



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 11:56 AM UTC

PDB ID : 6V35 / pdb_00006v35
EMDB ID : EMD-21028
Title : Cryo-EM structure of Ca²⁺-free hsSlo1-beta4 channel complex
Authors : Tao, X.; MacKinnon, R.
Deposited on : 2019-11-25
Resolution : 3.50 Å(reported)
Based on initial model : 6V22

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

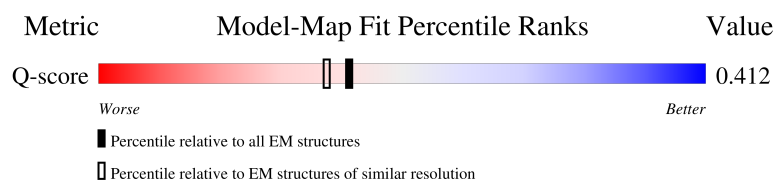
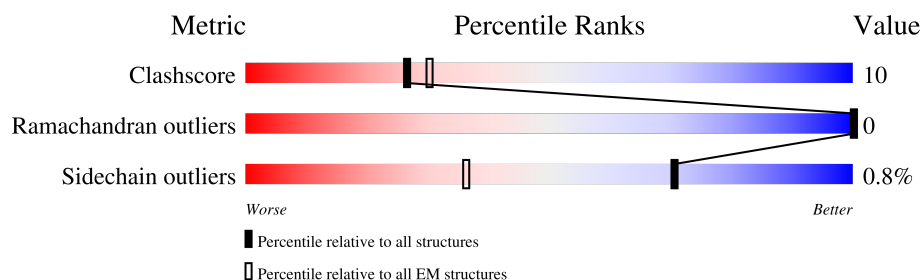
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	1065	17% 67% 18% • 14%
1	B	1065	17% 67% 18% • 14%
1	C	1065	16% 67% 18% • 14%
1	D	1065	17% 67% 18% 14%

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Mol	Chain	Length	Quality of chain
2	E	219	37% 77% 13% 10%
2	F	219	36% 78% 13% 10%
2	G	219	37% 77% 13% 10%
2	H	219	34% 77% 13% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 36488 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 Calcium-activated potassium channel subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	914	Total	C	N	O	S	0	0
			7287	4726	1193	1319	49		
1	B	914	Total	C	N	O	S	0	0
			7287	4726	1193	1319	49		
1	C	914	Total	C	N	O	S	0	0
			7287	4726	1193	1319	49		
1	D	914	Total	C	N	O	S	0	0
			7287	4726	1193	1319	49		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1057	SER	-	expression tag	UNP Q12791
A	1058	ASN	-	expression tag	UNP Q12791
A	1059	SER	-	expression tag	UNP Q12791
A	1060	LEU	-	expression tag	UNP Q12791
A	1061	GLU	-	expression tag	UNP Q12791
A	1062	VAL	-	expression tag	UNP Q12791
A	1063	LEU	-	expression tag	UNP Q12791
A	1064	PHE	-	expression tag	UNP Q12791
A	1065	GLN	-	expression tag	UNP Q12791
B	1057	SER	-	expression tag	UNP Q12791
B	1058	ASN	-	expression tag	UNP Q12791
B	1059	SER	-	expression tag	UNP Q12791
B	1060	LEU	-	expression tag	UNP Q12791
B	1061	GLU	-	expression tag	UNP Q12791
B	1062	VAL	-	expression tag	UNP Q12791
B	1063	LEU	-	expression tag	UNP Q12791
B	1064	PHE	-	expression tag	UNP Q12791
B	1065	GLN	-	expression tag	UNP Q12791
C	1057	SER	-	expression tag	UNP Q12791
C	1058	ASN	-	expression tag	UNP Q12791
C	1059	SER	-	expression tag	UNP Q12791
C	1060	LEU	-	expression tag	UNP Q12791

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1061	GLU	-	expression tag	UNP Q12791
C	1062	VAL	-	expression tag	UNP Q12791
C	1063	LEU	-	expression tag	UNP Q12791
C	1064	PHE	-	expression tag	UNP Q12791
C	1065	GLN	-	expression tag	UNP Q12791
D	1057	SER	-	expression tag	UNP Q12791
D	1058	ASN	-	expression tag	UNP Q12791
D	1059	SER	-	expression tag	UNP Q12791
D	1060	LEU	-	expression tag	UNP Q12791
D	1061	GLU	-	expression tag	UNP Q12791
D	1062	VAL	-	expression tag	UNP Q12791
D	1063	LEU	-	expression tag	UNP Q12791
D	1064	PHE	-	expression tag	UNP Q12791
D	1065	GLN	-	expression tag	UNP Q12791

- Molecule 2 is a protein called Calcium-activated potassium channel subunit beta-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	198	Total	C	N	O	S	0	0
			1581	1012	262	294	13		
2	F	198	Total	C	N	O	S	0	0
			1581	1012	262	294	13		
2	G	198	Total	C	N	O	S	0	0
			1581	1012	262	294	13		
2	H	198	Total	C	N	O	S	0	0
			1581	1012	262	294	13		

There are 36 discrepancies between the modelled and reference sequences:

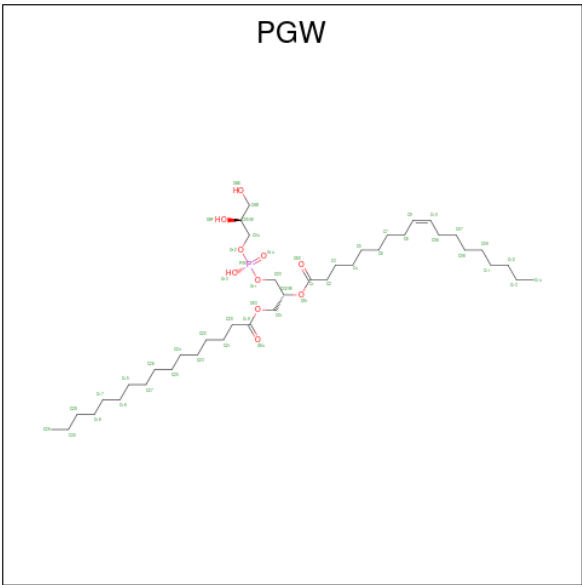
Chain	Residue	Modelled	Actual	Comment	Reference
E	2211	SER	-	expression tag	UNP Q86W47
E	2212	ASN	-	expression tag	UNP Q86W47
E	2213	SER	-	expression tag	UNP Q86W47
E	2214	LEU	-	expression tag	UNP Q86W47
E	2215	GLU	-	expression tag	UNP Q86W47
E	2216	VAL	-	expression tag	UNP Q86W47
E	2217	LEU	-	expression tag	UNP Q86W47
E	2218	PHE	-	expression tag	UNP Q86W47
E	2219	GLN	-	expression tag	UNP Q86W47
F	2211	SER	-	expression tag	UNP Q86W47
F	2212	ASN	-	expression tag	UNP Q86W47
F	2213	SER	-	expression tag	UNP Q86W47

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Chain	Residue	Modelled	Actual	Comment	Reference
F	2214	LEU	-	expression tag	UNP Q86W47
F	2215	GLU	-	expression tag	UNP Q86W47
F	2216	VAL	-	expression tag	UNP Q86W47
F	2217	LEU	-	expression tag	UNP Q86W47
F	2218	PHE	-	expression tag	UNP Q86W47
F	2219	GLN	-	expression tag	UNP Q86W47
G	2211	SER	-	expression tag	UNP Q86W47
G	2212	ASN	-	expression tag	UNP Q86W47
G	2213	SER	-	expression tag	UNP Q86W47
G	2214	LEU	-	expression tag	UNP Q86W47
G	2215	GLU	-	expression tag	UNP Q86W47
G	2216	VAL	-	expression tag	UNP Q86W47
G	2217	LEU	-	expression tag	UNP Q86W47
G	2218	PHE	-	expression tag	UNP Q86W47
G	2219	GLN	-	expression tag	UNP Q86W47
H	2211	SER	-	expression tag	UNP Q86W47
H	2212	ASN	-	expression tag	UNP Q86W47
H	2213	SER	-	expression tag	UNP Q86W47
H	2214	LEU	-	expression tag	UNP Q86W47
H	2215	GLU	-	expression tag	UNP Q86W47
H	2216	VAL	-	expression tag	UNP Q86W47
H	2217	LEU	-	expression tag	UNP Q86W47
H	2218	PHE	-	expression tag	UNP Q86W47
H	2219	GLN	-	expression tag	UNP Q86W47

- Molecule 3 is (1R)-2-{[(S)-{[(2S)-2,3-dihydroxypropyl]oxy}(hydroxy)phosphoryl]oxy}-1-[(hexadecanoyloxy)methyl]ethyl (9Z)-octadec-9-enoate (CCD ID: PGW) (formula: C₄₀H₇₇O₁₀P).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			29	20	8	1	
3	A	1	Total	C	O	P	0
			46	35	10	1	
3	A	1	Total	C			0
			9	9			
3	A	1	Total	C			0
			12	12			
3	A	1	Total	C			0
			12	12			
3	A	1	Total	C	O	P	0
			27	18	8	1	
3	A	1	Total	C	O		0
			13	11	2		
3	A	1	Total	C			0
			12	12			
3	E	1	Total	C			0
			7	7			
3	E	1	Total	C			0
			6	6			
3	B	1	Total	C	O	P	0
			27	18	8	1	
3	B	1	Total	C	O		0
			13	11	2		
3	B	1	Total	C			0
			9	9			
3	B	1	Total	C	O	P	0
			29	20	8	1	

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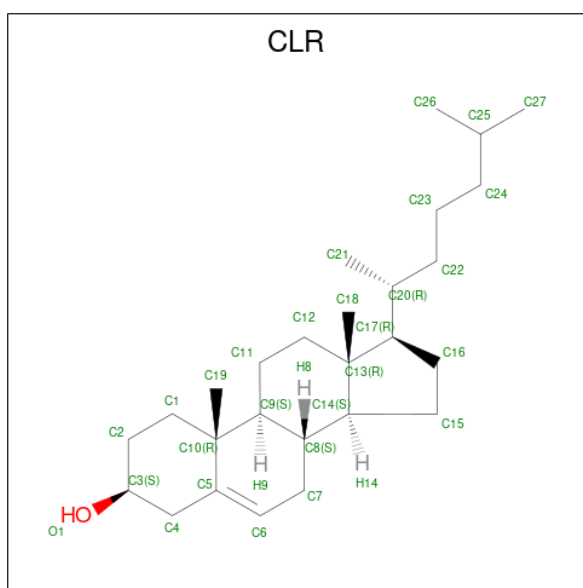
Mol	Chain	Residues	Atoms				AltConf
3	B	1	Total	C	O	P	0
			27	18	8	1	
3	B	1	Total	C	O	P	0
			46	35	10	1	
3	B	1	Total	C			0
			9	9			
3	B	1	Total	C			0
			12	12			
3	B	1	Total	C			0
			12	12			
3	F	1	Total	C			0
			9	9			
3	F	1	Total	C			0
			7	7			
3	F	1	Total	C			0
			6	6			
3	C	1	Total	C	O		0
			13	11	2		
3	C	1	Total	C	O	P	0
			29	20	8	1	
3	C	1	Total	C	O	P	0
			46	35	10	1	
3	C	1	Total	C			0
			9	9			
3	C	1	Total	C			0
			12	12			
3	C	1	Total	C			0
			12	12			
3	G	1	Total	C			0
			7	7			
3	G	1	Total	C			0
			6	6			
3	D	1	Total	C	O	P	0
			27	18	8	1	
3	D	1	Total	C	O		0
			13	11	2		
3	D	1	Total	C			0
			9	9			
3	D	1	Total	C	O	P	0
			29	20	8	1	
3	D	1	Total	C	O	P	0
			46	35	10	1	

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Mol	Chain	Residues	Atoms		AltConf
3	D	1	Total	C	0
			9	9	
3	D	1	Total	C	0
			12	12	
3	H	1	Total	C	0
			9	9	
3	H	1	Total	C	0
			7	7	
3	H	1	Total	C	0
			6	6	

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



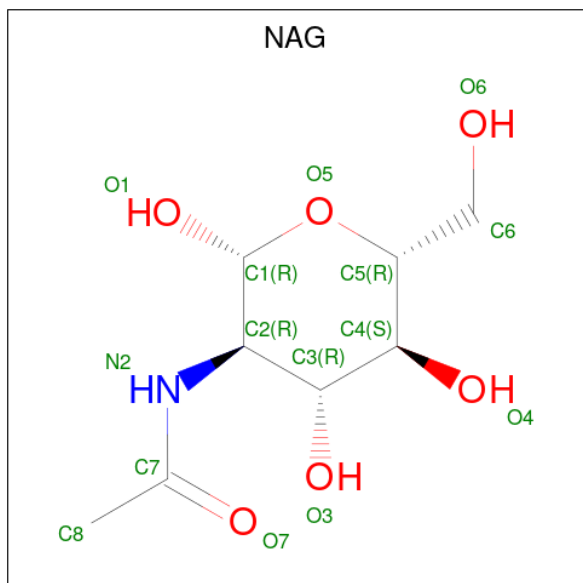
Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	C O	0
			28	27 1	
4	E	1	Total	C O	0
			28	27 1	
4	B	1	Total	C O	0
			28	27 1	
4	F	1	Total	C O	0
			28	27 1	
4	C	1	Total	C O	0
			28	27 1	
4	G	1	Total	C O	0
			28	27 1	

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Mol	Chain	Residues	Atoms			AltConf
4	D	1	Total	C	O	0
			28	27	1	
4	H	1	Total	C	O	0
			28	27	1	

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

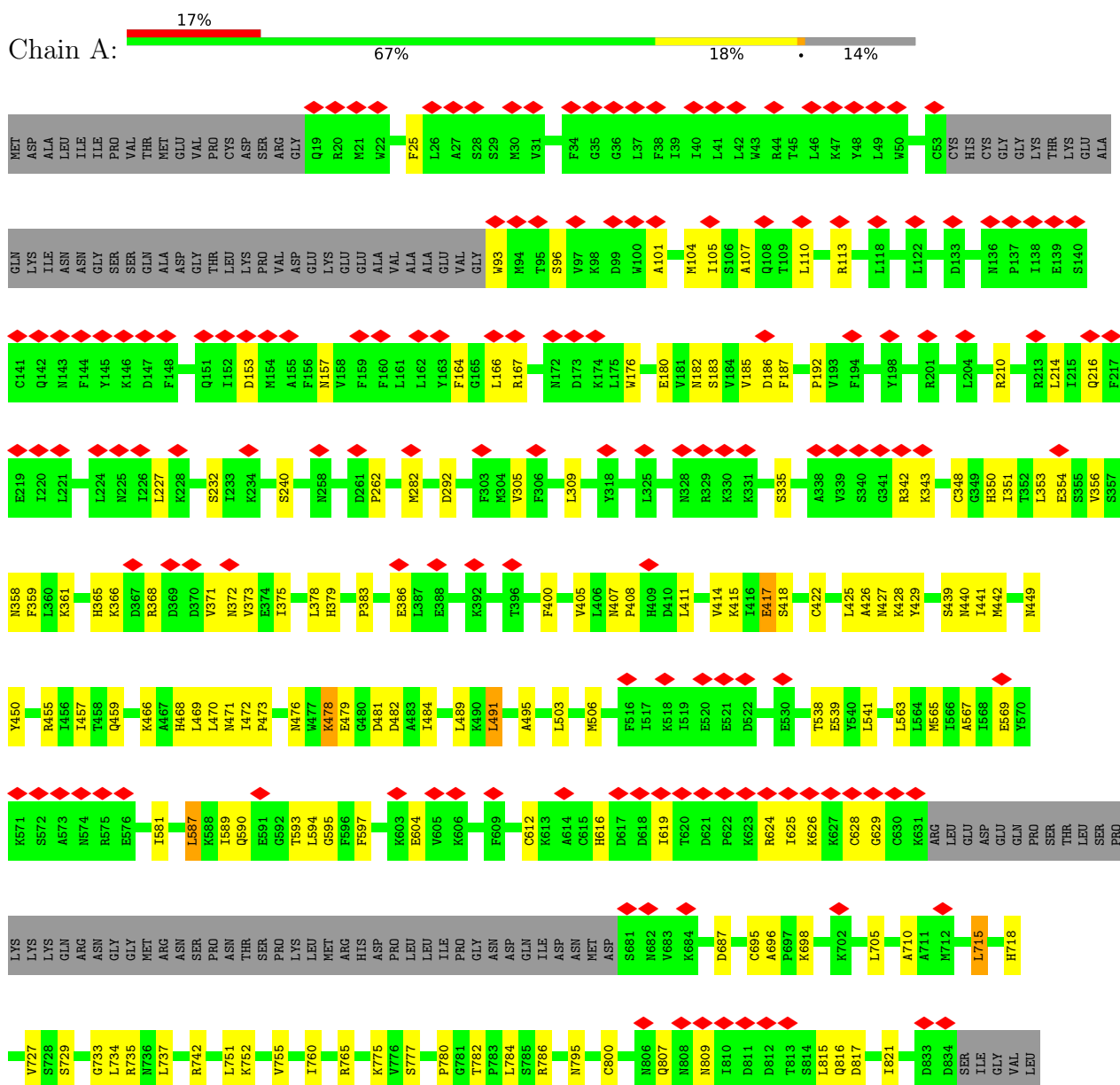


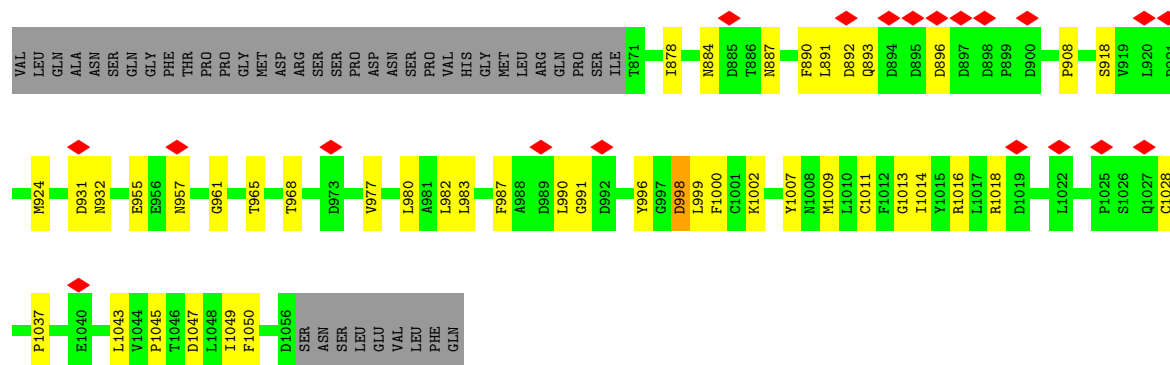
Mol	Chain	Residues	Atoms				AltConf
5	E	1	Total	C	N	O	0
			14	8	1	5	
5	E	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	G	1	Total	C	N	O	0
			14	8	1	5	
5	G	1	Total	C	N	O	0
			14	8	1	5	
5	H	1	Total	C	N	O	0
			14	8	1	5	
5	H	1	Total	C	N	O	0
			14	8	1	5	

3 Residue-property plots

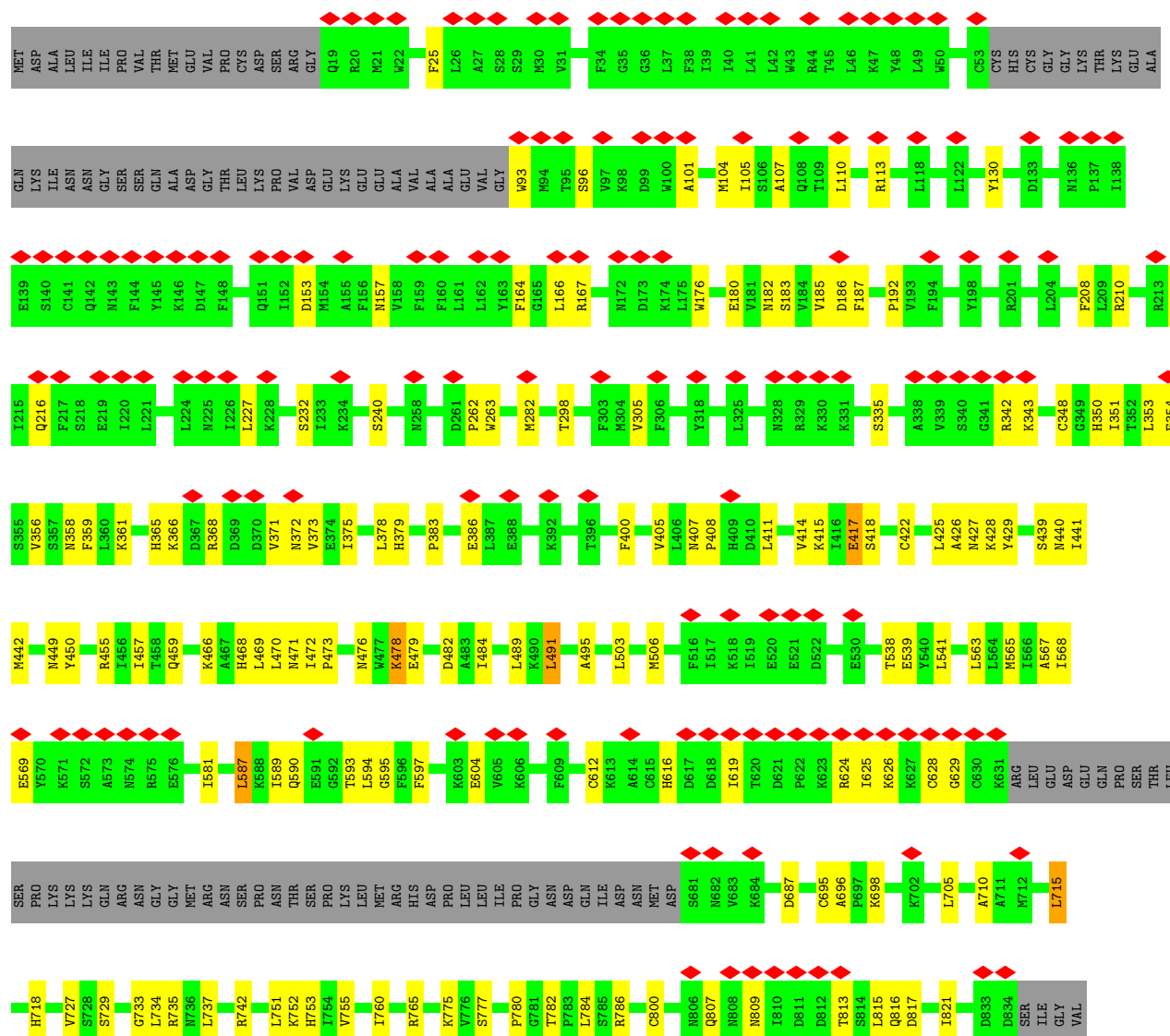
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

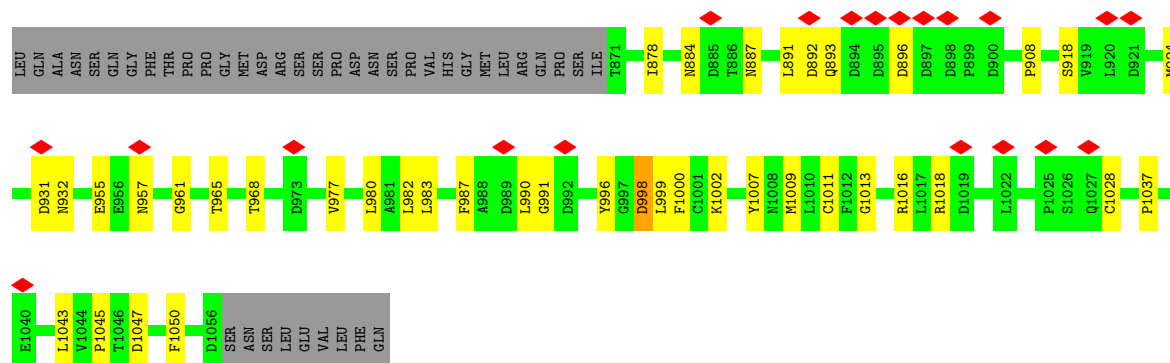
- Molecule 1: Calcium-activated potassium channel subunit alpha-1



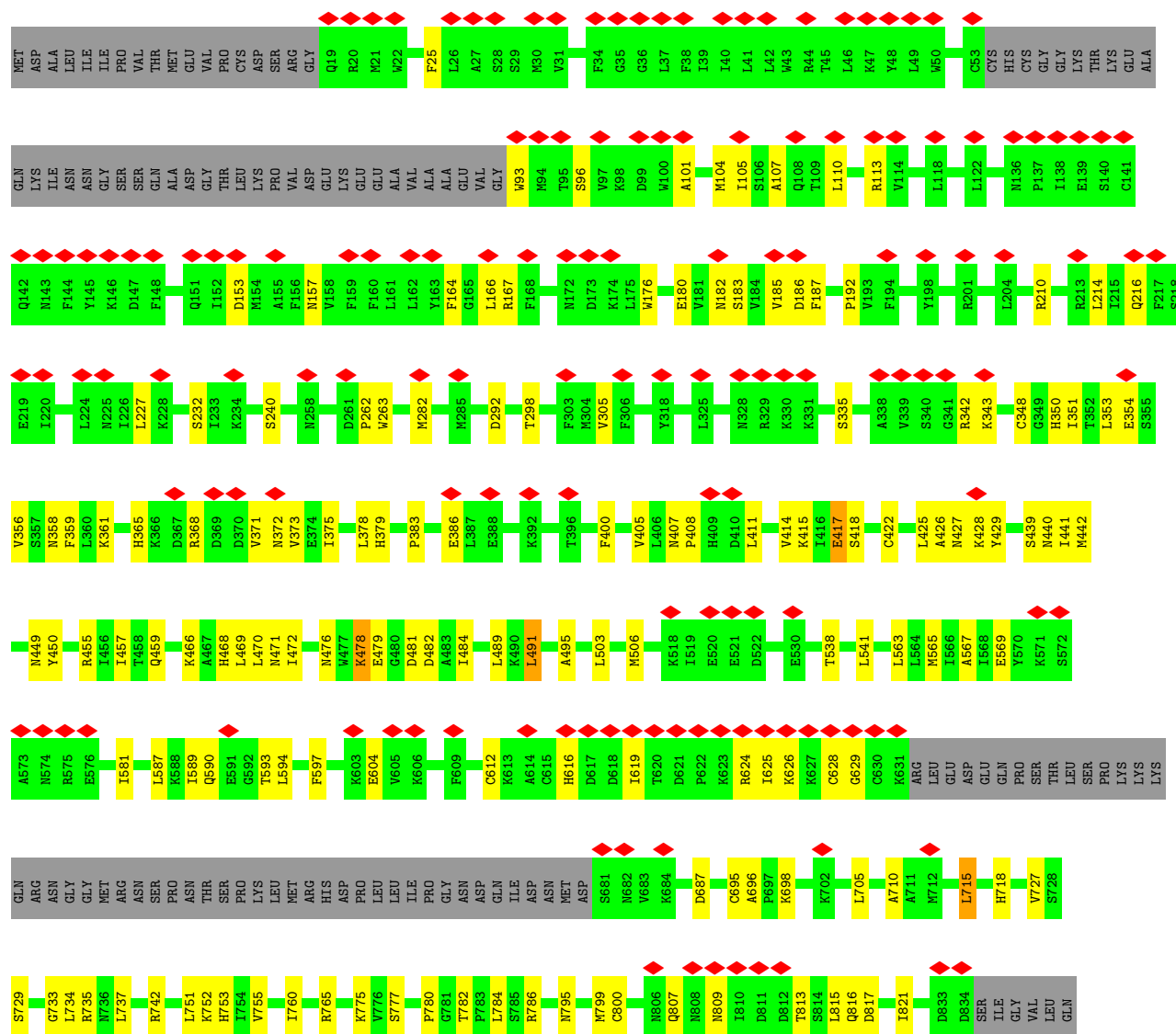


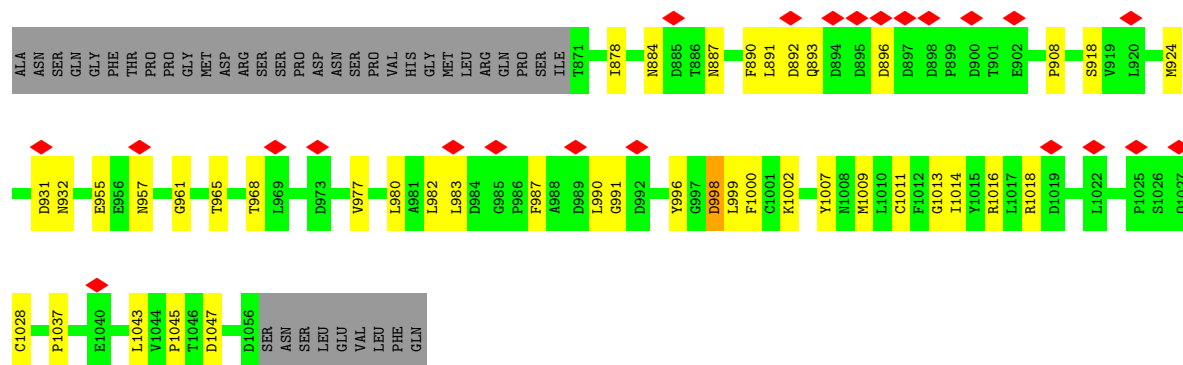
• Molecule 1: Calcium-activated potassium channel subunit alpha-1



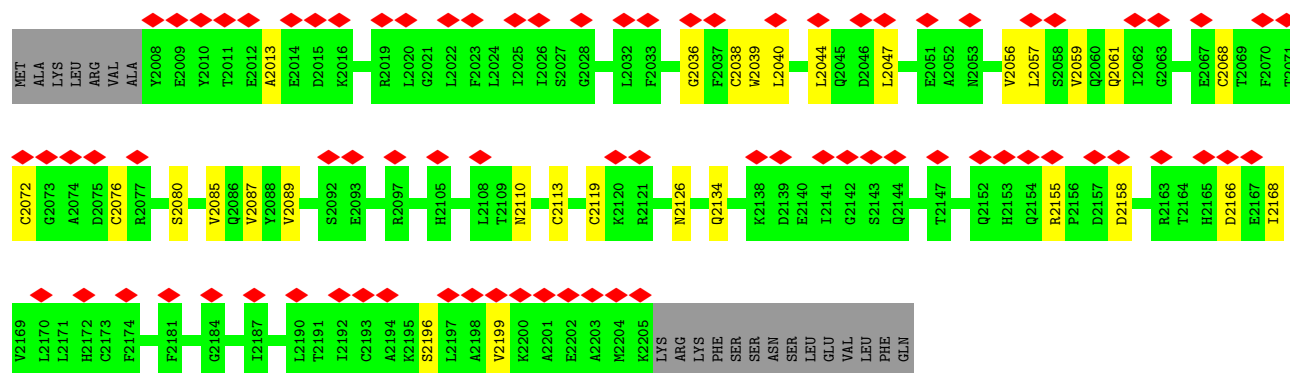
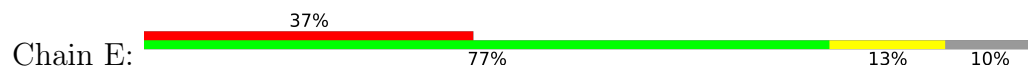


• Molecule 1: Calcium-activated potassium channel subunit alpha-1

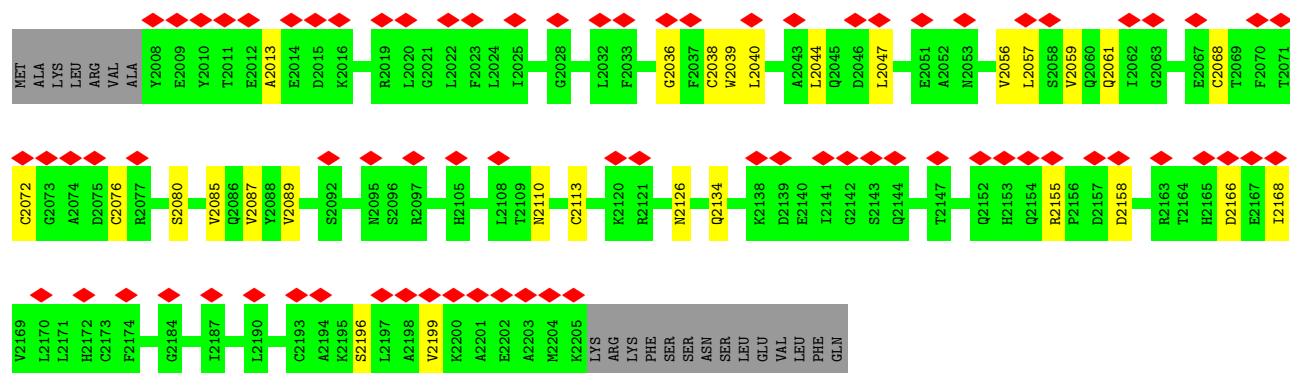
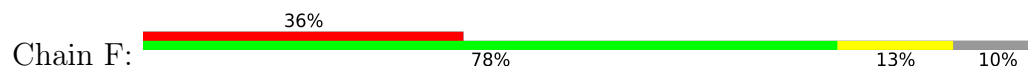




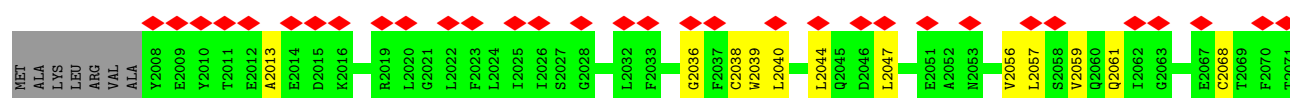
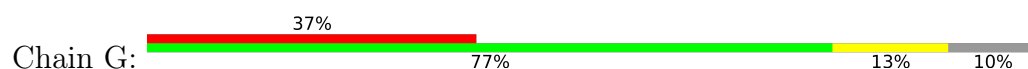
• Molecule 2: Calcium-activated potassium channel subunit beta-4

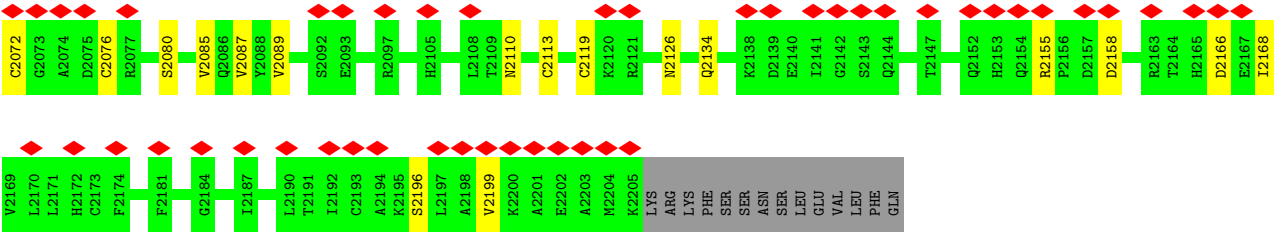


• Molecule 2: Calcium-activated potassium channel subunit beta-4

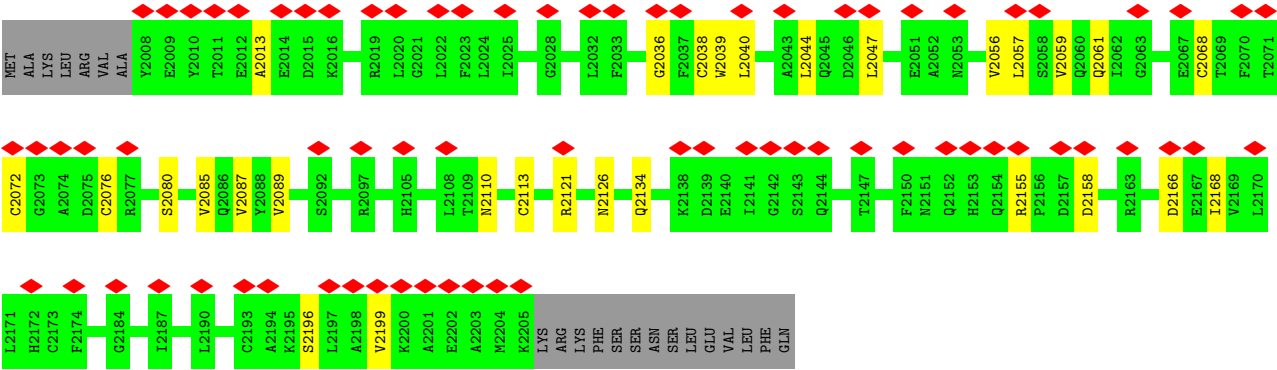
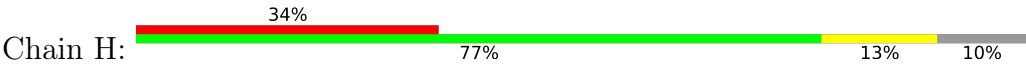


• Molecule 2: Calcium-activated potassium channel subunit beta-4





• Molecule 2: Calcium-activated potassium channel subunit beta-4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	42842	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	89	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	21.471	Depositor
Minimum map value	-9.618	Depositor
Average map value	-0.342	Depositor
Map value standard deviation	1.078	Depositor
Recommended contour level	6.7	Depositor
Map size ($\text{\AA}$)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3, 1.3, 1.3	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CLR, NAG, PGW

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	0.47	0/7456	0.70	0/10119
1	B	0.47	0/7456	0.70	0/10119
1	C	0.47	0/7456	0.70	0/10119
1	D	0.47	0/7456	0.70	0/10119
2	E	0.23	0/1619	0.49	1/2204 (0.0%)
2	F	0.24	0/1619	0.49	1/2204 (0.0%)
2	G	0.24	0/1619	0.49	1/2204 (0.0%)
2	H	0.24	0/1619	0.49	1/2204 (0.0%)
All	All	0.43	0/36300	0.67	4/49292 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	2038	CYS	N-CA-C	-5.44	107.30	114.31
2	E	2038	CYS	N-CA-C	-5.40	107.34	114.31
2	F	2038	CYS	N-CA-C	-5.40	107.35	114.31
2	H	2038	CYS	N-CA-C	-5.38	107.36	114.31

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	7287	0	7277	160	0
1	B	7287	0	7277	161	0
1	C	7287	0	7277	155	0
1	D	7287	0	7277	161	0
2	E	1581	0	1538	17	0
2	F	1581	0	1538	16	0
2	G	1581	0	1538	20	0
2	H	1581	0	1538	19	0
3	A	160	0	215	1	0
3	B	184	0	236	2	0
3	C	121	0	168	1	0
3	D	145	0	189	3	0
3	E	13	0	18	0	0
3	F	22	0	32	0	0
3	G	13	0	18	0	0
3	H	22	0	32	0	0
4	A	28	0	44	6	0
4	B	28	0	44	6	0
4	C	28	0	44	5	0
4	D	28	0	44	6	0
4	E	28	0	45	5	0
4	F	28	0	45	8	0
4	G	28	0	45	8	0
4	H	28	0	45	7	0
5	E	28	0	26	0	0
5	F	28	0	26	0	0
5	G	28	0	26	0	0
5	H	28	0	26	0	0
All	All	36488	0	36628	733	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 10.

All (733) 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:E:2305:CLR:C16	4:E:2305:CLR:C17	1.74	1.61
4:G:2305:CLR:C16	4:G:2305:CLR:C17	1.74	1.59
4:B:1110:CLR:C16	4:B:1110:CLR:C17	1.75	1.56
4:F:2306:CLR:C16	4:F:2306:CLR:C17	1.74	1.56
4:C:1107:CLR:C16	4:C:1107:CLR:C17	1.75	1.51
4:D:1108:CLR:C16	4:D:1108:CLR:C17	1.75	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:3006:CLR:C16	4:A:3006:CLR:C17	1.75	1.47
4:H:2306:CLR:C16	4:H:2306:CLR:C17	1.74	1.44
1:C:183:SER:O	1:C:187:PHE:HB2	1.68	0.93
1:A:183:SER:O	1:A:187:PHE:HB2	1.68	0.93
1:B:183:SER:O	1:B:187:PHE:HB2	1.68	0.93
1:C:491:LEU:HG	1:C:737:LEU:HB2	1.50	0.92
1:D:183:SER:O	1:D:187:PHE:HB2	1.68	0.92
1:A:491:LEU:HG	1:A:737:LEU:HB2	1.50	0.91
1:B:491:LEU:HG	1:B:737:LEU:HB2	1.50	0.90
1:D:104:MET:HE2	1:D:104:MET:HA	1.53	0.89
1:D:491:LEU:HG	1:D:737:LEU:HB2	1.50	0.89
1:A:104:MET:HE2	1:A:104:MET:HA	1.53	0.89
1:B:104:MET:HA	1:B:104:MET:HE2	1.53	0.89
1:C:104:MET:HE2	1:C:104:MET:HA	1.53	0.89
1:C:101:ALA:HB1	1:C:166:LEU:HD12	1.60	0.83
1:A:982:LEU:HD13	1:A:1043:LEU:HD21	1.61	0.83
1:A:101:ALA:HB1	1:A:166:LEU:HD12	1.60	0.83
1:B:982:LEU:HD13	1:B:1043:LEU:HD21	1.61	0.83
1:D:982:LEU:HD13	1:D:1043:LEU:HD21	1.61	0.82
1:B:101:ALA:HB1	1:B:166:LEU:HD12	1.61	0.82
1:C:982:LEU:HD13	1:C:1043:LEU:HD21	1.61	0.82
1:D:101:ALA:HB1	1:D:166:LEU:HD12	1.60	0.82
1:A:1002:LYS:CA	1:A:1002:LYS:HE2	2.11	0.81
1:B:1002:LYS:HE2	1:B:1002:LYS:CA	2.11	0.81
4:H:2306:CLR:C16	4:H:2306:CLR:C20	2.58	0.81
4:C:1107:CLR:C16	4:C:1107:CLR:C20	2.59	0.80
4:E:2305:CLR:C16	4:E:2305:CLR:C20	2.58	0.80
4:F:2306:CLR:C16	4:F:2306:CLR:C20	2.58	0.80
4:B:1110:CLR:C16	4:B:1110:CLR:C20	2.59	0.80
4:A:3006:CLR:C16	4:A:3006:CLR:C20	2.59	0.79
1:D:1002:LYS:CA	1:D:1002:LYS:HE2	2.11	0.79
1:C:1002:LYS:CA	1:C:1002:LYS:HE2	2.11	0.79
4:D:1108:CLR:C16	4:D:1108:CLR:C20	2.59	0.78
4:G:2305:CLR:C16	4:G:2305:CLR:C20	2.58	0.78
1:A:1002:LYS:HE2	1:A:1002:LYS:HA	1.67	0.76
1:B:1002:LYS:HE2	1:B:1002:LYS:HA	1.67	0.76
1:C:1002:LYS:HE2	1:C:1002:LYS:HA	1.67	0.76
1:D:1002:LYS:HE2	1:D:1002:LYS:HA	1.67	0.76
1:C:417:GLU:HG3	1:C:450:TYR:HE2	1.53	0.74
1:A:417:GLU:HG3	1:A:450:TYR:HE2	1.53	0.73
1:C:1002:LYS:HE2	1:C:1002:LYS:N	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:417:GLU:HG3	1:D:450:TYR:HE2	1.53	0.72
1:B:417:GLU:HG3	1:B:450:TYR:HE2	1.53	0.72
1:B:1002:LYS:HE2	1:B:1002:LYS:N	2.04	0.72
1:A:1002:LYS:HE2	1:A:1002:LYS:N	2.05	0.72
1:D:1002:LYS:HE2	1:D:1002:LYS:N	2.04	0.72
1:D:1000:PHE:HA	1:D:1011:CYS:SG	2.32	0.70
1:D:343:LYS:O	1:D:373:VAL:HA	1.91	0.70
1:A:1000:PHE:HA	1:A:1011:CYS:SG	2.32	0.69
1:B:343:LYS:O	1:B:373:VAL:HA	1.91	0.69
1:B:1000:PHE:HA	1:B:1011:CYS:SG	2.32	0.69
1:C:1000:PHE:HA	1:C:1011:CYS:SG	2.32	0.69
1:B:470:LEU:HD23	1:B:470:LEU:C	2.18	0.69
1:C:470:LEU:C	1:C:470:LEU:HD23	2.18	0.69
1:D:470:LEU:C	1:D:470:LEU:HD23	2.18	0.69
1:C:343:LYS:O	1:C:373:VAL:HA	1.91	0.69
1:A:343:LYS:O	1:A:373:VAL:HA	1.91	0.68
1:A:470:LEU:C	1:A:470:LEU:HD23	2.18	0.67
1:D:104:MET:HA	1:D:104:MET:CE	2.23	0.66
1:A:351:ILE:HG23	1:A:356:VAL:HG21	1.78	0.66
1:C:351:ILE:HG23	1:C:356:VAL:HG21	1.78	0.66
1:C:305:VAL:HG13	1:D:282:MET:HG2	1.77	0.66
1:B:351:ILE:HG23	1:B:356:VAL:HG21	1.78	0.66
1:D:351:ILE:HG23	1:D:356:VAL:HG21	1.78	0.66
1:A:104:MET:HA	1:A:104:MET:CE	2.23	0.65
2:F:2072:CYS:H	2:F:2076:CYS:HB2	1.61	0.65
2:E:2072:CYS:H	2:E:2076:CYS:HB2	1.61	0.65
1:C:358:ASN:HD22	1:C:918:SER:HB3	1.62	0.64
1:C:563:LEU:HD21	1:C:604:GLU:HB3	1.79	0.64
2:G:2072:CYS:H	2:G:2076:CYS:HB2	1.61	0.64
1:D:358:ASN:HD22	1:D:918:SER:HB3	1.62	0.64
2:H:2072:CYS:H	2:H:2076:CYS:HB2	1.61	0.64
1:A:353:LEU:HD22	1:A:386:GLU:OE1	1.98	0.64
1:A:358:ASN:HD22	1:A:918:SER:HB3	1.62	0.64
1:B:353:LEU:HD22	1:B:386:GLU:OE1	1.98	0.63
1:A:563:LEU:HD21	1:A:604:GLU:HB3	1.80	0.63
1:A:441:ILE:HD13	1:A:468:HIS:HB2	1.81	0.63
1:B:563:LEU:HD21	1:B:604:GLU:HB3	1.80	0.63
1:B:358:ASN:HD22	1:B:918:SER:HB3	1.62	0.62
1:C:353:LEU:HD22	1:C:386:GLU:OE1	1.98	0.62
1:D:353:LEU:HD22	1:D:386:GLU:OE1	1.98	0.62
1:D:563:LEU:HD21	1:D:604:GLU:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:439:SER:OG	1:D:815:LEU:HD21	1.99	0.62
1:B:441:ILE:HD13	1:B:468:HIS:HB2	1.81	0.62
2:F:2057:LEU:H	2:F:2089:VAL:HA	1.65	0.62
1:C:351:ILE:HG23	1:C:356:VAL:CG2	2.30	0.62
1:B:439:SER:OG	1:C:815:LEU:HD21	2.00	0.62
1:C:441:ILE:HD13	1:C:468:HIS:HB2	1.81	0.62
1:B:104:MET:HA	1:B:104:MET:CE	2.23	0.62
1:B:351:ILE:HG23	1:B:356:VAL:CG2	2.30	0.62
1:D:705:LEU:HD13	1:D:710:ALA:HB2	1.82	0.61
1:D:351:ILE:HG23	1:D:356:VAL:CG2	2.30	0.61
2:G:2057:LEU:H	2:G:2089:VAL:HA	1.65	0.61
1:D:441:ILE:HD13	1:D:468:HIS:HB2	1.81	0.61
1:A:351:ILE:HG23	1:A:356:VAL:CG2	2.30	0.61
1:A:705:LEU:HD13	1:A:710:ALA:HB2	1.82	0.61
1:C:612:CYS:H	1:C:616:HIS:HD2	1.49	0.61
2:H:2057:LEU:H	2:H:2089:VAL:HA	1.65	0.61
1:D:612:CYS:H	1:D:616:HIS:HD2	1.49	0.60
1:B:612:CYS:H	1:B:616:HIS:HD2	1.49	0.60
1:C:705:LEU:HD13	1:C:710:ALA:HB2	1.82	0.60
1:D:727:VAL:O	1:D:765:ARG:NH1	2.35	0.60
1:A:612:CYS:H	1:A:616:HIS:HD2	1.49	0.60
1:C:727:VAL:O	1:C:765:ARG:NH1	2.35	0.60
1:D:587:LEU:O	1:D:587:LEU:HD23	2.02	0.60
1:B:727:VAL:O	1:B:765:ARG:NH1	2.35	0.60
1:A:587:LEU:HD23	1:A:587:LEU:O	2.02	0.60
1:C:587:LEU:HD23	1:C:587:LEU:O	2.02	0.60
1:B:800:CYS:HB3	1:B:878:ILE:HG22	1.84	0.60
1:A:727:VAL:O	1:A:765:ARG:NH1	2.35	0.60
1:A:439:SER:OG	1:B:815:LEU:HD21	2.02	0.60
4:E:2305:CLR:C16	4:E:2305:CLR:H222	2.32	0.60
1:B:705:LEU:HD13	1:B:710:ALA:HB2	1.82	0.60
1:C:104:MET:HE2	1:C:104:MET:CA	2.30	0.60
1:A:305:VAL:HG13	1:B:282:MET:HG2	1.82	0.60
1:A:479:GLU:OE1	1:A:479:GLU:HA	2.02	0.59
4:H:2306:CLR:C16	4:H:2306:CLR:H222	2.32	0.59
2:E:2057:LEU:H	2:E:2089:VAL:HA	1.65	0.59
1:B:742:ARG:NH2	1:B:775:LYS:O	2.36	0.59
1:B:619:ILE:HA	1:B:624:ARG:HG3	1.85	0.59
1:C:186:ASP:OD1	1:C:210:ARG:NH1	2.36	0.59
1:C:619:ILE:HA	1:C:624:ARG:HG3	1.85	0.59
4:G:2305:CLR:C16	4:G:2305:CLR:H222	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:ASP:OD1	1:D:210:ARG:NH1	2.36	0.59
1:D:479:GLU:HA	1:D:479:GLU:OE1	2.02	0.59
4:F:2306:CLR:C16	4:F:2306:CLR:H222	2.32	0.59
1:C:742:ARG:NH2	1:C:775:LYS:O	2.36	0.59
1:C:800:CYS:HB3	1:C:878:ILE:HG22	1.84	0.59
1:C:815:LEU:O	1:C:815:LEU:HG	2.03	0.59
1:D:742:ARG:NH2	1:D:775:LYS:O	2.36	0.59
4:D:1108:CLR:C16	4:D:1108:CLR:H222	2.33	0.59
1:A:619:ILE:HA	1:A:624:ARG:HG3	1.85	0.59
1:A:742:ARG:NH2	1:A:775:LYS:O	2.36	0.59
1:D:619:ILE:HA	1:D:624:ARG:HG3	1.85	0.59
1:B:587:LEU:O	1:B:587:LEU:HD23	2.02	0.58
1:B:695:CYS:SG	1:B:696:ALA:N	2.76	0.58
4:A:3006:CLR:C16	4:A:3006:CLR:H222	2.33	0.58
1:B:479:GLU:HA	1:B:479:GLU:OE1	2.02	0.58
1:D:800:CYS:HB3	1:D:878:ILE:HG22	1.84	0.58
1:D:809:ASN:HD22	1:D:816:GLN:HG2	1.69	0.58
1:B:809:ASN:HD22	1:B:816:GLN:HG2	1.69	0.58
1:A:800:CYS:HB3	1:A:878:ILE:HG22	1.84	0.58
1:C:262:PRO:HB2	2:G:2039:TRP:HZ3	1.68	0.58
1:C:955:GLU:HG2	1:D:786:ARG:HD2	1.85	0.58
4:C:1107:CLR:C16	4:C:1107:CLR:H222	2.33	0.58
1:A:348:CYS:SG	1:A:422:CYS:SG	3.02	0.58
1:B:815:LEU:HG	1:B:815:LEU:O	2.03	0.58
1:D:982:LEU:HD11	1:D:1047:ASP:HB2	1.86	0.58
1:A:262:PRO:HB2	2:E:2039:TRP:HZ3	1.68	0.58
1:B:348:CYS:SG	1:B:422:CYS:SG	3.02	0.58
1:C:479:GLU:OE1	1:C:479:GLU:HA	2.02	0.58
1:D:695:CYS:SG	1:D:696:ALA:N	2.76	0.58
1:A:695:CYS:SG	1:A:696:ALA:N	2.76	0.58
1:B:186:ASP:OD1	1:B:210:ARG:NH1	2.36	0.58
1:C:753:HIS:HD1	1:C:775:LYS:HB2	1.67	0.58
1:B:982:LEU:HD11	1:B:1047:ASP:HB2	1.86	0.58
1:C:695:CYS:SG	1:C:696:ALA:N	2.76	0.58
1:D:348:CYS:SG	1:D:422:CYS:SG	3.02	0.58
1:A:982:LEU:HD11	1:A:1047:ASP:HB2	1.86	0.58
4:B:1110:CLR:C16	4:B:1110:CLR:H222	2.33	0.58
1:B:262:PRO:HB2	2:F:2039:TRP:HZ3	1.68	0.58
1:C:809:ASN:HD22	1:C:816:GLN:HG2	1.69	0.58
1:A:809:ASN:HD22	1:A:816:GLN:HG2	1.69	0.57
1:C:982:LEU:HD11	1:C:1047:ASP:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:ALA:CB	1:C:166:LEU:HD12	2.33	0.57
1:D:815:LEU:HG	1:D:815:LEU:O	2.03	0.57
1:C:348:CYS:SG	1:C:422:CYS:SG	3.02	0.57
1:D:104:MET:HE2	1:D:104:MET:CA	2.30	0.57
1:A:227:LEU:HD22	1:A:232:SER:HB3	1.87	0.57
1:A:815:LEU:HD21	1:D:439:SER:OG	2.05	0.57
1:D:262:PRO:HB2	2:H:2039:TRP:HZ3	1.68	0.57
1:A:815:LEU:O	1:A:815:LEU:HG	2.03	0.57
1:D:227:LEU:HD22	1:D:232:SER:HB3	1.87	0.57
2:F:2036:GLY:HA2	2:F:2040:LEU:HD12	1.87	0.57
1:C:104:MET:HA	1:C:104:MET:CE	2.23	0.57
1:A:405:VAL:HA	1:A:411:LEU:HD11	1.87	0.56
2:E:2036:GLY:HA2	2:E:2040:LEU:HD12	1.87	0.56
1:B:227:LEU:HD22	1:B:232:SER:HB3	1.87	0.56
1:C:227:LEU:HD22	1:C:232:SER:HB3	1.87	0.56
1:A:101:ALA:CB	1:A:166:LEU:HD12	2.34	0.56
1:C:569:GLU:HG2	1:C:594:LEU:HB3	1.88	0.56
1:D:351:ILE:HD12	1:D:379:HIS:HB2	1.88	0.56
1:B:105:ILE:HD11	1:B:166:LEU:HG	1.87	0.56
1:B:101:ALA:CB	1:B:166:LEU:HD12	2.34	0.56
1:A:153:ASP:OD1	1:A:157:ASN:ND2	2.38	0.56
1:B:687:ASP:HA	1:B:961:GLY:HA2	1.88	0.56
1:C:405:VAL:HA	1:C:411:LEU:HD11	1.87	0.56
1:A:569:GLU:HG2	1:A:594:LEU:HB3	1.88	0.56
1:C:351:ILE:HD12	1:C:379:HIS:HB2	1.88	0.56
1:D:353:LEU:HD22	1:D:386:GLU:HB3	1.88	0.56
1:A:687:ASP:HA	1:A:961:GLY:HA2	1.88	0.56
1:B:1018:ARG:NH2	1:B:1028:CYS:SG	2.79	0.56
1:D:735:ARG:NH2	1:D:957:ASN:OD1	2.39	0.56
1:A:186:ASP:OD1	1:A:210:ARG:NH1	2.36	0.56
1:C:590:GLN:HB2	1:C:593:THR:HG23	1.88	0.56
1:A:459:GLN:NE2	1:A:924:MET:SD	2.80	0.55
1:B:353:LEU:HD22	1:B:386:GLU:HB3	1.88	0.55
1:D:105:ILE:HD11	1:D:166:LEU:HG	1.88	0.55
1:D:405:VAL:HA	1:D:411:LEU:HD11	1.87	0.55
1:A:282:MET:HG2	1:D:305:VAL:HG13	1.88	0.55
1:A:892:ASP:HB2	1:A:908:PRO:HG3	1.88	0.55
1:B:153:ASP:OD1	1:B:157:ASN:ND2	2.38	0.55
1:C:353:LEU:HD22	1:C:386:GLU:HB3	1.88	0.55
1:C:735:ARG:NH2	1:C:957:ASN:OD1	2.39	0.55
1:D:1018:ARG:NH2	1:D:1028:CYS:SG	2.79	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:2036:GLY:HA2	2:H:2040:LEU:HD12	1.87	0.55
4:A:3006:CLR:C16	4:A:3006:CLR:C22	2.85	0.55
1:B:590:GLN:HB2	1:B:593:THR:HG23	1.88	0.55
4:F:2306:CLR:C16	4:F:2306:CLR:C22	2.85	0.55
1:D:892:ASP:HB2	1:D:908:PRO:HG3	1.88	0.55
1:C:459:GLN:NE2	1:C:924:MET:SD	2.79	0.55
1:A:105:ILE:HD11	1:A:166:LEU:HG	1.88	0.55
1:A:1018:ARG:NH2	1:A:1028:CYS:SG	2.79	0.55
1:C:782:THR:HG22	1:C:784:LEU:H	1.72	0.55
1:A:735:ARG:NH2	1:A:957:ASN:OD1	2.39	0.55
1:B:351:ILE:HD12	1:B:379:HIS:HB2	1.88	0.55
1:C:892:ASP:HB2	1:C:908:PRO:HG3	1.89	0.55
2:G:2036:GLY:HA2	2:G:2040:LEU:HD12	1.87	0.55
1:D:101:ALA:CB	1:D:166:LEU:HD12	2.34	0.55
1:D:569:GLU:HG2	1:D:594:LEU:HB3	1.88	0.55
1:A:782:THR:HG22	1:A:784:LEU:H	1.72	0.55
1:B:782:THR:HG22	1:B:784:LEU:H	1.72	0.55
1:C:1018:ARG:NH2	1:C:1028:CYS:SG	2.79	0.55
1:D:782:THR:HG22	1:D:784:LEU:H	1.72	0.55
1:B:735:ARG:NH2	1:B:957:ASN:OD1	2.39	0.55
1:A:351:ILE:HD12	1:A:379:HIS:HB2	1.88	0.55
1:B:405:VAL:HA	1:B:411:LEU:HD11	1.87	0.55
1:B:503:LEU:HD22	1:B:977:VAL:HG11	1.89	0.55
1:C:105:ILE:HD11	1:C:166:LEU:HG	1.88	0.55
1:C:628:CYS:SG	1:C:629:GLY:N	2.80	0.55
2:G:2056:VAL:HA	2:G:2089:VAL:HG12	1.89	0.55
1:D:982:LEU:CD1	1:D:1047:ASP:HB2	2.37	0.55
1:A:982:LEU:CD1	1:A:1047:ASP:HB2	2.37	0.55
1:B:982:LEU:CD1	1:B:1047:ASP:HB2	2.37	0.55
1:C:687:ASP:HA	1:C:961:GLY:HA2	1.88	0.55
1:C:715:LEU:O	1:C:718:HIS:ND1	2.40	0.55
1:D:459:GLN:NE2	1:D:924:MET:SD	2.80	0.55
1:D:590:GLN:HB2	1:D:593:THR:HG23	1.88	0.55
2:H:2056:VAL:HA	2:H:2089:VAL:HG12	1.89	0.55
1:A:590:GLN:HB2	1:A:593:THR:HG23	1.88	0.54
1:C:982:LEU:CD1	1:C:1047:ASP:HB2	2.37	0.54
1:D:350:HIS:CG	1:D:427:ASN:HB3	2.42	0.54
2:E:2056:VAL:HA	2:E:2089:VAL:HG12	1.89	0.54
2:F:2056:VAL:HA	2:F:2089:VAL:HG12	1.89	0.54
1:D:503:LEU:HD22	1:D:977:VAL:HG11	1.89	0.54
1:C:153:ASP:OD1	1:C:157:ASN:ND2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:ASN:ND2	1:C:918:SER:HB3	2.22	0.54
4:C:1107:CLR:C16	4:C:1107:CLR:C22	2.85	0.54
1:D:358:ASN:ND2	1:D:918:SER:HB3	2.22	0.54
4:E:2305:CLR:C16	4:E:2305:CLR:C22	2.85	0.54
1:B:538:THR:HG21	1:B:932:ASN:HB2	1.90	0.54
4:G:2305:CLR:C16	4:G:2305:CLR:C22	2.85	0.54
1:D:153:ASP:OD1	1:D:157:ASN:ND2	2.38	0.54
1:B:459:GLN:NE2	1:B:924:MET:SD	2.80	0.54
1:B:892:ASP:HB2	1:B:908:PRO:HG3	1.88	0.54
1:A:538:THR:HG21	1:A:932:ASN:HB2	1.90	0.54
1:B:358:ASN:ND2	1:B:918:SER:HB3	2.22	0.54
1:B:569:GLU:HG2	1:B:594:LEU:HB3	1.88	0.54
1:B:628:CYS:SG	1:B:629:GLY:N	2.80	0.54
1:C:538:THR:HG21	1:C:932:ASN:HB2	1.90	0.54
4:D:1108:CLR:C16	4:D:1108:CLR:C22	2.85	0.54
1:A:353:LEU:HD22	1:A:386:GLU:HB3	1.88	0.54
1:A:358:ASN:ND2	1:A:918:SER:HB3	2.22	0.54
1:A:817:ASP:OD1	1:A:887:ASN:ND2	2.41	0.54
1:D:687:ASP:HA	1:D:961:GLY:HA2	1.88	0.54
1:D:742:ARG:NH2	1:D:752:LYS:O	2.41	0.54
1:A:350:HIS:CG	1:A:427:ASN:HB3	2.42	0.54
1:D:817:ASP:OD1	1:D:887:ASN:ND2	2.41	0.54
1:A:503:LEU:HD22	1:A:977:VAL:HG11	1.89	0.54
1:B:350:HIS:CG	1:B:427:ASN:HB3	2.42	0.54
1:B:715:LEU:O	1:B:718:HIS:ND1	2.40	0.54
1:B:817:ASP:OD1	1:B:887:ASN:ND2	2.41	0.54
4:B:1110:CLR:C16	4:B:1110:CLR:C22	2.85	0.54
1:D:538:THR:HG21	1:D:932:ASN:HB2	1.90	0.54
4:H:2306:CLR:C16	4:H:2306:CLR:C22	2.85	0.54
1:C:182:ASN:OD1	1:C:216:GLN:NE2	2.41	0.53
1:C:350:HIS:CG	1:C:427:ASN:HB3	2.42	0.53
1:D:715:LEU:O	1:D:718:HIS:ND1	2.40	0.53
1:A:104:MET:HE2	1:A:104:MET:CA	2.30	0.53
1:A:742:ARG:NH2	1:A:752:LYS:O	2.41	0.53
2:G:2061:GLN:NE2	2:G:2134:GLN:OE1	2.42	0.53
1:D:182:ASN:OD1	1:D:216:GLN:NE2	2.41	0.53
1:B:742:ARG:NH2	1:B:752:LYS:O	2.41	0.53
1:C:503:LEU:HD22	1:C:977:VAL:HG11	1.89	0.53
1:C:742:ARG:NH2	1:C:752:LYS:O	2.41	0.53
1:C:817:ASP:OD1	1:C:887:ASN:ND2	2.41	0.53
1:A:715:LEU:O	1:A:718:HIS:ND1	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:996:TYR:CG	1:A:1037:PRO:HG2	2.44	0.53
1:B:996:TYR:CG	1:B:1037:PRO:HG2	2.44	0.53
2:H:2061:GLN:NE2	2:H:2134:GLN:OE1	2.41	0.53
2:E:2061:GLN:NE2	2:E:2134:GLN:OE1	2.42	0.53
2:E:2110:ASN:ND2	2:E:2113:CYS:SG	2.82	0.53
1:B:182:ASN:OD1	1:B:216:GLN:NE2	2.41	0.53
2:F:2110:ASN:ND2	2:F:2113:CYS:SG	2.82	0.53
1:C:996:TYR:CG	1:C:1037:PRO:HG2	2.44	0.53
1:D:755:VAL:HG22	1:D:777:SER:HB2	1.91	0.53
1:A:182:ASN:OD1	1:A:216:GLN:NE2	2.41	0.53
1:B:305:VAL:HG13	1:C:282:MET:HG2	1.89	0.53
2:H:2166:ASP:HB3	2:H:2168:ILE:HG22	1.91	0.53
1:A:1007:TYR:HB3	1:A:1009:MET:HE3	1.91	0.53
1:D:353:LEU:CD2	1:D:386:GLU:OE1	2.57	0.53
1:D:628:CYS:SG	1:D:629:GLY:N	2.80	0.53
2:E:2166:ASP:HB3	2:E:2168:ILE:HG22	1.91	0.53
1:B:353:LEU:CD2	1:B:386:GLU:OE1	2.57	0.53
1:C:495:ALA:HB2	1:C:737:LEU:HD12	1.91	0.53
1:D:996:TYR:CG	1:D:1037:PRO:HG2	2.44	0.53
2:F:2166:ASP:HB3	2:F:2168:ILE:HG22	1.91	0.52
1:C:755:VAL:HG22	1:C:777:SER:HB2	1.91	0.52
2:H:2110:ASN:ND2	2:H:2113:CYS:SG	2.82	0.52
1:A:729:SER:O	1:A:765:ARG:NH2	2.35	0.52
2:F:2061:GLN:NE2	2:F:2134:GLN:OE1	2.41	0.52
2:G:2158:ASP:OD1	2:H:2121:ARG:NH2	2.42	0.52
1:D:417:GLU:H	1:D:417:GLU:CD	2.17	0.52
1:D:495:ALA:HB2	1:D:737:LEU:HD12	1.91	0.52
1:B:1007:TYR:HB3	1:B:1009:MET:HE3	1.91	0.52
2:G:2110:ASN:ND2	2:G:2113:CYS:SG	2.82	0.52
1:A:495:ALA:HB2	1:A:737:LEU:HD12	1.91	0.52
1:B:495:ALA:HB2	1:B:737:LEU:HD12	1.91	0.52
1:C:342:ARG:HD3	1:C:372:ASN:HB3	1.92	0.52
1:C:353:LEU:CD2	1:C:386:GLU:OE1	2.57	0.52
2:G:2166:ASP:HB3	2:G:2168:ILE:HG22	1.90	0.52
1:A:890:PHE:HD1	1:D:449:ASN:HD22	1.58	0.52
1:A:353:LEU:CD2	1:A:386:GLU:OE1	2.57	0.52
1:A:755:VAL:HG22	1:A:777:SER:HB2	1.91	0.52
1:D:1007:TYR:HB3	1:D:1009:MET:HE3	1.91	0.52
1:B:729:SER:O	1:B:765:ARG:NH2	2.35	0.52
1:A:628:CYS:SG	1:A:629:GLY:N	2.80	0.52
1:A:815:LEU:CD1	1:D:442:MET:HG2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:587:LEU:HD23	1:D:587:LEU:C	2.36	0.51
1:A:983:LEU:CD2	1:A:1045:PRO:HB2	2.41	0.51
1:B:104:MET:HE2	1:B:104:MET:CA	2.30	0.51
1:C:1016:ARG:HH22	1:C:1043:LEU:HA	1.76	0.51
1:B:755:VAL:HG22	1:B:777:SER:HB2	1.91	0.51
1:C:983:LEU:CD2	1:C:1045:PRO:HB2	2.41	0.51
1:C:1000:PHE:HD1	1:C:1011:CYS:HB2	1.76	0.51
1:C:1007:TYR:HB3	1:C:1009:MET:HE3	1.91	0.51
1:D:342:ARG:HD3	1:D:372:ASN:HB3	1.92	0.51
1:D:1016:ARG:HH22	1:D:1043:LEU:HA	1.76	0.51
1:C:587:LEU:HD23	1:C:587:LEU:C	2.36	0.51
1:A:955:GLU:HG2	1:B:786:ARG:HD2	1.93	0.51
1:B:417:GLU:CD	1:B:417:GLU:H	2.17	0.51
1:B:476:ASN:OD1	1:B:478:LYS:HG3	2.11	0.51
1:B:983:LEU:CD2	1:B:1045:PRO:HB2	2.41	0.51
1:D:983:LEU:CD2	1:D:1045:PRO:HB2	2.41	0.51
1:A:342:ARG:HD3	1:A:372:ASN:HB3	1.92	0.51
1:B:587:LEU:HD23	1:B:587:LEU:C	2.36	0.50
1:A:476:ASN:OD1	1:A:478:LYS:HG3	2.11	0.50
1:A:1016:ARG:HH22	1:A:1043:LEU:HA	1.76	0.50
1:B:405:VAL:HA	1:B:411:LEU:CD1	2.42	0.50
1:C:405:VAL:HA	1:C:411:LEU:CD1	2.42	0.50
1:D:1000:PHE:HD1	1:D:1011:CYS:HB2	1.76	0.50
1:A:214:LEU:O	1:A:240:SER:OG	2.30	0.50
1:A:417:GLU:CD	1:A:417:GLU:H	2.17	0.50
1:C:153:ASP:O	1:C:157:ASN:ND2	2.44	0.50
1:A:587:LEU:HD23	1:A:587:LEU:C	2.36	0.50
1:A:1000:PHE:HD1	1:A:1011:CYS:HB2	1.76	0.50
1:B:110:LEU:HD12	1:B:110:LEU:O	2.12	0.50
1:C:417:GLU:CD	1:C:417:GLU:H	2.17	0.50
1:A:110:LEU:HD12	1:A:110:LEU:O	2.12	0.50
1:B:342:ARG:HD3	1:B:372:ASN:HB3	1.92	0.50
1:C:476:ASN:OD1	1:C:478:LYS:HG3	2.11	0.50
1:B:354:GLU:OE1	1:B:354:GLU:HA	2.12	0.50
1:B:1016:ARG:HH22	1:B:1043:LEU:HA	1.76	0.50
1:B:153:ASP:O	1:B:157:ASN:ND2	2.44	0.50
1:B:1000:PHE:HD1	1:B:1011:CYS:HB2	1.76	0.50
1:C:729:SER:O	1:C:765:ARG:NH2	2.35	0.50
1:D:153:ASP:O	1:D:157:ASN:ND2	2.45	0.50
1:D:405:VAL:HA	1:D:411:LEU:CD1	2.42	0.50
1:D:476:ASN:OD1	1:D:478:LYS:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:PRO:HD3	1:A:400:PHE:CE2	2.47	0.50
1:C:383:PRO:HD3	1:C:400:PHE:CE2	2.47	0.50
1:D:110:LEU:HD12	1:D:110:LEU:O	2.12	0.50
1:D:354:GLU:OE1	1:D:354:GLU:HA	2.12	0.50
1:D:214:LEU:O	1:D:240:SER:OG	2.30	0.50
1:D:383:PRO:HD3	1:D:400:PHE:CE2	2.47	0.50
1:A:354:GLU:HA	1:A:354:GLU:OE1	2.12	0.49
1:A:405:VAL:HA	1:A:411:LEU:CD1	2.42	0.49
1:B:214:LEU:O	1:B:240:SER:OG	2.30	0.49
1:B:383:PRO:HD3	1:B:400:PHE:CE2	2.47	0.49
1:B:955:GLU:HG2	1:C:786:ARG:HD2	1.94	0.49
1:C:354:GLU:HA	1:C:354:GLU:OE1	2.12	0.49
1:A:153:ASP:O	1:A:157:ASN:ND2	2.44	0.49
1:B:183:SER:O	1:B:187:PHE:CB	2.53	0.49
1:C:539:GLU:O	1:C:595:GLY:N	2.39	0.49
1:C:110:LEU:O	1:C:110:LEU:HD12	2.12	0.49
1:C:214:LEU:O	1:C:240:SER:OG	2.30	0.49
1:C:990:LEU:HD21	1:C:998:ASP:HB2	1.94	0.49
1:A:990:LEU:HD21	1:A:998:ASP:HB2	1.94	0.49
1:B:93:TRP:NE1	1:B:96:SER:OG	2.46	0.49
1:D:742:ARG:HG2	1:D:751:LEU:HD22	1.94	0.49
1:A:742:ARG:HG2	1:A:751:LEU:HD22	1.94	0.49
1:B:742:ARG:HG2	1:B:751:LEU:HD22	1.94	0.49
1:C:110:LEU:HD12	1:C:110:LEU:C	2.38	0.49
1:C:449:ASN:HD22	1:D:890:PHE:HD1	1.61	0.48
1:D:93:TRP:NE1	1:D:96:SER:OG	2.46	0.48
1:A:93:TRP:NE1	1:A:96:SER:OG	2.46	0.48
1:C:742:ARG:HG2	1:C:751:LEU:HD22	1.94	0.48
1:D:990:LEU:HD21	1:D:998:ASP:HB2	1.94	0.48
1:A:786:ARG:HD2	1:D:955:GLU:HG2	1.95	0.48
1:A:428:LYS:HD2	1:A:428:LYS:N	2.29	0.48
1:B:428:LYS:N	1:B:428:LYS:HD2	2.29	0.48
1:B:990:LEU:HD21	1:B:998:ASP:HB2	1.94	0.48
1:C:93:TRP:NE1	1:C:96:SER:OG	2.46	0.48
1:B:176:TRP:HB2	2:F:2013:ALA:HB2	1.96	0.48
1:C:428:LYS:HD2	1:C:428:LYS:N	2.29	0.48
1:D:110:LEU:HD12	1:D:110:LEU:C	2.38	0.48
1:A:425:LEU:HD23	1:A:924:MET:HE1	1.95	0.48
1:C:455:ARG:NH1	1:C:931:ASP:OD1	2.47	0.48
1:D:176:TRP:HB2	2:H:2013:ALA:HB2	1.96	0.48
1:A:176:TRP:HB2	2:E:2013:ALA:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:455:ARG:NH1	1:B:931:ASP:OD1	2.47	0.48
1:C:425:LEU:HD23	1:C:924:MET:HE1	1.95	0.48
1:B:110:LEU:HD12	1:B:110:LEU:C	2.38	0.47
1:B:1002:LYS:HA	1:B:1002:LYS:CE	2.40	0.47
1:C:491:LEU:HG	1:C:737:LEU:CB	2.35	0.47
1:A:983:LEU:HD21	1:A:1045:PRO:HB2	1.96	0.47
1:D:417:GLU:OE1	1:D:418:SER:N	2.47	0.47
1:D:425:LEU:HD23	1:D:924:MET:HE1	1.95	0.47
1:B:425:LEU:HD23	1:B:924:MET:HE1	1.95	0.47
1:D:983:LEU:HD21	1:D:1045:PRO:HB2	1.96	0.47
1:B:991:GLY:O	1:B:1043:LEU:HD23	2.14	0.47
1:C:991:GLY:O	1:C:1043:LEU:HD23	2.14	0.47
1:C:983:LEU:HD21	1:C:1045:PRO:HB2	1.96	0.47
1:D:455:ARG:NH1	1:D:931:ASP:OD1	2.47	0.47
1:A:991:GLY:O	1:A:1043:LEU:HD23	2.14	0.47
1:C:176:TRP:HB2	2:G:2013:ALA:HB2	1.96	0.47
1:D:991:GLY:O	1:D:1043:LEU:HD23	2.14	0.47
1:A:455:ARG:NH1	1:A:931:ASP:OD1	2.47	0.47
4:E:2305:CLR:C16	4:E:2305:CLR:H181	2.45	0.47
1:B:616:HIS:CE1	1:B:626:LYS:H	2.33	0.47
1:C:616:HIS:CE1	1:C:626:LYS:H	2.33	0.47
1:D:428:LYS:N	1:D:428:LYS:HD2	2.29	0.47
1:A:1002:LYS:HA	1:A:1002:LYS:CE	2.40	0.47
1:A:110:LEU:HD12	1:A:110:LEU:C	2.38	0.47
1:D:616:HIS:CE1	1:D:626:LYS:H	2.33	0.47
1:A:476:ASN:HB3	1:A:479:GLU:HB2	1.97	0.47
4:H:2306:CLR:C16	4:H:2306:CLR:H181	2.45	0.46
1:B:429:TYR:HD1	1:B:807:GLN:HB3	1.80	0.46
1:B:476:ASN:HB3	1:B:479:GLU:HB2	1.97	0.46
4:F:2306:CLR:C16	4:F:2306:CLR:H181	2.45	0.46
1:C:429:TYR:HD1	1:C:807:GLN:HB3	1.80	0.46
1:C:476:ASN:HB3	1:C:479:GLU:HB2	1.97	0.46
1:D:476:ASN:HB3	1:D:479:GLU:HB2	1.97	0.46
1:B:983:LEU:HD21	1:B:1045:PRO:HB2	1.96	0.46
1:C:965:THR:H	1:C:968:THR:HB	1.81	0.46
4:G:2305:CLR:C16	4:G:2305:CLR:H181	2.45	0.46
1:A:470:LEU:HD23	1:A:470:LEU:O	2.15	0.46
1:A:996:TYR:CD2	1:A:1037:PRO:HG2	2.51	0.46
1:B:470:LEU:HD23	1:B:470:LEU:O	2.15	0.46
1:C:491:LEU:CG	1:C:737:LEU:HB2	2.36	0.46
1:A:417:GLU:OE1	1:A:418:SER:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:616:HIS:CE1	1:A:626:LYS:H	2.33	0.46
1:C:25:PHE:HB3	1:C:192:PRO:HB3	1.98	0.46
1:D:965:THR:H	1:D:968:THR:HB	1.81	0.46
1:B:565:MET:HA	1:B:597:PHE:HB3	1.98	0.46
1:B:616:HIS:HE1	1:B:626:LYS:H	1.64	0.46
1:A:107:ALA:O	1:A:113:ARG:HG3	2.16	0.46
1:A:616:HIS:HE1	1:A:626:LYS:H	1.64	0.46
2:E:2059:VAL:HG22	2:E:2087:VAL:HG13	1.98	0.46
1:B:25:PHE:HB3	1:B:192:PRO:HB3	1.98	0.46
1:B:965:THR:H	1:B:968:THR:HB	1.81	0.46
1:C:616:HIS:HE1	1:C:626:LYS:H	1.64	0.46
1:D:506:MET:HE1	1:D:1013:GLY:HA3	1.98	0.46
1:D:616:HIS:HE1	1:D:626:LYS:H	1.64	0.46
2:H:2196:SER:HA	2:H:2199:VAL:HG12	1.98	0.46
1:C:999:LEU:HD12	1:C:999:LEU:O	2.16	0.46
2:G:2059:VAL:HG22	2:G:2087:VAL:HG13	1.98	0.46
1:D:25:PHE:HB3	1:D:192:PRO:HB3	1.98	0.46
2:E:2044:LEU:HD23	2:E:2047:LEU:HD12	1.98	0.46
1:C:506:MET:HE1	1:C:1013:GLY:HA3	1.98	0.46
1:D:729:SER:O	1:D:765:ARG:NH2	2.35	0.46
1:A:965:THR:H	1:A:968:THR:HB	1.81	0.45
2:G:2196:SER:HA	2:G:2199:VAL:HG12	1.98	0.45
1:D:565:MET:HA	1:D:597:PHE:HB3	1.98	0.45
1:B:996:TYR:CD2	1:B:1037:PRO:HG2	2.51	0.45
1:C:996:TYR:CD2	1:C:1037:PRO:HG2	2.51	0.45
1:D:429:TYR:HD1	1:D:807:GLN:HB3	1.80	0.45
1:B:110:LEU:HA	1:B:113:ARG:HE	1.82	0.45
1:B:506:MET:HE1	1:B:1013:GLY:HA3	1.98	0.45
1:B:999:LEU:O	1:B:999:LEU:HD12	2.16	0.45
1:C:110:LEU:HA	1:C:113:ARG:HE	1.82	0.45
2:G:2044:LEU:HD23	2:G:2047:LEU:HD12	1.98	0.45
1:D:996:TYR:CD2	1:D:1037:PRO:HG2	2.51	0.45
1:A:110:LEU:HA	1:A:113:ARG:HE	1.82	0.45
1:A:429:TYR:HD1	1:A:807:GLN:HB3	1.80	0.45
1:A:999:LEU:HD12	1:A:999:LEU:O	2.16	0.45
1:B:107:ALA:O	1:B:113:ARG:HG3	2.16	0.45
1:B:164:PHE:HA	1:B:167:ARG:HG2	1.99	0.45
1:B:417:GLU:OE1	1:B:418:SER:N	2.47	0.45
1:B:491:LEU:HG	1:B:737:LEU:CB	2.34	0.45
1:C:107:ALA:O	1:C:113:ARG:HG3	2.16	0.45
1:C:565:MET:HA	1:C:597:PHE:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:110:LEU:HA	1:D:113:ARG:HE	1.82	0.45
1:D:999:LEU:HD12	1:D:999:LEU:O	2.16	0.45
1:A:25:PHE:HB3	1:A:192:PRO:HB3	1.98	0.45
1:A:506:MET:HE1	1:A:1013:GLY:HA3	1.98	0.45
1:C:470:LEU:HD23	1:C:470:LEU:O	2.15	0.45
1:A:565:MET:HA	1:A:597:PHE:HB3	1.98	0.45
4:H:2306:CLR:H111	4:H:2306:CLR:H193	1.76	0.45
2:F:2059:VAL:HG22	2:F:2087:VAL:HG13	1.98	0.45
1:D:107:ALA:O	1:D:113:ARG:HG3	2.16	0.45
2:H:2044:LEU:HD23	2:H:2047:LEU:HD12	1.98	0.45
2:H:2059:VAL:HG22	2:H:2087:VAL:HG13	1.98	0.45
1:B:491:LEU:HD12	1:B:737:LEU:HD13	1.99	0.45
1:D:470:LEU:HD23	1:D:470:LEU:O	2.15	0.45
1:B:176:TRP:NE1	1:B:180:GLU:OE2	2.50	0.45
1:C:491:LEU:HD12	1:C:737:LEU:HD13	1.99	0.45
1:D:470:LEU:C	1:D:470:LEU:CD2	2.89	0.45
2:E:2196:SER:HA	2:E:2199:VAL:HG12	1.98	0.44
1:C:164:PHE:HA	1:C:167:ARG:HG2	1.99	0.44
1:C:896:ASP:N	1:C:896:ASP:OD1	2.51	0.44
1:D:335:SER:HB2	1:D:415:LYS:NZ	2.32	0.44
1:A:449:ASN:HD22	1:B:890:PHE:HD1	1.65	0.44
2:F:2044:LEU:HD23	2:F:2047:LEU:HD12	1.98	0.44
2:F:2196:SER:HA	2:F:2199:VAL:HG12	1.98	0.44
1:C:473:PRO:HG2	1:D:893:GLN:NE2	2.32	0.44
1:B:335:SER:HB2	1:B:415:LYS:NZ	2.32	0.44
1:A:491:LEU:HD12	1:A:737:LEU:HD13	1.99	0.44
1:C:176:TRP:NE1	1:C:180:GLU:OE2	2.50	0.44
1:C:335:SER:HB2	1:C:415:LYS:NZ	2.32	0.44
1:C:442:MET:HG2	1:D:815:LEU:CD1	2.47	0.44
1:D:183:SER:O	1:D:187:PHE:CB	2.53	0.44
1:A:164:PHE:HA	1:A:167:ARG:HG2	1.99	0.44
1:A:567:ALA:HB2	1:A:581:ILE:HD13	2.00	0.44
2:E:2080:SER:OG	2:E:2126:ASN:ND2	2.51	0.44
2:F:2080:SER:OG	2:F:2126:ASN:ND2	2.51	0.44
4:A:3006:CLR:H222	4:A:3006:CLR:H162	2.00	0.44
1:D:176:TRP:NE1	1:D:180:GLU:OE2	2.50	0.44
1:A:176:TRP:NE1	1:A:180:GLU:OE2	2.50	0.44
1:B:470:LEU:C	1:B:470:LEU:CD2	2.89	0.44
1:D:164:PHE:HA	1:D:167:ARG:HG2	1.99	0.44
1:D:491:LEU:HG	1:D:737:LEU:CB	2.35	0.44
1:D:491:LEU:HD12	1:D:737:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:815:LEU:HD13	1:D:442:MET:HG2	2.00	0.44
1:A:982:LEU:HA	1:A:987:PHE:CE2	2.53	0.44
2:G:2080:SER:OG	2:G:2126:ASN:ND2	2.51	0.44
4:H:2306:CLR:H183	4:H:2306:CLR:H20	1.90	0.44
2:H:2080:SER:OG	2:H:2126:ASN:ND2	2.51	0.44
1:B:471:ASN:N	1:B:471:ASN:HD22	2.16	0.43
1:B:567:ALA:HB2	1:B:581:ILE:HD13	2.00	0.43
1:B:1013:GLY:O	1:B:1050:PHE:N	2.46	0.43
1:A:539:GLU:O	1:A:595:GLY:N	2.39	0.43
1:B:541:LEU:HD22	1:B:589:ILE:HG21	2.00	0.43
1:B:982:LEU:HA	1:B:987:PHE:CE2	2.53	0.43
1:C:417:GLU:OE1	1:C:418:SER:N	2.47	0.43
1:A:473:PRO:HG2	1:B:893:GLN:NE2	2.33	0.43
1:A:760:ILE:HB	1:A:780:PRO:HB3	2.00	0.43
4:F:2306:CLR:H111	4:F:2306:CLR:H193	1.76	0.43
1:D:982:LEU:HA	1:D:987:PHE:CE2	2.53	0.43
4:D:1108:CLR:H222	4:D:1108:CLR:H162	2.00	0.43
1:A:335:SER:HB2	1:A:415:LYS:NZ	2.32	0.43
1:B:491:LEU:HD23	1:B:733:GLY:O	2.19	0.43
1:C:426:ALA:HB2	1:C:440:ASN:ND2	2.34	0.43
1:C:982:LEU:HA	1:C:987:PHE:CE2	2.53	0.43
2:G:2158:ASP:OD2	2:H:2121:ARG:NH1	2.50	0.43
2:F:2061:GLN:HG2	2:F:2085:VAL:HG22	2.00	0.43
1:D:471:ASN:N	1:D:471:ASN:HD22	2.16	0.43
1:D:541:LEU:HD22	1:D:589:ILE:HG21	2.00	0.43
1:D:567:ALA:HB2	1:D:581:ILE:HD13	2.00	0.43
1:A:491:LEU:HD23	1:A:733:GLY:O	2.19	0.43
2:E:2068:CYS:HB2	2:E:2119:CYS:HB2	1.93	0.43
1:B:491:LEU:CG	1:B:737:LEU:HB2	2.36	0.43
1:C:471:ASN:N	1:C:471:ASN:HD22	2.16	0.43
1:D:795:ASN:OD1	1:D:795:ASN:N	2.50	0.43
1:A:795:ASN:OD1	1:A:795:ASN:N	2.50	0.43
1:A:1013:GLY:O	1:A:1050:PHE:N	2.46	0.43
1:B:896:ASP:OD1	1:B:896:ASP:N	2.51	0.43
1:A:470:LEU:C	1:A:470:LEU:CD2	2.89	0.43
1:A:471:ASN:N	1:A:471:ASN:HD22	2.16	0.43
1:B:365:HIS:O	1:B:368:ARG:HB2	2.18	0.43
1:B:407:ASN:OD1	1:B:408:PRO:HD2	2.19	0.43
1:C:183:SER:O	1:C:187:PHE:CB	2.53	0.43
1:C:365:HIS:O	1:C:368:ARG:HB2	2.19	0.43
1:C:491:LEU:HD23	1:C:733:GLY:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:983:LEU:HG	1:C:1045:PRO:O	2.19	0.43
1:A:426:ALA:HB2	1:A:440:ASN:ND2	2.34	0.43
1:B:426:ALA:HB2	1:B:440:ASN:ND2	2.34	0.43
4:F:2306:CLR:H183	4:F:2306:CLR:H20	1.90	0.43
1:C:407:ASN:OD1	1:C:408:PRO:HD2	2.19	0.43
2:G:2061:GLN:HG2	2:G:2085:VAL:HG22	2.00	0.43
1:D:491:LEU:CG	1:D:737:LEU:HB2	2.36	0.43
1:D:760:ILE:HB	1:D:780:PRO:HB3	2.00	0.43
1:D:983:LEU:HG	1:D:1045:PRO:O	2.19	0.43
4:C:1107:CLR:H222	4:C:1107:CLR:H162	2.00	0.43
1:A:442:MET:HG2	1:B:815:LEU:CD1	2.49	0.42
1:C:760:ILE:HB	1:C:780:PRO:HB3	2.00	0.42
1:D:426:ALA:HB2	1:D:440:ASN:ND2	2.34	0.42
1:B:760:ILE:HB	1:B:780:PRO:HB3	2.00	0.42
1:C:567:ALA:HB2	1:C:581:ILE:HD13	2.00	0.42
1:D:407:ASN:OD1	1:D:408:PRO:HD2	2.19	0.42
1:D:491:LEU:HD23	1:D:733:GLY:O	2.19	0.42
1:A:619:ILE:HD11	1:A:625:ILE:HD11	2.01	0.42
2:E:2061:GLN:HG2	2:E:2085:VAL:HG22	2.00	0.42
1:D:698:LYS:H	1:D:698:LYS:HD2	1.84	0.42
1:A:371:VAL:O	1:A:371:VAL:HG23	2.20	0.42
1:A:541:LEU:HD22	1:A:589:ILE:HG21	2.00	0.42
1:B:619:ILE:HD11	1:B:625:ILE:HD11	2.01	0.42
1:B:983:LEU:HG	1:B:1045:PRO:O	2.19	0.42
3:B:1106:PGW:H26	3:B:1106:PGW:H23A	1.86	0.42
1:D:371:VAL:HG23	1:D:371:VAL:O	2.20	0.42
1:D:590:GLN:N	1:D:590:GLN:CD	2.78	0.42
1:A:365:HIS:O	1:A:368:ARG:HB2	2.19	0.42
1:A:698:LYS:H	1:A:698:LYS:HD2	1.84	0.42
1:A:983:LEU:HG	1:A:1045:PRO:O	2.19	0.42
3:A:3002:PGW:H09	3:A:3002:PGW:H06	1.86	0.42
1:B:361:LYS:HE2	1:B:361:LYS:HB3	1.84	0.42
1:C:813:THR:O	1:C:884:ASN:ND2	2.46	0.42
1:D:365:HIS:O	1:D:368:ARG:HB2	2.19	0.42
1:D:1002:LYS:HA	1:D:1002:LYS:CE	2.40	0.42
1:B:821:ILE:HG22	1:B:891:LEU:HD21	2.02	0.42
4:D:1108:CLR:C22	4:D:1108:CLR:H162	2.50	0.42
2:E:2068:CYS:SG	2:E:2080:SER:OG	2.78	0.42
1:D:817:ASP:OD1	1:D:817:ASP:N	2.53	0.42
2:H:2061:GLN:HG2	2:H:2085:VAL:HG22	2.00	0.42
1:A:405:VAL:CA	1:A:411:LEU:HD11	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:ASN:OD1	1:A:408:PRO:HD2	2.19	0.42
1:B:371:VAL:HG23	1:B:371:VAL:O	2.20	0.42
1:B:405:VAL:CA	1:B:411:LEU:HD11	2.50	0.42
1:C:590:GLN:CD	1:C:590:GLN:N	2.78	0.42
1:B:491:LEU:HD21	1:B:734:LEU:HD23	2.02	0.42
1:D:378:LEU:HD22	1:D:414:VAL:HG11	2.02	0.42
1:A:491:LEU:HD21	1:A:734:LEU:HD23	2.02	0.42
1:B:442:MET:HG2	1:C:815:LEU:CD1	2.50	0.42
1:B:469:LEU:HA	1:B:472:ILE:HD12	2.02	0.42
1:B:563:LEU:HD23	1:B:563:LEU:HA	1.88	0.42
2:F:2155:ARG:HB3	2:F:2158:ASP:HB2	2.02	0.42
1:C:1013:GLY:O	1:C:1050:PHE:N	2.46	0.42
4:G:2305:CLR:H183	4:G:2305:CLR:H20	1.90	0.42
1:D:405:VAL:CA	1:D:411:LEU:HD11	2.50	0.42
1:D:491:LEU:HD21	1:D:734:LEU:HD23	2.02	0.42
1:A:821:ILE:HG22	1:A:891:LEU:HD21	2.02	0.41
4:A:3006:CLR:C22	4:A:3006:CLR:H162	2.50	0.41
1:B:590:GLN:N	1:B:590:GLN:CD	2.78	0.41
1:A:491:LEU:HG	1:A:737:LEU:CB	2.35	0.41
1:A:590:GLN:N	1:A:590:GLN:CD	2.78	0.41
4:B:1110:CLR:H222	4:B:1110:CLR:H162	2.00	0.41
1:C:619:ILE:HD11	1:C:625:ILE:HD11	2.01	0.41
3:D:1105:PGW:H26	3:D:1105:PGW:H23A	1.86	0.41
1:A:183:SER:O	1:A:187:PHE:CB	2.53	0.41
1:A:996:TYR:CD1	1:A:1014:ILE:HD11	2.56	0.41
1:B:359:PHE:CE2	1:B:375:ILE:HD13	2.56	0.41
1:B:813:THR:O	1:B:884:ASN:ND2	2.46	0.41
1:D:896:ASP:OD1	1:D:896:ASP:N	2.51	0.41
1:A:366:LYS:H	1:A:366:LYS:HG3	1.53	0.41
1:A:484:ILE:HG23	1:A:489:LEU:HD12	2.02	0.41
1:C:469:LEU:HA	1:C:472:ILE:HD12	2.02	0.41
1:C:491:LEU:HD21	1:C:734:LEU:HD23	2.02	0.41
2:H:2155:ARG:HB3	2:H:2158:ASP:HB2	2.02	0.41
1:B:378:LEU:HD22	1:B:414:VAL:HG11	2.02	0.41
1:B:457:ILE:HA	1:B:482:ASP:O	2.20	0.41
1:B:484:ILE:HG23	1:B:489:LEU:HD12	2.02	0.41
1:B:980:LEU:HB3	1:B:987:PHE:HZ	1.86	0.41
1:C:371:VAL:HG23	1:C:371:VAL:O	2.20	0.41
2:G:2068:CYS:HB2	2:G:2119:CYS:HB2	1.93	0.41
1:D:359:PHE:CE2	1:D:375:ILE:HD13	2.56	0.41
1:D:996:TYR:CD1	1:D:1014:ILE:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:896:ASP:N	1:A:896:ASP:OD1	2.50	0.41
1:C:366:LYS:H	1:C:366:LYS:HG3	1.53	0.41
1:C:1002:LYS:CA	1:C:1002:LYS:CE	2.87	0.41
1:D:619:ILE:HD11	1:D:625:ILE:HD11	2.01	0.41
1:D:799:MET:HE3	1:D:799:MET:HB2	1.95	0.41
1:B:698:LYS:H	1:B:698:LYS:HD2	1.84	0.41
4:B:1110:CLR:C22	4:B:1110:CLR:H162	2.50	0.41
1:C:484:ILE:HG23	1:C:489:LEU:HD12	2.02	0.41
1:C:541:LEU:HD22	1:C:589:ILE:HG21	2.00	0.41
1:D:813:THR:O	1:D:884:ASN:ND2	2.46	0.41
3:D:1104:PGW:H4A	3:D:1104:PGW:H7	1.85	0.41
1:A:359:PHE:CE2	1:A:375:ILE:HD13	2.56	0.41
1:A:361:LYS:HB3	1:A:361:LYS:HE2	1.84	0.41
1:A:457:ILE:HA	1:A:482:ASP:O	2.20	0.41
1:A:980:LEU:HB3	1:A:987:PHE:CZ	2.56	0.41
3:B:1106:PGW:H09	3:B:1106:PGW:H06	1.86	0.41
1:C:359:PHE:CE2	1:C:375:ILE:HD13	2.56	0.41
1:C:378:LEU:HD22	1:C:414:VAL:HG11	2.02	0.41
1:C:457:ILE:HA	1:C:482:ASP:O	2.20	0.41
1:C:491:LEU:CD1	1:C:737:LEU:HD13	2.51	0.41
1:D:457:ILE:HA	1:D:482:ASP:O	2.20	0.41
1:A:309:LEU:HD23	1:A:309:LEU:HA	1.90	0.41
1:A:469:LEU:HA	1:A:472:ILE:HD12	2.02	0.41
1:B:980:LEU:HB3	1:B:987:PHE:CZ	2.56	0.41
2:F:2068:CYS:SG	2:F:2080:SER:OG	2.78	0.41
1:C:821:ILE:HG22	1:C:891:LEU:HD21	2.02	0.41
1:C:980:LEU:HB3	1:C:987:PHE:HZ	1.86	0.41
2:G:2068:CYS:SG	2:G:2080:SER:OG	2.78	0.41
2:G:2155:ARG:HB3	2:G:2158:ASP:HB2	2.02	0.41
4:G:2305:CLR:H193	4:G:2305:CLR:H111	1.76	0.41
1:D:292:ASP:OD1	1:D:292:ASP:N	2.54	0.41
1:D:476:ASN:O	1:D:481:ASP:HB2	2.21	0.41
1:D:484:ILE:HG23	1:D:489:LEU:HD12	2.02	0.41
1:D:491:LEU:CD1	1:D:737:LEU:HD13	2.51	0.41
1:D:753:HIS:NE2	1:D:777:SER:OG	2.54	0.41
1:D:821:ILE:HG22	1:D:891:LEU:HD21	2.02	0.41
1:A:292:ASP:OD1	1:A:292:ASP:N	2.54	0.41
1:A:378:LEU:HD22	1:A:414:VAL:HG11	2.02	0.41
1:B:539:GLU:O	1:B:595:GLY:N	2.39	0.41
1:C:361:LYS:HB3	1:C:361:LYS:HE2	1.84	0.41
1:D:263:TRP:HZ2	1:D:298:THR:HB	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:LEU:CD1	1:A:737:LEU:HD13	2.51	0.40
1:D:361:LYS:HB3	1:D:361:LYS:HE2	1.84	0.40
1:A:476:ASN:O	1:A:481:ASP:HB2	2.21	0.40
1:B:473:PRO:HG2	1:C:893:GLN:NE2	2.36	0.40
1:B:568:ILE:HG13	1:B:593:THR:HB	2.03	0.40
1:B:753:HIS:NE2	1:B:777:SER:OG	2.54	0.40
1:C:698:LYS:H	1:C:698:LYS:HD2	1.84	0.40
1:D:469:LEU:HA	1:D:472:ILE:HD12	2.02	0.40
1:A:417:GLU:CD	1:A:417:GLU:N	2.80	0.40
1:A:972:ARG:H	1:A:972:ARG:HG3	1.75	0.40
1:B:799:MET:HE3	1:B:799:MET:HB2	1.95	0.40
1:B:982:LEU:HD21	1:B:1049:ILE:HG22	2.03	0.40
4:F:2306:CLR:H222	4:F:2306:CLR:H161	2.04	0.40
1:C:130:TYR:CZ	1:C:208:PHE:HB3	2.57	0.40
1:C:263:TRP:HZ2	1:C:298:THR:HB	1.86	0.40
1:C:568:ILE:HG13	1:C:593:THR:HB	2.03	0.40
2:G:2155:ARG:HG3	2:H:2072:CYS:HB2	2.03	0.40
1:D:183:SER:HA	1:D:186:ASP:HB2	2.04	0.40
1:D:980:LEU:HB3	1:D:987:PHE:HZ	1.86	0.40
1:B:795:ASN:N	1:B:795:ASN:OD1	2.50	0.40
3:C:1103:PGW:H23A	3:C:1103:PGW:H26	1.86	0.40
4:G:2305:CLR:H222	4:G:2305:CLR:H161	2.04	0.40
1:D:980:LEU:HB3	1:D:987:PHE:CZ	2.56	0.40
1:A:183:SER:HA	1:A:186:ASP:HB2	2.04	0.40
2:E:2155:ARG:HB3	2:E:2158:ASP:HB2	2.02	0.40
1:B:348:CYS:SG	1:B:424:ILE:HG12	2.62	0.40
1:B:990:LEU:HD12	1:B:990:LEU:HA	1.95	0.40
1:B:996:TYR:CD1	1:B:1014:ILE:HD11	2.56	0.40
3:D:1105:PGW:H07A	3:D:1105:PGW:H11	1.93	0.40
2:H:2068:CYS:SG	2:H:2080:SER:OG	2.78	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	A	906/1065 (85%)	842 (93%)	64 (7%)	0	100	100
1	B	906/1065 (85%)	842 (93%)	64 (7%)	0	100	100
1	C	906/1065 (85%)	842 (93%)	64 (7%)	0	100	100
1	D	906/1065 (85%)	842 (93%)	64 (7%)	0	100	100
2	E	196/219 (90%)	183 (93%)	13 (7%)	0	100	100
2	F	196/219 (90%)	183 (93%)	13 (7%)	0	100	100
2	G	196/219 (90%)	183 (93%)	13 (7%)	0	100	100
2	H	196/219 (90%)	183 (93%)	13 (7%)	0	100	100
All	All	4408/5136 (86%)	4100 (93%)	308 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	804/937 (86%)	796 (99%)	8 (1%)	68	75
1	B	792/937 (84%)	784 (99%)	8 (1%)	68	75
1	C	804/937 (86%)	796 (99%)	8 (1%)	68	75
1	D	757/937 (81%)	750 (99%)	7 (1%)	70	76
2	E	180/199 (90%)	180 (100%)	0	100	100
2	F	180/199 (90%)	180 (100%)	0	100	100
2	G	180/199 (90%)	180 (100%)	0	100	100
2	H	180/199 (90%)	180 (100%)	0	100	100
All	All	3877/4544 (85%)	3846 (99%)	31 (1%)	70	77

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	185	VAL
1	A	417	GLU
1	A	466	LYS
1	A	478	LYS
1	A	491	LEU
1	A	587	LEU
1	A	715	LEU
1	A	998	ASP
1	B	185	VAL
1	B	417	GLU
1	B	466	LYS
1	B	478	LYS
1	B	491	LEU
1	B	587	LEU
1	B	715	LEU
1	B	998	ASP
1	C	185	VAL
1	C	417	GLU
1	C	466	LYS
1	C	478	LYS
1	C	491	LEU
1	C	587	LEU
1	C	715	LEU
1	C	998	ASP
1	D	185	VAL
1	D	417	GLU
1	D	466	LYS
1	D	478	LYS
1	D	491	LEU
1	D	715	LEU
1	D	998	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	ASN
1	A	157	ASN
1	A	182	ASN
1	A	216	GLN
1	A	258	ASN
1	A	358	ASN
1	A	394	HIS
1	A	440	ASN

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Mol	Chain	Res	Type
1	A	465	ASN
1	A	468	HIS
1	A	471	ASN
1	A	501	GLN
1	A	586	HIS
1	A	616	HIS
1	A	745	ASN
1	A	806	ASN
1	A	807	GLN
1	A	809	ASN
1	A	967	GLN
2	E	2152	GLN
1	B	143	ASN
1	B	157	ASN
1	B	172	ASN
1	B	182	ASN
1	B	216	GLN
1	B	258	ASN
1	B	358	ASN
1	B	394	HIS
1	B	440	ASN
1	B	465	ASN
1	B	468	HIS
1	B	471	ASN
1	B	501	GLN
1	B	586	HIS
1	B	745	ASN
1	B	806	ASN
1	B	807	GLN
1	B	809	ASN
1	B	967	GLN
2	F	2101	HIS
2	F	2106	GLN
2	F	2152	GLN
1	C	143	ASN
1	C	157	ASN
1	C	182	ASN
1	C	216	GLN
1	C	258	ASN
1	C	358	ASN
1	C	394	HIS
1	C	440	ASN

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Mol	Chain	Res	Type
1	C	449	ASN
1	C	465	ASN
1	C	468	HIS
1	C	471	ASN
1	C	501	GLN
1	C	586	HIS
1	C	616	HIS
1	C	745	ASN
1	C	806	ASN
1	C	807	GLN
1	C	809	ASN
1	C	967	GLN
2	G	2101	HIS
2	G	2106	GLN
1	D	143	ASN
1	D	157	ASN
1	D	182	ASN
1	D	216	GLN
1	D	258	ASN
1	D	358	ASN
1	D	394	HIS
1	D	440	ASN
1	D	465	ASN
1	D	468	HIS
1	D	471	ASN
1	D	501	GLN
1	D	616	HIS
1	D	745	ASN
1	D	806	ASN
1	D	807	GLN
1	D	809	ASN
1	D	967	GLN
2	H	2101	HIS
2	H	2106	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

56 ligands 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	E	2304	2	14,14,15	0.48	0	17,19,21	1.89	3 (17%)
3	PGW	H	2303	-	5,5,50	0.31	0	4,4,56	0.63	0
4	CLR	B	1110	-	31,31,31	4.38	14 (45%)	48,48,48	2.64	17 (35%)
5	NAG	H	2305	2	14,14,15	0.48	0	17,19,21	1.88	3 (17%)
3	PGW	G	2302	-	5,5,50	0.31	0	4,4,56	0.63	0
4	CLR	G	2305	-	31,31,31	4.33	13 (41%)	48,48,48	2.82	19 (39%)
5	NAG	H	2304	2	14,14,15	0.55	0	17,19,21	2.12	3 (17%)
4	CLR	F	2306	-	31,31,31	4.32	13 (41%)	48,48,48	2.82	19 (39%)
3	PGW	F	2302	-	6,6,50	0.31	0	5,5,56	0.67	0
3	PGW	C	1103	-	45,45,50	1.13	4 (8%)	48,51,56	1.13	3 (6%)
3	PGW	E	2302	-	5,5,50	0.31	0	4,4,56	0.63	0
3	PGW	D	1106	-	8,8,50	0.29	0	7,7,56	0.81	0
3	PGW	D	1105	-	45,45,50	1.13	5 (11%)	48,51,56	1.13	3 (6%)
3	PGW	B	1101	-	26,26,50	1.34	5 (19%)	29,31,56	1.49	4 (13%)
4	CLR	C	1107	-	31,31,31	4.39	14 (45%)	48,48,48	2.64	17 (35%)
3	PGW	A	3001	-	28,28,50	1.20	2 (7%)	30,32,56	1.07	2 (6%)
3	PGW	B	1107	-	8,8,50	0.29	0	7,7,56	0.81	0
3	PGW	A	3004	-	11,11,50	0.24	0	10,10,56	0.84	0
3	PGW	D	1107	-	11,11,50	0.24	0	10,10,56	0.84	0
3	PGW	B	1103	-	8,8,50	0.27	0	7,7,56	0.79	0
5	NAG	F	2304	2	14,14,15	0.55	0	17,19,21	2.13	3 (17%)
3	PGW	D	1103	-	8,8,50	0.27	0	7,7,56	0.79	0
3	PGW	D	1104	-	28,28,50	1.20	2 (7%)	30,32,56	1.07	2 (6%)
3	PGW	H	2302	-	6,6,50	0.31	0	5,5,56	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PGW	B	1108	-	11,11,50	0.25	0	10,10,56	0.84	0
3	PGW	C	1101	-	12,12,50	0.96	1 (8%)	12,12,56	1.16	0
4	CLR	A	3006	-	31,31,31	4.39	14 (45%)	48,48,48	2.64	17 (35%)
4	CLR	D	1108	-	31,31,31	4.39	14 (45%)	48,48,48	2.63	17 (35%)
4	CLR	H	2306	-	31,31,31	4.33	13 (41%)	48,48,48	2.83	19 (39%)
5	NAG	G	2303	2	14,14,15	0.54	0	17,19,21	2.13	3 (17%)
3	PGW	C	1106	-	11,11,50	0.29	0	10,10,56	0.75	0
3	PGW	A	3009	-	11,11,50	0.29	0	10,10,56	0.75	0
3	PGW	C	1105	-	11,11,50	0.24	0	10,10,56	0.84	0
5	NAG	E	2303	2	14,14,15	0.55	0	17,19,21	2.13	3 (17%)
3	PGW	D	1101	-	26,26,50	1.34	5 (19%)	29,31,56	1.49	4 (13%)
3	PGW	H	2301	-	8,8,50	0.27	0	7,7,56	0.79	0
3	PGW	B	1102	-	12,12,50	0.95	1 (8%)	12,12,56	1.16	0
4	CLR	E	2305	-	31,31,31	4.33	13 (41%)	48,48,48	2.82	19 (39%)
3	PGW	E	2301	-	6,6,50	0.31	0	5,5,56	0.67	0
3	PGW	B	1105	-	26,26,50	1.35	5 (19%)	29,31,56	1.49	4 (13%)
3	PGW	C	1104	-	8,8,50	0.29	0	7,7,56	0.81	0
3	PGW	B	1109	-	11,11,50	0.29	0	10,10,56	0.75	0
5	NAG	G	2304	2	14,14,15	0.49	0	17,19,21	1.89	3 (17%)
3	PGW	B	1106	-	45,45,50	1.13	4 (8%)	48,51,56	1.13	3 (6%)
3	PGW	A	3003	-	8,8,50	0.29	0	7,7,56	0.81	0
3	PGW	A	3005	-	11,11,50	0.29	0	10,10,56	0.75	0
3	PGW	F	2303	-	5,5,50	0.31	0	4,4,56	0.63	0
3	PGW	G	2301	-	6,6,50	0.31	0	5,5,56	0.67	0
3	PGW	B	1104	-	28,28,50	1.20	2 (7%)	30,32,56	1.07	2 (6%)
3	PGW	A	3008	-	12,12,50	0.94	1 (8%)	12,12,56	1.16	0
3	PGW	F	2301	-	8,8,50	0.27	0	7,7,56	0.79	0
3	PGW	A	3002	-	45,45,50	1.13	4 (8%)	48,51,56	1.13	3 (6%)
3	PGW	C	1102	-	28,28,50	1.20	2 (7%)	30,32,56	1.08	2 (6%)
3	PGW	A	3007	-	26,26,50	1.34	5 (19%)	29,31,56	1.49	4 (13%)
3	PGW	D	1102	-	12,12,50	0.95	1 (8%)	12,12,56	1.16	0
5	NAG	F	2305	2	14,14,15	0.47	0	17,19,21	1.88	3 (17%)

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	E	2304	2	-	2/6/23/26	0/1/1/1
3	PGW	H	2303	-	-	2/3/3/55	-
4	CLR	B	1110	-	-	6/10/68/68	0/4/4/4
5	NAG	H	2305	2	-	2/6/23/26	0/1/1/1
3	PGW	G	2302	-	-	2/3/3/55	-
4	CLR	G	2305	-	-	9/10/68/68	0/4/4/4
5	NAG	H	2304	2	-	0/6/23/26	0/1/1/1
4	CLR	F	2306	-	-	9/10/68/68	0/4/4/4
3	PGW	F	2302	-	-	0/4/4/55	-
3	PGW	C	1103	-	-	14/50/50/55	-
3	PGW	E	2302	-	-	2/3/3/55	-
3	PGW	D	1106	-	-	2/6/6/55	-
3	PGW	D	1105	-	-	14/50/50/55	-
3	PGW	B	1101	-	-	11/28/28/55	-
4	CLR	C	1107	-	-	6/10/68/68	0/4/4/4
3	PGW	A	3001	-	-	10/30/30/55	-
3	PGW	B	1107	-	-	2/6/6/55	-
3	PGW	A	3004	-	-	5/9/9/55	-
3	PGW	D	1107	-	-	5/9/9/55	-
3	PGW	B	1103	-	-	3/6/6/55	-
5	NAG	F	2304	2	-	0/6/23/26	0/1/1/1
3	PGW	D	1103	-	-	3/6/6/55	-
3	PGW	D	1104	-	-	10/30/30/55	-
3	PGW	H	2302	-	-	0/4/4/55	-
3	PGW	B	1108	-	-	5/9/9/55	-
3	PGW	C	1101	-	-	5/10/10/55	-
4	CLR	A	3006	-	-	6/10/68/68	0/4/4/4
4	CLR	D	1108	-	-	6/10/68/68	0/4/4/4
4	CLR	H	2306	-	-	9/10/68/68	0/4/4/4
5	NAG	G	2303	2	-	0/6/23/26	0/1/1/1
3	PGW	C	1106	-	-	4/9/9/55	-
3	PGW	A	3009	-	-	4/9/9/55	-
3	PGW	C	1105	-	-	5/9/9/55	-
5	NAG	E	2303	2	-	0/6/23/26	0/1/1/1
3	PGW	D	1101	-	-	11/28/28/55	-
3	PGW	H	2301	-	-	3/6/6/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PGW	B	1102	-	-	5/10/10/55	-
4	CLR	E	2305	-	-	9/10/68/68	0/4/4/4
3	PGW	E	2301	-	-	0/4/4/55	-
3	PGW	B	1105	-	-	11/28/28/55	-
3	PGW	C	1104	-	-	2/6/6/55	-
3	PGW	B	1109	-	-	4/9/9/55	-
5	NAG	G	2304	2	-	2/6/23/26	0/1/1/1
3	PGW	B	1106	-	-	14/50/50/55	-
3	PGW	A	3003	-	-	2/6/6/55	-
3	PGW	A	3005	-	-	4/9/9/55	-
3	PGW	F	2303	-	-	2/3/3/55	-
3	PGW	G	2301	-	-	0/4/4/55	-
3	PGW	B	1104	-	-	10/30/30/55	-
3	PGW	A	3008	-	-	5/10/10/55	-
3	PGW	F	2301	-	-	3/6/6/55	-
3	PGW	A	3002	-	-	14/50/50/55	-
3	PGW	C	1102	-	-	10/30/30/55	-
3	PGW	A	3007	-	-	11/28/28/55	-
3	PGW	D	1102	-	-	5/10/10/55	-
5	NAG	F	2305	2	-	2/6/23/26	0/1/1/1

All (157) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	2306	CLR	C6-C5	12.08	1.57	1.33
4	E	2305	CLR	C6-C5	12.08	1.57	1.33
4	G	2305	CLR	C6-C5	12.08	1.57	1.33
4	F	2306	CLR	C6-C5	12.06	1.57	1.33
4	A	3006	CLR	C6-C5	11.67	1.57	1.33
4	C	1107	CLR	C6-C5	11.67	1.57	1.33
4	D	1108	CLR	C6-C5	11.65	1.57	1.33
4	B	1110	CLR	C6-C5	11.64	1.57	1.33
4	D	1108	CLR	C16-C17	10.17	1.75	1.54
4	A	3006	CLR	C16-C17	10.17	1.75	1.54
4	C	1107	CLR	C16-C17	10.17	1.75	1.54
4	B	1110	CLR	C16-C17	10.16	1.75	1.54
4	F	2306	CLR	C16-C17	9.85	1.74	1.54
4	E	2305	CLR	C16-C17	9.85	1.74	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	2305	CLR	C16-C17	9.85	1.74	1.54
4	H	2306	CLR	C16-C17	9.84	1.74	1.54
4	H	2306	CLR	C20-C17	-9.83	1.37	1.54
4	E	2305	CLR	C20-C17	-9.82	1.37	1.54
4	G	2305	CLR	C20-C17	-9.82	1.37	1.54
4	F	2306	CLR	C20-C17	-9.80	1.37	1.54
4	B	1110	CLR	C20-C17	-9.77	1.37	1.54
4	A	3006	CLR	C20-C17	-9.76	1.37	1.54
4	C	1107	CLR	C20-C17	-9.76	1.37	1.54
4	D	1108	CLR	C20-C17	-9.76	1.37	1.54
4	C	1107	CLR	C8-C9	7.94	1.68	1.53
4	D	1108	CLR	C8-C9	7.92	1.68	1.53
4	B	1110	CLR	C8-C9	7.91	1.68	1.53
4	A	3006	CLR	C8-C9	7.91	1.68	1.53
4	F	2306	CLR	C8-C9	7.30	1.67	1.53
4	E	2305	CLR	C8-C9	7.28	1.67	1.53
4	G	2305	CLR	C8-C9	7.28	1.67	1.53
4	H	2306	CLR	C8-C9	7.25	1.67	1.53
4	E	2305	CLR	C12-C11	6.68	1.66	1.53
4	G	2305	CLR	C12-C11	6.68	1.66	1.53
4	H	2306	CLR	C12-C11	6.67	1.66	1.53
4	F	2306	CLR	C12-C11	6.66	1.66	1.53
4	A	3006	CLR	C12-C11	6.58	1.66	1.53
4	C	1107	CLR	C12-C11	6.58	1.66	1.53
4	D	1108	CLR	C12-C11	6.57	1.66	1.53
4	B	1110	CLR	C12-C11	6.56	1.66	1.53
4	D	1108	CLR	C7-C6	5.71	1.61	1.50
4	A	3006	CLR	C7-C6	5.70	1.61	1.50
4	C	1107	CLR	C7-C6	5.70	1.61	1.50
4	B	1110	CLR	C7-C6	5.70	1.61	1.50
4	B	1110	CLR	C13-C17	5.66	1.65	1.55
4	C	1107	CLR	C13-C17	5.66	1.65	1.55
4	D	1108	CLR	C13-C17	5.66	1.65	1.55
4	A	3006	CLR	C13-C17	5.65	1.65	1.55
4	E	2305	CLR	C7-C6	5.51	1.61	1.50
4	F	2306	CLR	C7-C6	5.51	1.61	1.50
4	G	2305	CLR	C7-C6	5.51	1.61	1.50
4	H	2306	CLR	C7-C6	5.50	1.61	1.50
4	F	2306	CLR	C13-C17	4.95	1.64	1.55
4	E	2305	CLR	C13-C17	4.94	1.64	1.55
4	H	2306	CLR	C13-C17	4.94	1.64	1.55
4	G	2305	CLR	C13-C17	4.92	1.64	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	2305	CLR	C15-C14	4.02	1.62	1.54
4	G	2305	CLR	C15-C14	4.02	1.62	1.54
4	F	2306	CLR	C15-C14	4.00	1.62	1.54
4	H	2306	CLR	C15-C14	4.00	1.62	1.54
4	D	1108	CLR	C15-C14	3.96	1.62	1.54
4	A	3006	CLR	C15-C14	3.94	1.62	1.54
4	C	1107	CLR	C15-C14	3.94	1.62	1.54
4	B	1110	CLR	C15-C14	3.94	1.62	1.54
3	B	1106	PGW	C10-C9	3.71	1.52	1.31
3	D	1105	PGW	C10-C9	3.71	1.52	1.31
3	D	1104	PGW	C10-C9	3.70	1.52	1.31
3	A	3002	PGW	C10-C9	3.69	1.52	1.31
3	C	1103	PGW	C10-C9	3.69	1.52	1.31
3	B	1104	PGW	C10-C9	3.68	1.52	1.31
3	A	3001	PGW	C10-C9	3.68	1.52	1.31
3	C	1102	PGW	C10-C9	3.68	1.52	1.31
4	C	1107	CLR	C13-C14	3.65	1.61	1.55
4	D	1108	CLR	C13-C14	3.65	1.61	1.55
4	B	1110	CLR	C13-C14	3.64	1.61	1.55
4	A	3006	CLR	C13-C14	3.62	1.61	1.55
4	H	2306	CLR	C13-C14	3.48	1.61	1.55
4	E	2305	CLR	C13-C14	3.47	1.61	1.55
4	G	2305	CLR	C13-C14	3.47	1.61	1.55
4	F	2306	CLR	C13-C14	3.45	1.61	1.55
4	B	1110	CLR	C22-C20	3.19	1.62	1.54
4	A	3006	CLR	C22-C20	3.16	1.62	1.54
4	C	1107	CLR	C22-C20	3.16	1.62	1.54
4	D	1108	CLR	C22-C20	3.16	1.62	1.54
4	H	2306	CLR	C22-C20	3.09	1.62	1.54
4	F	2306	CLR	C22-C20	3.09	1.62	1.54
4	E	2305	CLR	C22-C20	3.08	1.62	1.54
4	G	2305	CLR	C22-C20	3.06	1.61	1.54
4	H	2306	CLR	C21-C20	2.87	1.60	1.53
4	E	2305	CLR	C21-C20	2.86	1.60	1.53
3	B	1105	PGW	O01-C02	-2.86	1.39	1.46
3	C	1101	PGW	O03-C19	2.85	1.40	1.30
3	B	1102	PGW	O03-C19	2.85	1.40	1.30
3	D	1102	PGW	O03-C19	2.85	1.40	1.30
4	G	2305	CLR	C21-C20	2.85	1.60	1.53
4	A	3006	CLR	C21-C20	2.85	1.60	1.53
4	B	1110	CLR	C21-C20	2.85	1.60	1.53
4	C	1107	CLR	C21-C20	2.85	1.60	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	2306	CLR	C21-C20	2.85	1.60	1.53
3	B	1101	PGW	O01-C02	-2.84	1.39	1.46
3	A	3007	PGW	O01-C02	-2.84	1.39	1.46
3	A	3008	PGW	O03-C19	2.84	1.40	1.30
4	D	1108	CLR	C21-C20	2.83	1.60	1.53
3	D	1101	PGW	O01-C02	-2.81	1.40	1.46
3	A	3007	PGW	P-O12	2.76	1.65	1.54
3	B	1105	PGW	P-O12	2.76	1.65	1.54
3	B	1101	PGW	P-O12	2.75	1.65	1.54
3	D	1101	PGW	P-O12	2.75	1.65	1.54
4	H	2306	CLR	C8-C14	-2.74	1.48	1.53
4	E	2305	CLR	C8-C14	-2.73	1.48	1.53
4	G	2305	CLR	C8-C14	-2.73	1.48	1.53
4	F	2306	CLR	C8-C14	-2.69	1.48	1.53
3	A	3002	PGW	O03-C19	2.68	1.41	1.33
3	C	1103	PGW	O03-C19	2.68	1.41	1.33
4	A	3006	CLR	C8-C14	-2.68	1.48	1.53
4	C	1107	CLR	C8-C14	-2.68	1.48	1.53
4	D	1108	CLR	C8-C14	-2.68	1.48	1.53
3	B	1106	PGW	O03-C19	2.68	1.41	1.33
3	D	1105	PGW	O03-C19	2.67	1.41	1.33
4	B	1110	CLR	C8-C14	-2.65	1.48	1.53
3	C	1103	PGW	O01-C02	-2.59	1.40	1.46
3	D	1105	PGW	O01-C02	-2.59	1.40	1.46
3	A	3002	PGW	O01-C02	-2.59	1.40	1.46
3	B	1106	PGW	O01-C02	-2.58	1.40	1.46
3	B	1105	PGW	O03-C19	2.45	1.40	1.33
4	D	1108	CLR	C7-C8	2.43	1.57	1.53
3	B	1101	PGW	O03-C19	2.42	1.40	1.33
3	D	1101	PGW	O03-C19	2.42	1.40	1.33
3	B	1104	PGW	O01-C1	2.42	1.40	1.33
3	A	3007	PGW	O03-C19	2.42	1.40	1.33
4	A	3006	CLR	C7-C8	2.41	1.57	1.53
3	D	1104	PGW	O01-C1	2.40	1.40	1.33
3	C	1102	PGW	O01-C1	2.40	1.40	1.33
3	A	3001	PGW	O01-C1	2.39	1.40	1.33
4	B	1110	CLR	C7-C8	2.39	1.57	1.53
4	C	1107	CLR	C7-C8	2.37	1.56	1.53
3	A	3007	PGW	P-O13	-2.28	1.46	1.54
3	B	1101	PGW	P-O13	-2.27	1.46	1.54
3	D	1101	PGW	P-O13	-2.27	1.46	1.54
3	B	1105	PGW	P-O13	-2.26	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3002	PGW	O01-C1	2.25	1.40	1.34
3	C	1103	PGW	O01-C1	2.25	1.40	1.34
3	D	1105	PGW	O01-C1	2.24	1.40	1.34
3	B	1106	PGW	O01-C1	2.24	1.40	1.34
3	A	3007	PGW	O03-C01	-2.22	1.40	1.45
3	B	1105	PGW	O03-C01	-2.21	1.40	1.45
4	B	1110	CLR	C4-C5	2.18	1.56	1.51
3	B	1101	PGW	O03-C01	-2.18	1.40	1.45
3	D	1101	PGW	O03-C01	-2.18	1.40	1.45
4	D	1108	CLR	C4-C5	2.16	1.56	1.51
4	H	2306	CLR	C4-C5	2.16	1.56	1.51
4	F	2306	CLR	C4-C5	2.16	1.56	1.51
4	A	3006	CLR	C4-C5	2.15	1.56	1.51
4	C	1107	CLR	C4-C5	2.15	1.56	1.51
4	E	2305	CLR	C4-C5	2.14	1.56	1.51
4	G	2305	CLR	C4-C5	2.14	1.56	1.51
3	D	1105	PGW	O03-C01	-2.02	1.40	1.45

All (204) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1110	CLR	C4-C5-C6	-9.07	108.27	120.57
4	A	3006	CLR	C4-C5-C6	-9.07	108.27	120.57
4	C	1107	CLR	C4-C5-C6	-9.07	108.27	120.57
4	D	1108	CLR	C4-C5-C6	-9.04	108.32	120.57
4	H	2306	CLR	C4-C5-C6	-8.51	109.04	120.57
4	E	2305	CLR	C4-C5-C6	-8.48	109.08	120.57
4	G	2305	CLR	C4-C5-C6	-8.48	109.08	120.57
4	F	2306	CLR	C4-C5-C6	-8.45	109.12	120.57
4	C	1107	CLR	C10-C5-C6	-6.82	112.97	122.93
4	A	3006	CLR	C10-C5-C6	-6.81	112.98	122.93
4	B	1110	CLR	C10-C5-C6	-6.80	113.00	122.93
5	E	2304	NAG	C1-O5-C5	6.80	121.30	112.19
5	G	2304	NAG	C1-O5-C5	6.80	121.30	112.19
4	D	1108	CLR	C10-C5-C6	-6.80	113.01	122.93
5	F	2305	NAG	C1-O5-C5	6.78	121.28	112.19
5	H	2305	NAG	C1-O5-C5	6.78	121.27	112.19
5	F	2304	NAG	C1-O5-C5	6.66	121.12	112.19
5	G	2303	NAG	C1-O5-C5	6.66	121.11	112.19
4	A	3006	CLR	C7-C6-C5	-6.65	113.79	125.02
4	C	1107	CLR	C7-C6-C5	-6.65	113.79	125.02
4	D	1108	CLR	C7-C6-C5	-6.64	113.81	125.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1110	CLR	C7-C6-C5	-6.64	113.81	125.02
5	E	2303	NAG	C1-O5-C5	6.64	121.08	112.19
5	H	2304	NAG	C1-O5-C5	6.62	121.05	112.19
4	H	2306	CLR	C7-C8-C9	-5.19	103.72	109.72
4	E	2305	CLR	C7-C8-C9	-5.17	103.74	109.72
4	G	2305	CLR	C7-C8-C9	-5.17	103.74	109.72
4	G	2305	CLR	C12-C13-C17	5.16	124.21	116.60
4	F	2306	CLR	C7-C8-C9	-5.15	103.77	109.72
4	F	2306	CLR	C12-C13-C17	5.15	124.18	116.60
4	H	2306	CLR	C12-C13-C17	5.14	124.17	116.60
4	E	2305	CLR	C12-C13-C17	5.14	124.17	116.60
4	G	2305	CLR	C7-C6-C5	-5.03	116.53	125.02
4	E	2305	CLR	C7-C6-C5	-5.00	116.58	125.02
4	F	2306	CLR	C7-C6-C5	-5.00	116.58	125.02
4	H	2306	CLR	C7-C6-C5	-4.99	116.59	125.02
4	B	1110	CLR	C14-C8-C9	4.78	115.33	109.09
4	A	3006	CLR	C14-C8-C9	4.77	115.32	109.09
4	D	1108	CLR	C14-C8-C9	4.76	115.30	109.09
4	C	1107	CLR	C14-C8-C9	4.73	115.27	109.09
4	E	2305	CLR	C18-C13-C17	-4.61	103.31	111.68
4	G	2305	CLR	C18-C13-C17	-4.61	103.32	111.68
4	H	2306	CLR	C18-C13-C17	-4.61	103.33	111.68
4	F	2306	CLR	C18-C13-C17	-4.60	103.33	111.68
4	H	2306	CLR	C1-C2-C3	4.48	116.42	110.48
4	E	2305	CLR	C1-C2-C3	4.48	116.41	110.48
4	H	2306	CLR	C14-C8-C9	4.47	114.92	109.09
4	G	2305	CLR	C1-C2-C3	4.45	116.38	110.48
4	E	2305	CLR	C14-C8-C9	4.45	114.90	109.09
4	G	2305	CLR	C14-C8-C9	4.45	114.90	109.09
4	F	2306	CLR	C1-C2-C3	4.45	116.37	110.48
4	F	2306	CLR	C14-C8-C9	4.42	114.85	109.09
4	B	1110	CLR	C12-C13-C17	4.36	123.03	116.60
4	C	1107	CLR	C12-C13-C17	4.35	123.01	116.60
4	D	1108	CLR	C12-C13-C17	4.35	123.00	116.60
4	A	3006	CLR	C12-C13-C17	4.34	122.99	116.60
3	A	3007	PGW	O01-C1-C2	4.32	120.83	111.48
3	D	1101	PGW	O01-C1-C2	4.32	120.83	111.48
3	B	1101	PGW	O01-C1-C2	4.32	120.83	111.48
3	B	1105	PGW	O01-C1-C2	4.32	120.82	111.48
4	G	2305	CLR	C18-C13-C14	-4.20	104.07	111.68
4	G	2305	CLR	C9-C10-C5	4.19	115.79	109.65
4	E	2305	CLR	C18-C13-C14	-4.18	104.09	111.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	2306	CLR	C18-C13-C14	-4.18	104.09	111.68
4	F	2306	CLR	C18-C13-C14	-4.18	104.10	111.68
4	H	2306	CLR	C9-C10-C5	4.18	115.77	109.65
4	D	1108	CLR	C7-C8-C9	-4.17	104.90	109.72
4	C	1107	CLR	C7-C8-C9	-4.17	104.90	109.72
4	A	3006	CLR	C7-C8-C9	-4.17	104.90	109.72
4	F	2306	CLR	C9-C10-C5	4.17	115.75	109.65
4	E	2305	CLR	C9-C10-C5	4.16	115.74	109.65
4	B	1110	CLR	C7-C8-C9	-4.16	104.91	109.72
4	H	2306	CLR	C21-C20-C22	-4.03	104.11	110.34
4	G	2305	CLR	C17-C13-C14	4.02	104.71	100.10
4	H	2306	CLR	C17-C13-C14	4.01	104.70	100.10
4	F	2306	CLR	C17-C13-C14	4.00	104.69	100.10
4	E	2305	CLR	C17-C13-C14	4.00	104.69	100.10
4	E	2305	CLR	C21-C20-C22	-4.00	104.15	110.34
4	G	2305	CLR	C21-C20-C22	-4.00	104.16	110.34
4	F	2306	CLR	C21-C20-C22	-3.98	104.18	110.34
4	H	2306	CLR	C10-C5-C6	-3.92	117.21	122.93
4	E	2305	CLR	C10-C5-C6	-3.89	117.25	122.93
4	G	2305	CLR	C10-C5-C6	-3.89	117.25	122.93
4	F	2306	CLR	C10-C5-C6	-3.89	117.25	122.93
4	B	1110	CLR	C18-C13-C14	-3.81	104.77	111.68
4	D	1108	CLR	C18-C13-C14	-3.79	104.80	111.68
4	C	1107	CLR	C18-C13-C14	-3.78	104.81	111.68
4	A	3006	CLR	C18-C13-C14	-3.78	104.81	111.68
3	D	1105	PGW	O01-C1-C2	3.64	119.35	111.48
3	A	3002	PGW	O01-C1-C2	3.63	119.33	111.48
3	C	1103	PGW	O01-C1-C2	3.63	119.33	111.48
3	B	1106	PGW	O01-C1-C2	3.61	119.30	111.48
4	B	1110	CLR	C21-C20-C22	-3.60	104.76	110.34
4	A	3006	CLR	C21-C20-C22	-3.58	104.79	110.34
4	C	1107	CLR	C21-C20-C22	-3.58	104.79	110.34
4	D	1108	CLR	C21-C20-C22	-3.58	104.80	110.34
5	E	2303	NAG	O5-C1-C2	3.51	116.73	111.29
5	F	2304	NAG	O5-C1-C2	3.51	116.72	111.29
5	H	2304	NAG	O5-C1-C2	3.50	116.71	111.29
5	G	2303	NAG	O5-C1-C2	3.49	116.69	111.29
5	G	2303	NAG	C4-C3-C2	3.37	115.95	111.02
5	E	2303	NAG	C4-C3-C2	3.34	115.92	111.02
5	F	2304	NAG	C4-C3-C2	3.33	115.89	111.02
5	H	2304	NAG	C4-C3-C2	3.32	115.89	111.02
4	F	2306	CLR	C1-C10-C5	3.28	114.39	108.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	2305	CLR	C1-C10-C5	3.26	114.37	108.74
4	H	2306	CLR	C1-C10-C5	3.26	114.36	108.74
4	G	2305	CLR	C1-C10-C5	3.25	114.34	108.74
4	A	3006	CLR	C18-C13-C12	-3.14	105.97	110.61
4	C	1107	CLR	C18-C13-C12	-3.14	105.97	110.61
4	F	2306	CLR	C16-C17-C13	-3.14	100.15	103.84
4	G	2305	CLR	C16-C17-C13	-3.13	100.16	103.84
4	B	1110	CLR	C18-C13-C12	-3.13	105.99	110.61
4	H	2306	CLR	C16-C17-C13	-3.13	100.16	103.84
4	E	2305	CLR	C16-C17-C13	-3.13	100.16	103.84
4	D	1108	CLR	C18-C13-C12	-3.12	106.00	110.61
4	E	2305	CLR	C19-C10-C9	-3.02	108.27	111.66
4	F	2306	CLR	C19-C10-C9	-3.02	108.27	111.66
4	H	2306	CLR	C19-C10-C9	-3.01	108.28	111.66
4	G	2305	CLR	C19-C10-C9	-3.01	108.28	111.66
4	F	2306	CLR	C4-C5-C10	-2.78	112.87	116.42
4	H	2306	CLR	C4-C5-C10	-2.76	112.88	116.42
4	E	2305	CLR	C4-C5-C10	-2.76	112.89	116.42
4	G	2305	CLR	C4-C5-C10	-2.76	112.89	116.42
3	D	1101	PGW	O03-C19-C20	2.69	120.05	111.83
3	A	3007	PGW	O03-C19-C20	2.69	120.04	111.83
3	B	1101	PGW	O03-C19-C20	2.68	120.02	111.83
3	B	1105	PGW	O03-C19-C20	2.68	120.02	111.83
3	C	1102	PGW	O01-C1-C2	2.65	119.91	111.83
3	A	3001	PGW	O01-C1-C2	2.64	119.89	111.83
3	D	1104	PGW	O01-C1-C2	2.63	119.87	111.83
3	B	1104	PGW	O01-C1-C2	2.63	119.86	111.83
4	A	3006	CLR	C17-C13-C14	2.62	103.11	100.10
4	C	1107	CLR	C17-C13-C14	2.62	103.10	100.10
4	D	1108	CLR	C17-C13-C14	2.61	103.10	100.10
4	B	1110	CLR	C12-C13-C14	2.59	111.13	107.25
4	D	1108	CLR	C12-C13-C14	2.58	111.10	107.25
4	A	3006	CLR	C12-C13-C14	2.58	111.10	107.25
4	B	1110	CLR	C17-C13-C14	2.58	103.06	100.10
4	C	1107	CLR	C9-C10-C5	2.56	113.41	109.65
4	C	1107	CLR	C12-C13-C14	2.56	111.07	107.25
4	A	3006	CLR	C9-C10-C5	2.54	113.37	109.65
4	B	1110	CLR	C9-C10-C5	2.53	113.36	109.65
3	D	1101	PGW	O13-P-O14	-2.53	100.97	110.83
4	D	1108	CLR	C9-C10-C5	2.52	113.34	109.65
3	B	1105	PGW	O13-P-O14	-2.52	101.01	110.83
3	B	1104	PGW	O13-P-O14	-2.52	100.73	112.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1101	PGW	O13-P-O14	-2.52	101.02	110.83
3	D	1104	PGW	O13-P-O14	-2.52	100.73	112.44
3	A	3007	PGW	O13-P-O14	-2.52	101.03	110.83
3	A	3001	PGW	O13-P-O14	-2.51	100.75	112.44
3	C	1102	PGW	O13-P-O14	-2.51	100.75	112.44
3	B	1106	PGW	O13-P-O14	-2.46	100.99	112.44
3	A	3002	PGW	O13-P-O14	-2.45	101.03	112.44
3	D	1105	PGW	O13-P-O14	-2.45	101.04	112.44
3	C	1103	PGW	O13-P-O14	-2.45	101.07	112.44
4	A	3006	CLR	C1-C10-C5	2.42	112.92	108.74
4	D	1108	CLR	C1-C10-C5	2.42	112.91	108.74
4	B	1110	CLR	C1-C10-C5	2.41	112.90	108.74
4	C	1107	CLR	C1-C10-C5	2.40	112.89	108.74
3	B	1106	PGW	O03-C19-C20	2.38	119.10	111.83
3	D	1105	PGW	O03-C19-C20	2.37	119.08	111.83
3	A	3002	PGW	O03-C19-C20	2.37	119.06	111.83
3	C	1103	PGW	O03-C19-C20	2.37	119.05	111.83
4	G	2305	CLR	C19-C10-C5	-2.35	104.79	108.38
4	H	2306	CLR	C19-C10-C5	-2.34	104.81	108.38
4	E	2305	CLR	C19-C10-C5	-2.34	104.81	108.38
4	F	2306	CLR	C19-C10-C5	-2.32	104.84	108.38
4	D	1108	CLR	C18-C13-C17	-2.31	107.49	111.68
3	A	3007	PGW	C02-O01-C1	-2.30	112.30	117.80
4	B	1110	CLR	C18-C13-C17	-2.29	107.52	111.68
4	A	3006	CLR	C18-C13-C17	-2.29	107.53	111.68
4	F	2306	CLR	C1-C10-C9	-2.29	105.71	108.74
3	B	1101	PGW	C02-O01-C1	-2.29	112.32	117.80
3	D	1101	PGW	C02-O01-C1	-2.29	112.32	117.80
3	B	1105	PGW	C02-O01-C1	-2.29	112.32	117.80
4	C	1107	CLR	C18-C13-C17	-2.29	107.53	111.68
4	H	2306	CLR	C2-C3-C4	2.28	113.49	110.29
4	G	2305	CLR	C2-C3-C4	2.27	113.49	110.29
4	F	2306	CLR	C2-C3-C4	2.26	113.47	110.29
4	G	2305	CLR	C1-C10-C9	-2.26	105.75	108.74
4	E	2305	CLR	C1-C10-C9	-2.25	105.75	108.74
4	E	2305	CLR	C2-C3-C4	2.25	113.45	110.29
4	H	2306	CLR	C1-C10-C9	-2.24	105.77	108.74
4	D	1108	CLR	C1-C2-C3	2.13	113.30	110.48
4	B	1110	CLR	C1-C2-C3	2.13	113.30	110.48
4	C	1107	CLR	C1-C2-C3	2.13	113.30	110.48
4	A	3006	CLR	C1-C2-C3	2.13	113.30	110.48
5	H	2305	NAG	O5-C1-C2	2.12	114.58	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	2305	NAG	O5-C1-C2	2.12	114.56	111.29
5	E	2304	NAG	O5-C1-C2	2.11	114.56	111.29
5	G	2304	NAG	O5-C1-C2	2.11	114.56	111.29
4	B	1110	CLR	C1-C10-C9	-2.11	105.95	108.74
4	A	3006	CLR	C1-C10-C9	-2.10	105.96	108.74
4	C	1107	CLR	C1-C10-C9	-2.10	105.96	108.74
4	D	1108	CLR	C1-C10-C9	-2.07	105.99	108.74
4	B	1110	CLR	C4-C5-C10	-2.07	113.77	116.42
4	D	1108	CLR	C4-C5-C10	-2.07	113.77	116.42
4	A	3006	CLR	C4-C5-C10	-2.05	113.80	116.42
4	C	1107	CLR	C4-C5-C10	-2.02	113.83	116.42
5	H	2305	NAG	C2-N2-C7	-2.01	120.20	122.90
5	F	2305	NAG	C2-N2-C7	-2.01	120.21	122.90
5	E	2304	NAG	C2-N2-C7	-2.00	120.22	122.90
5	G	2304	NAG	C2-N2-C7	-2.00	120.22	122.90

There are no chirality outliers.

All (292) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3001	PGW	C04-C05-CAD-OAE
3	A	3001	PGW	C03-O11-P-O12
3	A	3001	PGW	C03-O11-P-O13
3	A	3001	PGW	C03-O11-P-O14
3	A	3001	PGW	O01-C02-C03-O11
3	A	3002	PGW	OAF-C05-CAD-OAE
3	A	3002	PGW	C04-C05-CAD-OAE
3	A	3007	PGW	C03-O11-P-O12
3	A	3007	PGW	C03-O11-P-O13
3	A	3007	PGW	C03-O11-P-O14
3	A	3007	PGW	C2-C1-O01-C02
3	B	1101	PGW	C03-O11-P-O12
3	B	1101	PGW	C03-O11-P-O13
3	B	1101	PGW	C03-O11-P-O14
3	B	1101	PGW	C2-C1-O01-C02
3	B	1104	PGW	C04-C05-CAD-OAE
3	B	1104	PGW	C03-O11-P-O12
3	B	1104	PGW	C03-O11-P-O13
3	B	1104	PGW	C03-O11-P-O14
3	B	1104	PGW	O01-C02-C03-O11
3	B	1105	PGW	C03-O11-P-O12
3	B	1105	PGW	C03-O11-P-O13

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Mol	Chain	Res	Type	Atoms
3	B	1105	PGW	C03-O11-P-O14
3	B	1105	PGW	C2-C1-O01-C02
3	B	1106	PGW	OAF-C05-CAD-OAE
3	B	1106	PGW	C04-C05-CAD-OAE
3	C	1102	PGW	C04-C05-CAD-OAE
3	C	1102	PGW	C03-O11-P-O12
3	C	1102	PGW	C03-O11-P-O13
3	C	1102	PGW	C03-O11-P-O14
3	C	1102	PGW	O01-C02-C03-O11
3	C	1103	PGW	OAF-C05-CAD-OAE
3	C	1103	PGW	C04-C05-CAD-OAE
3	D	1101	PGW	C03-O11-P-O12
3	D	1101	PGW	C03-O11-P-O13
3	D	1101	PGW	C03-O11-P-O14
3	D	1101	PGW	C2-C1-O01-C02
3	D	1104	PGW	C04-C05-CAD-OAE
3	D	1104	PGW	C03-O11-P-O12
3	D	1104	PGW	C03-O11-P-O13
3	D	1104	PGW	C03-O11-P-O14
3	D	1104	PGW	O01-C02-C03-O11
3	D	1105	PGW	OAF-C05-CAD-OAE
3	D	1105	PGW	C04-C05-CAD-OAE
3	A	3007	PGW	O02-C1-O01-C02
3	B	1101	PGW	O02-C1-O01-C02
3	B	1105	PGW	O02-C1-O01-C02
3	D	1101	PGW	O02-C1-O01-C02
3	A	3002	PGW	C20-C19-O03-C01
3	B	1106	PGW	C20-C19-O03-C01
3	C	1103	PGW	C20-C19-O03-C01
3	D	1105	PGW	C20-C19-O03-C01
3	A	3002	PGW	O04-C19-O03-C01
3	B	1106	PGW	O04-C19-O03-C01
3	C	1103	PGW	O04-C19-O03-C01
3	D	1105	PGW	O04-C19-O03-C01
4	A	3006	CLR	C17-C20-C22-C23
4	B	1110	CLR	C17-C20-C22-C23
4	C	1107	CLR	C17-C20-C22-C23
4	D	1108	CLR	C17-C20-C22-C23
4	A	3006	CLR	C21-C20-C22-C23
4	B	1110	CLR	C21-C20-C22-C23
4	C	1107	CLR	C21-C20-C22-C23
4	D	1108	CLR	C21-C20-C22-C23

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Mol	Chain	Res	Type	Atoms
4	E	2305	CLR	C17-C20-C22-C23
4	F	2306	CLR	C17-C20-C22-C23
4	G	2305	CLR	C17-C20-C22-C23
4	H	2306	CLR	C17-C20-C22-C23
4	E	2305	CLR	C21-C20-C22-C23
4	F	2306	CLR	C21-C20-C22-C23
4	G	2305	CLR	C21-C20-C22-C23
4	H	2306	CLR	C21-C20-C22-C23
5	E	2304	NAG	O5-C5-C6-O6
5	F	2305	NAG	O5-C5-C6-O6
5	G	2304	NAG	O5-C5-C6-O6
5	H	2305	NAG	O5-C5-C6-O6
5	E	2304	NAG	C4-C5-C6-O6
5	F	2305	NAG	C4-C5-C6-O6
5	G	2304	NAG	C4-C5-C6-O6
5	H	2305	NAG	C4-C5-C6-O6
4	E	2305	CLR	C20-C22-C23-C24
4	F	2306	CLR	C20-C22-C23-C24
4	G	2305	CLR	C20-C22-C23-C24
4	H	2306	CLR	C20-C22-C23-C24
4	C	1107	CLR	C22-C23-C24-C25
4	A	3006	CLR	C22-C23-C24-C25
4	B	1110	CLR	C22-C23-C24-C25
4	D	1108	CLR	C22-C23-C24-C25
3	A	3007	PGW	C1-C2-C3-C4
3	B	1101	PGW	C1-C2-C3-C4
3	B	1105	PGW	C1-C2-C3-C4
3	D	1101	PGW	C1-C2-C3-C4
4	E	2305	CLR	C22-C23-C24-C25
4	F	2306	CLR	C22-C23-C24-C25
4	G	2305	CLR	C22-C23-C24-C25
4	H	2306	CLR	C22-C23-C24-C25
3	A	3002	PGW	C5-C6-C7-C8
3	B	1106	PGW	C5-C6-C7-C8
3	C	1103	PGW	C5-C6-C7-C8
3	A	3004	PGW	C22-C23-C24-C25
3	A	3007	PGW	C2-C3-C4-C5
3	B	1101	PGW	C2-C3-C4-C5
3	B	1105	PGW	C2-C3-C4-C5
3	B	1108	PGW	C22-C23-C24-C25
3	C	1105	PGW	C22-C23-C24-C25
3	D	1101	PGW	C2-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
3	D	1105	PGW	C5-C6-C7-C8
3	D	1107	PGW	C22-C23-C24-C25
3	A	3005	PGW	C16-C15-C27-C26
3	C	1106	PGW	C16-C15-C27-C26
3	A	3009	PGW	C16-C15-C27-C26
3	B	1109	PGW	C16-C15-C27-C26
3	A	3004	PGW	C21-C22-C23-C24
3	B	1108	PGW	C21-C22-C23-C24
3	C	1105	PGW	C21-C22-C23-C24
3	D	1107	PGW	C21-C22-C23-C24
3	E	2302	PGW	C2-C3-C4-C5
3	F	2303	PGW	C2-C3-C4-C5
3	H	2303	PGW	C2-C3-C4-C5
3	A	3001	PGW	C10-C06-C07-C08
3	B	1104	PGW	C10-C06-C07-C08
3	C	1102	PGW	C10-C06-C07-C08
3	D	1104	PGW	C10-C06-C07-C08
3	G	2302	PGW	C2-C3-C4-C5
3	D	1103	PGW	C3-C4-C5-C6
3	B	1103	PGW	C3-C4-C5-C6
3	F	2301	PGW	C3-C4-C5-C6
3	H	2301	PGW	C3-C4-C5-C6
3	A	3008	PGW	C23-C24-C25-C26
3	B	1102	PGW	C23-C24-C25-C26
3	C	1101	PGW	C23-C24-C25-C26
3	D	1102	PGW	C23-C24-C25-C26
3	A	3005	PGW	C25-C26-C27-C15
3	A	3009	PGW	C25-C26-C27-C15
3	B	1109	PGW	C25-C26-C27-C15
3	C	1106	PGW	C25-C26-C27-C15
3	B	1102	PGW	C21-C22-C23-C24
3	D	1102	PGW	C21-C22-C23-C24
3	A	3008	PGW	C21-C22-C23-C24
3	C	1101	PGW	C21-C22-C23-C24
3	A	3001	PGW	OAF-C05-CAD-OAE
3	B	1104	PGW	OAF-C05-CAD-OAE
3	C	1102	PGW	OAF-C05-CAD-OAE
3	D	1104	PGW	OAF-C05-CAD-OAE
3	A	3004	PGW	C23-C24-C25-C26
3	C	1105	PGW	C23-C24-C25-C26
3	D	1107	PGW	C23-C24-C25-C26
3	B	1108	PGW	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
3	D	1102	PGW	C25-C26-C27-C15
3	A	3008	PGW	C25-C26-C27-C15
3	B	1102	PGW	C25-C26-C27-C15
3	C	1101	PGW	C25-C26-C27-C15
3	A	3001	PGW	C06-C10-C9-C8
3	B	1104	PGW	C06-C10-C9-C8
3	C	1102	PGW	C06-C10-C9-C8
3	D	1104	PGW	C06-C10-C9-C8
3	B	1104	PGW	C06-C07-C08-C09
3	D	1104	PGW	C06-C07-C08-C09
3	A	3001	PGW	C06-C07-C08-C09
3	C	1102	PGW	C06-C07-C08-C09
3	A	3003	PGW	C5-C6-C7-C8
3	B	1107	PGW	C5-C6-C7-C8
3	C	1104	PGW	C5-C6-C7-C8
3	D	1106	PGW	C5-C6-C7-C8
3	A	3002	PGW	C07-C06-C10-C9
3	B	1106	PGW	C07-C06-C10-C9
3	C	1103	PGW	C07-C06-C10-C9
3	D	1105	PGW	C07-C06-C10-C9
3	A	3004	PGW	C25-C26-C27-C15
3	B	1108	PGW	C25-C26-C27-C15
3	C	1105	PGW	C25-C26-C27-C15
3	D	1107	PGW	C25-C26-C27-C15
4	E	2305	CLR	C13-C17-C20-C21
4	F	2306	CLR	C13-C17-C20-C21
4	G	2305	CLR	C13-C17-C20-C21
4	H	2306	CLR	C13-C17-C20-C21
3	A	3005	PGW	C23-C24-C25-C26
3	A	3009	PGW	C23-C24-C25-C26
3	B	1109	PGW	C23-C24-C25-C26
3	C	1106	PGW	C23-C24-C25-C26
3	A	3005	PGW	C21-C22-C23-C24
3	A	3009	PGW	C21-C22-C23-C24
3	C	1106	PGW	C21-C22-C23-C24
3	B	1109	PGW	C21-C22-C23-C24
3	B	1101	PGW	C3-C4-C5-C6
3	B	1105	PGW	C3-C4-C5-C6
3	D	1101	PGW	C3-C4-C5-C6
3	A	3007	PGW	C3-C4-C5-C6
4	E	2305	CLR	C23-C24-C25-C26
4	F	2306	CLR	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
4	G	2305	CLR	C23-C24-C25-C26
4	H	2306	CLR	C23-C24-C25-C26
3	A	3007	PGW	O03-C01-C02-O01
3	B	1101	PGW	O03-C01-C02-O01
3	B	1105	PGW	O03-C01-C02-O01
3	D	1101	PGW	O03-C01-C02-O01
3	E	2302	PGW	C3-C4-C5-C6
3	F	2303	PGW	C3-C4-C5-C6
3	G	2302	PGW	C3-C4-C5-C6
3	H	2303	PGW	C3-C4-C5-C6
4	A	3006	CLR	C13-C17-C20-C21
4	B	1110	CLR	C13-C17-C20-C21
4	C	1107	CLR	C13-C17-C20-C21
4	D	1108	CLR	C13-C17-C20-C21
3	A	3007	PGW	C20-C21-C22-C23
3	B	1101	PGW	C20-C21-C22-C23
3	B	1105	PGW	C20-C21-C22-C23
3	D	1101	PGW	C20-C21-C22-C23
3	A	3002	PGW	C09-C11-C12-C13
3	B	1106	PGW	C09-C11-C12-C13
3	C	1103	PGW	C09-C11-C12-C13
3	D	1105	PGW	C09-C11-C12-C13
3	B	1103	PGW	C4-C5-C6-C7
3	F	2301	PGW	C4-C5-C6-C7
3	D	1103	PGW	C4-C5-C6-C7
3	H	2301	PGW	C4-C5-C6-C7
4	A	3006	CLR	C23-C24-C25-C27
4	B	1110	CLR	C23-C24-C25-C27
4	C	1107	CLR	C23-C24-C25-C27
4	D	1108	CLR	C23-C24-C25-C27
3	B	1106	PGW	C08-C09-C11-C12
3	C	1103	PGW	C08-C09-C11-C12
3	A	3002	PGW	C08-C09-C11-C12
3	D	1105	PGW	C08-C09-C11-C12
3	A	3007	PGW	O03-C01-C02-C03
3	B	1101	PGW	O03-C01-C02-C03
3	B	1105	PGW	O03-C01-C02-C03
3	D	1101	PGW	O03-C01-C02-C03
3	A	3001	PGW	C04-O12-P-O14
3	B	1104	PGW	C04-O12-P-O14
3	C	1102	PGW	C04-O12-P-O14
3	D	1104	PGW	C04-O12-P-O14

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Mol	Chain	Res	Type	Atoms
3	A	3002	PGW	C05-C04-O12-P
3	B	1106	PGW	C05-C04-O12-P
3	C	1103	PGW	C05-C04-O12-P
3	D	1105	PGW	C05-C04-O12-P
4	E	2305	CLR	C13-C17-C20-C22
4	F	2306	CLR	C13-C17-C20-C22
4	H	2306	CLR	C13-C17-C20-C22
3	A	3004	PGW	C20-C21-C22-C23
3	B	1108	PGW	C20-C21-C22-C23
3	C	1105	PGW	C20-C21-C22-C23
3	D	1107	PGW	C20-C21-C22-C23
4	G	2305	CLR	C13-C17-C20-C22
4	C	1107	CLR	C20-C22-C23-C24
4	A	3006	CLR	C20-C22-C23-C24
4	B	1110	CLR	C20-C22-C23-C24
4	D	1108	CLR	C20-C22-C23-C24
4	E	2305	CLR	C23-C24-C25-C27
4	F	2306	CLR	C23-C24-C25-C27
4	G	2305	CLR	C23-C24-C25-C27
4	H	2306	CLR	C23-C24-C25-C27
3	A	3002	PGW	C7-C8-C9-C10
3	B	1106	PGW	C7-C8-C9-C10
3	C	1103	PGW	C7-C8-C9-C10
3	D	1105	PGW	C7-C8-C9-C10
3	B	1103	PGW	C6-C7-C8-C9
3	F	2301	PGW	C6-C7-C8-C9
3	D	1103	PGW	C6-C7-C8-C9
3	H	2301	PGW	C6-C7-C8-C9
3	A	3008	PGW	O03-C19-C20-C21
3	B	1102	PGW	O03-C19-C20-C21
3	C	1101	PGW	O03-C19-C20-C21
3	D	1102	PGW	O03-C19-C20-C21
3	B	1102	PGW	O04-C19-C20-C21
3	D	1102	PGW	O04-C19-C20-C21
3	A	3008	PGW	O04-C19-C20-C21
3	C	1101	PGW	O04-C19-C20-C21
3	A	3002	PGW	O01-C02-C03-O11
3	B	1106	PGW	O01-C02-C03-O11
3	C	1103	PGW	O01-C02-C03-O11
3	D	1105	PGW	O01-C02-C03-O11
3	C	1103	PGW	O03-C19-C20-C21
3	A	3002	PGW	O03-C19-C20-C21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	1106	PGW	O03-C19-C20-C21
3	D	1105	PGW	O03-C19-C20-C21
3	C	1103	PGW	C2-C3-C4-C5
3	A	3002	PGW	C2-C3-C4-C5
3	D	1105	PGW	C2-C3-C4-C5
3	B	1106	PGW	C2-C3-C4-C5
3	A	3002	PGW	O04-C19-C20-C21
3	C	1103	PGW	O04-C19-C20-C21
3	D	1105	PGW	O04-C19-C20-C21
3	B	1106	PGW	O04-C19-C20-C21
4	E	2305	CLR	C16-C17-C20-C21
4	F	2306	CLR	C16-C17-C20-C21
4	G	2305	CLR	C16-C17-C20-C21
4	H	2306	CLR	C16-C17-C20-C21
3	A	3003	PGW	C6-C7-C8-C9
3	C	1104	PGW	C6-C7-C8-C9
3	B	1107	PGW	C6-C7-C8-C9
3	D	1106	PGW	C6-C7-C8-C9

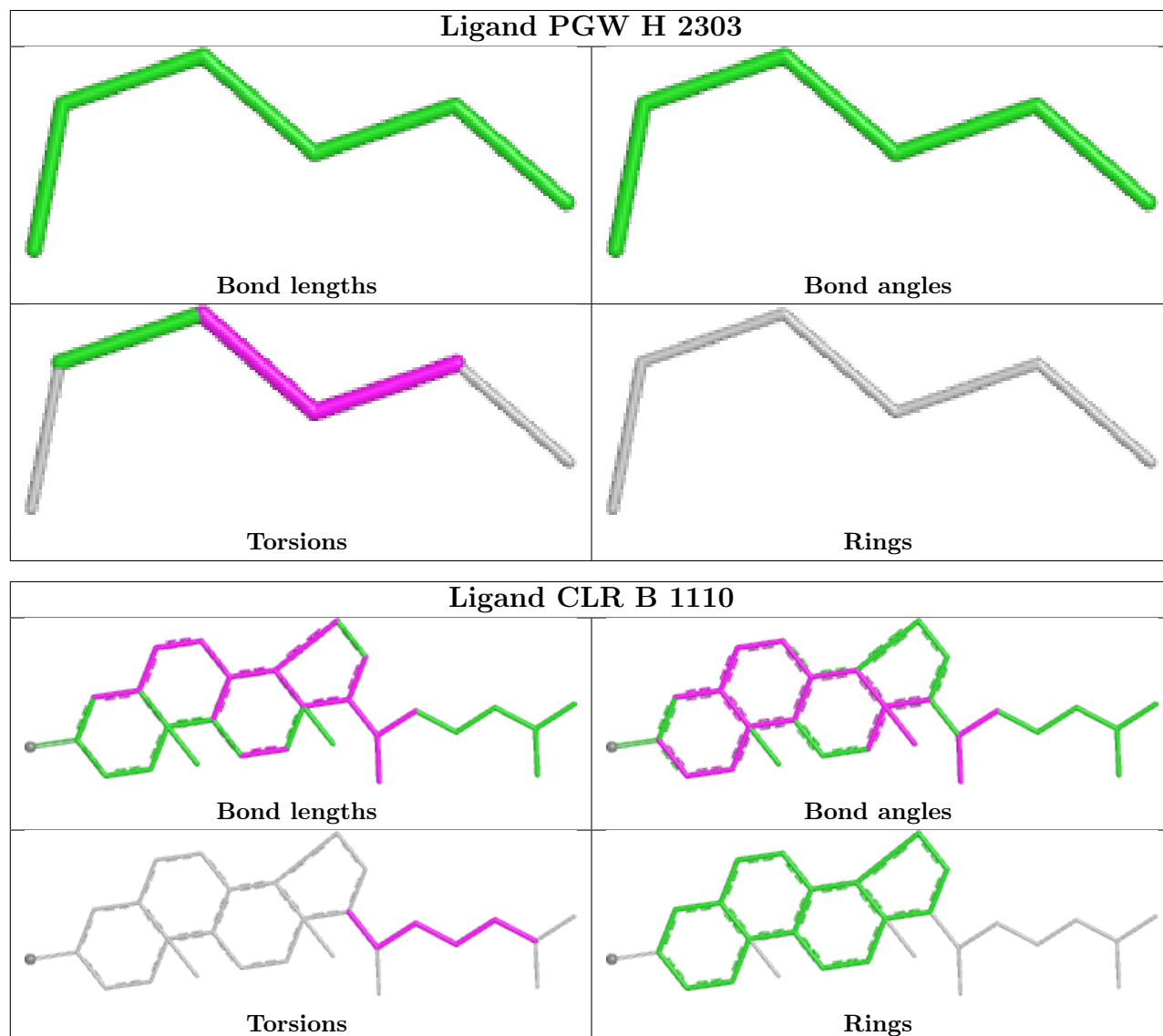
There are no ring outliers.

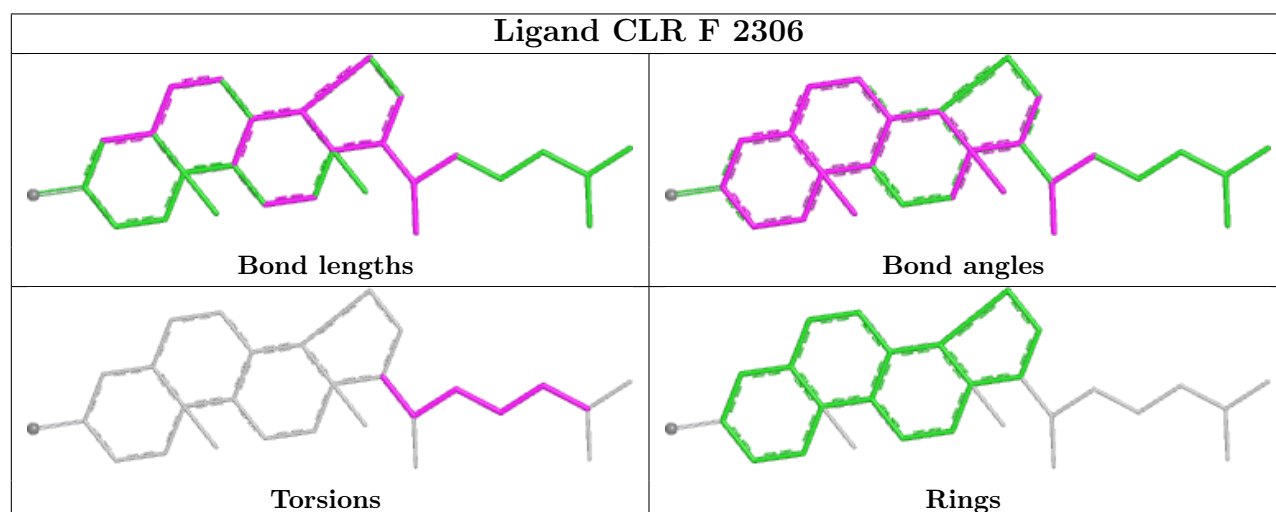
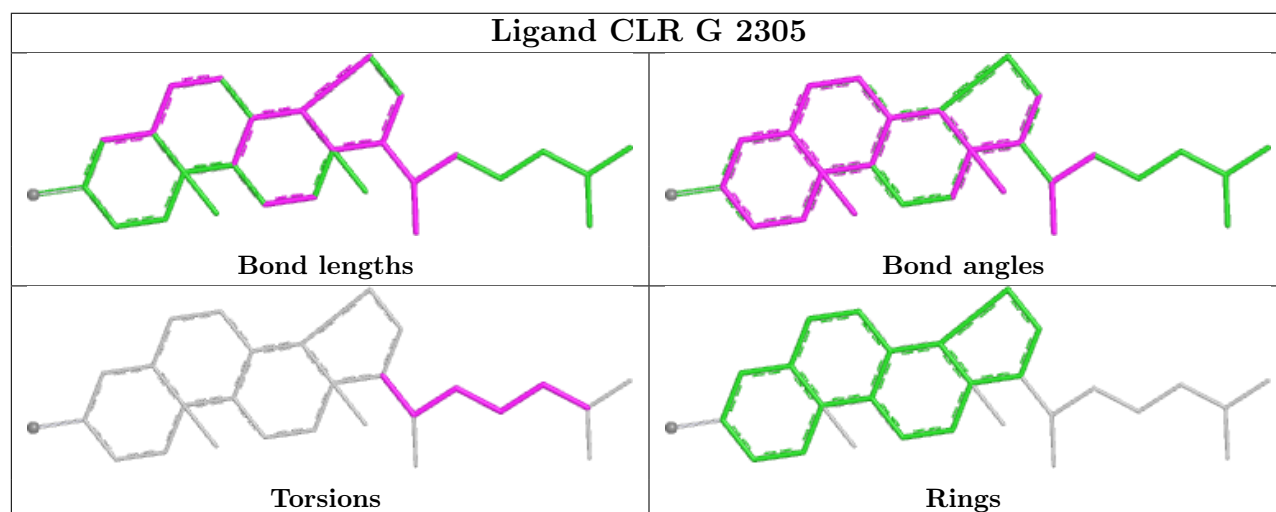
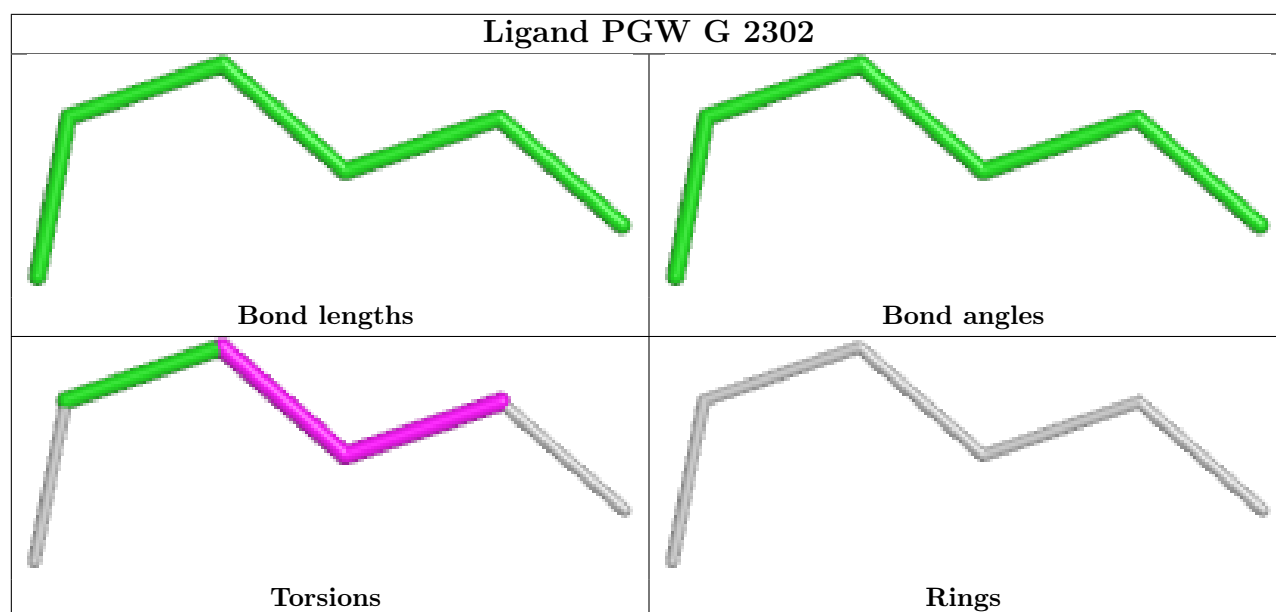
13 monomers are involved in 58 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1110	CLR	6	0
4	G	2305	CLR	8	0
4	F	2306	CLR	8	0
3	C	1103	PGW	1	0
3	D	1105	PGW	2	0
4	C	1107	CLR	5	0
3	D	1104	PGW	1	0
4	A	3006	CLR	6	0
4	D	1108	CLR	6	0
4	H	2306	CLR	7	0
4	E	2305	CLR	5	0
3	B	1106	PGW	2	0
3	A	3002	PGW	1	0

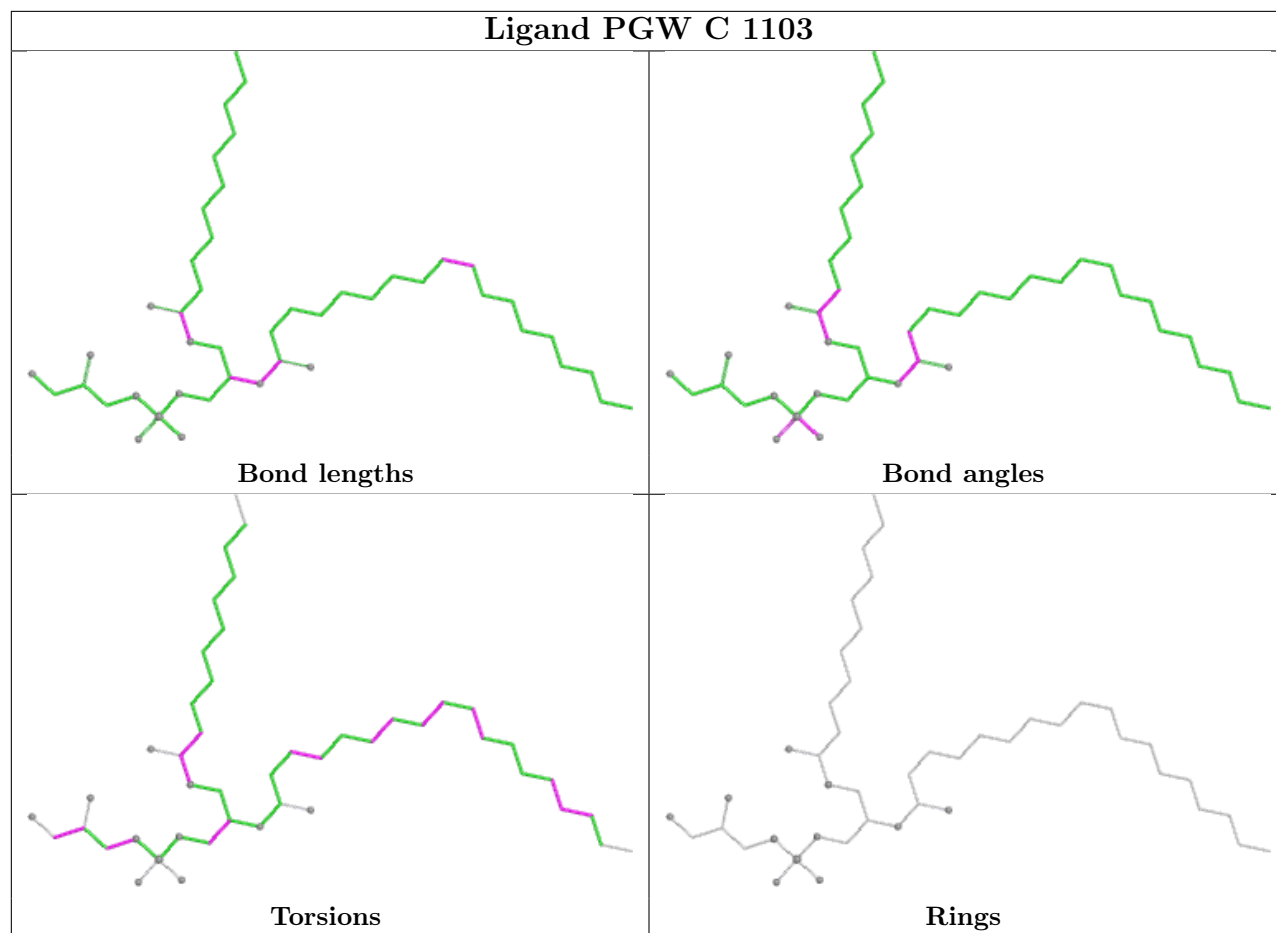
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

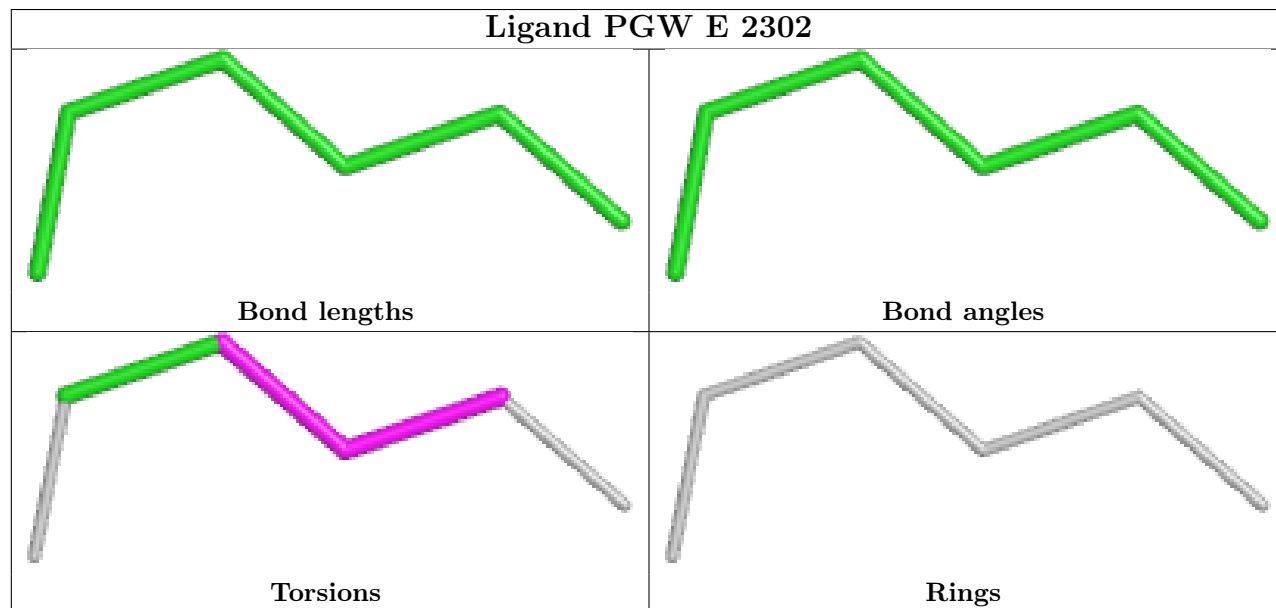


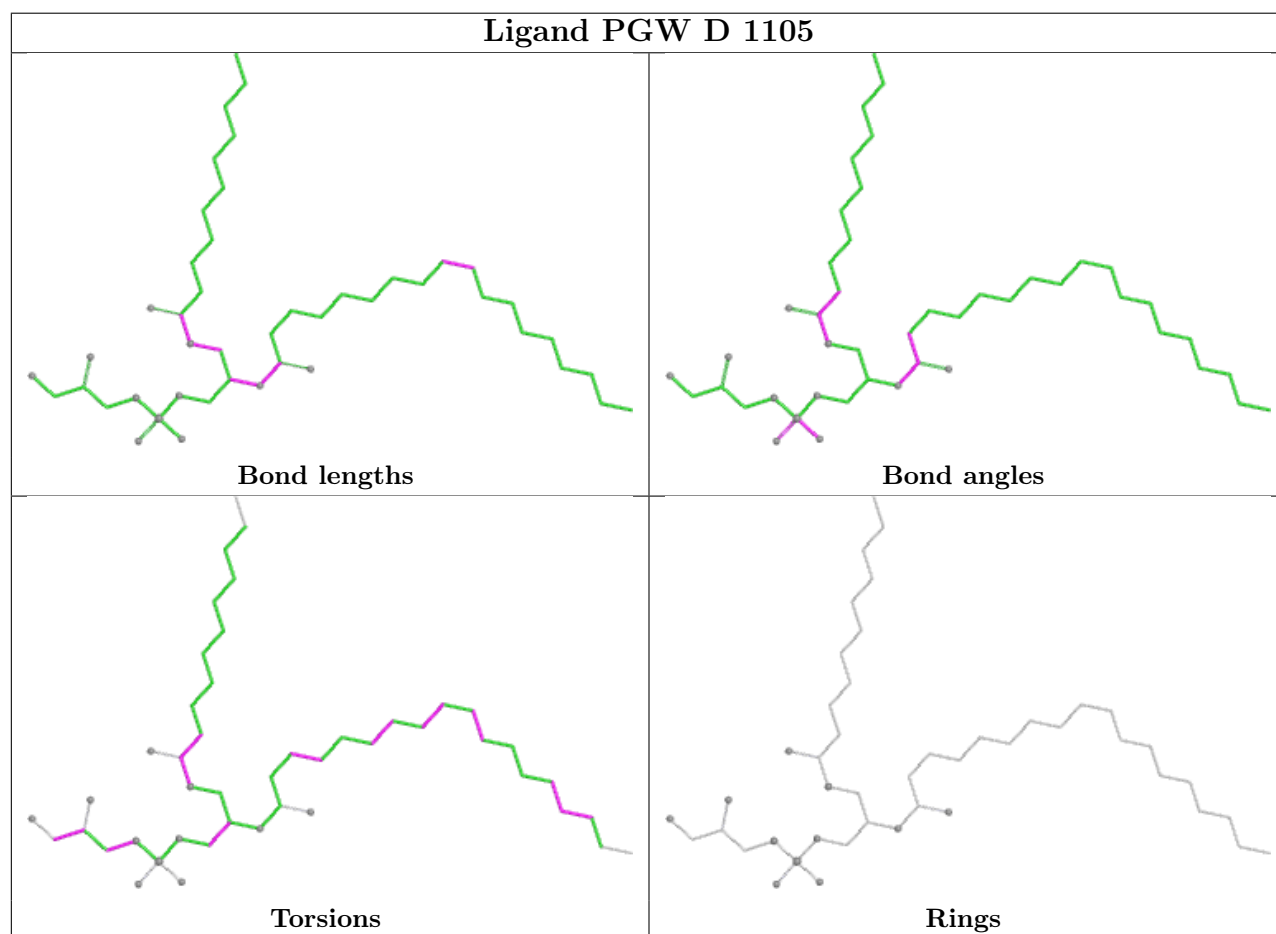
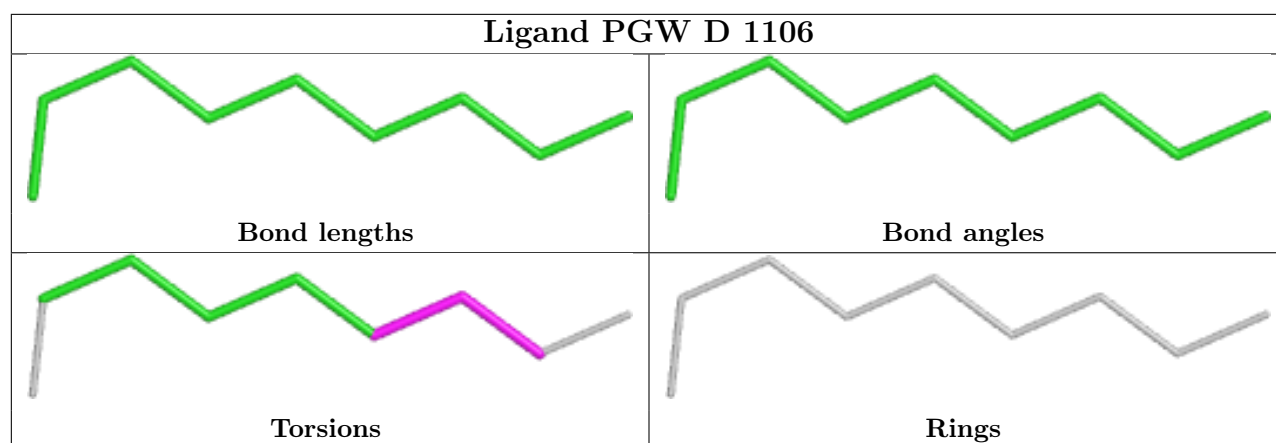


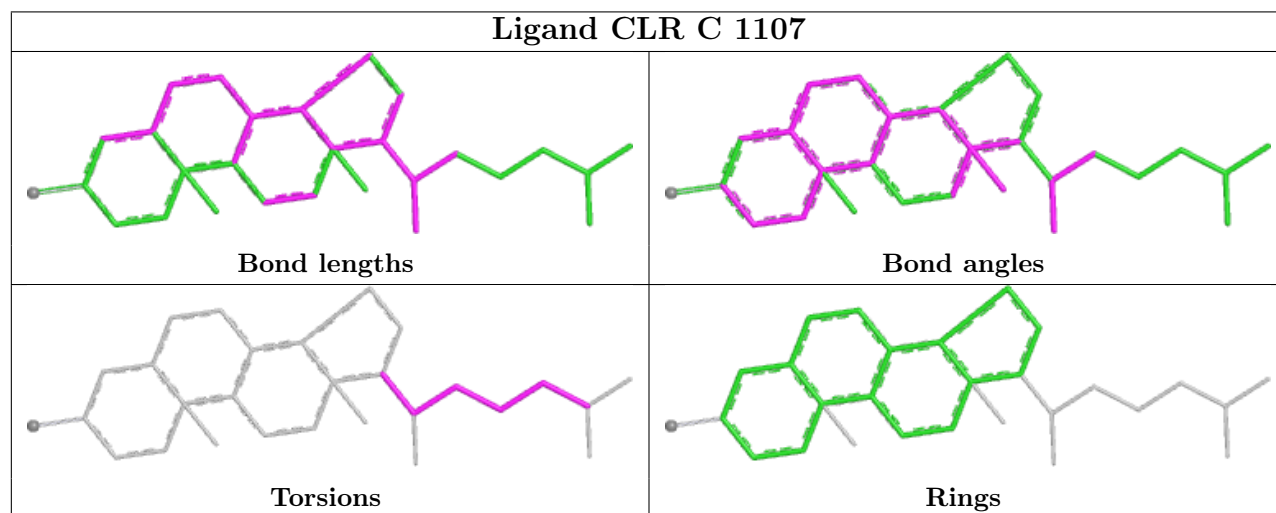
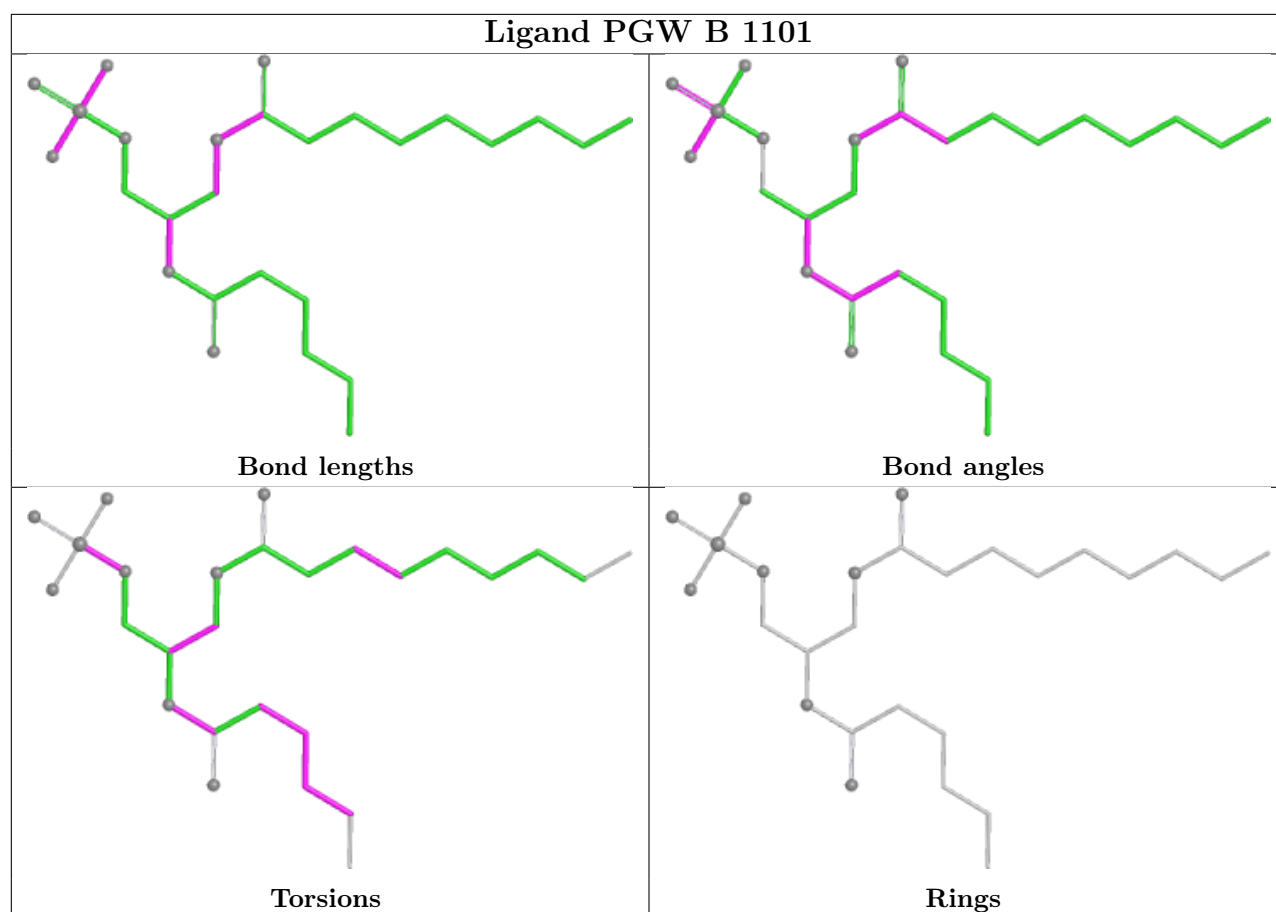
Ligand PGW C 1103

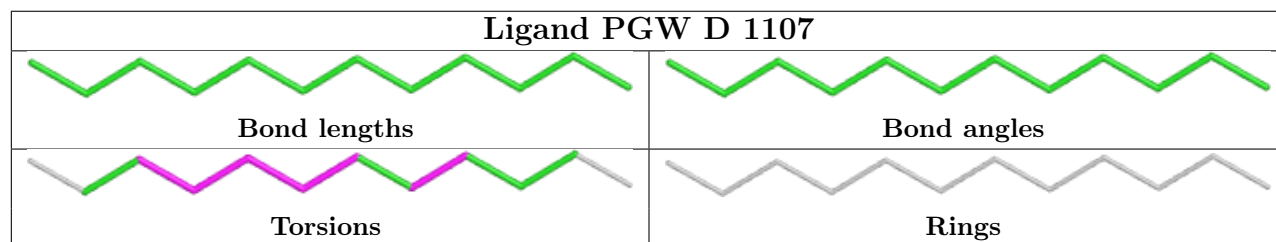
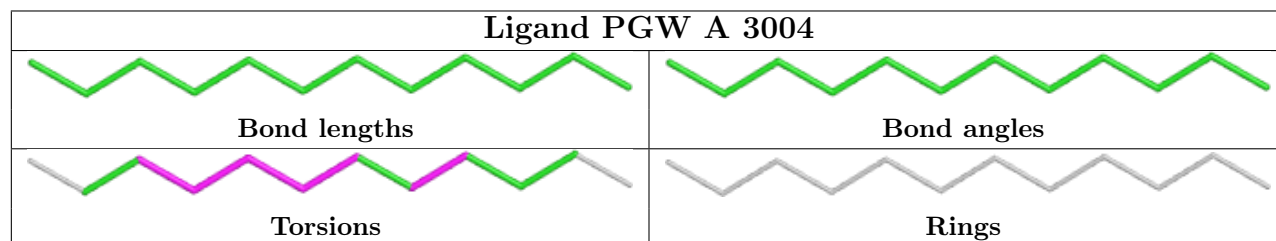
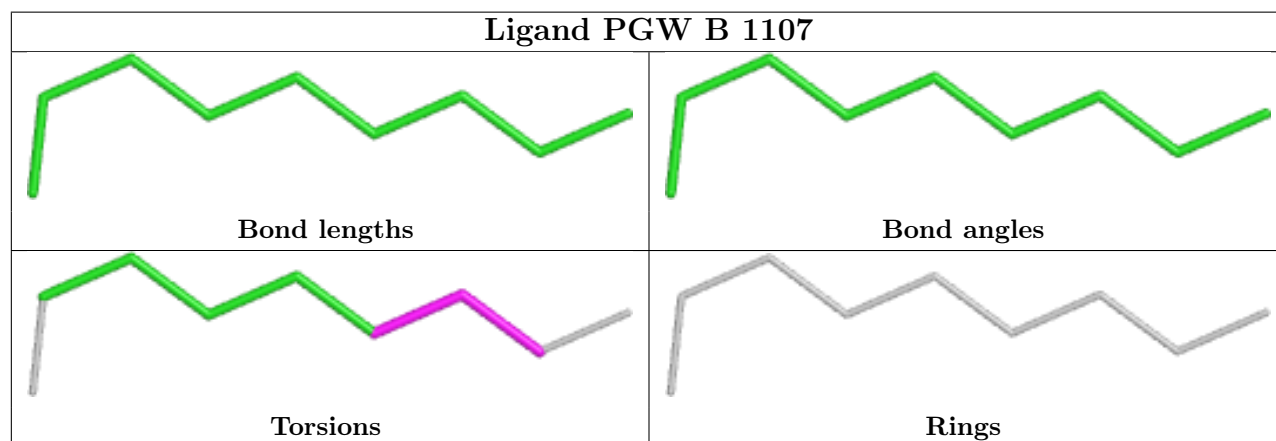
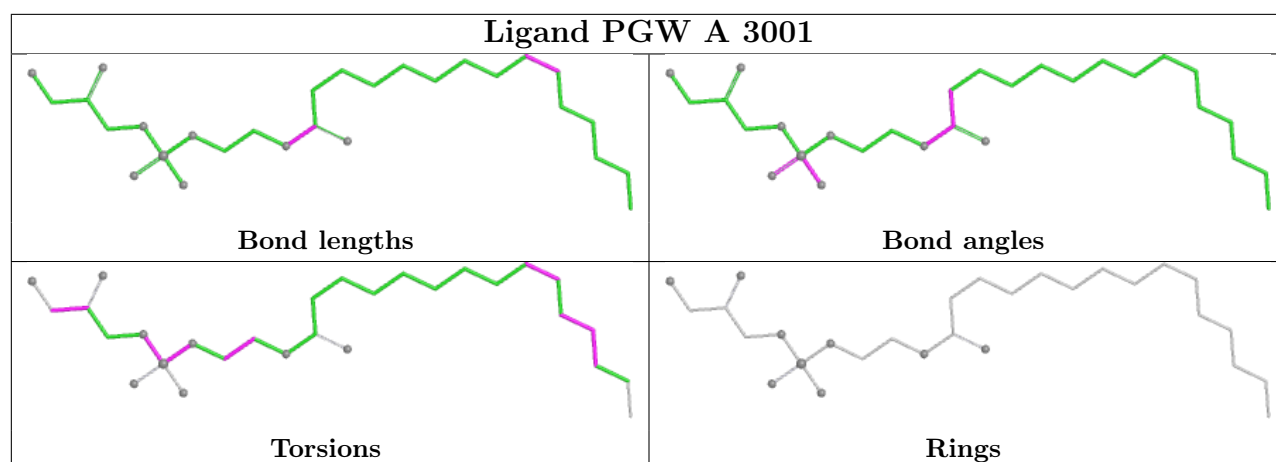


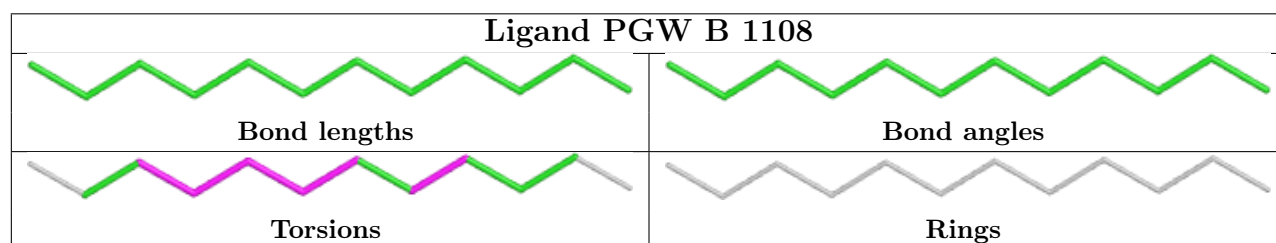
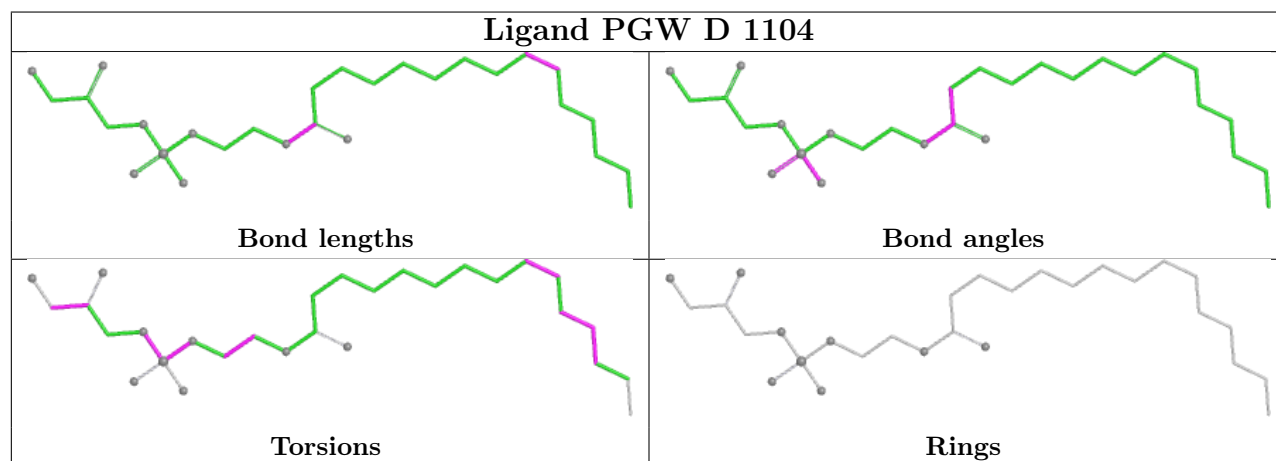
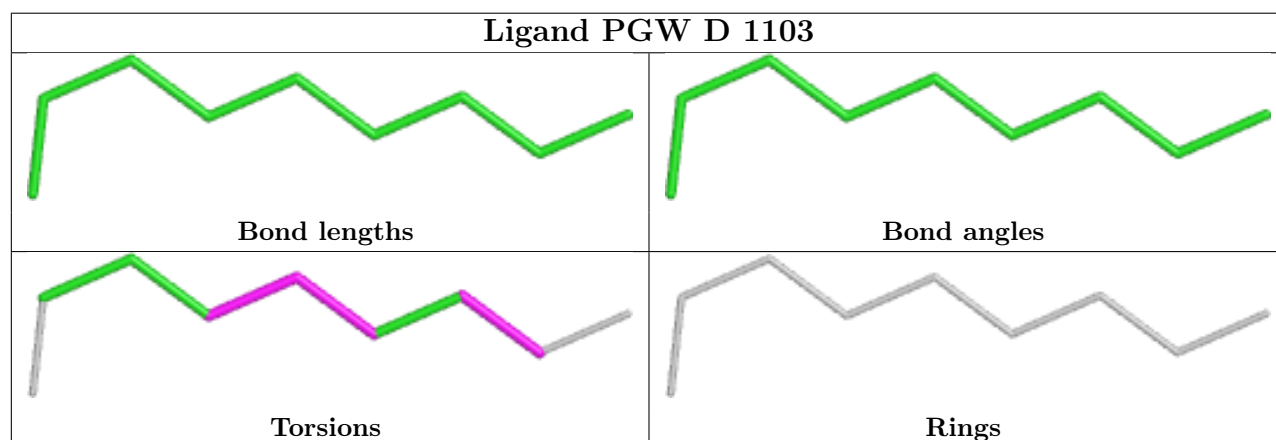
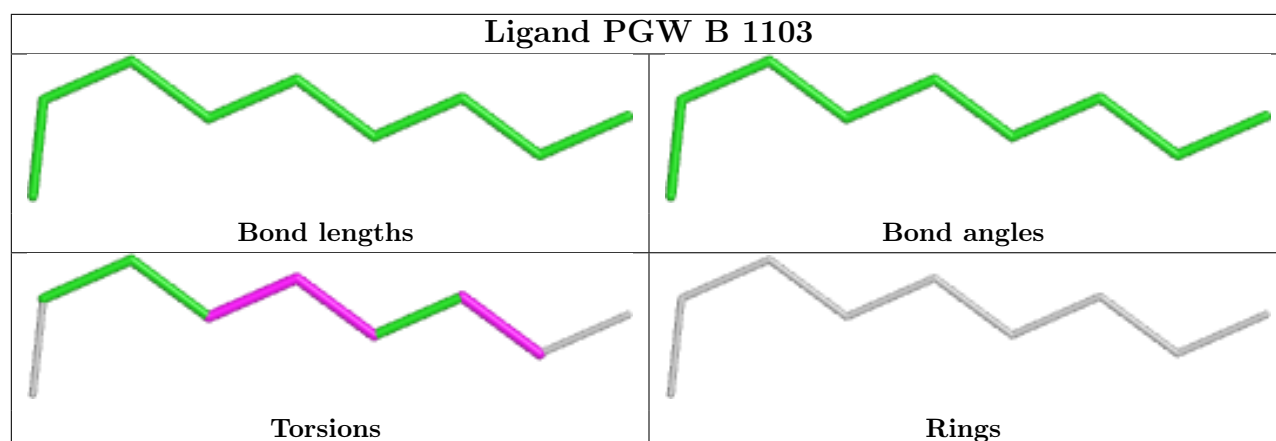
Ligand PGW E 2302

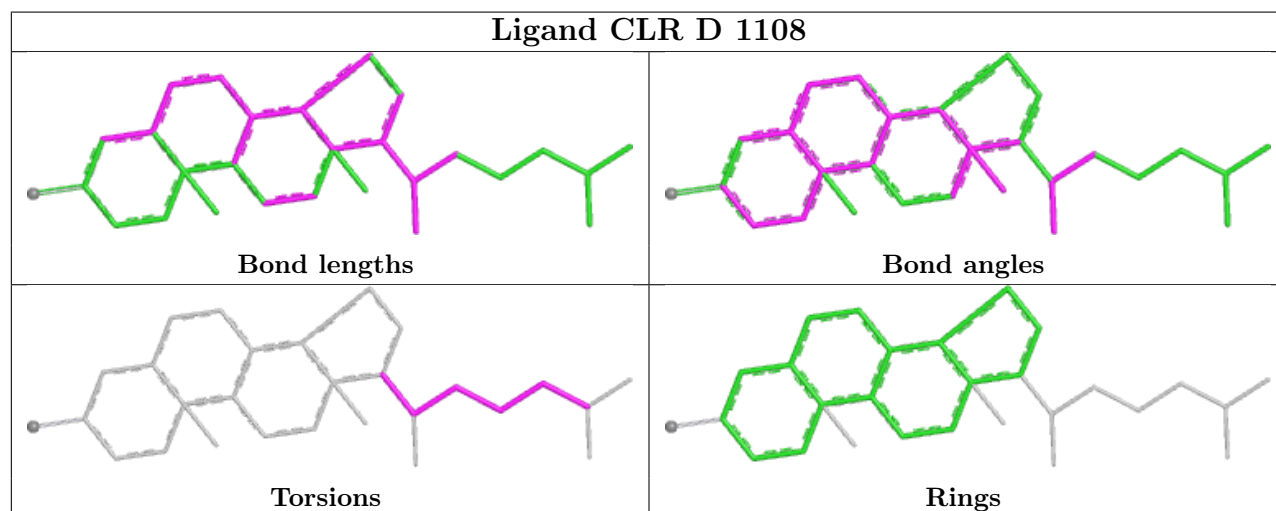
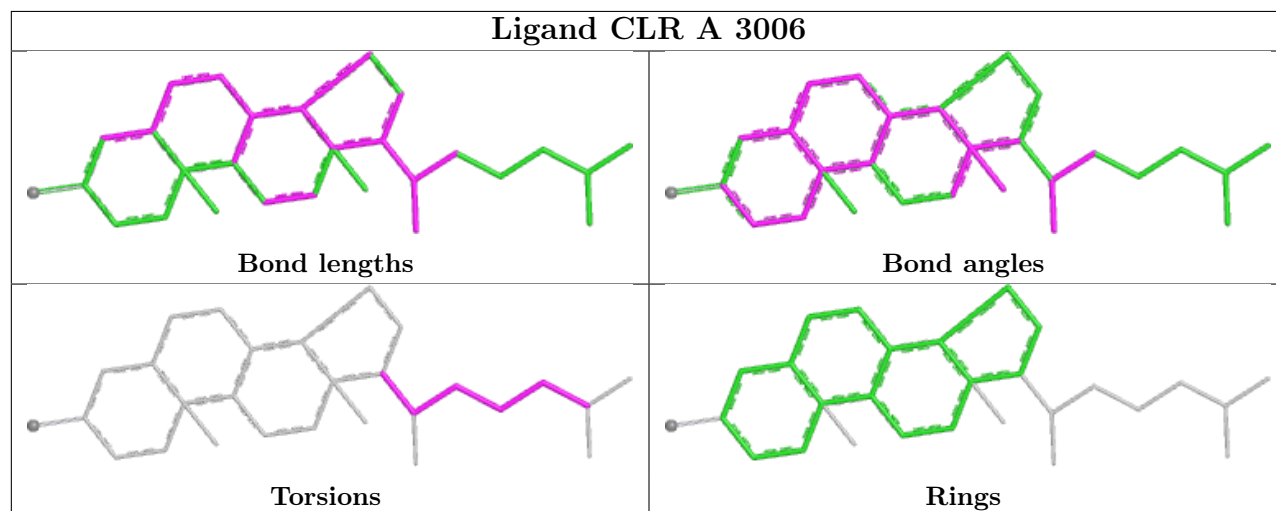
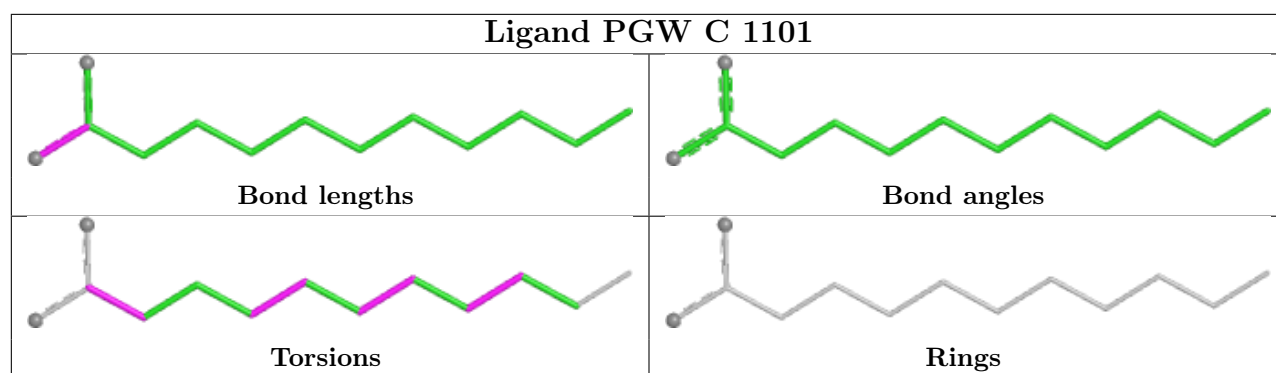


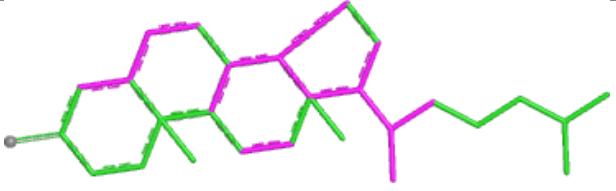
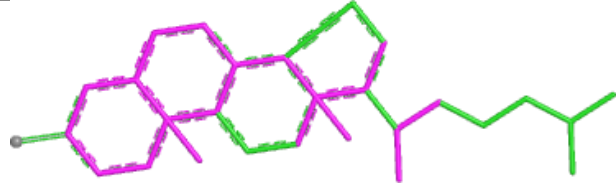
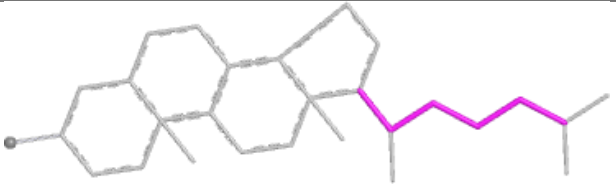
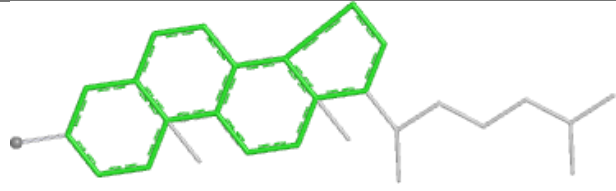








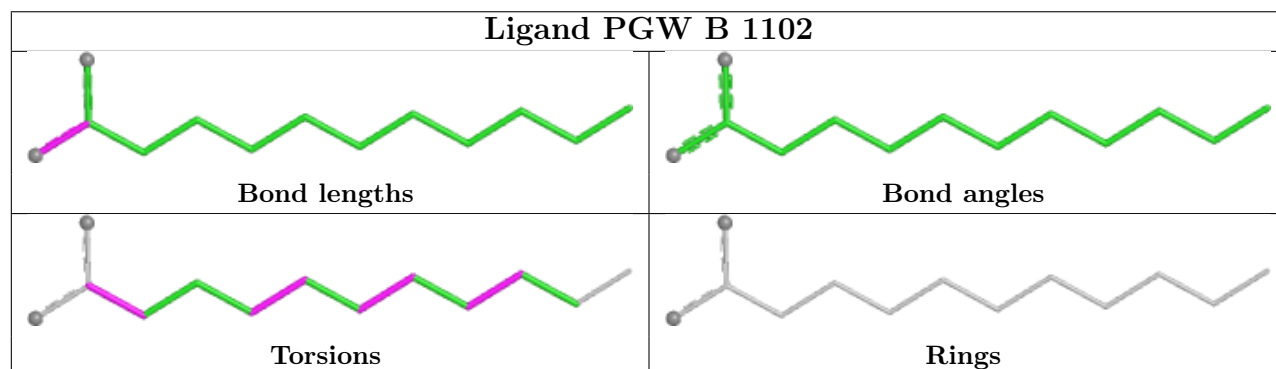
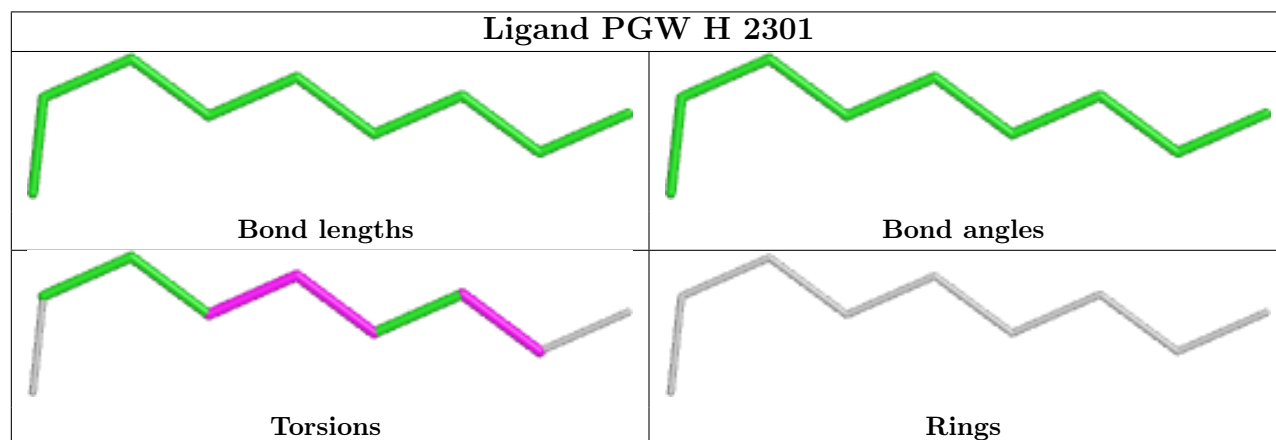
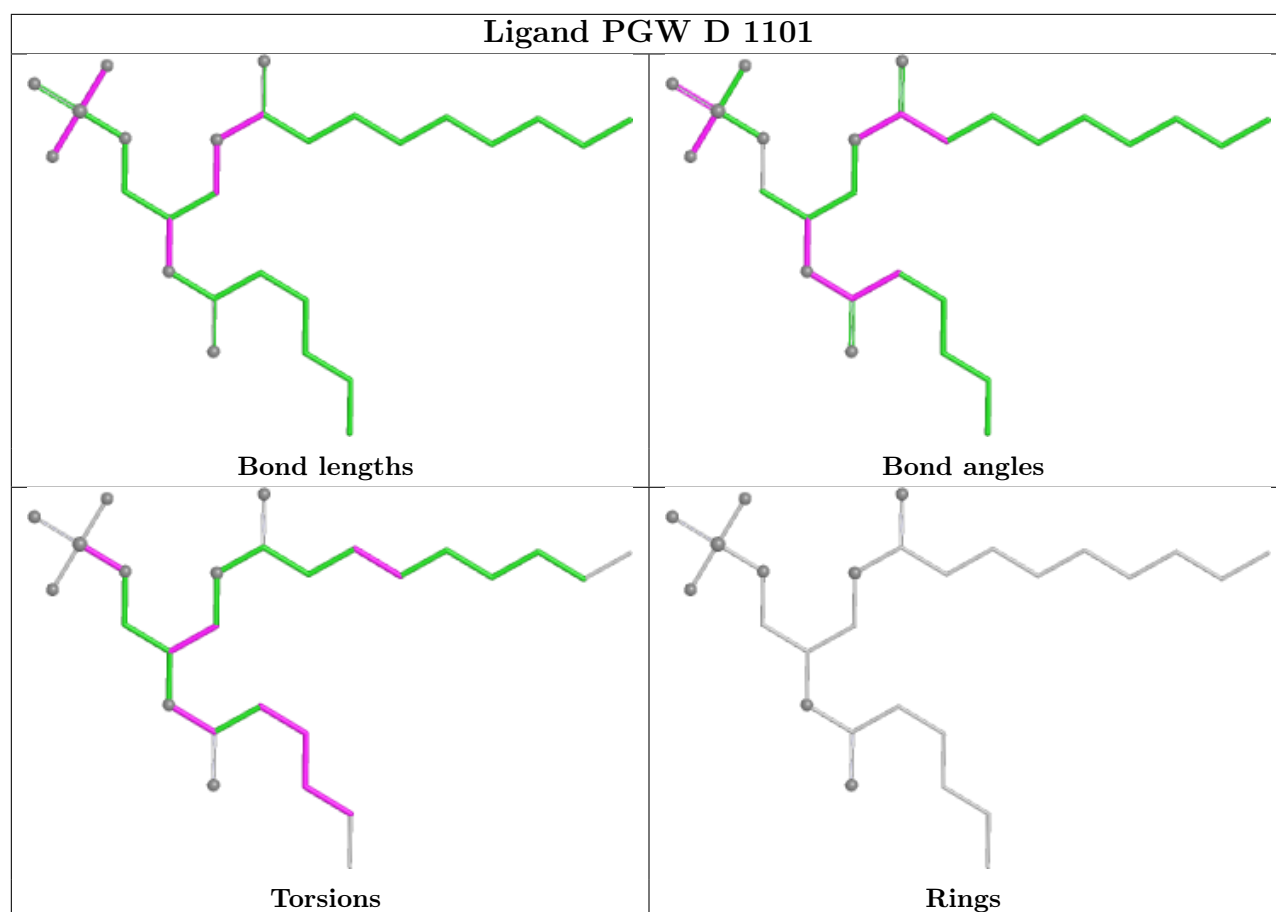


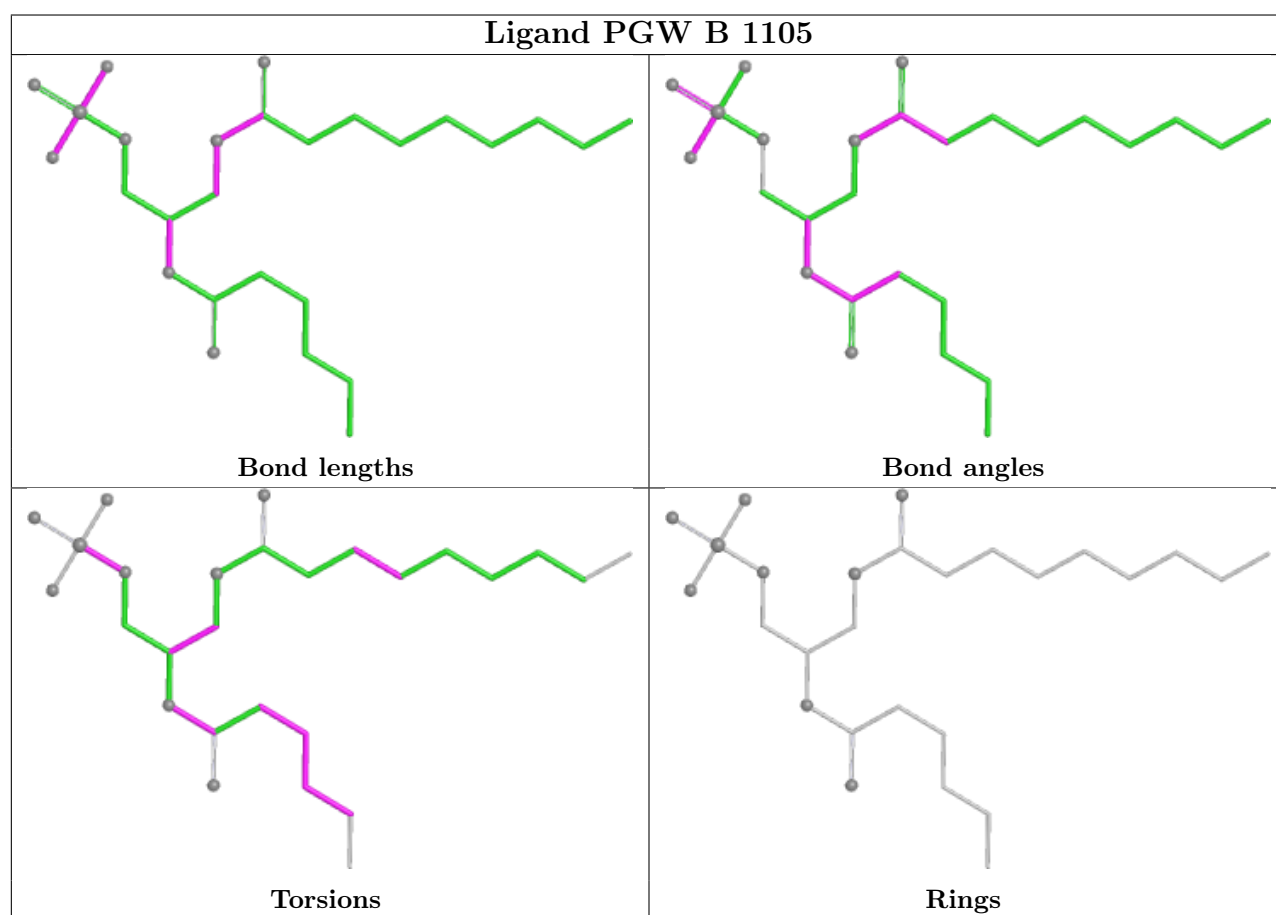
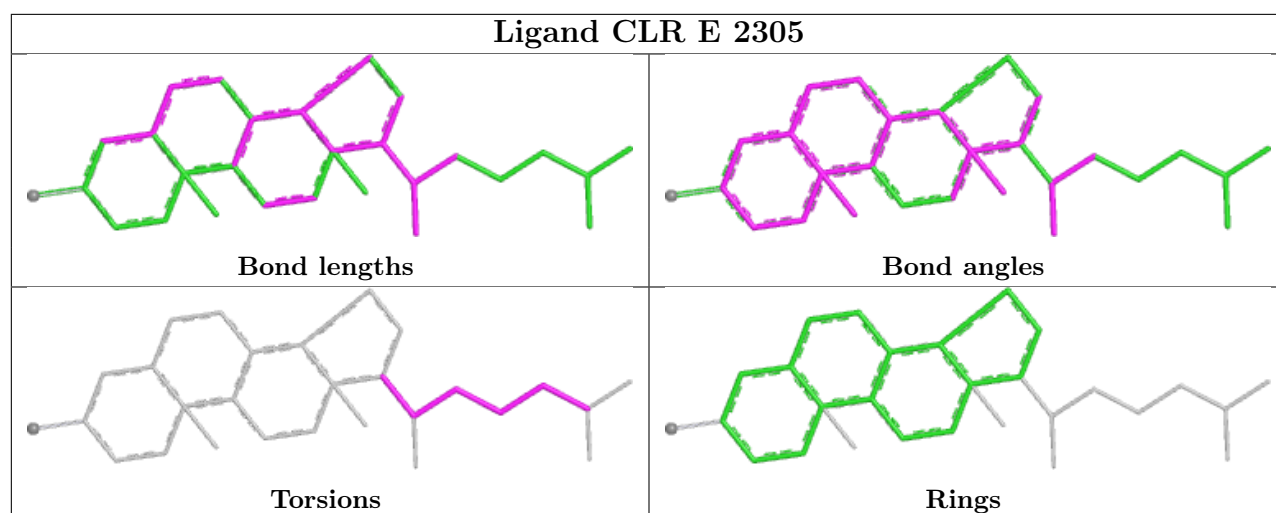
Ligand CLR H 2306			
			
Bond lengths		Bond angles	
			
Torsions		Rings	

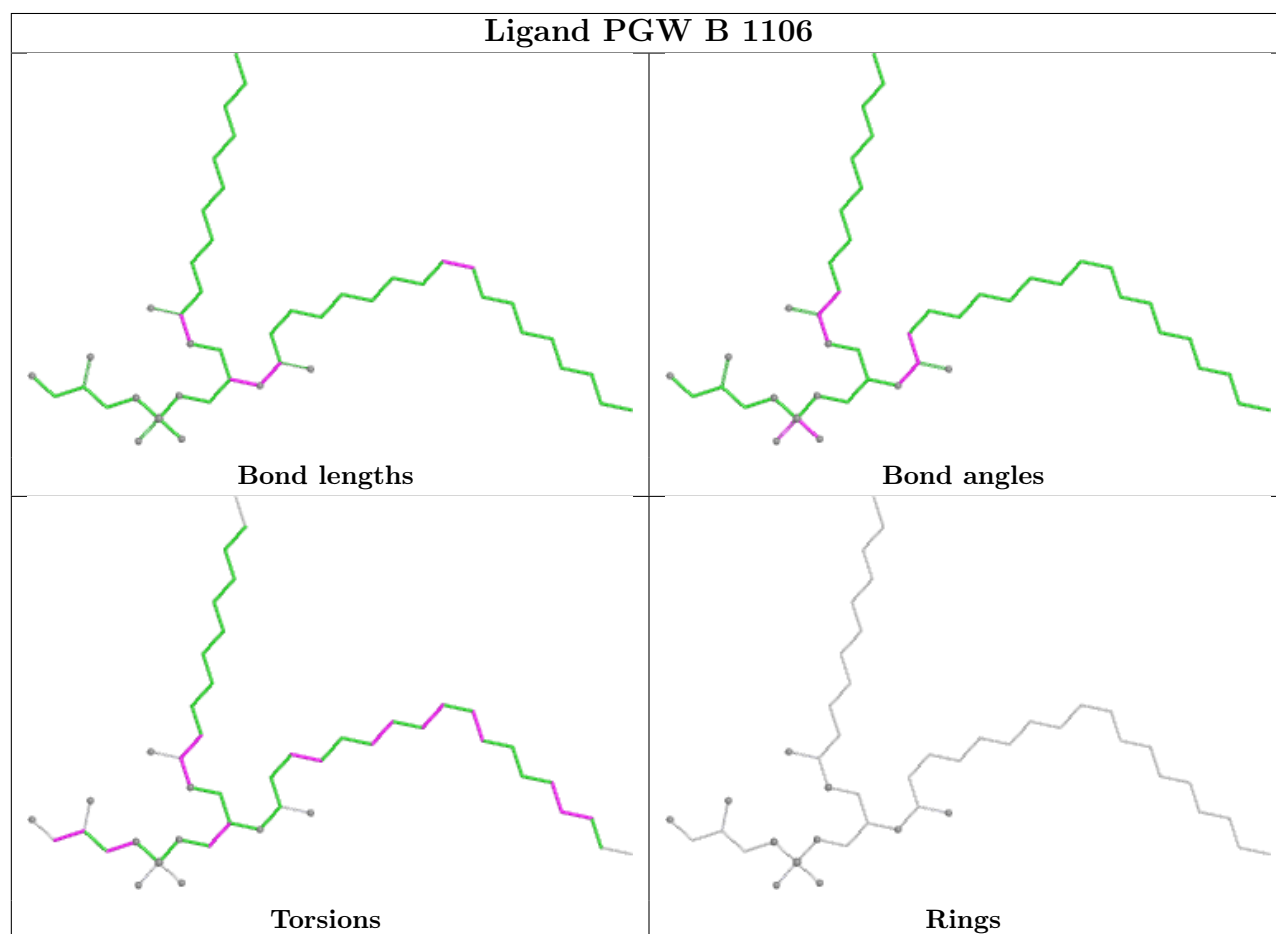
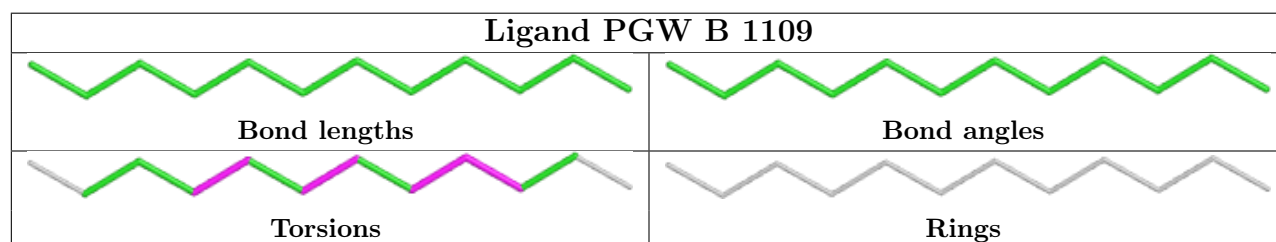
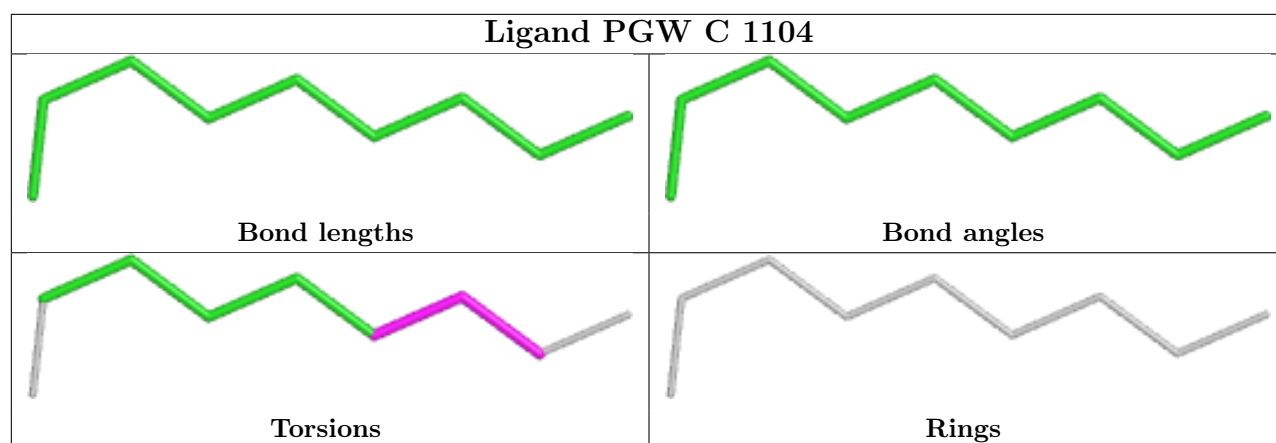
Ligand PGW C 1106			
			
Bond lengths		Bond angles	
			
Torsions		Rings	

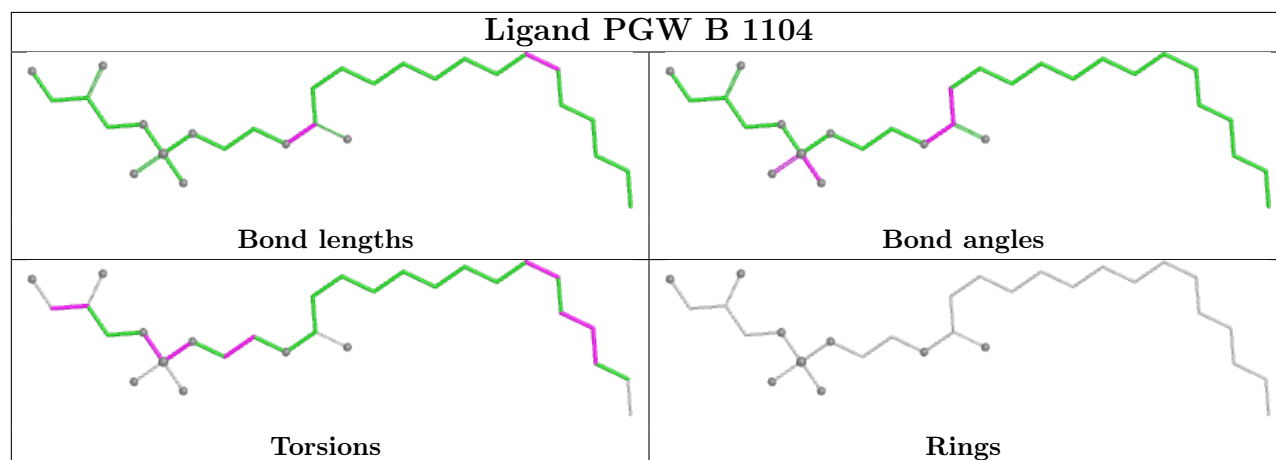
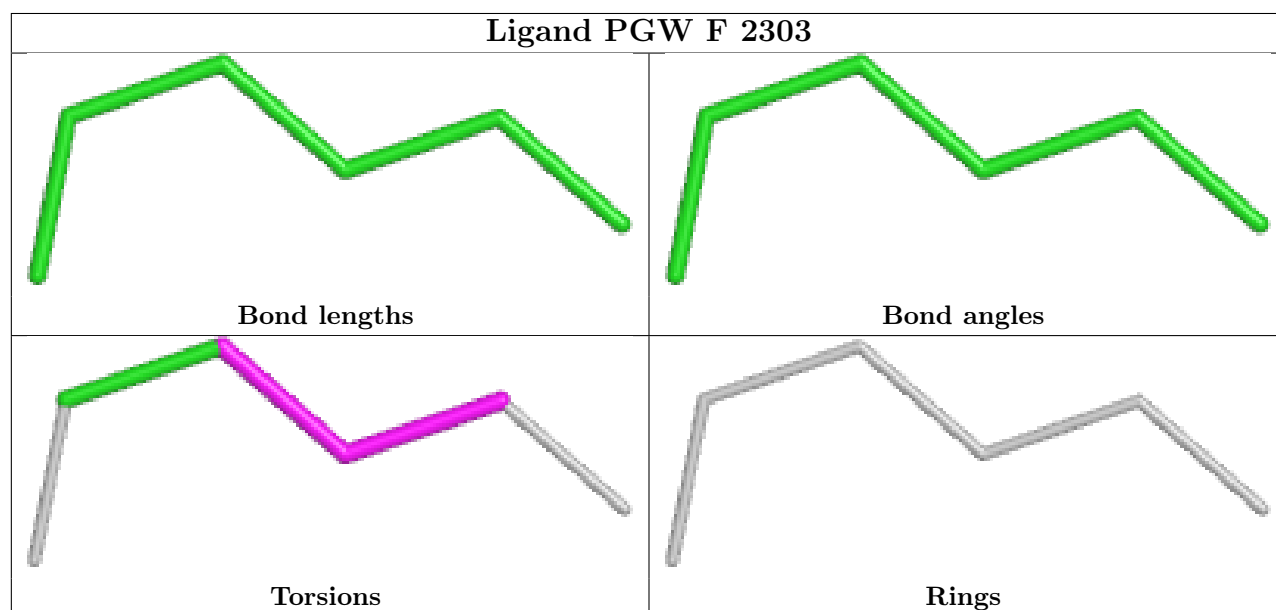
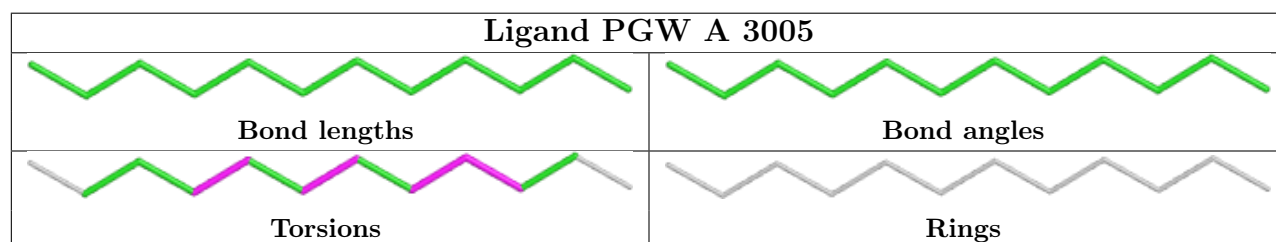
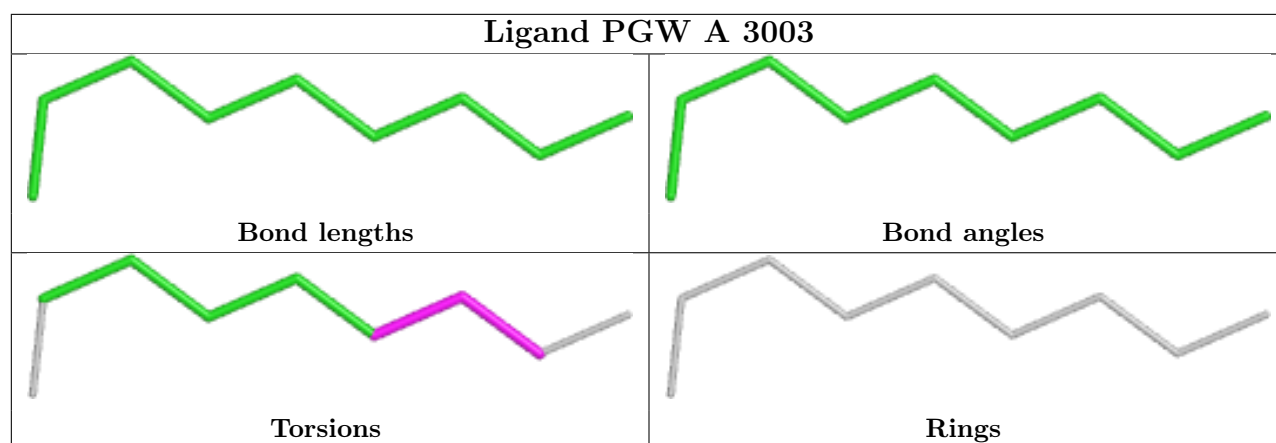
Ligand PGW A 3009			
			
Bond lengths		Bond angles	
			
Torsions		Rings	

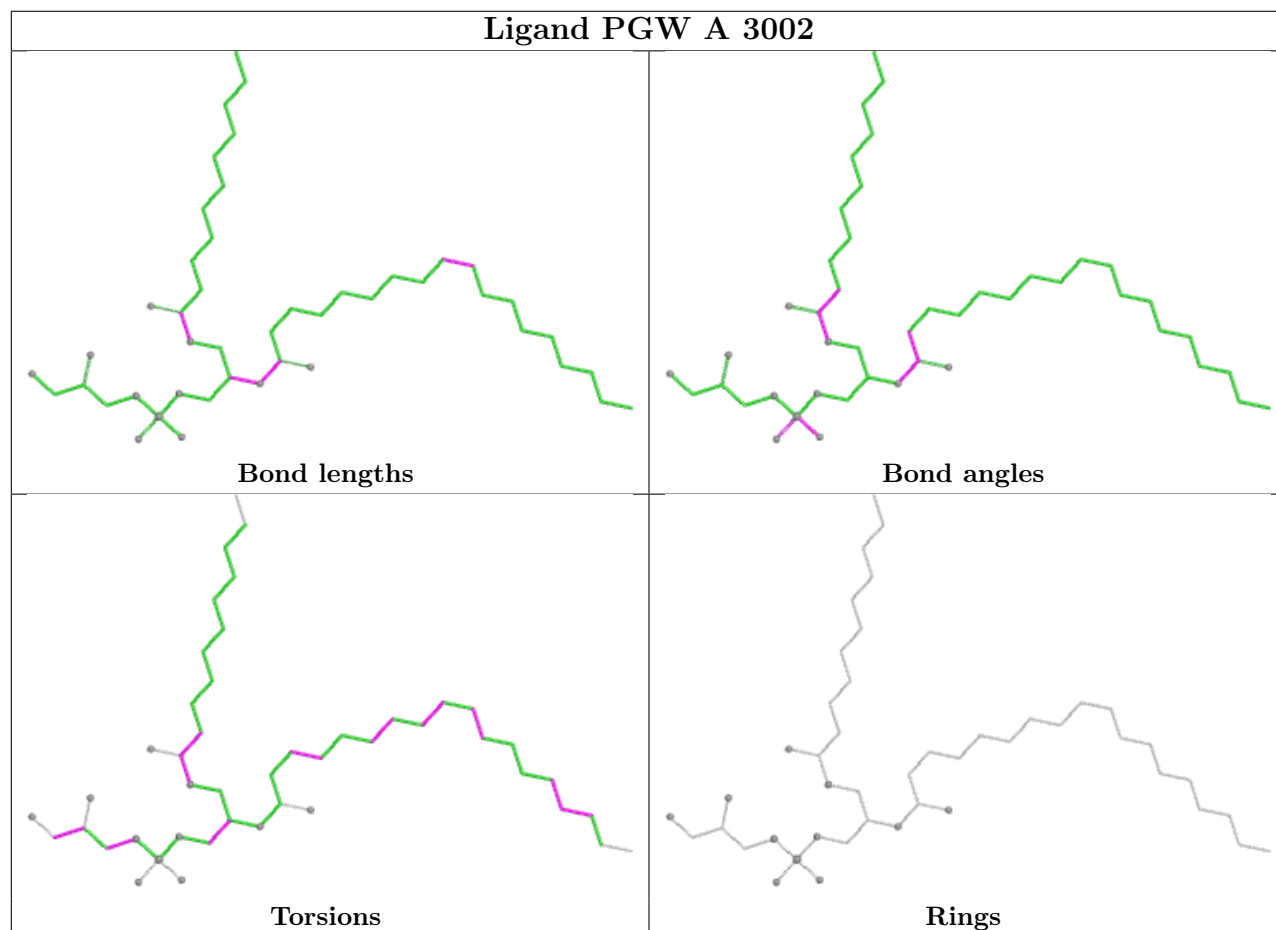
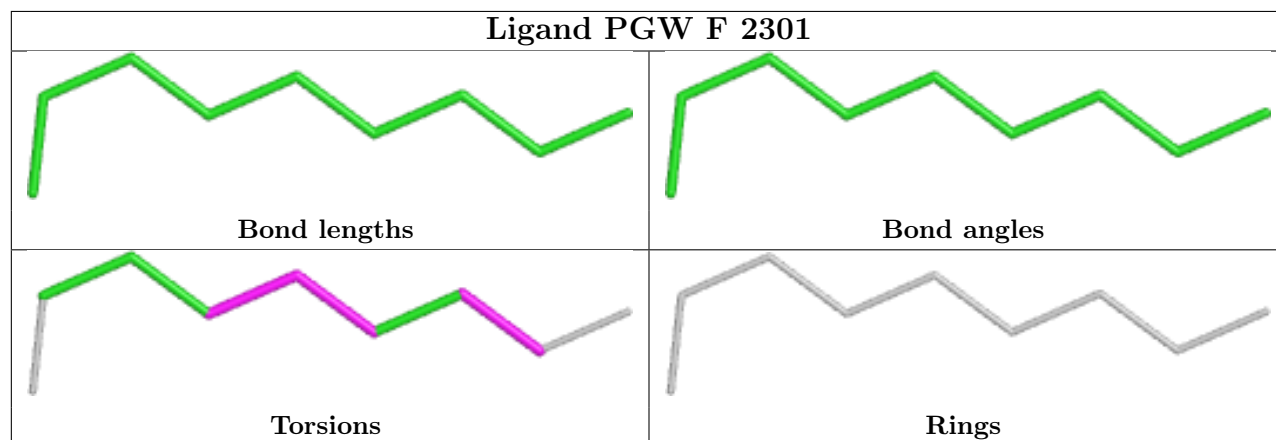
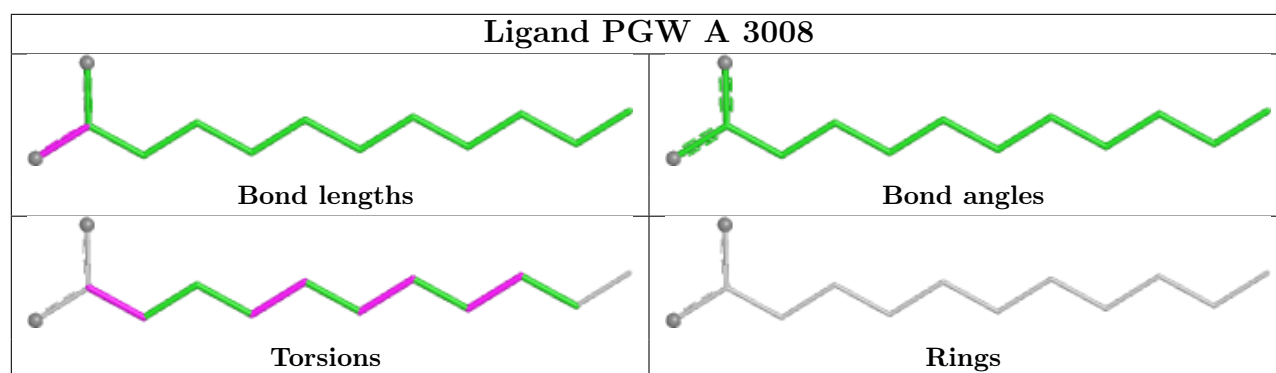
Ligand PGW C 1105			
			
Bond lengths		Bond angles	
			
Torsions		Rings	

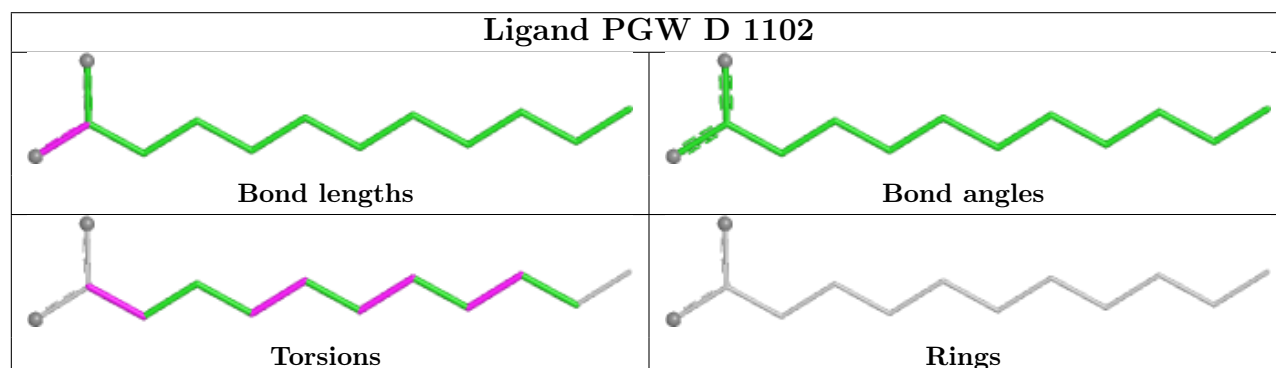
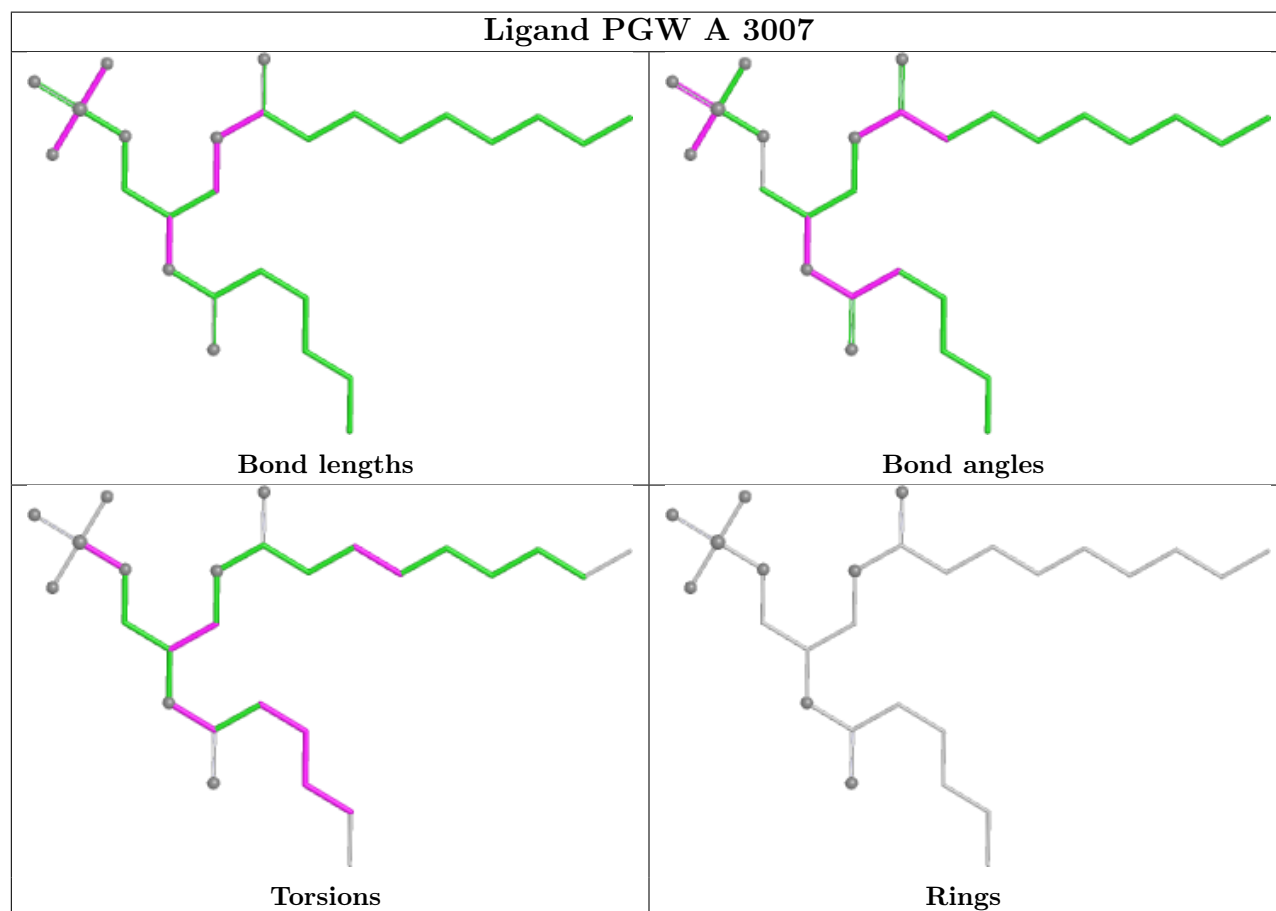
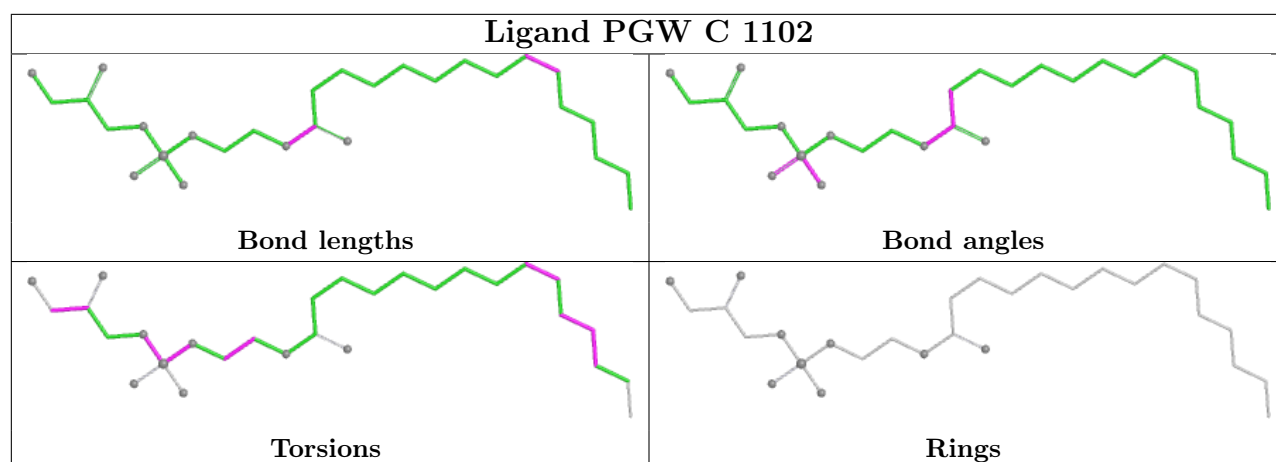












5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

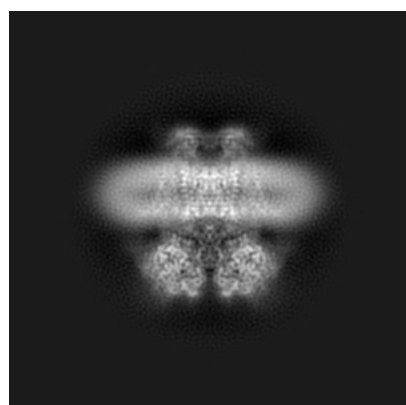
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21028. These allow visual inspection of the internal detail of the map and identification of artifacts.

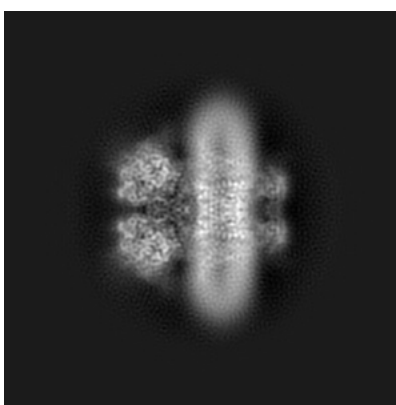
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

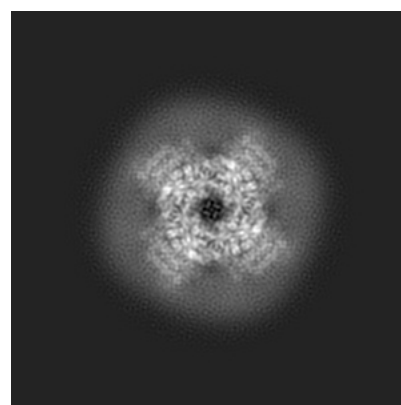
6.1.1 Primary map



X



Y

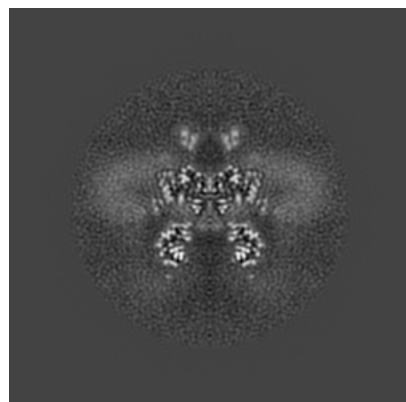


Z

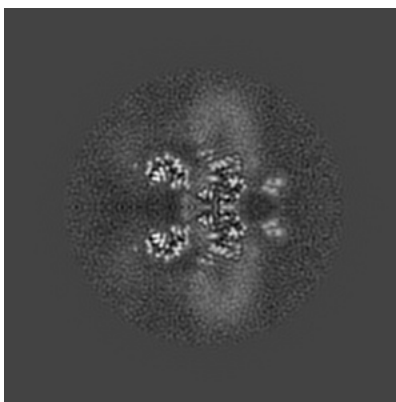
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

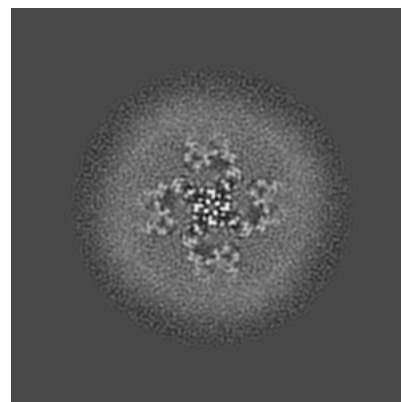
6.2.1 Primary map



X Index: 128



Y Index: 128

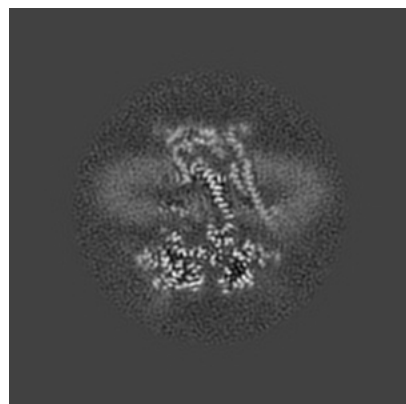


Z Index: 128

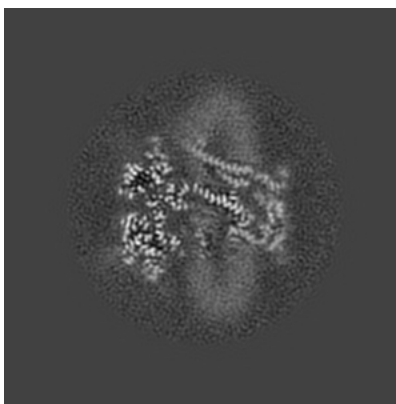
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

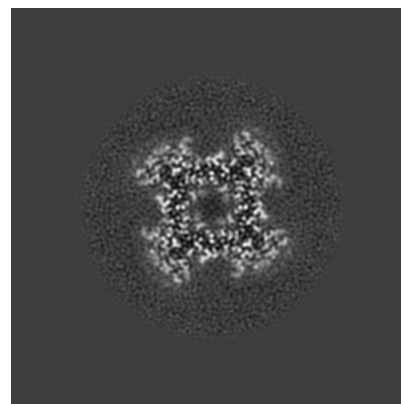
6.3.1 Primary map



X Index: 112



Y Index: 144

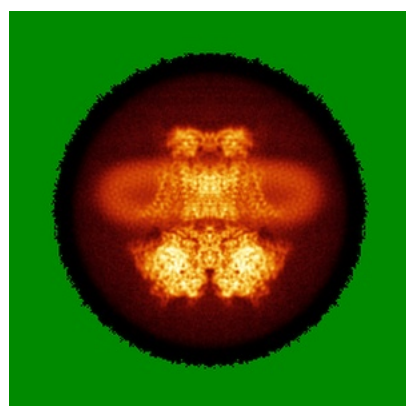


Z Index: 97

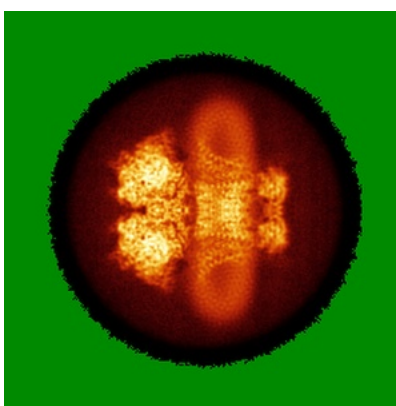
The images above show the largest variance slices of the map in three orthogonal directions.

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

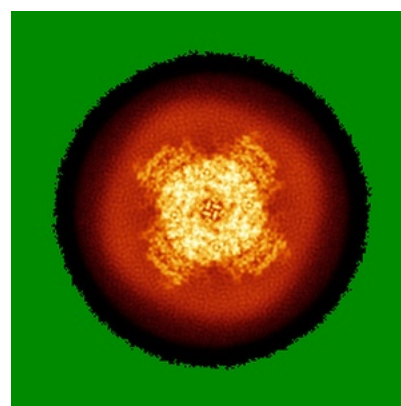
6.4.1 Primary map



X



Y

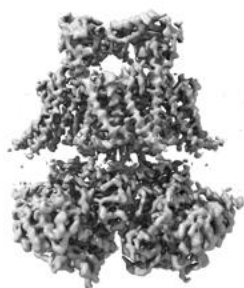


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

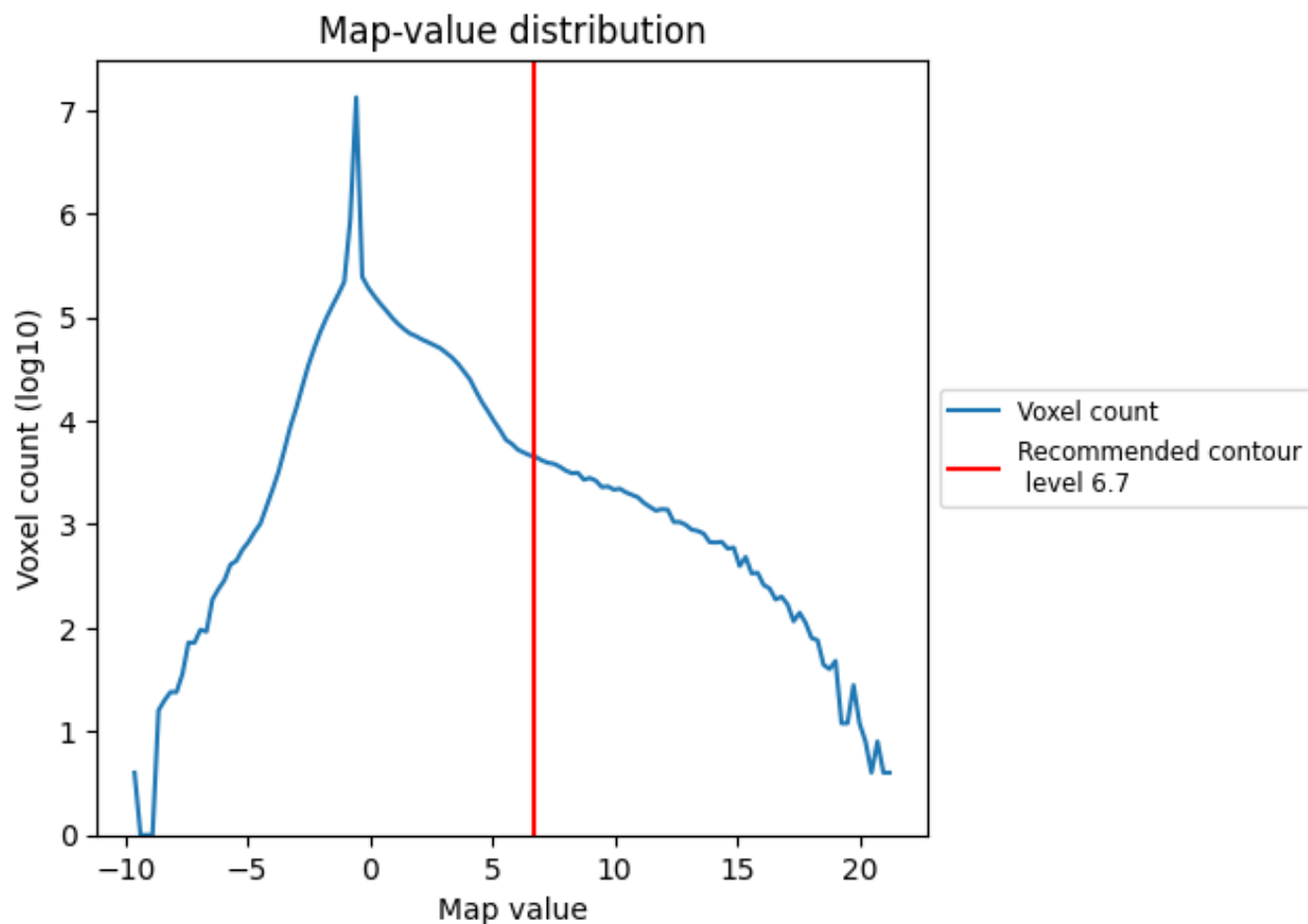
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

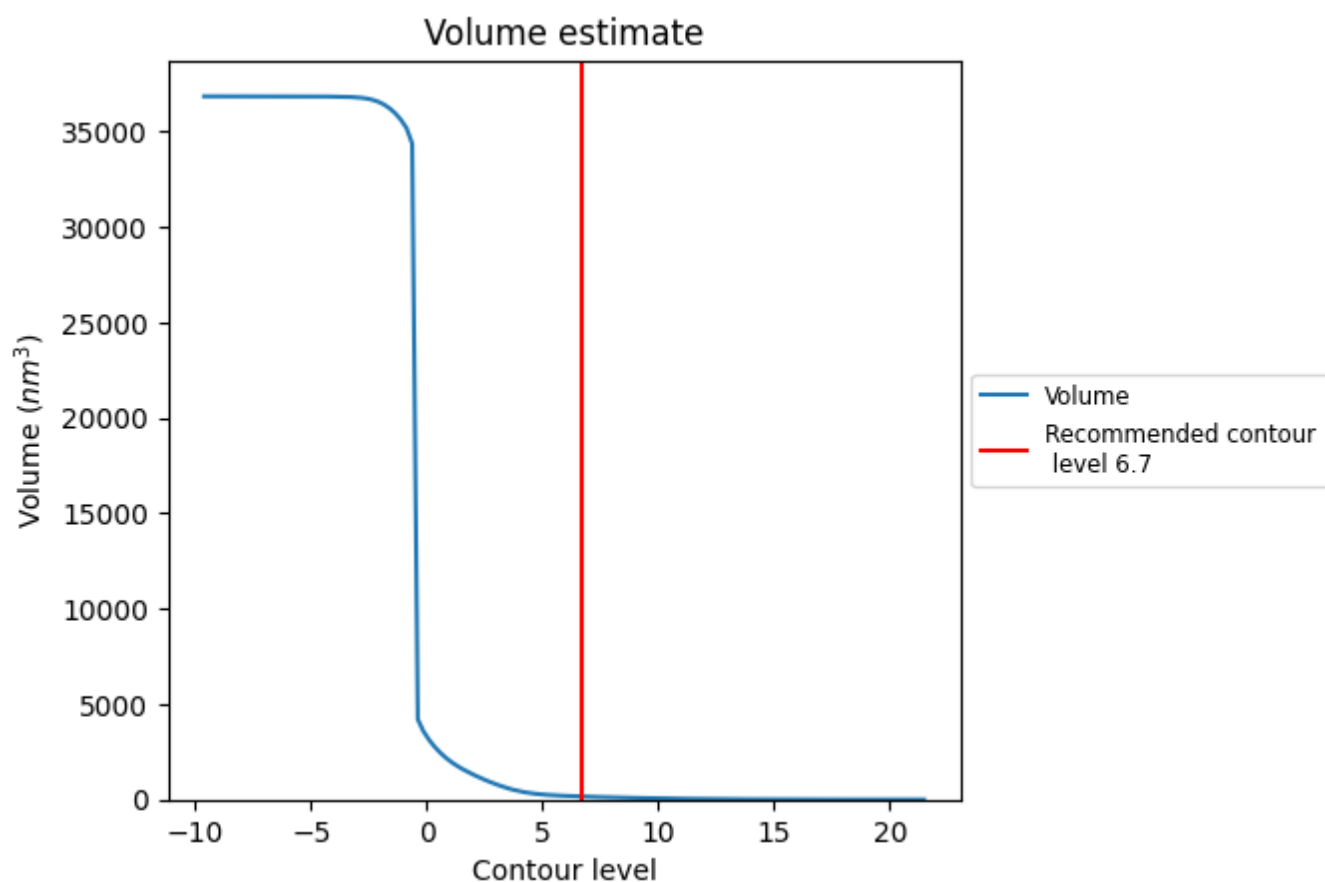
This section contains the results of statistical analysis of the map.

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.

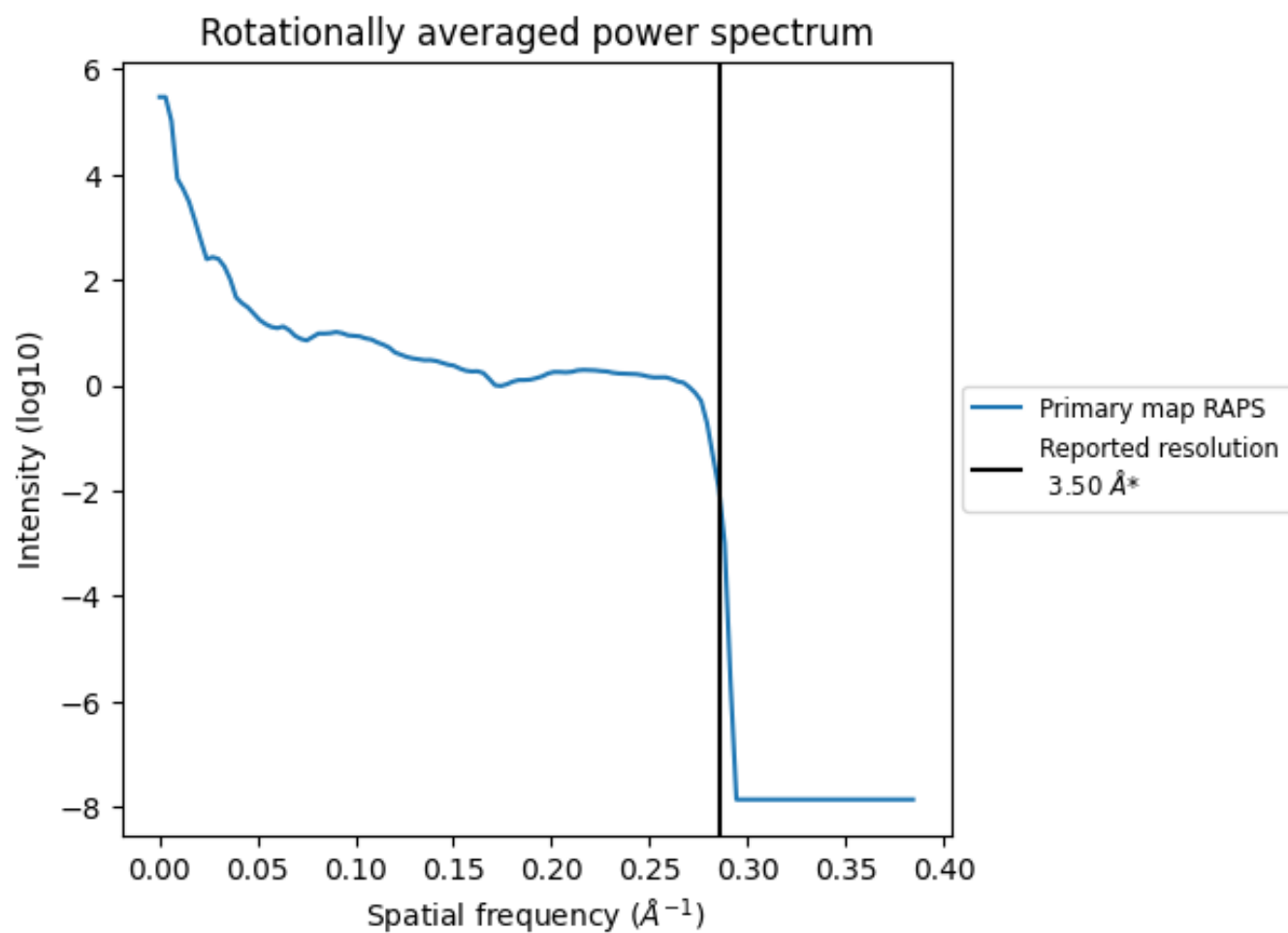
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 161 nm^3 ; this corresponds to an approximate mass of 146 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 0.286 Å⁻¹

8 Fourier-Shell correlation

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

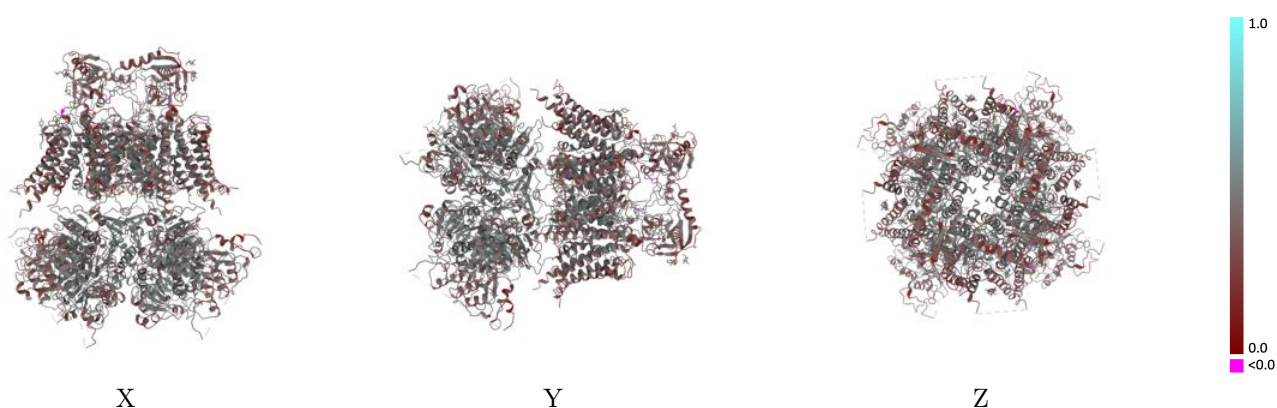
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-21028 and PDB model 6V35. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

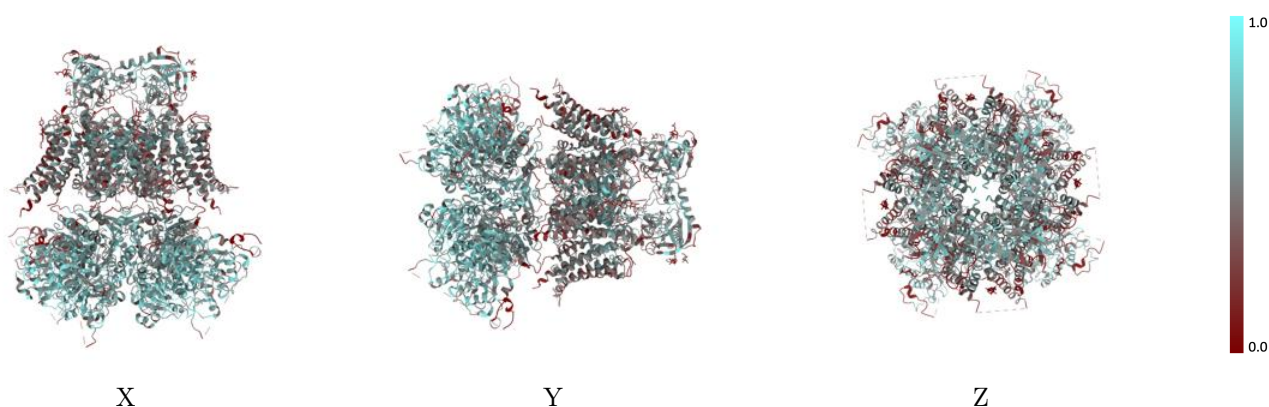
This section was not generated.

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



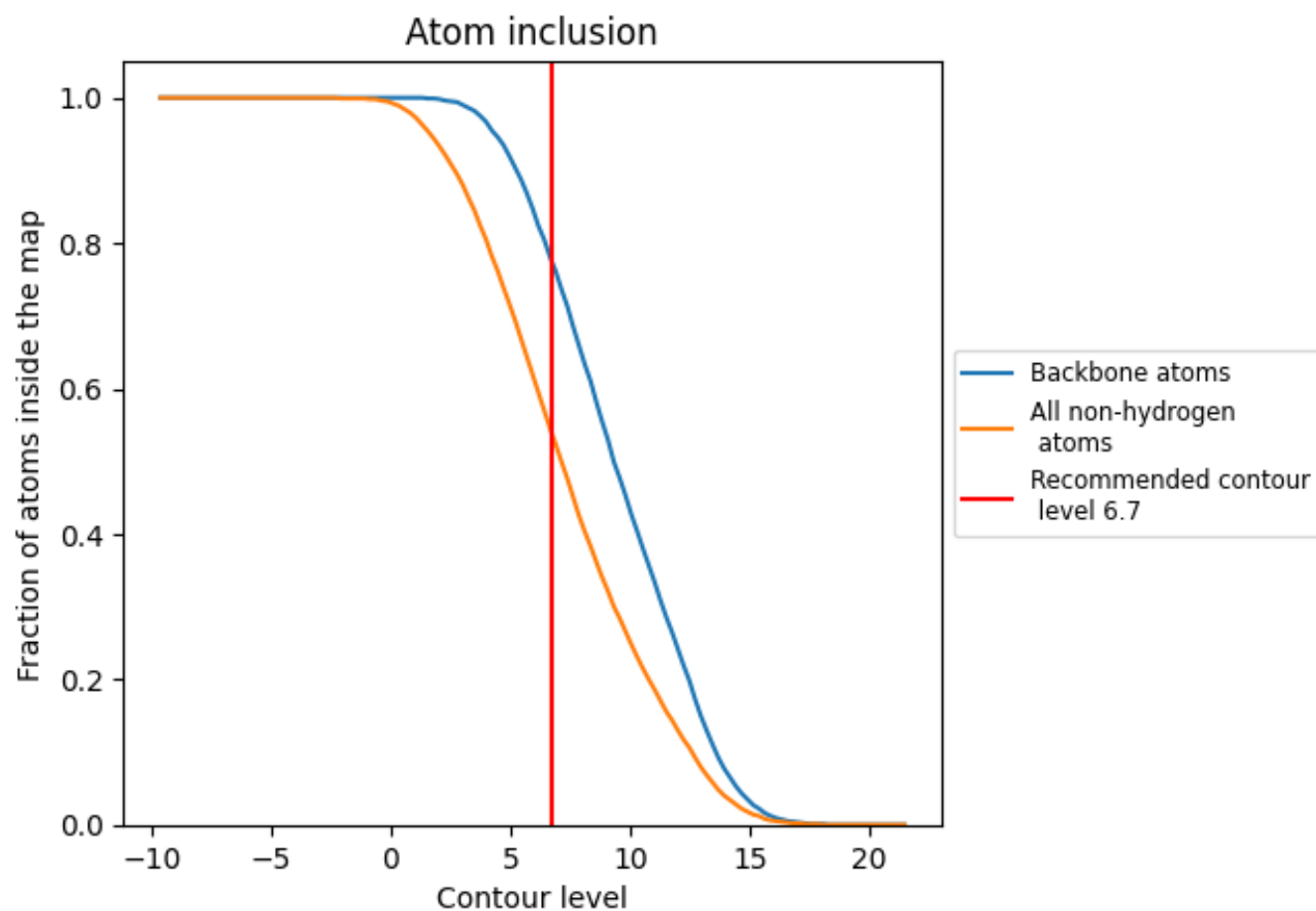
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (6.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 54% 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 (6.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5410	0.4120
A	0.5640	0.4240
B	0.5650	0.4240
C	0.5660	0.4220
D	0.5660	0.4230
E	0.4310	0.3620
F	0.4300	0.3650
G	0.4310	0.3610
H	0.4330	0.3620

