



Full wwPDB EM Validation Report ⓘ

Nov 15, 2022 – 01:35 AM JST

PDB ID : 6JP8
EMDB ID : EMD-9867
Title : Rabbit Cav1.1-Bay K8644 Complex
Authors : Zhao, Y.; Huang, G.; Wu, J.; Yan, N.
Deposited on : 2019-03-26
Resolution : 2.70 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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

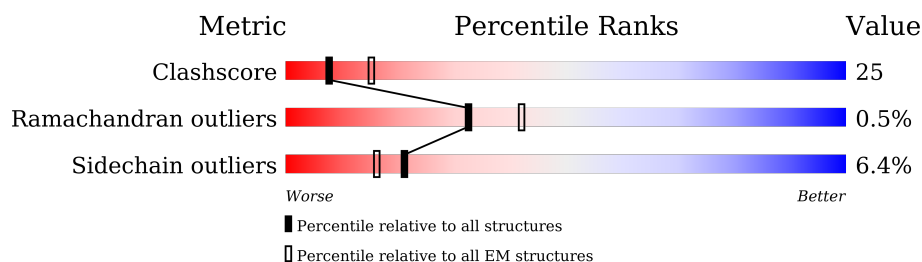
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	E	222	
2	B	450	
2	C	450	
3	A	1873	
4	F	1046	
5	D	2	
5	G	2	
5	J	2	

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Mol	Chain	Length	Quality of chain
5	K	2	<div>100%</div>
6	H	3	<div>67%</div>
6	I	3	<div>33%</div>
7	L	3	<div>100%</div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	ETA	F	1101	-	-	X	-
5	NAG	D	1	-	-	X	-
7	NAG	L	1	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 21801 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 Voltage-dependent calcium channel gamma-1 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	169	Total	C	N	O	S	0	0
			1326	872	216	220	18		

- Molecule 2 is a protein called Voltage-dependent L-type calcium channel subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	100	Total	C	N	O	S	0	0
			710	455	125	129	1		
2	C	178	Total	C	N	O	S	0	0
			1367	876	232	254	5		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	75	GLN	-	expression tag	UNP P19517
B	76	GLY	-	expression tag	UNP P19517
B	77	PRO	-	expression tag	UNP P19517
B	78	HIS	-	expression tag	UNP P19517
B	79	MET	-	expression tag	UNP P19517
C	75	GLN	-	expression tag	UNP P19517
C	76	GLY	-	expression tag	UNP P19517
C	77	PRO	-	expression tag	UNP P19517
C	78	HIS	-	expression tag	UNP P19517
C	79	MET	-	expression tag	UNP P19517

- Molecule 3 is a protein called Voltage-dependent L-type calcium channel subunit alpha-1S.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1274	Total	C	N	O	S	0	0
			10219	6728	1668	1753	70		

- Molecule 4 is a protein called Voltage-dependent calcium channel subunit alpha-2/delta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	973	Total	C	N	O	S	1	0
			7804	4942	1320	1510	32		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	SER	See sequence details	UNP P13806

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	D	2	Total	C	N	O	0	0
			28	16	2	10		
5	G	2	Total	C	N	O	0	0
			28	16	2	10		
5	J	2	Total	C	N	O	0	0
			28	16	2	10		
5	K	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



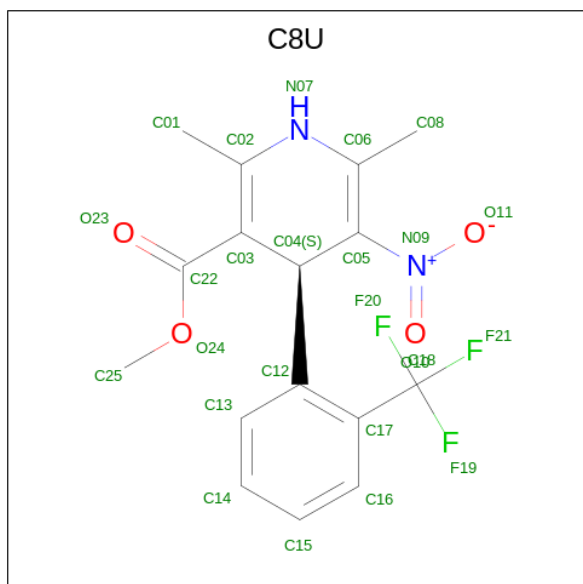
Mol	Chain	Residues	Atoms				AltConf	Trace
6	H	3	Total	C	N	O	0	0
			39	22	2	15		
6	I	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
7	L	3	Total	C	N	O	0	0
			42	24	3	15		

- Molecule 8 is methyl (4 {S})-2,6-dimethyl-5-nitro-4-[2-(trifluoromethyl)phenyl]-1,4-dihydro pyridine-3-carboxylate (three-letter code: C8U) (formula: $C_{16}H_{15}F_3N_2O_4$).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	F	N	O	0
			25	16	3	2	4	

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

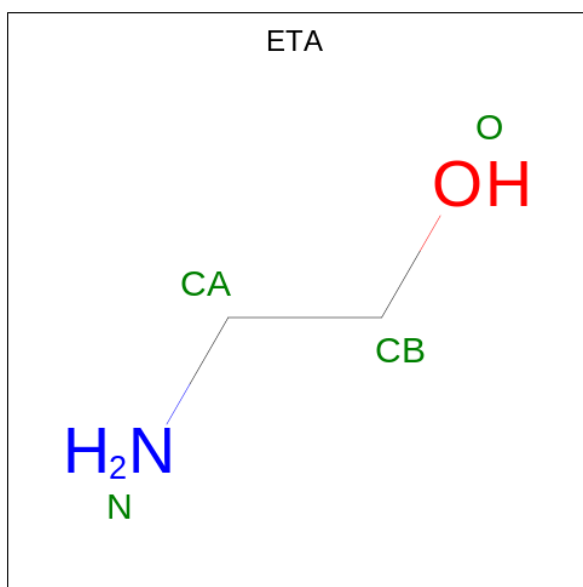


Mol	Chain	Residues	Atoms				AltConf
9	A	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			98	56	7	35	
9	F	1	Total	C	N	O	0
			98	56	7	35	
9	F	1	Total	C	N	O	0
			98	56	7	35	
9	F	1	Total	C	N	O	0
			98	56	7	35	
9	F	1	Total	C	N	O	0
			98	56	7	35	
9	F	1	Total	C	N	O	0
			98	56	7	35	

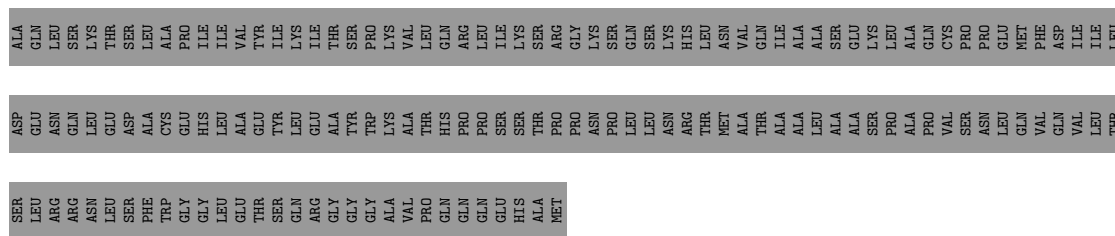
- Molecule 10 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
10	A	2	Total	Ca	0
			2	2	

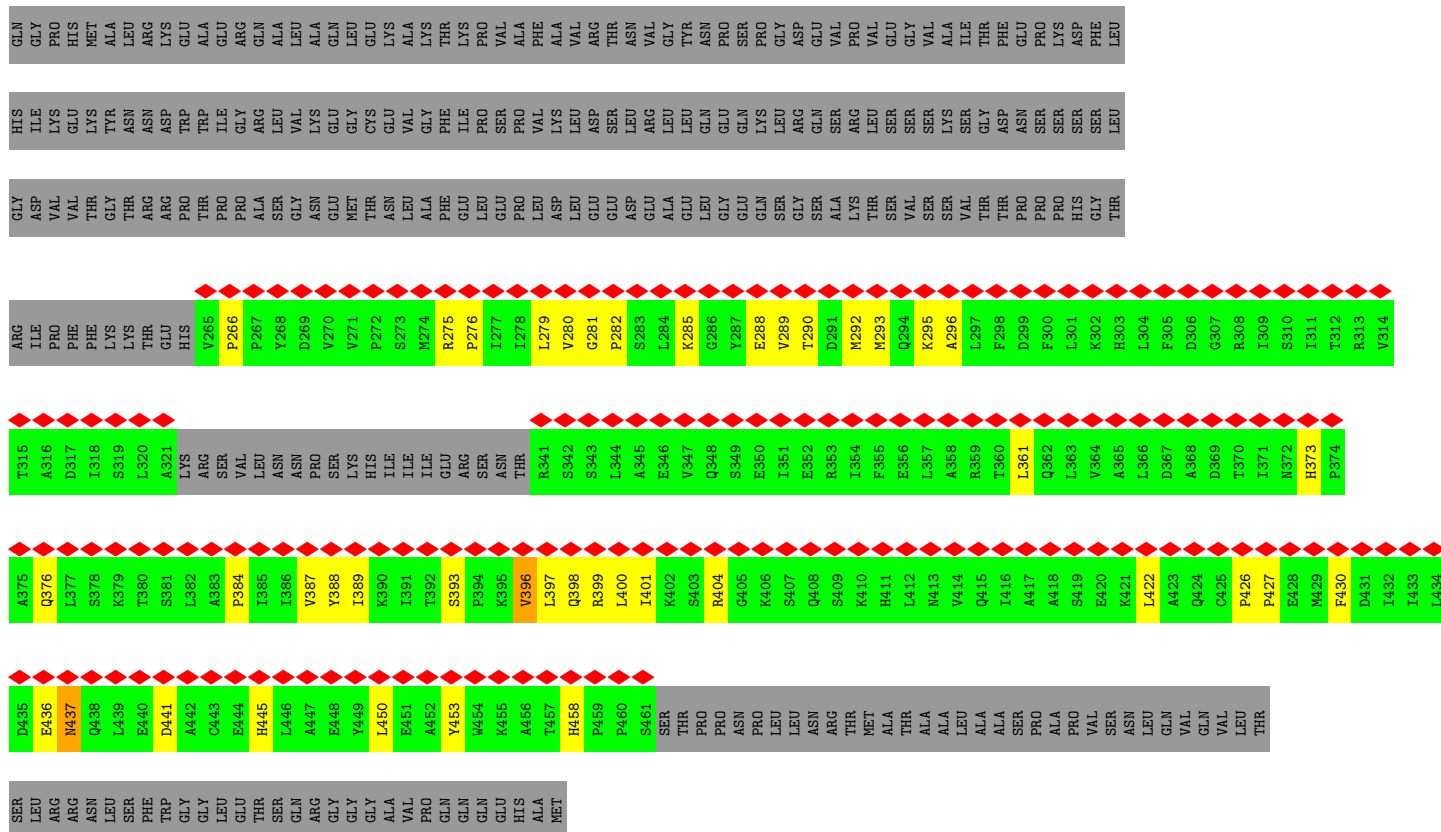
- Molecule 11 is ETHANOLAMINE (three-letter code: ETA) (formula: C₂H₇NO).



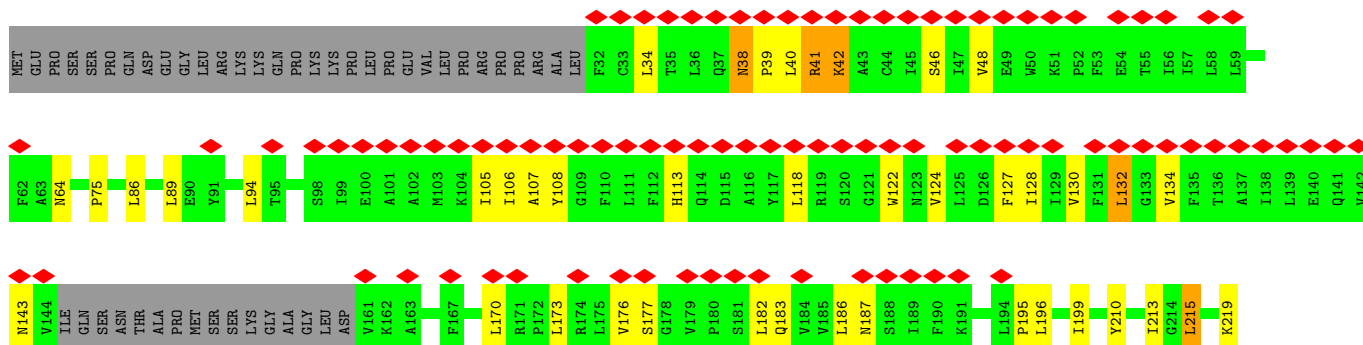
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
11	F	1	4	2	1	1	0



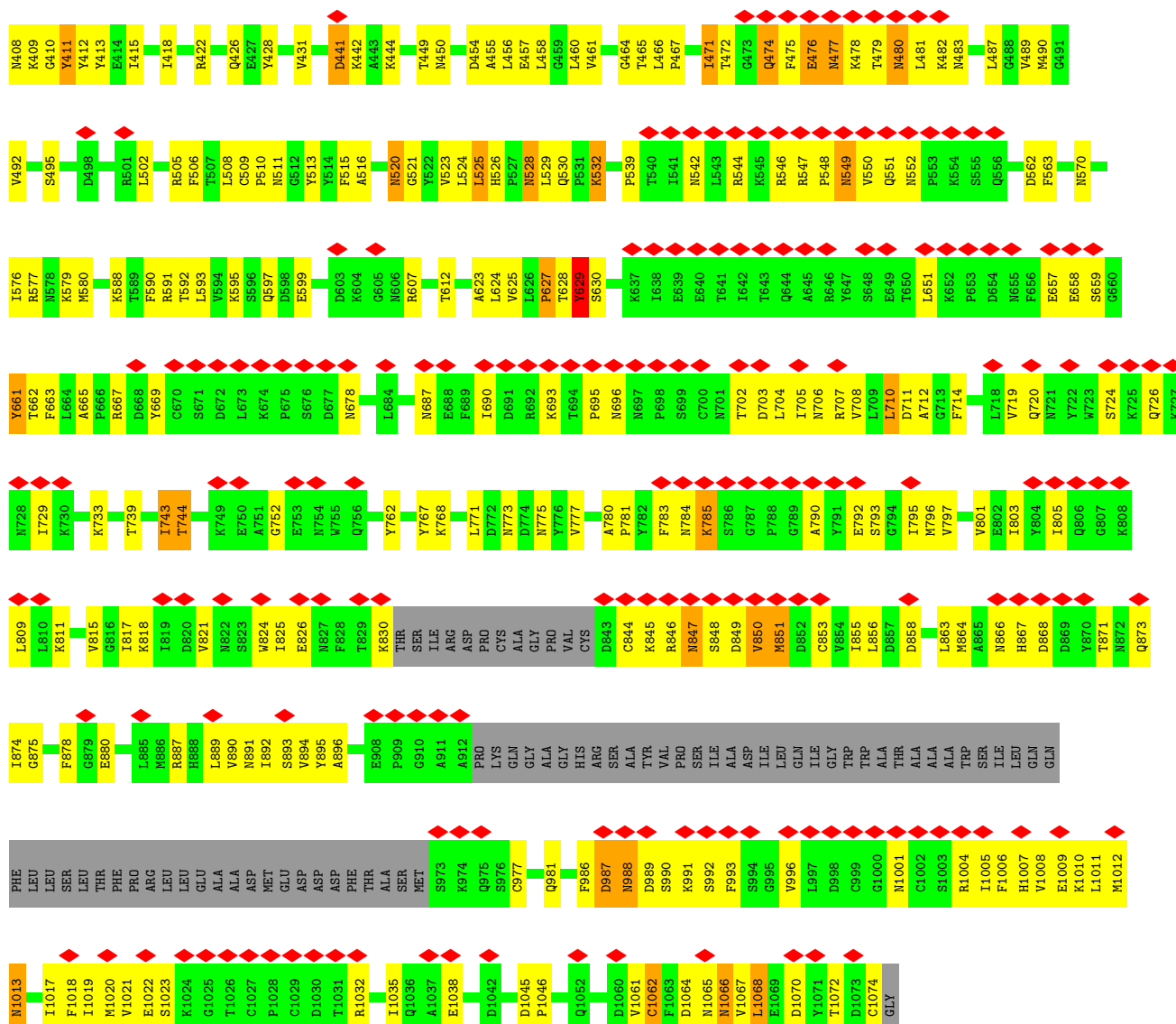
- Molecule 2: Voltage-dependent L-type calcium channel subunit beta-1



- Molecule 3: Voltage-dependent L-type calcium channel subunit alpha-1S







- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



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- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	542394	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.284	Depositor
Minimum map value	-0.187	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.044	Depositor
Map size (\AA)	349.12, 349.12, 349.12	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.091, 1.091, 1.091	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: NAG, ETA, C8U, CA, BMA

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	E	0.52	0/1358	0.71	0/1832
2	B	0.28	0/723	0.45	0/979
2	C	0.30	0/1394	0.49	0/1892
3	A	0.46	0/10463	0.71	0/14191
4	F	0.81	1/7974 (0.0%)	0.78	0/10816
All	All	0.60	1/21912 (0.0%)	0.72	0/29710

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	665	ALA	C-N	-6.95	1.21	1.34

There are no bond angle outliers.

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	E	1326	0	1345	162	0
2	B	710	0	633	7	0
2	C	1367	0	1343	78	0
3	A	10219	0	10309	420	0
4	F	7804	0	7608	546	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	28	0	25	8	0
5	G	28	0	25	1	0
5	J	28	0	25	0	0
5	K	28	0	25	7	0
6	H	39	0	34	4	0
6	I	39	0	34	1	0
7	L	42	0	37	12	0
8	A	25	0	0	1	0
9	A	14	0	13	0	0
9	F	98	0	91	15	0
10	A	2	0	0	0	0
11	F	4	0	7	4	0
All	All	21801	0	21554	1099	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 25.

All (1099) 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)
4:F:784:ASN:ND2	9:F:1120:NAG:C1	1.68	1.53
4:F:678:ASN:HD21	5:K:1:NAG:C1	1.19	1.52
3:A:226:CYS:HB3	3:A:254:CYS:SG	1.48	1.50
4:F:326:ASN:ND2	9:F:1104:NAG:C1	1.72	1.50
4:F:988:ASN:HD21	9:F:1122:NAG:C1	1.18	1.48
4:F:1001:ASN:HD21	9:F:1121:NAG:C1	1.27	1.43
4:F:1001:ASN:ND2	9:F:1121:NAG:C1	1.80	1.40
4:F:678:ASN:ND2	5:K:1:NAG:C1	1.87	1.34
1:E:212:TRP:HA	3:A:1091:TYR:CE1	1.60	1.34
4:F:988:ASN:ND2	9:F:1122:NAG:C1	1.87	1.33
1:E:149:LEU:HD13	3:A:1234:PHE:CE2	1.63	1.32
3:A:656:PHE:HB3	3:A:1058:ASN:ND2	1.45	1.30
1:E:218:ALA:HB2	3:A:1098:LEU:N	1.49	1.27
1:E:218:ALA:HB2	3:A:1098:LEU:CA	1.66	1.25
4:F:326:ASN:ND2	9:F:1104:NAG:O5	1.62	1.24
3:A:928:ILE:HG21	3:A:1060:PHE:CE1	1.73	1.23
4:F:1070:ASP:OD1	4:F:1072:THR:HG22	1.36	1.22
1:E:212:TRP:HB3	3:A:1091:TYR:CD1	1.74	1.21
3:A:331:GLY:HA2	3:A:1380:ILE:CD1	1.69	1.21
4:F:255:ASP:OD1	4:F:354:ALA:HB3	1.42	1.19
1:E:127:MET:HG3	1:E:136:LEU:CD2	1.73	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:20:ILE:HG13	1:E:118:LEU:CD2	1.73	1.18
7:L:3:NAG:H82	7:L:3:NAG:C1	1.71	1.18
3:A:39:PRO:CG	3:A:41:ARG:HH11	1.56	1.17
1:E:20:ILE:CG1	1:E:118:LEU:HD21	1.74	1.17
1:E:142:MET:SD	3:A:1187:PHE:HD2	1.66	1.17
1:E:212:TRP:CA	3:A:1091:TYR:CE1	2.27	1.16
4:F:132:ASP:OD2	4:F:137:LYS:HG2	1.45	1.16
3:A:226:CYS:CB	3:A:254:CYS:SG	2.35	1.15
2:C:296:ALA:HB2	3:A:369:TRP:O	1.41	1.15
4:F:100:LEU:CD1	4:F:198:ASN:HD21	1.59	1.15
4:F:359:ILE:HG22	4:F:385:ARG:HB2	1.16	1.14
1:E:207:MET:CE	3:A:1258:TRP:HD1	1.60	1.13
1:E:218:ALA:CB	3:A:1098:LEU:H	1.61	1.13
3:A:928:ILE:CG2	3:A:1060:PHE:CE1	2.31	1.12
3:A:921:VAL:HG13	3:A:1370:PHE:CE2	1.84	1.12
4:F:47:LEU:HG	7:L:1:NAG:H81	1.27	1.12
4:F:161:VAL:HG21	4:F:221:PRO:HG2	1.19	1.12
3:A:331:GLY:CA	3:A:1380:ILE:CD1	2.28	1.12
4:F:465:THR:CG2	4:F:489:VAL:CG1	2.28	1.12
1:E:133:ARG:HB2	1:E:135:TYR:CE1	1.85	1.11
2:C:295:LYS:HE3	3:A:373:GLY:O	1.49	1.11
4:F:100:LEU:HD11	4:F:198:ASN:HD21	1.13	1.11
3:A:656:PHE:CB	3:A:1058:ASN:HD22	1.62	1.11
2:C:437:ASN:ND2	3:A:361:GLU:HB2	1.66	1.10
3:A:39:PRO:HG2	3:A:41:ARG:NH1	1.65	1.10
3:A:39:PRO:HG2	3:A:41:ARG:HH11	1.15	1.10
3:A:656:PHE:CB	3:A:1058:ASN:ND2	2.13	1.10
1:E:32:TRP:NE1	1:E:158:MET:HG3	1.68	1.09
3:A:921:VAL:HG13	3:A:1370:PHE:HE2	1.09	1.09
4:F:889:LEU:HD12	4:F:892:ILE:CD1	1.83	1.09
1:E:207:MET:HE3	3:A:1258:TRP:HD1	1.14	1.08
5:K:2:NAG:H82	5:K:2:NAG:H3	1.36	1.07
1:E:32:TRP:HE1	1:E:158:MET:HG3	0.99	1.07
3:A:1277:LEU:HD22	3:A:1371:LEU:HD22	1.31	1.07
3:A:331:GLY:HA2	3:A:1380:ILE:HD12	1.25	1.07
1:E:142:MET:SD	3:A:1187:PHE:CD2	2.48	1.06
1:E:117:PHE:CZ	3:A:1195:ILE:HD11	1.90	1.05
1:E:212:TRP:CA	3:A:1091:TYR:HE1	1.67	1.05
4:F:846:ARG:O	4:F:847:ASN:ND2	1.88	1.05
1:E:127:MET:HG3	1:E:136:LEU:HD21	1.36	1.05
4:F:1074:CYS:O	11:F:1101:ETA:N	1.88	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:208:PRO:HB3	1:E:213:GLU:HB2	1.39	1.04
2:C:282:PRO:HG2	2:C:290:THR:HG23	1.34	1.03
4:F:889:LEU:O	4:F:894:VAL:HG12	1.56	1.03
3:A:39:PRO:CG	3:A:41:ARG:NH1	2.20	1.03
3:A:331:GLY:CA	3:A:1380:ILE:HD11	1.86	1.03
4:F:100:LEU:HD11	4:F:198:ASN:ND2	1.71	1.03
3:A:294:TRP:HE1	3:A:1321:THR:HG21	1.21	1.03
2:C:280:VAL:HG12	2:C:285:LYS:HE3	1.41	1.03
3:A:39:PRO:CG	3:A:41:ARG:HE	1.70	1.03
4:F:178:SER:HB3	4:F:181:VAL:HG12	1.39	1.03
7:L:3:NAG:C1	7:L:3:NAG:C8	2.31	1.03
1:E:218:ALA:HB2	3:A:1098:LEU:HA	1.38	1.02
1:E:116:GLY:HA2	1:E:119:ILE:CD1	1.90	1.02
4:F:480:ASN:O	4:F:480:ASN:ND2	1.92	1.02
4:F:889:LEU:HG	4:F:894:VAL:HG11	1.39	1.01
2:C:281:GLY:HA2	2:C:422:LEU:HD13	1.36	1.01
3:A:39:PRO:HG2	3:A:41:ARG:CZ	1.91	1.00
3:A:199:ILE:HD11	3:A:332:VAL:HG21	1.42	1.00
2:C:396:VAL:HB	3:A:366:TYR:CE2	1.97	1.00
1:E:127:MET:CG	1:E:136:LEU:HD21	1.92	1.00
4:F:161:VAL:CG2	4:F:221:PRO:HG2	1.92	1.00
4:F:889:LEU:CD1	4:F:892:ILE:HD11	1.91	0.99
3:A:39:PRO:HG2	3:A:41:ARG:NE	1.75	0.99
4:F:993:PHE:HB2	4:F:1008:VAL:CG1	1.91	0.99
1:E:20:ILE:HG13	1:E:118:LEU:HD21	1.00	0.99
4:F:362:LEU:HD11	4:F:401:ILE:HD11	1.42	0.99
4:F:889:LEU:HD12	4:F:892:ILE:HD11	1.00	0.99
1:E:149:LEU:HD13	3:A:1234:PHE:HE2	1.21	0.98
4:F:168:VAL:CG1	4:F:216:LEU:HD21	1.94	0.97
1:E:116:GLY:HA2	1:E:119:ILE:HD12	1.41	0.97
3:A:423:TRP:CD1	3:A:423:TRP:C	2.34	0.97
3:A:1277:LEU:HD22	3:A:1371:LEU:CD2	1.94	0.97
3:A:1366:MET:HG2	8:A:1901:C8U:O11	1.64	0.96
4:F:114:ARG:NH2	6:H:1:NAG:H62	1.79	0.96
4:F:510:PRO:HG2	4:F:767:TYR:CE2	1.99	0.96
1:E:210:ASN:HB2	1:E:213:GLU:HG3	1.47	0.96
1:E:207:MET:HE3	3:A:1258:TRP:CD1	2.00	0.95
3:A:39:PRO:HD2	3:A:41:ARG:NE	1.80	0.95
4:F:336:LYS:HE3	4:F:369:GLU:OE2	1.67	0.95
4:F:465:THR:HG21	4:F:489:VAL:HG11	1.45	0.95
3:A:976:LYS:HG2	4:F:547:ARG:NH2	1.81	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:263:SER:O	4:F:266:VAL:HG22	1.66	0.95
1:E:207:MET:CE	3:A:1258:TRP:CD1	2.49	0.95
1:E:142:MET:CE	3:A:1184:VAL:HG13	1.96	0.94
1:E:218:ALA:HB2	3:A:1098:LEU:H	1.12	0.94
4:F:476:GLU:OE1	4:F:478:LYS:HB2	1.65	0.94
4:F:159:ARG:HH22	4:F:226:VAL:HG12	1.32	0.94
4:F:356:CYS:SG	4:F:1062:CYS:HB2	2.07	0.94
3:A:1277:LEU:CD2	3:A:1371:LEU:HD22	1.97	0.94
4:F:291:VAL:HG12	4:F:312:ALA:HB2	1.49	0.94
4:F:659:SER:O	4:F:719:VAL:HG11	1.67	0.94
3:A:226:CYS:CB	3:A:254:CYS:HG	1.79	0.93
1:E:133:ARG:CB	1:E:135:TYR:CE1	2.53	0.92
2:C:280:VAL:HG12	2:C:285:LYS:CE	1.99	0.92
3:A:423:TRP:C	3:A:423:TRP:HD1	1.70	0.92
3:A:1338:CYS:HG	3:A:1352:CYS:HG	1.07	0.92
4:F:993:PHE:O	4:F:1008:VAL:HG12	1.70	0.92
4:F:161:VAL:HG21	4:F:221:PRO:CG	1.99	0.92
3:A:928:ILE:CG2	3:A:1060:PHE:HE1	1.84	0.91
4:F:824:TRP:CG	4:F:864:MET:CE	2.52	0.91
3:A:289:ILE:CD1	3:A:317:LEU:HD11	2.00	0.91
4:F:388:THR:HB	4:F:401:ILE:HG13	1.50	0.91
4:F:266:VAL:O	4:F:270:THR:HG23	1.71	0.91
4:F:669:TYR:CD1	4:F:704:LEU:CD2	2.53	0.91
3:A:39:PRO:HG2	3:A:41:ARG:HE	1.27	0.90
4:F:824:TRP:CG	4:F:864:MET:HE1	2.07	0.90
4:F:846:ARG:NH1	4:F:868:ASP:HB2	1.85	0.90
1:E:105:ILE:HG21	3:A:1206:LEU:HD13	1.52	0.90
4:F:159:ARG:NH2	4:F:226:VAL:HG12	1.86	0.90
4:F:117:PHE:CG	4:F:182:LEU:HD12	2.07	0.90
4:F:993:PHE:HB2	4:F:1008:VAL:HG13	1.54	0.89
4:F:1070:ASP:CG	4:F:1072:THR:HG22	1.91	0.89
1:E:218:ALA:CB	3:A:1098:LEU:HA	2.01	0.89
3:A:976:LYS:HE3	4:F:547:ARG:HH12	1.32	0.89
4:F:892:ILE:HG13	4:F:894:VAL:HG12	1.55	0.89
2:C:396:VAL:HB	3:A:366:TYR:HE2	1.35	0.88
4:F:710:LEU:HD21	4:F:714:PHE:CZ	2.07	0.88
1:E:115:LEU:HD13	1:E:119:ILE:HD11	1.55	0.88
3:A:656:PHE:HB3	3:A:1058:ASN:HD22	0.75	0.88
4:F:350:ASN:HD21	5:D:1:NAG:C1	1.87	0.88
4:F:367:GLY:O	4:F:400:PRO:HG2	1.73	0.88
1:E:149:LEU:HD13	3:A:1234:PHE:CZ	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:276:THR:O	4:F:280:GLU:HG2	1.74	0.87
4:F:510:PRO:HG2	4:F:767:TYR:CD2	2.08	0.87
3:A:39:PRO:CG	3:A:41:ARG:NE	2.32	0.87
1:E:4:THR:CG2	1:E:134:ASP:OD2	2.23	0.87
1:E:138:ARG:HH12	3:A:1179:GLY:HA2	1.38	0.87
3:A:38:ASN:ND2	3:A:39:PRO:HD3	1.89	0.87
3:A:440:LEU:O	3:A:444:LEU:HG	1.74	0.87
3:A:924:ALA:O	3:A:928:ILE:HG13	1.75	0.86
1:E:212:TRP:CB	3:A:1091:TYR:CD1	2.58	0.86
1:E:132:LYS:HD3	1:E:132:LYS:N	1.88	0.86
3:A:1237:LEU:O	3:A:1240:VAL:HG12	1.75	0.86
1:E:127:MET:HG3	1:E:136:LEU:HD23	1.57	0.86
4:F:361:MET:HE2	4:F:387:PHE:CD1	2.11	0.85
3:A:39:PRO:CD	3:A:41:ARG:NE	2.38	0.85
4:F:480:ASN:HA	4:F:483:ASN:HB2	1.58	0.85
4:F:591:ARG:HH22	9:F:1115:NAG:HN2	1.23	0.85
3:A:215:LEU:O	3:A:219:LYS:HB2	1.76	0.85
3:A:1367:LEU:O	3:A:1371:LEU:HD13	1.76	0.85
4:F:889:LEU:O	4:F:894:VAL:CG1	2.24	0.85
2:C:400:LEU:HD13	3:A:366:TYR:HB3	1.57	0.85
4:F:465:THR:CG2	4:F:489:VAL:HG11	2.04	0.85
3:A:215:LEU:HD22	3:A:219:LYS:HD3	1.56	0.85
1:E:127:MET:CG	1:E:136:LEU:CD2	2.53	0.84
5:D:1:NAG:H83	5:D:2:NAG:C7	2.07	0.84
2:C:293:MET:HB3	3:A:369:TRP:HE3	1.42	0.83
4:F:168:VAL:CG1	4:F:216:LEU:CD2	2.56	0.83
4:F:206:LEU:CD2	4:F:458:LEU:HD21	2.08	0.83
4:F:168:VAL:HG13	4:F:216:LEU:HD21	1.60	0.83
4:F:361:MET:CE	4:F:387:PHE:CD1	2.61	0.83
2:C:393:SER:O	2:C:396:VAL:HG23	1.78	0.83
4:F:134:ASP:HB2	4:F:137:LYS:HD3	1.60	0.83
3:A:928:ILE:HG22	3:A:1060:PHE:HE1	1.43	0.83
4:F:170:ILE:HD13	4:F:216:LEU:HD23	1.58	0.83
4:F:515:PHE:HE2	4:F:580:MET:HE3	1.44	0.82
1:E:212:TRP:CB	3:A:1091:TYR:CE1	2.62	0.82
2:C:296:ALA:CB	3:A:369:TRP:O	2.27	0.82
3:A:423:TRP:HD1	3:A:423:TRP:O	1.61	0.82
3:A:928:ILE:HG21	3:A:1060:PHE:CZ	2.14	0.82
3:A:1369:ALA:O	3:A:1373:ILE:HG23	1.79	0.82
3:A:1053:ALA:HA	3:A:1057:MET:CE	2.10	0.82
4:F:243:ARG:HH21	4:F:243:ARG:HG3	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:350:ASN:ND2	5:D:1:NAG:C1	2.41	0.82
4:F:824:TRP:C	4:F:864:MET:HE1	1.99	0.82
4:F:1010:LYS:CG	4:F:1017:ILE:HG13	2.09	0.82
3:A:1242:ARG:O	3:A:1245:LYS:HG3	1.79	0.81
1:E:117:PHE:CE2	3:A:1195:ILE:CD1	2.63	0.81
4:F:824:TRP:CD1	4:F:864:MET:HE1	2.16	0.81
4:F:47:LEU:HG	7:L:1:NAG:C8	2.09	0.81
4:F:845:LYS:O	4:F:848:SER:OG	1.97	0.81
1:E:117:PHE:CZ	3:A:1195:ILE:CD1	2.63	0.81
4:F:781:PRO:O	4:F:875:GLY:HA3	1.81	0.81
4:F:1070:ASP:OD1	4:F:1072:THR:CG2	2.24	0.81
4:F:43:ASP:OD1	7:L:1:NAG:H2	1.81	0.81
4:F:465:THR:CG2	4:F:489:VAL:HG12	2.11	0.80
2:C:295:LYS:CE	3:A:373:GLY:O	2.29	0.80
2:C:293:MET:HE2	3:A:369:TRP:CZ3	2.15	0.80
4:F:858:ASP:HA	4:F:986:PHE:CZ	2.17	0.80
3:A:39:PRO:CG	3:A:41:ARG:CZ	2.58	0.80
4:F:887:ARG:O	4:F:890:VAL:HG22	1.82	0.80
3:A:331:GLY:HA3	3:A:1380:ILE:HD11	1.63	0.80
3:A:39:PRO:CD	3:A:41:ARG:CZ	2.60	0.80
3:A:199:ILE:HD11	3:A:332:VAL:CG2	2.12	0.80
3:A:331:GLY:HA3	3:A:1380:ILE:CD1	2.11	0.80
1:E:212:TRP:HA	3:A:1091:TYR:HE1	1.05	0.80
4:F:481:LEU:HD23	4:F:482:LYS:H	1.46	0.80
3:A:1338:CYS:HG	3:A:1352:CYS:CB	1.95	0.79
1:E:138:ARG:NH1	3:A:1179:GLY:HA2	1.98	0.79
4:F:546:ARG:NH2	4:F:552:ASN:HD22	1.81	0.79
1:E:32:TRP:HE1	1:E:158:MET:CG	1.91	0.79
1:E:209:GLN:HA	3:A:1262:LYS:HG3	1.65	0.79
1:E:218:ALA:CB	3:A:1098:LEU:N	2.27	0.78
3:A:981:THR:CG2	4:F:546:ARG:HH12	1.96	0.78
1:E:124:CYS:HB2	1:E:140:ALA:HB2	1.65	0.78
3:A:1068:PHE:HB3	3:A:1381:MET:SD	2.24	0.78
4:F:168:VAL:HG22	4:F:218:ARG:HG2	1.64	0.78
4:F:465:THR:HG23	4:F:489:VAL:HG12	1.66	0.78
4:F:1010:LYS:HG3	4:F:1017:ILE:HG13	1.64	0.78
4:F:590:PHE:CD2	4:F:592:THR:HG23	2.18	0.78
1:E:152:PHE:CZ	3:A:309:TRP:CZ2	2.72	0.78
3:A:928:ILE:HG22	3:A:1060:PHE:CE1	2.19	0.77
4:F:356:CYS:SG	4:F:1062:CYS:CB	2.71	0.77
1:E:212:TRP:HB3	3:A:1091:TYR:CE1	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1097:PRO:HG2	3:A:1413:ALA:HB1	1.65	0.77
1:E:218:ALA:CA	3:A:1098:LEU:HA	2.14	0.77
1:E:20:ILE:CD1	1:E:118:LEU:HD21	2.14	0.77
4:F:669:TYR:CE1	4:F:704:LEU:HD21	2.20	0.77
4:F:663:PHE:HB2	4:F:744:THR:HG23	1.63	0.77
2:C:396:VAL:HG13	3:A:359:LEU:HD23	1.67	0.77
3:A:1096:ARG:HD3	3:A:1097:PRO:HD2	1.65	0.77
1:E:30:ASP:OD2	1:E:55:ARG:HG3	1.85	0.77
4:F:591:ARG:NH2	9:F:1115:NAG:HN2	1.82	0.77
1:E:208:PRO:HB3	1:E:213:GLU:CB	2.15	0.77
3:A:617:ASN:N	3:A:617:ASN:HD22	1.83	0.77
4:F:669:TYR:CE1	4:F:704:LEU:CD2	2.68	0.77
3:A:617:ASN:HD22	3:A:617:ASN:H	1.34	0.76
2:C:437:ASN:O	3:A:365:GLY:HA2	1.86	0.76
2:C:282:PRO:CG	2:C:290:THR:HG23	2.14	0.76
7:L:1:NAG:O3	7:L:1:NAG:H83	1.86	0.76
4:F:359:ILE:CG2	4:F:385:ARG:HB2	2.08	0.76
4:F:465:THR:HG22	4:F:489:VAL:CG1	2.16	0.76
3:A:46:SER:HB2	3:A:107:ALA:HB1	1.67	0.76
4:F:359:ILE:HG22	4:F:385:ARG:CB	2.07	0.76
4:F:1008:VAL:HG23	4:F:1019:ILE:HG22	1.67	0.76
2:C:279:LEU:HD23	2:C:387:VAL:HB	1.67	0.75
3:A:213:ILE:HG13	3:A:1240:VAL:HG21	1.68	0.75
1:E:20:ILE:CG1	1:E:118:LEU:CD2	2.49	0.75
2:C:289:VAL:HG13	2:C:400:LEU:CD2	2.16	0.75
4:F:178:SER:HB3	4:F:181:VAL:CG1	2.14	0.75
1:E:20:ILE:CD1	1:E:118:LEU:CD2	2.65	0.75
4:F:388:THR:CB	4:F:401:ILE:HG13	2.16	0.75
1:E:117:PHE:CE2	3:A:1195:ILE:HD11	2.22	0.75
2:C:396:VAL:CG1	3:A:359:LEU:HD23	2.17	0.75
4:F:1074:CYS:C	11:F:1101:ETA:HB1	2.08	0.75
3:A:39:PRO:HD2	3:A:41:ARG:CZ	2.15	0.75
3:A:1263:SER:HB2	3:A:1383:ASN:HD21	1.50	0.75
1:E:115:LEU:O	1:E:119:ILE:HG13	1.86	0.74
4:F:256:MET:HB2	4:F:359:ILE:CD1	2.18	0.74
4:F:855:ILE:O	4:F:856:LEU:HD12	1.87	0.74
2:C:396:VAL:HG13	3:A:359:LEU:CD2	2.18	0.74
3:A:39:PRO:HG3	3:A:41:ARG:HH11	1.49	0.74
2:C:280:VAL:CG1	2:C:285:LYS:NZ	2.51	0.74
3:A:40:LEU:HD23	3:A:40:LEU:O	1.86	0.74
3:A:46:SER:HB2	3:A:107:ALA:CB	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:275:ARG:HD2	4:F:325:ASN:HA	1.69	0.73
4:F:590:PHE:HD2	4:F:592:THR:HG23	1.52	0.73
3:A:1241:MET:O	3:A:1244:ILE:HG12	1.88	0.73
3:A:445:ASN:O	3:A:449:ILE:HG12	1.88	0.73
4:F:117:PHE:CD1	4:F:182:LEU:HD12	2.23	0.73
4:F:515:PHE:HE2	4:F:580:MET:CE	2.00	0.73
4:F:206:LEU:HD23	4:F:458:LEU:CD2	2.19	0.73
4:F:824:TRP:CG	4:F:864:MET:HE3	2.24	0.73
4:F:889:LEU:CG	4:F:894:VAL:HG11	2.17	0.72
4:F:590:PHE:HE2	4:F:592:THR:HG21	1.53	0.72
1:E:142:MET:HE2	3:A:1184:VAL:HG13	1.71	0.72
3:A:289:ILE:HD11	3:A:317:LEU:CD1	2.20	0.72
4:F:100:LEU:CD1	4:F:198:ASN:ND2	2.38	0.72
3:A:1239:ARG:O	3:A:1242:ARG:HG2	1.89	0.72
4:F:205:LEU:HD21	4:F:492:VAL:CG2	2.20	0.72
1:E:124:CYS:CB	1:E:140:ALA:HB2	2.18	0.72
2:C:282:PRO:HG2	2:C:290:THR:CG2	2.17	0.72
3:A:289:ILE:CD1	3:A:317:LEU:CD1	2.68	0.71
4:F:133:LEU:H	4:F:133:LEU:CD2	2.03	0.71
4:F:229:SER:O	4:F:235:ILE:HG22	1.91	0.71
4:F:243:ARG:HG3	4:F:243:ARG:NH2	2.00	0.71
1:E:130:ARG:O	1:E:133:ARG:HD3	1.90	0.71
4:F:513:TYR:O	4:F:624:LEU:HD12	1.90	0.71
4:F:255:ASP:OD1	4:F:354:ALA:CB	2.31	0.71
4:F:478:LYS:HD3	4:F:478:LYS:C	2.11	0.71
4:F:669:TYR:CD1	4:F:704:LEU:HD22	2.24	0.71
3:A:928:ILE:O	3:A:932:VAL:HG23	1.90	0.71
3:A:1053:ALA:HA	3:A:1057:MET:HE2	1.72	0.71
4:F:235:ILE:O	4:F:235:ILE:HD12	1.91	0.71
3:A:931:ILE:HD11	3:A:1060:PHE:HD1	1.55	0.71
4:F:846:ARG:NH1	4:F:868:ASP:CB	2.53	0.71
4:F:159:ARG:NH2	4:F:226:VAL:CG1	2.54	0.71
1:E:149:LEU:CD1	3:A:1234:PHE:CE2	2.59	0.70
4:F:595:LYS:HD3	4:F:599:GLU:OE1	1.91	0.70
1:E:117:PHE:CE2	3:A:1195:ILE:HD13	2.26	0.70
4:F:510:PRO:HG2	4:F:767:TYR:HE2	1.57	0.70
4:F:705:ILE:HD12	4:F:706:ASN:N	2.07	0.70
1:E:4:THR:HG22	1:E:134:ASP:OD2	1.89	0.70
4:F:850:VAL:HG22	4:F:851:MET:HG2	1.72	0.70
4:F:93:ARG:NH1	4:F:202:ASP:OD2	2.25	0.70
4:F:988:ASN:CG	9:F:1122:NAG:C1	2.60	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1472:ARG:HH11	3:A:1478:LYS:HD2	1.58	0.69
3:A:289:ILE:HD11	3:A:317:LEU:HD11	1.74	0.69
3:A:294:TRP:NE1	3:A:1321:THR:HG21	2.01	0.69
4:F:411:TYR:CD1	4:F:1074:CYS:HA	2.27	0.69
1:E:207:MET:HE2	3:A:1258:TRP:CD1	2.26	0.69
1:E:132:LYS:HD3	1:E:132:LYS:H	1.57	0.69
1:E:218:ALA:N	3:A:1098:LEU:HA	2.06	0.69
1:E:130:ARG:O	1:E:131:LYS:HB2	1.92	0.69
3:A:196:LEU:CD1	3:A:332:VAL:CG1	2.71	0.69
4:F:546:ARG:HH21	4:F:552:ASN:HD22	1.40	0.69
4:F:996:VAL:HG23	4:F:1004:ARG:O	1.92	0.69
4:F:339:PHE:CZ	4:F:362:LEU:HD23	2.28	0.69
4:F:388:THR:HB	4:F:401:ILE:CG1	2.23	0.69
4:F:478:LYS:HD3	4:F:478:LYS:O	1.93	0.69
4:F:1074:CYS:C	11:F:1101:ETA:HN1	1.95	0.69
3:A:196:LEU:HD12	3:A:332:VAL:HG11	1.73	0.68
3:A:812:SER:O	3:A:903:ARG:NH1	2.26	0.68
2:C:289:VAL:HG13	2:C:400:LEU:HD23	1.76	0.68
4:F:124:VAL:HG21	4:F:182:LEU:HD13	1.75	0.68
4:F:461:VAL:HG12	4:F:495:SER:HA	1.73	0.68
4:F:206:LEU:CD2	4:F:458:LEU:CD2	2.71	0.68
4:F:311:GLN:HE22	4:F:520:ASN:HD21	1.41	0.68
1:E:218:ALA:HB3	3:A:1098:LEU:H	1.56	0.68
3:A:358:GLN:O	3:A:361:GLU:HG3	1.93	0.68
4:F:370:ARG:CD	4:F:372:GLN:HE21	2.06	0.68
4:F:590:PHE:CE2	4:F:592:THR:HG21	2.28	0.68
4:F:889:LEU:O	4:F:892:ILE:HG13	1.92	0.68
4:F:515:PHE:CE2	4:F:580:MET:HE3	2.28	0.68
4:F:993:PHE:HB2	4:F:1008:VAL:HG11	1.75	0.68
3:A:1098:LEU:HD23	3:A:1098:LEU:C	2.14	0.68
3:A:1430:GLN:HG3	3:A:1432:PRO:HD2	1.75	0.68
4:F:889:LEU:HA	4:F:892:ILE:HD11	1.75	0.68
4:F:411:TYR:CE1	4:F:1074:CYS:HA	2.29	0.68
4:F:478:LYS:HD2	4:F:479:THR:HG23	1.74	0.68
4:F:162:SER:O	4:F:221:PRO:HB2	1.93	0.67
4:F:398:ARG:O	4:F:402:GLN:HG3	1.94	0.67
1:E:152:PHE:HZ	3:A:309:TRP:CZ2	2.12	0.67
1:E:209:GLN:NE2	3:A:1262:LYS:HG2	2.09	0.67
4:F:44:LEU:HD11	4:F:824:TRP:CZ2	2.29	0.67
1:E:127:MET:SD	1:E:136:LEU:HD21	2.35	0.67
3:A:447:LEU:HD13	3:A:447:LEU:C	2.14	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:359:ILE:HD13	4:F:361:MET:HE3	1.75	0.67
4:F:132:ASP:OD2	4:F:137:LYS:CG	2.36	0.67
1:E:216:MET:O	1:E:216:MET:HG3	1.94	0.67
3:A:976:LYS:HE3	4:F:547:ARG:NH1	2.08	0.67
3:A:974:VAL:O	3:A:983:MET:HB2	1.95	0.66
1:E:136:LEU:C	1:E:139:PRO:HD2	2.15	0.66
2:C:437:ASN:HB2	3:A:361:GLU:O	1.96	0.66
3:A:128:ILE:O	3:A:132:LEU:HB2	1.95	0.66
3:A:39:PRO:CD	3:A:41:ARG:NH1	2.58	0.66
4:F:705:ILE:HD12	4:F:705:ILE:C	2.16	0.66
4:F:858:ASP:HA	4:F:986:PHE:CE1	2.30	0.66
3:A:274:HIS:HD2	3:A:276:ASP:H	1.43	0.66
4:F:858:ASP:HB3	4:F:986:PHE:CE2	2.30	0.66
3:A:196:LEU:HD12	3:A:332:VAL:CG1	2.25	0.66
4:F:783:PHE:CE1	4:F:873:GLN:HB2	2.31	0.66
4:F:348:ASN:O	4:F:350:ASN:N	2.29	0.66
1:E:105:ILE:HG21	3:A:1206:LEU:CD1	2.25	0.66
4:F:478:LYS:CD	4:F:479:THR:HG23	2.26	0.66
1:E:209:GLN:CD	3:A:1262:LYS:HG2	2.17	0.65
1:E:212:TRP:N	3:A:1091:TYR:HE1	1.94	0.65
3:A:423:TRP:CD1	3:A:423:TRP:O	2.45	0.65
4:F:783:PHE:HE1	4:F:873:GLN:CB	2.09	0.65
1:E:214:SER:O	1:E:217:ASP:HB2	1.95	0.65
4:F:256:MET:HB2	4:F:359:ILE:HD11	1.79	0.65
4:F:339:PHE:O	4:F:343:PHE:HD2	1.79	0.65
2:C:396:VAL:HB	3:A:366:TYR:CZ	2.31	0.65
3:A:981:THR:HG21	4:F:546:ARG:HH12	1.61	0.65
4:F:28:PRO:HD3	4:F:851:MET:HE3	1.78	0.65
4:F:361:MET:HE2	4:F:387:PHE:HD1	1.62	0.65
4:F:366:GLY:HA3	4:F:396:TYR:CB	2.26	0.65
4:F:114:ARG:HH21	6:H:1:NAG:H62	1.61	0.65
4:F:339:PHE:HZ	4:F:362:LEU:HD23	1.62	0.65
4:F:783:PHE:HE1	4:F:873:GLN:HA	1.62	0.65
4:F:891:ASN:OD1	9:F:1107:NAG:O5	2.08	0.65
4:F:114:ARG:CZ	6:H:1:NAG:H62	2.27	0.64
4:F:506:PHE:CZ	4:F:667:ARG:HG3	2.32	0.64
4:F:892:ILE:O	4:F:893:SER:HB3	1.97	0.64
5:K:1:NAG:H82	5:K:2:NAG:H2	1.79	0.64
2:C:293:MET:HB3	3:A:369:TRP:CE3	2.30	0.64
3:A:1384:PHE:HE1	3:A:1388:THR:HG21	1.61	0.64
4:F:28:PRO:HD3	4:F:851:MET:CE	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:168:VAL:HG11	4:F:216:LEU:HD21	1.76	0.64
2:C:393:SER:O	2:C:396:VAL:CG2	2.46	0.64
4:F:130:LYS:HA	4:F:228:ASN:HD22	1.63	0.64
4:F:159:ARG:HH22	4:F:226:VAL:CG1	2.06	0.63
2:C:279:LEU:O	2:C:280:VAL:HG13	1.98	0.63
4:F:340:SER:O	4:F:344:GLU:HG2	1.97	0.63
1:E:146:PHE:CE1	3:A:1238:PHE:CZ	2.86	0.63
3:A:931:ILE:HD11	3:A:1060:PHE:CD1	2.33	0.63
1:E:146:PHE:CZ	3:A:1238:PHE:CZ	2.86	0.63
3:A:1068:PHE:CB	3:A:1381:MET:SD	2.86	0.63
4:F:269:LEU:HD22	4:F:269:LEU:O	1.99	0.63
1:E:218:ALA:H	3:A:1098:LEU:HA	1.63	0.63
1:E:146:PHE:CD1	3:A:1235:PHE:HE1	2.17	0.63
1:E:107:ALA:N	1:E:157:VAL:HG11	2.13	0.63
3:A:1092:ALA:O	3:A:1464:ASN:ND2	2.32	0.63
7:L:3:NAG:H83	7:L:3:NAG:O5	1.97	0.63
3:A:48:VAL:HG12	3:A:48:VAL:O	1.98	0.63
4:F:895:TYR:CZ	4:F:986:PHE:HE1	2.17	0.63
1:E:133:ARG:CB	1:E:135:TYR:HE1	2.08	0.63
2:C:280:VAL:CG1	2:C:285:LYS:HZ2	2.09	0.63
4:F:103:GLU:HG3	4:F:194:VAL:HG21	1.81	0.63
1:E:149:LEU:CD1	3:A:1234:PHE:CZ	2.80	0.62
4:F:159:ARG:NH1	4:F:224:PRO:O	2.32	0.62
4:F:783:PHE:CE1	4:F:873:GLN:CB	2.82	0.62
7:L:3:NAG:C8	7:L:3:NAG:O5	2.47	0.62
2:C:293:MET:HE2	3:A:369:TRP:HZ3	1.64	0.62
4:F:178:SER:OG	4:F:180:ILE:HG22	2.00	0.62
4:F:267:SER:HB3	4:F:329:ALA:HB3	1.80	0.62
3:A:215:LEU:HD23	3:A:275:PHE:O	2.00	0.62
3:A:980:PRO:HB3	4:F:418:ILE:HG21	1.82	0.62
4:F:528:ASN:HD22	4:F:528:ASN:C	2.02	0.62
4:F:847:ASN:C	4:F:847:ASN:HD22	2.03	0.62
4:F:880:GLU:HG2	4:F:1035:ILE:HG22	1.82	0.62
3:A:199:ILE:CD1	3:A:332:VAL:HG21	2.25	0.62
3:A:1028:GLU:HB2	3:A:1031:MET:HG3	1.81	0.62
1:E:105:ILE:CG2	3:A:1206:LEU:CD1	2.78	0.62
4:F:206:LEU:HD21	4:F:458:LEU:HD21	1.81	0.62
4:F:1008:VAL:CG2	4:F:1019:ILE:HG22	2.29	0.62
4:F:97:LEU:HD11	4:F:464:GLY:O	1.99	0.61
4:F:993:PHE:O	4:F:1008:VAL:CG1	2.47	0.61
1:E:208:PRO:O	1:E:209:GLN:HB2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:370:ARG:HD3	4:F:372:GLN:HE21	1.65	0.61
4:F:376:ALA:O	4:F:380:LYS:HB2	2.01	0.61
3:A:1027:ASN:ND2	3:A:1032:GLY:O	2.33	0.61
3:A:1053:ALA:HA	3:A:1057:MET:HE3	1.81	0.61
3:A:1384:PHE:CE1	3:A:1388:THR:HG23	2.36	0.61
4:F:210:PHE:HB2	4:F:490:MET:HE2	1.82	0.61
1:E:208:PRO:CB	1:E:213:GLU:HB2	2.24	0.61
3:A:245:CYS:SG	3:A:261:CYS:CB	2.89	0.61
3:A:656:PHE:HB2	3:A:1058:ASN:ND2	2.09	0.61
4:F:856:LEU:O	4:F:1017:ILE:HG22	2.01	0.61
4:F:1010:LYS:HG2	4:F:1017:ILE:HG13	1.83	0.61
4:F:256:MET:HB2	4:F:359:ILE:HD12	1.83	0.61
5:D:1:NAG:H83	5:D:2:NAG:C8	2.31	0.61
3:A:196:LEU:CD1	3:A:332:VAL:HG12	2.31	0.61
4:F:781:PRO:CG	4:F:795:ILE:HG13	2.31	0.61
4:F:868:ASP:HA	4:F:871:THR:HG22	1.82	0.61
1:E:142:MET:HG2	3:A:1188:LEU:HD12	1.82	0.60
4:F:465:THR:HG22	4:F:489:VAL:HG13	1.81	0.60
3:A:1236:ARG:HD2	3:A:1239:ARG:HH21	1.64	0.60
4:F:133:LEU:H	4:F:133:LEU:HD23	1.66	0.60
4:F:889:LEU:HG	4:F:894:VAL:CG1	2.23	0.60
4:F:161:VAL:CG2	4:F:221:PRO:CG	2.70	0.60
3:A:938:LEU:HD21	3:A:1051:LEU:HD23	1.82	0.60
3:A:38:ASN:CG	3:A:39:PRO:HD3	2.22	0.60
3:A:295:THR:HG21	3:A:1318:ARG:HG3	1.83	0.60
3:A:1384:PHE:HE1	3:A:1388:THR:CG2	2.15	0.60
3:A:1384:PHE:CE1	3:A:1388:THR:CG2	2.85	0.60
4:F:391:VAL:HG12	4:F:415:ILE:HB	1.84	0.60
4:F:168:VAL:HG13	4:F:216:LEU:CD2	2.24	0.60
4:F:1045:ASP:OD1	4:F:1046:PRO:HD2	2.02	0.60
3:A:617:ASN:H	3:A:617:ASN:ND2	1.98	0.59
4:F:109:ALA:HB2	4:F:471:ILE:O	2.02	0.59
4:F:710:LEU:CD2	4:F:714:PHE:CZ	2.82	0.59
4:F:1068:LEU:HD12	4:F:1068:LEU:O	2.01	0.59
1:E:215:CYS:O	1:E:216:MET:HG2	2.02	0.59
4:F:43:ASP:CG	7:L:1:NAG:H2	2.23	0.59
3:A:196:LEU:HD11	3:A:332:VAL:HG12	1.84	0.59
4:F:411:TYR:HD2	4:F:413:TYR:HH	1.49	0.59
4:F:449:THR:HG22	4:F:450:ASN:N	2.17	0.59
4:F:792:GLU:OE1	4:F:792:GLU:N	2.22	0.59
1:E:142:MET:HE1	3:A:1184:VAL:HG13	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:476:GLU:OE1	4:F:478:LYS:CB	2.47	0.59
3:A:196:LEU:CD1	3:A:332:VAL:HG11	2.31	0.59
3:A:1051:LEU:O	3:A:1056:MET:HG2	2.01	0.59
4:F:590:PHE:CE2	4:F:592:THR:CG2	2.86	0.59
4:F:704:LEU:C	4:F:704:LEU:HD23	2.23	0.59
4:F:217:ALA:HB2	4:F:240:VAL:HG21	1.85	0.59
4:F:590:PHE:CD2	4:F:592:THR:CG2	2.85	0.59
4:F:796:MET:HB3	4:F:818:LYS:HD2	1.83	0.59
2:C:393:SER:HB3	2:C:396:VAL:CG2	2.33	0.59
3:A:1100:CYS:O	3:A:1101:TYR:C	2.41	0.59
4:F:521:GLY:O	4:F:562:ASP:OD1	2.21	0.59
4:F:889:LEU:HA	4:F:892:ILE:CD1	2.32	0.59
3:A:562:LEU:HB3	3:A:655:VAL:HG22	1.85	0.59
1:E:105:ILE:CG2	3:A:1206:LEU:HD13	2.29	0.59
3:A:976:LYS:HD3	4:F:547:ARG:NH1	2.18	0.59
4:F:33:ILE:HG21	4:F:1007:HIS:ND1	2.17	0.59
1:E:131:LYS:HB2	1:E:133:ARG:HD3	1.85	0.58
3:A:450:ALA:O	3:A:1000:VAL:HG21	2.03	0.58
2:C:293:MET:CE	3:A:369:TRP:CE3	2.86	0.58
4:F:887:ARG:NH2	4:F:1032:ARG:O	2.36	0.58
3:A:908:ILE:HD12	3:A:918:VAL:HG21	1.84	0.58
4:F:851:MET:SD	4:F:1020:MET:SD	3.01	0.58
1:E:217:ASP:OD1	1:E:218:ALA:N	2.36	0.58
3:A:976:LYS:HG2	4:F:547:ARG:CZ	2.33	0.58
4:F:85:ASP:HB3	4:F:502:LEU:HD22	1.84	0.58
4:F:170:ILE:CD1	4:F:216:LEU:HD23	2.31	0.58
4:F:780:ALA:HB2	4:F:863:LEU:HD21	1.85	0.58
1:E:130:ARG:O	1:E:133:ARG:CD	2.52	0.58
3:A:909:ASN:OD1	3:A:915:LYS:NZ	2.37	0.58
4:F:408:ASN:C	4:F:409:LYS:HG3	2.24	0.58
4:F:651:LEU:O	4:F:687:ASN:ND2	2.37	0.58
3:A:545:LEU:HD11	3:A:931:ILE:HA	1.86	0.58
2:C:293:MET:CE	3:A:369:TRP:CZ3	2.85	0.58
4:F:523:VAL:HG21	4:F:526:HIS:HB2	1.85	0.58
4:F:702:THR:O	4:F:706:ASN:HB2	2.03	0.58
4:F:291:VAL:CG1	4:F:312:ALA:HB2	2.28	0.58
4:F:456:LEU:O	4:F:457:GLU:HB2	2.03	0.57
1:E:134:ASP:N	1:E:134:ASP:OD1	2.36	0.57
4:F:693:LYS:NZ	4:F:696:ASN:OD1	2.37	0.57
4:F:846:ARG:NH1	4:F:868:ASP:CG	2.58	0.57
4:F:1011:LEU:HD12	4:F:1011:LEU:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:209:GLN:H	3:A:1258:TRP:HZ2	1.53	0.57
3:A:39:PRO:CB	3:A:41:ARG:HE	2.17	0.57
3:A:309:TRP:O	3:A:312:ILE:HG13	2.04	0.57
3:A:1097:PRO:CG	3:A:1413:ALA:HB1	2.32	0.57
3:A:1098:LEU:HG	3:A:1099:ARG:N	2.20	0.57
4:F:256:MET:HE3	4:F:258:ILE:HG13	1.84	0.57
3:A:494:SER:HB3	3:A:497:ASN:HB2	1.85	0.57
4:F:132:ASP:CG	4:F:137:LYS:HG2	2.23	0.57
4:F:357:ASN:ND2	4:F:1064:ASP:HB3	2.18	0.57
4:F:366:GLY:HA3	4:F:396:TYR:HB3	1.84	0.57
1:E:152:PHE:CZ	3:A:309:TRP:HZ2	2.20	0.57
3:A:1100:CYS:HB2	3:A:1407:ALA:HB1	1.86	0.57
4:F:256:MET:CB	4:F:359:ILE:HD11	2.33	0.57
4:F:824:TRP:CB	4:F:864:MET:CE	2.83	0.57
2:C:281:GLY:HA2	2:C:422:LEU:CD1	2.24	0.57
3:A:225:THR:HB	3:A:265:TRP:CD2	2.39	0.57
3:A:1100:CYS:O	3:A:1102:ILE:N	2.37	0.57
3:A:447:LEU:HD13	3:A:447:LEU:O	2.03	0.57
3:A:1288:MET:SD	3:A:1356:PHE:CE2	2.97	0.57
4:F:824:TRP:C	4:F:864:MET:CE	2.71	0.57
4:F:824:TRP:O	4:F:864:MET:HE1	2.04	0.57
3:A:127:PHE:HA	3:A:130:VAL:HG22	1.87	0.57
2:C:280:VAL:HG12	2:C:285:LYS:NZ	2.18	0.57
4:F:100:LEU:HD13	4:F:198:ASN:HD21	1.62	0.57
4:F:844:CYS:HB3	4:F:866:ASN:ND2	2.20	0.56
1:E:133:ARG:HB2	1:E:135:TYR:CZ	2.37	0.56
2:C:396:VAL:CG2	3:A:366:TYR:OH	2.53	0.56
4:F:339:PHE:O	4:F:343:PHE:CD2	2.58	0.56
4:F:361:MET:HE1	4:F:387:PHE:CD1	2.39	0.56
4:F:523:VAL:HG13	4:F:523:VAL:O	2.05	0.56
1:E:208:PRO:HD2	3:A:1258:TRP:NE1	2.19	0.56
4:F:205:LEU:HD21	4:F:492:VAL:HG21	1.88	0.56
4:F:889:LEU:O	4:F:892:ILE:CG1	2.54	0.56
1:E:146:PHE:CE1	3:A:1235:PHE:HE1	2.24	0.56
2:C:289:VAL:CG1	2:C:400:LEU:HD23	2.35	0.56
4:F:37:VAL:HG13	4:F:1011:LEU:HG	1.88	0.56
1:E:4:THR:HG21	1:E:134:ASP:OD2	2.05	0.56
3:A:544:SER:OG	3:A:930:ASN:ND2	2.38	0.56
4:F:121:GLU:HA	4:F:121:GLU:OE1	2.05	0.56
4:F:784:ASN:CG	9:F:1120:NAG:C1	2.65	0.56
4:F:895:TYR:CE1	4:F:986:PHE:HE1	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:38:ASN:CB	3:A:39:PRO:CD	2.83	0.56
4:F:366:GLY:HA3	4:F:396:TYR:HB2	1.88	0.56
1:E:210:ASN:ND2	1:E:213:GLU:OE1	2.32	0.56
2:C:399:ARG:HH12	3:A:356:LYS:NZ	2.04	0.56
4:F:365:ASP:OD1	4:F:366:GLY:N	2.38	0.56
4:F:546:ARG:HH21	4:F:552:ASN:ND2	2.03	0.56
4:F:1010:LYS:HG3	4:F:1017:ILE:CG1	2.34	0.56
2:C:396:VAL:HB	3:A:366:TYR:OH	2.06	0.56
3:A:929:GLY:O	3:A:933:LEU:HG	2.06	0.56
3:A:1070:GLU:HA	3:A:1073:GLU:HB2	1.88	0.56
4:F:476:GLU:CD	4:F:478:LYS:HB2	2.26	0.56
4:F:444:LYS:NZ	4:F:467:PRO:O	2.39	0.55
4:F:773:ASN:HD22	4:F:777:VAL:HG21	1.71	0.55
4:F:1061:VAL:HG23	4:F:1061:VAL:O	2.05	0.55
1:E:117:PHE:HE2	3:A:1195:ILE:HD13	1.67	0.55
4:F:326:ASN:ND2	9:F:1104:NAG:C2	2.65	0.55
4:F:474:GLN:O	4:F:475:PHE:C	2.44	0.55
1:E:142:MET:SD	3:A:1187:PHE:CE2	2.99	0.55
4:F:243:ARG:HH21	4:F:243:ARG:CG	2.15	0.55
3:A:439:ILE:HA	3:A:442:VAL:HB	1.88	0.55
4:F:449:THR:HG22	4:F:450:ASN:H	1.71	0.55
1:E:146:PHE:HZ	3:A:1238:PHE:CE1	2.24	0.55
3:A:39:PRO:CD	3:A:41:ARG:HE	2.11	0.55
3:A:1249:ARG:NH2	3:A:1251:GLU:OE2	2.39	0.55
1:E:53:LEU:HD23	1:E:158:MET:HE2	1.88	0.55
1:E:133:ARG:O	1:E:133:ARG:HG2	2.06	0.55
1:E:116:GLY:HA2	1:E:119:ILE:HD11	1.86	0.55
2:C:279:LEU:CD2	2:C:387:VAL:HG11	2.36	0.55
3:A:358:GLN:O	3:A:361:GLU:CG	2.55	0.55
3:A:423:TRP:CD1	3:A:424:LYS:N	2.74	0.55
3:A:904:PRO:O	3:A:1276:MET:HE1	2.06	0.55
4:F:227:ASP:HB2	4:F:236:ASP:HB3	1.89	0.55
5:D:1:NAG:C8	5:D:2:NAG:C7	2.83	0.55
3:A:917:VAL:HG12	3:A:1273:LEU:HD11	1.88	0.55
3:A:1196:ASP:HB2	3:A:1235:PHE:HB3	1.88	0.55
4:F:297:ASN:ND2	4:F:330:LYS:O	2.37	0.55
1:E:115:LEU:CD1	1:E:119:ILE:HD11	2.32	0.55
4:F:37:VAL:CG2	4:F:1018:PHE:CD2	2.90	0.55
3:A:108:TYR:HB3	3:A:113:HIS:HB3	1.89	0.55
3:A:199:ILE:HG21	3:A:329:VAL:HG23	1.88	0.55
1:E:136:LEU:O	1:E:139:PRO:HD2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:542:TRP:CH2	3:A:933:LEU:HB3	2.42	0.54
4:F:370:ARG:HG3	4:F:372:GLN:HG3	1.89	0.54
3:A:976:LYS:CE	4:F:547:ARG:HH12	2.13	0.54
4:F:216:LEU:C	4:F:216:LEU:HD13	2.28	0.54
4:F:528:ASN:O	4:F:528:ASN:ND2	2.27	0.54
4:F:570:ASN:HD21	4:F:592:THR:CG2	2.20	0.54
3:A:225:THR:HB	3:A:265:TRP:CE3	2.42	0.54
3:A:1277:LEU:CD2	3:A:1371:LEU:CD2	2.71	0.54
4:F:129:ALA:O	4:F:130:LYS:HG2	2.07	0.54
3:A:449:ILE:CG2	3:A:532:LEU:CD2	2.86	0.54
3:A:617:ASN:N	3:A:617:ASN:ND2	2.55	0.54
4:F:359:ILE:HD13	4:F:361:MET:CE	2.37	0.54
3:A:230:GLY:O	4:F:544:ARG:NH2	2.41	0.54
3:A:938:LEU:HD23	3:A:1052:ILE:HD11	1.89	0.54
4:F:385:ARG:HH12	4:F:431:VAL:HG12	1.73	0.54
2:C:293:MET:HE3	3:A:369:TRP:CE3	2.43	0.54
3:A:1097:PRO:O	3:A:1098:LEU:HB3	2.08	0.54
4:F:570:ASN:ND2	4:F:592:THR:CG2	2.70	0.54
1:E:30:ASP:OD2	1:E:55:ARG:CG	2.54	0.54
2:B:143:ASP:HB3	2:B:164:LYS:HD3	1.89	0.54
3:A:974:VAL:CG2	3:A:984:GLU:CG	2.86	0.54
2:B:145:TRP:HB2	2:B:159:ILE:HB	1.90	0.54
3:A:1406:TRP:NE1	3:A:1410:ASP:OD2	2.41	0.54
4:F:361:MET:CE	4:F:387:PHE:HD1	2.19	0.54
4:F:896:ALA:CB	4:F:987:ASP:HB3	2.38	0.54
5:K:2:NAG:H3	5:K:2:NAG:C8	2.19	0.54
4:F:171:PRO:HG2	4:F:174:ILE:HD12	1.88	0.53
4:F:284:THR:HG21	4:F:428:TYR:OH	2.09	0.53
4:F:441:ASP:N	4:F:441:ASP:OD1	2.40	0.53
4:F:546:ARG:NH2	4:F:552:ASN:ND2	2.55	0.53
3:A:1338:CYS:HG	3:A:1352:CYS:HB2	1.72	0.53
4:F:780:ALA:CB	4:F:863:LEU:HD21	2.38	0.53
1:E:32:TRP:HB2	1:E:182:PHE:HB2	1.90	0.53
3:A:215:LEU:HD22	3:A:219:LYS:CD	2.34	0.53
3:A:901:VAL:HG11	3:A:1284:ILE:HD11	1.91	0.53
1:E:217:ASP:O	1:E:218:ALA:C	2.47	0.53
2:C:279:LEU:HD23	2:C:387:VAL:CB	2.38	0.53
3:A:183:GLN:O	3:A:187:ASN:ND2	2.41	0.53
4:F:597:GLN:OE1	4:F:768:LYS:NZ	2.38	0.53
4:F:795:ILE:HD11	4:F:874:ILE:HD11	1.91	0.53
2:C:280:VAL:O	2:C:388:TYR:HA	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:46:SER:HB2	3:A:107:ALA:HB2	1.91	0.53
4:F:858:ASP:CA	4:F:986:PHE:CZ	2.88	0.53
4:F:992:SER:O	4:F:993:PHE:CD1	2.62	0.53
4:F:783:PHE:CE1	4:F:873:GLN:HA	2.44	0.53
1:E:209:GLN:N	3:A:1258:TRP:HZ2	2.07	0.53
3:A:1052:ILE:HD13	3:A:1056:MET:HG3	1.91	0.53
4:F:230:ARG:N	4:F:230:ARG:HD3	2.22	0.53
4:F:824:TRP:HB3	4:F:864:MET:HE3	1.91	0.53
1:E:121:GLY:O	1:E:140:ALA:HB1	2.09	0.52
1:E:135:TYR:CD2	1:E:136:LEU:N	2.77	0.52
3:A:105:ILE:HG13	3:A:106:ILE:HG23	1.91	0.52
4:F:178:SER:O	4:F:181:VAL:HG13	2.09	0.52
4:F:339:PHE:CZ	4:F:362:LEU:CD2	2.92	0.52
4:F:515:PHE:CE2	4:F:580:MET:CE	2.88	0.52
4:F:993:PHE:CB	4:F:1008:VAL:CG1	2.77	0.52
3:A:454:HIS:HB2	3:A:951:LYS:HG2	1.91	0.52
3:A:974:VAL:HG23	3:A:984:GLU:HG2	1.91	0.52
1:E:131:LYS:CB	1:E:133:ARG:CD	2.88	0.52
3:A:556:ILE:HD11	3:A:557:ARG:NH1	2.24	0.52
1:E:131:LYS:HB2	1:E:133:ARG:CD	2.39	0.52
3:A:245:CYS:HG	3:A:261:CYS:CB	2.12	0.52
3:A:1098:LEU:HG	3:A:1099:ARG:H	1.74	0.52
4:F:1010:LYS:CG	4:F:1017:ILE:CG1	2.85	0.52
3:A:38:ASN:CG	3:A:39:PRO:CD	2.77	0.52
3:A:1098:LEU:CG	3:A:1099:ARG:N	2.73	0.52
3:A:1108:GLN:HE22	3:A:1173:LYS:HB2	1.74	0.52
4:F:777:VAL:O	4:F:797:VAL:HA	2.10	0.52
2:C:389:ILE:CG1	3:A:369:TRP:CH2	2.92	0.52
3:A:38:ASN:HD22	3:A:39:PRO:HD3	1.74	0.52
3:A:1271:ALA:HB2	3:A:1375:LEU:HD11	1.92	0.52
3:A:1363:SER:O	3:A:1367:LEU:HG	2.09	0.52
3:A:450:ALA:O	3:A:1000:VAL:CG2	2.58	0.52
4:F:826:GLU:O	4:F:830:LYS:HG2	2.09	0.52
4:F:1011:LEU:N	4:F:1011:LEU:CD1	2.73	0.52
4:F:1066:ASN:HD22	4:F:1067:VAL:H	1.57	0.52
1:E:216:MET:HB3	3:A:1181:PRO:HD3	1.92	0.52
3:A:542:TRP:CZ3	3:A:933:LEU:HB3	2.45	0.52
4:F:824:TRP:CD1	4:F:864:MET:CE	2.87	0.52
3:A:245:CYS:SG	3:A:261:CYS:HB2	2.50	0.51
3:A:535:LEU:HD11	3:A:941:MET:HG3	1.91	0.51
4:F:532:LYS:NZ	4:F:532:LYS:CB	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:75:PRO:HG2	4:F:265:SER:HA	1.91	0.51
3:A:177:SER:HA	3:A:183:GLN:HE21	1.76	0.51
3:A:542:TRP:CZ3	3:A:933:LEU:CB	2.94	0.51
3:A:656:PHE:CB	3:A:1058:ASN:HD21	2.17	0.51
4:F:34:LYS:CD	4:F:1009:GLU:OE2	2.59	0.51
2:C:293:MET:HE2	3:A:369:TRP:CE3	2.44	0.51
4:F:127:TYR:HB2	4:F:147:ILE:HB	1.92	0.51
4:F:177:GLY:HA2	4:F:182:LEU:HD23	1.91	0.51
4:F:867:HIS:O	4:F:868:ASP:CB	2.57	0.51
4:F:346:LEU:O	4:F:353:ARG:NH2	2.43	0.51
3:A:34:LEU:O	3:A:113:HIS:NE2	2.43	0.51
3:A:127:PHE:HA	3:A:130:VAL:CG2	2.41	0.51
4:F:889:LEU:HA	4:F:892:ILE:CG1	2.41	0.51
4:F:367:GLY:O	4:F:400:PRO:CG	2.51	0.51
1:E:20:ILE:HD11	1:E:118:LEU:CD2	2.41	0.51
1:E:212:TRP:N	3:A:1091:TYR:CE1	2.71	0.51
4:F:386:VAL:O	4:F:410:GLY:HA3	2.10	0.51
4:F:487:LEU:HD22	6:I:1:NAG:H82	1.93	0.51
3:A:599:ASN:HB3	3:A:601:PRO:HD2	1.93	0.51
3:A:1380:ILE:HD13	3:A:1387:LEU:HD21	1.93	0.51
4:F:1008:VAL:HG23	4:F:1019:ILE:CG2	2.37	0.51
4:F:690:ILE:HG23	4:F:695:PRO:HG3	1.93	0.50
4:F:783:PHE:HE1	4:F:873:GLN:CA	2.22	0.50
3:A:981:THR:CB	4:F:546:ARG:HH12	2.25	0.50
3:A:1005:MET:SD	3:A:1362:ILE:HD11	2.51	0.50
3:A:1430:GLN:O	3:A:1434:GLY:N	2.42	0.50
4:F:1021:VAL:HG22	4:F:1022:GLU:N	2.26	0.50
4:F:1070:ASP:OD1	4:F:1072:THR:N	2.40	0.50
2:C:296:ALA:CB	3:A:369:TRP:HA	2.41	0.50
4:F:629:TYR:CB	4:F:809:LEU:HD23	2.41	0.50
4:F:712:ALA:HB2	4:F:743:ILE:HD13	1.93	0.50
3:A:974:VAL:CG2	3:A:984:GLU:HG2	2.41	0.50
4:F:167:ALA:HB3	4:F:219:TYR:CZ	2.46	0.50
4:F:336:LYS:CE	4:F:369:GLU:OE2	2.52	0.50
4:F:339:PHE:HZ	4:F:362:LEU:CD2	2.24	0.50
4:F:479:THR:O	4:F:480:ASN:HB3	2.12	0.50
4:F:510:PRO:CG	4:F:767:TYR:CE2	2.84	0.50
4:F:454:ASP:OD1	4:F:455:ALA:N	2.44	0.50
4:F:726:GLN:HB3	4:F:729:ILE:HD11	1.94	0.50
4:F:1074:CYS:O	11:F:1101:ETA:HB1	2.11	0.50
1:E:133:ARG:HB3	1:E:135:TYR:HE1	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:373:HIS:HB3	2:C:376:GLN:HB2	1.93	0.50
1:E:135:TYR:CG	1:E:136:LEU:N	2.79	0.50
4:F:33:ILE:HG23	4:F:1018:PHE:HE2	1.77	0.50
3:A:977:ASP:CG	4:F:547:ARG:HH21	2.14	0.50
3:A:1406:TRP:CH2	3:A:1417:ILE:HG23	2.47	0.50
4:F:237:LEU:HD12	4:F:237:LEU:H	1.76	0.50
4:F:781:PRO:HD3	4:F:795:ILE:HG13	1.93	0.50
1:E:32:TRP:NE1	1:E:158:MET:CG	2.59	0.50
3:A:924:ALA:O	3:A:928:ILE:CG1	2.55	0.50
3:A:1476:LYS:HD3	3:A:1478:LYS:HE3	1.93	0.50
4:F:385:ARG:NH1	4:F:431:VAL:HG12	2.27	0.50
4:F:824:TRP:CB	4:F:864:MET:HE1	2.40	0.50
2:C:280:VAL:CG1	2:C:285:LYS:CE	2.80	0.49
4:F:476:GLU:OE1	4:F:478:LYS:N	2.45	0.49
4:F:1008:VAL:CB	4:F:1019:ILE:HG22	2.41	0.49
4:F:629:TYR:CD1	4:F:629:TYR:C	2.84	0.49
3:A:656:PHE:HB2	3:A:1058:ASN:HD21	1.77	0.49
3:A:1454:PRO:HG2	3:A:1465:ALA:HB1	1.93	0.49
4:F:291:VAL:O	4:F:291:VAL:HG13	2.11	0.49
4:F:506:PHE:CZ	4:F:667:ARG:CG	2.94	0.49
4:F:663:PHE:CB	4:F:744:THR:HG23	2.39	0.49
3:A:1277:LEU:HD22	3:A:1371:LEU:HD21	1.90	0.49
4:F:210:PHE:HB2	4:F:490:MET:CE	2.42	0.49
4:F:775:ASN:HB2	4:F:1013:ASN:O	2.12	0.49
4:F:993:PHE:CB	4:F:1008:VAL:HG13	2.37	0.49
4:F:242:ARG:NH1	4:F:426:GLN:HB3	2.28	0.49
1:E:5:GLU:OE1	1:E:10:ARG:NH2	2.45	0.49
3:A:1236:ARG:HD2	3:A:1239:ARG:NH2	2.27	0.49
5:D:1:NAG:H83	5:D:2:NAG:O7	2.12	0.49
4:F:205:LEU:HD21	4:F:492:VAL:HG23	1.95	0.49
4:F:206:LEU:HD23	4:F:458:LEU:HD23	1.93	0.49
4:F:481:LEU:HD23	4:F:482:LYS:N	2.22	0.49
1:E:131:LYS:HB3	1:E:133:ARG:NE	2.28	0.49
3:A:976:LYS:CD	4:F:547:ARG:NH1	2.75	0.49
3:A:358:GLN:HA	3:A:361:GLU:HG2	1.95	0.49
4:F:256:MET:HE2	4:F:258:ILE:HD11	1.94	0.49
4:F:460:LEU:HD13	4:F:529:LEU:CD1	2.42	0.49
1:E:19:GLY:HA3	1:E:191:LEU:HD22	1.95	0.48
2:C:281:GLY:HA3	2:C:388:TYR:CD1	2.48	0.48
4:F:57:LEU:HD23	4:F:801:VAL:HG21	1.94	0.48
4:F:281:MET:O	4:F:284:THR:HB	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:477:ASN:N	4:F:477:ASN:ND2	2.60	0.48
4:F:516:ALA:HB3	4:F:525:LEU:N	2.28	0.48
3:A:326:LEU:O	3:A:330:LEU:HB2	2.12	0.48
4:F:216:LEU:HD13	4:F:216:LEU:O	2.12	0.48
4:F:348:ASN:C	4:F:350:ASN:H	2.16	0.48
4:F:710:LEU:HD23	4:F:710:LEU:O	2.12	0.48
3:A:440:LEU:O	3:A:444:LEU:CG	2.55	0.48
4:F:151:PHE:CZ	4:F:224:PRO:HD3	2.48	0.48
1:E:136:LEU:O	1:E:139:PRO:HG2	2.14	0.48
3:A:357:GLN:HG2	3:A:670:LEU:HD11	1.94	0.48
3:A:848:VAL:HA	3:A:851:MET:HG2	1.95	0.48
4:F:562:ASP:OD1	4:F:563:PHE:N	2.46	0.48
4:F:627:PRO:HG2	4:F:630:SER:HB3	1.94	0.48
1:E:146:PHE:CZ	3:A:1238:PHE:CE1	3.01	0.48
2:C:289:VAL:HG13	2:C:400:LEU:HD21	1.94	0.48
4:F:357:ASN:ND2	4:F:1064:ASP:CB	2.76	0.48
4:F:481:LEU:CD2	4:F:482:LYS:H	2.22	0.48
1:E:107:ALA:HB2	1:E:157:VAL:HG12	1.95	0.48
1:E:212:TRP:HB3	3:A:1091:TYR:HD1	1.63	0.48
4:F:161:VAL:HG23	4:F:223:SER:OG	2.14	0.48
4:F:34:LYS:HD2	4:F:1009:GLU:OE2	2.13	0.48
4:F:365:ASP:O	4:F:394:HIS:CE1	2.67	0.48
1:E:124:CYS:HB2	1:E:140:ALA:CB	2.41	0.48
4:F:889:LEU:HA	4:F:892:ILE:HG12	1.95	0.48
2:C:397:LEU:O	2:C:400:LEU:HB3	2.14	0.47
1:E:212:TRP:HA	3:A:1091:TYR:CZ	2.35	0.47
2:C:393:SER:HB3	2:C:396:VAL:HG22	1.95	0.47
4:F:390:SER:HB2	4:F:412:TYR:OH	2.14	0.47
4:F:669:TYR:HE1	4:F:708:VAL:HG21	1.78	0.47
3:A:41:ARG:HG2	3:A:42:LYS:N	2.29	0.47
3:A:46:SER:CB	3:A:107:ALA:HB1	2.41	0.47
4:F:191:LEU:HD22	4:F:490:MET:HE1	1.95	0.47
4:F:284:THR:CG2	4:F:428:TYR:OH	2.62	0.47
4:F:285:LEU:CD1	4:F:291:VAL:HG21	2.45	0.47
1:E:119:ILE:HG13	1:E:119:ILE:H	1.55	0.47
4:F:51:ALA:HB3	4:F:817:ILE:HD11	1.96	0.47
4:F:262:VAL:HG23	4:F:297:ASN:HB3	1.96	0.47
4:F:720:GLN:O	4:F:724:SER:OG	2.32	0.47
1:E:107:ALA:HB2	1:E:157:VAL:CG1	2.44	0.47
2:C:276:PRO:HG2	2:C:384:PRO:HB3	1.97	0.47
3:A:356:LYS:HE2	3:A:359:LEU:HD13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1338:CYS:SG	3:A:1352:CYS:HB2	2.54	0.47
3:A:1466:THR:O	3:A:1470:LEU:N	2.46	0.47
3:A:1359:TYR:O	3:A:1363:SER:HB3	2.14	0.47
4:F:570:ASN:ND2	4:F:592:THR:HG22	2.30	0.47
4:F:711:ASP:OD2	4:F:739:THR:CG2	2.63	0.47
4:F:824:TRP:CB	4:F:864:MET:HE3	2.43	0.47
3:A:291:MET:HB3	3:A:1321:THR:HG23	1.97	0.47
3:A:333:LEU:HD21	3:A:653:LEU:HB3	1.96	0.47
4:F:532:LYS:HZ3	4:F:532:LYS:HB3	1.80	0.47
4:F:710:LEU:HD21	4:F:714:PHE:CE1	2.46	0.47
4:F:710:LEU:CD2	4:F:714:PHE:CE1	2.98	0.47
3:A:449:ILE:HG21	3:A:532:LEU:CD2	2.45	0.47
4:F:259:LEU:HD11	4:F:342:ALA:HB2	1.95	0.47
4:F:285:LEU:HD11	4:F:291:VAL:HG21	1.97	0.47
4:F:510:PRO:CG	4:F:767:TYR:HE2	2.22	0.47
2:C:437:ASN:HD22	3:A:361:GLU:HB2	1.69	0.47
4:F:33:ILE:HG23	4:F:1018:PHE:CE2	2.50	0.47
4:F:370:ARG:HD2	4:F:372:GLN:HE21	1.78	0.47
4:F:669:TYR:CE1	4:F:708:VAL:HG21	2.50	0.47
4:F:781:PRO:CD	4:F:795:ILE:HG13	2.45	0.47
4:F:54:VAL:HG22	4:F:815:VAL:HG21	1.97	0.47
4:F:896:ALA:HB2	4:F:987:ASP:HB3	1.95	0.47
4:F:1010:LYS:HG3	4:F:1017:ILE:CD1	2.45	0.47
5:G:1:NAG:H62	5:G:2:NAG:HN2	1.80	0.47
2:C:292:MET:SD	2:C:404:ARG:NH2	2.88	0.46
3:A:170:LEU:HD12	3:A:173:LEU:HD12	1.98	0.46
3:A:186:LEU:HG	3:A:565:LEU:HD11	1.97	0.46
3:A:1447:ARG:HG2	3:A:1451:MET:HG2	1.97	0.46
4:F:466:LEU:HD12	4:F:467:PRO:HD2	1.97	0.46
4:F:1070:ASP:OD2	4:F:1072:THR:HG22	2.14	0.46
3:A:289:ILE:HD12	3:A:317:LEU:HD11	1.92	0.46
3:A:556:ILE:HA	3:A:559:ILE:HB	1.97	0.46
4:F:711:ASP:OD2	4:F:739:THR:HG23	2.15	0.46
3:A:1369:ALA:O	3:A:1373:ILE:CG2	2.59	0.46
3:A:245:CYS:HG	3:A:261:CYS:HG	0.47	0.46
3:A:1292:ILE:HD13	3:A:1352:CYS:HB3	1.98	0.46
4:F:33:ILE:HG21	4:F:1007:HIS:CE1	2.50	0.46
4:F:133:LEU:HD23	4:F:133:LEU:N	2.29	0.46
4:F:234:LYS:HB2	4:F:551:GLN:HG2	1.96	0.46
3:A:892:VAL:HG12	3:A:894:LYS:H	1.81	0.46
3:A:973:TYR:HB3	3:A:983:MET:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:364:THR:O	4:F:390:SER:HA	2.15	0.46
4:F:516:ALA:CB	4:F:524:LEU:HB3	2.46	0.46
4:F:1012:MET:O	4:F:1013:ASN:CB	2.63	0.46
1:E:205:PRO:O	1:E:206:ARG:HG2	2.16	0.46
4:F:283:GLU:OE1	4:F:283:GLU:HA	2.16	0.46
4:F:628:THR:O	4:F:629:TYR:CD2	2.68	0.46
4:F:846:ARG:HH12	4:F:868:ASP:CB	2.27	0.46
2:B:129:GLU:N	2:B:132:ASP:OD2	2.47	0.46
3:A:196:LEU:HD11	3:A:332:VAL:CG1	2.43	0.46
3:A:335:GLY:HA3	3:A:1387:LEU:O	2.16	0.46
4:F:126:TYR:HE1	4:F:144:SER:HB2	1.81	0.46
4:F:178:SER:CB	4:F:181:VAL:HG12	2.28	0.46
4:F:856:LEU:HD21	4:F:878:PHE:CG	2.51	0.46
4:F:895:TYR:CE1	4:F:986:PHE:CE1	3.03	0.46
1:E:110:ILE:HD11	3:A:1199:LEU:HG	1.98	0.46
2:B:99:LYS:NZ	2:B:138:GLU:OE1	2.40	0.46
4:F:629:TYR:HB2	4:F:809:LEU:HD23	1.98	0.46
4:F:792:GLU:H	4:F:792:GLU:CD	2.12	0.46
2:C:288:GLU:HB3	2:C:404:ARG:HH21	1.81	0.46
1:E:134:ASP:O	1:E:137:LEU:CB	2.64	0.46
3:A:94:LEU:HD11	3:A:134:VAL:HG12	1.97	0.46
3:A:976:LYS:CE	4:F:547:ARG:NH1	2.75	0.46
4:F:41:GLN:HB3	4:F:1011:LEU:HB3	1.97	0.46
4:F:320:LEU:O	4:F:324:VAL:HG23	2.16	0.46
4:F:607:ARG:HA	4:F:607:ARG:HD3	1.80	0.46
1:E:149:LEU:CD1	3:A:1234:PHE:HE2	2.10	0.45
4:F:539:PRO:HD3	4:F:977:CYS:HB3	1.98	0.45
2:C:436:GLU:HG2	2:C:441:ASP:HB3	1.98	0.45
3:A:548:LEU:O	3:A:552:LEU:N	2.42	0.45
4:F:161:VAL:HG22	4:F:162:SER:N	2.30	0.45
4:F:285:LEU:HD13	4:F:291:VAL:HB	1.99	0.45
4:F:362:LEU:HD12	4:F:362:LEU:O	2.16	0.45
4:F:784:ASN:HB3	4:F:785:LYS:H	1.59	0.45
1:E:35:LEU:HG	1:E:37:PRO:HD3	1.98	0.45
2:C:437:ASN:ND2	3:A:361:GLU:OE1	2.49	0.45
4:F:548:PRO:O	4:F:549:ASN:HB3	2.17	0.45
7:L:1:NAG:H61	7:L:2:NAG:O5	2.16	0.45
1:E:209:GLN:CD	3:A:1262:LYS:CG	2.84	0.45
2:C:393:SER:HB3	2:C:396:VAL:HG21	1.99	0.45
4:F:628:THR:O	4:F:629:TYR:CG	2.69	0.45
3:A:256:ILE:HG23	3:A:257:ASN:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:336:LYS:HG3	4:F:369:GLU:OE2	2.16	0.45
4:F:75:ALA:O	4:F:79:VAL:HG23	2.17	0.45
4:F:79:VAL:HG12	4:F:612:THR:HG22	1.99	0.45
4:F:319:VAL:HG21	4:F:1046:PRO:HG3	1.98	0.45
4:F:705:ILE:CD1	4:F:706:ASN:N	2.79	0.45
2:C:275:ARG:NH2	2:C:384:PRO:O	2.50	0.45
2:C:426:PRO:HA	2:C:427:PRO:HD3	1.90	0.45
4:F:41:GLN:OE1	4:F:1012:MET:O	2.34	0.45
4:F:771:LEU:O	4:F:811:LYS:NZ	2.49	0.45
4:F:773:ASN:HD22	4:F:777:VAL:CG2	2.30	0.45
1:E:35:LEU:HB3	1:E:49:ALA:H	1.81	0.45
4:F:27:PHE:CE1	4:F:1020:MET:HG2	2.52	0.45
4:F:368:GLU:O	4:F:368:GLU:HG2	2.16	0.45
3:A:86:LEU:HD13	3:A:89:LEU:HD23	1.97	0.45
3:A:947:VAL:O	3:A:951:LYS:HB2	2.16	0.45
4:F:511:ASN:HB2	4:F:627:PRO:HG3	1.99	0.45
4:F:516:ALA:HB3	4:F:525:LEU:H	1.82	0.45
4:F:523:VAL:CG2	4:F:526:HIS:HB2	2.46	0.45
4:F:1001:ASN:HD22	9:F:1121:NAG:C1	2.08	0.45
4:F:1006:PHE:O	4:F:1006:PHE:CD1	2.70	0.45
3:A:1338:CYS:SG	3:A:1352:CYS:CB	3.02	0.45
4:F:304:SER:HB2	4:F:305:CYS:H	1.54	0.45
4:F:821:VAL:O	4:F:825:ILE:HG13	2.17	0.45
4:F:292:ASN:OD1	4:F:293:VAL:N	2.47	0.44
4:F:515:PHE:CZ	4:F:623:ALA:HB3	2.52	0.44
4:F:669:TYR:CD1	4:F:704:LEU:HD21	2.37	0.44
1:E:217:ASP:O	1:E:218:ALA:O	2.35	0.44
3:A:588:GLU:HG2	4:F:268:GLY:O	2.17	0.44
3:A:1052:ILE:HD13	3:A:1052:ILE:HA	1.89	0.44
4:F:576:ILE:HD11	4:F:588:LYS:HG2	1.99	0.44
4:F:702:THR:HG23	4:F:703:ASP:N	2.32	0.44
4:F:867:HIS:O	4:F:868:ASP:HB3	2.16	0.44
4:F:1010:LYS:CG	4:F:1017:ILE:CD1	2.95	0.44
4:F:214:THR:HG22	4:F:214:THR:O	2.16	0.44
3:A:600:PHE:O	3:A:604:LEU:HB2	2.17	0.44
3:A:931:ILE:CD1	3:A:1060:PHE:HD1	2.28	0.44
3:A:1233:ALA:HA	3:A:1236:ARG:HE	1.83	0.44
3:A:908:ILE:HG22	3:A:914:LEU:HD13	1.98	0.44
3:A:938:LEU:CD2	3:A:1052:ILE:HD11	2.47	0.44
4:F:94:SER:O	4:F:98:VAL:HG23	2.17	0.44
4:F:381:ASP:OD1	4:F:381:ASP:N	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:669:TYR:HD1	4:F:704:LEU:CD2	2.24	0.44
4:F:739:THR:HG22	4:F:743:ILE:O	2.17	0.44
4:F:824:TRP:CD2	4:F:864:MET:HE3	2.53	0.44
1:E:110:ILE:HD13	1:E:110:ILE:HA	1.78	0.44
3:A:289:ILE:HD12	3:A:317:LEU:HG	2.00	0.44
3:A:454:HIS:HB3	3:A:998:ASP:OD2	2.17	0.44
3:A:1383:ASN:O	3:A:1387:LEU:HD13	2.18	0.44
4:F:465:THR:HG22	4:F:466:LEU:N	2.32	0.44
4:F:803:ILE:HD12	4:F:805:ILE:HD11	1.99	0.44
1:E:152:PHE:CE1	3:A:309:TRP:HZ2	2.35	0.44
3:A:539:THR:HA	3:A:542:TRP:HD1	1.82	0.44
3:A:1276:MET:O	3:A:1280:ILE:HG13	2.17	0.44
4:F:182:LEU:HD22	4:F:182:LEU:HA	1.80	0.44
4:F:704:LEU:HD23	4:F:704:LEU:O	2.18	0.44
3:A:981:THR:HB	4:F:546:ARG:HH12	1.82	0.44
4:F:243:ARG:HA	4:F:243:ARG:HD2	1.74	0.44
3:A:331:GLY:N	3:A:1380:ILE:HD11	2.32	0.43
3:A:958:ASN:HD22	3:A:988:ARG:HA	1.83	0.43
4:F:826:GLU:OE1	4:F:826:GLU:HA	2.17	0.43
5:D:1:NAG:H82	5:D:1:NAG:H3	2.00	0.43
3:A:1244:ILE:N	3:A:1244:ILE:HD13	2.33	0.43
4:F:198:ASN:HB2	4:F:208:GLN:OE1	2.18	0.43
4:F:253:PRO:O	4:F:356:CYS:HB3	2.19	0.43
4:F:481:LEU:HD23	4:F:481:LEU:N	2.33	0.43
2:C:389:ILE:CG1	3:A:369:TRP:CZ3	3.01	0.43
3:A:215:LEU:CD2	3:A:219:LYS:HD3	2.39	0.43
4:F:350:ASN:CG	5:D:1:NAG:C1	2.85	0.43
4:F:390:SER:CB	4:F:412:TYR:OH	2.66	0.43
2:C:279:LEU:CD2	2:C:387:VAL:CG1	2.96	0.43
3:A:289:ILE:HD12	3:A:317:LEU:CG	2.48	0.43
3:A:1100:CYS:HB3	3:A:1102:ILE:HD12	2.00	0.43
4:F:208:GLN:O	4:F:219:TYR:HA	2.18	0.43
4:F:516:ALA:HB3	4:F:524:LEU:HB3	2.01	0.43
2:C:296:ALA:HB2	3:A:369:TRP:C	2.29	0.43
2:C:361:LEU:HB3	2:C:458:HIS:HE2	1.84	0.43
3:A:341:ARG:HG3	3:A:345:LYS:HB2	1.99	0.43
4:F:169:HIS:CE1	4:F:238:TYR:HD1	2.36	0.43
4:F:281:MET:CE	4:F:363:PHE:HZ	2.31	0.43
4:F:513:TYR:CZ	4:F:625:VAL:HG21	2.54	0.43
3:A:1318:ARG:CD	3:A:1328:ILE:HD11	2.47	0.43
4:F:1010:LYS:HG2	4:F:1017:ILE:CG1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:32:TRP:HH2	1:E:53:LEU:HG	1.83	0.43
3:A:996:HIS:ND1	3:A:998:ASP:HB2	2.34	0.43
3:A:1296:ASP:OD1	3:A:1302:ARG:NH1	2.52	0.43
3:A:1406:TRP:HZ2	3:A:1415:GLY:O	2.01	0.43
4:F:100:LEU:HD12	4:F:194:VAL:HG12	2.00	0.43
4:F:400:PRO:O	4:F:404:MET:HG3	2.18	0.43
4:F:532:LYS:H	4:F:532:LYS:HG3	1.56	0.43
4:F:733:LYS:HE3	4:F:733:LYS:HB2	1.82	0.43
1:E:20:ILE:HG13	1:E:118:LEU:HD22	1.86	0.43
3:A:224:LYS:HG2	3:A:263:GLY:CA	2.49	0.43
3:A:822:ILE:HG13	3:A:823:ARG:HG3	2.01	0.43
3:A:914:LEU:HD21	3:A:1272:LEU:CD2	2.48	0.43
4:F:133:LEU:H	4:F:133:LEU:HD22	1.80	0.43
4:F:346:LEU:HD21	4:F:360:ILE:CG2	2.49	0.43
4:F:661:TYR:HD2	4:F:752:GLY:HA3	1.83	0.43
3:A:420:VAL:HG13	3:A:423:TRP:CD2	2.53	0.43
3:A:542:TRP:CZ3	3:A:933:LEU:HB2	2.54	0.43
4:F:33:ILE:CG2	4:F:1007:HIS:CE1	3.02	0.43
4:F:205:LEU:HD23	4:F:206:LEU:N	2.34	0.43
4:F:781:PRO:O	4:F:875:GLY:CA	2.60	0.43
4:F:824:TRP:HB3	4:F:864:MET:CE	2.48	0.43
1:E:127:MET:CG	1:E:136:LEU:HD23	2.35	0.43
1:E:205:PRO:O	1:E:206:ARG:CB	2.67	0.43
2:C:445:HIS:HB2	3:A:685:LYS:HE2	2.01	0.43
3:A:475:PHE:HE2	3:A:534:ARG:HD3	1.84	0.43
3:A:921:VAL:CG1	3:A:1370:PHE:CE2	2.77	0.43
3:A:971:TYR:HB3	3:A:985:LEU:HD11	2.01	0.43
4:F:41:GLN:CB	4:F:1011:LEU:HB3	2.49	0.43
4:F:44:LEU:HD11	4:F:824:TRP:HZ2	1.82	0.43
4:F:242:ARG:NH2	4:F:280:GLU:O	2.52	0.43
3:A:118:LEU:HD22	3:A:124:VAL:HG22	2.01	0.42
2:C:293:MET:HA	3:A:369:TRP:HB3	2.01	0.42
3:A:1125:PHE:HE2	3:A:1249:ARG:HB2	1.84	0.42
4:F:346:LEU:HD12	4:F:346:LEU:HA	1.86	0.42
4:F:590:PHE:CD1	4:F:590:PHE:N	2.87	0.42
4:F:988:ASN:OD1	9:F:1122:NAG:O5	2.37	0.42
3:A:1114:VAL:O	3:A:1117:SER:OG	2.27	0.42
4:F:41:GLN:HB3	4:F:1011:LEU:CG	2.49	0.42
4:F:319:VAL:CG2	4:F:1046:PRO:HG3	2.49	0.42
3:A:333:LEU:HD23	3:A:657:LEU:HD22	2.02	0.42
3:A:959:ASP:HB3	3:A:972:TYR:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1106:PRO:HA	3:A:1109:TYR:HB3	2.01	0.42
4:F:981:GLN:HG2	4:F:1038:GLU:HG2	2.01	0.42
1:E:218:ALA:CB	3:A:1098:LEU:CA	2.55	0.42
4:F:1008:VAL:HB	4:F:1019:ILE:HG22	2.02	0.42
1:E:4:THR:CB	1:E:134:ASP:OD2	2.68	0.42
1:E:32:TRP:CH2	1:E:53:LEU:HG	2.54	0.42
1:E:205:PRO:C	1:E:206:ARG:HG2	2.40	0.42
3:A:447:LEU:C	3:A:447:LEU:CD1	2.86	0.42
3:A:452:GLU:OE2	3:A:528:ARG:NH2	2.53	0.42
4:F:471:ILE:O	4:F:471:ILE:HG13	2.18	0.42
5:K:1:NAG:H82	5:K:2:NAG:C2	2.47	0.42
4:F:212:SER:CB	4:F:216:LEU:O	2.67	0.42
4:F:1005:ILE:HG23	4:F:1005:ILE:O	2.19	0.42
4:F:1011:LEU:CD1	4:F:1011:LEU:H	2.33	0.42
1:E:146:PHE:CE1	3:A:1235:PHE:CE1	3.05	0.42
2:C:396:VAL:HG23	3:A:366:TYR:OH	2.20	0.42
3:A:850:LYS:O	3:A:853:THR:OG1	2.28	0.42
3:A:1150:SER:O	3:A:1154:ASN:OD1	2.37	0.42
4:F:704:LEU:O	4:F:708:VAL:HG23	2.20	0.42
3:A:368:SER:HA	3:A:371:THR:HG22	2.02	0.42
4:F:178:SER:O	4:F:181:VAL:CG1	2.68	0.42
2:B:108:ASN:ND2	2:C:266:PRO:O	2.53	0.42
4:F:206:LEU:CD2	4:F:495:SER:HB2	2.49	0.42
4:F:478:LYS:HD3	4:F:479:THR:HG23	2.01	0.42
4:F:1066:ASN:HD22	4:F:1067:VAL:N	2.17	0.42
3:A:195:PRO:HB2	3:A:196:LEU:HD12	2.00	0.41
3:A:796:VAL:HA	3:A:801:PHE:CG	2.55	0.41
4:F:481:LEU:CD2	4:F:481:LEU:H	2.33	0.41
4:F:570:ASN:ND2	4:F:592:THR:HG21	2.34	0.41
4:F:844:CYS:HB3	4:F:866:ASN:HD21	1.85	0.41
3:A:819:GLU:OE2	3:A:897:ARG:NH2	2.53	0.41
3:A:1060:PHE:O	3:A:1064:VAL:HG23	2.20	0.41
4:F:509:CYS:HB2	4:F:510:PRO:CD	2.49	0.41
4:F:510:PRO:HG3	4:F:762:TYR:CD1	2.55	0.41
1:E:60:ARG:NE	1:E:77:GLU:OE1	2.49	0.41
2:B:136:ILE:HA	2:B:147:GLY:HA3	2.01	0.41
3:A:1383:ASN:ND2	3:A:1383:ASN:N	2.69	0.41
2:C:427:PRO:HA	2:C:430:PHE:HD2	1.86	0.41
3:A:679:GLU:HG3	3:A:682:LYS:HD2	2.03	0.41
1:E:163:LYS:HA	1:E:163:LYS:HD2	1.31	0.41
2:C:396:VAL:CB	3:A:366:TYR:OH	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:122:TRP:HH2	3:A:186:LEU:HD12	1.84	0.41
4:F:629:TYR:C	4:F:629:TYR:HD1	2.23	0.41
2:C:281:GLY:CA	2:C:422:LEU:HD13	2.28	0.41
3:A:942:PHE:HE2	3:A:1051:LEU:HD22	1.85	0.41
3:A:958:ASN:HB2	3:A:989:GLN:H	1.86	0.41
3:A:1144:GLU:OE2	3:A:1148:HIS:NE2	2.53	0.41
4:F:369:GLU:HG2	4:F:371:ALA:H	1.85	0.41
4:F:705:ILE:HD12	4:F:706:ASN:CA	2.51	0.41
4:F:851:MET:HA	4:F:1023:SER:N	2.36	0.41
2:B:137:LYS:N	2:B:146:ILE:O	2.54	0.41
2:C:450:LEU:HA	2:C:453:TYR:HB3	2.02	0.41
4:F:58:VAL:HG13	4:F:803:ILE:HG22	2.01	0.41
4:F:817:ILE:HG21	4:F:817:ILE:HD13	1.86	0.41
3:A:132:LEU:HD12	3:A:132:LEU:HA	1.85	0.41
4:F:61:TYR:O	4:F:68:TYR:OH	2.24	0.41
4:F:230:ARG:N	4:F:230:ARG:CD	2.82	0.41
4:F:232:PRO:HB2	4:F:234:LYS:HD3	2.01	0.41
4:F:290:PHE:HD1	4:F:354:ALA:HB2	1.86	0.41
4:F:361:MET:HE2	4:F:387:PHE:HB2	2.02	0.41
1:E:209:GLN:OE1	3:A:1262:LYS:HG2	2.21	0.41
3:A:599:ASN:CB	3:A:601:PRO:HD2	2.50	0.41
4:F:185:LEU:O	4:F:189:SER:OG	2.36	0.41
4:F:191:LEU:CD2	4:F:490:MET:HE1	2.51	0.41
4:F:346:LEU:CD2	4:F:360:ILE:CG2	2.98	0.41
4:F:351:VAL:HG23	4:F:353:ARG:HG3	2.03	0.41
4:F:579:LYS:HE2	4:F:579:LYS:HB2	1.85	0.41
2:C:437:ASN:CB	3:A:361:GLU:O	2.67	0.41
3:A:1059:ILE:O	3:A:1059:ILE:CG2	2.69	0.41
5:K:1:NAG:H83	5:K:1:NAG:H2	1.91	0.41
3:A:176:VAL:HG23	3:A:182:LEU:HB3	2.02	0.40
4:F:114:ARG:HH21	6:H:1:NAG:C6	2.30	0.40
4:F:151:PHE:CE2	4:F:224:PRO:HD3	2.56	0.40
4:F:217:ALA:HB2	4:F:240:VAL:CG2	2.50	0.40
4:F:274:ILE:CG1	4:F:391:VAL:HG21	2.51	0.40
4:F:477:ASN:N	4:F:477:ASN:HD22	2.18	0.40
4:F:729:ILE:CG2	7:L:2:NAG:H82	2.51	0.40
4:F:847:ASN:ND2	4:F:847:ASN:C	2.73	0.40
4:F:889:LEU:HD12	4:F:889:LEU:HA	1.88	0.40
3:A:503:VAL:HG13	3:A:534:ARG:HG2	2.04	0.40
4:F:43:ASP:OD2	7:L:1:NAG:C1	2.70	0.40
4:F:262:VAL:HG22	4:F:296:PHE:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:272:ILE:HD13	3:A:630:PRO:HG3	2.04	0.40
3:A:1007:LEU:HA	3:A:1010:VAL:HG13	2.04	0.40
4:F:780:ALA:HA	4:F:863:LEU:HD21	2.04	0.40
2:C:295:LYS:CD	3:A:373:GLY:O	2.70	0.40
3:A:210:TYR:CG	3:A:317:LEU:HD13	2.56	0.40
3:A:1100:CYS:SG	3:A:1102:ILE:HD11	2.62	0.40
3:A:1406:TRP:CZ2	3:A:1417:ILE:HG23	2.56	0.40
4:F:887:ARG:O	4:F:890:VAL:CG2	2.62	0.40
2:C:398:GLN:HA	2:C:401:ILE:HD12	2.02	0.40
3:A:982:GLN:HG2	4:F:550:VAL:HG21	2.04	0.40
3:A:1029:GLU:O	3:A:1029:GLU:HG2	2.21	0.40
4:F:315:ARG:HD3	4:F:315:ARG:HA	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	159/222 (72%)	147 (92%)	9 (6%)	3 (2%)	8	20
2	B	98/450 (22%)	89 (91%)	9 (9%)	0	100	100
2	C	174/450 (39%)	162 (93%)	12 (7%)	0	100	100
3	A	1260/1873 (67%)	1181 (94%)	76 (6%)	3 (0%)	47	73
4	F	968/1046 (92%)	876 (90%)	86 (9%)	6 (1%)	25	50
All	All	2659/4041 (66%)	2455 (92%)	192 (7%)	12 (0%)	32	54

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	206	ARG
3	A	1101	TYR

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Mol	Chain	Res	Type
4	F	349	TYR
1	E	218	ALA
3	A	1174	ALA
4	F	629	TYR
4	F	661	TYR
4	F	790	ALA
4	F	549	ASN
3	A	1098	LEU
4	F	627	PRO
1	E	37	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	143/192 (74%)	128 (90%)	15 (10%)	7	16
2	B	58/391 (15%)	57 (98%)	1 (2%)	60	84
2	C	143/391 (37%)	141 (99%)	2 (1%)	67	86
3	A	1097/1628 (67%)	1039 (95%)	58 (5%)	22	48
4	F	868/924 (94%)	797 (92%)	71 (8%)	11	26
All	All	2309/3526 (66%)	2162 (94%)	147 (6%)	21	39

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	82	TYR
1	E	105	ILE
1	E	110	ILE
1	E	118	LEU
1	E	119	ILE
1	E	127	MET
1	E	131	LYS
1	E	132	LYS
1	E	133	ARG

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Mol	Chain	Res	Type
1	E	134	ASP
1	E	137	LEU
1	E	141	SER
1	E	158	MET
1	E	163	LYS
1	E	215	CYS
2	B	115	PRO
2	C	396	VAL
2	C	437	ASN
3	A	38	ASN
3	A	41	ARG
3	A	42	LYS
3	A	64	ASN
3	A	132	LEU
3	A	143	ASN
3	A	215	LEU
3	A	225	THR
3	A	226	CYS
3	A	239	ASN
3	A	252	ARG
3	A	289	ILE
3	A	327	ASN
3	A	359	LEU
3	A	423	TRP
3	A	445	ASN
3	A	455	ASN
3	A	543	THR
3	A	584	ARG
3	A	617	ASN
3	A	912	LYS
3	A	931	ILE
3	A	935	THR
3	A	937	LEU
3	A	938	LEU
3	A	939	GLN
3	A	941	MET
3	A	983	MET
3	A	988	ARG
3	A	998	ASP
3	A	1010	VAL
3	A	1014	GLU
3	A	1029	GLU

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Mol	Chain	Res	Type
3	A	1031	MET
3	A	1037	ASN
3	A	1051	LEU
3	A	1059	ILE
3	A	1098	LEU
3	A	1131	ASN
3	A	1237	LEU
3	A	1243	LEU
3	A	1262	LYS
3	A	1272	LEU
3	A	1295	VAL
3	A	1302	ARG
3	A	1318	ARG
3	A	1323	GLU
3	A	1333	SER
3	A	1337	LEU
3	A	1352	CYS
3	A	1373	ILE
3	A	1381	MET
3	A	1382	ASP
3	A	1383	ASN
3	A	1385	ASP
3	A	1416	ARG
3	A	1427	ARG
3	A	1464	ASN
4	F	40	MET
4	F	93	ARG
4	F	133	LEU
4	F	158	ARG
4	F	181	VAL
4	F	182	LEU
4	F	186	ASN
4	F	197	LYS
4	F	205	LEU
4	F	216	LEU
4	F	230	ARG
4	F	234	LYS
4	F	237	LEU
4	F	243	ARG
4	F	254	LYS
4	F	269	LEU
4	F	270	THR

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Mol	Chain	Res	Type
4	F	302	ASP
4	F	303	VAL
4	F	315	ARG
4	F	318	LYS
4	F	346	LEU
4	F	361	MET
4	F	381	ASP
4	F	406	CYS
4	F	407	GLU
4	F	411	TYR
4	F	422	ARG
4	F	441	ASP
4	F	442	LYS
4	F	471	ILE
4	F	472	THR
4	F	474	GLN
4	F	476	GLU
4	F	477	ASN
4	F	480	ASN
4	F	505	ARG
4	F	508	LEU
4	F	520	ASN
4	F	525	LEU
4	F	528	ASN
4	F	530	GLN
4	F	532	LYS
4	F	542	ASN
4	F	577	ARG
4	F	593	LEU
4	F	629	TYR
4	F	657	GLU
4	F	658	GLU
4	F	662	THR
4	F	707	ARG
4	F	710	LEU
4	F	743	ILE
4	F	744	THR
4	F	785	LYS
4	F	793	SER
4	F	847	ASN
4	F	849	ASP
4	F	850	VAL

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Mol	Chain	Res	Type
4	F	851	MET
4	F	853	CYS
4	F	987	ASP
4	F	988	ASN
4	F	989	ASP
4	F	990	SER
4	F	991	LYS
4	F	1013	ASN
4	F	1062	CYS
4	F	1065	ASN
4	F	1066	ASN
4	F	1068	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	50	HIS
3	A	38	ASN
3	A	143	ASN
3	A	183	GLN
3	A	239	ASN
3	A	274	HIS
3	A	418	ASN
3	A	455	ASN
3	A	617	ASN
3	A	869	ASN
3	A	930	ASN
3	A	939	GLN
3	A	1058	ASN
3	A	1108	GLN
3	A	1138	GLN
3	A	1287	GLN
3	A	1374	ASN
3	A	1383	ASN
3	A	1464	ASN
4	F	56	GLN
4	F	108	GLN
4	F	228	ASN
4	F	299	ASN
4	F	357	ASN
4	F	372	GLN
4	F	395	ASN

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Mol	Chain	Res	Type
4	F	450	ASN
4	F	477	ASN
4	F	511	ASN
4	F	520	ASN
4	F	530	GLN
4	F	552	ASN
4	F	570	ASN
4	F	678	ASN
4	F	697	ASN
4	F	773	ASN
4	F	847	ASN
4	F	866	ASN
4	F	988	ASN
4	F	1001	ASN
4	F	1013	ASN
4	F	1065	ASN
4	F	1066	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

17 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	D	1	5	14,14,15	0.29	0	17,19,21	1.02	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	D	2	5	14,14,15	0.31	0	17,19,21	0.54	0
5	NAG	G	1	5,4	14,14,15	0.31	0	17,19,21	0.61	0
5	NAG	G	2	5	14,14,15	0.29	0	17,19,21	0.61	0
6	NAG	H	1	6,4	14,14,15	0.71	1 (7%)	17,19,21	0.70	0
6	NAG	H	2	6	14,14,15	0.37	0	17,19,21	0.77	0
6	BMA	H	3	6	11,11,12	0.75	0	15,15,17	0.97	1 (6%)
6	NAG	I	1	6,4	14,14,15	0.83	1 (7%)	17,19,21	0.83	0
6	NAG	I	2	6	14,14,15	1.60	1 (7%)	17,19,21	0.92	1 (5%)
6	BMA	I	3	6	11,11,12	0.93	0	15,15,17	1.05	1 (6%)
5	NAG	J	1	5,4	14,14,15	0.53	0	17,19,21	0.62	0
5	NAG	J	2	5	14,14,15	0.31	0	17,19,21	0.39	0
5	NAG	K	1	5	14,14,15	0.29	0	17,19,21	0.66	0
5	NAG	K	2	5	14,14,15	0.29	0	17,19,21	0.58	0
7	NAG	L	1	7,4	14,14,15	0.29	0	17,19,21	0.65	0
7	NAG	L	2	7	14,14,15	0.31	0	17,19,21	0.69	0
7	NAG	L	3	7	14,14,15	0.27	0	17,19,21	1.33	1 (5%)

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
5	NAG	D	1	5	-	5/6/23/26	0/1/1/1
5	NAG	D	2	5	-	2/6/23/26	0/1/1/1
5	NAG	G	1	5,4	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	3/6/23/26	0/1/1/1
6	NAG	H	1	6,4	-	0/6/23/26	0/1/1/1
6	NAG	H	2	6	-	2/6/23/26	0/1/1/1
6	BMA	H	3	6	-	0/2/19/22	0/1/1/1
6	NAG	I	1	6,4	-	2/6/23/26	0/1/1/1
6	NAG	I	2	6	-	2/6/23/26	0/1/1/1
6	BMA	I	3	6	-	2/2/19/22	0/1/1/1
5	NAG	J	1	5,4	-	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	0/6/23/26	0/1/1/1
5	NAG	K	1	5	-	4/6/23/26	0/1/1/1
5	NAG	K	2	5	-	6/6/23/26	0/1/1/1
7	NAG	L	1	7,4	-	2/6/23/26	0/1/1/1
7	NAG	L	2	7	-	5/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	L	3	7	-	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	I	2	NAG	O5-C1	-5.83	1.34	1.43
6	I	1	NAG	O5-C1	-2.62	1.39	1.43
6	H	1	NAG	O5-C1	-2.33	1.40	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	3	NAG	C1-O5-C5	4.34	118.08	112.19
5	D	1	NAG	C3-C4-C5	2.52	114.73	110.24
6	H	3	BMA	C1-O5-C5	2.47	115.53	112.19
6	I	2	NAG	C4-C3-C2	2.28	114.35	111.02
6	I	3	BMA	O5-C1-C2	-2.01	107.66	110.77

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1	NAG	C8-C7-N2-C2
5	D	1	NAG	O7-C7-N2-C2
5	K	1	NAG	C8-C7-N2-C2
5	K	1	NAG	O7-C7-N2-C2
7	L	1	NAG	C8-C7-N2-C2
7	L	1	NAG	O7-C7-N2-C2
7	L	3	NAG	C1-C2-N2-C7
7	L	3	NAG	C8-C7-N2-C2
7	L	3	NAG	O7-C7-N2-C2
5	K	2	NAG	C8-C7-N2-C2
7	L	2	NAG	C8-C7-N2-C2
7	L	2	NAG	O7-C7-N2-C2
5	K	2	NAG	C1-C2-N2-C7
5	J	1	NAG	O5-C5-C6-O6
7	L	2	NAG	C4-C5-C6-O6
5	K	2	NAG	O7-C7-N2-C2
5	K	1	NAG	O5-C5-C6-O6
5	K	1	NAG	C4-C5-C6-O6
5	D	1	NAG	O5-C5-C6-O6

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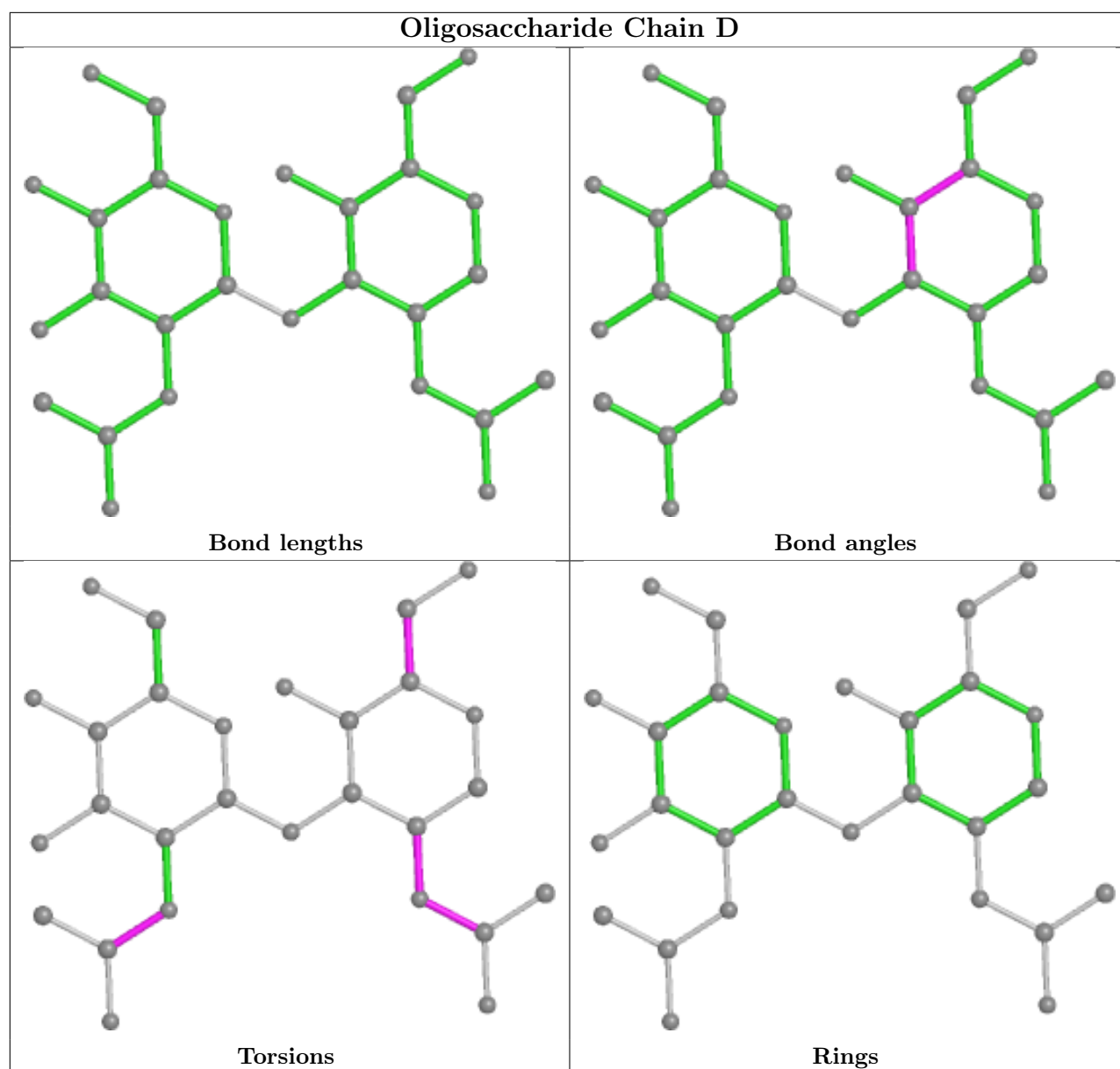
Mol	Chain	Res	Type	Atoms
5	D	1	NAG	C4-C5-C6-O6
7	L	2	NAG	O5-C5-C6-O6
5	J	1	NAG	C4-C5-C6-O6
7	L	2	NAG	C1-C2-N2-C7
6	H	2	NAG	O5-C5-C6-O6
6	H	2	NAG	C4-C5-C6-O6
5	K	2	NAG	C4-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6
6	I	3	BMA	C4-C5-C6-O6
5	D	2	NAG	C8-C7-N2-C2
5	D	1	NAG	C1-C2-N2-C7
5	K	2	NAG	O5-C5-C6-O6
6	I	3	BMA	O5-C5-C6-O6
6	I	1	NAG	O5-C5-C6-O6
5	D	2	NAG	O7-C7-N2-C2
7	L	3	NAG	O5-C5-C6-O6
5	G	2	NAG	C1-C2-N2-C7
6	I	2	NAG	C4-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
6	I	1	NAG	C4-C5-C6-O6
5	K	2	NAG	C3-C2-N2-C7
5	G	2	NAG	C3-C2-N2-C7

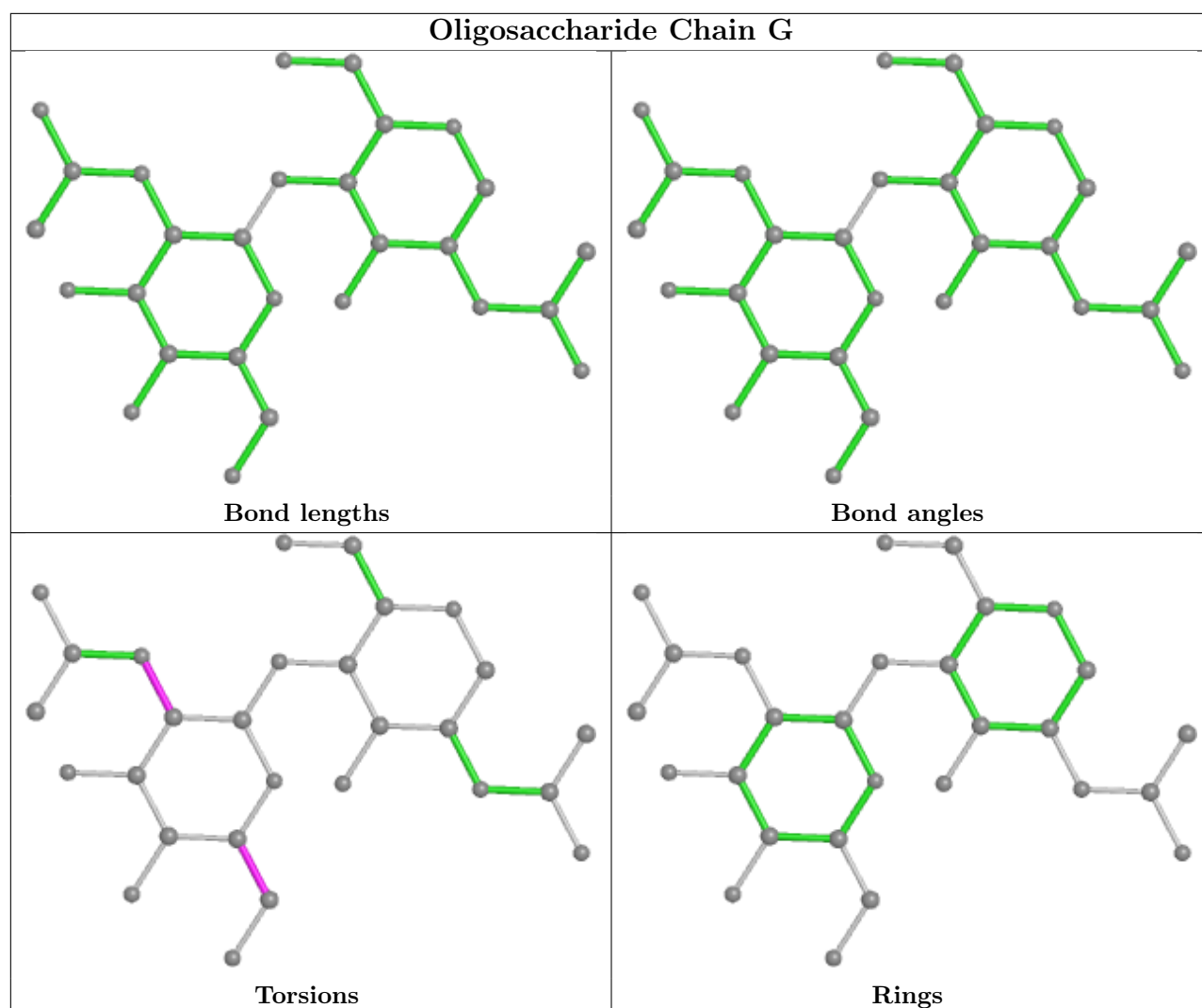
There are no ring outliers.

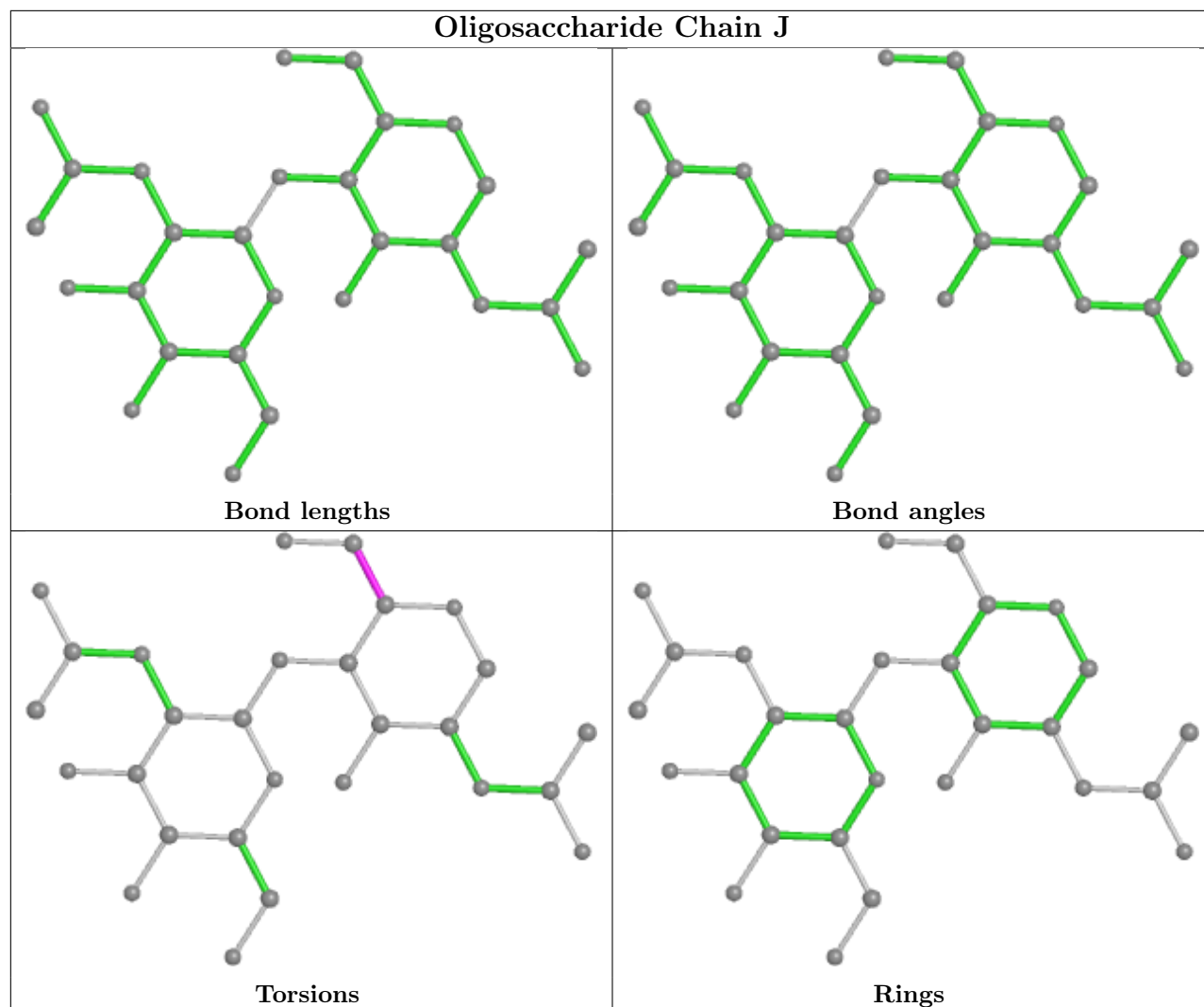
11 monomers are involved in 33 short contacts:

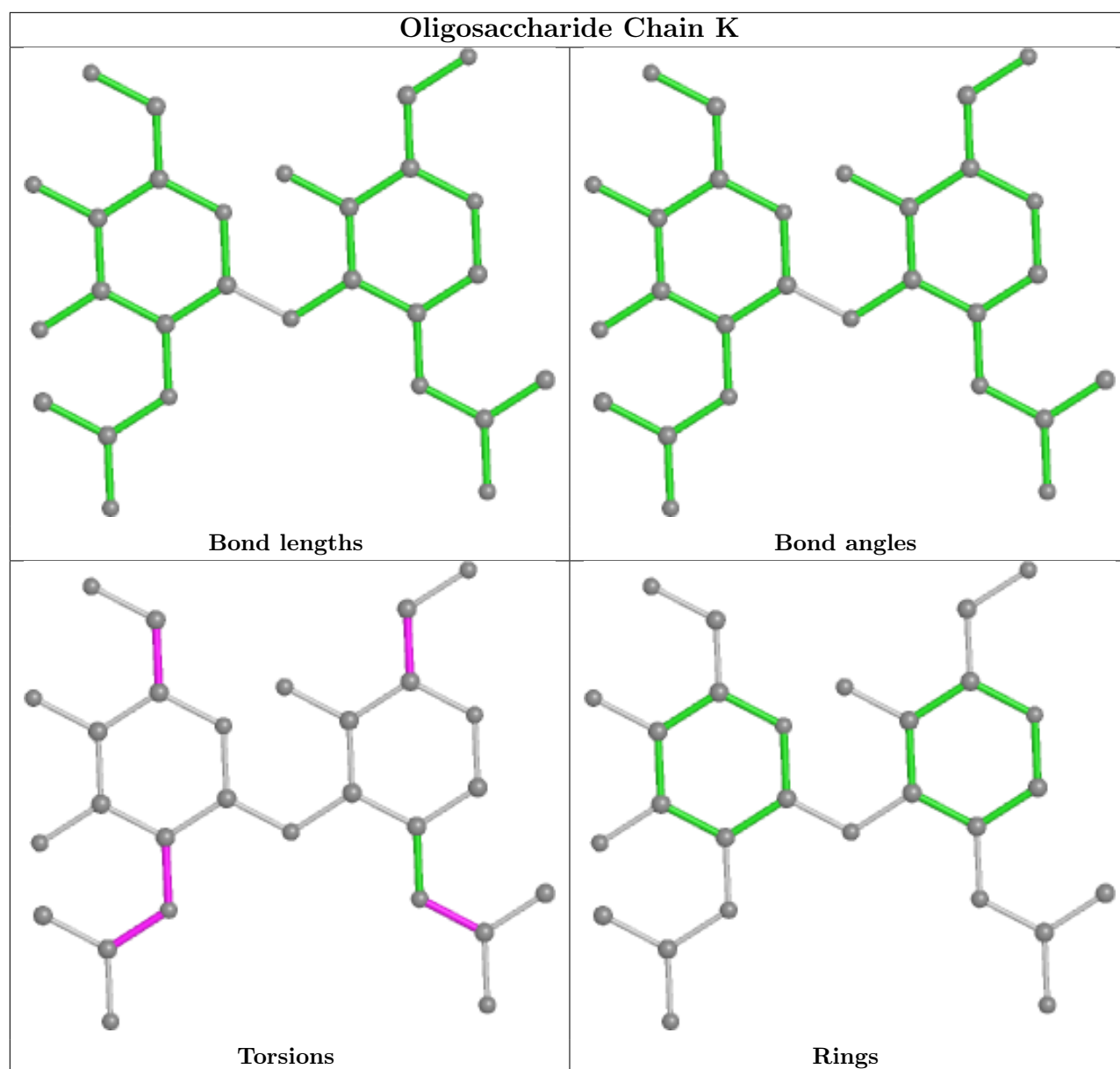
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	1	NAG	1	0
5	K	1	NAG	5	0
7	L	2	NAG	2	0
7	L	3	NAG	4	0
7	L	1	NAG	7	0
5	G	2	NAG	1	0
5	K	2	NAG	4	0
6	I	1	NAG	1	0
5	D	2	NAG	4	0
5	D	1	NAG	8	0
6	H	1	NAG	4	0

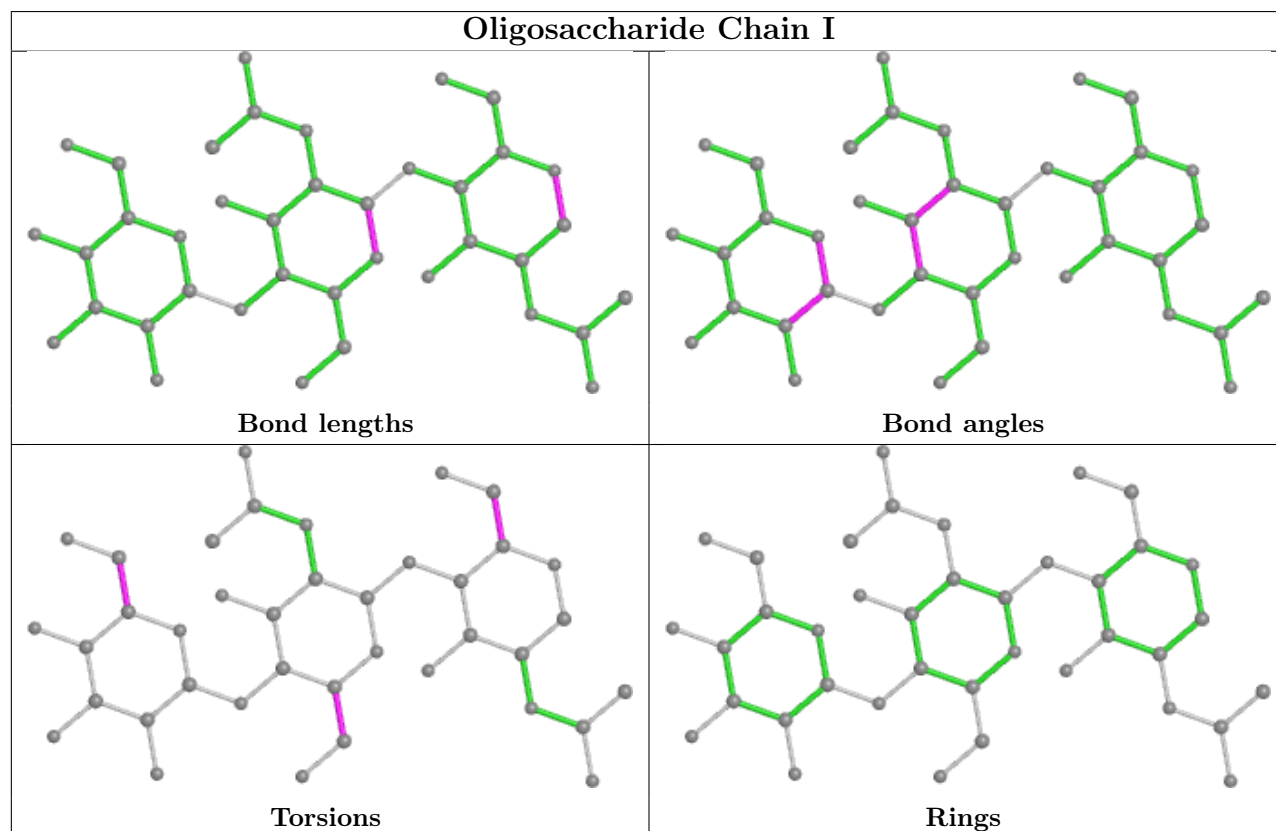
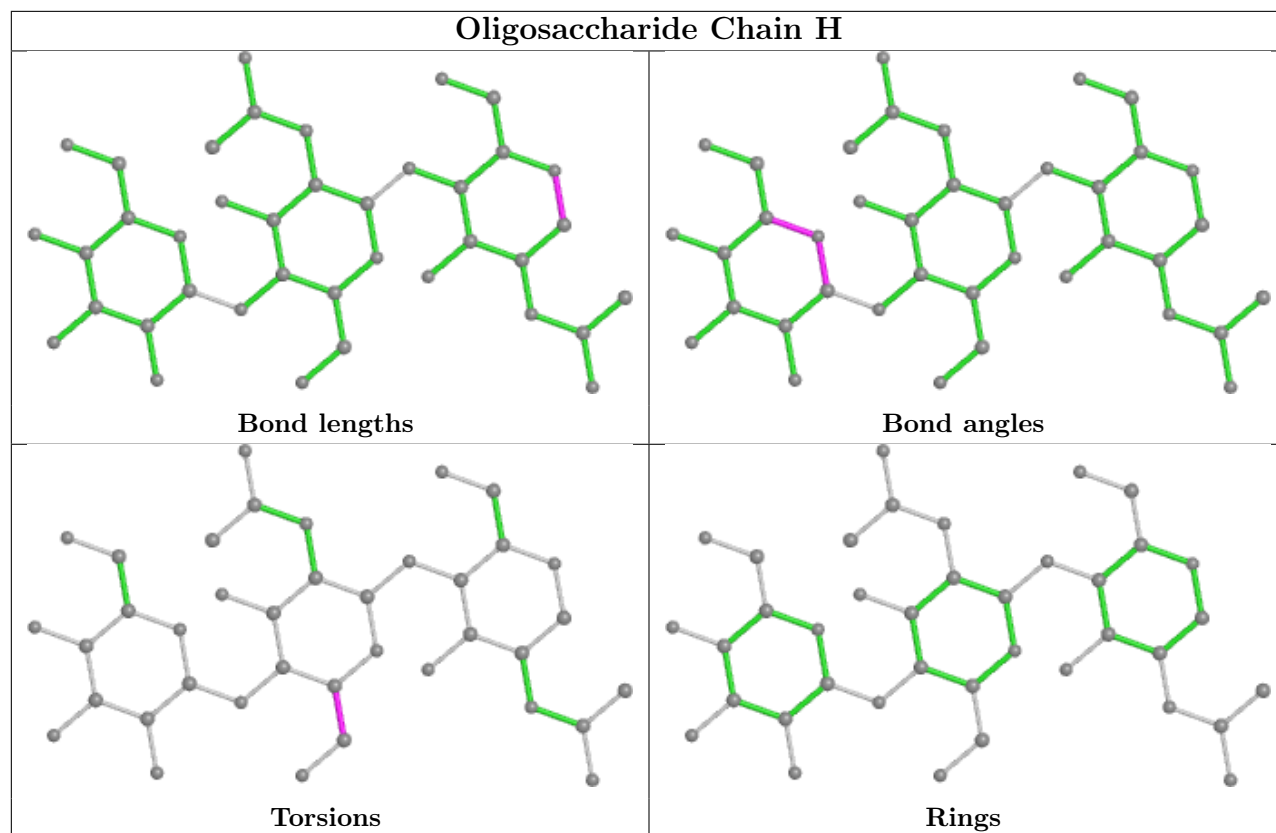
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

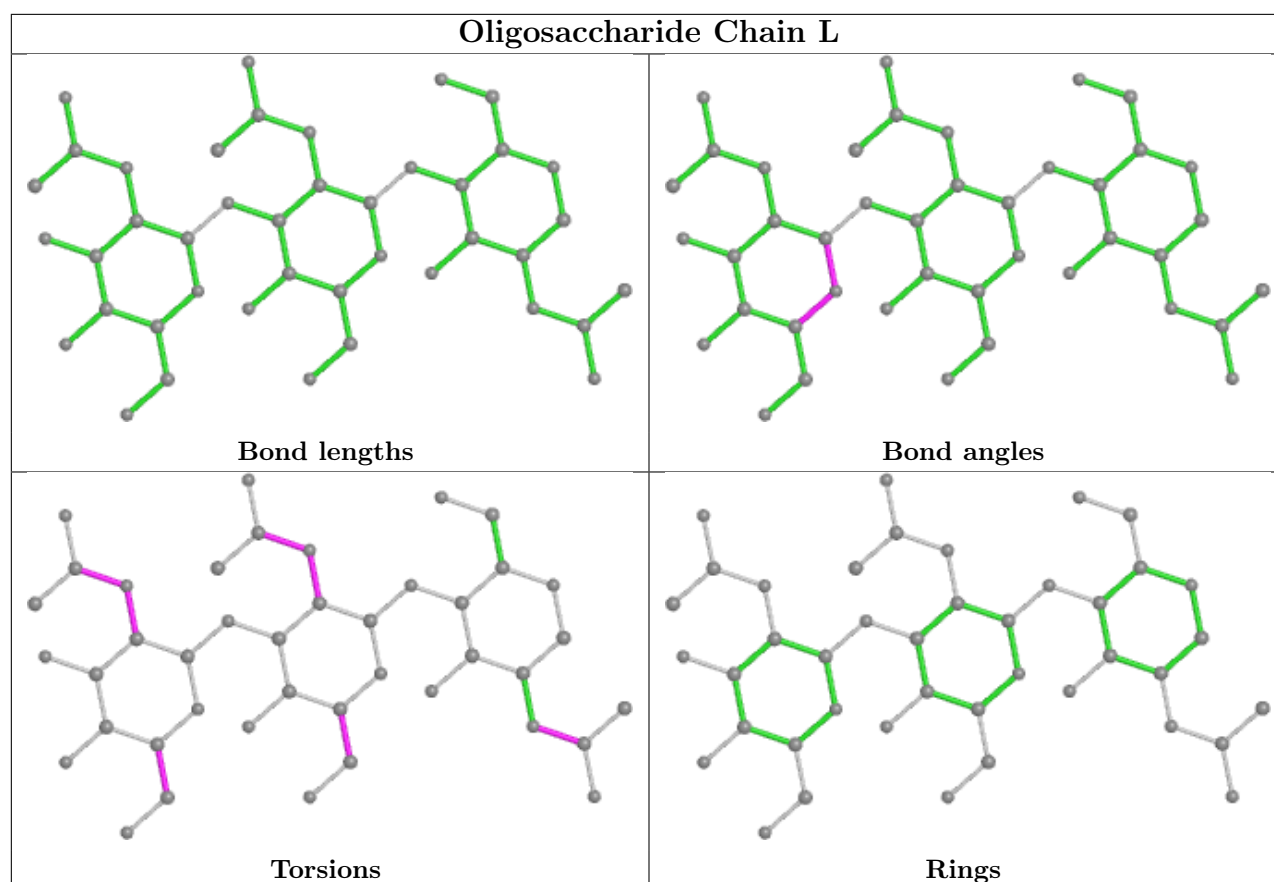












5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\# Z > 2$
9	NAG	F	1114	4	14,14,15	0.25	0	17,19,21	0.66	1 (5%)
9	NAG	F	1104	-	14,14,15	0.29	0	17,19,21	0.70	0
11	ETA	F	1101	-	3,3,3	0.39	0	2,2,2	0.52	0
9	NAG	F	1122	-	14,14,15	0.29	0	17,19,21	0.62	0
9	NAG	F	1107	4	14,14,15	0.30	0	17,19,21	0.61	0
9	NAG	A	1902	-	14,14,15	0.30	0	17,19,21	0.55	0
8	C8U	A	1901	-	22,26,26	3.59	7 (31%)	30,39,39	2.61	11 (36%)
9	NAG	F	1120	-	14,14,15	0.30	0	17,19,21	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	F	1121	-	14,14,15	0.45	0	17,19,21	0.51	0
9	NAG	F	1115	4	14,14,15	0.80	1 (7%)	17,19,21	1.01	1 (5%)

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
9	NAG	F	1114	4	-	0/6/23/26	0/1/1/1
9	NAG	F	1104	-	-	3/6/23/26	0/1/1/1
11	ETA	F	1101	-	-	1/1/1/1	-
9	NAG	F	1122	-	-	2/6/23/26	0/1/1/1
9	NAG	F	1107	4	-	2/6/23/26	0/1/1/1
9	NAG	A	1902	-	-	2/6/23/26	0/1/1/1
8	C8U	A	1901	-	-	9/18/40/40	0/2/2/2
9	NAG	F	1120	-	-	2/6/23/26	0/1/1/1
9	NAG	F	1121	-	-	0/6/23/26	0/1/1/1
9	NAG	F	1115	4	-	0/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1901	C8U	C02-C03	13.86	1.52	1.35
8	A	1901	C8U	C02-N07	4.85	1.45	1.38
8	A	1901	C8U	C06-N07	4.79	1.44	1.38
8	A	1901	C8U	O10-N09	-3.12	1.17	1.22
8	A	1901	C8U	O24-C22	2.86	1.39	1.33
8	A	1901	C8U	C22-C03	2.78	1.52	1.47
9	F	1115	NAG	C1-C2	2.41	1.55	1.52
8	A	1901	C8U	O24-C25	-2.24	1.40	1.45

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1901	C8U	C01-C02-C03	-8.34	119.28	127.62
8	A	1901	C8U	C08-C06-N07	5.16	119.59	113.45
8	A	1901	C8U	C01-C02-N07	5.12	119.53	113.45
8	A	1901	C8U	O24-C22-C03	4.45	120.23	112.30
9	F	1115	NAG	C1-O5-C5	3.63	117.11	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1901	C8U	C06-N07-C02	-3.49	120.17	123.40
8	A	1901	C8U	C05-C04-C03	2.91	112.29	108.65
8	A	1901	C8U	F19-C18-C17	-2.66	108.06	112.70
8	A	1901	C8U	O23-C22-C03	-2.47	120.09	125.20
8	A	1901	C8U	C04-C05-N09	2.39	119.60	116.37
9	F	1114	NAG	C1-O5-C5	2.36	115.39	112.19
8	A	1901	C8U	F20-C18-C17	-2.04	109.14	112.70
8	A	1901	C8U	O24-C22-O23	-2.00	119.67	123.53

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1901	C8U	C06-C05-N09-O10
9	F	1104	NAG	C8-C7-N2-C2
9	F	1104	NAG	O7-C7-N2-C2
8	A	1901	C8U	C03-C22-O24-C25
9	A	1902	NAG	O5-C5-C6-O6
9	F	1120	NAG	O5-C5-C6-O6
9	F	1120	NAG	C4-C5-C6-O6
8	A	1901	C8U	C02-C03-C22-O23
8	A	1901	C8U	C02-C03-C22-O24
8	A	1901	C8U	O23-C22-O24-C25
9	A	1902	NAG	C4-C5-C6-O6
8	A	1901	C8U	C04-C05-N09-O10
8	A	1901	C8U	C04-C03-C22-O23
8	A	1901	C8U	C04-C03-C22-O24
9	F	1104	NAG	C1-C2-N2-C7
9	F	1122	NAG	C4-C5-C6-O6
9	F	1107	NAG	C4-C5-C6-O6
9	F	1122	NAG	O5-C5-C6-O6
9	F	1107	NAG	O5-C5-C6-O6
11	F	1101	ETA	N-CA-CB-O
8	A	1901	C8U	C12-C17-C18-F20

There are no ring outliers.

8 monomers are involved in 20 short contacts:

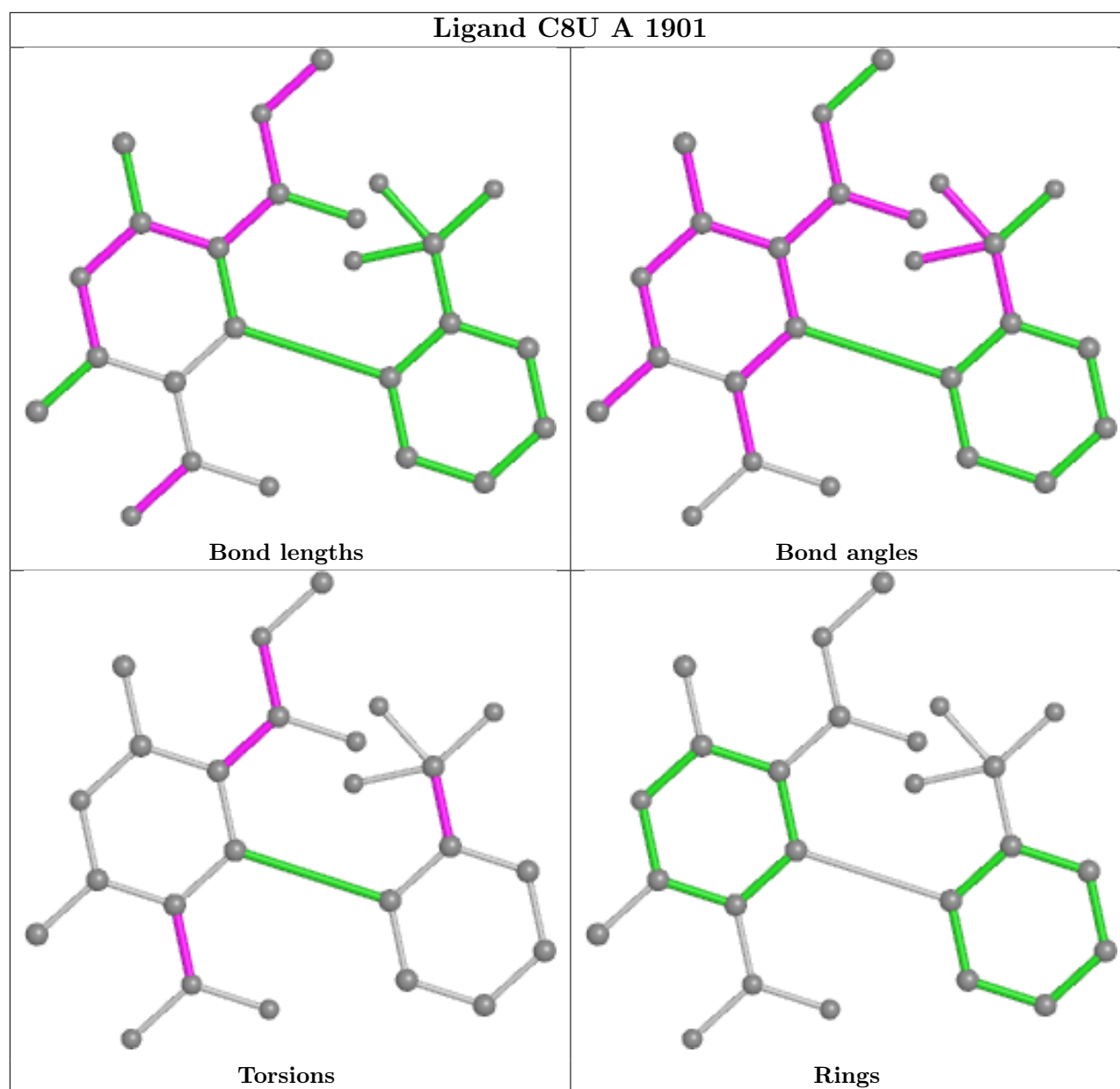
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	F	1104	NAG	3	0
11	F	1101	ETA	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	F	1122	NAG	4	0
9	F	1107	NAG	1	0
8	A	1901	C8U	1	0
9	F	1120	NAG	2	0
9	F	1121	NAG	3	0
9	F	1115	NAG	2	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

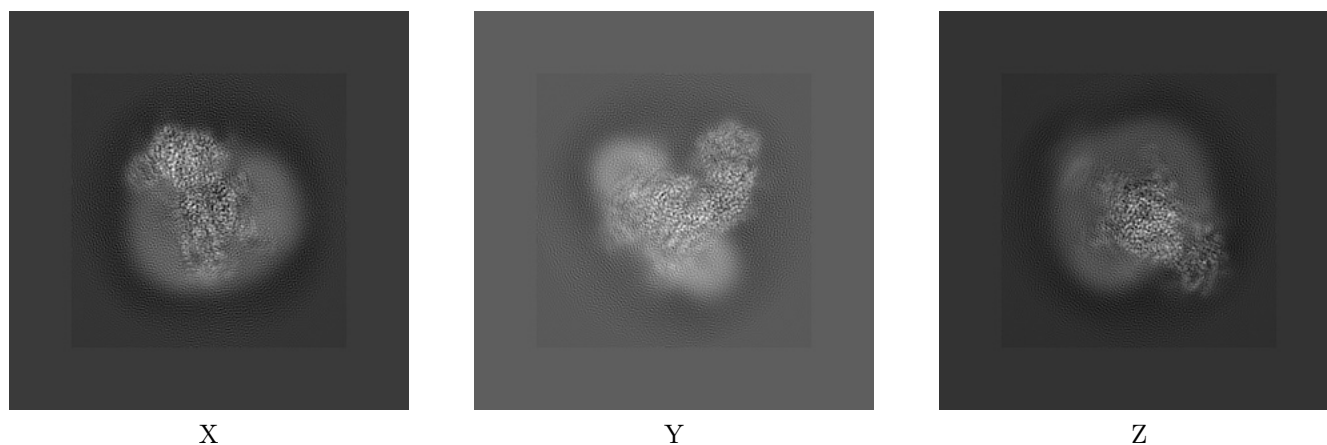
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9867. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

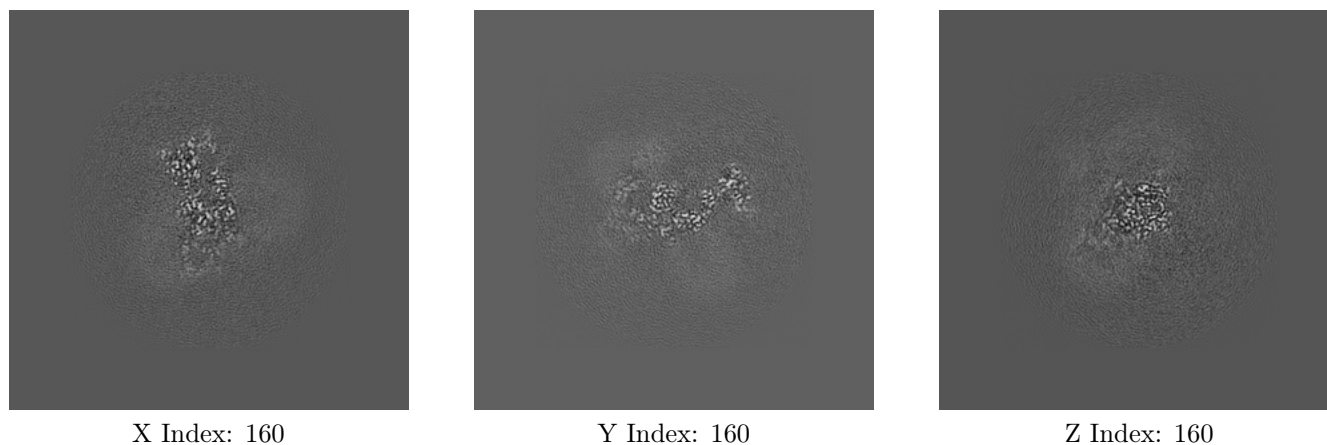
6.1.1 Primary map



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

6.2 Central slices [i](#)

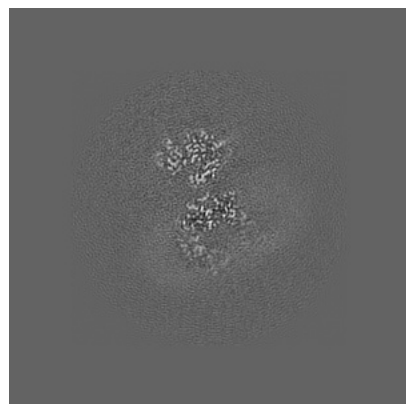
6.2.1 Primary map



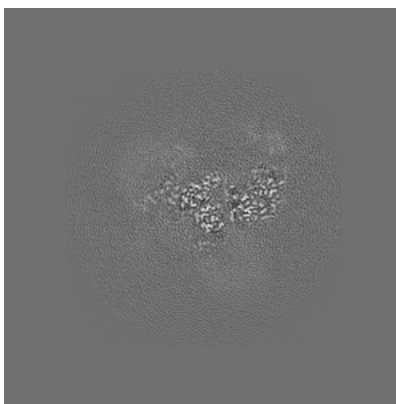
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

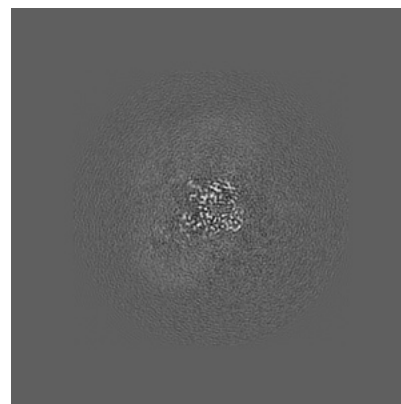
6.3.1 Primary map



X Index: 172



Y Index: 148



Z Index: 161

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.044. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

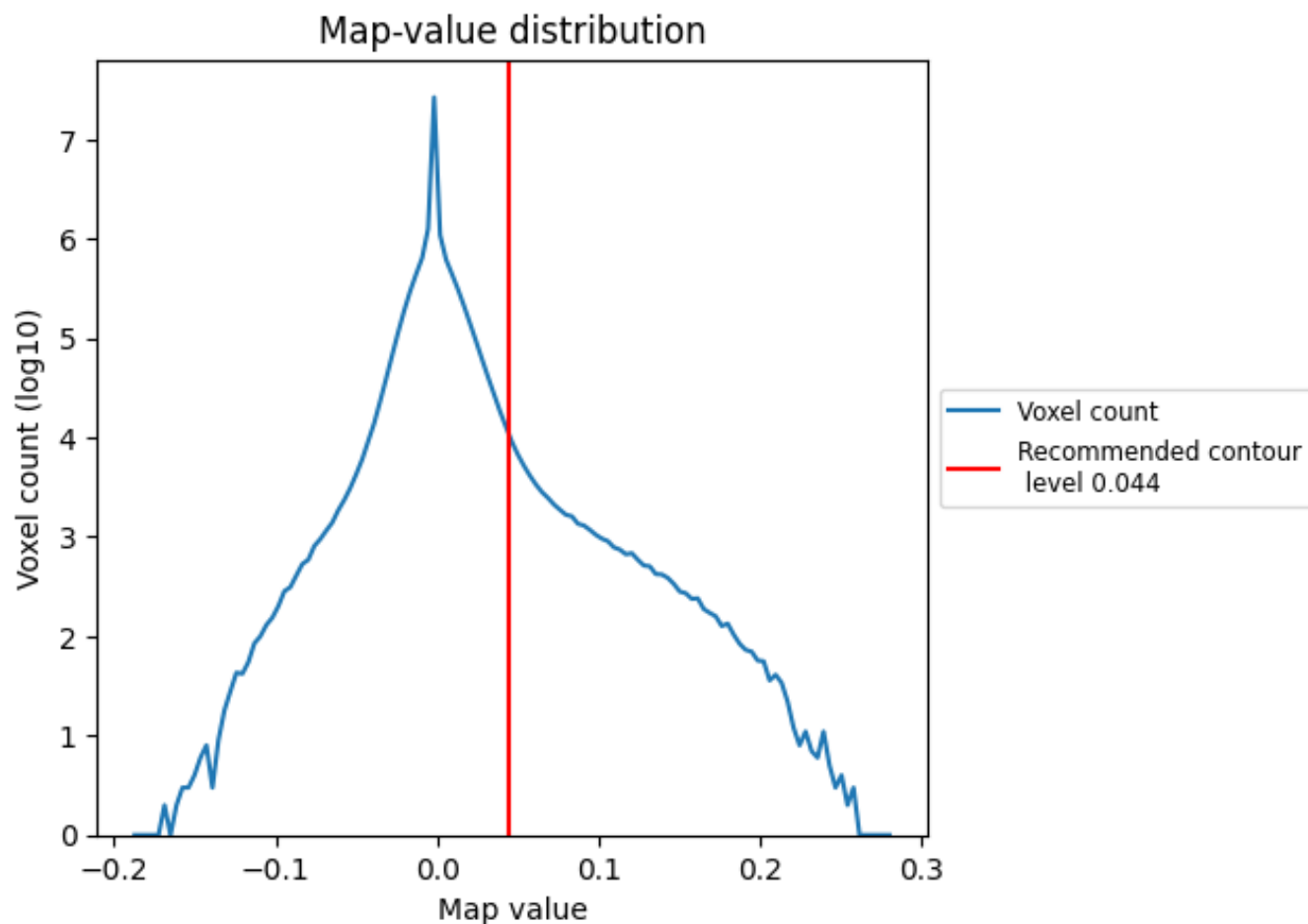
6.5 Mask visualisation

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

7 Map analysis [i](#)

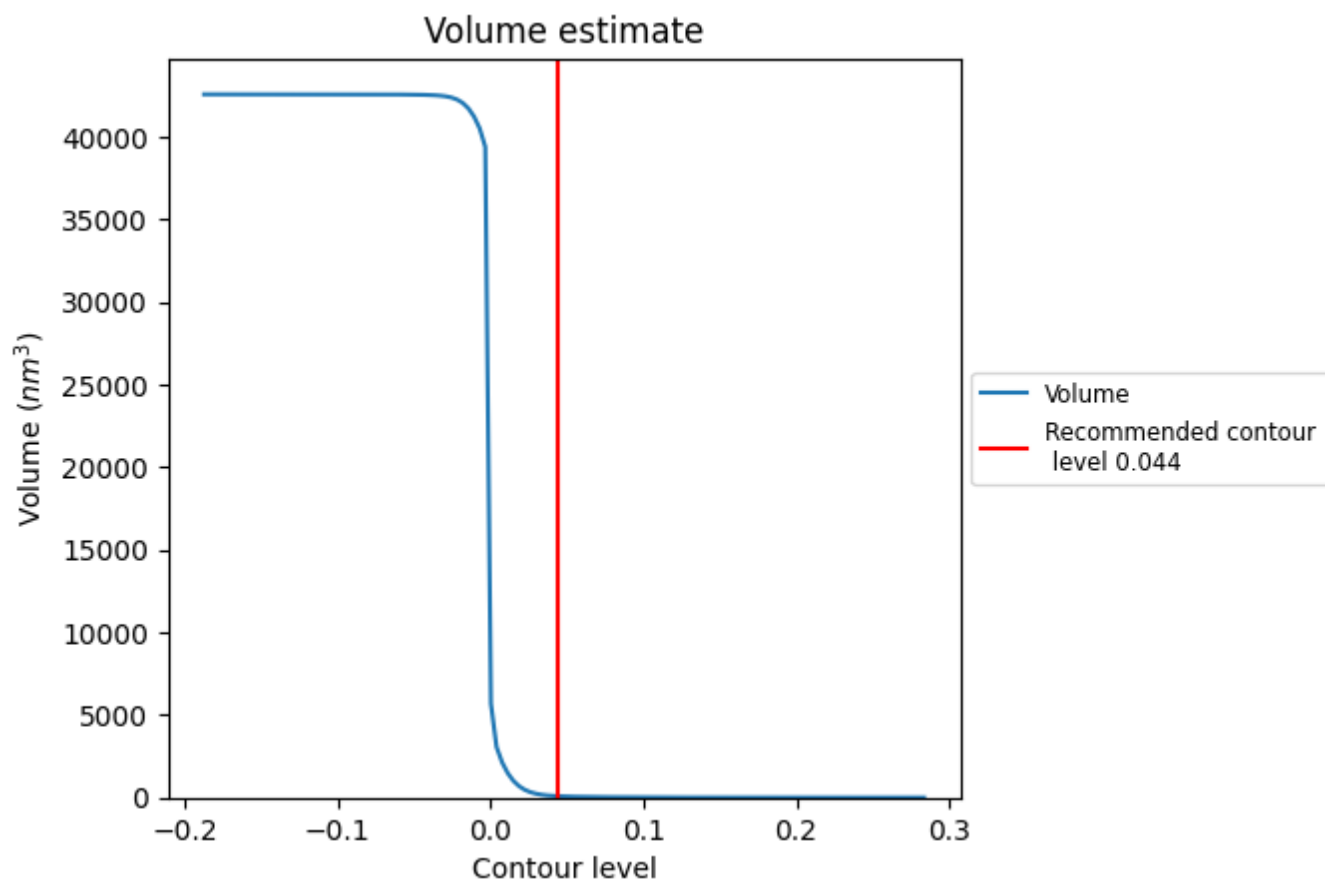
This section contains the results of statistical analysis of the map.

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.

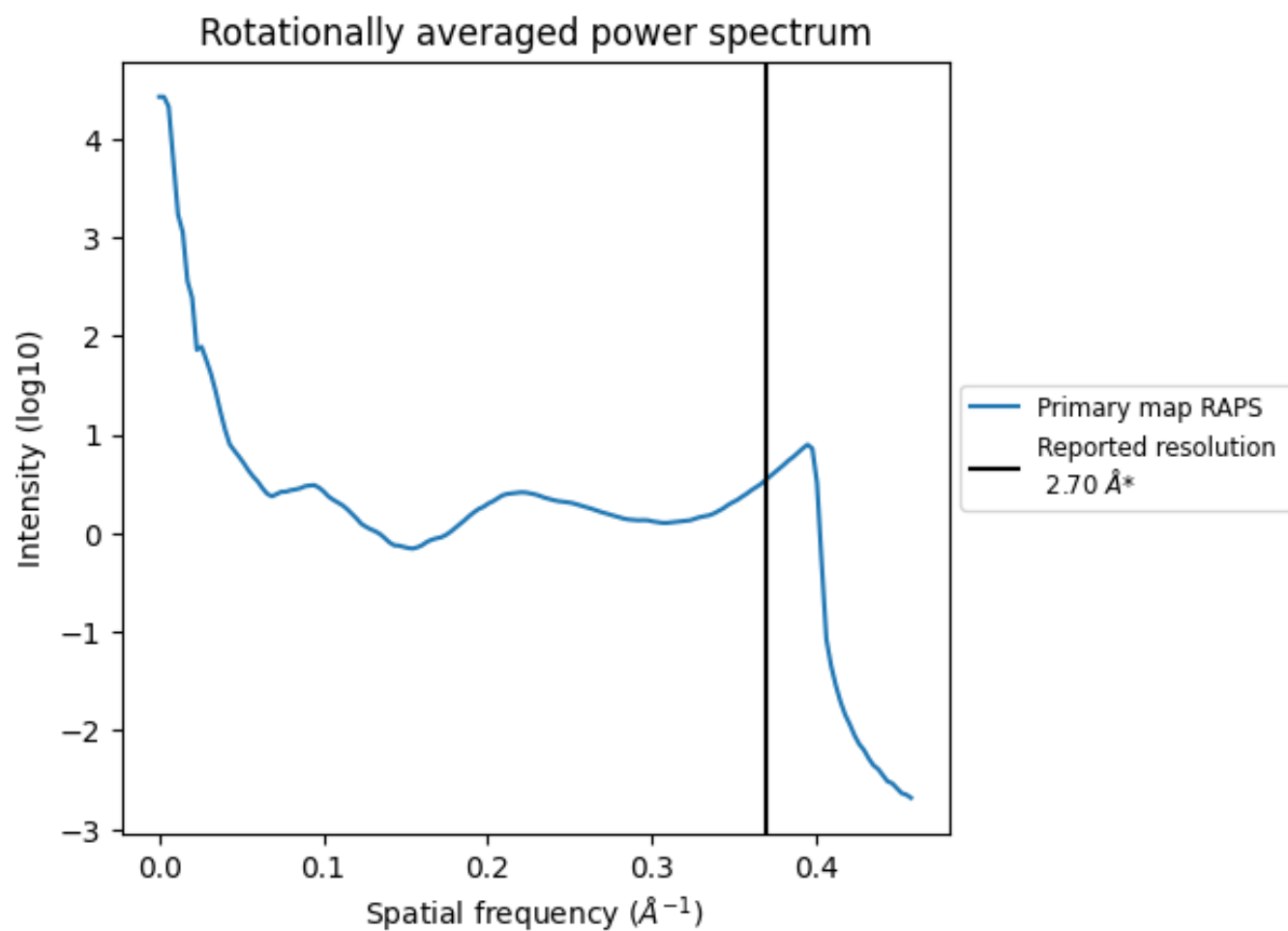
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 83 nm³; this corresponds to an approximate mass of 75 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 0.370 Å⁻¹

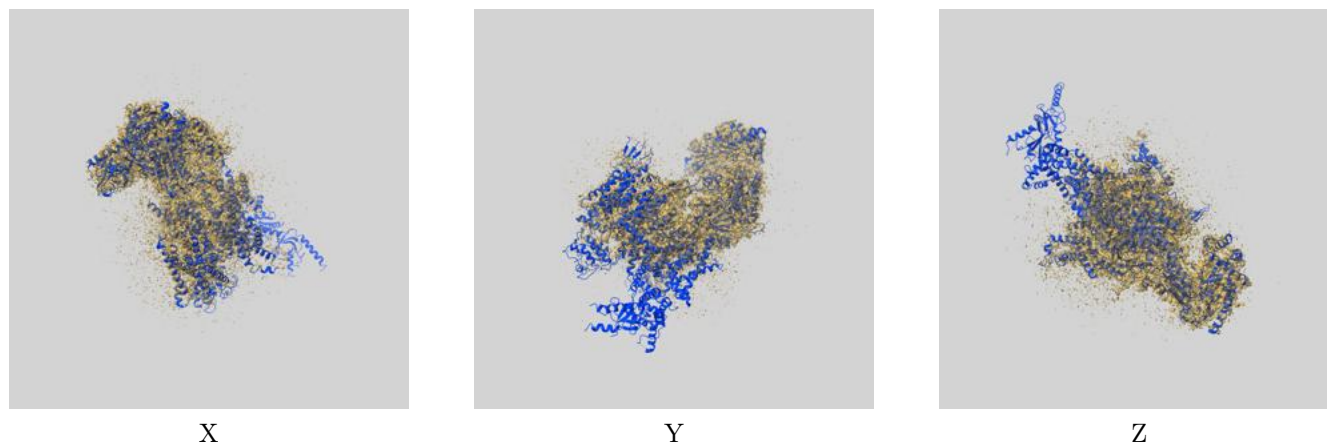
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

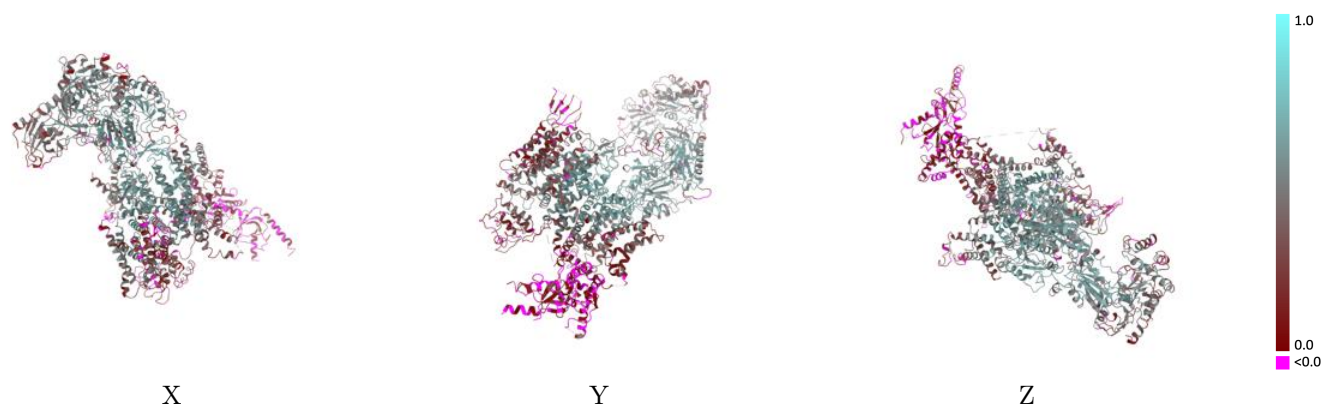
This section contains information regarding the fit between EMDB map EMD-9867 and PDB model 6JP8. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



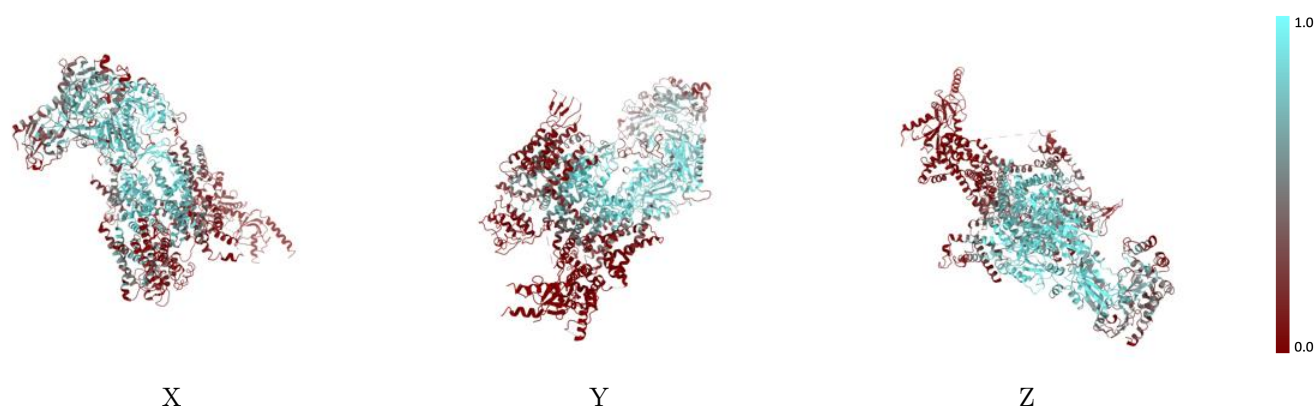
The images above show the 3D surface view of the map at the recommended contour level 0.044 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



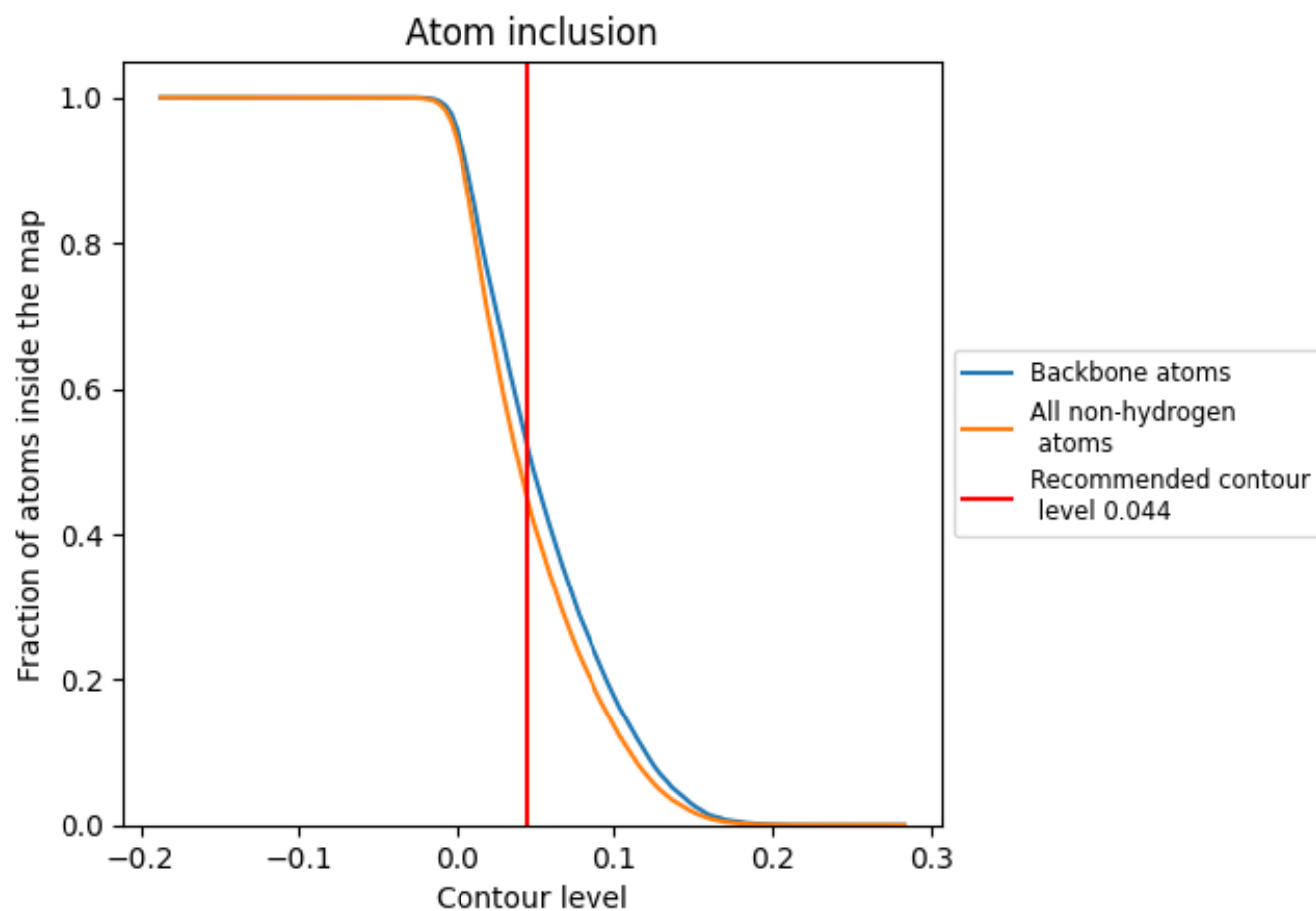
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.044).

9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 46% 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 (0.044) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4551	<div></div> 0.3850
A	<div></div> 0.4679	<div></div> 0.4240
B	<div></div> 0.0000	<div></div> 0.0130
C	<div></div> 0.0000	<div></div> 0.0010
D	<div></div> 0.0714	<div></div> 0.2270
E	<div></div> 0.1302	<div></div> 0.1990
F	<div></div> 0.6203	<div></div> 0.4680
G	<div></div> 0.0714	<div></div> 0.1420
H	<div></div> 0.2821	<div></div> 0.2780
I	<div></div> 0.5385	<div></div> 0.4390
J	<div></div> 0.2500	<div></div> 0.3470
K	<div></div> 0.1071	<div></div> 0.2580
L	<div></div> 0.1190	<div></div> 0.2190

