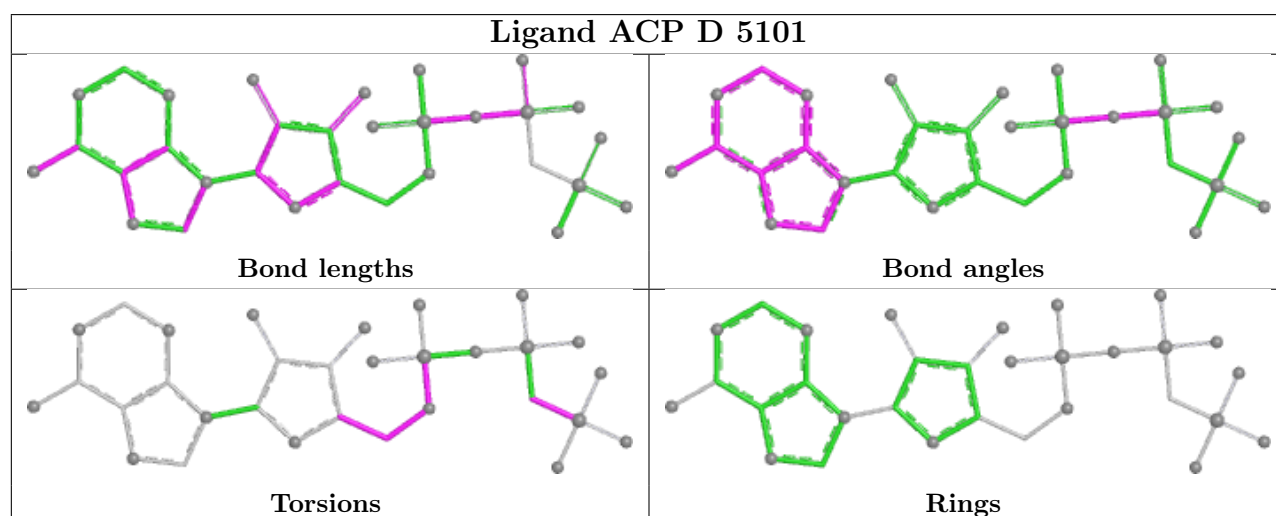
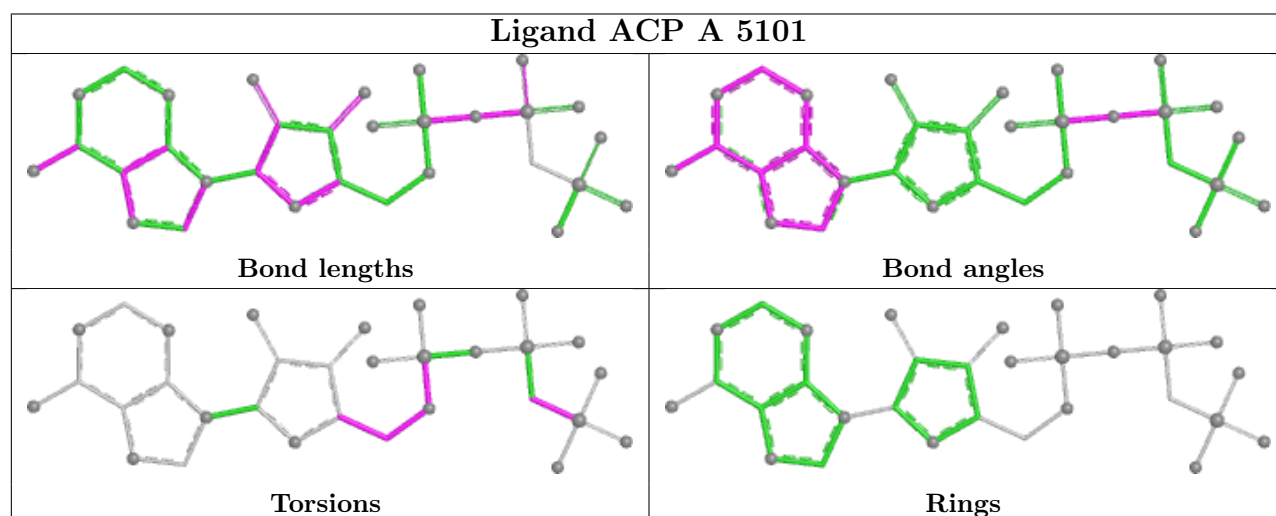
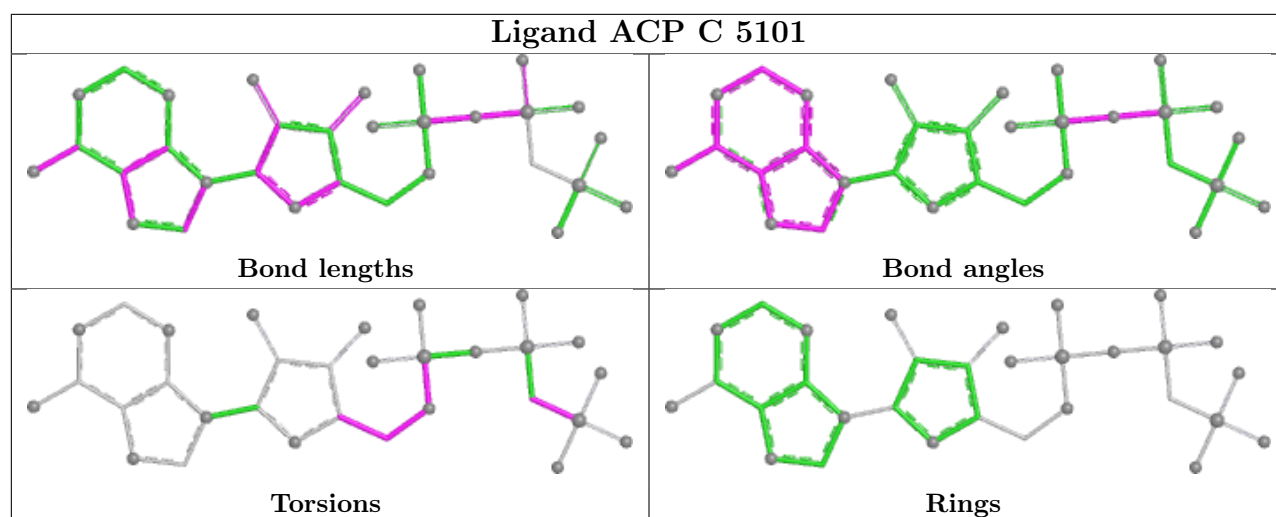
Mol	Chain	Res	Type	Atoms
2	D	5101	ACP	C5'-O5'-PA-O3A
2	D	5101	ACP	C4'-C5'-O5'-PA
2	A	5101	ACP	C5'-O5'-PA-O2A
2	A	5101	ACP	C5'-O5'-PA-O3A
2	A	5101	ACP	C4'-C5'-O5'-PA
2	D	5101	ACP	O4'-C4'-C5'-O5'
2	D	5101	ACP	C3'-C4'-C5'-O5'
2	A	5101	ACP	O4'-C4'-C5'-O5'
2	A	5101	ACP	C3'-C4'-C5'-O5'
2	B	5101	ACP	O4'-C4'-C5'-O5'
2	B	5101	ACP	C3'-C4'-C5'-O5'
2	C	5101	ACP	O4'-C4'-C5'-O5'
2	C	5101	ACP	C3'-C4'-C5'-O5'
2	B	5101	ACP	PB-C3B-PG-O1G
2	C	5101	ACP	PB-C3B-PG-O1G
2	D	5101	ACP	PB-C3B-PG-O1G
2	A	5101	ACP	PB-C3B-PG-O1G

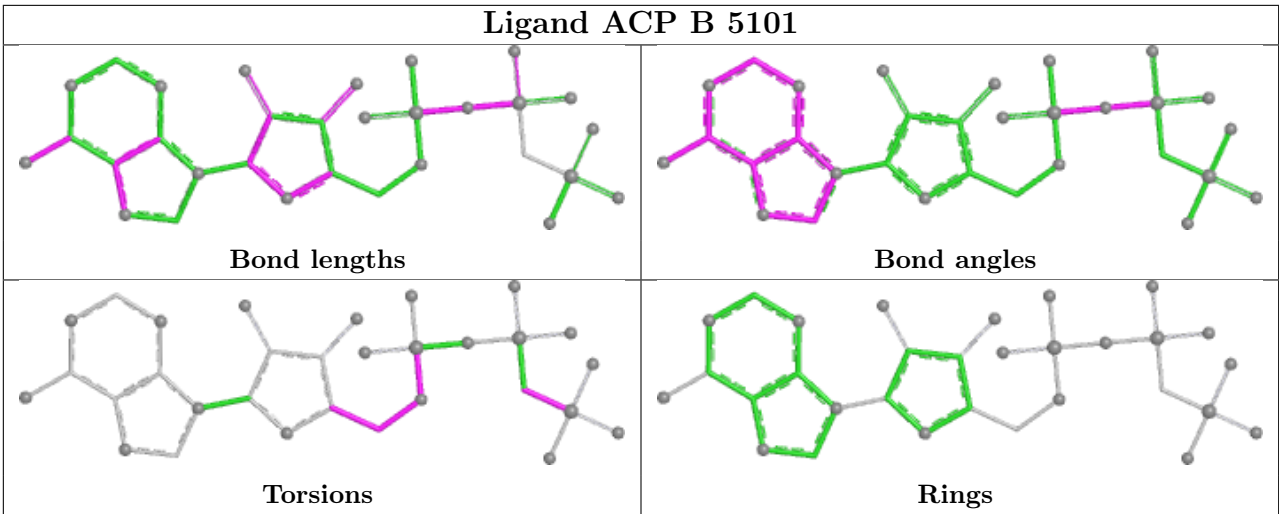
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	5101	ACP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	7
1	B	7
1	C	7
1	A	7

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	3288:UNK	C	3289:UNK	N	13.33
1	B	3288:UNK	C	3289:UNK	N	13.32
1	C	3288:UNK	C	3289:UNK	N	13.32
1	A	3288:UNK	C	3289:UNK	N	13.25
1	A	3510:UNK	C	3511:UNK	N	13.22
1	D	3510:UNK	C	3511:UNK	N	13.12
1	B	3510:UNK	C	3511:UNK	N	13.11
1	C	3510:UNK	C	3511:UNK	N	13.11
1	D	3122:UNK	C	3123:UNK	N	12.59
1	A	3122:UNK	C	3123:UNK	N	12.59
1	B	3122:UNK	C	3123:UNK	N	12.51
1	C	3122:UNK	C	3123:UNK	N	12.50
1	A	3221:UNK	C	3222:UNK	N	11.37

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3221:UNK	C	3222:UNK	N	11.35
1	C	3221:UNK	C	3222:UNK	N	11.35
1	D	3221:UNK	C	3222:UNK	N	11.34
1	B	3191:UNK	C	3192:UNK	N	11.13
1	C	3191:UNK	C	3192:UNK	N	11.13
1	D	3191:UNK	C	3192:UNK	N	11.13
1	A	3191:UNK	C	3192:UNK	N	11.10
1	B	3302:UNK	C	3303:UNK	N	10.58
1	D	3302:UNK	C	3303:UNK	N	10.58
1	C	3302:UNK	C	3303:UNK	N	10.57
1	A	3302:UNK	C	3303:UNK	N	10.43
1	B	1297:UNK	C	1298:UNK	N	7.04
1	C	1297:UNK	C	1298:UNK	N	7.04
1	D	1297:UNK	C	1298:UNK	N	7.04
1	A	1297:UNK	C	1298:UNK	N	6.91

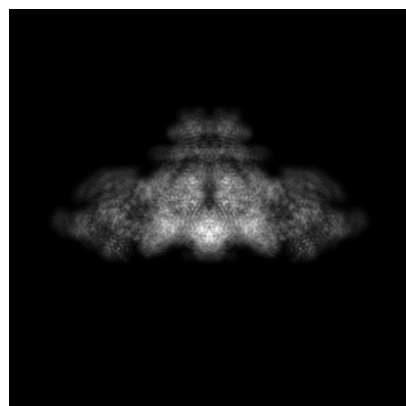
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25830. These allow visual inspection of the internal detail of the map and identification of artifacts.

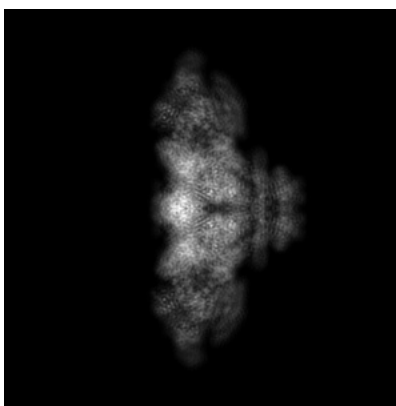
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

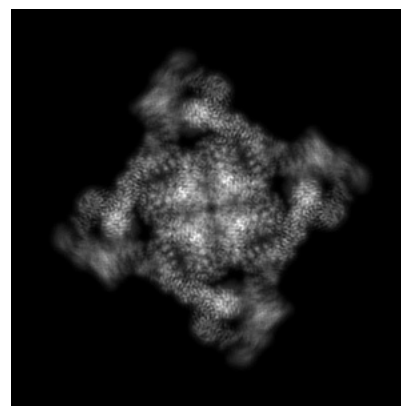
6.1.1 Primary map



X

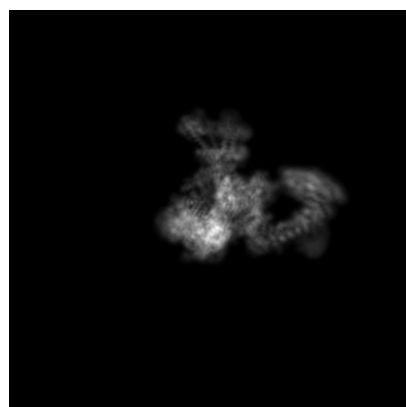


Y

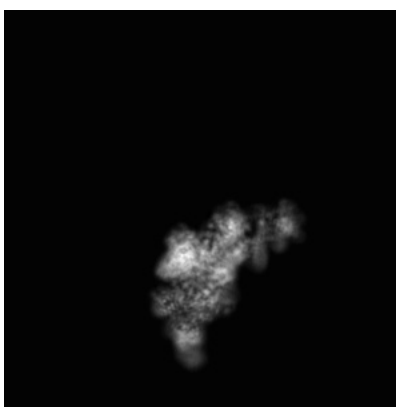


Z

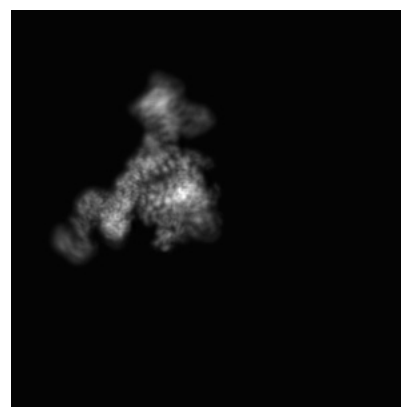
6.1.2 Raw map



X



Y



Z

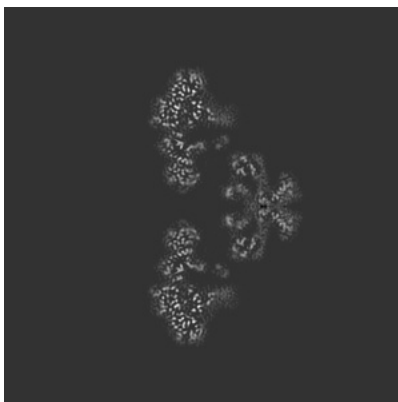
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

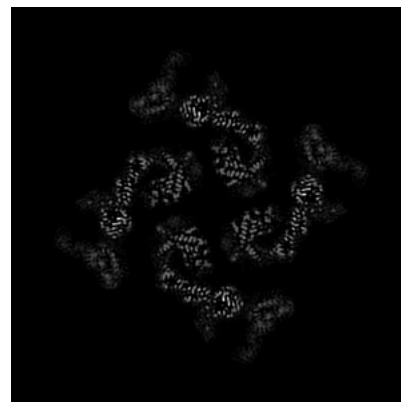
6.2.1 Primary map



X Index: 216



Y Index: 216

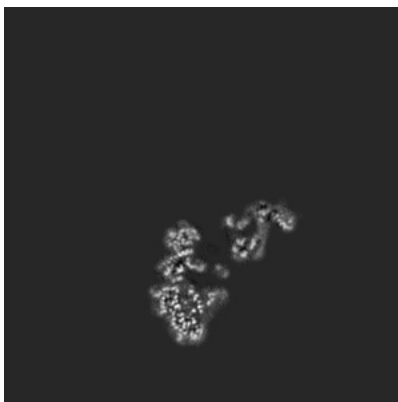


Z Index: 216

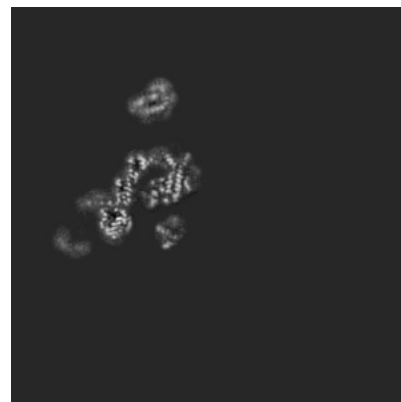
6.2.2 Raw map



X Index: 216



Y Index: 216

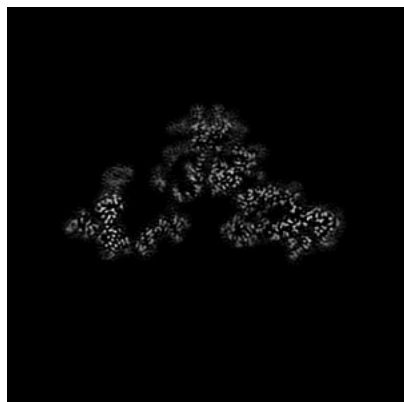


Z Index: 216

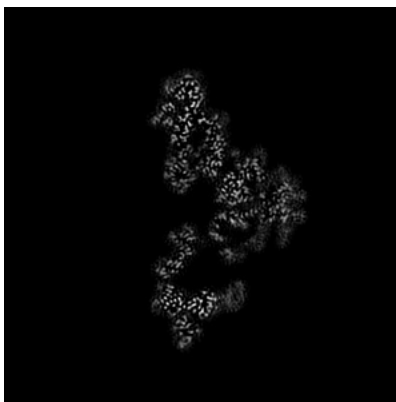
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

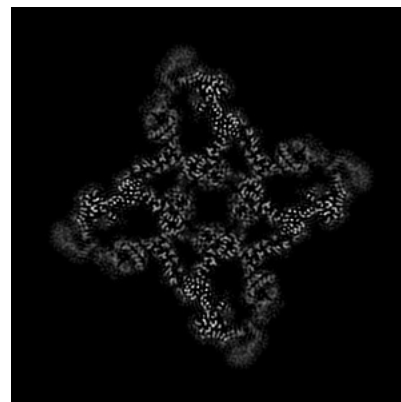
6.3.1 Primary map



X Index: 226



Y Index: 206

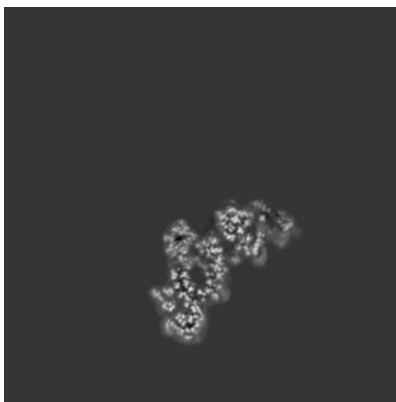


Z Index: 198

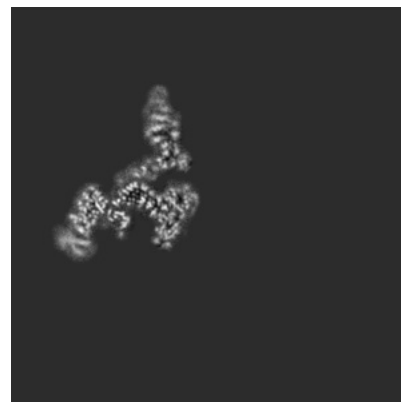
6.3.2 Raw map



X Index: 167



Y Index: 226

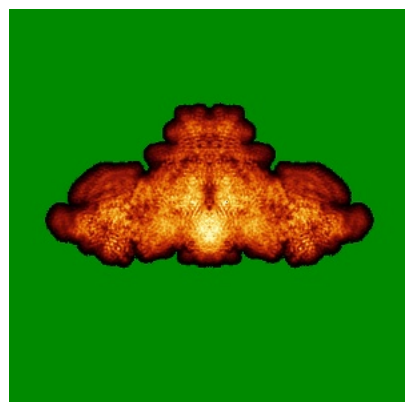


Z Index: 192

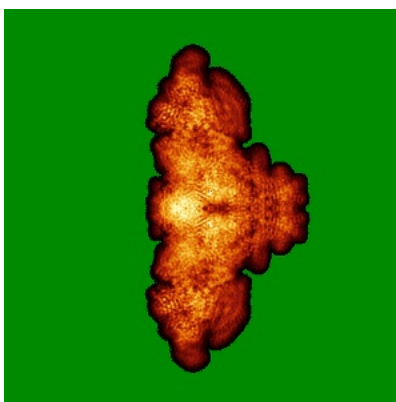
The images above show the largest variance slices of the map in three orthogonal directions.

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

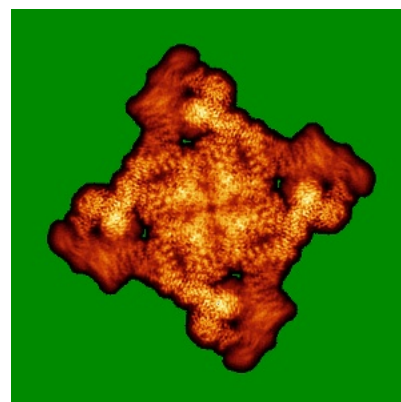
6.4.1 Primary map



X

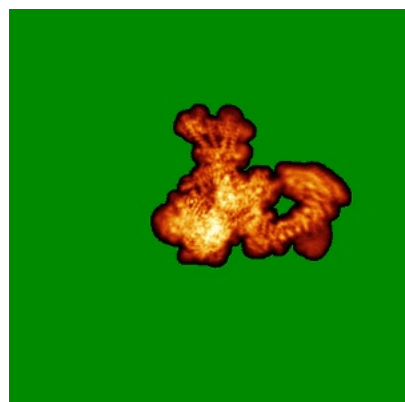


Y

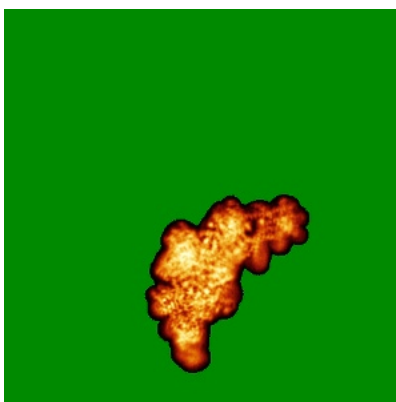


Z

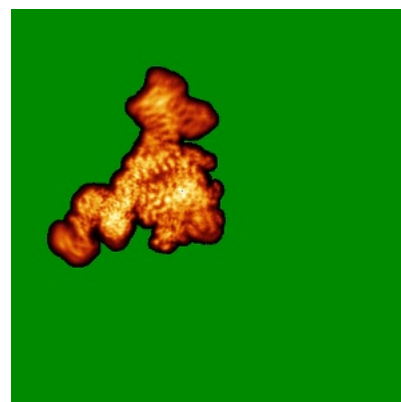
6.4.2 Raw map



X



Y

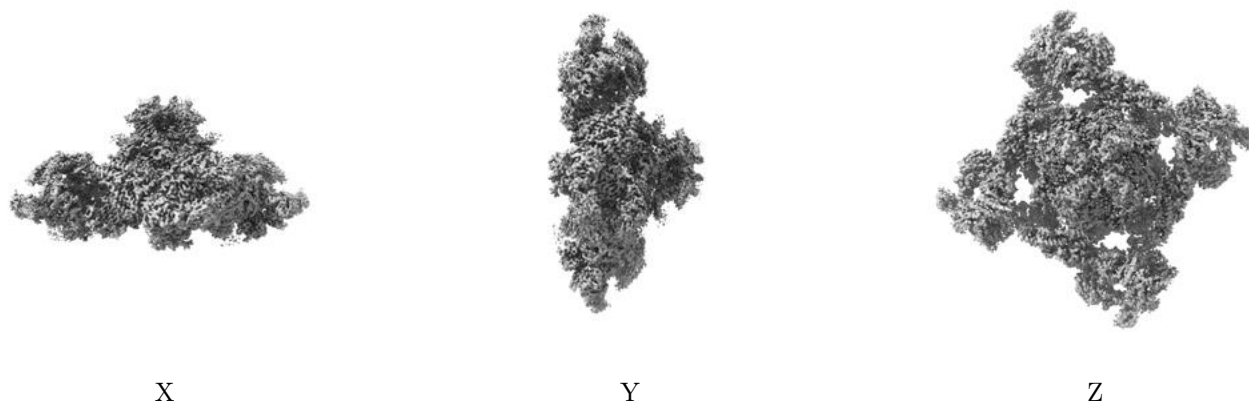


Z

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.

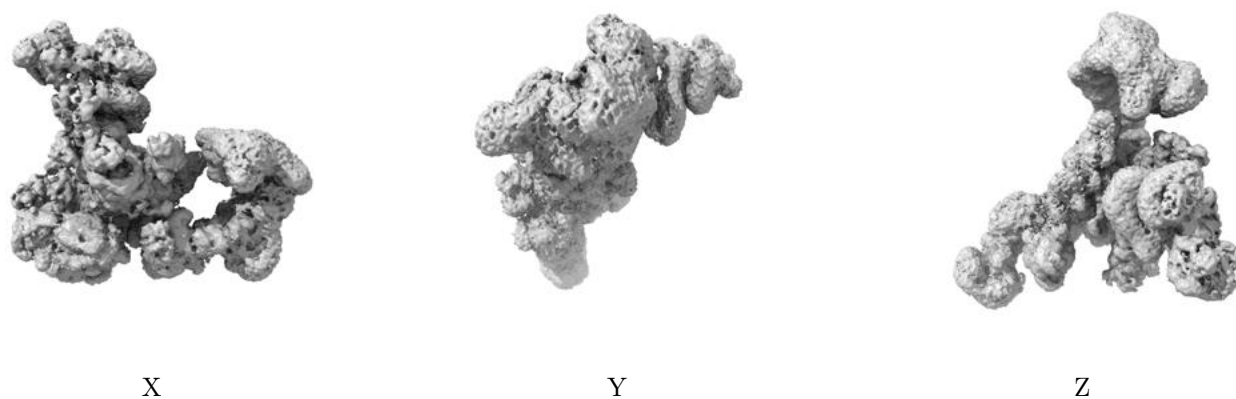
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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



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.

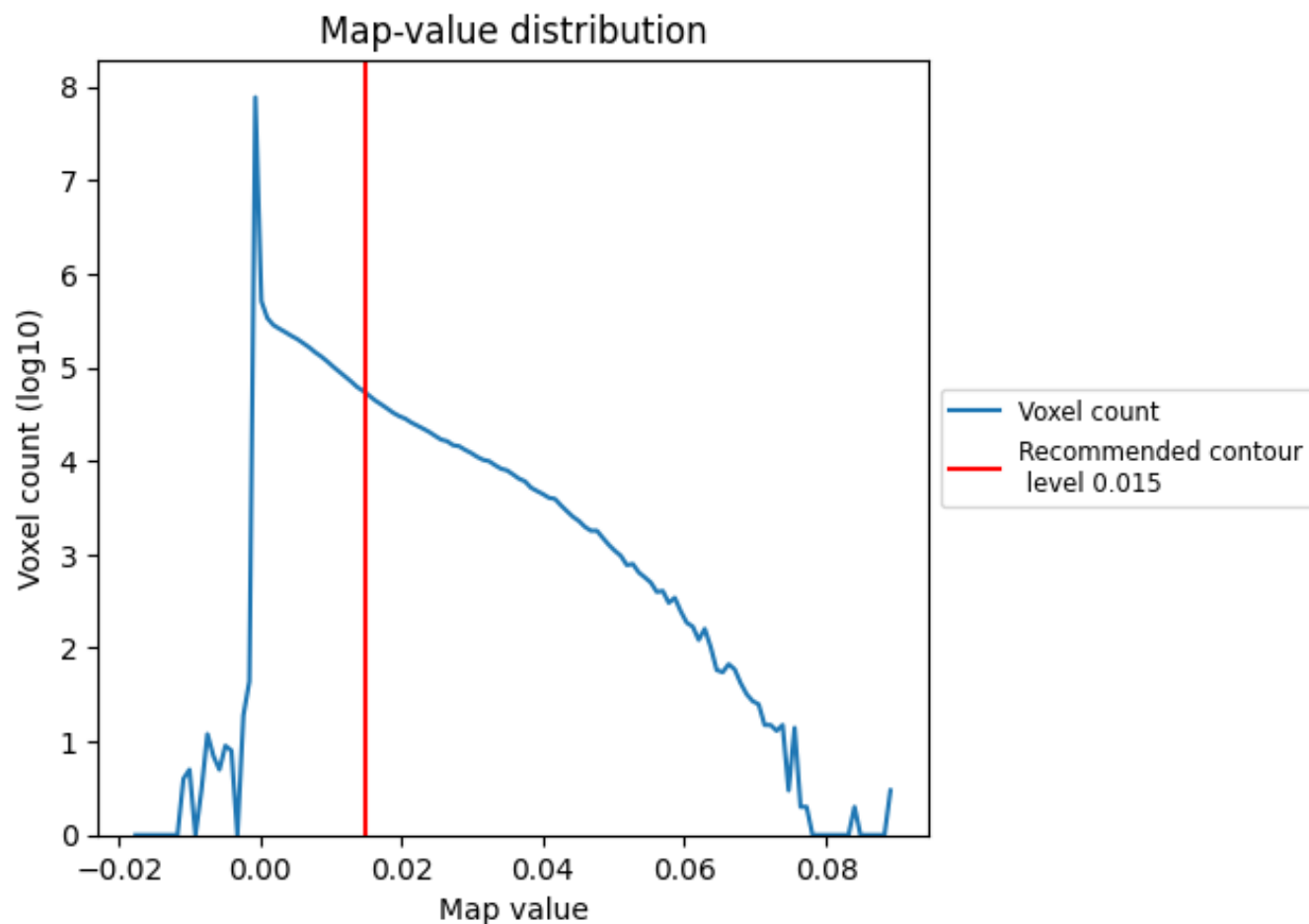
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

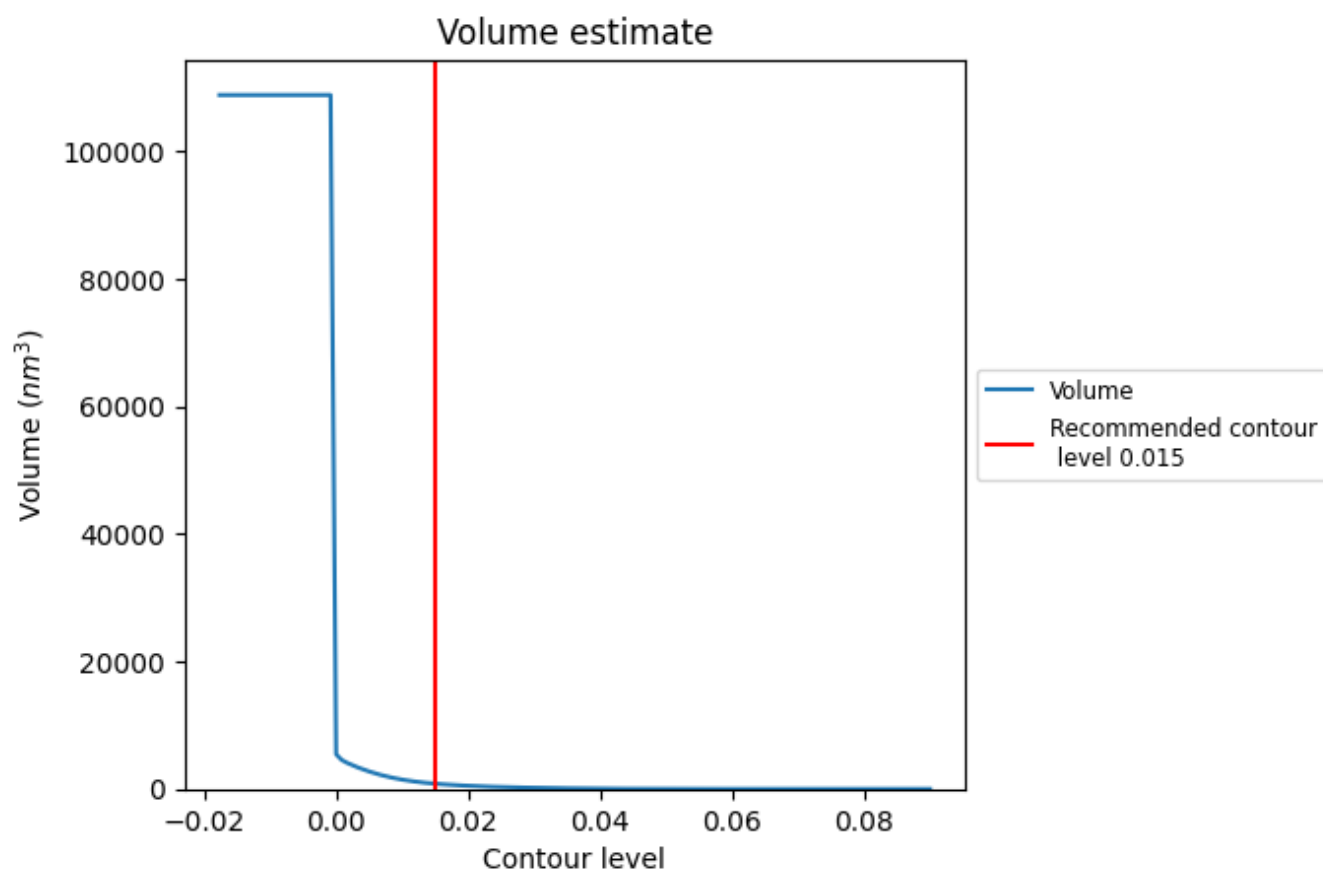
This section contains the results of statistical analysis of the map.

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.

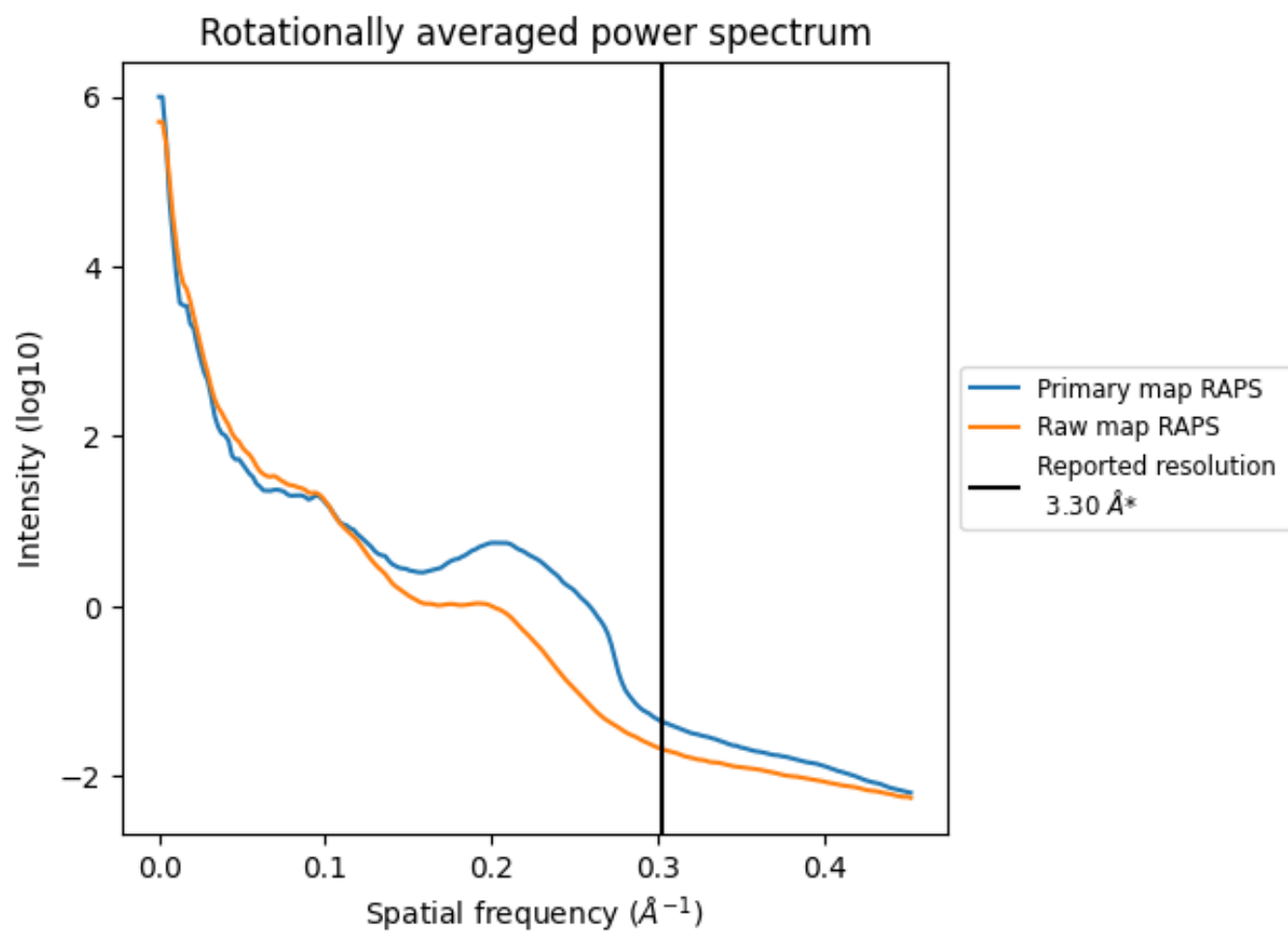
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 826 nm^3 ; this corresponds to an approximate mass of 746 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 ⓘ

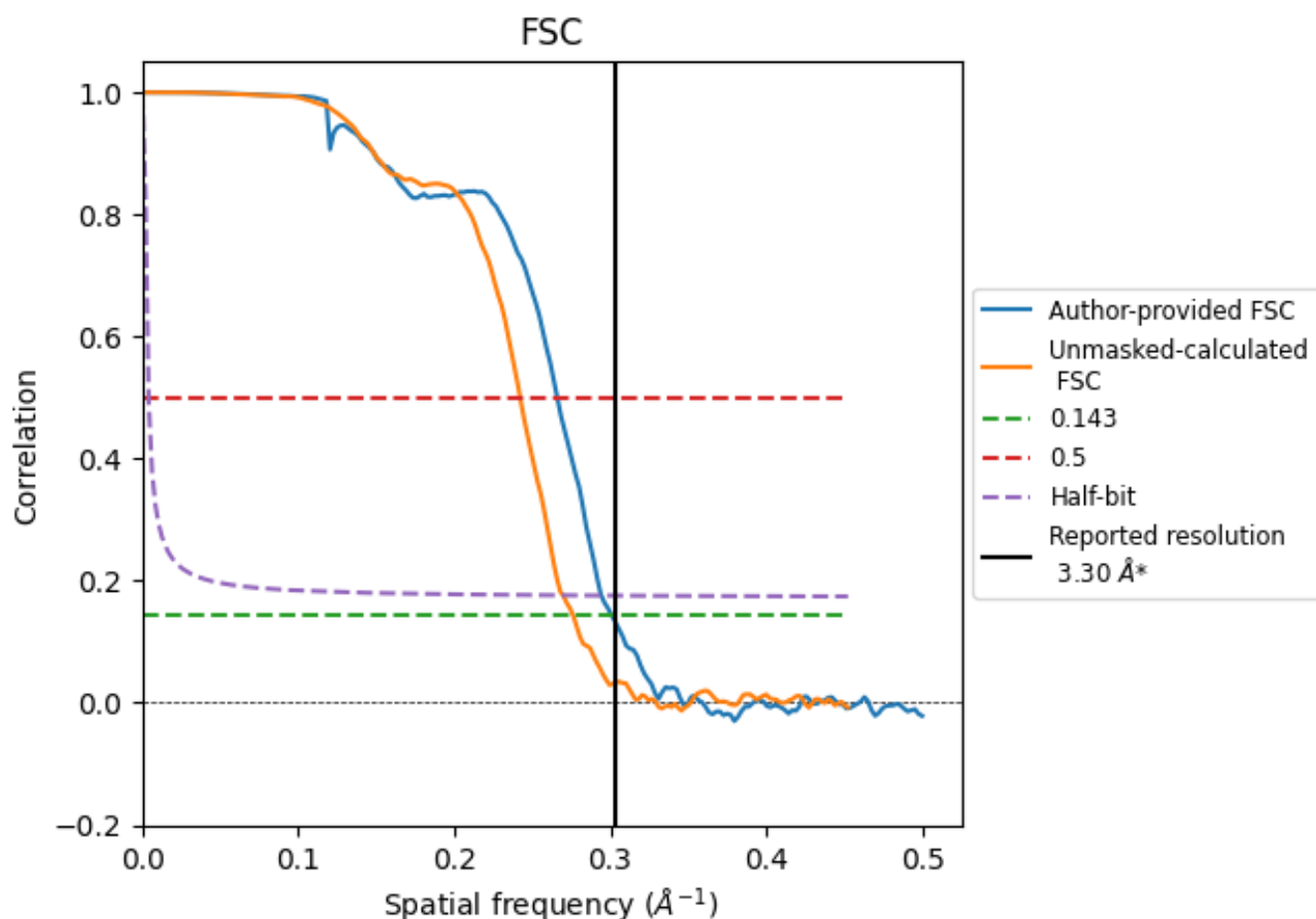


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

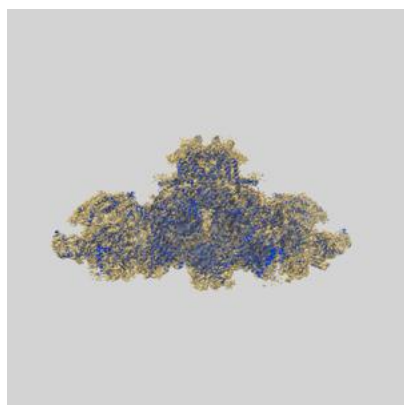
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.32	3.76	3.40
Unmasked-calculated*	3.62	4.13	3.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

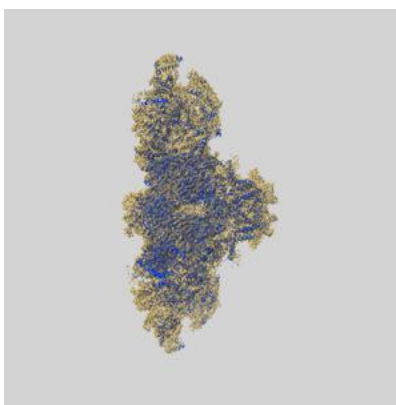
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25830 and PDB model 7TDI. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

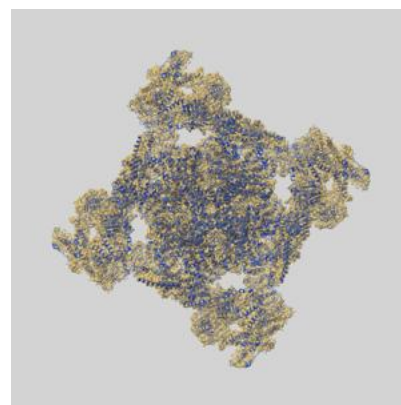
9.1 Map-model overlay [i](#)



X



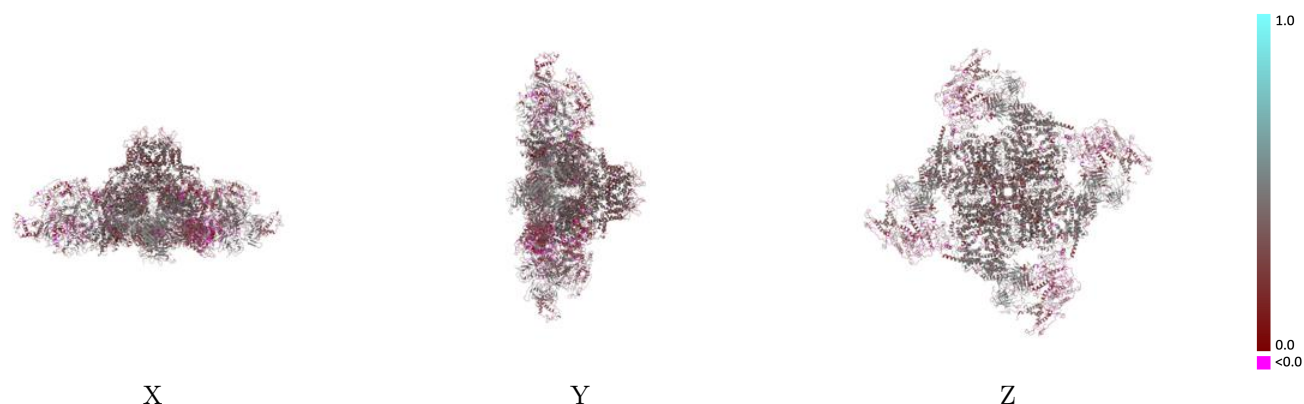
Y



Z

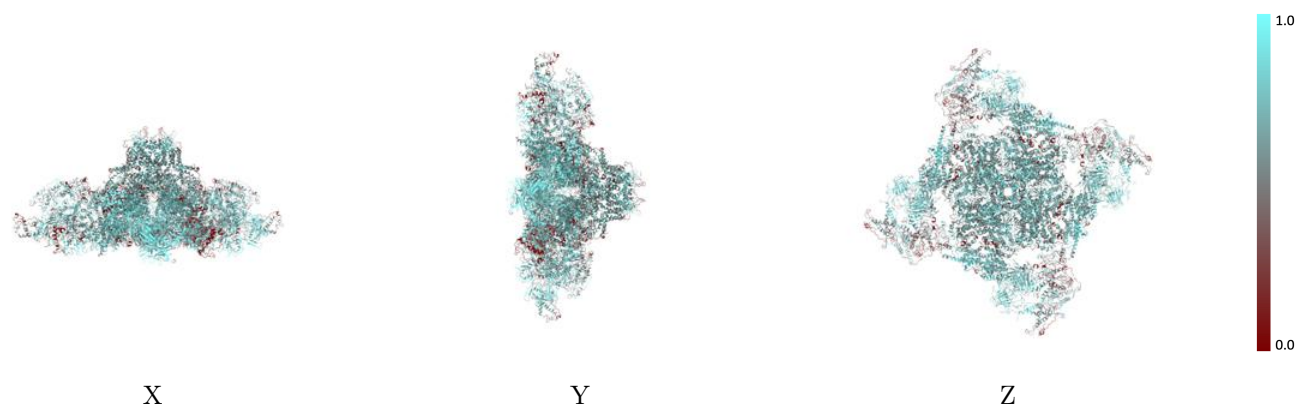
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



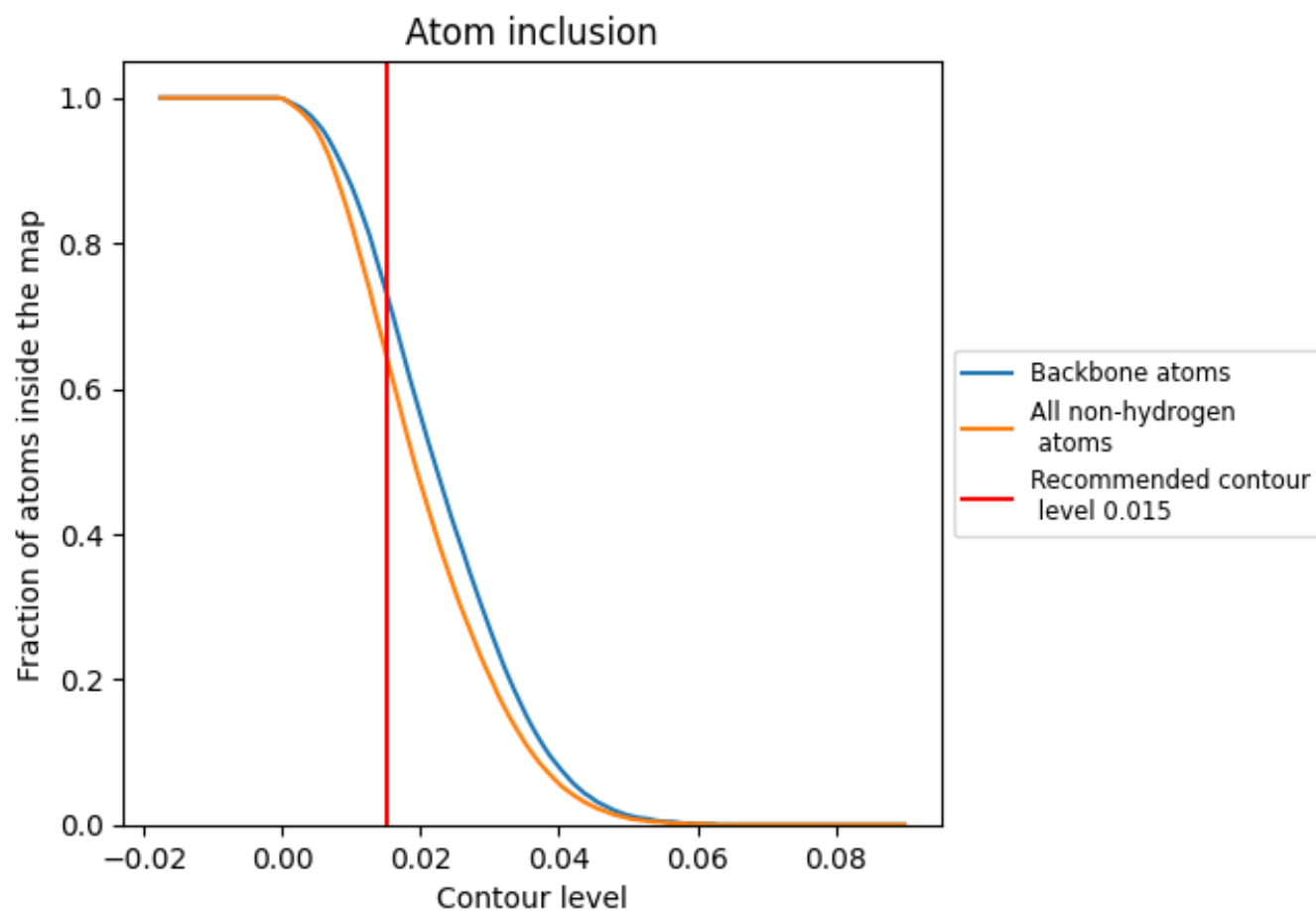
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion ⓘ



At the recommended contour level, 73% of all backbone atoms, 65% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6480	0.3320
A	0.6390	0.3250
B	0.6490	0.3350
C	0.6510	0.3350
D	0.6520	0.3350

