



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 10:27 PM UTC

PDB ID : 6JPB / pdb_00006jpb
EMDB ID : EMD-9869
Title : Rabbit Cav1.1-Diltiazem Complex
Authors : Zhao, Y.; Huang, G.; Wu, J.; Yan, N.
Deposited on : 2019-03-26
Resolution : 2.90 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

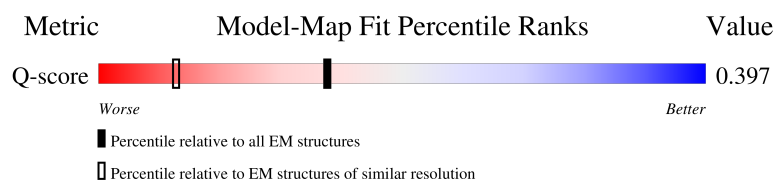
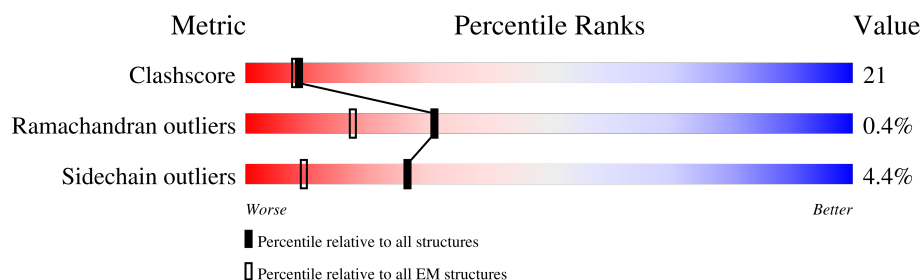
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



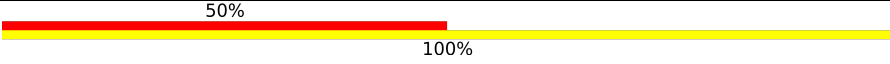
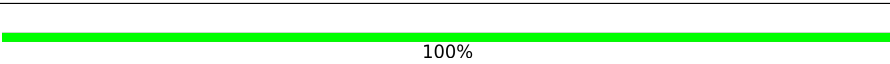
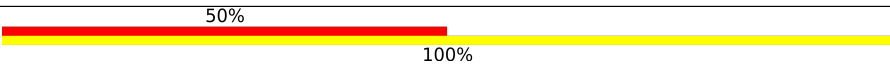
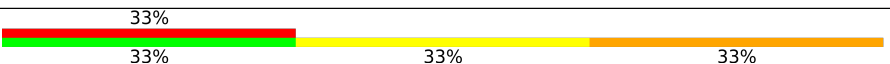
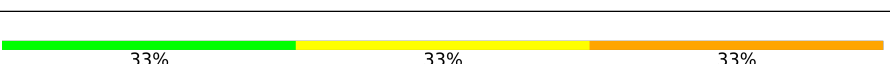
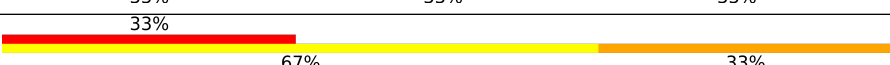
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	1873	20% 54% 13% 32%
2	E	222	45% 56% 19% 24%
3	B	450	22% 22% 78%
4	C	524	34% 32% 66%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	F	1046	
6	D	2	
6	G	2	
6	J	2	
6	K	2	
7	H	3	
7	I	3	
8	L	3	

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
6	NAG	D	1	-	-	X	-
8	NAG	L	1	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 21989 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 L-type calcium channel subunit alpha-1S.

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

- Molecule 2 is a protein called Voltage-dependent calcium channel gamma-1 subunit.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	100	Total	C	N	O	S	0	0
			710	455	125	129	1		

There are 5 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

- Molecule 4 is a protein called Voltage-dependent L-type calcium channel subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	178	Total	C	N	O	S	0	0
			1367	876	232	254	5		

- Molecule 5 is a protein called Voltage-dependent calcium channel subunit alpha-2/delta-1.

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

There is a discrepancy between the modelled and reference sequences:

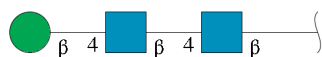
Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	SER	See sequence details	UNP P13806

- Molecule 6 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
6	D	2	Total	C	N	O	0	0
			28	16	2	10		
6	G	2	Total	C	N	O	0	0
			28	16	2	10		
6	J	2	Total	C	N	O	0	0
			28	16	2	10		
6	K	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 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.



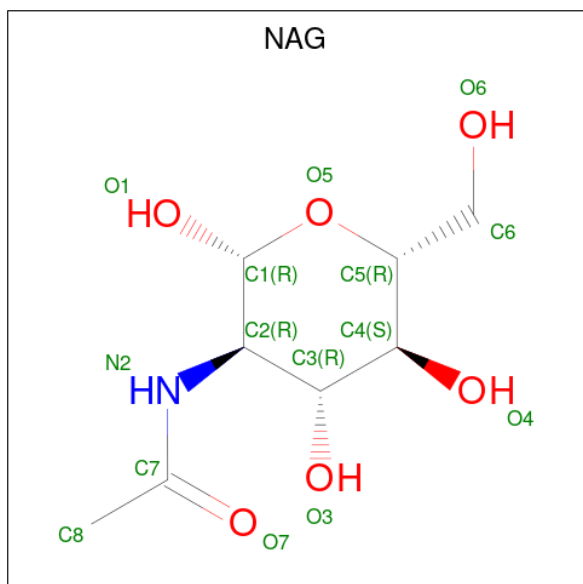
Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	3	Total	C	N	O	0	0
			39	22	2	15		
7	I	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 8 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
8	L	3	Total	C	N	O	0	0
			42	24	3	15		

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

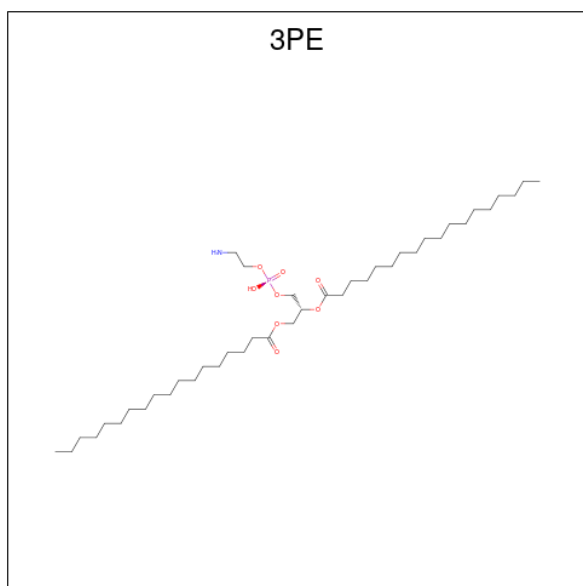


Mol	Chain	Residues	Atoms				AltConf
9	A	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			14	8	1	5	
9	F	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca).

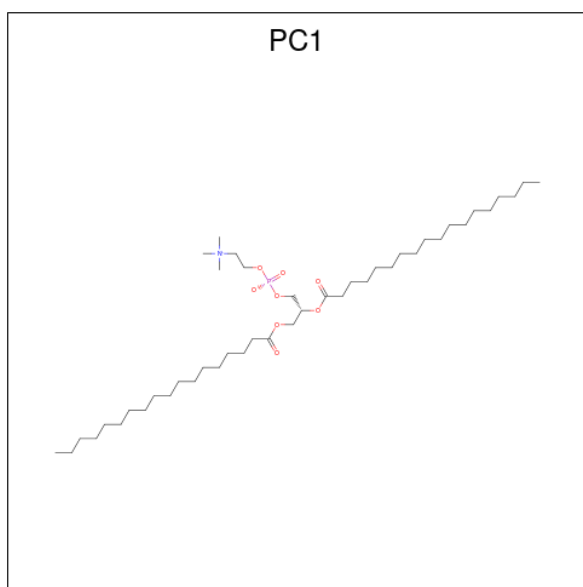
Mol	Chain	Residues	Atoms		AltConf
10	A	2	Total	Ca	0
			2	2	
10	F	1	Total	Ca	0
			1	1	

- Molecule 11 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



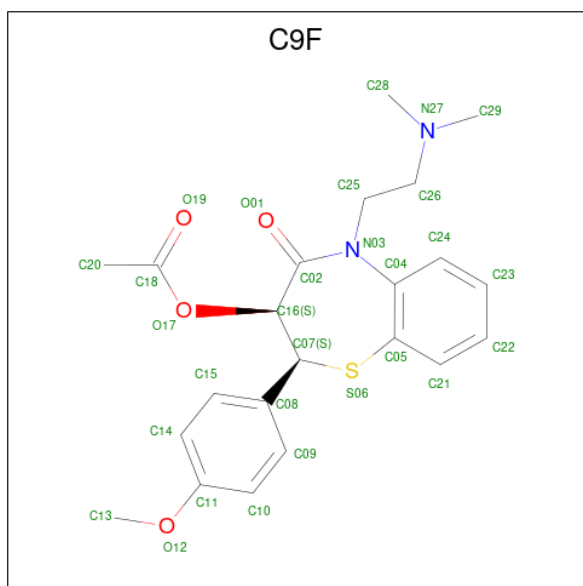
Mol	Chain	Residues	Atoms					AltConf
11	A	1	Total	C	N	O	P	0
			33	23	1	8	1	
11	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
11	A	1	Total	C	N	O	P	0
			34	24	1	8	1	
11	A	1	Total	C	N	O	P	0
			42	32	1	8	1	

- Molecule 12 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



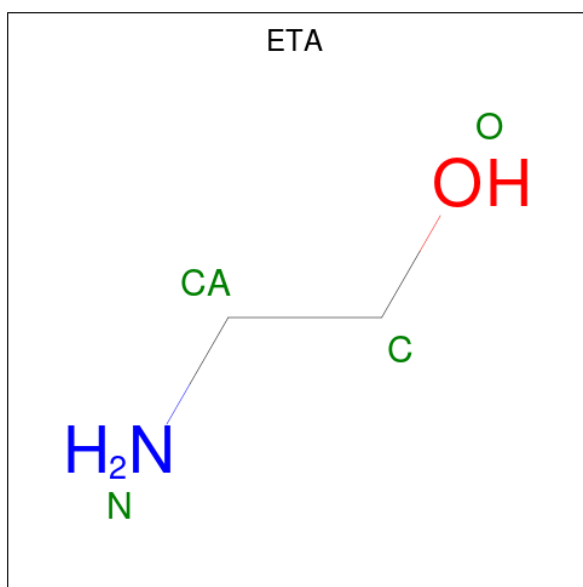
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
12	A	1	39	29	1	8	1	0

- Molecule 13 is Diltiazem (CCD ID: C9F) (formula: $C_{22}H_{26}N_2O_4S$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
13	A	1	29	22	2	4	1	0

- Molecule 14 is ETHANOLAMINE (CCD ID: ETA) (formula: C_2H_7NO).

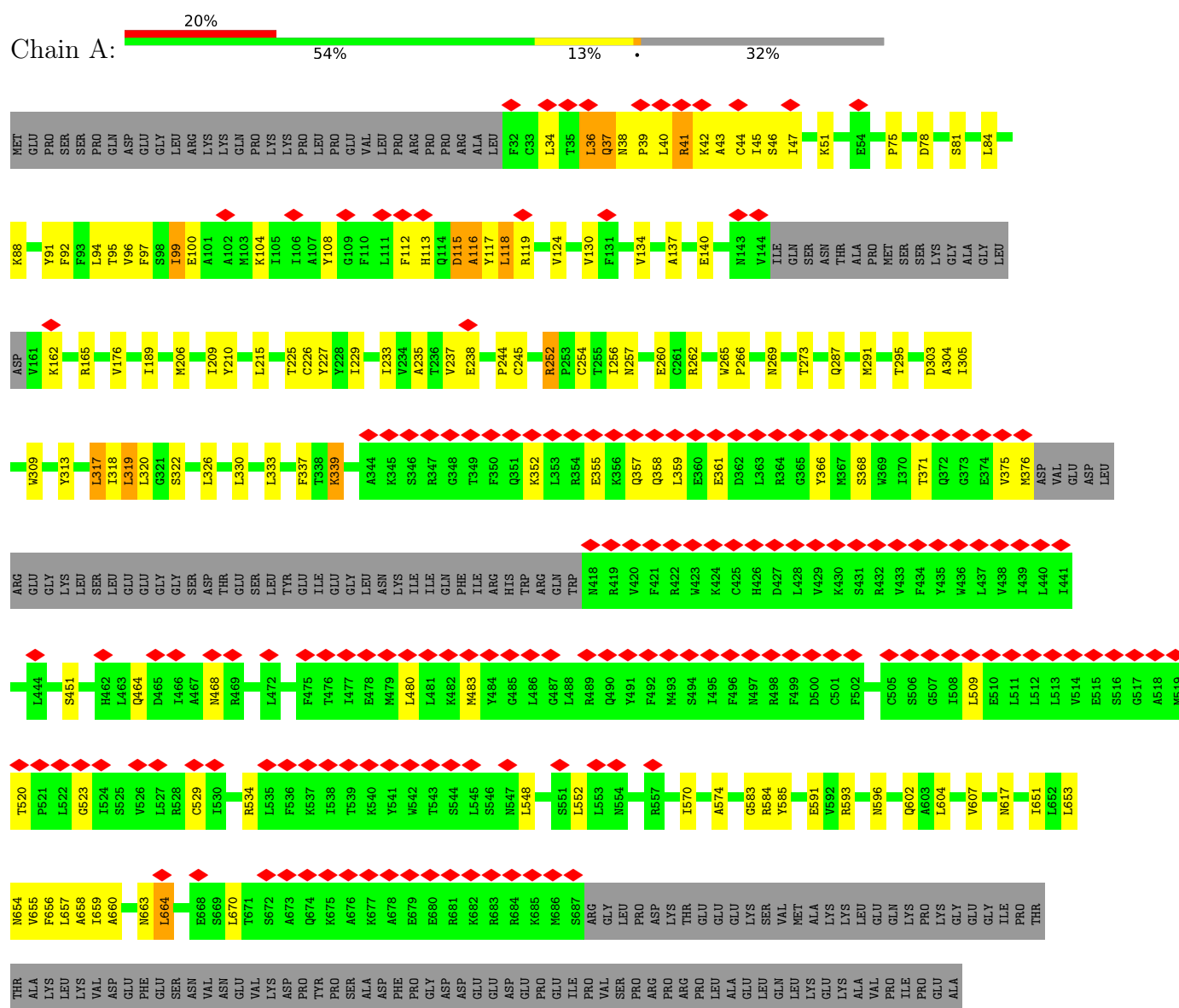


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
14	F	1	4	2	1	1	0

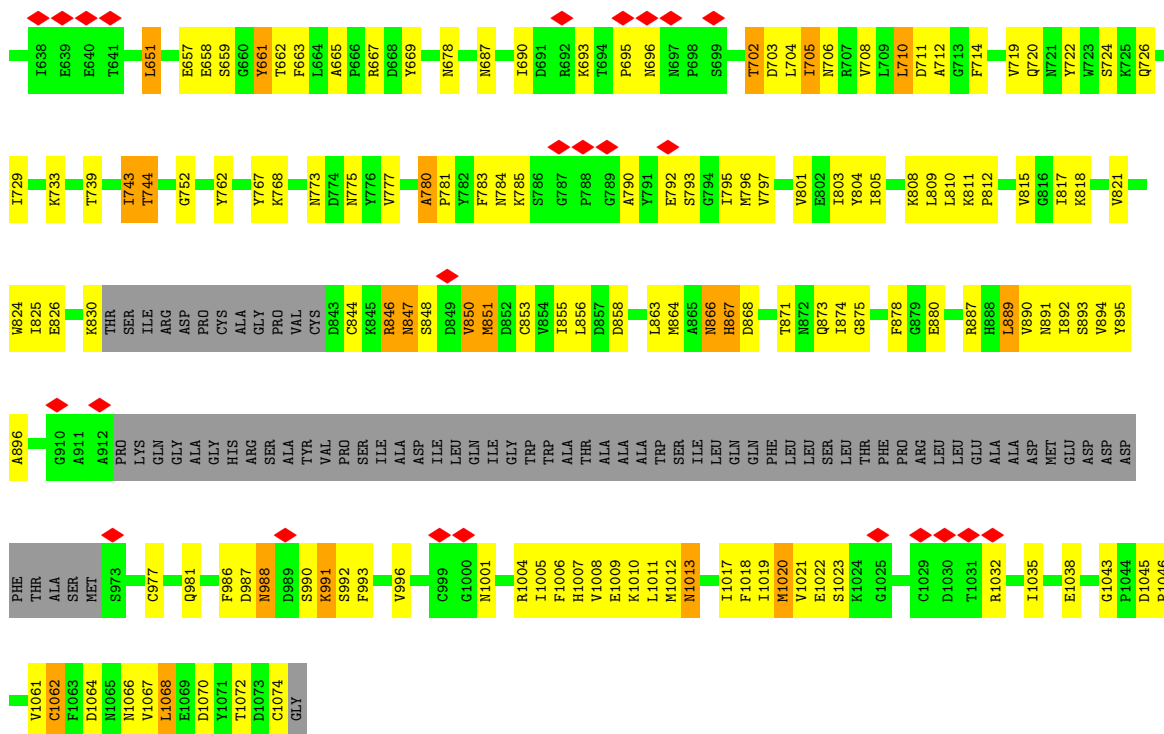
3 Residue-property plots

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







- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



- Molecule 8: 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	267633	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	0.204	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	349.12, 349.12, 349.12	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: ETA, BMA, CA, C9F, NAG, PC1, 3PE

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	0.63	1/10463 (0.0%)	0.84	7/14191 (0.0%)
2	E	0.42	0/1358	0.79	2/1832 (0.1%)
3	B	0.13	0/723	0.31	0/979
4	C	0.18	0/1394	0.46	0/1892
5	F	0.81	1/7974 (0.0%)	1.02	23/10816 (0.2%)
All	All	0.67	2/21912 (0.0%)	0.88	32/29710 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	665	ALA	C-N	-5.43	1.21	1.33
1	A	997	PHE	CA-CB	-5.15	1.44	1.53

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	867	HIS	N-CA-C	10.02	122.20	111.28
5	F	478	LYS	N-CA-C	9.76	121.92	111.28
2	E	181	SER	N-CA-C	9.04	121.14	111.28
5	F	991	LYS	N-CA-C	8.01	120.02	111.28
5	F	325	ASN	N-CA-C	7.92	120.82	111.71
1	A	37	GLN	N-CA-C	7.69	121.34	110.50
5	F	303	VAL	N-CA-C	7.49	121.50	111.17
5	F	399	GLY	O-C-N	7.00	123.59	121.07
5	F	1043	GLY	C-N-CD	6.92	135.82	120.60
5	F	220	TYR	C-N-CD	6.86	135.69	120.60
5	F	347	LEU	N-CA-C	6.73	120.40	112.72
5	F	422	ARG	N-CA-C	6.67	120.51	112.38
1	A	115	ASP	N-CA-C	-6.63	104.14	111.36
5	F	506	PHE	N-CA-C	6.57	118.44	111.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	243	ARG	N-CA-C	6.42	116.99	109.60
5	F	476	GLU	N-CA-C	6.42	121.25	113.17
5	F	254	LYS	N-CA-C	6.30	119.52	108.75
5	F	866	ASN	N-CA-C	6.17	118.01	111.28
2	E	215	CYS	N-CA-C	-6.17	101.15	110.28
5	F	247	ILE	N-CA-C	6.17	116.95	110.72
5	F	124	VAL	N-CA-C	-5.96	99.29	107.99
1	A	36	LEU	N-CA-C	-5.71	104.06	111.71
5	F	373	GLU	N-CA-C	5.70	117.49	111.28
1	A	1090	GLN	N-CA-C	-5.59	105.19	111.28
5	F	780	ALA	CA-C-N	-5.53	114.55	120.03
5	F	780	ALA	C-N-CA	-5.53	114.55	120.03
1	A	237	VAL	N-CA-C	-5.49	101.89	109.46
5	F	702	THR	N-CA-C	5.47	117.32	111.36
1	A	116	ALA	N-CA-C	5.33	117.17	111.36
1	A	320	LEU	N-CA-C	5.14	116.88	111.28
5	F	846	ARG	N-CA-C	-5.07	100.90	108.96
5	F	157	PHE	N-CA-C	-5.07	100.20	108.76

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	10219	0	10305	316	0
2	E	1326	0	1345	37	0
3	B	710	0	633	0	0
4	C	1367	0	1343	5	0
5	F	7804	0	7605	548	0
6	D	28	0	25	8	0
6	G	28	0	25	1	0
6	J	28	0	25	0	0
6	K	28	0	25	8	0
7	H	39	0	34	4	0
7	I	39	0	34	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	42	0	37	12	0
9	A	14	0	13	2	0
9	F	98	0	91	15	0
10	A	2	0	0	0	0
10	F	1	0	0	0	0
11	A	144	0	187	19	0
12	A	39	0	52	1	0
13	A	29	0	0	5	0
14	F	4	0	0	2	0
All	All	21989	0	21779	917	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 21.

All (917) 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:38:ASN:HD22	1:A:39:PRO:CD	1.16	1.56
5:F:784:ASN:ND2	9:F:1121:NAG:C1	1.68	1.54
5:F:678:ASN:HD21	6:K:1:NAG:C1	1.19	1.53
5:F:326:ASN:ND2	9:F:1105:NAG:C1	1.72	1.50
1:A:257:ASN:ND2	9:A:1901:NAG:C1	1.72	1.49
5:F:988:ASN:HD21	9:F:1123:NAG:C1	1.18	1.49
5:F:1001:ASN:HD21	9:F:1122:NAG:C1	1.27	1.43
5:F:1001:ASN:ND2	9:F:1122:NAG:C1	1.81	1.39
1:A:38:ASN:ND2	1:A:39:PRO:HD2	1.05	1.37
5:F:678:ASN:ND2	6:K:1:NAG:C1	1.86	1.34
5:F:988:ASN:ND2	9:F:1123:NAG:C1	1.87	1.34
1:A:226:CYS:SG	1:A:254:CYS:SG	1.35	1.30
1:A:226:CYS:SG	1:A:254:CYS:CB	2.20	1.28
1:A:1181:PRO:O	11:A:1904:3PE:H332	1.35	1.26
5:F:326:ASN:ND2	9:F:1105:NAG:O5	1.62	1.24
5:F:1070:ASP:OD1	5:F:1072:THR:HG22	1.36	1.21
1:A:1181:PRO:CB	11:A:1904:3PE:H331	1.70	1.20
5:F:255:ASP:OD1	5:F:354:ALA:HB3	1.42	1.19
1:A:1181:PRO:HB2	11:A:1904:3PE:C33	1.74	1.18
8:L:3:NAG:H82	8:L:3:NAG:C1	1.71	1.18
1:A:1081:LEU:HD13	1:A:1086:ARG:CD	1.75	1.17
5:F:132:ASP:OD2	5:F:137:LYS:HG2	1.45	1.16
5:F:100:LEU:CD1	5:F:198:ASN:HD21	1.59	1.14
5:F:359:ILE:HG22	5:F:385:ARG:HB2	1.16	1.14

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:548:LEU:HD21	1:A:1059:ILE:HD11	1.28	1.12
5:F:465:THR:CG2	5:F:489:VAL:CG1	2.28	1.12
5:F:47:LEU:HG	8:L:1:NAG:H81	1.27	1.11
5:F:161:VAL:HG21	5:F:221:PRO:HG2	1.19	1.11
1:A:40:LEU:HA	1:A:43:ALA:HB3	1.25	1.10
1:A:1085:GLN:HE22	1:A:1475:LEU:HB3	1.15	1.10
5:F:100:LEU:HD11	5:F:198:ASN:HD21	1.13	1.10
1:A:38:ASN:ND2	1:A:39:PRO:CD	1.86	1.09
5:F:889:LEU:HD12	5:F:892:ILE:CD1	1.83	1.09
1:A:1081:LEU:HD13	1:A:1086:ARG:HD3	1.31	1.08
6:K:2:NAG:H82	6:K:2:NAG:H3	1.37	1.07
1:A:333:LEU:HD23	1:A:657:LEU:HD23	1.31	1.06
5:F:515:PHE:HE2	5:F:580:MET:HE1	1.14	1.06
1:A:796:VAL:HG23	1:A:801:PHE:CE2	1.92	1.05
1:A:34:LEU:CB	1:A:37:GLN:CB	2.34	1.05
5:F:1074:CYS:O	14:F:1102:ETA:N	1.88	1.05
1:A:548:LEU:HD21	1:A:1059:ILE:CD1	1.86	1.04
5:F:889:LEU:O	5:F:894:VAL:HG12	1.56	1.04
5:F:178:SER:HB3	5:F:181:VAL:HG12	1.39	1.03
8:L:3:NAG:C1	8:L:3:NAG:C8	2.31	1.03
5:F:100:LEU:HD11	5:F:198:ASN:ND2	1.71	1.03
1:A:1185:PHE:HB2	11:A:1904:3PE:H362	1.38	1.03
5:F:515:PHE:CE2	5:F:580:MET:HE1	1.94	1.02
5:F:824:TRP:CG	5:F:864:MET:HE1	1.95	1.02
5:F:28:PRO:HD3	5:F:851:MET:HE1	1.41	1.02
5:F:480:ASN:O	5:F:480:ASN:ND2	1.92	1.02
5:F:889:LEU:HG	5:F:894:VAL:HG11	1.39	1.02
5:F:161:VAL:CG2	5:F:221:PRO:HG2	1.92	1.00
5:F:889:LEU:CD1	5:F:892:ILE:HD11	1.91	0.99
1:A:548:LEU:CD2	1:A:1059:ILE:HD11	1.91	0.99
5:F:362:LEU:HD11	5:F:401:ILE:HD11	1.42	0.99
5:F:993:PHE:HB2	5:F:1008:VAL:CG1	1.92	0.99
1:A:1085:GLN:NE2	1:A:1475:LEU:HB3	1.75	0.99
5:F:889:LEU:HD12	5:F:892:ILE:HD11	1.00	0.99
1:A:38:ASN:HD21	1:A:39:PRO:HD2	1.17	0.98
5:F:168:VAL:CG1	5:F:216:LEU:HD21	1.94	0.97
5:F:510:PRO:HG2	5:F:767:TYR:CE2	1.99	0.96
5:F:114:ARG:NH2	7:H:1:NAG:H62	1.79	0.96
1:A:1337:LEU:HD22	1:A:1338:CYS:N	1.81	0.96
1:A:1337:LEU:HB2	1:A:1350:TYR:CE1	2.01	0.95
5:F:336:LYS:HE3	5:F:369:GLU:OE2	1.67	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:465:THR:HG21	5:F:489:VAL:HG11	1.46	0.95
1:A:1057:MET:CE	13:A:1909:C9F:S06	2.54	0.95
5:F:263:SER:O	5:F:266:VAL:HG22	1.66	0.95
5:F:159:ARG:HH22	5:F:226:VAL:HG12	1.32	0.94
1:A:798:ALA:HB1	1:A:800:TRP:CE2	2.03	0.94
5:F:476:GLU:OE1	5:F:478:LYS:HB2	1.65	0.94
5:F:1070:ASP:CG	5:F:1072:THR:HG22	1.91	0.94
5:F:291:VAL:HG12	5:F:312:ALA:HB2	1.49	0.94
5:F:659:SER:O	5:F:719:VAL:HG11	1.67	0.94
5:F:356:CYS:SG	5:F:1062:CYS:HB2	2.07	0.93
1:A:1181:PRO:HB2	11:A:1904:3PE:H331	0.95	0.93
1:A:660:ALA:O	1:A:664:LEU:HB2	1.68	0.93
1:A:1081:LEU:HD22	1:A:1086:ARG:HG2	1.50	0.93
1:A:791:LEU:HD23	1:A:791:LEU:H	1.32	0.93
1:A:1057:MET:HE2	13:A:1909:C9F:S06	2.09	0.92
1:A:793:HIS:O	1:A:797:ASN:HB2	1.70	0.92
5:F:993:PHE:O	5:F:1008:VAL:HG12	1.70	0.92
5:F:388:THR:HB	5:F:401:ILE:HG13	1.50	0.92
5:F:161:VAL:HG21	5:F:221:PRO:CG	1.99	0.92
5:F:824:TRP:CG	5:F:864:MET:CE	2.52	0.91
5:F:669:TYR:CD1	5:F:704:LEU:CD2	2.53	0.90
1:A:1181:PRO:C	11:A:1904:3PE:H332	1.96	0.90
5:F:266:VAL:O	5:F:270:THR:HG23	1.71	0.90
5:F:117:PHE:CG	5:F:182:LEU:HD12	2.07	0.90
5:F:159:ARG:NH2	5:F:226:VAL:HG12	1.86	0.89
1:A:1337:LEU:HB2	1:A:1350:TYR:HE1	1.33	0.89
1:A:94:LEU:HD11	1:A:134:VAL:HG12	1.53	0.89
1:A:1181:PRO:CB	11:A:1904:3PE:C33	2.43	0.89
5:F:824:TRP:CD1	5:F:864:MET:HE1	2.08	0.89
5:F:892:ILE:HG13	5:F:894:VAL:HG12	1.55	0.89
5:F:993:PHE:HB2	5:F:1008:VAL:HG13	1.54	0.89
5:F:710:LEU:HD21	5:F:714:PHE:CZ	2.08	0.88
5:F:809:LEU:O	5:F:810:LEU:HD22	1.74	0.88
5:F:350:ASN:HD21	6:D:1:NAG:C1	1.87	0.88
1:A:38:ASN:HD22	1:A:39:PRO:N	1.71	0.88
5:F:276:THR:O	5:F:280:GLU:HG2	1.74	0.88
5:F:367:GLY:O	5:F:400:PRO:HG2	1.73	0.87
5:F:510:PRO:HG2	5:F:767:TYR:CD2	2.08	0.87
5:F:591:ARG:HH22	9:F:1116:NAG:HN2	1.23	0.86
5:F:480:ASN:HA	5:F:483:ASN:HB2	1.58	0.86
5:F:889:LEU:O	5:F:894:VAL:CG1	2.24	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:465:THR:CG2	5:F:489:VAL:HG11	2.04	0.85
5:F:256:MET:HE2	5:F:258:ILE:HD11	1.57	0.85
1:A:981:THR:HG22	5:F:552:ASN:HB3	1.55	0.84
1:A:39:PRO:HB2	1:A:41:ARG:HE	1.40	0.84
6:D:1:NAG:H83	6:D:2:NAG:C7	2.07	0.84
1:A:39:PRO:HG2	1:A:41:ARG:HH11	1.42	0.84
5:F:168:VAL:HG13	5:F:216:LEU:HD21	1.60	0.84
5:F:826:GLU:OE2	5:F:846:ARG:NH2	2.11	0.84
5:F:206:LEU:CD2	5:F:458:LEU:HD21	2.08	0.84
5:F:134:ASP:HB2	5:F:137:LYS:HD3	1.60	0.83
5:F:168:VAL:CG1	5:F:216:LEU:CD2	2.56	0.83
5:F:361:MET:HE2	5:F:387:PHE:CD1	2.13	0.83
5:F:361:MET:CE	5:F:387:PHE:CD1	2.61	0.83
1:A:257:ASN:ND2	9:A:1901:NAG:C2	2.41	0.83
5:F:350:ASN:ND2	6:D:1:NAG:C1	2.41	0.83
5:F:170:ILE:HD13	5:F:216:LEU:HD23	1.58	0.82
5:F:809:LEU:C	5:F:810:LEU:HD22	2.04	0.82
5:F:243:ARG:HH21	5:F:243:ARG:HG3	1.45	0.82
5:F:1010:LYS:CG	5:F:1017:ILE:HG13	2.09	0.82
1:A:1082:ASP:O	1:A:1086:ARG:HG3	1.80	0.81
1:A:91:TYR:HE1	1:A:137:ALA:HB1	1.43	0.81
5:F:28:PRO:CD	5:F:851:MET:HE1	2.11	0.81
1:A:94:LEU:HD13	1:A:94:LEU:O	1.79	0.81
1:A:39:PRO:HG2	1:A:41:ARG:NH1	1.95	0.81
5:F:781:PRO:O	5:F:875:GLY:HA3	1.81	0.81
5:F:43:ASP:OD1	8:L:1:NAG:H2	1.81	0.81
5:F:47:LEU:HG	8:L:1:NAG:C8	2.09	0.81
5:F:465:THR:CG2	5:F:489:VAL:HG12	2.11	0.80
5:F:1070:ASP:OD1	5:F:1072:THR:CG2	2.24	0.80
5:F:824:TRP:C	5:F:864:MET:HE1	2.05	0.80
5:F:858:ASP:HA	5:F:986:PHE:CZ	2.17	0.80
5:F:887:ARG:O	5:F:890:VAL:HG22	1.82	0.80
1:A:659:ILE:O	1:A:663:ASN:HB2	1.82	0.79
5:F:481:LEU:HD23	5:F:482:LYS:H	1.46	0.79
1:A:94:LEU:HD11	1:A:134:VAL:CG1	2.13	0.78
5:F:1010:LYS:HG3	5:F:1017:ILE:HG13	1.64	0.78
5:F:590:PHE:CD2	5:F:592:THR:HG23	2.18	0.78
1:A:796:VAL:HG23	1:A:801:PHE:HE2	1.44	0.78
5:F:168:VAL:HG22	5:F:218:ARG:HG2	1.64	0.78
5:F:465:THR:HG23	5:F:489:VAL:HG12	1.66	0.78
5:F:356:CYS:SG	5:F:1062:CYS:CB	2.71	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1334:TYR:HA	1:A:1353:GLY:C	2.10	0.77
1:A:226:CYS:CB	1:A:254:CYS:SG	2.72	0.77
5:F:669:TYR:CE1	5:F:704:LEU:HD21	2.20	0.77
5:F:591:ARG:NH2	9:F:1116:NAG:HN2	1.81	0.77
5:F:663:PHE:HB2	5:F:744:THR:HG23	1.63	0.77
5:F:669:TYR:CE1	5:F:704:LEU:CD2	2.68	0.77
1:A:260:GLU:OE2	1:A:262:ARG:HD3	1.85	0.77
5:F:846:ARG:C	5:F:847:ASN:HD22	1.93	0.77
1:A:796:VAL:HG23	1:A:801:PHE:CD2	2.19	0.77
1:A:1334:TYR:O	1:A:1352:CYS:O	2.03	0.77
5:F:359:ILE:HG22	5:F:385:ARG:CB	2.07	0.76
8:L:1:NAG:O3	8:L:1:NAG:H83	1.86	0.76
5:F:478:LYS:HD3	5:F:478:LYS:C	2.11	0.76
1:A:226:CYS:SG	1:A:254:CYS:HB3	2.25	0.76
1:A:1334:TYR:HA	1:A:1353:GLY:O	1.85	0.76
5:F:359:ILE:CG2	5:F:385:ARG:HB2	2.08	0.76
1:A:1474:ALA:C	1:A:1475:LEU:HD12	2.09	0.76
5:F:465:THR:HG22	5:F:489:VAL:CG1	2.16	0.76
5:F:178:SER:HB3	5:F:181:VAL:CG1	2.14	0.75
5:F:1008:VAL:HG23	5:F:1019:ILE:HG22	1.67	0.75
1:A:99:ILE:HD12	1:A:100:GLU:N	2.02	0.75
1:A:1083:LYS:HA	1:A:1086:ARG:CZ	2.16	0.75
5:F:388:THR:CB	5:F:401:ILE:HG13	2.16	0.75
1:A:1084:ASN:HA	1:A:1087:GLN:HG2	1.68	0.75
1:A:39:PRO:HB2	1:A:41:ARG:NE	2.01	0.75
1:A:791:LEU:H	1:A:791:LEU:CD2	1.99	0.74
5:F:256:MET:HB2	5:F:359:ILE:CD1	2.18	0.74
5:F:988:ASN:CG	9:F:1123:NAG:C1	2.60	0.74
5:F:804:TYR:CZ	5:F:809:LEU:HD13	2.23	0.74
5:F:855:ILE:O	5:F:856:LEU:HD12	1.87	0.74
5:F:275:ARG:HD2	5:F:325:ASN:HA	1.69	0.73
5:F:206:LEU:HD23	5:F:458:LEU:CD2	2.19	0.73
5:F:590:PHE:HD2	5:F:592:THR:HG23	1.52	0.73
5:F:117:PHE:CD1	5:F:182:LEU:HD12	2.23	0.73
1:A:41:ARG:CD	1:A:42:LYS:H	2.02	0.73
1:A:1430:GLN:HG3	1:A:1432:PRO:HD2	1.71	0.73
5:F:889:LEU:CG	5:F:894:VAL:HG11	2.17	0.73
1:A:40:LEU:HD23	1:A:40:LEU:C	2.14	0.72
1:A:252:ARG:HG2	1:A:1302:ARG:HH21	1.52	0.72
1:A:1081:LEU:CD2	1:A:1086:ARG:HG2	2.20	0.72
5:F:590:PHE:HE2	5:F:592:THR:HG21	1.53	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:255:ASP:OD1	5:F:354:ALA:CB	2.31	0.72
5:F:243:ARG:HG3	5:F:243:ARG:NH2	2.00	0.72
1:A:252:ARG:HG2	1:A:1302:ARG:NH2	2.04	0.72
5:F:205:LEU:HD21	5:F:492:VAL:CG2	2.20	0.72
1:A:337:PHE:CE2	1:A:658:ALA:HB2	2.24	0.72
5:F:513:TYR:O	5:F:624:LEU:HD12	1.90	0.71
5:F:229:SER:O	5:F:235:ILE:HG22	1.91	0.71
5:F:359:ILE:HD13	5:F:361:MET:HE3	1.71	0.71
5:F:669:TYR:CD1	5:F:704:LEU:HD22	2.24	0.71
1:A:333:LEU:HD23	1:A:657:LEU:CD2	2.16	0.71
5:F:133:LEU:H	5:F:133:LEU:CD2	2.03	0.71
5:F:235:ILE:O	5:F:235:ILE:HD12	1.91	0.71
5:F:803:ILE:HG13	5:F:810:LEU:HB2	1.71	0.71
5:F:159:ARG:NH2	5:F:226:VAL:CG1	2.54	0.71
5:F:705:ILE:HD12	5:F:705:ILE:C	2.15	0.71
1:A:225:THR:HG22	1:A:227:TYR:CE2	2.26	0.70
1:A:1061:VAL:O	1:A:1065:ILE:HG13	1.90	0.70
1:A:1081:LEU:HB2	1:A:1086:ARG:HG2	1.73	0.70
1:A:99:ILE:HD12	1:A:99:ILE:C	2.16	0.70
5:F:100:LEU:CD1	5:F:198:ASN:ND2	2.38	0.70
5:F:705:ILE:HD12	5:F:706:ASN:N	2.06	0.70
1:A:798:ALA:HB1	1:A:800:TRP:CZ2	2.26	0.70
5:F:210:PHE:HB2	5:F:490:MET:HE3	1.72	0.70
5:F:595:LYS:HD3	5:F:599:GLU:OE1	1.91	0.70
1:A:1181:PRO:O	11:A:1904:3PE:C33	2.29	0.70
5:F:93:ARG:NH1	5:F:202:ASP:OD2	2.25	0.70
5:F:510:PRO:HG2	5:F:767:TYR:HE2	1.57	0.70
1:A:118:LEU:HD13	1:A:118:LEU:O	1.92	0.70
5:F:411:TYR:CD1	5:F:1074:CYS:HA	2.27	0.70
5:F:850:VAL:HG22	5:F:851:MET:HG2	1.72	0.69
5:F:339:PHE:CZ	5:F:362:LEU:HD23	2.28	0.69
5:F:478:LYS:HD3	5:F:478:LYS:O	1.93	0.69
5:F:996:VAL:HG23	5:F:1004:ARG:O	1.92	0.69
5:F:388:THR:HB	5:F:401:ILE:CG1	2.23	0.69
1:A:95:THR:O	1:A:99:ILE:HG23	1.93	0.68
5:F:461:VAL:HG12	5:F:495:SER:HA	1.73	0.68
5:F:124:VAL:HG21	5:F:182:LEU:HD13	1.75	0.68
1:A:118:LEU:CD1	1:A:124:VAL:HG22	2.24	0.68
2:E:214:SER:HB2	2:E:217:ASP:OD1	1.93	0.68
5:F:206:LEU:CD2	5:F:458:LEU:CD2	2.71	0.68
5:F:515:PHE:HE2	5:F:580:MET:CE	2.01	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:478:LYS:HD2	5:F:479:THR:HG23	1.74	0.68
5:F:889:LEU:O	5:F:892:ILE:HG13	1.92	0.68
1:A:40:LEU:HD23	1:A:40:LEU:O	1.94	0.68
5:F:370:ARG:CD	5:F:372:GLN:HE21	2.06	0.68
5:F:889:LEU:HA	5:F:892:ILE:HD11	1.75	0.68
1:A:962:LYS:HD2	1:A:967:GLU:HB3	1.76	0.68
5:F:311:GLN:HE22	5:F:520:ASN:HD21	1.41	0.68
5:F:398:ARG:O	5:F:402:GLN:HG3	1.94	0.68
5:F:411:TYR:CE1	5:F:1074:CYS:HA	2.29	0.68
5:F:590:PHE:CE2	5:F:592:THR:HG21	2.28	0.68
5:F:993:PHE:HB2	5:F:1008:VAL:HG11	1.75	0.68
5:F:162:SER:O	5:F:221:PRO:HB2	1.93	0.67
1:A:1060:PHE:CZ	1:A:1373:ILE:HD11	2.30	0.67
1:A:94:LEU:CD1	1:A:134:VAL:HG12	2.22	0.67
1:A:791:LEU:HD23	1:A:791:LEU:N	2.06	0.67
5:F:44:LEU:HD11	5:F:824:TRP:CZ2	2.29	0.67
5:F:132:ASP:OD2	5:F:137:LYS:CG	2.36	0.67
5:F:528:ASN:HD22	5:F:528:ASN:C	2.01	0.67
1:A:1081:LEU:HD13	1:A:1086:ARG:CG	2.25	0.67
1:A:235:ALA:HB1	1:A:256:ILE:HG21	1.77	0.66
5:F:858:ASP:HA	5:F:986:PHE:CE1	2.30	0.66
5:F:348:ASN:O	5:F:350:ASN:N	2.29	0.66
5:F:465:THR:HG23	5:F:489:VAL:CG1	2.23	0.66
5:F:478:LYS:CD	5:F:479:THR:HG23	2.26	0.66
5:F:783:PHE:CE1	5:F:873:GLN:HB2	2.31	0.66
5:F:339:PHE:O	5:F:343:PHE:HD2	1.79	0.66
5:F:858:ASP:HB3	5:F:986:PHE:CE2	2.30	0.66
1:A:1334:TYR:H	1:A:1353:GLY:C	2.04	0.65
1:A:1084:ASN:O	1:A:1088:CYS:HB2	1.96	0.65
2:E:32:TRP:HH2	2:E:53:LEU:HD21	1.62	0.65
5:F:256:MET:HB2	5:F:359:ILE:HD11	1.79	0.65
5:F:804:TYR:CE1	5:F:809:LEU:HD13	2.32	0.65
1:A:1081:LEU:HD12	1:A:1081:LEU:H	1.61	0.65
5:F:366:GLY:HA3	5:F:396:TYR:CB	2.26	0.65
5:F:783:PHE:HE1	5:F:873:GLN:CB	2.09	0.65
1:A:41:ARG:HD2	1:A:42:LYS:H	1.60	0.65
1:A:791:LEU:O	1:A:795:ILE:HG13	1.95	0.65
1:A:210:TYR:CE1	1:A:317:LEU:HB2	2.31	0.65
5:F:114:ARG:HH21	7:H:1:NAG:H62	1.62	0.65
5:F:783:PHE:HE1	5:F:873:GLN:HA	1.62	0.65
6:K:1:NAG:H82	6:K:2:NAG:H2	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:339:PHE:HZ	5:F:362:LEU:HD23	1.62	0.64
5:F:361:MET:HE2	5:F:387:PHE:HD1	1.62	0.64
5:F:506:PHE:CZ	5:F:667:ARG:HG3	2.32	0.64
5:F:892:ILE:O	5:F:893:SER:HB3	1.97	0.64
1:A:94:LEU:HD13	1:A:94:LEU:C	2.22	0.64
1:A:788:VAL:O	1:A:791:LEU:HD21	1.96	0.64
1:A:295:THR:HG21	1:A:1318:ARG:HG3	1.78	0.64
5:F:43:ASP:CG	8:L:1:NAG:H2	2.23	0.64
5:F:114:ARG:CZ	7:H:1:NAG:H62	2.27	0.64
2:E:32:TRP:CE3	2:E:181:SER:HB3	2.32	0.64
5:F:159:ARG:HH22	5:F:226:VAL:CG1	2.06	0.64
1:A:97:PHE:HB3	1:A:130:VAL:HG11	1.80	0.64
5:F:130:LYS:HA	5:F:228:ASN:HD22	1.63	0.64
5:F:704:LEU:C	5:F:704:LEU:HD23	2.23	0.64
1:A:1012:THR:O	1:A:1013:PHE:HB2	1.98	0.64
1:A:1083:LYS:HB2	1:A:1086:ARG:NH2	2.13	0.64
5:F:824:TRP:C	5:F:864:MET:CE	2.71	0.63
11:A:1904:3PE:H341	11:A:1904:3PE:O32	1.95	0.63
5:F:168:VAL:HG11	5:F:216:LEU:HD21	1.76	0.63
8:L:3:NAG:H83	8:L:3:NAG:O5	1.97	0.63
5:F:269:LEU:HD22	5:F:269:LEU:O	1.98	0.63
1:A:1315:LEU:C	1:A:1315:LEU:HD23	2.23	0.63
5:F:340:SER:O	5:F:344:GLU:HG2	1.97	0.63
1:A:118:LEU:HD13	1:A:124:VAL:HG22	1.80	0.63
5:F:103:GLU:HG3	5:F:194:VAL:HG21	1.81	0.63
5:F:408:ASN:C	5:F:409:LYS:HG3	2.24	0.63
5:F:895:TYR:CZ	5:F:986:PHE:HE1	2.17	0.63
5:F:178:SER:OG	5:F:180:ILE:HG22	2.00	0.62
5:F:783:PHE:CE1	5:F:873:GLN:CB	2.82	0.62
1:A:162:LYS:HE3	1:A:165:ARG:HH21	1.65	0.62
1:A:1092:ALA:O	1:A:1464:ASN:ND2	2.32	0.62
1:A:1181:PRO:C	11:A:1904:3PE:C33	2.69	0.62
5:F:159:ARG:NH1	5:F:224:PRO:O	2.32	0.62
8:L:3:NAG:C8	8:L:3:NAG:O5	2.47	0.62
1:A:1083:LYS:HD3	1:A:1086:ARG:HH21	1.63	0.62
5:F:267:SER:HB3	5:F:329:ALA:HB3	1.80	0.62
5:F:891:ASN:OD1	9:F:1108:NAG:O5	2.08	0.62
1:A:41:ARG:HD2	1:A:41:ARG:N	2.13	0.62
5:F:206:LEU:HD21	5:F:458:LEU:HD21	1.81	0.62
5:F:880:GLU:HG2	5:F:1035:ILE:HG22	1.82	0.62
5:F:132:ASP:CG	5:F:137:LYS:HG2	2.23	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:256:MET:HE2	5:F:258:ILE:CD1	2.29	0.62
1:A:796:VAL:HG22	1:A:796:VAL:O	2.00	0.61
5:F:97:LEU:HD11	5:F:464:GLY:O	1.99	0.61
5:F:993:PHE:O	5:F:1008:VAL:CG1	2.47	0.61
5:F:1008:VAL:CG2	5:F:1019:ILE:HG22	2.29	0.61
5:F:376:ALA:O	5:F:380:LYS:HB2	2.01	0.61
1:A:656:PHE:CD1	1:A:1054:PHE:O	2.54	0.61
1:A:1081:LEU:HD22	1:A:1086:ARG:CG	2.28	0.61
1:A:84:LEU:O	1:A:88:LYS:HE3	2.00	0.61
5:F:370:ARG:HD3	5:F:372:GLN:HE21	1.65	0.61
5:F:784:ASN:CG	9:F:1121:NAG:C1	2.66	0.61
5:F:1010:LYS:HG2	5:F:1017:ILE:HG13	1.83	0.61
5:F:256:MET:HB2	5:F:359:ILE:HD12	1.83	0.61
5:F:856:LEU:O	5:F:1017:ILE:HG22	2.01	0.61
1:A:788:VAL:HB	1:A:791:LEU:HD21	1.83	0.61
5:F:781:PRO:CG	5:F:795:ILE:HG13	2.31	0.61
5:F:868:ASP:HA	5:F:871:THR:HG22	1.82	0.61
5:F:133:LEU:H	5:F:133:LEU:HD23	1.66	0.60
5:F:824:TRP:CG	5:F:864:MET:HE3	2.36	0.60
1:A:1337:LEU:HB2	1:A:1350:TYR:CD1	2.36	0.60
5:F:889:LEU:HG	5:F:894:VAL:CG1	2.23	0.60
5:F:161:VAL:CG2	5:F:221:PRO:CG	2.70	0.60
5:F:476:GLU:CD	5:F:478:LYS:HB2	2.26	0.60
5:F:465:THR:HG22	5:F:489:VAL:HG13	1.81	0.60
1:A:291:MET:HG2	1:A:318:ILE:HD11	1.84	0.60
1:A:798:ALA:CB	1:A:800:TRP:CE2	2.82	0.60
5:F:1068:LEU:HD12	5:F:1068:LEU:O	2.01	0.60
6:D:1:NAG:H83	6:D:2:NAG:C8	2.31	0.60
1:A:1081:LEU:CG	1:A:1086:ARG:HG2	2.32	0.60
1:A:1337:LEU:HD23	1:A:1349:GLU:HB3	1.83	0.60
2:E:178:TYR:CD2	2:E:182:PHE:HB3	2.36	0.60
5:F:391:VAL:HG12	5:F:415:ILE:HB	1.84	0.60
5:F:474:GLN:O	5:F:475:PHE:C	2.45	0.60
5:F:1045:ASP:OD1	5:F:1046:PRO:HD2	2.02	0.60
1:A:451:SER:OG	1:A:464:GLN:NE2	2.35	0.60
5:F:449:THR:HG22	5:F:450:ASN:N	2.17	0.59
1:A:252:ARG:HG3	1:A:303:ASP:HB3	1.83	0.59
1:A:1081:LEU:HD12	1:A:1081:LEU:N	2.17	0.59
5:F:109:ALA:HB2	5:F:471:ILE:O	2.02	0.59
1:A:1337:LEU:HD22	1:A:1337:LEU:C	2.26	0.59
5:F:792:GLU:OE1	5:F:792:GLU:N	2.21	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:216:LEU:C	5:F:216:LEU:HD13	2.28	0.59
5:F:590:PHE:CE2	5:F:592:THR:CG2	2.86	0.59
5:F:710:LEU:CD2	5:F:714:PHE:CZ	2.82	0.59
5:F:824:TRP:CB	5:F:864:MET:HE1	2.32	0.59
5:F:889:LEU:HA	5:F:892:ILE:CD1	2.32	0.59
1:A:108:TYR:HB3	1:A:113:HIS:HB3	1.85	0.59
5:F:33:ILE:HG21	5:F:1007:HIS:ND1	2.17	0.59
5:F:476:GLU:OE1	5:F:478:LYS:CB	2.47	0.59
5:F:796:MET:HB3	5:F:818:LYS:HD2	1.83	0.59
5:F:521:GLY:O	5:F:562:ASP:OD1	2.21	0.59
5:F:217:ALA:HB2	5:F:240:VAL:HG21	1.85	0.59
1:A:1007:LEU:HA	1:A:1010:VAL:CG1	2.33	0.59
1:A:1057:MET:HE1	13:A:1909:C9F:S06	2.42	0.59
5:F:361:MET:HE1	5:F:387:PHE:CD1	2.36	0.59
5:F:590:PHE:CD2	5:F:592:THR:CG2	2.85	0.59
5:F:85:ASP:HB3	5:F:502:LEU:HD22	1.84	0.58
1:A:78:ASP:OD2	5:F:263:SER:HB2	2.03	0.58
5:F:168:VAL:HG13	5:F:216:LEU:CD2	2.24	0.58
5:F:887:ARG:NH2	5:F:1032:ARG:O	2.36	0.58
5:F:170:ILE:CD1	5:F:216:LEU:HD23	2.31	0.58
5:F:780:ALA:HB2	5:F:863:LEU:HD21	1.84	0.58
5:F:851:MET:SD	5:F:1020:MET:SD	3.01	0.58
5:F:291:VAL:CG1	5:F:312:ALA:HB2	2.28	0.58
1:A:357:GLN:HG2	1:A:670:LEU:HD11	1.85	0.58
5:F:456:LEU:O	5:F:457:GLU:HB2	2.03	0.58
5:F:523:VAL:HG21	5:F:526:HIS:HB2	1.85	0.58
5:F:651:LEU:O	5:F:687:ASN:ND2	2.37	0.58
5:F:702:THR:O	5:F:706:ASN:HB2	2.03	0.58
1:A:375:VAL:HG12	1:A:376:MET:HG2	1.85	0.58
1:A:1396:PRO:HA	1:A:1399:LEU:HB2	1.86	0.58
1:A:40:LEU:HA	1:A:43:ALA:CB	2.18	0.58
1:A:91:TYR:O	1:A:95:THR:HG23	2.03	0.57
1:A:981:THR:HG22	5:F:552:ASN:CB	2.30	0.57
5:F:357:ASN:ND2	5:F:1064:ASP:HB3	2.18	0.57
5:F:366:GLY:HA3	5:F:396:TYR:HB3	1.84	0.57
5:F:693:LYS:NZ	5:F:696:ASN:OD1	2.37	0.57
1:A:957:CYS:SG	1:A:958:ASN:N	2.75	0.57
6:K:2:NAG:H82	6:K:2:NAG:C3	2.21	0.57
1:A:75:PRO:HG2	5:F:265:SER:HA	1.84	0.57
1:A:1081:LEU:O	1:A:1086:ARG:HD3	2.04	0.57
5:F:1011:LEU:HD12	5:F:1011:LEU:N	2.20	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:835:PHE:HA	1:A:838:ALA:HB3	1.86	0.57
1:A:1081:LEU:HD13	1:A:1086:ARG:HD2	1.79	0.57
5:F:256:MET:CB	5:F:359:ILE:HD11	2.34	0.57
2:E:141:SER:OG	2:E:196:GLY:O	2.20	0.57
5:F:824:TRP:CB	5:F:864:MET:CE	2.83	0.57
1:A:596:ASN:O	1:A:602:GLN:HG3	2.03	0.57
5:F:100:LEU:HD13	5:F:198:ASN:HD21	1.62	0.57
1:A:480:LEU:HA	1:A:483:MET:HG2	1.87	0.57
1:A:1060:PHE:CE2	1:A:1373:ILE:CD1	2.88	0.57
2:E:32:TRP:CD1	2:E:182:PHE:HD1	2.23	0.57
5:F:339:PHE:O	5:F:343:PHE:CD2	2.58	0.56
5:F:844:CYS:HB3	5:F:866:ASN:ND2	2.20	0.56
1:A:226:CYS:SG	1:A:254:CYS:CA	2.94	0.56
11:A:1904:3PE:O22	11:A:1904:3PE:H31	2.03	0.56
5:F:205:LEU:HD21	5:F:492:VAL:HG21	1.87	0.56
5:F:889:LEU:O	5:F:892:ILE:CG1	2.54	0.56
1:A:1085:GLN:O	1:A:1089:VAL:HG23	2.05	0.56
1:A:1339:ASP:OD1	1:A:1339:ASP:N	2.29	0.56
1:A:245:CYS:CB	1:A:252:ARG:HD2	2.35	0.56
1:A:1056:MET:O	1:A:1059:ILE:HG22	2.05	0.56
2:E:35:LEU:HG	2:E:37:PRO:HD3	1.88	0.56
5:F:37:VAL:HG13	5:F:1011:LEU:HG	1.88	0.56
5:F:895:TYR:CE1	5:F:986:PHE:HE1	2.22	0.56
1:A:1081:LEU:CB	1:A:1086:ARG:HG2	2.36	0.56
5:F:121:GLU:HA	5:F:121:GLU:OE1	2.04	0.56
5:F:365:ASP:OD1	5:F:366:GLY:N	2.38	0.56
5:F:366:GLY:HA3	5:F:396:TYR:HB2	1.88	0.56
5:F:1061:VAL:HG23	5:F:1061:VAL:O	2.05	0.56
1:A:41:ARG:CD	1:A:42:LYS:N	2.69	0.56
1:A:1181:PRO:HB3	11:A:1904:3PE:H331	1.80	0.56
2:E:215:CYS:O	2:E:216:MET:HG2	2.06	0.56
1:A:1475:LEU:HD12	1:A:1475:LEU:N	2.21	0.56
5:F:326:ASN:ND2	9:F:1105:NAG:C2	2.65	0.56
5:F:1010:LYS:HG3	5:F:1017:ILE:CG1	2.34	0.56
1:A:38:ASN:HB3	1:A:42:LYS:HE2	1.87	0.56
1:A:809:ILE:HG21	1:A:907:ALA:HB2	1.87	0.56
5:F:444:LYS:NZ	5:F:467:PRO:O	2.39	0.56
5:F:449:THR:HG22	5:F:450:ASN:H	1.71	0.55
5:F:773:ASN:HD22	5:F:777:VAL:HG21	1.71	0.55
6:D:1:NAG:C8	6:D:2:NAG:C7	2.83	0.55
1:A:256:ILE:HG22	1:A:256:ILE:O	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1181:PRO:CB	11:A:1904:3PE:H332	2.36	0.55
5:F:243:ARG:HH21	5:F:243:ARG:CG	2.15	0.55
1:A:1084:ASN:CA	1:A:1087:GLN:HG2	2.34	0.55
1:A:96:VAL:O	1:A:99:ILE:HG13	2.07	0.55
1:A:1083:LYS:HD3	1:A:1086:ARG:NH2	2.22	0.55
5:F:33:ILE:HD11	5:F:1020:MET:HE3	1.88	0.55
5:F:37:VAL:CG2	5:F:1018:PHE:CD2	2.90	0.55
5:F:227:ASP:HB2	5:F:236:ASP:HB3	1.89	0.55
5:F:297:ASN:ND2	5:F:330:LYS:O	2.37	0.55
5:F:370:ARG:HG3	5:F:372:GLN:HG3	1.89	0.55
5:F:523:VAL:HG13	5:F:523:VAL:O	2.05	0.55
5:F:570:ASN:HD21	5:F:592:THR:CG2	2.20	0.55
1:A:210:TYR:O	1:A:313:TYR:OH	2.25	0.54
1:A:788:VAL:HG12	1:A:791:LEU:CD2	2.37	0.54
1:A:928:ILE:HD13	1:A:1060:PHE:HE1	1.72	0.54
1:A:981:THR:CG2	5:F:552:ASN:HB3	2.33	0.54
2:E:34:VAL:HB	2:E:177:TYR:HB3	1.88	0.54
1:A:104:LYS:HD3	1:A:117:TYR:CE1	2.42	0.54
5:F:129:ALA:O	5:F:130:LYS:HG2	2.07	0.54
5:F:256:MET:HE1	5:F:281:MET:CG	2.38	0.54
1:A:1083:LYS:HB2	1:A:1086:ARG:HH22	1.73	0.54
5:F:629:TYR:CD1	5:F:629:TYR:C	2.84	0.54
5:F:385:ARG:HH12	5:F:431:VAL:HG12	1.73	0.54
5:F:824:TRP:CD1	5:F:864:MET:CE	2.87	0.54
1:A:1334:TYR:N	1:A:1353:GLY:C	2.65	0.54
1:A:788:VAL:HG12	1:A:791:LEU:HD22	1.90	0.54
1:A:1395:GLY:H	1:A:1398:HIS:HD2	1.55	0.54
5:F:441:ASP:N	5:F:441:ASP:OD1	2.40	0.54
5:F:528:ASN:O	5:F:528:ASN:ND2	2.27	0.54
5:F:361:MET:CE	5:F:387:PHE:HD1	2.19	0.54
5:F:780:ALA:CB	5:F:863:LEU:HD21	2.38	0.54
5:F:570:ASN:ND2	5:F:592:THR:CG2	2.70	0.53
5:F:896:ALA:CB	5:F:987:ASP:HB3	2.38	0.53
5:F:284:THR:HG21	5:F:428:TYR:OH	2.09	0.53
5:F:858:ASP:CA	5:F:986:PHE:CZ	2.88	0.53
1:A:1173:LYS:O	1:A:1174:ALA:HB3	2.08	0.53
4:C:390:LYS:HD3	4:C:435:ASP:HB3	1.89	0.53
1:A:788:VAL:CG1	1:A:791:LEU:HD22	2.38	0.53
1:A:1151:ASP:HA	1:A:1154:ASN:HD22	1.73	0.53
5:F:171:PRO:HG2	5:F:174:ILE:HD12	1.88	0.53
5:F:348:ASN:C	5:F:350:ASN:H	2.16	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1007:LEU:HA	1:A:1010:VAL:HG12	1.90	0.53
2:E:28:VAL:O	2:E:55:ARG:NH2	2.42	0.53
1:A:1054:PHE:O	1:A:1058:ASN:ND2	2.42	0.53
1:A:1281:TYR:O	1:A:1360:TYR:OH	2.22	0.53
1:A:40:LEU:O	1:A:41:ARG:C	2.50	0.53
1:A:189:ILE:HG23	1:A:654:ASN:HD22	1.74	0.53
5:F:992:SER:O	5:F:993:PHE:CD1	2.62	0.53
1:A:112:PHE:HA	1:A:115:ASP:HB3	1.90	0.53
1:A:1088:CYS:O	1:A:1091:TYR:HB3	2.08	0.53
5:F:61:TYR:O	5:F:68:TYR:OH	2.24	0.53
5:F:230:ARG:N	5:F:230:ARG:HD3	2.23	0.53
1:A:44:CYS:SG	1:A:45:ILE:N	2.82	0.53
1:A:368:SER:HA	1:A:371:THR:HG22	1.90	0.53
5:F:597:GLN:OE1	5:F:768:LYS:NZ	2.38	0.53
5:F:795:ILE:HD11	5:F:874:ILE:HD11	1.91	0.53
1:A:358:GLN:HA	1:A:361:GLU:HG2	1.90	0.53
1:A:40:LEU:O	1:A:44:CYS:N	2.42	0.52
6:K:2:NAG:H3	6:K:2:NAG:C8	2.19	0.52
1:A:252:ARG:HD2	1:A:252:ARG:O	2.09	0.52
1:A:1315:LEU:HD23	1:A:1315:LEU:O	2.09	0.52
5:F:178:SER:O	5:F:181:VAL:HG13	2.09	0.52
5:F:339:PHE:CZ	5:F:362:LEU:CD2	2.92	0.52
5:F:1010:LYS:CG	5:F:1017:ILE:CG1	2.85	0.52
1:A:256:ILE:O	1:A:257:ASN:HB2	2.09	0.52
1:A:1337:LEU:HD22	1:A:1338:CYS:H	1.71	0.52
5:F:1066:ASN:HD22	5:F:1067:VAL:H	1.57	0.52
1:A:118:LEU:HD11	1:A:124:VAL:HG22	1.92	0.52
1:A:958:ASN:HB2	1:A:989:GLN:H	1.74	0.52
1:A:1060:PHE:O	1:A:1064:VAL:HG23	2.10	0.52
5:F:359:ILE:HD13	5:F:361:MET:CE	2.37	0.52
5:F:777:VAL:O	5:F:797:VAL:HA	2.10	0.52
5:F:826:GLU:O	5:F:830:LYS:HG2	2.09	0.52
5:F:993:PHE:CB	5:F:1008:VAL:CG1	2.77	0.52
5:F:1011:LEU:N	5:F:1011:LEU:CD1	2.73	0.52
1:A:1007:LEU:O	1:A:1010:VAL:HG13	2.09	0.52
2:E:57:CYS:HA	2:E:80:CYS:HA	1.91	0.52
5:F:127:TYR:HB2	5:F:147:ILE:HB	1.92	0.51
5:F:367:GLY:O	5:F:400:PRO:CG	2.51	0.51
1:A:92:PHE:C	1:A:92:PHE:CD2	2.88	0.51
1:A:245:CYS:HB2	1:A:252:ARG:HD2	1.92	0.51
5:F:34:LYS:CD	5:F:1009:GLU:OE2	2.59	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1084:ASN:HA	1:A:1087:GLN:CG	2.40	0.51
5:F:177:GLY:HA2	5:F:182:LEU:HD23	1.91	0.51
5:F:532:LYS:NZ	5:F:532:LYS:CB	2.73	0.51
5:F:510:PRO:CG	5:F:767:TYR:CE2	2.84	0.51
5:F:867:HIS:O	5:F:868:ASP:CB	2.57	0.51
5:F:889:LEU:HA	5:F:892:ILE:CG1	2.41	0.51
5:F:1070:ASP:OD1	5:F:1072:THR:N	2.40	0.51
1:A:548:LEU:HD21	1:A:1059:ILE:HD12	1.88	0.51
1:A:1475:LEU:N	1:A:1475:LEU:CD1	2.73	0.51
2:E:187:ALA:O	2:E:191:LEU:N	2.43	0.51
5:F:346:LEU:O	5:F:353:ARG:NH2	2.43	0.51
1:A:1057:MET:SD	13:A:1909:C9F:S06	3.09	0.51
2:E:50:HIS:N	2:E:57:CYS:O	2.44	0.51
5:F:846:ARG:O	5:F:847:ASN:HB2	2.10	0.51
5:F:386:VAL:O	5:F:410:GLY:HA3	2.10	0.51
5:F:487:LEU:HD22	7:I:1:NAG:H82	1.93	0.51
5:F:792:GLU:H	5:F:792:GLU:CD	2.12	0.51
1:A:116:ALA:O	1:A:119:ARG:HB2	2.11	0.50
5:F:690:ILE:HG23	5:F:695:PRO:HG3	1.93	0.50
1:A:1083:LYS:CA	1:A:1086:ARG:CZ	2.89	0.50
5:F:783:PHE:HE1	5:F:873:GLN:CA	2.23	0.50
5:F:1008:VAL:HG23	5:F:1019:ILE:CG2	2.37	0.50
5:F:336:LYS:CE	5:F:369:GLU:OE2	2.52	0.50
5:F:712:ALA:HB2	5:F:743:ILE:HD13	1.93	0.50
5:F:167:ALA:HB3	5:F:219:TYR:CZ	2.46	0.50
5:F:339:PHE:HZ	5:F:362:LEU:CD2	2.24	0.50
1:A:40:LEU:O	1:A:43:ALA:N	2.44	0.50
1:A:819:GLU:OE2	1:A:897:ARG:NH2	2.45	0.50
2:E:27:VAL:HG13	2:E:28:VAL:HG13	1.94	0.50
5:F:479:THR:O	5:F:480:ASN:HB3	2.12	0.50
1:A:38:ASN:CB	1:A:42:LYS:HE2	2.41	0.50
1:A:238:GLU:HG3	1:A:986:ARG:HH22	1.77	0.50
1:A:1334:TYR:H	1:A:1354:THR:N	2.08	0.50
1:A:1426:LEU:HD13	1:A:1429:ILE:HD12	1.94	0.50
2:E:50:HIS:HB2	2:E:57:CYS:HB3	1.93	0.50
5:F:33:ILE:HG23	5:F:1018:PHE:HE2	1.77	0.50
2:E:32:TRP:HB3	2:E:181:SER:HB3	1.93	0.50
5:F:237:LEU:HD12	5:F:237:LEU:H	1.76	0.50
5:F:291:VAL:O	5:F:291:VAL:HG13	2.11	0.50
5:F:454:ASP:OD1	5:F:455:ALA:N	2.44	0.50
5:F:506:PHE:CZ	5:F:667:ARG:CG	2.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:726:GLN:HB3	5:F:729:ILE:HD11	1.94	0.50
1:A:655:VAL:O	1:A:659:ILE:HG13	2.12	0.50
5:F:476:GLU:OE1	5:F:478:LYS:N	2.45	0.50
1:A:36:LEU:C	1:A:113:HIS:NE2	2.70	0.49
1:A:140:GLU:OE2	1:A:165:ARG:NH2	2.43	0.49
5:F:385:ARG:NH1	5:F:431:VAL:HG12	2.27	0.49
5:F:781:PRO:HD3	5:F:795:ILE:HG13	1.93	0.49
5:F:1008:VAL:CB	5:F:1019:ILE:HG22	2.41	0.49
1:A:355:GLU:O	1:A:359:LEU:N	2.39	0.49
5:F:256:MET:HE1	5:F:281:MET:HG2	1.93	0.49
1:A:656:PHE:HB3	1:A:1058:ASN:CG	2.37	0.49
5:F:481:LEU:HD23	5:F:482:LYS:N	2.22	0.49
5:F:206:LEU:HD23	5:F:458:LEU:HD23	1.93	0.49
5:F:1021:VAL:HG22	5:F:1022:GLU:N	2.26	0.49
5:F:350:ASN:CG	6:D:1:NAG:C1	2.85	0.49
5:F:663:PHE:CB	5:F:744:THR:HG23	2.39	0.49
5:F:775:ASN:HB2	5:F:1013:ASN:O	2.12	0.49
1:A:94:LEU:CD1	1:A:94:LEU:C	2.86	0.49
1:A:1081:LEU:CD1	1:A:1086:ARG:HD3	2.23	0.49
5:F:242:ARG:NH1	5:F:426:GLN:HB3	2.28	0.49
2:E:112:VAL:O	2:E:116:GLY:N	2.43	0.49
5:F:205:LEU:HD21	5:F:492:VAL:HG23	1.95	0.49
1:A:38:ASN:HD22	1:A:38:ASN:C	2.18	0.49
1:A:548:LEU:HD22	1:A:1059:ILE:HD11	1.89	0.49
6:D:1:NAG:H83	6:D:2:NAG:O7	2.12	0.49
4:C:284:LEU:HD11	4:C:418:ALA:HB3	1.93	0.49
5:F:993:PHE:CB	5:F:1008:VAL:HG13	2.37	0.49
1:A:1083:LYS:CD	1:A:1086:ARG:HH21	2.25	0.49
1:A:1334:TYR:CA	1:A:1353:GLY:C	2.82	0.49
5:F:57:LEU:HD23	5:F:801:VAL:HG21	1.94	0.49
5:F:516:ALA:HB3	5:F:525:LEU:N	2.28	0.49
5:F:710:LEU:HD23	5:F:710:LEU:O	2.12	0.49
1:A:927:THR:OG1	1:A:928:ILE:N	2.45	0.48
1:A:206:MET:HE3	1:A:206:MET:HB2	1.74	0.48
1:A:1108:GLN:NE2	1:A:1170:LEU:O	2.39	0.48
5:F:216:LEU:HD13	5:F:216:LEU:O	2.12	0.48
1:A:244:PRO:O	1:A:303:ASP:HB3	2.13	0.48
1:A:318:ILE:O	1:A:322:SER:HB3	2.13	0.48
1:A:548:LEU:CD2	1:A:1059:ILE:CD1	2.68	0.48
1:A:1472:ARG:HH11	1:A:1478:LYS:HB2	1.78	0.48
2:E:32:TRP:HB2	2:E:182:PHE:HB2	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:281:MET:O	5:F:284:THR:HB	2.12	0.48
5:F:460:LEU:HD13	5:F:529:LEU:CD1	2.42	0.48
5:F:477:ASN:N	5:F:477:ASN:ND2	2.60	0.48
5:F:151:PHE:CZ	5:F:224:PRO:HD3	2.48	0.48
5:F:163:TYR:O	5:F:220:TYR:OH	2.28	0.48
5:F:357:ASN:ND2	5:F:1064:ASP:CB	2.76	0.48
5:F:161:VAL:HG23	5:F:223:SER:OG	2.14	0.48
5:F:808:LYS:O	5:F:810:LEU:HD23	2.13	0.48
1:A:330:LEU:CD2	13:A:1909:C9F:C20	2.92	0.48
1:A:651:ILE:O	1:A:655:VAL:HG23	2.12	0.48
1:A:1063:PHE:CD1	1:A:1063:PHE:C	2.92	0.48
5:F:627:PRO:HG2	5:F:630:SER:HB3	1.94	0.48
5:F:210:PHE:HB2	5:F:490:MET:CE	2.42	0.48
5:F:365:ASP:O	5:F:394:HIS:CE1	2.66	0.48
5:F:481:LEU:CD2	5:F:482:LYS:H	2.22	0.48
1:A:40:LEU:C	1:A:43:ALA:H	2.21	0.48
5:F:562:ASP:OD1	5:F:563:PHE:N	2.46	0.48
1:A:574:ALA:HB2	1:A:604:LEU:HD12	1.95	0.48
2:E:30:ASP:OD1	2:E:30:ASP:N	2.47	0.48
5:F:34:LYS:HD2	5:F:1009:GLU:OE2	2.13	0.48
5:F:889:LEU:HA	5:F:892:ILE:HG12	1.95	0.48
5:F:262:VAL:HG23	5:F:297:ASN:HB3	1.96	0.47
5:F:390:SER:HB2	5:F:412:TYR:OH	2.14	0.47
1:A:981:THR:CG2	5:F:552:ASN:CB	2.91	0.47
5:F:285:LEU:CD1	5:F:291:VAL:HG21	2.45	0.47
5:F:510:PRO:CG	5:F:767:TYR:HE2	2.22	0.47
5:F:720:GLN:O	5:F:724:SER:OG	2.32	0.47
5:F:824:TRP:O	5:F:864:MET:HE1	2.12	0.47
1:A:1085:GLN:HE22	1:A:1475:LEU:CB	2.06	0.47
5:F:284:THR:CG2	5:F:428:TYR:OH	2.62	0.47
5:F:532:LYS:HZ2	5:F:532:LYS:HB2	1.79	0.47
5:F:570:ASN:ND2	5:F:592:THR:HG22	2.30	0.47
5:F:259:LEU:HD11	5:F:342:ALA:HB2	1.95	0.47
5:F:783:PHE:CE1	5:F:873:GLN:HA	2.44	0.47
5:F:896:ALA:HB2	5:F:987:ASP:HB3	1.95	0.47
1:A:309:TRP:HB3	12:A:1905:PC1:H222	1.96	0.47
1:A:1446:LYS:O	1:A:1450:GLY:N	2.36	0.47
5:F:28:PRO:HD3	5:F:851:MET:CE	2.28	0.47
5:F:51:ALA:HB3	5:F:817:ILE:HD11	1.96	0.47
5:F:133:LEU:CD2	5:F:133:LEU:N	2.73	0.47
5:F:710:LEU:CD2	5:F:714:PHE:CE1	2.98	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:781:PRO:CD	5:F:795:ILE:HG13	2.45	0.47
5:F:54:VAL:HG22	5:F:815:VAL:HG21	1.97	0.47
5:F:669:TYR:HE1	5:F:708:VAL:HG21	1.78	0.47
5:F:711:ASP:OD2	5:F:739:THR:CG2	2.63	0.47
5:F:1010:LYS:HG3	5:F:1017:ILE:CD1	2.45	0.47
5:F:33:ILE:HG23	5:F:1018:PHE:CE2	2.50	0.47
5:F:178:SER:CB	5:F:181:VAL:HG12	2.28	0.47
5:F:370:ARG:HD2	5:F:372:GLN:HE21	1.78	0.47
1:A:99:ILE:C	1:A:99:ILE:CD1	2.85	0.47
5:F:285:LEU:HD11	5:F:291:VAL:HG21	1.97	0.47
1:A:225:THR:CG2	1:A:227:TYR:CE2	2.97	0.46
1:A:1012:THR:O	1:A:1013:PHE:CB	2.62	0.46
1:A:1496:LYS:O	1:A:1497:ILE:C	2.57	0.46
2:E:32:TRP:HE3	2:E:181:SER:HB3	1.76	0.46
5:F:480:ASN:HD22	5:F:480:ASN:C	2.14	0.46
5:F:669:TYR:CE1	5:F:708:VAL:HG21	2.50	0.46
6:G:1:NAG:H62	6:G:2:NAG:HN2	1.80	0.46
1:A:659:ILE:HG23	1:A:663:ASN:OD1	2.16	0.46
1:A:796:VAL:HA	1:A:801:PHE:CD2	2.51	0.46
5:F:133:LEU:HD23	5:F:133:LEU:N	2.28	0.46
1:A:1324:ALA:HB1	1:A:1327:GLU:HB3	1.97	0.46
5:F:710:LEU:HD21	5:F:714:PHE:CE1	2.46	0.46
5:F:824:TRP:HB3	5:F:864:MET:HE3	1.97	0.46
5:F:466:LEU:HD12	5:F:467:PRO:HD2	1.98	0.46
5:F:1012:MET:O	5:F:1013:ASN:CB	2.63	0.46
1:A:1081:LEU:CD1	1:A:1086:ARG:CD	2.69	0.46
5:F:126:TYR:HE1	5:F:144:SER:HB2	1.81	0.46
5:F:283:GLU:OE1	5:F:283:GLU:HA	2.16	0.46
5:F:1070:ASP:OD2	5:F:1072:THR:HG22	2.14	0.46
1:A:118:LEU:HD13	1:A:118:LEU:C	2.40	0.46
1:A:1334:TYR:H	1:A:1353:GLY:CA	2.28	0.46
2:E:217:ASP:O	2:E:218:ALA:C	2.58	0.46
5:F:33:ILE:HG21	5:F:1007:HIS:CE1	2.50	0.46
5:F:516:ALA:CB	5:F:524:LEU:HB3	2.46	0.46
5:F:711:ASP:OD2	5:F:739:THR:HG23	2.15	0.46
5:F:856:LEU:HD21	5:F:878:PHE:CG	2.51	0.46
1:A:99:ILE:CD1	1:A:100:GLU:N	2.75	0.46
5:F:629:TYR:C	5:F:629:TYR:HD1	2.23	0.46
5:F:826:GLU:CD	5:F:846:ARG:HH21	2.21	0.46
5:F:234:LYS:HB2	5:F:551:GLN:HG2	1.96	0.46
5:F:364:THR:O	5:F:390:SER:HA	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1074:CYS:C	14:F:1102:ETA:C	2.89	0.46
1:A:318:ILE:CG2	1:A:319:LEU:N	2.79	0.46
2:E:1:MET:O	2:E:5:GLU:N	2.48	0.46
5:F:41:GLN:HB3	5:F:1011:LEU:HB3	1.98	0.46
5:F:895:TYR:CE1	5:F:986:PHE:CE1	3.03	0.46
1:A:269:ASN:HB2	1:A:273:THR:HG22	1.97	0.46
1:A:928:ILE:HD13	1:A:1060:PHE:CE1	2.50	0.46
1:A:1001:LEU:HG	11:A:1908:3PE:H31	1.97	0.46
1:A:1083:LYS:CD	1:A:1086:ARG:NH2	2.79	0.46
5:F:320:LEU:O	5:F:324:VAL:HG23	2.16	0.46
5:F:628:THR:O	5:F:629:TYR:CD2	2.69	0.46
5:F:50:THR:O	5:F:722:TYR:OH	2.29	0.45
5:F:539:PRO:HD3	5:F:977:CYS:HB3	1.98	0.45
5:F:607:ARG:HA	5:F:607:ARG:HD3	1.80	0.45
5:F:847:ASN:HD22	5:F:847:ASN:N	2.13	0.45
1:A:39:PRO:CG	1:A:41:ARG:NH1	2.73	0.45
5:F:285:LEU:HD13	5:F:291:VAL:HB	1.99	0.45
1:A:366:TYR:HB3	4:C:400:LEU:HD21	1.99	0.45
1:A:1060:PHE:HZ	1:A:1373:ILE:HD11	1.79	0.45
1:A:1085:GLN:CD	1:A:1475:LEU:HB3	2.40	0.45
1:A:1396:PRO:O	1:A:1400:ASP:N	2.48	0.45
5:F:304:SER:HB2	5:F:305:CYS:H	1.54	0.45
5:F:336:LYS:HG3	5:F:369:GLU:OE2	2.16	0.45
5:F:362:LEU:HD12	5:F:362:LEU:O	2.16	0.45
1:A:352:LYS:HE2	1:A:352:LYS:HB3	1.84	0.45
1:A:520:THR:O	1:A:523:GLY:N	2.49	0.45
1:A:1456:ASN:HD22	1:A:1461:VAL:HA	1.80	0.45
5:F:801:VAL:O	5:F:811:LYS:HA	2.16	0.45
1:A:798:ALA:CB	1:A:800:TRP:NE1	2.79	0.45
5:F:368:GLU:O	5:F:368:GLU:HG2	2.16	0.45
5:F:516:ALA:HB3	5:F:525:LEU:H	1.81	0.45
8:L:1:NAG:H61	8:L:2:NAG:O5	2.16	0.45
2:E:81:SER:OG	2:E:82:TYR:N	2.48	0.45
5:F:75:ALA:O	5:F:79:VAL:HG23	2.17	0.45
5:F:319:VAL:HG21	5:F:1046:PRO:HG3	1.98	0.45
5:F:773:ASN:HD22	5:F:777:VAL:CG2	2.30	0.45
1:A:1060:PHE:CE2	1:A:1373:ILE:HD13	2.52	0.45
1:A:1141:HIS:O	11:A:1906:3PE:N	2.39	0.45
5:F:79:VAL:HG12	5:F:612:THR:HG22	1.99	0.45
5:F:161:VAL:HG22	5:F:162:SER:N	2.30	0.45
5:F:523:VAL:CG2	5:F:526:HIS:HB2	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:628:THR:O	5:F:629:TYR:CG	2.69	0.45
5:F:705:ILE:CD1	5:F:706:ASN:N	2.78	0.45
5:F:825:ILE:HA	5:F:864:MET:HE2	1.98	0.45
1:A:38:ASN:HD21	1:A:41:ARG:CZ	2.30	0.45
1:A:104:LYS:HD3	1:A:117:TYR:HE1	1.81	0.45
1:A:574:ALA:HB2	1:A:604:LEU:CD1	2.47	0.45
5:F:292:ASN:OD1	5:F:293:VAL:N	2.47	0.45
5:F:821:VAL:O	5:F:825:ILE:HG13	2.17	0.45
5:F:1006:PHE:O	5:F:1006:PHE:CD1	2.70	0.45
1:A:1342:SER:OG	1:A:1343:ASP:N	2.50	0.45
5:F:41:GLN:OE1	5:F:1012:MET:O	2.34	0.45
5:F:511:ASN:HB2	5:F:627:PRO:HG3	1.99	0.45
5:F:515:PHE:CZ	5:F:623:ALA:HB3	2.52	0.45
5:F:525:LEU:C	5:F:525:LEU:CD2	2.90	0.45
2:E:37:PRO:HG2	2:E:47:GLU:HB2	1.98	0.44
5:F:27:PHE:CE1	5:F:1020:MET:HG2	2.52	0.44
5:F:235:ILE:HD12	5:F:235:ILE:C	2.41	0.44
5:F:576:ILE:HD11	5:F:588:LYS:HG2	1.99	0.44
5:F:669:TYR:CD1	5:F:704:LEU:HD21	2.37	0.44
5:F:710:LEU:CD2	5:F:710:LEU:C	2.90	0.44
4:C:284:LEU:HD12	4:C:415:GLN:HA	1.99	0.44
1:A:1007:LEU:HA	1:A:1007:LEU:HD23	1.83	0.44
1:A:1175:ARG:HG3	2:E:135:TYR:CE1	2.52	0.44
5:F:1010:LYS:CG	5:F:1017:ILE:CD1	2.95	0.44
1:A:1083:LYS:CB	1:A:1086:ARG:NH2	2.78	0.44
5:F:243:ARG:HA	5:F:243:ARG:HD2	1.74	0.44
5:F:465:THR:HG22	5:F:466:LEU:N	2.32	0.44
5:F:702:THR:HG23	5:F:703:ASP:N	2.32	0.44
5:F:867:HIS:O	5:F:868:ASP:HB3	2.16	0.44
1:A:837:ILE:HB	1:A:883:MET:HE2	1.99	0.44
1:A:1060:PHE:CZ	1:A:1373:ILE:CD1	2.99	0.44
2:E:19:GLY:HA3	2:E:191:LEU:HD22	1.99	0.44
5:F:381:ASP:OD1	5:F:381:ASP:N	2.37	0.44
1:A:788:VAL:O	1:A:791:LEU:CD2	2.64	0.44
1:A:812:SER:HB3	1:A:903:ARG:HD3	1.99	0.44
1:A:1081:LEU:HB2	1:A:1086:ARG:CG	2.46	0.44
5:F:94:SER:O	5:F:98:VAL:HG23	2.17	0.44
1:A:84:LEU:O	1:A:88:LYS:CE	2.66	0.44
5:F:704:LEU:HD23	5:F:704:LEU:O	2.18	0.44
5:F:739:THR:HG22	5:F:743:ILE:O	2.17	0.44
5:F:803:ILE:HD12	5:F:805:ILE:HD11	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:855:ILE:C	5:F:856:LEU:HD12	2.42	0.44
1:A:788:VAL:HB	1:A:791:LEU:CD2	2.47	0.44
5:F:281:MET:HE3	5:F:363:PHE:HZ	1.83	0.44
5:F:848:SER:OG	5:F:850:VAL:CG1	2.66	0.44
1:A:1334:TYR:H	1:A:1353:GLY:HA3	1.83	0.44
5:F:214:THR:HG22	5:F:214:THR:O	2.16	0.44
5:F:1001:ASN:HD22	9:F:1122:NAG:C1	2.08	0.44
1:A:99:ILE:HD12	1:A:100:GLU:CA	2.48	0.43
1:A:233:ILE:HD13	5:F:547:ARG:HB3	1.99	0.43
5:F:198:ASN:HB2	5:F:208:GLN:OE1	2.18	0.43
5:F:669:TYR:HD1	5:F:704:LEU:CD2	2.24	0.43
5:F:781:PRO:O	5:F:875:GLY:CA	2.60	0.43
5:F:253:PRO:O	5:F:356:CYS:HB3	2.19	0.43
5:F:390:SER:CB	5:F:412:TYR:OH	2.66	0.43
5:F:481:LEU:HD23	5:F:481:LEU:N	2.33	0.43
1:A:1084:ASN:O	1:A:1087:GLN:HG2	2.18	0.43
5:F:133:LEU:H	5:F:133:LEU:HD22	1.80	0.43
5:F:1006:PHE:CD1	5:F:1006:PHE:C	2.96	0.43
1:A:1081:LEU:HD13	1:A:1086:ARG:HG2	1.98	0.43
5:F:182:LEU:HD22	5:F:182:LEU:HA	1.80	0.43
5:F:516:ALA:HB3	5:F:524:LEU:HB3	2.01	0.43
5:F:733:LYS:HE3	5:F:733:LYS:HB2	1.82	0.43
5:F:826:GLU:OE1	5:F:826:GLU:HA	2.17	0.43
5:F:1010:LYS:HG2	5:F:1017:ILE:CG1	2.47	0.43
6:D:1:NAG:H82	6:D:1:NAG:H3	2.00	0.43
5:F:191:LEU:CD2	5:F:490:MET:HE1	2.49	0.43
5:F:208:GLN:O	5:F:219:TYR:HA	2.19	0.43
5:F:238:TYR:CD1	5:F:238:TYR:C	2.96	0.43
5:F:517:ILE:HD12	5:F:580:MET:HE3	2.00	0.43
5:F:169:HIS:CE1	5:F:238:TYR:HD1	2.37	0.43
5:F:242:ARG:NH2	5:F:280:GLU:O	2.52	0.43
5:F:281:MET:CE	5:F:363:PHE:HZ	2.31	0.43
5:F:400:PRO:O	5:F:404:MET:HG3	2.18	0.43
5:F:460:LEU:C	5:F:461:VAL:HG13	2.44	0.43
1:A:1099:ARG:HE	2:E:218:ALA:HA	1.83	0.43
4:C:351:ILE:HG23	4:C:382:LEU:HD21	2.00	0.43
5:F:513:TYR:CZ	5:F:625:VAL:HG21	2.54	0.43
5:F:824:TRP:HB3	5:F:864:MET:CE	2.48	0.43
1:A:41:ARG:CG	1:A:42:LYS:N	2.81	0.43
1:A:1081:LEU:H	1:A:1081:LEU:CD1	2.26	0.43
1:A:1292:ILE:HD12	1:A:1336:LYS:HB2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:21:VAL:O	2:E:25:THR:N	2.46	0.43
2:E:32:TRP:CH2	2:E:53:LEU:HD21	2.46	0.43
5:F:100:LEU:HD12	5:F:194:VAL:HG12	2.00	0.43
5:F:205:LEU:HD23	5:F:206:LEU:N	2.34	0.43
5:F:661:TYR:HD2	5:F:752:GLY:HA3	1.83	0.43
1:A:1008:PHE:O	1:A:1012:THR:HG23	2.19	0.43
5:F:346:LEU:HD21	5:F:360:ILE:CG2	2.49	0.43
5:F:590:PHE:CD1	5:F:590:PHE:N	2.87	0.43
1:A:333:LEU:HD21	1:A:653:LEU:O	2.19	0.43
1:A:1181:PRO:O	11:A:1904:3PE:H361	2.18	0.43
2:E:27:VAL:HA	2:E:53:LEU:HD12	2.01	0.43
5:F:33:ILE:CG2	5:F:1007:HIS:CE1	3.02	0.43
1:A:118:LEU:CD1	1:A:118:LEU:C	2.92	0.42
1:A:583:GLY:O	1:A:585:TYR:N	2.47	0.42
1:A:1175:ARG:HG3	2:E:135:TYR:CD1	2.54	0.42
5:F:41:GLN:HB3	5:F:1011:LEU:CG	2.49	0.42
5:F:41:GLN:CB	5:F:1011:LEU:HB3	2.49	0.42
5:F:847:ASN:N	5:F:847:ASN:ND2	2.67	0.42
1:A:1394:LEU:HD23	1:A:1475:LEU:HD22	2.01	0.42
5:F:981:GLN:HG2	5:F:1038:GLU:HG2	2.01	0.42
5:F:988:ASN:OD1	9:F:1123:NAG:O5	2.37	0.42
1:A:529:CYS:HB3	11:A:1907:3PE:H342	2.00	0.42
1:A:788:VAL:CG1	1:A:791:LEU:CD2	2.97	0.42
1:A:1431:PRO:HB3	1:A:1436:GLY:HA2	2.00	0.42
2:E:1:MET:HG3	2:E:5:GLU:HG3	2.01	0.42
5:F:44:LEU:HD11	5:F:824:TRP:HZ2	1.83	0.42
5:F:319:VAL:CG2	5:F:1046:PRO:HG3	2.49	0.42
5:F:1008:VAL:HB	5:F:1019:ILE:HG22	2.02	0.42
1:A:570:ILE:O	1:A:574:ALA:N	2.43	0.42
1:A:591:GLU:OE2	1:A:593:ARG:NH2	2.53	0.42
1:A:604:LEU:HD12	1:A:604:LEU:HA	1.84	0.42
1:A:798:ALA:CB	1:A:800:TRP:CZ2	3.01	0.42
1:A:287:GLN:NE2	1:A:617:ASN:HD22	2.18	0.42
5:F:346:LEU:HD12	5:F:346:LEU:HA	1.86	0.42
5:F:1005:ILE:HG23	5:F:1005:ILE:O	2.19	0.42
1:A:115:ASP:O	1:A:119:ARG:HG3	2.20	0.42
5:F:532:LYS:H	5:F:532:LYS:HG3	1.56	0.42
1:A:812:SER:O	1:A:903:ARG:NH1	2.50	0.42
1:A:958:ASN:HD22	1:A:988:ARG:HA	1.85	0.42
1:A:1165:MET:HE3	1:A:1187:PHE:HD1	1.85	0.42
5:F:704:LEU:O	5:F:708:VAL:HG23	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1908:3PE:H2	11:A:1908:3PE:H221	1.83	0.42
5:F:212:SER:CB	5:F:216:LEU:O	2.67	0.42
5:F:1011:LEU:CD1	5:F:1011:LEU:H	2.33	0.42
6:K:1:NAG:H82	6:K:2:NAG:C2	2.47	0.42
1:A:226:CYS:SG	1:A:254:CYS:HA	2.60	0.42
1:A:244:PRO:O	1:A:303:ASP:CB	2.68	0.42
2:E:32:TRP:HH2	2:E:53:LEU:CD2	2.32	0.42
5:F:178:SER:O	5:F:181:VAL:CG1	2.68	0.42
1:A:209:ILE:HD11	1:A:1243:LEU:HD22	2.02	0.41
1:A:548:LEU:O	1:A:552:LEU:N	2.50	0.41
2:E:149:LEU:HA	2:E:149:LEU:HD23	1.85	0.41
5:F:570:ASN:ND2	5:F:592:THR:HG21	2.33	0.41
5:F:844:CYS:HB3	5:F:866:ASN:HD21	1.85	0.41
5:F:1066:ASN:HD22	5:F:1067:VAL:N	2.17	0.41
1:A:1084:ASN:C	1:A:1087:GLN:HG2	2.45	0.41
2:E:117:PHE:O	2:E:121:GLY:N	2.44	0.41
5:F:206:LEU:CD2	5:F:495:SER:HB2	2.49	0.41
5:F:481:LEU:CD2	5:F:481:LEU:H	2.33	0.41
5:F:509:CYS:HB2	5:F:510:PRO:CD	2.49	0.41
1:A:318:ILE:HD12	1:A:318:ILE:HA	1.98	0.41
1:A:318:ILE:HG23	1:A:319:LEU:N	2.36	0.41
5:F:185:LEU:O	5:F:189:SER:OG	2.36	0.41
5:F:478:LYS:HD3	5:F:479:THR:HG23	2.01	0.41
5:F:705:ILE:HD12	5:F:706:ASN:CA	2.50	0.41
1:A:339:LYS:HD3	1:A:1388:THR:HA	2.01	0.41
2:E:35:LEU:HD11	2:E:174:ILE:HG12	2.02	0.41
5:F:369:GLU:HG2	5:F:371:ALA:H	1.85	0.41
5:F:510:PRO:HG3	5:F:762:TYR:CD1	2.55	0.41
5:F:705:ILE:C	5:F:705:ILE:CD1	2.85	0.41
5:F:817:ILE:HD13	5:F:817:ILE:HG21	1.86	0.41
1:A:265:TRP:CD1	1:A:266:PRO:HD2	2.56	0.41
5:F:114:ARG:HH21	7:H:1:NAG:C6	2.30	0.41
5:F:351:VAL:HG23	5:F:353:ARG:HG3	2.03	0.41
5:F:471:ILE:O	5:F:471:ILE:HG13	2.18	0.41
5:F:810:LEU:C	5:F:812:PRO:HD3	2.46	0.41
5:F:851:MET:HA	5:F:1023:SER:N	2.36	0.41
1:A:43:ALA:O	1:A:46:SER:OG	2.26	0.41
1:A:1105:ASN:O	1:A:1108:GLN:N	2.49	0.41
1:A:1373:ILE:HA	1:A:1376:PHE:HB2	2.02	0.41
5:F:58:VAL:HG13	5:F:803:ILE:HG22	2.01	0.41
5:F:232:PRO:HB2	5:F:234:LYS:HD3	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:290:PHE:HD1	5:F:354:ALA:HB2	1.86	0.41
5:F:346:LEU:CD2	5:F:360:ILE:CG2	2.98	0.41
5:F:477:ASN:N	5:F:477:ASN:HD22	2.18	0.41
5:F:809:LEU:C	5:F:810:LEU:CD2	2.86	0.41
1:A:226:CYS:CA	1:A:254:CYS:SG	3.08	0.41
1:A:468:ASN:OD1	1:A:534:ARG:NH1	2.49	0.41
5:F:151:PHE:CE2	5:F:224:PRO:HD3	2.56	0.41
1:A:44:CYS:O	1:A:47:ILE:N	2.47	0.40
1:A:91:TYR:HE1	1:A:137:ALA:CB	2.23	0.40
1:A:574:ALA:HA	1:A:607:VAL:HG21	2.03	0.40
1:A:1470:LEU:HD22	1:A:1470:LEU:HA	1.89	0.40
5:F:262:VAL:HG22	5:F:296:PHE:O	2.21	0.40
5:F:889:LEU:HD12	5:F:889:LEU:HA	1.88	0.40
1:A:91:TYR:CE1	1:A:137:ALA:HB1	2.35	0.40
1:A:1153:LEU:HA	1:A:1156:ALA:HB3	2.01	0.40
5:F:729:ILE:CG2	8:L:2:NAG:H82	2.51	0.40
1:A:788:VAL:CB	1:A:791:LEU:HD21	2.51	0.40
5:F:117:PHE:CD2	5:F:182:LEU:HD12	2.52	0.40
5:F:217:ALA:HB2	5:F:240:VAL:CG2	2.50	0.40
5:F:230:ARG:N	5:F:230:ARG:CD	2.83	0.40
5:F:274:ILE:CG1	5:F:391:VAL:HG21	2.52	0.40
5:F:303:VAL:HG13	5:F:323:ALA:CB	2.51	0.40
5:F:315:ARG:HD3	5:F:315:ARG:HA	1.97	0.40
6:K:1:NAG:H83	6:K:1:NAG:H2	1.91	0.40
1:A:1259:THR:HG22	1:A:1383:ASN:ND2	2.36	0.40
1:A:1334:TYR:N	1:A:1354:THR:N	2.70	0.40
11:A:1906:3PE:H322	11:A:1906:3PE:H222	2.03	0.40
2:E:111:SER:HA	2:E:114:SER:HB3	2.03	0.40
5:F:43:ASP:OD2	8:L:1:NAG:C1	2.70	0.40
5:F:398:ARG:O	5:F:401:ILE:HG22	2.21	0.40
5:F:579:LYS:HE2	5:F:579:LYS:HB2	1.84	0.40
5:F:780:ALA:HA	5:F:863:LEU:HD21	2.04	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	1260/1873 (67%)	1144 (91%)	111 (9%)	5 (0%)	30	59
2	E	159/222 (72%)	142 (89%)	16 (10%)	1 (1%)	21	51
3	B	98/450 (22%)	93 (95%)	5 (5%)	0	100	100
4	C	174/524 (33%)	167 (96%)	7 (4%)	0	100	100
5	F	968/1046 (92%)	876 (90%)	87 (9%)	5 (0%)	24	54
All	All	2659/4115 (65%)	2422 (91%)	226 (8%)	11 (0%)	31	59

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1013	PHE
5	F	349	TYR
5	F	629	TYR
5	F	661	TYR
1	A	304	ALA
2	E	205	PRO
5	F	790	ALA
1	A	584	ARG
1	A	305	ILE
1	A	51	LYS
5	F	627	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	1097/1628 (67%)	1070 (98%)	27 (2%)	42	74
2	E	143/192 (74%)	140 (98%)	3 (2%)	47	77
3	B	58/391 (15%)	57 (98%)	1 (2%)	53	82
4	C	143/460 (31%)	143 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	868/924 (94%)	798 (92%)	70 (8%)	11	33
All	All	2309/3595 (64%)	2208 (96%)	101 (4%)	27	59

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	81	SER
1	A	99	ILE
1	A	118	LEU
1	A	176	VAL
1	A	215	LEU
1	A	229	ILE
1	A	252	ARG
1	A	317	LEU
1	A	319	LEU
1	A	326	LEU
1	A	339	LYS
1	A	509	LEU
1	A	664	LEU
1	A	791	LEU
1	A	988	ARG
1	A	1010	VAL
1	A	1056	MET
1	A	1058	ASN
1	A	1081	LEU
1	A	1088	CYS
1	A	1277	LEU
1	A	1333	SER
1	A	1337	LEU
1	A	1339	ASP
1	A	1470	LEU
1	A	1475	LEU
2	E	13	LEU
2	E	137	LEU
2	E	181	SER
3	B	115	PRO
5	F	93	ARG
5	F	107	VAL
5	F	133	LEU
5	F	181	VAL
5	F	182	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	F	197	LYS
5	F	205	LEU
5	F	216	LEU
5	F	230	ARG
5	F	237	LEU
5	F	240	VAL
5	F	243	ARG
5	F	254	LYS
5	F	256	MET
5	F	269	LEU
5	F	270	THR
5	F	271	LEU
5	F	302	ASP
5	F	303	VAL
5	F	315	ARG
5	F	318	LYS
5	F	346	LEU
5	F	361	MET
5	F	381	ASP
5	F	382	LYS
5	F	406	CYS
5	F	407	GLU
5	F	422	ARG
5	F	437	VAL
5	F	441	ASP
5	F	442	LYS
5	F	471	ILE
5	F	472	THR
5	F	474	GLN
5	F	476	GLU
5	F	477	ASN
5	F	480	ASN
5	F	490	MET
5	F	508	LEU
5	F	517	ILE
5	F	524	LEU
5	F	525	LEU
5	F	528	ASN
5	F	529	LEU
5	F	530	GLN
5	F	532	LYS
5	F	593	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	F	629	TYR
5	F	651	LEU
5	F	657	GLU
5	F	658	GLU
5	F	662	THR
5	F	705	ILE
5	F	710	LEU
5	F	743	ILE
5	F	744	THR
5	F	785	LYS
5	F	793	SER
5	F	847	ASN
5	F	850	VAL
5	F	851	MET
5	F	853	CYS
5	F	889	LEU
5	F	988	ASN
5	F	990	SER
5	F	991	LYS
5	F	1013	ASN
5	F	1020	MET
5	F	1062	CYS
5	F	1068	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	143	ASN
1	A	239	ASN
1	A	274	HIS
1	A	287	GLN
1	A	307	ASN
1	A	327	ASN
1	A	357	GLN
1	A	455	ASN
1	A	464	GLN
1	A	547	ASN
1	A	1037	ASN
1	A	1058	ASN
1	A	1071	GLN
1	A	1085	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1138	GLN
1	A	1154	ASN
1	A	1287	GLN
1	A	1311	GLN
1	A	1398	HIS
1	A	1456	ASN
1	A	1464	ASN
2	E	31	HIS
5	F	108	GLN
5	F	228	ASN
5	F	308	HIS
5	F	357	ASN
5	F	372	GLN
5	F	379	ASN
5	F	395	ASN
5	F	408	ASN
5	F	450	ASN
5	F	477	ASN
5	F	511	ASN
5	F	520	ASN
5	F	530	GLN
5	F	570	ASN
5	F	678	ASN
5	F	697	ASN
5	F	773	ASN
5	F	847	ASN
5	F	866	ASN
5	F	988	ASN
5	F	1001	ASN
5	F	1013	ASN
5	F	1065	ASN
5	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$
6	NAG	D	1	6	14,14,15	0.27	0	17,19,21	0.99	1 (5%)
6	NAG	D	2	6	14,14,15	0.32	0	17,19,21	0.50	0
6	NAG	G	1	6,5	14,14,15	0.29	0	17,19,21	0.56	0
6	NAG	G	2	6	14,14,15	0.27	0	17,19,21	0.55	0
7	NAG	H	1	5,7	14,14,15	0.68	1 (7%)	17,19,21	0.70	0
7	NAG	H	2	7	14,14,15	0.36	0	17,19,21	0.80	0
7	BMA	H	3	7	11,11,12	0.73	0	15,15,17	0.94	1 (6%)
7	NAG	I	1	5,7	14,14,15	0.80	1 (7%)	17,19,21	0.84	0
7	NAG	I	2	7	14,14,15	1.55	1 (7%)	17,19,21	0.93	1 (5%)
7	BMA	I	3	7	11,11,12	0.89	0	15,15,17	0.92	0
6	NAG	J	1	6,5	14,14,15	0.53	0	17,19,21	0.64	0
6	NAG	J	2	6	14,14,15	0.30	0	17,19,21	0.41	0
6	NAG	K	1	6	14,14,15	0.28	0	17,19,21	0.62	0
6	NAG	K	2	6	14,14,15	0.29	0	17,19,21	0.51	0
8	NAG	L	1	5,8	14,14,15	0.28	0	17,19,21	0.59	0
8	NAG	L	2	8	14,14,15	0.31	0	17,19,21	0.65	0
8	NAG	L	3	8	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
6	NAG	D	1	6	-	5/6/23/26	0/1/1/1
6	NAG	D	2	6	-	2/6/23/26	0/1/1/1
6	NAG	G	1	6,5	-	0/6/23/26	0/1/1/1
6	NAG	G	2	6	-	2/6/23/26	0/1/1/1
7	NAG	H	1	5,7	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	H	2	7	-	2/6/23/26	0/1/1/1
7	BMA	H	3	7	-	0/2/19/22	0/1/1/1
7	NAG	I	1	5,7	-	2/6/23/26	0/1/1/1
7	NAG	I	2	7	-	2/6/23/26	0/1/1/1
7	BMA	I	3	7	-	2/2/19/22	0/1/1/1
6	NAG	J	1	6,5	-	2/6/23/26	0/1/1/1
6	NAG	J	2	6	-	0/6/23/26	0/1/1/1
6	NAG	K	1	6	-	4/6/23/26	0/1/1/1
6	NAG	K	2	6	-	6/6/23/26	0/1/1/1
8	NAG	L	1	5,8	-	2/6/23/26	0/1/1/1
8	NAG	L	2	8	-	5/6/23/26	0/1/1/1
8	NAG	L	3	8	-	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)
7	I	2	NAG	O5-C1	-5.60	1.34	1.43
7	I	1	NAG	O5-C1	-2.51	1.39	1.43
7	H	1	NAG	O5-C1	-2.21	1.40	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L	3	NAG	C1-O5-C5	4.39	118.07	112.19
6	D	1	NAG	C3-C4-C5	2.50	114.77	110.23
7	H	3	BMA	C1-O5-C5	2.50	115.53	112.19
7	I	2	NAG	C4-C3-C2	2.31	114.40	111.02

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	1	NAG	C1-C2-N2-C7
6	D	1	NAG	C8-C7-N2-C2
6	D	1	NAG	O7-C7-N2-C2
6	K	1	NAG	C8-C7-N2-C2
6	K	1	NAG	O7-C7-N2-C2
8	L	1	NAG	C8-C7-N2-C2
8	L	1	NAG	O7-C7-N2-C2

Continued on next page...

Continued from previous page...

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

There are no ring outliers.

11 monomers are involved in 34 short contacts:

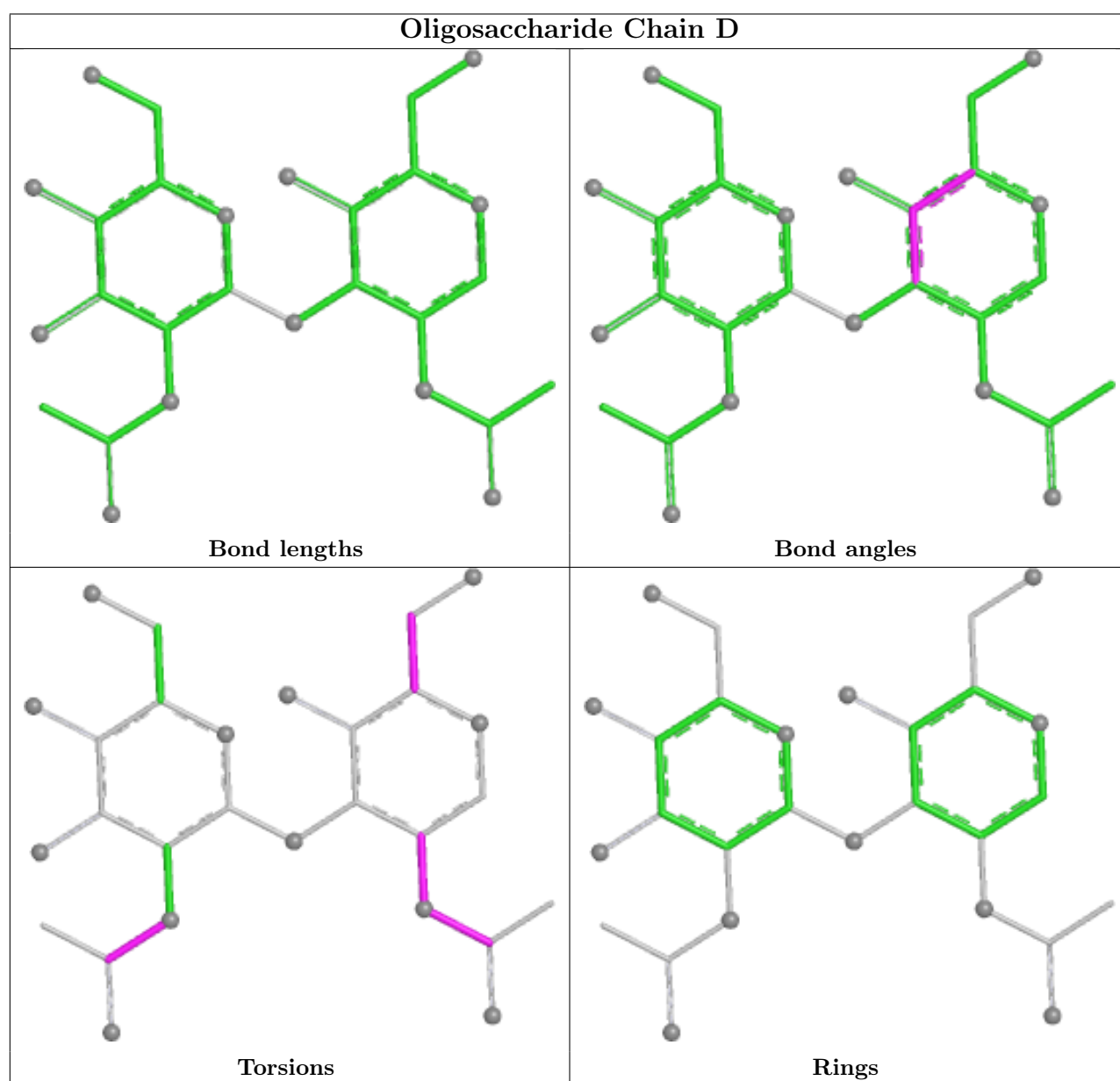
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	I	1	NAG	1	0
6	K	2	NAG	5	0
6	K	1	NAG	5	0
8	L	1	NAG	7	0

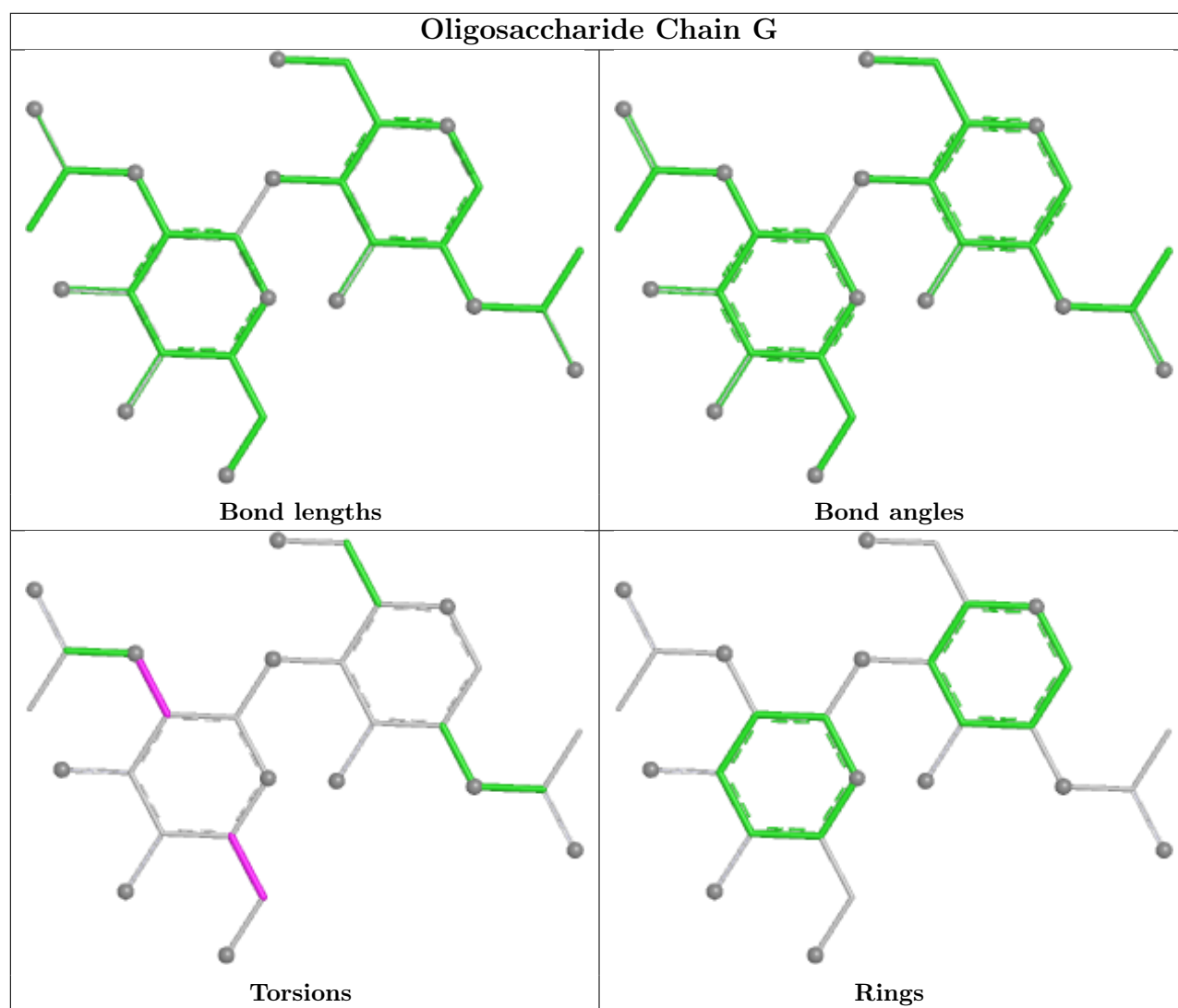
Continued on next page...

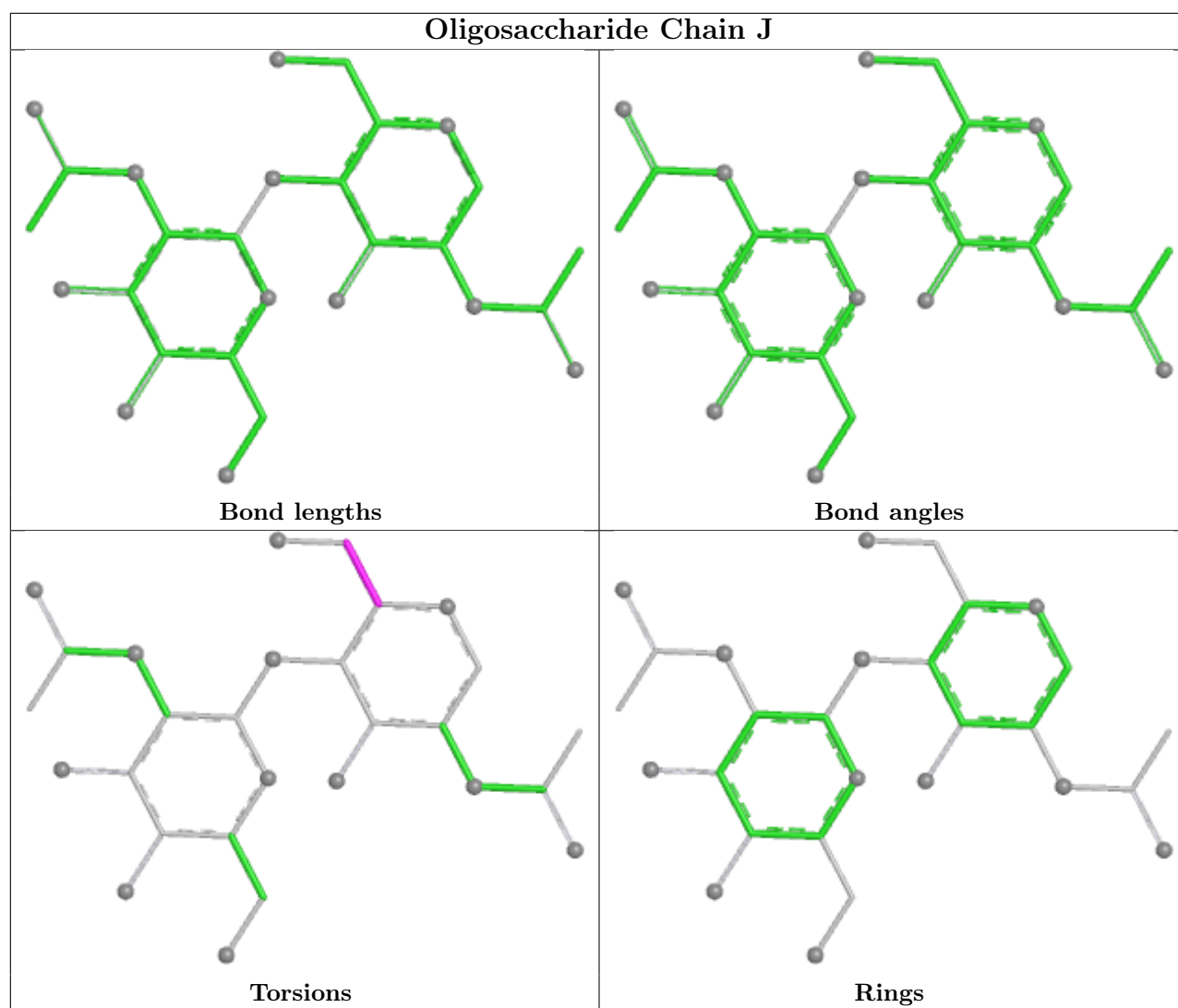
Continued from previous page...

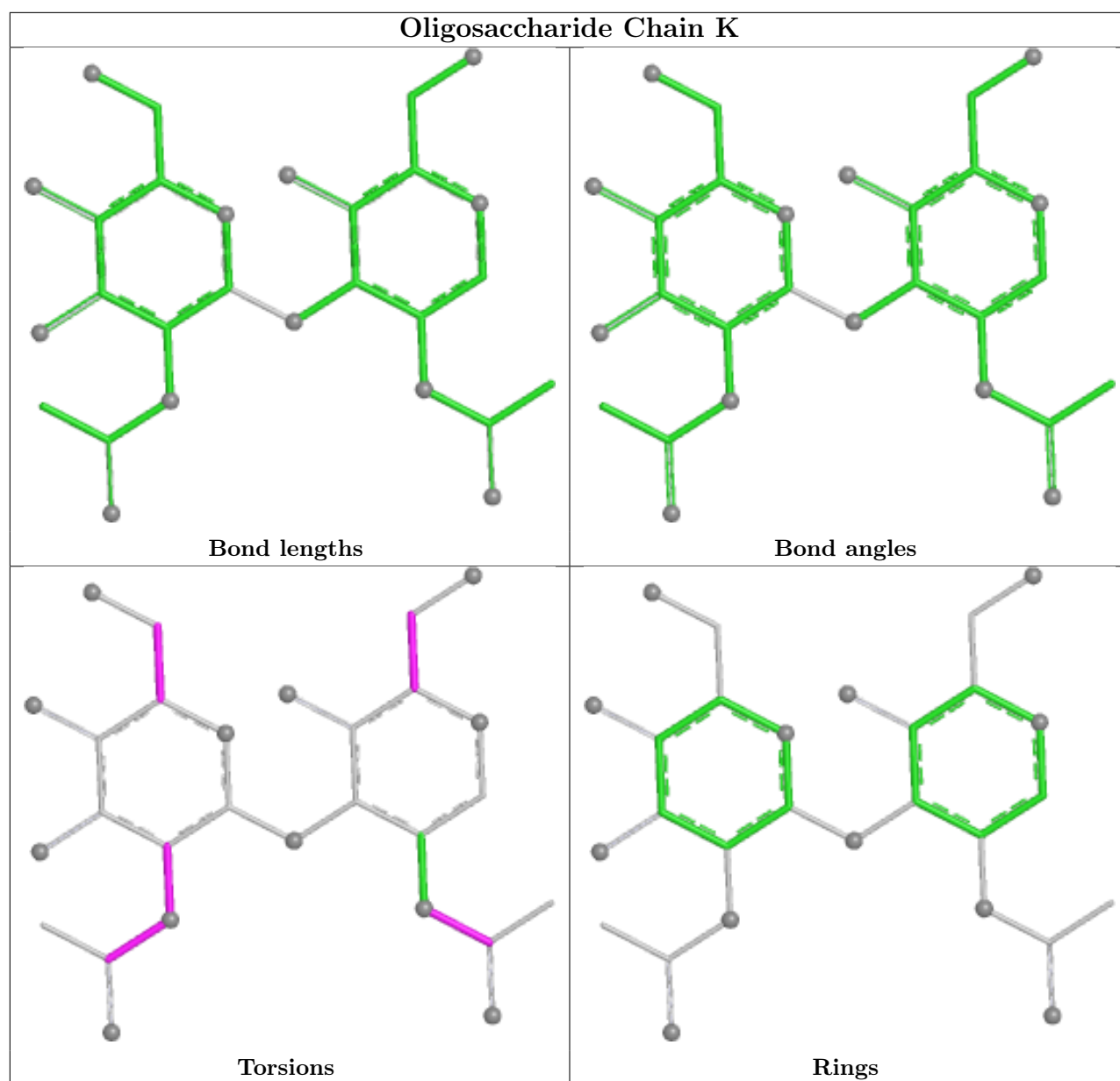
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	L	3	NAG	4	0
8	L	2	NAG	2	0
6	D	2	NAG	4	0
6	D	1	NAG	8	0
6	G	1	NAG	1	0
6	G	2	NAG	1	0
7	H	1	NAG	4	0

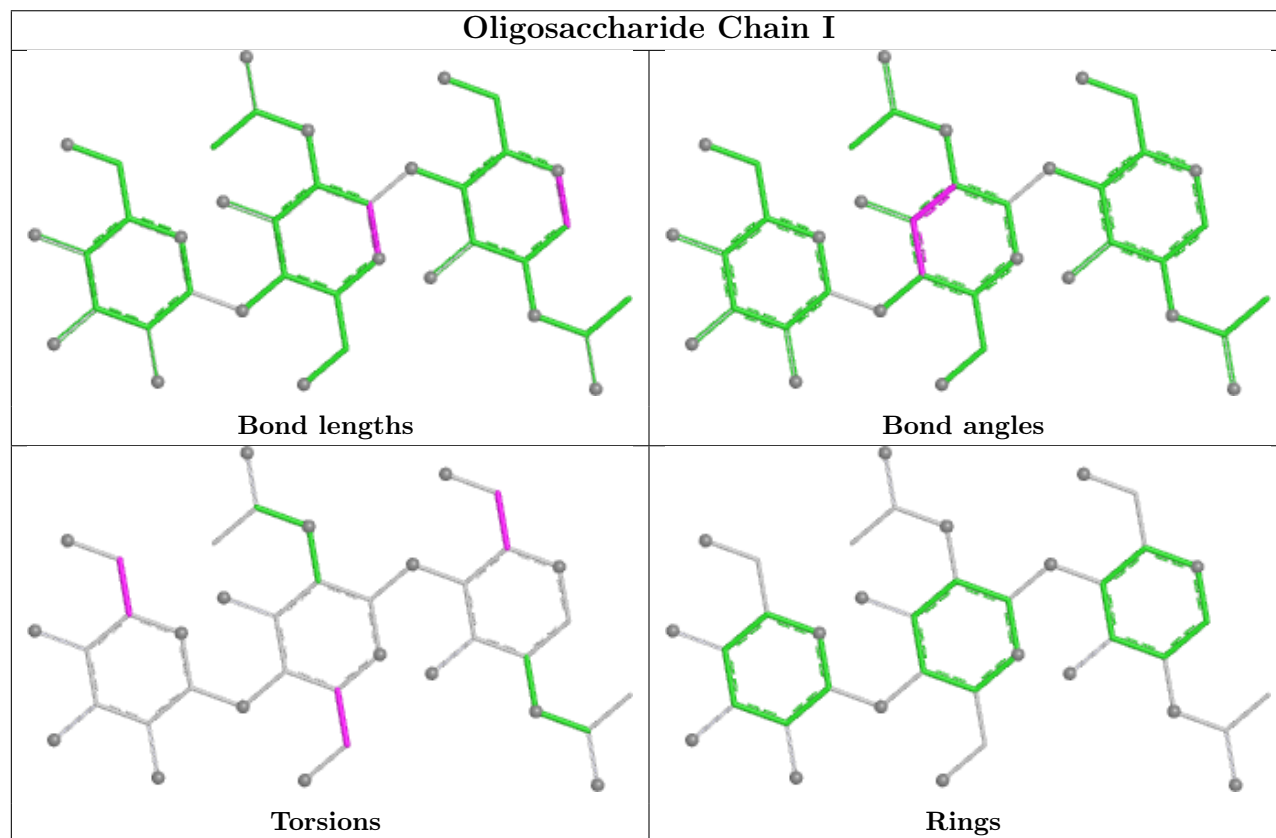
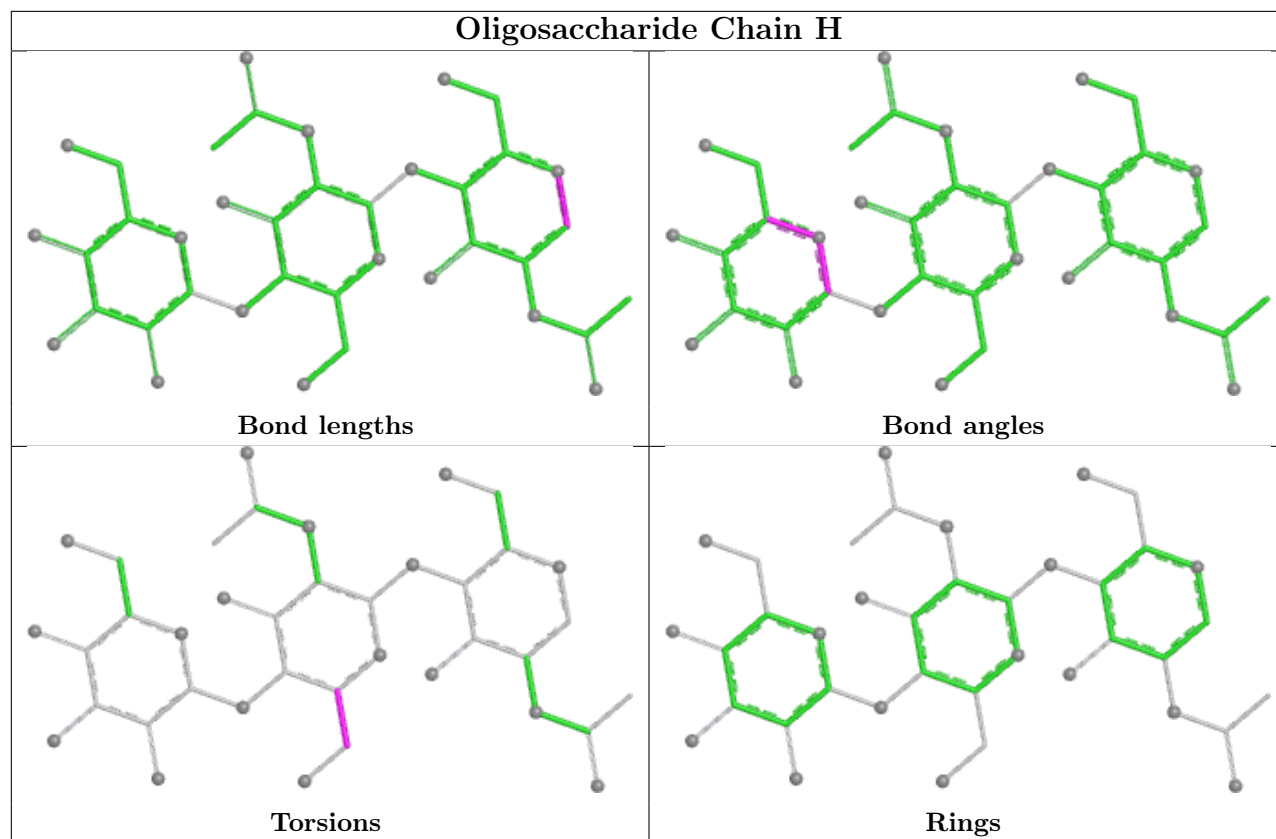
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

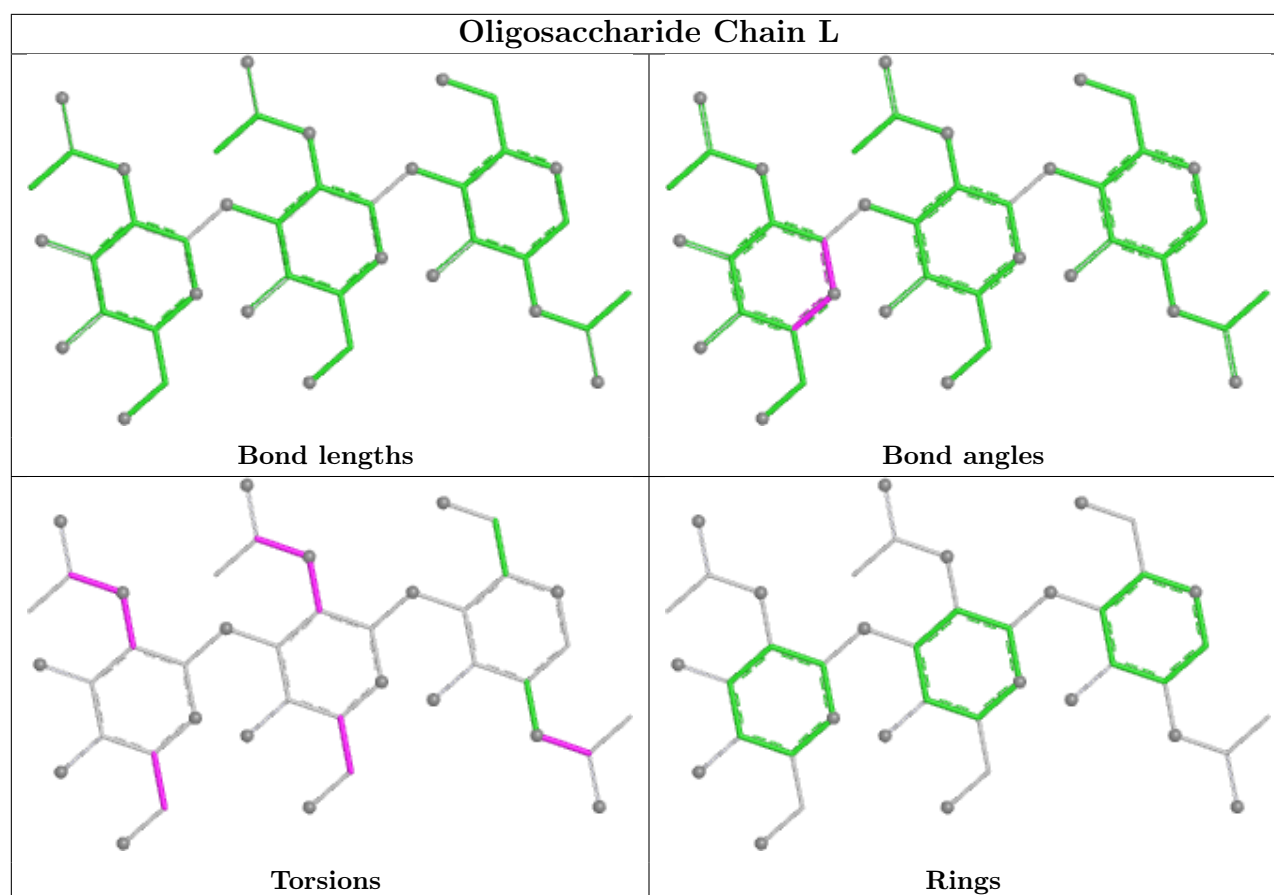












5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 3 are monoatomic - leaving 15 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	1108	5	14,14,15	0.30	0	17,19,21	0.57	0
9	NAG	F	1115	5	14,14,15	0.25	0	17,19,21	0.67	1 (5%)
9	NAG	F	1105	-	14,14,15	0.30	0	17,19,21	0.63	0
9	NAG	F	1123	-	14,14,15	0.28	0	17,19,21	0.57	0
9	NAG	F	1116	5	14,14,15	0.86	1 (7%)	17,19,21	1.02	1 (5%)
11	3PE	A	1906	-	34,34,50	1.05	2 (5%)	37,39,55	1.11	3 (8%)
11	3PE	A	1904	-	32,32,50	1.15	2 (6%)	35,37,55	1.14	2 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	F	1122	-	14,14,15	0.46	0	17,19,21	0.53	0
9	NAG	A	1901	-	14,14,15	0.30	0	17,19,21	0.56	0
14	ETA	F	1102	-	3,3,3	0.41	0	2,2,2	0.49	0
12	PC1	A	1905	-	38,38,53	1.18	3 (7%)	44,46,61	1.21	3 (6%)
11	3PE	A	1907	-	33,33,50	1.05	4 (12%)	36,38,55	1.14	2 (5%)
11	3PE	A	1908	-	41,41,50	0.98	3 (7%)	44,46,55	0.97	2 (4%)
13	C9F	A	1909	-	31,31,31	2.95	11 (35%)	43,43,43	3.34	14 (32%)
9	NAG	F	1121	-	14,14,15	0.31	0	17,19,21	0.55	0

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	1108	5	-	2/6/23/26	0/1/1/1
9	NAG	F	1115	5	-	0/6/23/26	0/1/1/1
9	NAG	F	1105	-	-	2/6/23/26	0/1/1/1
9	NAG	F	1123	-	-	2/6/23/26	0/1/1/1
9	NAG	F	1116	5	-	0/6/23/26	0/1/1/1
11	3PE	A	1906	-	-	20/38/38/54	-
11	3PE	A	1904	-	-	20/36/36/54	-
9	NAG	F	1122	-	-	0/6/23/26	0/1/1/1
9	NAG	A	1901	-	-	2/6/23/26	0/1/1/1
14	ETA	F	1102	-	-	1/1/1/1	-
12	PC1	A	1905	-	-	15/42/42/57	-
11	3PE	A	1907	-	-	16/37/37/54	-
11	3PE	A	1908	-	-	25/45/45/54	-
13	C9F	A	1909	-	-	8/15/35/35	0/3/3/3
9	NAG	F	1121	-	-	2/6/23/26	0/1/1/1

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	1909	C9F	C04-N03	10.83	1.53	1.43
13	A	1909	C9F	C02-N03	6.11	1.48	1.37
13	A	1909	C9F	C07-S06	-4.79	1.79	1.84
11	A	1904	3PE	O31-C31	4.34	1.46	1.33
13	A	1909	C9F	O12-C11	4.07	1.45	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	1904	3PE	O21-C21	4.05	1.45	1.34
13	A	1909	C9F	C08-C07	3.76	1.58	1.51
13	A	1909	C9F	C24-C04	3.21	1.44	1.39
11	A	1908	3PE	O21-C2	-3.21	1.39	1.46
13	A	1909	C9F	C05-S06	3.17	1.80	1.77
11	A	1906	3PE	O21-C2	-3.12	1.39	1.46
12	A	1905	PC1	O31-C31	2.98	1.42	1.33
13	A	1909	C9F	O17-C16	-2.93	1.39	1.44
12	A	1905	PC1	O21-C2	-2.89	1.39	1.46
9	F	1116	NAG	C1-C2	2.67	1.56	1.52
12	A	1905	PC1	O21-C21	2.67	1.41	1.34
13	A	1909	C9F	O01-C02	-2.52	1.17	1.22
13	A	1909	C9F	C16-C02	2.51	1.56	1.53
11	A	1907	3PE	O31-C3	-2.41	1.39	1.45
11	A	1906	3PE	O31-C3	-2.40	1.39	1.45
13	A	1909	C9F	C22-C21	2.40	1.43	1.38
11	A	1907	3PE	O21-C2	-2.38	1.41	1.46
11	A	1908	3PE	O31-C31	2.37	1.40	1.33
11	A	1907	3PE	O21-C21	2.31	1.40	1.34
11	A	1907	3PE	O31-C31	2.30	1.40	1.33
11	A	1908	3PE	O31-C3	-2.08	1.40	1.45

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	1909	C9F	C16-C02-N03	12.16	128.36	115.49
13	A	1909	C9F	C04-N03-C02	8.76	136.98	122.98
13	A	1909	C9F	C05-C04-N03	6.42	125.82	121.05
13	A	1909	C9F	C07-C16-C02	6.41	119.70	113.99
13	A	1909	C9F	C05-S06-C07	5.92	110.91	102.57
13	A	1909	C9F	O17-C18-C20	5.04	120.08	111.09
13	A	1909	C9F	O01-C02-C16	-4.69	114.17	121.25
11	A	1907	3PE	O21-C21-C22	4.48	121.17	111.48
13	A	1909	C9F	C25-N03-C04	-4.40	109.78	118.09
11	A	1908	3PE	O21-C21-C22	4.01	120.16	111.48
11	A	1904	3PE	O21-C21-C22	3.93	119.98	111.48
12	A	1905	PC1	O21-C21-C22	3.75	119.60	111.48
11	A	1906	3PE	O21-C21-C22	3.66	119.40	111.48
9	F	1116	NAG	C1-O5-C5	3.64	117.07	112.19
12	A	1905	PC1	C15-N-C14	3.61	118.46	108.98
13	A	1909	C9F	C25-N03-C02	-3.26	113.23	117.90
12	A	1905	PC1	O31-C31-C32	3.13	121.38	111.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	1909	C9F	O01-C02-N03	-3.02	117.47	122.18
13	A	1909	C9F	C16-C07-S06	2.96	112.03	109.10
13	A	1909	C9F	C24-C04-N03	-2.92	115.73	119.31
11	A	1906	3PE	O31-C31-C32	2.84	120.50	111.83
13	A	1909	C9F	C08-C07-C16	-2.83	110.81	116.69
11	A	1908	3PE	O31-C31-C32	2.73	120.15	111.83
11	A	1904	3PE	O31-C31-C32	2.73	120.15	111.83
11	A	1907	3PE	O31-C31-C32	2.70	120.07	111.83
9	F	1115	NAG	C1-O5-C5	2.37	115.36	112.19
11	A	1906	3PE	O31-C31-O32	-2.17	118.20	123.63
13	A	1909	C9F	C16-O17-C18	-2.05	113.26	116.64

There are no chirality outliers.

All (115) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	F	1105	NAG	C8-C7-N2-C2
9	F	1105	NAG	O7-C7-N2-C2
11	A	1904	3PE	C1-O11-P-O12
11	A	1904	3PE	C1-O11-P-O13
11	A	1904	3PE	C1-O11-P-O14
11	A	1904	3PE	C11-O13-P-O11
11	A	1904	3PE	C11-O13-P-O12
11	A	1904	3PE	C11-O13-P-O14
11	A	1906	3PE	C11-O13-P-O11
11	A	1906	3PE	C11-O13-P-O14
11	A	1907	3PE	C11-O13-P-O11
11	A	1907	3PE	C11-O13-P-O12
11	A	1907	3PE	C11-O13-P-O14
11	A	1908	3PE	C1-O11-P-O12
11	A	1908	3PE	C1-O11-P-O13
11	A	1908	3PE	C1-O11-P-O14
11	A	1908	3PE	O22-C21-O21-C2
11	A	1908	3PE	C22-C21-O21-C2
12	A	1905	PC1	O21-C2-C3-O31
12	A	1905	PC1	C22-C21-O21-C2
12	A	1905	PC1	O22-C21-O21-C2
13	A	1909	C9F	C10-C11-O12-C13
13	A	1909	C9F	C20-C18-O17-C16
13	A	1909	C9F	C14-C11-O12-C13
11	A	1907	3PE	O32-C31-O31-C3
11	A	1907	3PE	C32-C31-O31-C3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
9	F	1121	NAG	O5-C5-C6-O6
9	F	1121	NAG	C4-C5-C6-O6
11	A	1906	3PE	C22-C21-O21-C2
11	A	1906	3PE	O22-C21-O21-C2
11	A	1906	3PE	C32-C31-O31-C3
9	A	1901	NAG	C8-C7-N2-C2
9	A	1901	NAG	O7-C7-N2-C2
11	A	1908	3PE	C32-C31-O31-C3
11	A	1906	3PE	O32-C31-O31-C3
13	A	1909	C9F	N03-C25-C26-N27
11	A	1908	3PE	O32-C31-O31-C3
13	A	1909	C9F	O19-C18-O17-C16
11	A	1908	3PE	C31-C32-C33-C34
11	A	1908	3PE	O11-C1-C2-O21
11	A	1906	3PE	O21-C2-C3-O31
12	A	1905	PC1	C27-C28-C29-C2A
12	A	1905	PC1	C28-C29-C2A-C2B
11	A	1908	3PE	C24-C25-C26-C27
11	A	1904	3PE	C22-C21-O21-C2
11	A	1906	3PE	C33-C34-C35-C36
11	A	1904	3PE	C34-C35-C36-C37
11	A	1904	3PE	C1-C2-C3-O31
12	A	1905	PC1	C25-C26-C27-C28
11	A	1904	3PE	C21-C22-C23-C24
11	A	1906	3PE	C22-C23-C24-C25
11	A	1906	3PE	C25-C26-C27-C28
11	A	1904	3PE	O22-C21-O21-C2
11	A	1904	3PE	C22-C23-C24-C25
11	A	1908	3PE	C2A-C2B-C2C-C2D
11	A	1906	3PE	C27-C28-C29-C2A
11	A	1908	3PE	C25-C26-C27-C28
11	A	1906	3PE	C24-C25-C26-C27
11	A	1908	3PE	C2E-C2F-C2G-C2H
11	A	1904	3PE	C23-C24-C25-C26
11	A	1904	3PE	C35-C36-C37-C38
11	A	1908	3PE	O11-C1-C2-C3
11	A	1907	3PE	C23-C24-C25-C26
11	A	1908	3PE	C1-C2-C3-O31
11	A	1908	3PE	C2C-C2D-C2E-C2F
12	A	1905	PC1	C32-C31-O31-C3
11	A	1904	3PE	C3-C2-O21-C21
11	A	1908	3PE	C23-C24-C25-C26

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
11	A	1908	3PE	C33-C34-C35-C36
11	A	1906	3PE	C23-C24-C25-C26
11	A	1904	3PE	C24-C25-C26-C27
11	A	1904	3PE	C2-C1-O11-P
11	A	1906	3PE	O11-C1-C2-C3
11	A	1906	3PE	C1-C2-C3-O31
12	A	1905	PC1	C1-C2-C3-O31
11	A	1908	3PE	C36-C37-C38-C39
11	A	1908	3PE	C32-C33-C34-C35
11	A	1907	3PE	C27-C28-C29-C2A
12	A	1905	PC1	C33-C34-C35-C36
11	A	1906	3PE	C34-C35-C36-C37
12	A	1905	PC1	C2A-C2B-C2C-C2D
12	A	1905	PC1	O32-C31-O31-C3
11	A	1908	3PE	C29-C2A-C2B-C2C
11	A	1907	3PE	C24-C25-C26-C27
11	A	1907	3PE	C28-C29-C2A-C2B
11	A	1906	3PE	O11-C1-C2-O21
11	A	1904	3PE	O21-C2-C3-O31
12	A	1905	PC1	O13-C11-C12-N
11	A	1908	3PE	O21-C2-C3-O31
11	A	1904	3PE	O13-C11-C12-N
11	A	1906	3PE	C11-O13-P-O12
11	A	1907	3PE	C1-O11-P-O13
11	A	1907	3PE	C1-O11-P-O14
13	A	1909	C9F	C26-C25-N03-C02
11	A	1908	3PE	C34-C35-C36-C37
11	A	1907	3PE	C2-C1-O11-P
11	A	1907	3PE	C34-C35-C36-C37
12	A	1905	PC1	C2C-C2D-C2E-C2F
11	A	1907	3PE	C26-C27-C28-C29
9	F	1123	NAG	C4-C5-C6-O6
9	F	1108	NAG	C4-C5-C6-O6
13	A	1909	C9F	C26-C25-N03-C04
11	A	1906	3PE	C32-C33-C34-C35
9	F	1123	NAG	O5-C5-C6-O6
14	F	1102	ETA	O-C-CA-N
11	A	1908	3PE	C22-C23-C24-C25
9	F	1108	NAG	O5-C5-C6-O6
11	A	1907	3PE	C29-C2A-C2B-C2C
11	A	1908	3PE	C27-C28-C29-C2A
13	A	1909	C9F	C02-C16-O17-C18

Continued on next page...

Continued from previous page...

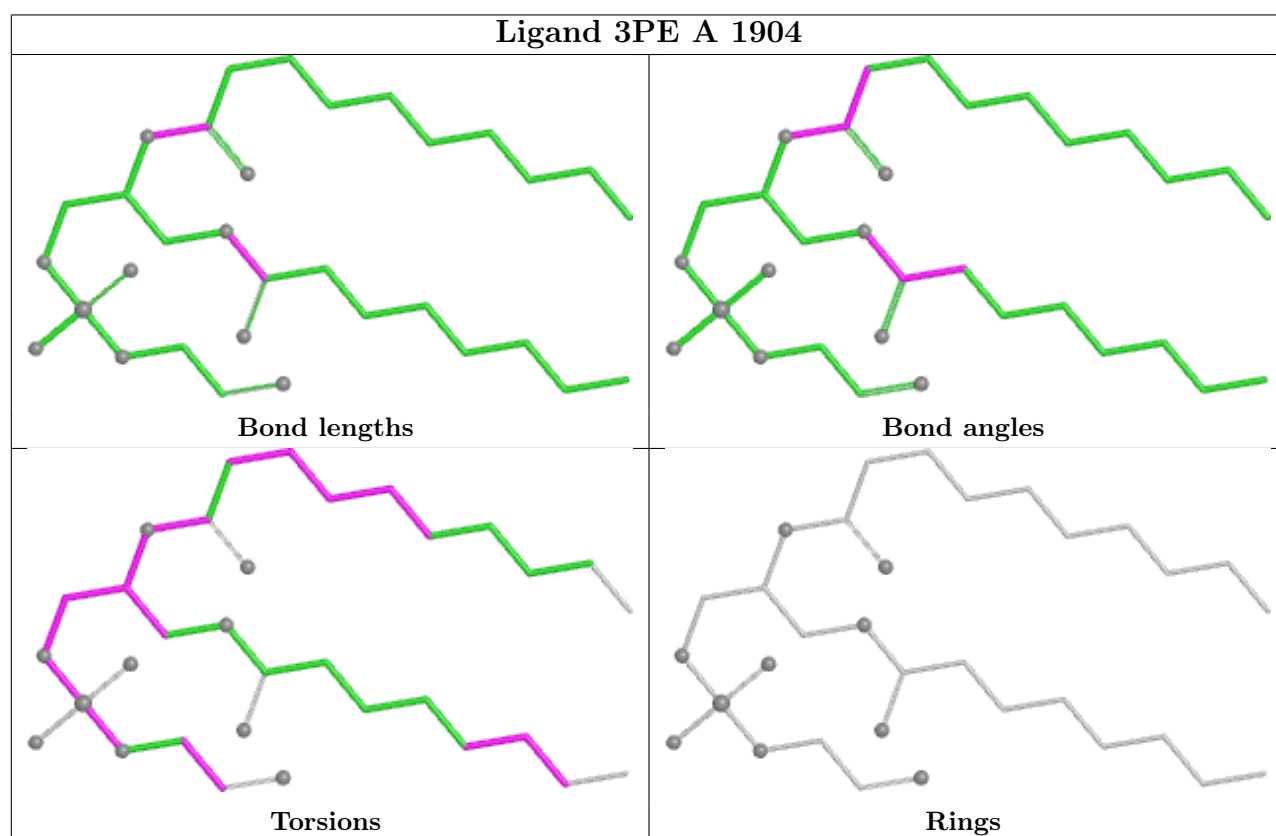
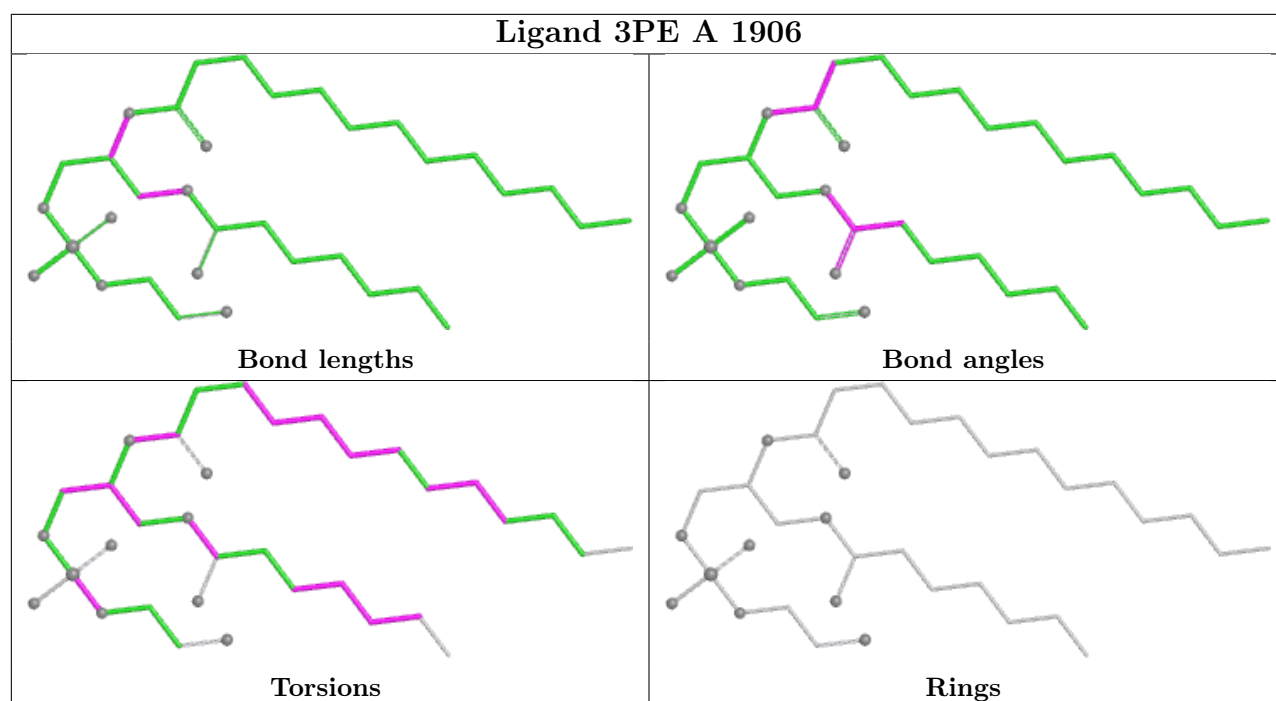
Mol	Chain	Res	Type	Atoms
11	A	1904	3PE	O11-C1-C2-O21
12	A	1905	PC1	C11-C12-N-C15
11	A	1906	3PE	C28-C29-C2A-C2B
12	A	1905	PC1	C22-C23-C24-C25
11	A	1907	3PE	O21-C21-C22-C23

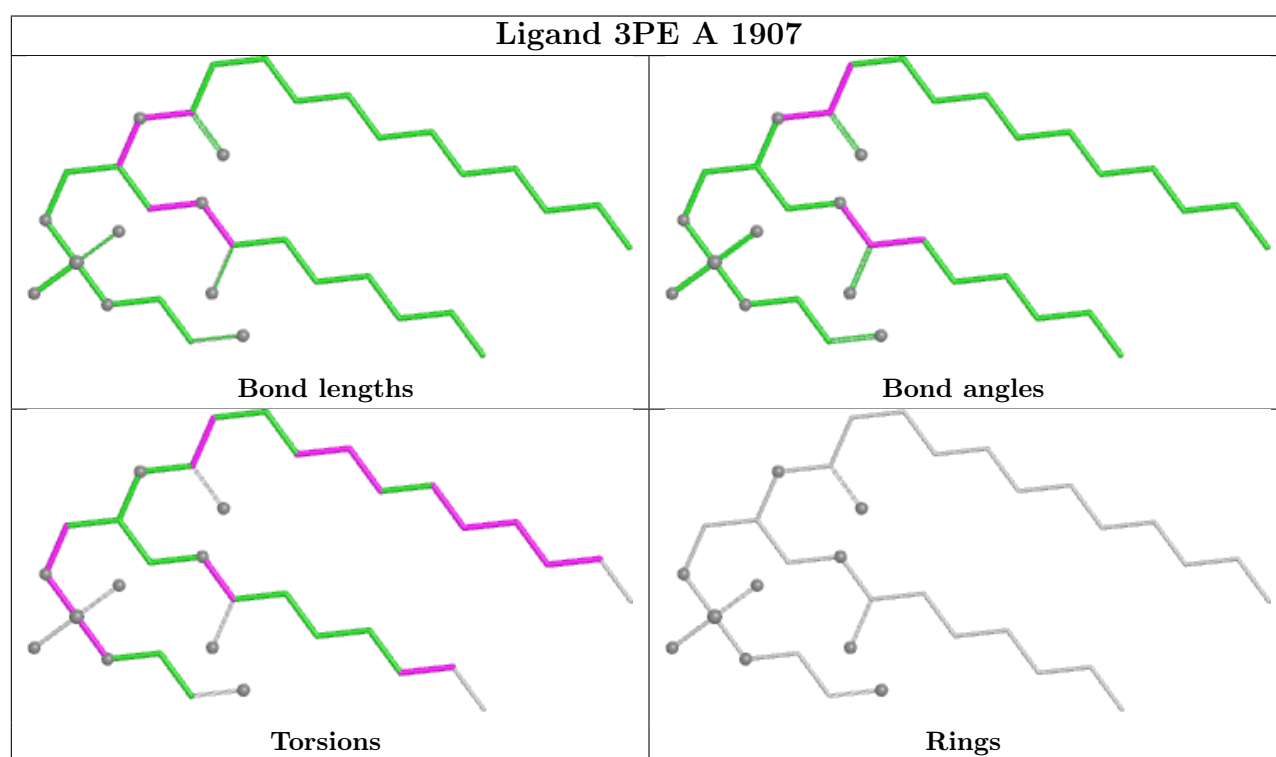
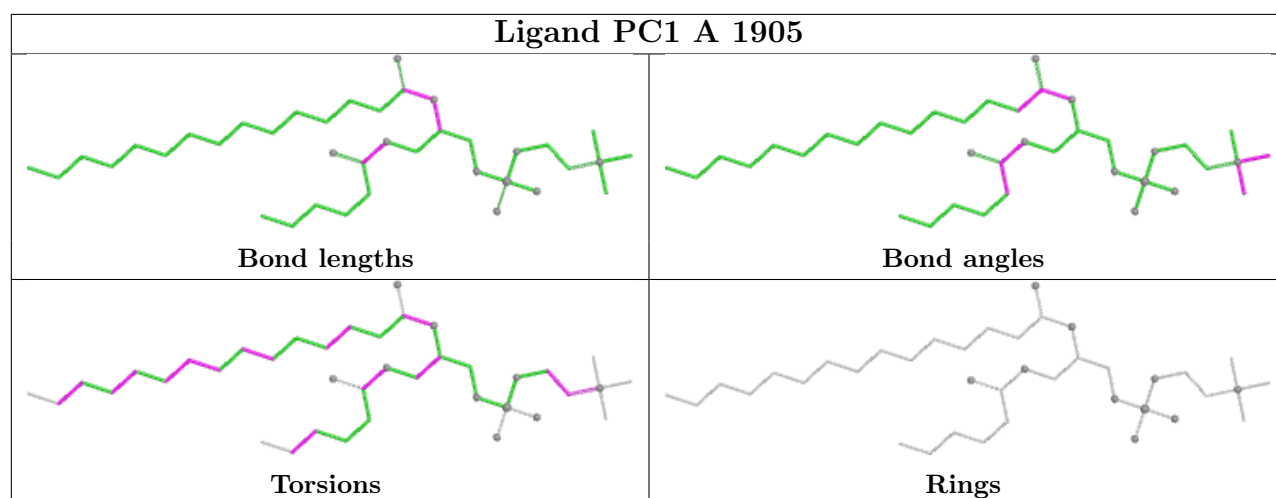
There are no ring outliers.

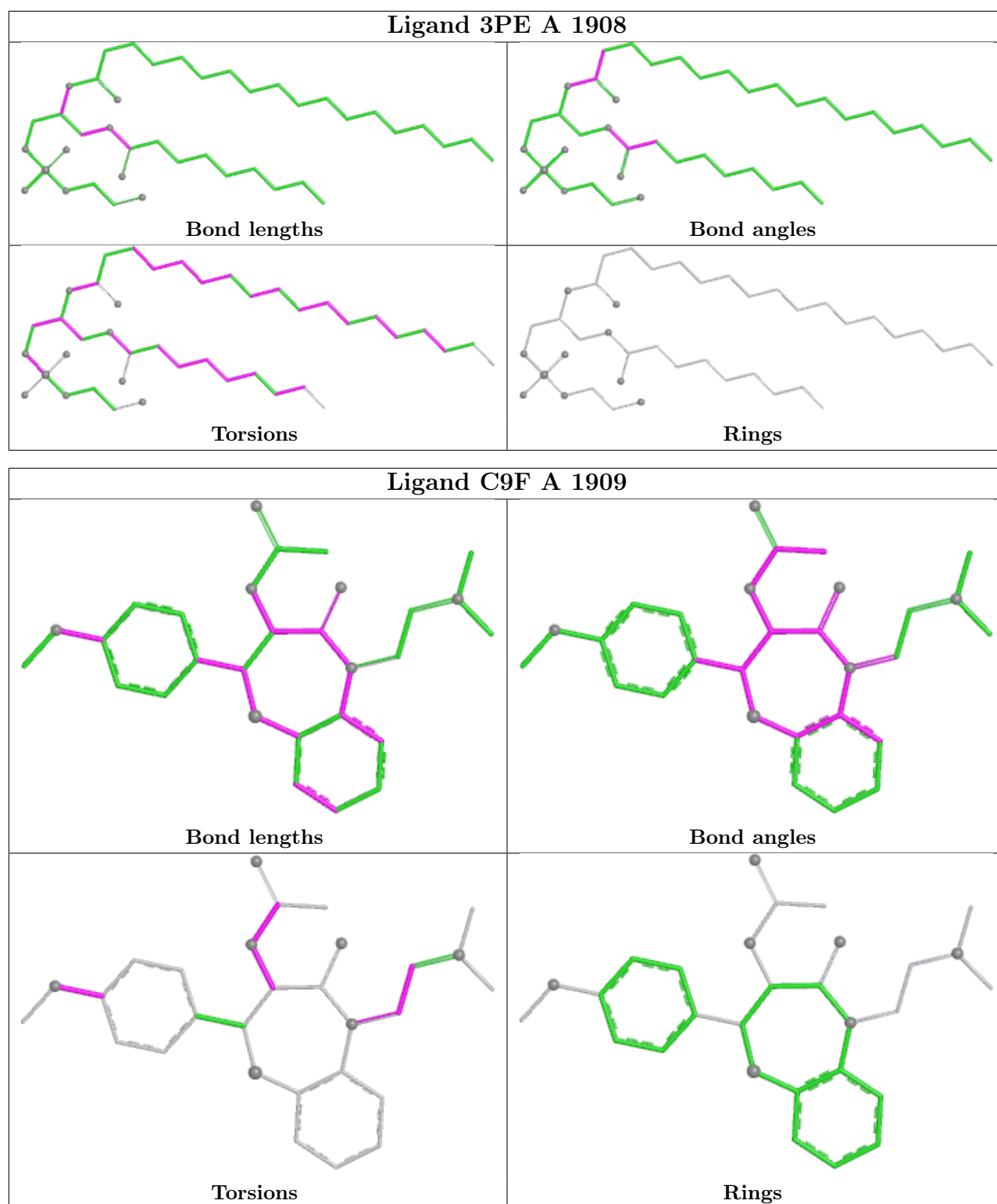
14 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	F	1108	NAG	1	0
9	F	1105	NAG	3	0
9	F	1123	NAG	4	0
9	F	1116	NAG	2	0
11	A	1906	3PE	2	0
11	A	1904	3PE	14	0
9	F	1122	NAG	3	0
9	A	1901	NAG	2	0
14	F	1102	ETA	2	0
12	A	1905	PC1	1	0
11	A	1907	3PE	1	0
11	A	1908	3PE	2	0
13	A	1909	C9F	5	0
9	F	1121	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

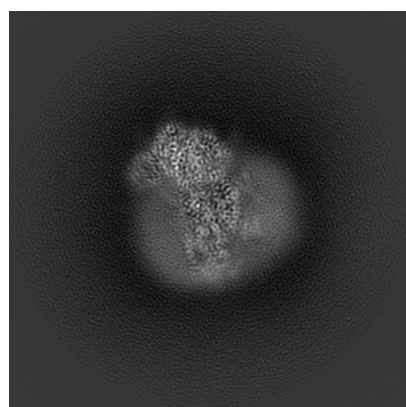
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9869. These allow visual inspection of the internal detail of the map and identification of artifacts.

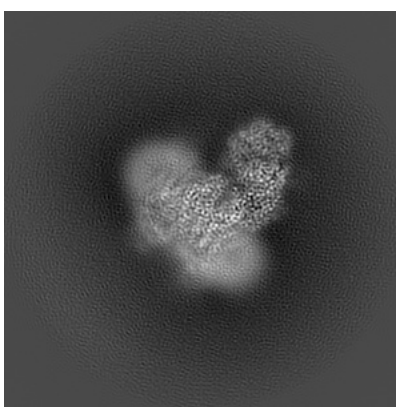
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

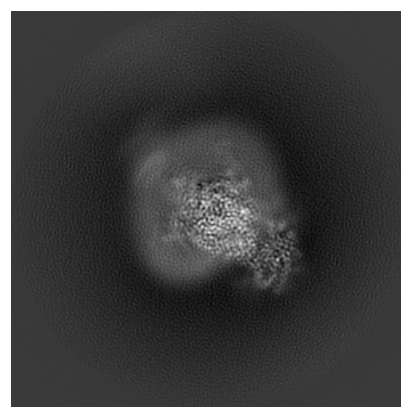
6.1.1 Primary map



X



Y

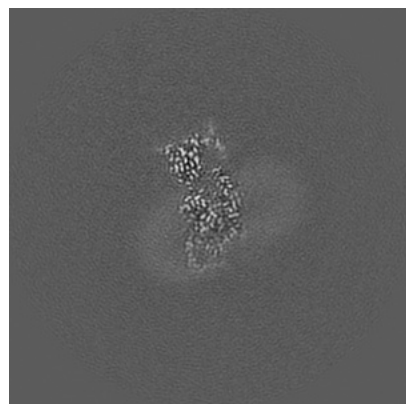


Z

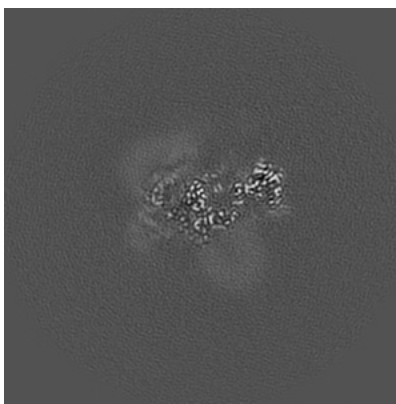
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

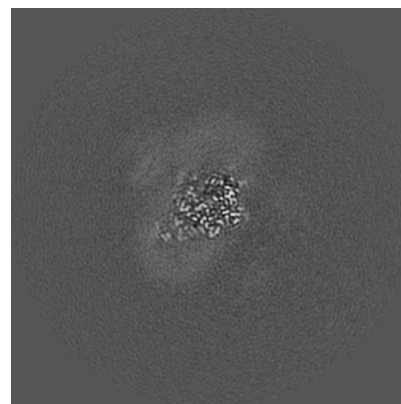
6.2.1 Primary map



X Index: 160



Y Index: 160

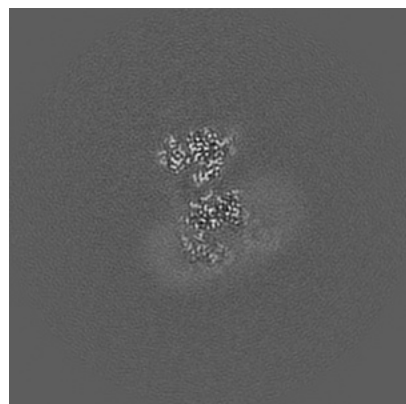


Z Index: 160

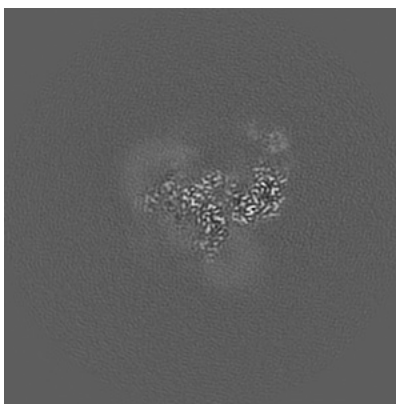
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

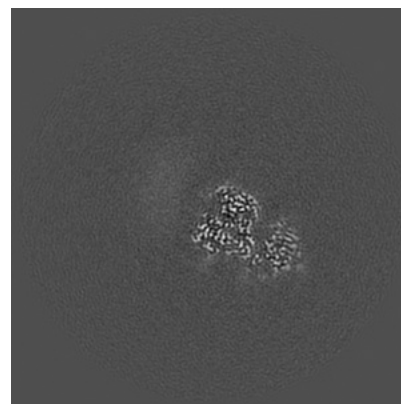
6.3.1 Primary map



X Index: 173



Y Index: 150

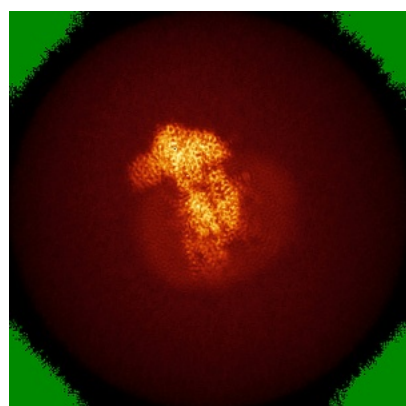


Z Index: 205

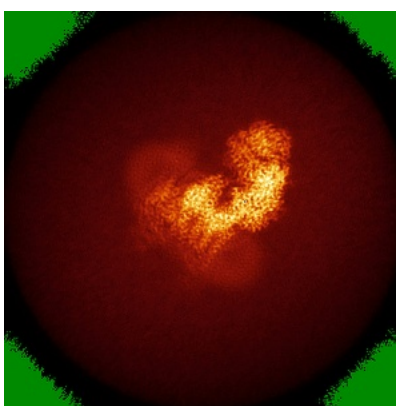
The images above show the largest variance slices of the map in three orthogonal directions.

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

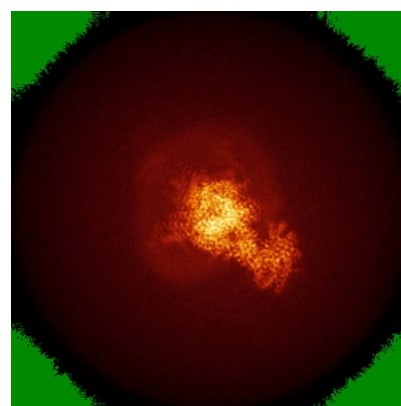
6.4.1 Primary map



X



Y

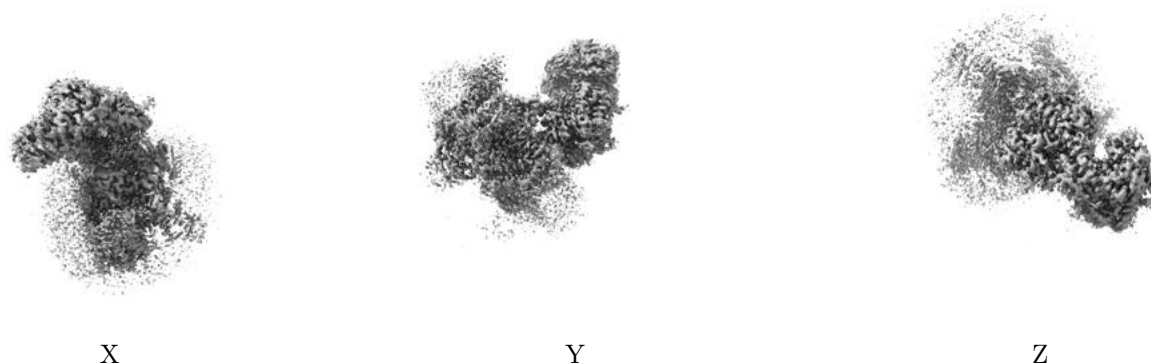


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.023. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

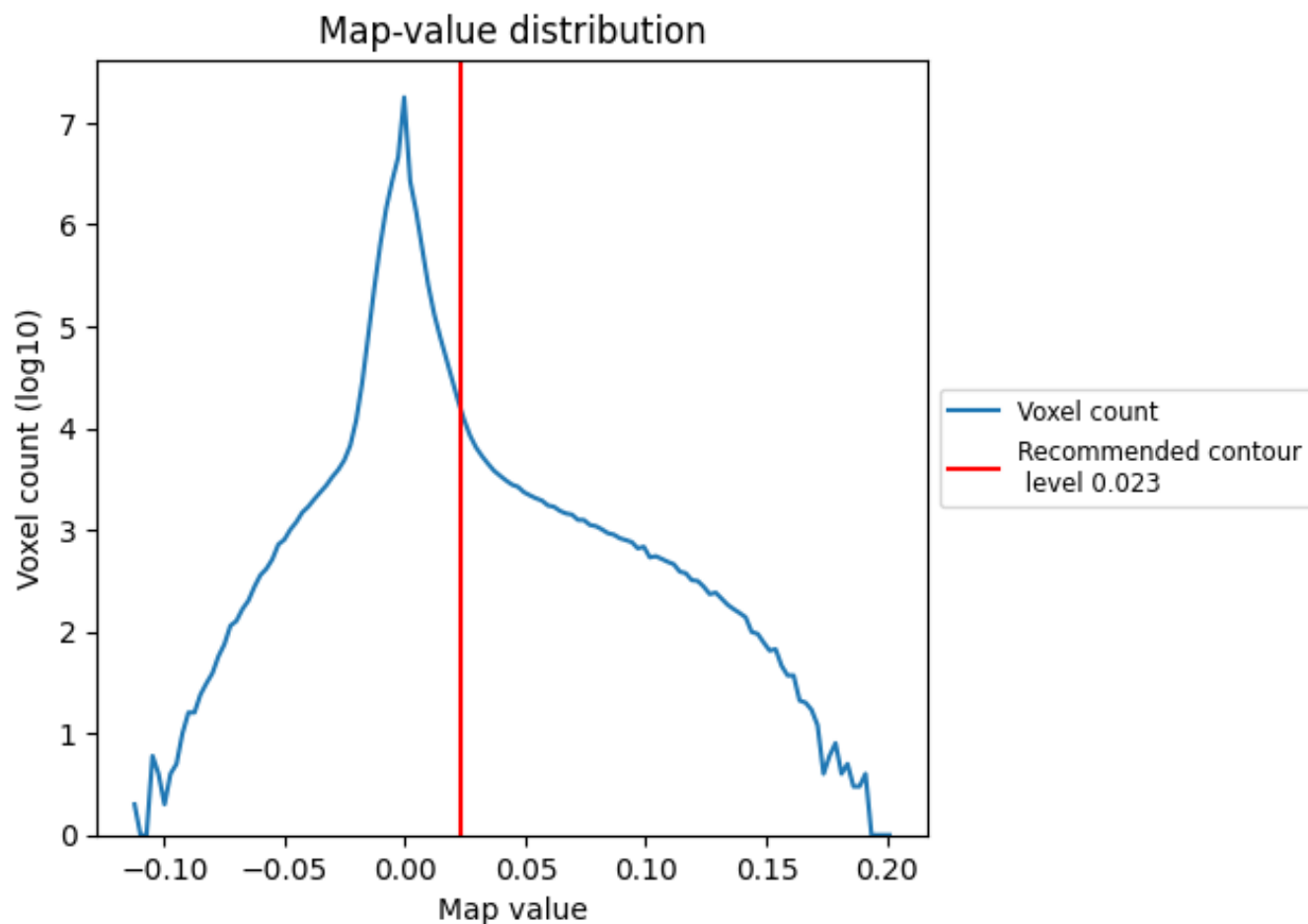
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

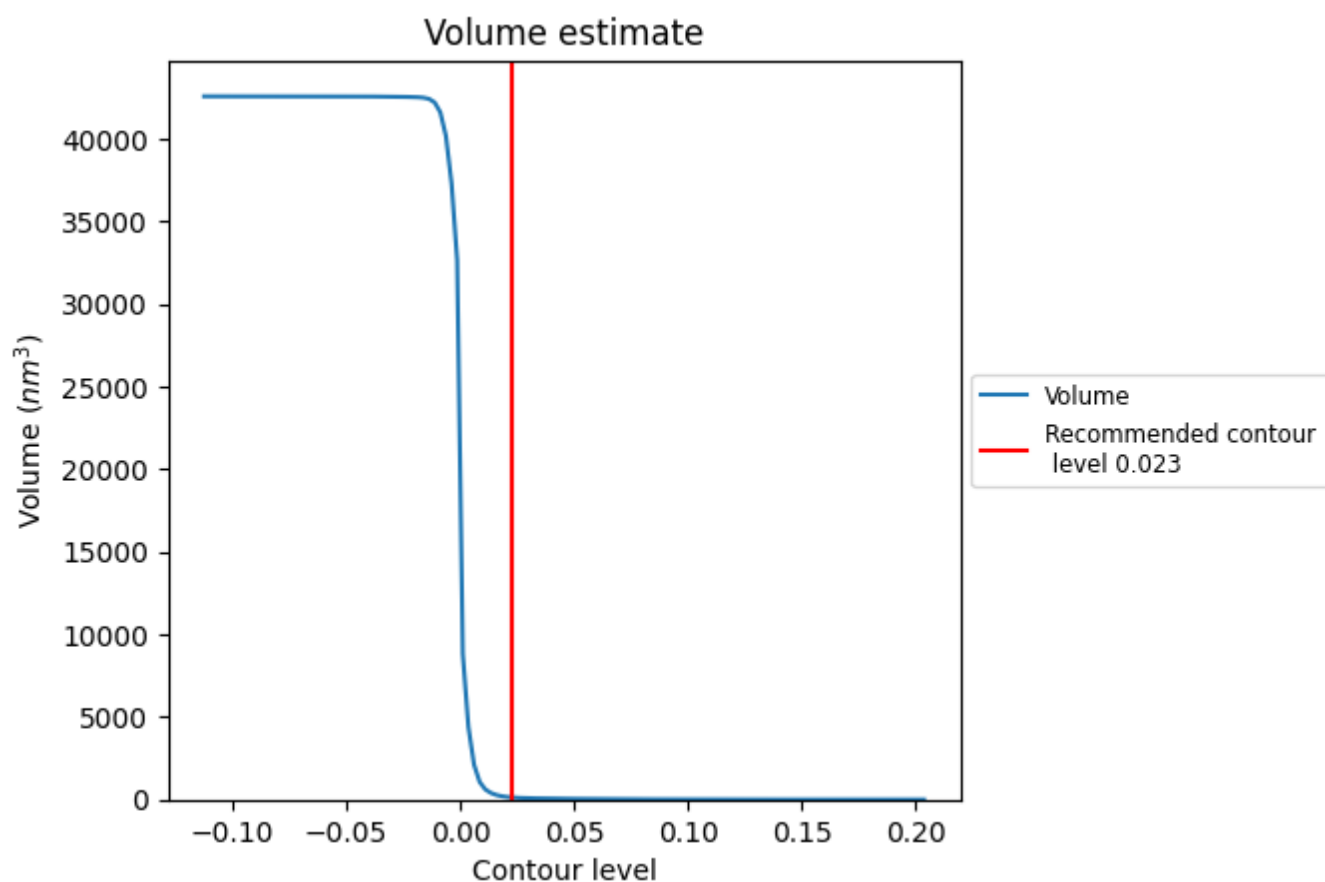
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

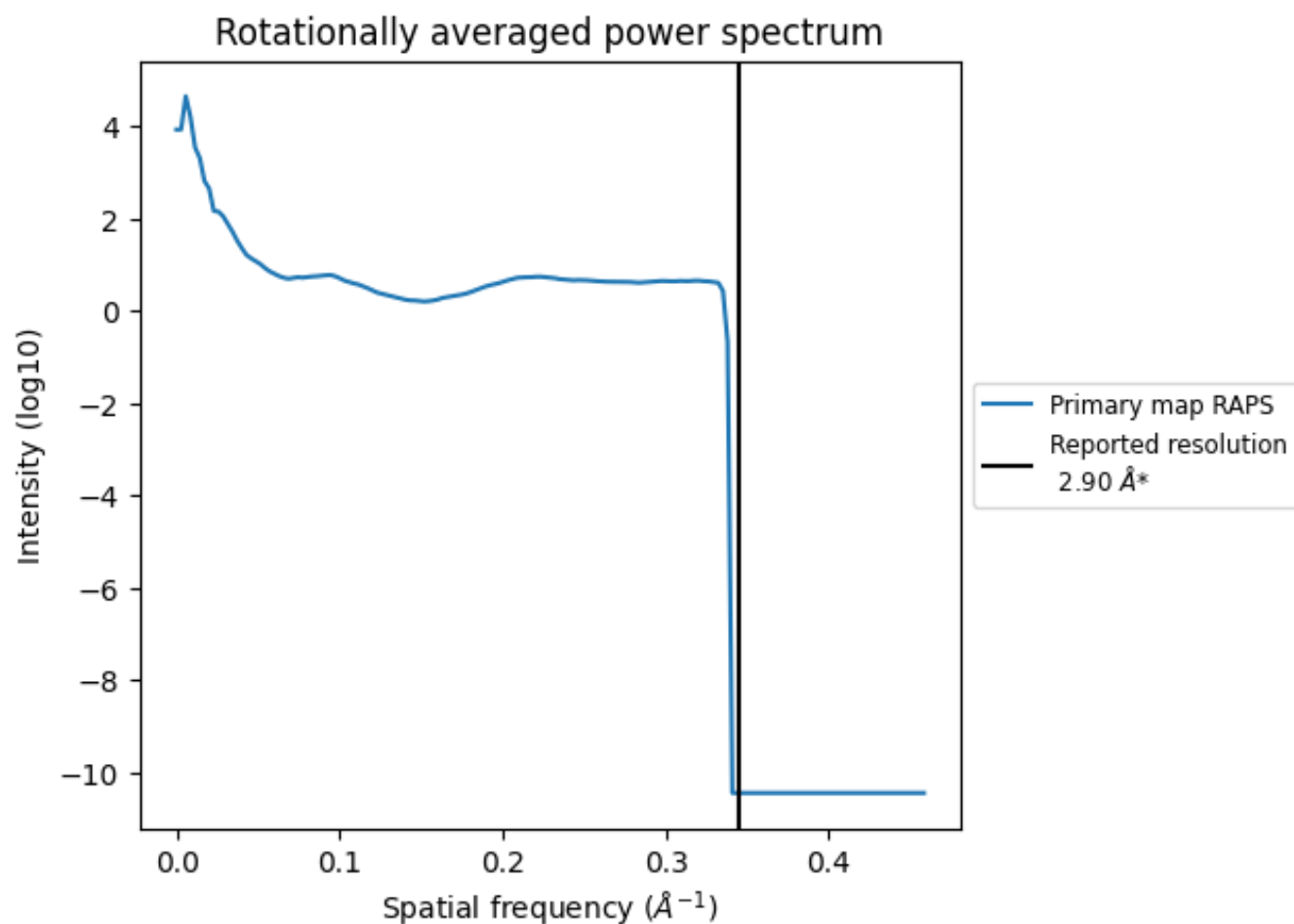
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 126 nm³; this corresponds to an approximate mass of 114 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 0.345 Å⁻¹

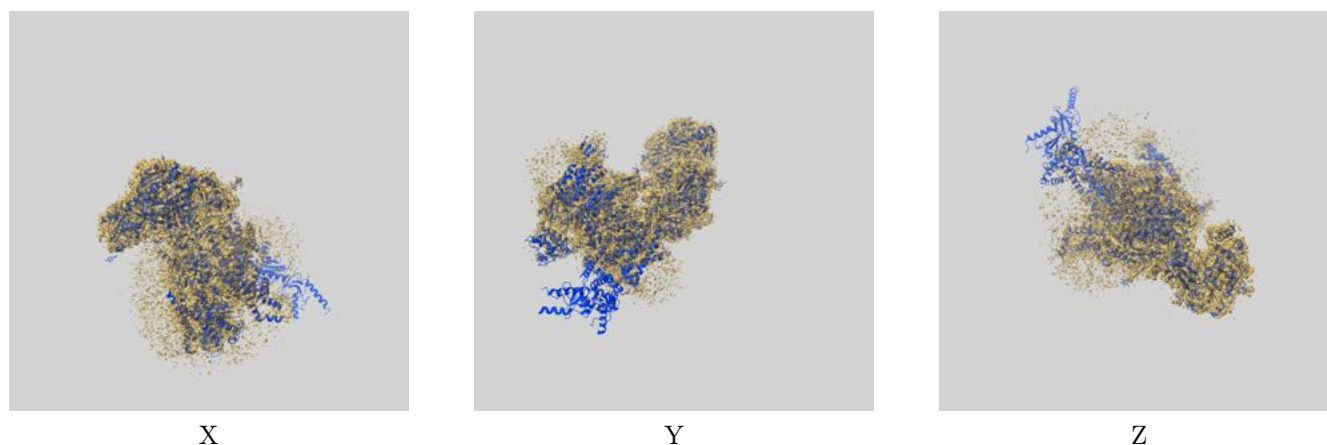
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

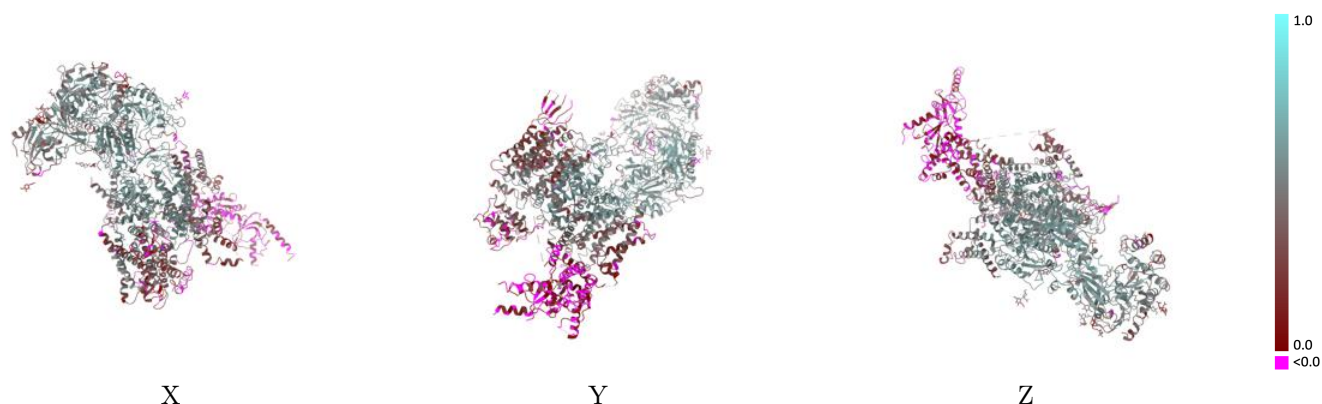
This section contains information regarding the fit between EMDB map EMD-9869 and PDB model 6JPB. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



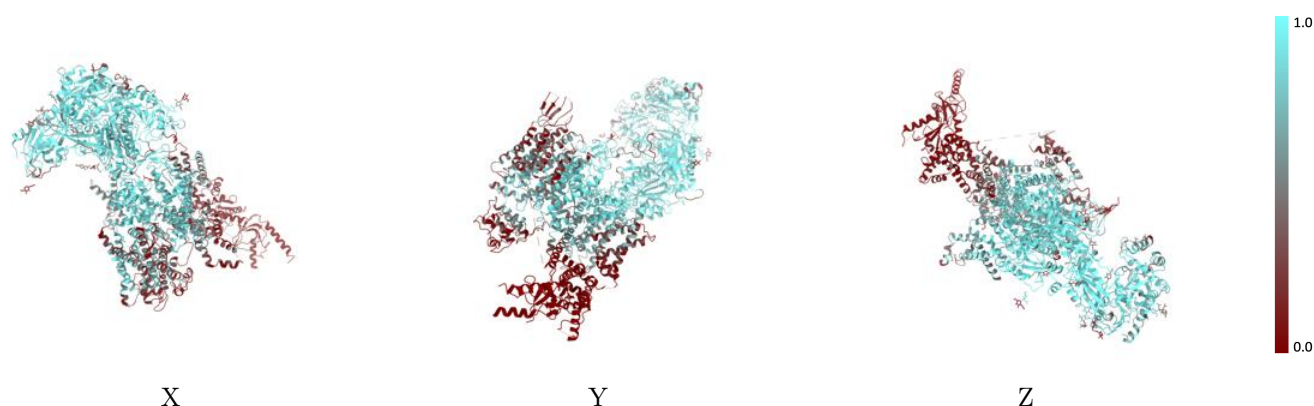
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



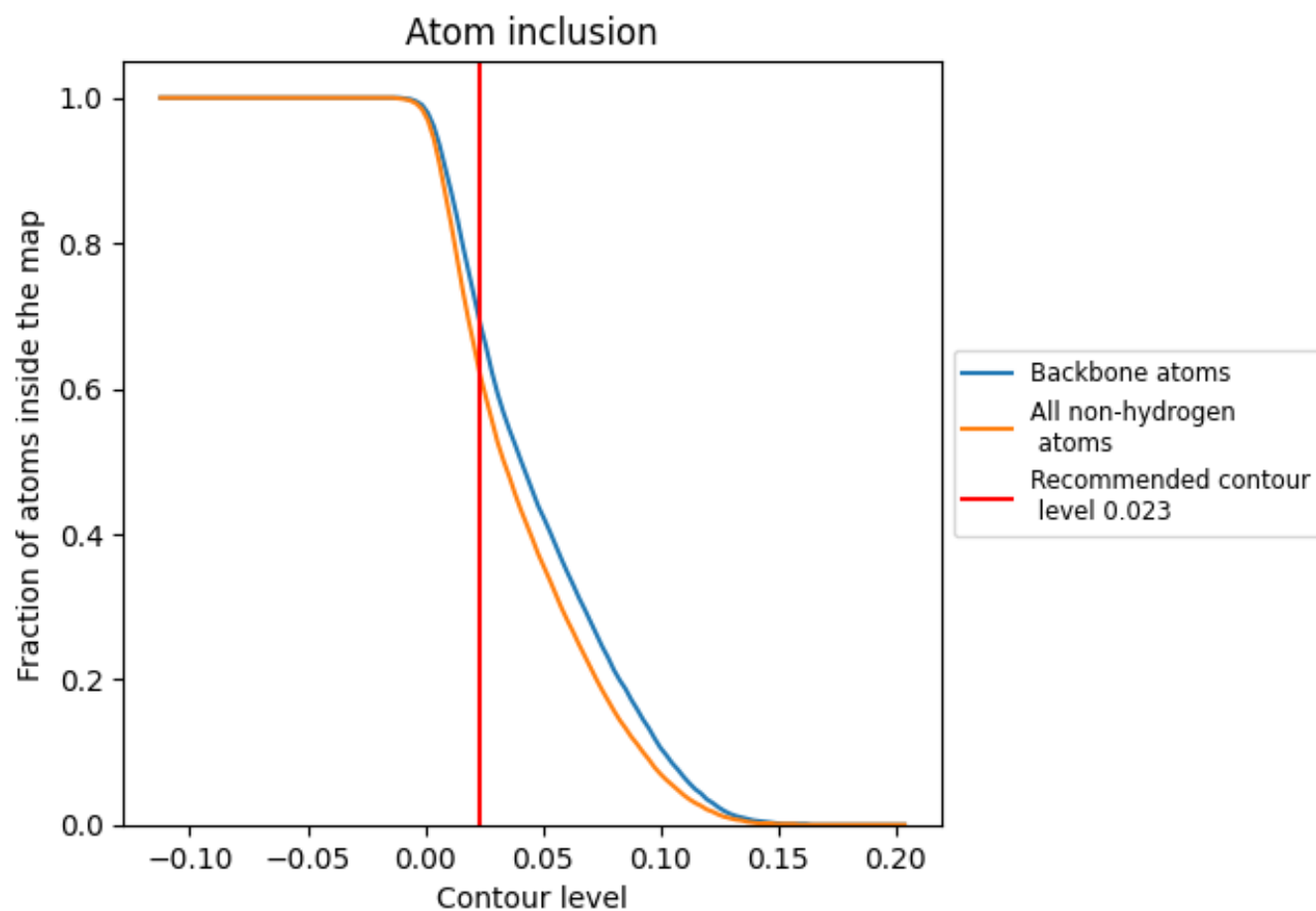
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 62% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6240	0.3970
A	0.6220	0.4110
B	0.0000	0.0010
C	0.0020	0.0040
D	0.3930	0.3500
E	0.3650	0.2520
F	0.8360	0.5070
G	0.5360	0.3730
H	0.5380	0.2860
I	0.8720	0.4950
J	0.7140	0.4280
K	0.5000	0.3350
L	0.5480	0.2390

1.0

0.0

<0.0