



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 11:32 AM JST

PDB ID : 5X1B / pdb_00005x1b
Title : CO bound cytochrome c oxidase at 20 nsec after pump laser irradiation to release CO from O2 reduction center
Authors : Shimada, A.; Kubo, M.; Baba, S.; Yamashita, K.; Hirata, K.; Ueno, G.; Nomura, T.; Kimura, T.; Shinzawa-Itoh, K.; Baba, J.; Hatano, K.; Eto, Y.; Miyamoto, A.; Murakami, H.; Kumasaka, T.; Owada, S.; Tono, K.; Yabashi, M.; Yamaguchi, Y.; Yanagisawa, S.; Sakaguchi, M.; Ogura, T.; Komiya, R.; Yan, J.; Yamashita, E.; Yamamoto, M.; Ago, H.; Yoshikawa, S.; Tsukihara, T.
Deposited on : 2017-01-25
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>
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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12

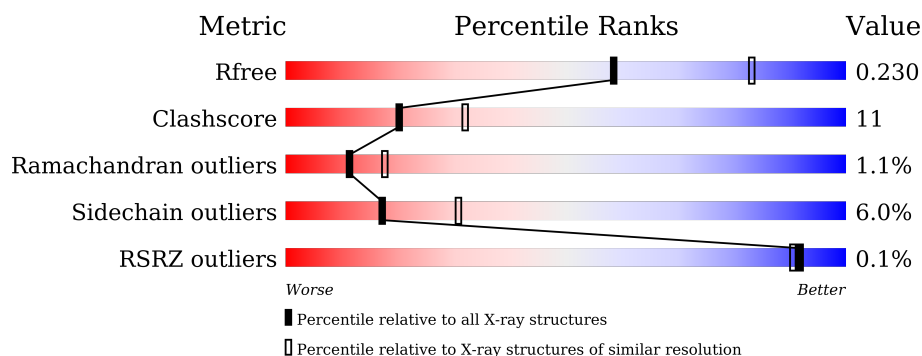
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	514	
1	N	514	
2	B	227	

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Ideal geometry (proteins) : Engh & Huber (2001)
 Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.50

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Mol	Chain	Length	Quality of chain
2	O	227	
3	C	261	
3	P	261	
4	D	147	
4	Q	147	
5	E	109	
5	R	109	
6	F	98	
6	S	98	
7	G	85	
7	T	85	
8	H	85	
8	U	85	
9	I	73	
9	V	73	
10	J	59	
10	W	59	
11	K	56	
11	X	56	
12	L	47	
12	Y	47	
13	M	46	
13	Z	46	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
21	EDO	A	614	-	-	X	-

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 31717 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	1	0
			4030	2694	623	678	35			
1	N	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			

- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	227	Total	C	N	O	S	0	0	0
			1824	1185	281	340	18			
2	O	227	Total	C	N	O	S	0	0	0
			1824	1185	281	340	18			

- Molecule 3 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	259	Total	C	N	O	S	0	0	0
			2110	1412	336	350	12			
3	P	259	Total	C	N	O	S	0	0	0
			2110	1412	336	350	12			

- Molecule 4 is a protein called Cytochrome c oxidase subunit 4 isoform 1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			
4	Q	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			

- Molecule 5 is a protein called Cytochrome c oxidase subunit 5A, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			
5	R	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			

- Molecule 6 is a protein called Cytochrome c oxidase subunit 5B, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			
6	S	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			

- Molecule 7 is a protein called Cytochrome c oxidase subunit 6A2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	84	Total	C	N	O	P	S	0	0
			675	431	129	113	1	1		
7	T	84	Total	C	N	O	P	S	0	0
			675	431	129	113	1	1		

- Molecule 8 is a protein called Cytochrome c oxidase subunit 6B1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			
8	U	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			

- Molecule 9 is a protein called Cytochrome c oxidase subunit 6C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			
9	V	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			

- Molecule 10 is a protein called Cytochrome c oxidase subunit 7A1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

- Molecule 11 is a protein called Cytochrome c oxidase subunit 7B, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	49	Total	C	N	O	S	0	0	0
			384	250	65	67	2			
11	X	49	Total	C	N	O	S	0	0	0
			384	250	65	67	2			

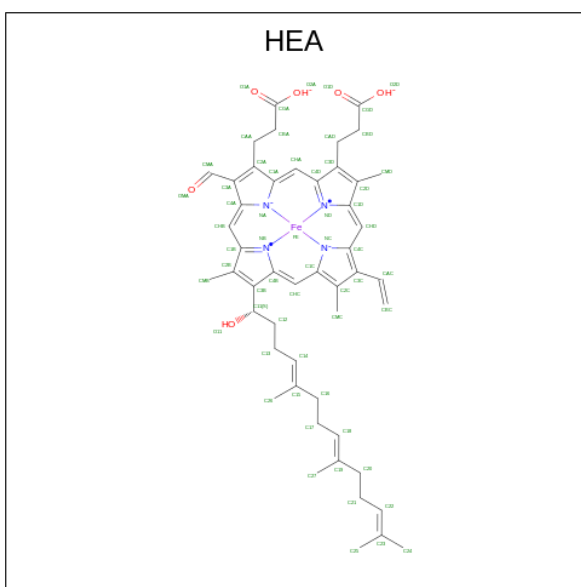
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	46	Total	C	N	O	S	0	0	0
			380	254	64	60	2			
12	Y	46	Total	C	N	O	S	0	0	0
			380	254	64	60	2			

- Molecule 13 is a protein called Cytochrome c oxidase subunit 8B, mitochondrial.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	43	Total	C	N	O	0	0	0
			335	223	53	59			
13	Z	43	Total	C	N	O	0	0	0
			335	223	53	59			

- Molecule 14 is HEME-A (CCD ID: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
14	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
14	N	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
14	N	1	Total 60	C 49	Fe 1	N 4	O 6	0	0

- Molecule 15 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total	Cu	0	0
			1	1		
15	N	1	Total	Cu	0	0
			1	1		

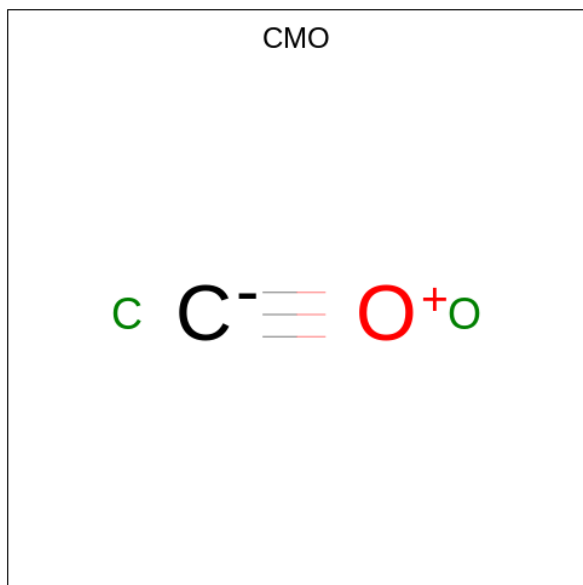
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		

- Molecule 17 is SODIUM ION (CCD ID: NA) (formula: Na).

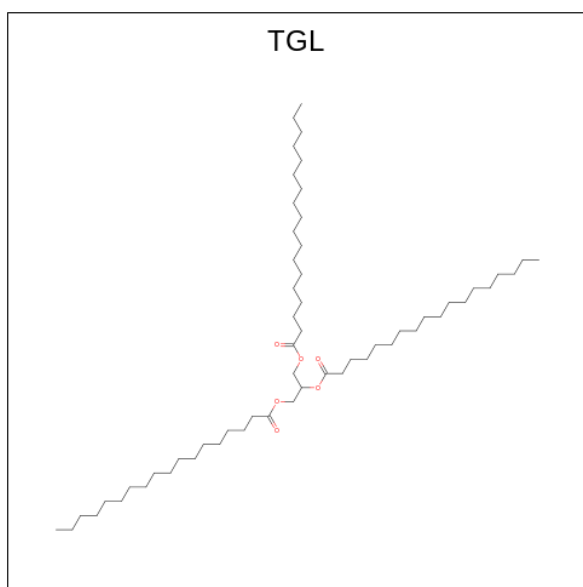
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Na	0	0
			1	1		
17	N	1	Total	Na	0	0
			1	1		

- Molecule 18 is CARBON MONOXIDE (CCD ID: CMO) (formula: CO).



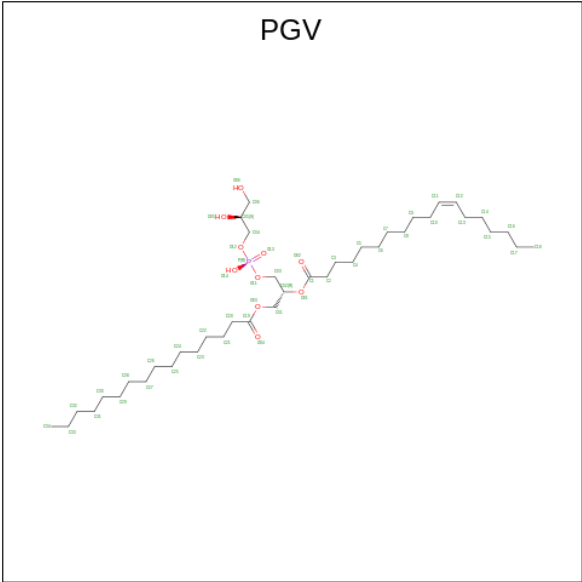
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	A	1	Total	C	O	0	0
			2	1	1		
18	N	1	Total	C	O	0	0
			2	1	1		

- Molecule 19 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: C₅₇H₁₁₀O₆).



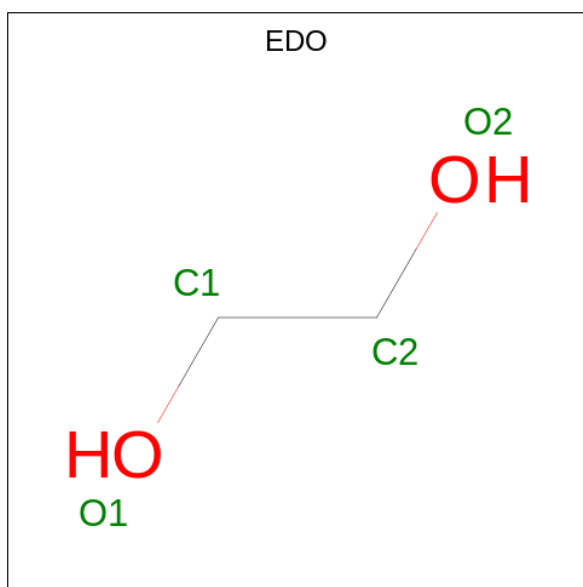
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	A	1	Total	C	O	0	0
			63	57	6		
19	D	1	Total	C	O	0	0
			63	57	6		
19	L	1	Total	C	O	0	0
			63	57	6		
19	N	1	Total	C	O	0	0
			63	57	6		
19	N	1	Total	C	O	0	0
			63	57	6		
19	N	1	Total	C	O	0	0
			63	57	6		

- Molecule 20 is (1R)-2-{{[[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
20	A	1	Total	C	O	P	0	0
			51	40	10	1		
20	A	1	Total	C	O	P	0	0
			51	40	10	1		
20	C	1	Total	C	O	P	0	0
			51	40	10	1		
20	C	1	Total	C	O	P	0	0
			51	40	10	1		
20	G	1	Total	C	O	P	0	0
			51	40	10	1		
20	N	1	Total	C	O	P	0	0
			51	40	10	1		
20	N	1	Total	C	O	P	0	0
			51	40	10	1		
20	P	1	Total	C	O	P	0	0
			51	40	10	1		

- Molecule 21 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



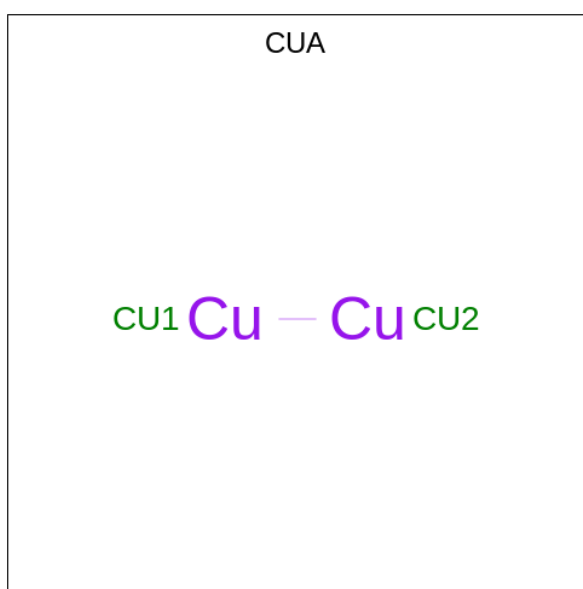
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	B	1	Total	C	O	0	0
			4	2	2		
21	B	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	F	1	Total	C	O	0	0
			4	2	2		
21	G	1	Total	C	O	0	0
			4	2	2		
21	K	1	Total	C	O	0	0
			4	2	2		
21	K	1	Total	C	O	0	0
			4	2	2		

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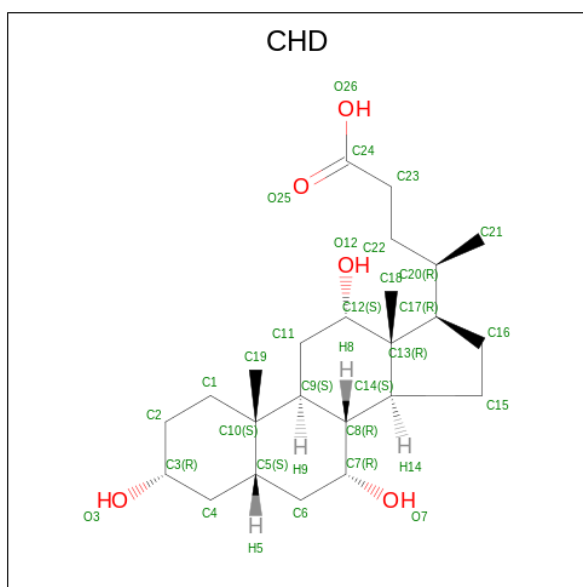
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
21	K	1	Total C O 4 2 2	0	0
21	L	1	Total C O 4 2 2	0	0
21	N	1	Total C O 4 2 2	0	0
21	T	1	Total C O 4 2 2	0	0

- Molecule 22 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



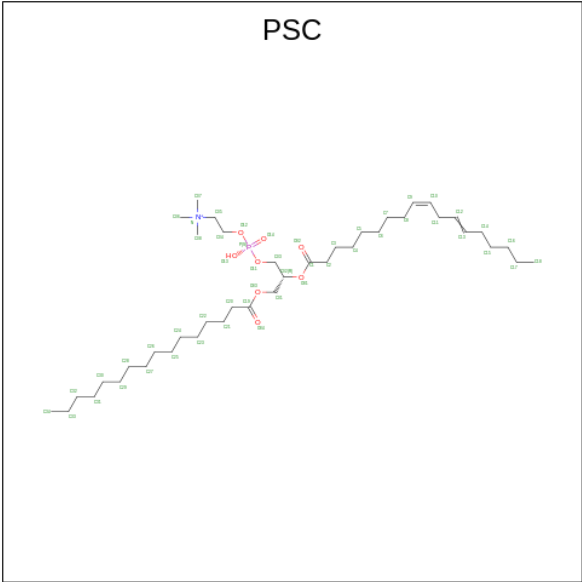
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
22	B	1	Total Cu 2 2	0	0
22	O	1	Total Cu 2 2	0	0

- Molecule 23 is CHOLIC ACID (CCD ID: CHD) (formula: C₂₄H₄₀O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	B	1	Total C O 29 24 5	0	0
23	C	1	Total C O 29 24 5	0	0
23	C	1	Total C O 29 24 5	0	0
23	J	1	Total C O 29 24 5	0	0
23	O	1	Total C O 29 24 5	0	0
23	P	1	Total C O 29 24 5	0	0
23	P	1	Total C O 29 24 5	0	0
23	W	1	Total C O 29 24 5	0	0

- Molecule 24 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (CCD ID: PSC) (formula: C₄₂H₈₁NO₈P).

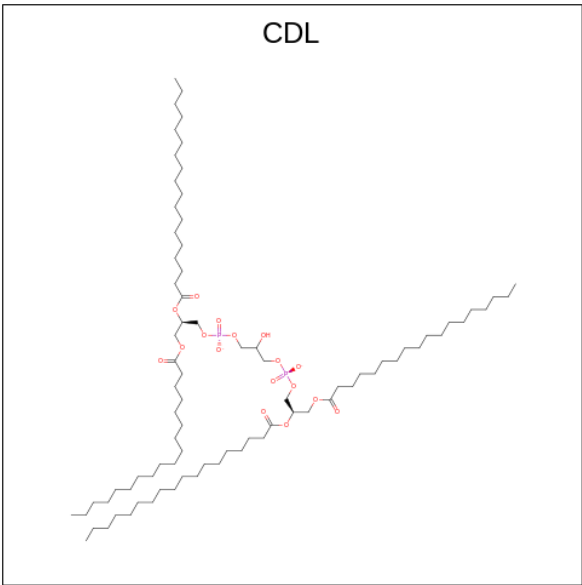


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	B	1	Total	C	N	O	P	0	0
			52	42	1	8	1		
24	R	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

- Molecule 25 is UNKNOWN LIGAND (CCD ID: UNX) (formula: X).

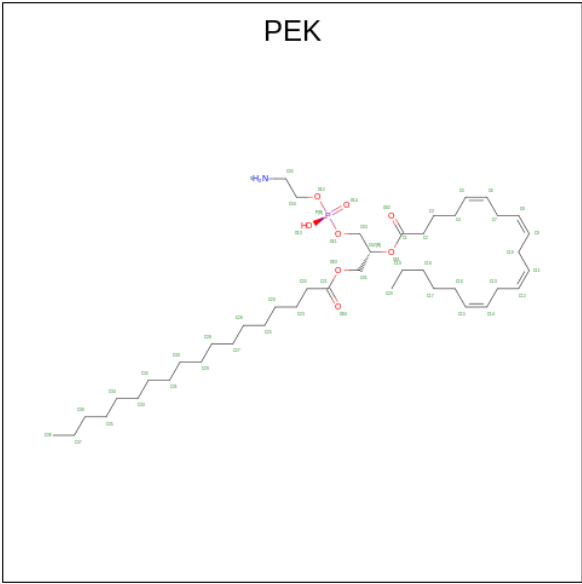
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	C	1	Total	X	0	0
			1	1		
25	P	1	Total	X	0	0
			1	1		

- Molecule 26 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
26	C	1	Total	C	O	P	0	0
			100	81	17	2		
26	C	1	Total	C	O	P	0	0
			100	81	17	2		
26	P	1	Total	C	O	P	0	0
			100	81	17	2		
26	T	1	Total	C	O	P	0	0
			100	81	17	2		

- Molecule 27 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (CCD ID: PEK) (formula: C₄₃H₇₈NO₈P).

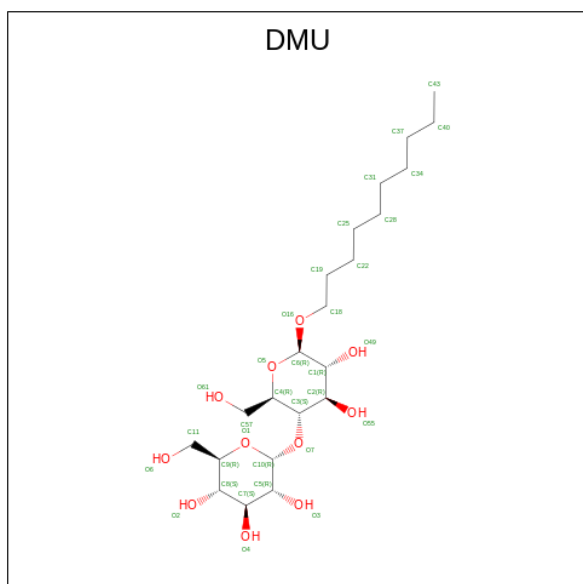


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
27	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
27	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
27	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
27	P	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
27	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
27	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		

- Molecule 28 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	F	1	Total	Zn	0	0
			1	1		
28	S	1	Total	Zn	0	0
			1	1		

- Molecule 29 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
29	M	1	Total	C	O	0	0
			33	22	11		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
29	Z	1	Total	C	O	0	0
			33	22	11		

- Molecule 30 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	A	125	Total	O	0	0
			125	125		
30	B	77	Total	O	0	1
			78	78		
30	C	70	Total	O	0	0
			70	70		
30	D	41	Total	O	0	0
			41	41		
30	E	24	Total	O	0	0
			24	24		
30	F	36	Total	O	0	0
			36	36		
30	G	31	Total	O	0	0
			31	31		
30	H	33	Total	O	0	0
			33	33		
30	I	12	Total	O	0	0
			12	12		
30	J	19	Total	O	0	0
			19	19		
30	K	19	Total	O	0	0
			19	19		
30	L	14	Total	O	0	0
			14	14		
30	M	15	Total	O	0	0
			15	15		
30	N	117	Total	O	0	0
			117	117		
30	O	76	Total	O	0	1
			77	77		
30	P	54	Total	O	0	0
			54	54		
30	Q	29	Total	O	0	0
			29	29		
30	R	29	Total	O	0	0
			29	29		

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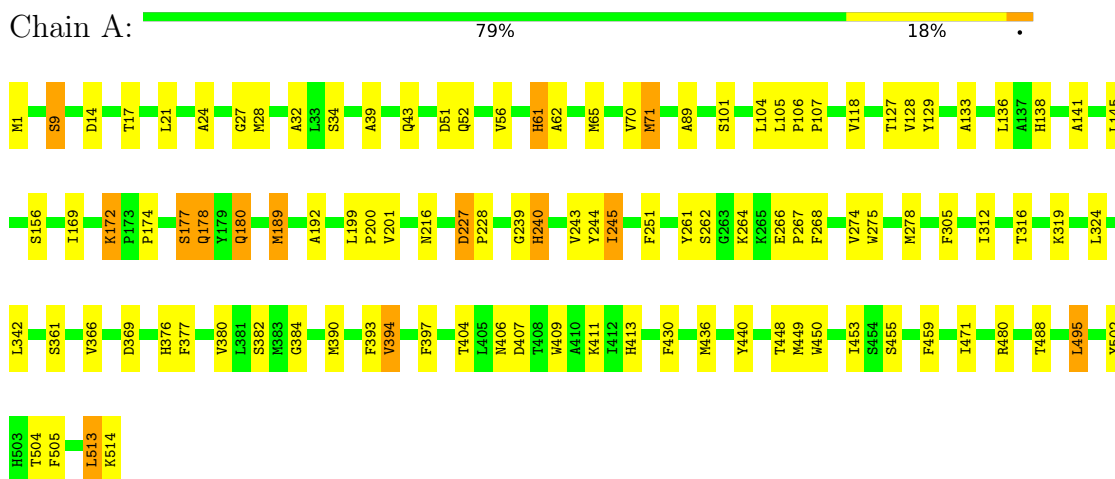
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	S	43	Total 43	O 43	0	0
30	T	20	Total 20	O 20	0	0
30	U	31	Total 31	O 31	0	0
30	V	19	Total 19	O 19	0	0
30	W	17	Total 17	O 17	0	0
30	X	9	Total 9	O 9	0	0
30	Y	6	Total 6	O 6	0	0
30	Z	4	Total 4	O 4	0	0

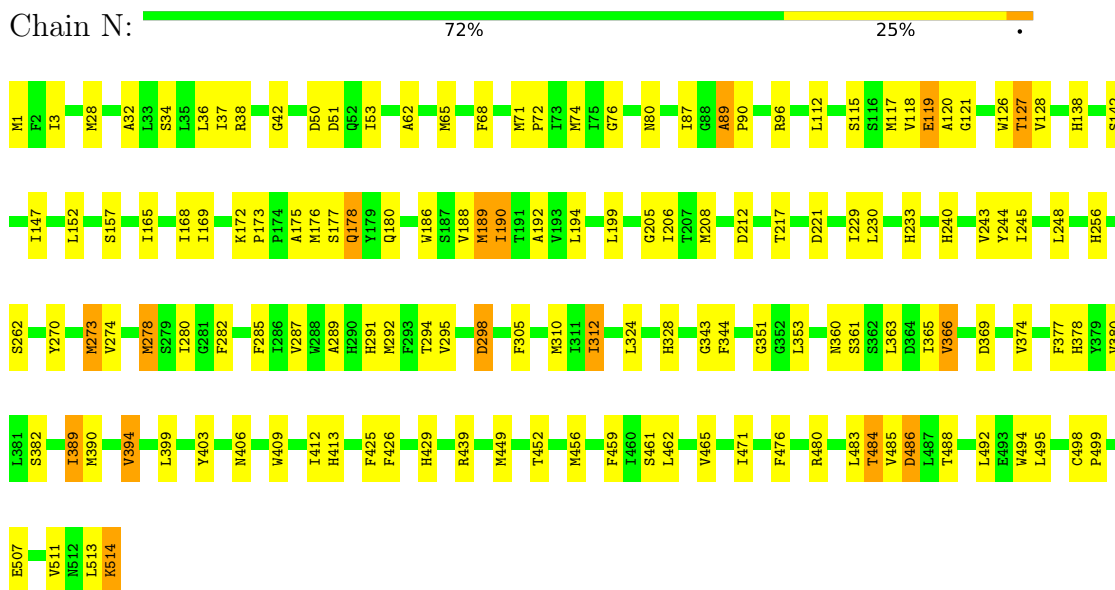
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Cytochrome c oxidase subunit 1

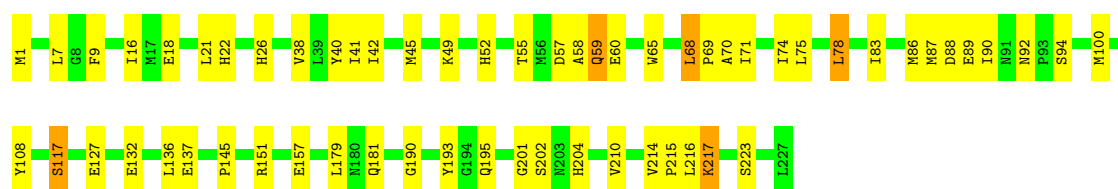


• Molecule 1: Cytochrome c oxidase subunit 1



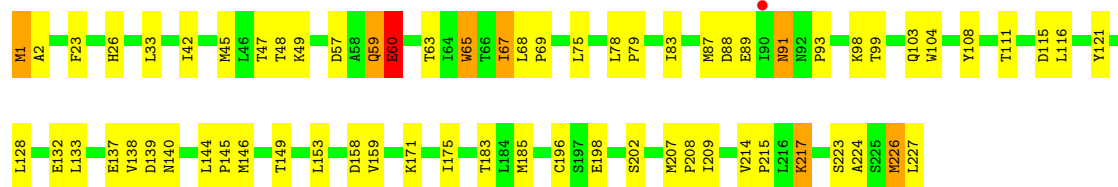
• Molecule 2: Cytochrome c oxidase subunit 2

Chain B:  74% 24% .



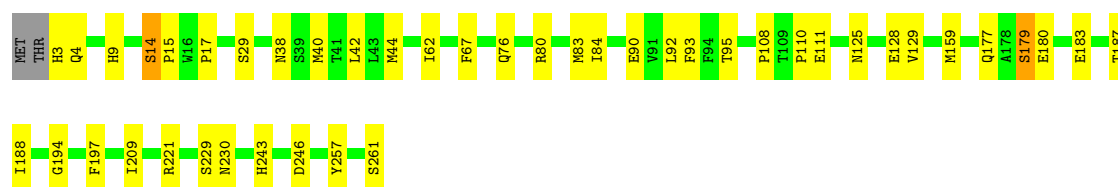
• Molecule 2: Cytochrome c oxidase subunit 2

Chain O:  70% 26% .



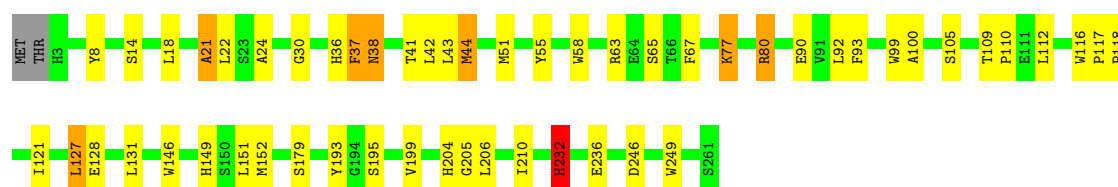
• Molecule 3: Cytochrome c oxidase subunit 3

Chain C:  82% 16% ..



• Molecule 3: Cytochrome c oxidase subunit 3

Chain P:  79% 18% ..

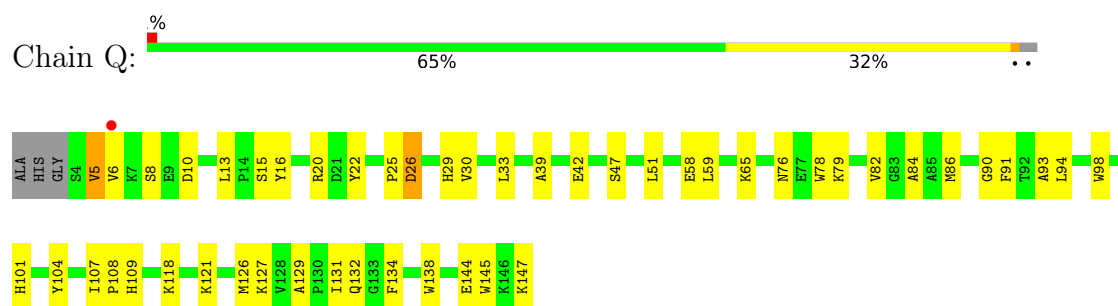


• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial

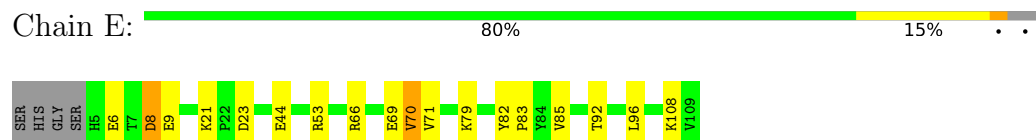
Chain D:  76% 21% ..



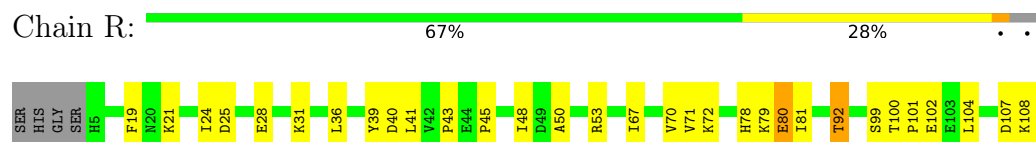
• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



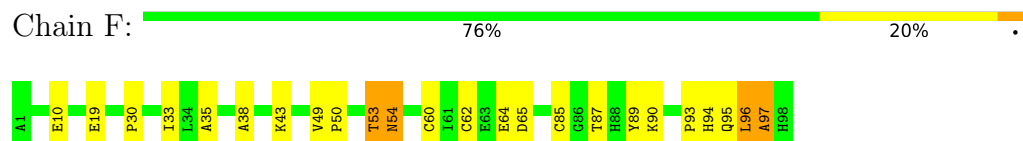
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



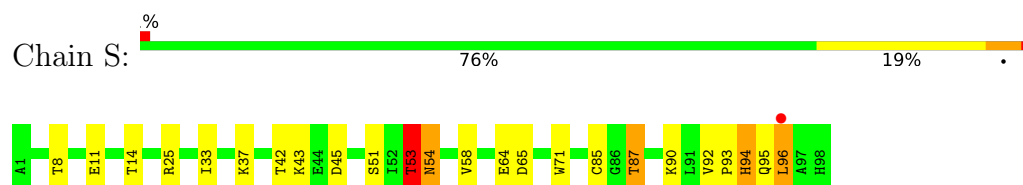
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



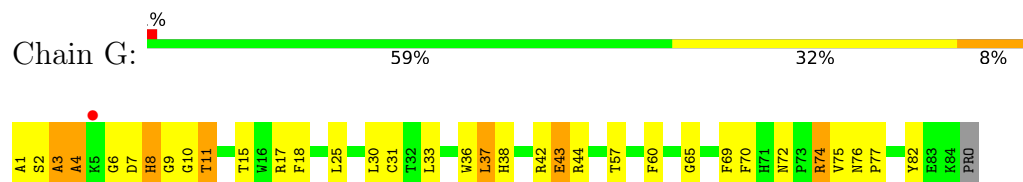
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial

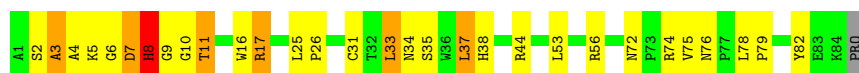


- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial





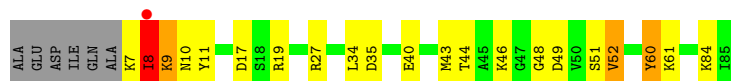
- Molecule 8: Cytochrome c oxidase subunit 6B1

Chain H: 73% 15% 7%



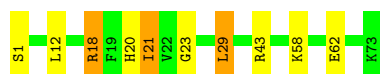
- Molecule 8: Cytochrome c oxidase subunit 6B1

Chain U: 68% 20% 7%



- Molecule 9: Cytochrome c oxidase subunit 6C

Chain I: 86% 10% 7%



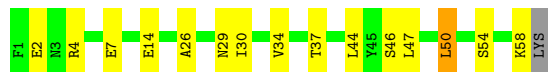
- Molecule 9: Cytochrome c oxidase subunit 6C

Chain V: 66% 29% 7%



- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial

Chain J: 73% 24% 7%



- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial

Chain W: 73% 22% 7%



- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial

Chain K: 71% 12% 12%



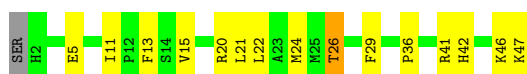
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial

Chain X: 57% 29% 12%



- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial

Chain L: 66% 30% 2%



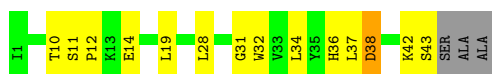
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial

Chain Y: 68% 28% 2%



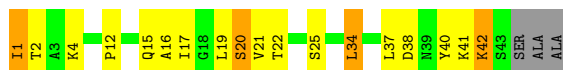
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial

Chain M: 63% 28% 7%



- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial

Chain Z: 54% 30% 9% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	185.85Å 209.49Å 179.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 15.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.7 (15.00-2.40) 97.7 (15.00-2.40)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0048	Depositor
R, R_{free}	0.182 , 0.230 0.182 , 0.230	Depositor DCC
R_{free} test set	13569 reflections (1.08%)	wwPDB-VP
Wilson B-factor (Å ²)	56.1	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.045 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	31717	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CHD, FME, CMO, HEA, ZN, DMU, PSC, TGL, PEK, CUA, CU, MG, PGV, EDO, NA, SAC, UNX, CDL, TPO

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	1.16	5/4164 (0.1%)	1.22	21/5689 (0.4%)
1	N	1.09	5/4156 (0.1%)	1.14	12/5678 (0.2%)
2	B	1.07	3/1860 (0.2%)	1.18	5/2534 (0.2%)
2	O	0.97	1/1860 (0.1%)	1.14	4/2534 (0.2%)
3	C	1.12	1/2197 (0.0%)	1.10	7/3005 (0.2%)
3	P	1.12	2/2197 (0.1%)	1.11	5/3005 (0.2%)
4	D	0.96	0/1229	1.05	2/1658 (0.1%)
4	Q	0.88	1/1229 (0.1%)	1.07	5/1658 (0.3%)
5	E	0.87	0/871	1.06	0/1182
5	R	0.84	0/871	1.02	2/1182 (0.2%)
6	F	0.99	0/765	1.09	1/1038 (0.1%)
6	S	1.01	0/765	1.12	1/1038 (0.1%)
7	G	1.18	1/690 (0.1%)	1.07	1/937 (0.1%)
7	T	1.09	0/690	1.08	2/937 (0.2%)
8	H	0.97	0/682	1.18	1/921 (0.1%)
8	U	0.95	0/682	1.05	1/921 (0.1%)
9	I	0.87	0/605	1.09	0/802
9	V	0.77	0/605	1.07	3/802 (0.4%)
10	J	0.92	0/471	1.05	0/636
10	W	0.85	0/471	1.01	0/636
11	K	0.94	0/398	1.07	0/546
11	X	0.89	0/398	1.12	2/546 (0.4%)
12	L	1.01	0/393	1.16	2/526 (0.4%)
12	Y	0.97	0/393	1.11	0/526
13	M	1.08	0/345	1.17	1/470 (0.2%)
13	Z	0.83	0/345	1.08	0/470
All	All	1.04	19/29332 (0.1%)	1.12	78/39877 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
7	G	0	1
7	T	0	2
All	All	0	3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	198	GLU	CA-C	-6.83	1.44	1.52
1	A	133	ALA	CA-C	6.18	1.61	1.52
1	A	376	HIS	CG-CD2	6.16	1.42	1.35
1	A	376	HIS	ND1-CE1	6.12	1.38	1.32
1	N	256	HIS	CG-CD2	5.63	1.42	1.35
2	B	204	HIS	CG-CD2	5.61	1.42	1.35
1	A	61	HIS	CG-CD2	5.61	1.42	1.35
1	N	429	HIS	CG-CD2	5.56	1.42	1.35
3	P	232	HIS	CG-CD2	5.53	1.42	1.35
1	N	96	ARG	CA-C	5.41	1.59	1.52
1	A	240	HIS	CD2-NE2	-5.31	1.32	1.37
3	P	58	TRP	CD2-CE2	5.26	1.50	1.41
3	C	9	HIS	CD2-NE2	-5.23	1.32	1.37
1	N	126	TRP	CD2-CE2	5.17	1.50	1.41
7	G	6	GLY	N-CA	5.14	1.51	1.45
2	B	26	HIS	CG-CD2	5.06	1.41	1.35
4	Q	109	HIS	CG-CD2	5.06	1.41	1.35
2	B	22	HIS	CG-CD2	5.04	1.41	1.35
1	N	291	HIS	CG-CD2	5.04	1.41	1.35

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	MET	CA-C-N	-8.59	110.08	119.19
1	A	71	MET	C-N-CA	-8.59	110.08	119.19
1	N	287	VAL	N-CA-C	7.98	119.77	112.43
2	B	201	GLY	N-CA-C	7.65	122.70	111.76
6	F	96	LEU	N-CA-C	-7.63	100.92	113.50
1	A	436	MET	CA-C-N	-7.55	112.00	119.78
1	A	436	MET	C-N-CA	-7.55	112.00	119.78
1	A	169	ILE	CB-CA-C	-7.41	102.31	112.24
1	N	89	ALA	CA-C-N	7.37	127.08	119.56
1	N	89	ALA	C-N-CA	7.37	127.08	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	221	ASP	CA-C-N	-7.28	112.14	119.56
1	N	221	ASP	C-N-CA	-7.28	112.14	119.56
1	A	89	ALA	CA-C-N	7.21	126.83	119.19
1	A	89	ALA	C-N-CA	7.21	126.83	119.19
1	A	105	LEU	CA-C-N	-7.04	113.12	120.38
1	A	105	LEU	C-N-CA	-7.04	113.12	120.38
3	P	21	ALA	N-CA-C	-6.93	103.66	111.14
3	P	8	TYR	N-CA-C	6.91	119.44	110.53
9	V	31	PHE	N-CA-C	-6.90	96.10	110.80
11	X	6	ALA	CA-C-N	6.77	128.30	119.84
11	X	6	ALA	C-N-CA	6.77	128.30	119.84
9	V	29	LEU	N-CA-C	-6.75	105.16	113.19
4	D	5	VAL	N-CA-C	6.74	118.28	108.58
2	B	38	VAL	N-CA-C	-6.44	104.21	110.72
6	S	53	THR	CB-CA-C	-6.27	106.56	114.40
2	B	65	TRP	N-CA-C	6.23	120.72	113.18
12	L	11	ILE	CA-C-N	-6.18	113.59	120.45
12	L	11	ILE	C-N-CA	-6.18	113.59	120.45
3	C	129	VAL	CB-CA-C	-6.15	107.83	114.35
3	P	14	SER	CA-C-N	6.14	125.84	119.64
3	P	14	SER	C-N-CA	6.14	125.84	119.64
1	A	192	ALA	N-CA-C	-6.11	104.62	111.28
2	O	214	VAL	CA-C-N	5.99	126.00	119.89
2	O	214	VAL	C-N-CA	5.99	126.00	119.89
3	C	209	ILE	N-CA-C	5.94	116.41	110.23
1	A	9	SER	N-CA-C	5.89	118.36	110.35
13	M	31	GLY	N-CA-C	-5.86	105.27	112.77
5	R	100	THR	CA-C-N	5.85	127.15	119.84
5	R	100	THR	C-N-CA	5.85	127.15	119.84
2	B	190	GLY	N-CA-C	5.68	118.10	110.43
1	A	448	THR	N-CA-C	5.68	117.15	111.07
1	A	141	ALA	N-CA-C	5.64	119.42	112.54
3	C	4	GLN	N-CA-C	5.63	118.61	110.28
1	A	305	PHE	N-CA-C	5.53	117.31	111.28
1	A	70	VAL	N-CA-C	5.51	115.72	110.42
8	H	50	VAL	N-CA-C	-5.46	107.48	113.43
7	G	57	THR	N-CA-C	-5.43	106.57	114.12
1	N	278	MET	N-CA-C	5.41	117.87	111.33
3	P	205	GLY	N-CA-C	-5.38	106.13	112.64
2	O	65	TRP	CB-CA-C	5.38	119.65	110.56
4	Q	22	TYR	CA-C-N	5.31	125.38	119.32
4	Q	22	TYR	C-N-CA	5.31	125.38	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	229	SER	N-CA-C	-5.28	106.81	113.20
1	N	461	SER	N-CA-C	-5.26	105.54	111.28
4	D	116	VAL	N-CA-C	5.24	115.97	110.62
1	N	248	LEU	CA-C-N	-5.23	114.22	119.56
1	N	248	LEU	C-N-CA	-5.23	114.22	119.56
1	A	239	GLY	N-CA-C	5.23	119.21	112.83
4	Q	76	ASN	N-CA-C	5.22	119.28	113.02
9	V	54	TYR	N-CA-C	5.19	117.43	109.07
1	N	192	ALA	N-CA-C	-5.18	105.54	111.14
1	A	453	ILE	N-CA-C	-5.15	105.52	110.72
7	T	75	VAL	N-CA-C	5.14	118.66	113.47
1	A	262	SER	N-CA-C	-5.12	106.72	113.17
2	O	67	ILE	CB-CA-C	-5.11	105.33	112.02
1	A	227	ASP	CA-C-N	5.09	124.88	119.28
1	A	227	ASP	C-N-CA	5.09	124.88	119.28
3	C	14	SER	CA-C-N	5.08	124.70	119.56
3	C	14	SER	C-N-CA	5.08	124.70	119.56
1	N	157	SER	N-CA-C	5.08	116.63	111.14
1	A	216	ASN	N-CA-C	5.06	118.58	111.90
2	B	89	GLU	N-CA-C	5.05	117.22	110.35
8	U	11	TYR	N-CA-C	5.05	117.49	109.96
3	C	194	GLY	N-CA-C	-5.04	106.63	113.24
7	T	8	HIS	N-CA-C	5.03	121.52	110.80
1	N	262	SER	N-CA-C	-5.02	106.85	113.17
4	Q	13	LEU	CA-C-N	5.01	125.29	119.93
4	Q	13	LEU	C-N-CA	5.01	125.29	119.93

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	G	11	TPO	Peptide
7	T	10	GLY	Peptide
7	T	11	TPO	Peptide

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	4030	0	4009	78	0
1	N	4027	0	4002	113	0
2	B	1824	0	1833	37	0
2	O	1824	0	1833	45	0
3	C	2110	0	2027	33	0
3	P	2110	0	2027	45	0
4	D	1195	0	1183	22	0
4	Q	1195	0	1183	32	0
5	E	852	0	845	9	0
5	R	852	0	845	22	0
6	F	748	0	728	13	0
6	S	748	0	728	19	0
7	G	675	0	643	30	0
7	T	675	0	643	24	0
8	H	662	0	623	13	0
8	U	662	0	623	11	0
9	I	601	0	613	9	0
9	V	601	0	613	25	0
10	J	460	0	459	9	0
10	W	460	0	459	11	0
11	K	384	0	366	6	0
11	X	384	0	366	14	0
12	L	380	0	380	13	0
12	Y	380	0	380	16	0
13	M	335	0	352	8	0
13	Z	335	0	352	19	0
14	A	120	0	108	12	0
14	N	120	0	108	13	0
15	A	1	0	0	0	0
15	N	1	0	0	0	0
16	A	1	0	0	0	0
16	N	1	0	0	0	0
17	A	1	0	0	0	0
17	N	1	0	0	0	0
18	A	2	0	0	1	0
18	N	2	0	0	0	0
19	A	63	0	110	3	0
19	D	63	0	110	1	0
19	L	63	0	110	4	0
19	N	189	0	330	12	0
20	A	102	0	152	3	0
20	C	102	0	152	0	0
20	G	51	0	76	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	N	102	0	152	8	0
20	P	51	0	76	3	0
21	A	20	0	30	9	0
21	B	8	0	12	1	0
21	C	12	0	18	0	0
21	F	4	0	6	0	0
21	G	4	0	6	0	0
21	K	12	0	18	0	0
21	L	4	0	6	0	0
21	N	4	0	6	1	0
21	T	4	0	6	2	0
22	B	2	0	0	0	0
22	O	2	0	0	0	0
23	B	29	0	39	1	0
23	C	58	0	78	3	0
23	J	29	0	39	1	0
23	O	29	0	39	1	0
23	P	58	0	78	2	0
23	W	29	0	38	1	0
24	B	52	0	80	12	0
24	R	52	0	80	6	0
25	C	1	0	0	0	0
25	P	1	0	0	0	0
26	C	200	0	312	15	0
26	P	100	0	156	8	0
26	T	100	0	156	13	0
27	C	53	0	77	3	0
27	G	106	0	154	10	0
27	P	53	0	77	4	0
27	T	106	0	154	4	0
28	F	1	0	0	0	0
28	S	1	0	0	0	0
29	M	33	0	42	1	0
29	Z	33	0	42	1	0
30	A	125	0	0	22	0
30	B	78	0	0	6	0
30	C	70	0	0	18	0
30	D	41	0	0	2	0
30	E	24	0	0	2	0
30	F	36	0	0	2	0
30	G	31	0	0	2	0
30	H	33	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	I	12	0	0	0	0
30	J	19	0	0	2	0
30	K	19	0	0	3	0
30	L	14	0	0	2	0
30	M	15	0	0	1	0
30	N	117	0	0	16	0
30	O	77	0	0	8	0
30	P	54	0	0	5	0
30	Q	29	0	0	7	0
30	R	29	0	0	3	0
30	S	43	0	0	4	0
30	T	20	0	0	6	0
30	U	31	0	0	3	0
30	V	19	0	0	4	0
30	W	17	0	0	1	0
30	X	9	0	0	4	0
30	Y	6	0	0	1	0
30	Z	4	0	0	0	0
All	All	31717	0	31348	701	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 11.

All (701) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:240:HIS:NE2	1:N:244:TYR:CE2	1.73	1.45
1:A:240:HIS:NE2	1:A:244:TYR:HE2	1.01	1.42
1:A:240:HIS:NE2	1:A:244:TYR:CE2	1.78	1.30
1:A:240:HIS:CD2	1:A:244:TYR:HE2	1.49	1.29
1:N:240:HIS:NE2	1:N:244:TYR:HE2	0.80	1.28
5:R:50:ALA:HB3	30:R:303:HOH:O	1.43	1.18
6:S:85:CYS:SG	6:S:87:THR:CG2	2.30	1.18
9:V:26:MET:O	9:V:30:GLY:HA3	1.44	1.15
1:N:298:ASP:HB2	30:N:724:HOH:O	1.49	1.11
6:S:85:CYS:SG	6:S:87:THR:HG22	1.90	1.10
3:P:118:PRO:HD2	30:P:403:HOH:O	1.53	1.08
8:H:9:LYS:HD3	8:H:10:ASN:H	1.12	1.08
5:R:41:LEU:HD23	24:R:201:PSC:H082	1.31	1.08
26:C:307:CDL:H221	26:C:307:CDL:H511	1.12	1.05
1:A:240:HIS:CD2	1:A:244:TYR:CE2	2.33	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:50:ASP:HB3	1:N:53:ILE:HD12	1.39	1.02
6:F:19:GLU:HG2	30:F:231:HOH:O	1.60	1.01
2:O:223:SER:HA	30:O:414:HOH:O	1.61	1.01
24:R:201:PSC:H031	24:R:201:PSC:H211	1.44	0.99
9:V:15:ARG:HD3	30:V:113:HOH:O	1.62	0.98
1:A:104:LEU:HB2	30:A:788:HOH:O	1.64	0.97
1:N:353:LEU:HA	30:N:715:HOH:O	1.65	0.96
26:C:307:CDL:H221	26:C:307:CDL:C51	1.94	0.96
7:G:76:ASN:HD21	27:G:101:PEK:HN2	1.14	0.95
6:S:85:CYS:SG	6:S:87:THR:HG23	2.04	0.95
19:N:609:TGL:OC1	30:N:701:HOH:O	1.84	0.94
8:H:9:LYS:HD3	8:H:10:ASN:N	1.82	0.94
2:B:57:ASP:H	24:B:303:PSC:H241	1.33	0.94
12:L:47:LYS:HB2	13:M:43:SER:HB3	1.48	0.94
3:C:90:GLU:HA	30:C:413:HOH:O	1.67	0.92
1:N:240:HIS:CE1	1:N:244:TYR:HE2	1.86	0.92
1:N:439:ARG:NH2	30:N:702:HOH:O	2.01	0.92
6:S:54:ASN:HD22	6:S:54:ASN:H	1.18	0.91
30:A:799:HOH:O	12:L:36:PRO:HB2	1.72	0.89
1:N:240:HIS:CD2	1:N:244:TYR:HE2	1.88	0.89
19:N:609:TGL:CC1	30:N:701:HOH:O	2.19	0.89
2:B:90:ILE:HA	30:B:464:HOH:O	1.71	0.88
4:Q:107:ILE:HB	30:Q:202:HOH:O	1.73	0.88
11:K:24:PHE:O	11:K:28:VAL:HG12	1.74	0.87
11:X:42:PRO:HD2	30:X:101:HOH:O	1.72	0.87
9:V:32:ALA:O	30:V:101:HOH:O	1.93	0.87
19:A:607:TGL:H201	19:A:607:TGL:H361	1.55	0.86
7:G:10:GLY:HA3	1:N:177:SER:HB2	1.55	0.86
30:A:751:HOH:O	8:H:23:GLN:HG3	1.74	0.86
1:A:39:ALA:HA	21:A:614:EDO:H21	1.56	0.85
11:K:48:VAL:HB	30:K:207:HOH:O	1.77	0.84
4:Q:93:ALA:HB1	30:X:102:HOH:O	1.76	0.84
26:T:103:CDL:H531	26:T:103:CDL:H241	1.60	0.84
7:G:3:ALA:HB2	27:G:102:PEK:H292	1.60	0.84
1:A:243:VAL:HG21	18:A:606:CMO:C	2.08	0.83
9:V:30:GLY:C	9:V:32:ALA:N	2.28	0.83
1:N:240:HIS:CD2	1:N:244:TYR:CE2	2.63	0.83
11:X:54:ARG:HH21	11:X:54:ARG:HG3	1.44	0.82
19:N:611:TGL:OC1	19:N:611:TGL:HC42	1.80	0.81
19:N:611:TGL:H231	19:N:611:TGL:H282	1.62	0.81
20:N:607:PGV:H011	13:Z:15:GLN:HE22	1.43	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:226:MET:HB2	30:O:414:HOH:O	1.81	0.81
7:T:79:PRO:HD3	30:T:201:HOH:O	1.80	0.80
3:C:90:GLU:HG2	30:C:413:HOH:O	1.80	0.80
7:G:9:GLY:HA3	1:N:172:LYS:HZ1	1.47	0.80
26:C:307:CDL:H771	26:C:307:CDL:H542	1.64	0.80
26:T:103:CDL:H222	26:T:103:CDL:H511	1.63	0.79
1:A:513:LEU:O	1:A:514:LYS:HB2	1.82	0.79
21:A:613:EDO:H11	11:K:39:GLU:H	1.45	0.79
9:V:26:MET:O	9:V:30:GLY:CA	2.30	0.79
24:B:303:PSC:H202	24:B:303:PSC:H272	1.64	0.78
1:A:61:HIS:CD2	30:A:754:HOH:O	2.36	0.78
2:B:210:VAL:HG13	30:B:415:HOH:O	1.84	0.78
3:C:62:ILE:HG12	30:C:404:HOH:O	1.84	0.77
12:Y:17:ASN:HB3	12:Y:20:ARG:NH1	2.00	0.77
6:S:54:ASN:H	6:S:54:ASN:ND2	1.82	0.76
9:V:29:LEU:O	9:V:32:ALA:HB2	1.85	0.75
6:F:64:GLU:O	6:F:65:ASP:HB2	1.84	0.75
7:T:17:ARG:HH22	27:T:102:PEK:H041	1.51	0.75
5:R:31:LYS:HE2	30:S:229:HOH:O	1.85	0.74
12:L:47:LYS:HB2	13:M:43:SER:CB	2.18	0.74
1:N:513:LEU:O	1:N:514:LYS:HB2	1.86	0.74
11:X:29:TRP:HA	30:X:102:HOH:O	1.88	0.73
1:N:406:ASN:HD21	20:N:607:PGV:C03	2.00	0.73
13:Z:1:ILE:O	13:Z:1:ILE:HG13	1.86	0.73
10:W:30:ILE:O	10:W:34:VAL:HG23	1.88	0.73
26:T:103:CDL:H381	26:T:103:CDL:H141	1.70	0.73
6:S:92:VAL:HG11	30:S:240:HOH:O	1.89	0.72
3:C:221:ARG:CZ	30:C:404:HOH:O	2.38	0.72
9:V:30:GLY:O	9:V:31:PHE:C	2.33	0.72
1:A:104:LEU:CB	30:A:788:HOH:O	2.29	0.72
26:C:307:CDL:H511	26:C:307:CDL:C22	2.06	0.72
14:N:602:HEA:HBC1	14:N:602:HEA:HMC1	1.72	0.71
1:N:406:ASN:HD21	20:N:607:PGV:H031	1.53	0.71
7:G:44:ARG:HG2	30:G:224:HOH:O	1.90	0.71
6:F:93:PRO:HA	30:F:225:HOH:O	1.90	0.71
14:A:602:HEA:HBC1	14:A:602:HEA:HMC1	1.73	0.71
9:V:29:LEU:C	9:V:32:ALA:HB2	2.15	0.71
26:C:307:CDL:H871	27:G:102:PEK:H322	1.72	0.71
1:N:240:HIS:CE1	1:N:244:TYR:CE2	2.69	0.71
2:O:57:ASP:HB2	24:R:201:PSC:H202	1.72	0.70
1:N:274:VAL:HG12	1:N:278:MET:HE2	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Y:17:ASN:HB3	12:Y:20:ARG:HH12	1.54	0.70
1:N:115:SER:O	1:N:121:GLY:HA2	1.92	0.70
2:O:139:ASP:OD1	2:O:140:ASN:N	2.23	0.70
2:O:217:LYS:NZ	2:O:217:LYS:H	1.89	0.70
3:C:29:SER:HB3	3:C:42:LEU:HD13	1.74	0.70
1:N:50:ASP:HB3	1:N:53:ILE:CD1	2.21	0.69
1:A:62:ALA:HA	30:A:754:HOH:O	1.91	0.69
8:U:9:LYS:HB2	30:U:114:HOH:O	1.92	0.69
1:N:65:MET:HB3	14:N:601:HEA:CBC	2.23	0.69
1:N:406:ASN:ND2	20:N:607:PGV:H031	2.07	0.69
3:P:18:LEU:O	3:P:22:LEU:HD12	1.93	0.68
20:A:608:PGV:H332	30:C:413:HOH:O	1.93	0.68
27:P:302:PEK:H131	20:P:303:PGV:H181	1.75	0.68
9:V:28:SER:C	9:V:30:GLY:H	1.98	0.68
12:Y:47:LYS:HB2	13:Z:42:LYS:CD	2.23	0.68
7:T:72:ASN:H	7:T:76:ASN:HD22	1.39	0.68
10:W:9:GLN:O	10:W:13:GLN:HG3	1.94	0.68
4:D:112:GLU:HB3	30:D:328:HOH:O	1.93	0.67
6:S:54:ASN:HD22	6:S:54:ASN:N	1.86	0.67
1:N:390:MET:HE2	1:N:413:HIS:HE1	1.59	0.67
3:P:36:HIS:C	3:P:38:ASN:H	2.02	0.67
1:A:32:ALA:HB1	30:A:799:HOH:O	1.94	0.67
2:B:18:GLU:OE1	21:B:305:EDO:O1	2.11	0.67
14:A:601:HEA:H212	30:A:743:HOH:O	1.95	0.66
7:G:3:ALA:HA	27:G:102:PEK:H331	1.78	0.66
26:C:307:CDL:OA7	26:C:307:CDL:H351	1.96	0.66
1:N:165:ILE:HA	30:N:805:HOH:O	1.93	0.66
1:N:194:LEU:HD22	1:N:285:PHE:CE2	2.31	0.66
9:V:30:GLY:C	9:V:32:ALA:H	2.00	0.66
1:A:156:SER:HB2	30:A:788:HOH:O	1.96	0.66
26:C:307:CDL:OB4	26:C:307:CDL:H161	1.96	0.66
2:B:127:GLU:HG2	30:B:432:HOH:O	1.95	0.65
1:A:505:PHE:HA	30:A:702:HOH:O	1.96	0.65
4:D:109:HIS:HD2	30:D:317:HOH:O	1.79	0.65
4:Q:121:LYS:HB2	11:X:50:PRO:HB3	1.78	0.65
1:N:194:LEU:HD22	1:N:285:PHE:HE2	1.61	0.65
3:C:257:TYR:O	3:C:261:SER:HB3	1.97	0.64
7:G:72:ASN:H	7:G:76:ASN:HD22	1.45	0.64
1:N:312:ILE:HD13	1:N:312:ILE:O	1.97	0.64
27:C:306:PEK:H031	30:C:412:HOH:O	1.97	0.64
3:P:36:HIS:O	3:P:38:ASN:N	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:147:ILE:HG23	1:N:206:ILE:HD12	1.78	0.63
2:O:207:MET:HG3	30:O:402:HOH:O	1.98	0.63
1:A:455:SER:HB3	21:A:614:EDO:H12	1.79	0.63
1:A:390:MET:HE2	1:A:413:HIS:HE1	1.63	0.63
1:N:353:LEU:HD23	30:N:715:HOH:O	1.97	0.63
1:N:488:THR:HB	1:N:495:LEU:HD13	1.79	0.63
1:A:24:ALA:HB2	30:A:723:HOH:O	1.98	0.62
5:R:80:GLU:H	5:R:80:GLU:CD	2.06	0.62
26:C:307:CDL:H541	26:C:307:CDL:H752	1.79	0.62
2:O:196:CYS:HB3	30:O:402:HOH:O	1.98	0.62
13:Z:17:ILE:O	13:Z:21:VAL:HG23	1.98	0.62
1:N:484:THR:HB	13:Z:2:THR:OG1	2.00	0.62
11:X:39:GLU:HB3	30:X:106:HOH:O	1.98	0.62
1:A:240:HIS:O	1:A:243:VAL:HG22	1.98	0.61
8:H:7:LYS:C	8:H:8:ILE:HG13	2.26	0.61
4:Q:108:PRO:HD2	30:Q:202:HOH:O	1.98	0.61
12:Y:47:LYS:HB2	13:Z:42:LYS:HD3	1.81	0.61
7:G:17:ARG:HD3	30:O:433:HOH:O	2.00	0.61
27:P:302:PEK:HN2	7:T:76:ASN:HD21	1.48	0.61
26:C:307:CDL:H511	26:C:307:CDL:H241	1.83	0.61
3:P:112:LEU:HD13	3:P:118:PRO:HG3	1.83	0.61
6:F:85:CYS:SG	6:F:87:THR:HG23	2.41	0.60
14:N:602:HEA:C26	30:N:715:HOH:O	2.49	0.60
9:V:31:PHE:C	9:V:31:PHE:CD1	2.78	0.60
26:T:103:CDL:H241	26:T:103:CDL:C53	2.31	0.60
14:N:601:HEA:HBC1	14:N:601:HEA:CMC	2.31	0.60
1:N:175:ALA:HB3	1:N:511:VAL:HG12	1.83	0.60
7:G:10:GLY:HA3	1:N:177:SER:CB	2.31	0.60
4:Q:78:TRP:O	4:Q:82:VAL:HG23	2.00	0.60
3:P:146:TRP:CZ2	7:T:17:ARG:HG3	2.37	0.60
4:Q:26:ASP:OD1	4:Q:26:ASP:N	2.33	0.60
14:A:601:HEA:C1D	30:A:754:HOH:O	2.49	0.60
12:L:20:ARG:NH2	19:L:101:TGL:HC31	2.16	0.60
1:N:390:MET:HE2	1:N:413:HIS:CE1	2.37	0.60
3:P:116:TRP:HA	3:P:117:PRO:C	2.26	0.60
6:S:43:LYS:HG3	30:S:236:HOH:O	2.02	0.60
12:Y:35:ALA:HB3	12:Y:36:PRO:HD3	1.83	0.60
1:A:488:THR:HB	1:A:495:LEU:HD11	1.84	0.59
3:C:125:ASN:HB3	3:C:128:GLU:OE2	2.01	0.59
3:C:221:ARG:NH2	30:C:404:HOH:O	2.35	0.59
1:N:32:ALA:HB3	12:Y:36:PRO:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:68:PHE:HE2	1:N:112:LEU:HD22	1.67	0.59
3:P:146:TRP:HB2	7:T:16:TRP:HB3	1.84	0.59
10:J:4:ARG:HD2	10:J:7:GLU:OE1	2.03	0.59
13:Z:16:ALA:O	13:Z:20:SER:OG	2.20	0.59
30:A:812:HOH:O	26:T:103:CDL:HB22	2.03	0.59
3:P:246:ASP:HB2	30:P:442:HOH:O	2.03	0.59
1:N:62:ALA:HB2	14:N:601:HEA:HBD1	1.84	0.58
1:N:280:ILE:HG12	1:N:312:ILE:HD11	1.83	0.58
1:A:156:SER:CB	30:A:788:HOH:O	2.49	0.58
5:E:71:VAL:HG11	5:E:85:VAL:HG11	1.85	0.58
1:N:390:MET:O	1:N:394:VAL:HG13	2.03	0.58
7:T:31:CYS:SG	26:T:103:CDL:H532	2.42	0.58
30:B:404:HOH:O	9:I:23:GLY:HA3	2.04	0.58
2:O:116:LEU:HD11	2:O:226:MET:HG2	1.84	0.58
2:B:52:HIS:HE1	24:B:303:PSC:H201	1.69	0.58
3:C:188:ILE:HG22	27:G:101:PEK:O13	2.04	0.58
5:E:8:ASP:HB2	30:E:219:HOH:O	2.04	0.58
14:N:601:HEA:HBC1	14:N:601:HEA:HMC3	1.86	0.58
20:N:607:PGV:H202	13:Z:12:PRO:HG3	1.85	0.57
9:V:19:PHE:CD1	9:V:19:PHE:C	2.82	0.57
1:N:37:ILE:CG2	14:N:601:HEA:HMA	2.34	0.57
1:N:476:PHE:HZ	19:N:611:TGL:H251	1.70	0.57
19:N:610:TGL:H302	4:Q:86:MET:HE3	1.85	0.57
8:U:7:LYS:C	8:U:8:ILE:HG13	2.30	0.57
1:A:27:GLY:HA3	30:A:743:HOH:O	2.02	0.57
1:A:488:THR:HB	1:A:495:LEU:CD1	2.35	0.57
6:S:64:GLU:HB2	30:S:230:HOH:O	2.05	0.56
10:W:9:GLN:O	10:W:13:GLN:CG	2.53	0.56
1:N:142:SER:HB2	30:N:785:HOH:O	2.03	0.56
5:R:108:LYS:O	5:R:109:VAL:C	2.48	0.56
12:Y:46:LYS:HA	30:Y:102:HOH:O	2.04	0.56
2:B:41:ILE:O	2:B:45:MET:HG2	2.06	0.56
1:N:310:MET:HE1	1:N:360:ASN:OD1	2.04	0.56
1:A:43:GLN:HG2	4:D:104:TYR:CD1	2.40	0.56
1:A:251:PHE:CD2	1:A:319:LYS:HE2	2.41	0.56
3:P:206:LEU:HD22	27:P:302:PEK:H102	1.87	0.56
7:T:56:ARG:NH2	30:T:201:HOH:O	2.39	0.56
4:Q:108:PRO:CD	30:Q:202:HOH:O	2.54	0.56
7:G:7:ASP:O	7:G:8:HIS:HB2	2.06	0.56
3:C:3:HIS:HB2	30:C:444:HOH:O	2.05	0.55
7:G:31:CYS:HA	30:G:207:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:V:28:SER:C	9:V:30:GLY:N	2.64	0.55
4:Q:39:ALA:O	4:Q:42:GLU:HB2	2.05	0.55
4:Q:101:HIS:HB3	30:Q:218:HOH:O	2.06	0.55
3:P:118:PRO:CD	30:P:403:HOH:O	2.27	0.55
7:G:8:HIS:HE1	27:G:102:PEK:H051	1.71	0.55
11:K:44:PRO:HB2	30:K:207:HOH:O	2.07	0.55
2:O:98:LYS:HG2	2:O:153:LEU:HB2	1.89	0.55
7:G:8:HIS:CE1	27:G:102:PEK:H051	2.41	0.55
1:A:449:MET:HE2	11:K:40:TRP:HB3	1.89	0.55
19:N:609:TGL:H222	19:N:609:TGL:HA71	1.88	0.55
23:P:306:CHD:H12	23:P:306:CHD:H212	1.89	0.55
10:W:26:ALA:O	10:W:30:ILE:HD13	2.07	0.55
9:V:31:PHE:CD1	9:V:32:ALA:N	2.74	0.54
2:B:151:ARG:HD3	2:B:181:GLN:HE21	1.73	0.54
9:V:30:GLY:O	9:V:32:ALA:N	2.39	0.54
2:B:217:LYS:HG3	30:B:458:HOH:O	2.06	0.54
3:C:90:GLU:CA	30:C:413:HOH:O	2.37	0.54
3:C:246:ASP:HB2	30:C:455:HOH:O	2.06	0.54
1:N:229:ILE:HD11	2:O:175:ILE:HD13	1.90	0.54
1:N:233:HIS:CE1	1:N:292:MET:HE1	2.43	0.54
7:T:78:LEU:HB3	7:T:79:PRO:HD2	1.90	0.54
1:A:409:TRP:HB3	1:A:471:ILE:HG12	1.89	0.54
1:A:240:HIS:CD2	1:A:244:TYR:CD2	2.94	0.54
2:B:9:PHE:HB2	2:B:21:LEU:HD21	1.90	0.54
8:U:40:GLU:HB2	30:U:105:HOH:O	2.08	0.54
9:V:64:ARG:NH1	9:V:73:LYS:O	2.40	0.54
12:Y:24:MET:HA	12:Y:24:MET:HE2	1.88	0.53
3:P:65:SER:HB2	20:P:303:PGV:H041	1.90	0.53
26:C:307:CDL:H662	20:G:103:PGV:H172	1.90	0.53
1:N:483:LEU:HG	13:Z:4:LYS:HG2	1.90	0.53
12:Y:20:ARG:HB3	12:Y:20:ARG:CZ	2.38	0.53
1:N:127:THR:HG23	30:N:702:HOH:O	2.07	0.53
1:A:51:ASP:HB2	2:B:202:SER:O	2.09	0.53
2:O:91:ASN:HD22	2:O:93:PRO:HD3	1.72	0.53
3:C:67:PHE:HE2	26:C:303:CDL:H1	1.74	0.53
20:N:608:PGV:H251	20:N:608:PGV:H51	1.91	0.53
2:O:1:FME:HE1	2:O:133:LEU:HD22	1.90	0.53
2:O:89:GLU:O	2:O:91:ASN:OD1	2.27	0.53
7:T:3:ALA:HB2	27:T:101:PEK:H351	1.89	0.53
2:O:226:MET:HA	2:O:226:MET:HE3	1.89	0.53
4:D:110:THR:HG22	4:D:115:TRP:CE2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:486:ASP:OD1	1:N:486:ASP:N	2.38	0.53
1:A:502:TYR:OH	21:A:612:EDO:H22	2.09	0.53
7:G:72:ASN:N	7:G:76:ASN:HD22	2.07	0.53
7:G:37:LEU:O	7:G:38:HIS:ND1	2.42	0.52
1:N:374:VAL:HA	1:N:377:PHE:CE2	2.43	0.52
26:P:304:CDL:H432	26:P:304:CDL:H331	1.90	0.52
10:W:29:ASN:HD22	10:W:29:ASN:H	1.57	0.52
1:A:177:SER:H	1:A:180:GLN:NE2	2.07	0.52
1:N:365:ILE:HB	30:N:704:HOH:O	2.09	0.52
5:R:102:GLU:OE1	5:R:102:GLU:N	2.40	0.52
23:J:101:CHD:H183	23:J:101:CHD:H212	1.91	0.52
7:T:37:LEU:HD21	26:T:103:CDL:H401	1.91	0.52
5:R:99:SER:HB2	5:R:104:LEU:HD21	1.91	0.52
26:C:307:CDL:H522	26:C:307:CDL:H712	1.92	0.52
1:N:87:ILE:O	1:N:173:PRO:HD3	2.09	0.52
21:A:613:EDO:O2	4:D:100:LYS:HE2	2.10	0.52
4:D:99:GLU:O	4:D:103:VAL:HB	2.09	0.52
2:B:90:ILE:HD12	2:B:90:ILE:H	1.74	0.52
2:O:63:THR:O	2:O:67:ILE:HG12	2.09	0.52
3:P:18:LEU:HG	3:P:22:LEU:CD1	2.40	0.52
5:R:45:PRO:HD3	9:V:9:MET:HE1	1.90	0.52
10:J:54:SER:O	12:L:46:LYS:HE3	2.10	0.52
1:N:459:PHE:O	1:N:462:LEU:HB3	2.09	0.52
7:G:4:ALA:HB1	1:N:282:PHE:HA	1.91	0.51
2:O:139:ASP:O	9:V:70:GLN:NE2	2.43	0.51
2:O:217:LYS:H	2:O:217:LYS:HZ3	1.56	0.51
1:A:514:LYS:HA	6:F:38:ALA:HB3	1.90	0.51
9:V:19:PHE:C	9:V:19:PHE:HD1	2.18	0.51
4:D:130:PRO:HA	4:D:135:SER:HB2	1.92	0.51
3:P:63:ARG:HE	26:P:304:CDL:HA22	1.75	0.51
2:B:108:TYR:O	2:B:117:SER:HA	2.11	0.51
7:T:8:HIS:CE1	27:T:101:PEK:H312	2.46	0.51
8:H:44:THR:C	8:H:46:LYS:H	2.19	0.51
11:X:42:PRO:O	11:X:47:ARG:NH2	2.43	0.51
1:A:177:SER:H	1:A:180:GLN:HE21	1.59	0.50
7:G:60:PHE:O	7:G:65:GLY:HA2	2.12	0.50
1:A:393:PHE:O	1:A:397:PHE:HB2	2.11	0.50
1:N:492:LEU:HD13	6:S:71:TRP:CD2	2.47	0.50
14:A:602:HEA:HMC1	14:A:602:HEA:CBC	2.40	0.50
4:D:34:SER:H	4:D:37:GLN:NE2	2.08	0.50
2:O:83:ILE:O	2:O:87:MET:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:SER:CA	30:A:788:HOH:O	2.60	0.50
1:N:366:VAL:N	30:N:704:HOH:O	2.34	0.50
1:A:14:ASP:O	1:A:17:THR:HB	2.11	0.50
8:H:60:TYR:CD1	8:H:60:TYR:C	2.90	0.50
5:R:109:VAL:HG23	5:R:109:VAL:O	2.10	0.50
1:N:68:PHE:O	1:N:72:PRO:HG2	2.11	0.50
5:R:53:ARG:NH2	5:R:92:THR:HG23	2.27	0.50
1:A:201:VAL:HA	30:A:720:HOH:O	2.10	0.50
3:C:187:THR:HG22	27:G:101:PEK:H051	1.94	0.50
12:L:15:VAL:HG12	12:L:21:LEU:HD22	1.94	0.50
1:N:76:GLY:O	1:N:80:ASN:HB2	2.11	0.50
14:N:602:HEA:H263	30:N:715:HOH:O	2.12	0.50
8:H:10:ASN:HA	30:H:117:HOH:O	2.11	0.49
3:P:18:LEU:HG	3:P:22:LEU:HD12	1.94	0.49
5:E:21:LYS:HE2	5:E:23:ASP:OD1	2.12	0.49
13:M:28:LEU:HD23	29:M:101:DMU:H7	1.94	0.49
1:N:117:MET:HB3	10:W:54:SER:OG	2.12	0.49
1:N:168:ILE:HD12	30:N:805:HOH:O	2.13	0.49
1:N:186:TRP:O	1:N:190:ILE:HG13	2.12	0.49
3:P:112:LEU:HB3	3:P:118:PRO:HB3	1.93	0.49
6:S:42:THR:OG1	6:S:45:ASP:HB3	2.12	0.49
10:W:50:LEU:O	10:W:50:LEU:HD22	2.12	0.49
12:Y:26:THR:CG2	13:Z:25:SER:HB3	2.42	0.49
1:A:505:PHE:HD1	30:A:702:HOH:O	1.94	0.49
1:A:52:GLN:O	1:A:56:VAL:HG23	2.12	0.49
2:B:83:ILE:O	2:B:87:MET:HG3	2.12	0.49
1:N:37:ILE:HG22	14:N:601:HEA:HMA	1.93	0.49
4:Q:129:ALA:HB3	4:Q:134:PHE:HB3	1.94	0.49
6:F:64:GLU:O	6:F:65:ASP:CB	2.57	0.49
2:B:136:LEU:HB3	2:B:193:TYR:CD2	2.47	0.49
3:C:180:GLU:HG3	30:C:402:HOH:O	2.13	0.49
23:C:305:CHD:H212	23:C:305:CHD:H12	1.94	0.49
1:N:270:TYR:O	1:N:273:MET:HB2	2.12	0.49
10:W:12:PHE:O	10:W:23:LYS:HE2	2.12	0.49
1:A:199:LEU:N	1:A:200:PRO:CD	2.75	0.49
4:D:33:LEU:HA	4:D:37:GLN:HE21	1.77	0.49
1:N:118:VAL:O	1:N:119:GLU:C	2.55	0.49
3:P:127:LEU:HD12	3:P:131:LEU:HD22	1.95	0.49
24:R:201:PSC:H252	24:R:201:PSC:H21	1.95	0.49
3:C:3:HIS:CB	30:C:444:HOH:O	2.60	0.49
3:P:67:PHE:HE2	26:P:304:CDL:H1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:8:SER:C	4:Q:10:ASP:H	2.20	0.49
12:Y:5:GLU:O	12:Y:9:LYS:HG3	2.12	0.49
2:O:132:GLU:HB3	2:O:137:GLU:HG3	1.95	0.48
5:R:43:PRO:HG2	5:R:48:ILE:HD11	1.94	0.48
1:A:430:PHE:CE1	19:A:607:TGL:HB22	2.48	0.48
7:G:9:GLY:H	1:N:178:GLN:HE21	1.60	0.48
11:X:54:ARG:HG3	11:X:54:ARG:NH2	2.21	0.48
1:N:240:HIS:O	1:N:243:VAL:HG22	2.13	0.48
5:R:40:ASP:H	24:R:201:PSC:H071	1.79	0.48
1:A:380:VAL:O	1:A:384:GLY:HA3	2.14	0.48
3:C:17:PRO:HG2	30:C:445:HOH:O	2.13	0.48
26:T:103:CDL:H331	26:T:103:CDL:OA7	2.13	0.48
7:G:9:GLY:H	1:N:178:GLN:NE2	2.12	0.48
1:N:240:HIS:CD2	1:N:244:TYR:CD2	3.00	0.48
2:O:49:LYS:HE2	4:Q:20:ARG:CZ	2.44	0.48
4:Q:131:ILE:HG22	4:Q:132:GLN:HG3	1.96	0.48
10:W:25:GLY:HA2	30:W:203:HOH:O	2.13	0.48
1:A:34:SER:HB3	1:A:61:HIS:CE1	2.48	0.48
1:A:189:MET:O	1:A:189:MET:HG3	2.10	0.48
21:A:614:EDO:H22	4:D:99:GLU:OE1	2.14	0.48
2:B:151:ARG:CD	2:B:181:GLN:HE21	2.26	0.48
12:L:22:LEU:O	12:L:26:THR:HB	2.13	0.48
2:B:52:HIS:CE1	24:B:303:PSC:H201	2.49	0.48
2:B:100:MET:HE2	2:B:157:GLU:HG3	1.95	0.48
7:T:78:LEU:HA	30:T:201:HOH:O	2.13	0.48
12:Y:26:THR:HG23	13:Z:25:SER:HB3	1.95	0.48
3:P:80:ARG:NH2	3:P:236:GLU:OE1	2.47	0.48
1:A:180:GLN:HE21	1:A:180:GLN:HB2	1.54	0.47
24:B:303:PSC:H011	24:B:303:PSC:H261	1.95	0.47
8:H:7:LYS:O	8:U:46:LYS:NZ	2.47	0.47
1:N:324:LEU:HD21	2:O:42:ILE:HG13	1.96	0.47
10:W:29:ASN:HD22	10:W:29:ASN:N	2.12	0.47
1:N:294:THR:HG22	1:N:365:ILE:HD13	1.96	0.47
5:R:72:LYS:NZ	5:R:102:GLU:OE2	2.39	0.47
1:A:21:LEU:HD23	19:L:101:TGL:H211	1.97	0.47
1:A:450:TRP:HA	1:A:450:TRP:CE3	2.50	0.47
26:C:307:CDL:H871	27:G:102:PEK:C32	2.42	0.47
1:N:328:HIS:HB2	2:O:45:MET:SD	2.54	0.47
2:B:78:LEU:HD12	2:B:78:LEU:HA	1.61	0.47
1:N:507:GLU:OE1	6:S:51:SER:HA	2.14	0.47
12:Y:26:THR:HG23	13:Z:25:SER:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:38:ASN:ND2	30:C:406:HOH:O	2.47	0.47
10:J:50:LEU:C	10:J:50:LEU:HD22	2.40	0.47
1:N:409:TRP:HB3	1:N:471:ILE:HG12	1.96	0.47
4:Q:138:TRP:CH2	11:X:50:PRO:HG2	2.50	0.47
23:W:101:CHD:H183	23:W:101:CHD:H222	1.97	0.47
23:C:304:CHD:H12	23:C:304:CHD:H212	1.95	0.47
6:F:96:LEU:O	6:F:97:ALA:HB2	2.14	0.47
1:N:378:HIS:O	1:N:382:SER:HB2	2.15	0.47
3:P:36:HIS:C	3:P:38:ASN:N	2.70	0.47
14:A:601:HEA:OMA	14:A:601:HEA:HHB	2.15	0.47
7:G:44:ARG:HD2	7:G:74:ARG:O	2.15	0.47
1:N:425:PHE:O	1:N:426:PHE:C	2.55	0.47
19:N:609:TGL:HC31	30:N:815:HOH:O	2.14	0.47
10:W:50:LEU:HD22	10:W:50:LEU:C	2.40	0.47
14:A:601:HEA:HMC3	14:A:601:HEA:HBC1	1.97	0.47
1:A:278:MET:HB3	21:T:104:EDO:H22	1.97	0.46
1:N:205:GLY:HA2	1:N:208:MET:HE3	1.98	0.46
13:Z:34:LEU:HD12	13:Z:34:LEU:HA	1.77	0.46
5:E:53:ARG:NH2	5:E:92:THR:HG23	2.30	0.46
9:I:18:ARG:HH11	9:I:18:ARG:HB2	1.80	0.46
4:D:40:LEU:CD2	4:D:58:GLU:HG2	2.46	0.46
4:D:82:VAL:O	4:D:86:MET:HG3	2.14	0.46
6:F:53:THR:HB	6:F:54:ASN:H	1.56	0.46
21:N:612:EDO:C1	13:Z:1:ILE:HG21	2.46	0.46
2:O:146:MET:HE2	2:O:215:PRO:HD3	1.97	0.46
2:B:215:PRO:O	2:B:216:LEU:C	2.57	0.46
4:Q:127:LYS:HE2	30:Q:225:HOH:O	2.15	0.46
5:R:80:GLU:CD	5:R:80:GLU:N	2.73	0.46
24:B:303:PSC:H202	24:B:303:PSC:C27	2.39	0.46
1:N:42:GLY:HA3	4:Q:104:TYR:OH	2.16	0.46
20:N:608:PGV:C03	20:N:608:PGV:H042	2.45	0.46
3:P:149:HIS:HA	3:P:152:MET:HE3	1.97	0.46
5:R:25:ASP:HB2	30:R:307:HOH:O	2.14	0.46
5:R:39:TYR:HB3	24:R:201:PSC:H073	1.96	0.46
4:D:48:TRP:HA	4:D:51:LEU:HD22	1.98	0.46
8:H:54:GLU:CD	8:H:57:ARG:HH21	2.24	0.46
10:J:50:LEU:HD22	10:J:50:LEU:O	2.15	0.46
13:M:38:ASP:HB3	30:M:210:HOH:O	2.15	0.46
1:N:37:ILE:HG21	14:N:601:HEA:HMA	1.97	0.46
1:A:440:TYR:OH	2:B:195:GLN:HB3	2.16	0.46
9:I:12:LEU:HD12	9:I:12:LEU:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:21:ILE:HD13	9:I:21:ILE:HA	1.71	0.46
3:P:77:LYS:O	3:P:80:ARG:HB2	2.16	0.46
8:U:60:TYR:CD1	8:U:60:TYR:C	2.94	0.46
9:V:33:THR:O	9:V:34:PHE:C	2.57	0.46
5:E:82:TYR:HB3	5:E:83:PRO:HD3	1.97	0.46
2:O:158:ASP:OD1	2:O:159:VAL:N	2.43	0.46
1:A:145:LEU:HD23	1:A:145:LEU:HA	1.83	0.46
1:N:74:MET:HE3	1:N:389:ILE:HD11	1.97	0.46
1:N:449:MET:HE2	11:X:40:TRP:HB3	1.98	0.46
3:P:21:ALA:O	3:P:24:ALA:HB3	2.16	0.46
3:P:41:THR:O	3:P:44:MET:HB2	2.15	0.46
7:T:17:ARG:HD2	30:T:206:HOH:O	2.15	0.46
4:D:60:TYR:OH	5:E:69:GLU:OE1	2.33	0.46
2:O:224:ALA:HA	30:O:466:HOH:O	2.15	0.46
27:P:302:PEK:H101	27:P:302:PEK:H181	1.97	0.45
19:A:607:TGL:H151	19:A:607:TGL:HC61	1.97	0.45
3:C:243:HIS:HD2	30:C:430:HOH:O	1.99	0.45
8:U:10:ASN:HA	30:U:115:HOH:O	2.16	0.45
1:A:43:GLN:HG2	4:D:104:TYR:CE1	2.52	0.45
1:A:316:THR:HG21	14:A:602:HEA:H14	1.98	0.45
9:I:29:LEU:HA	9:I:29:LEU:HD13	1.71	0.45
11:K:12:LYS:HB2	11:K:12:LYS:NZ	2.31	0.45
13:M:36:HIS:O	13:M:37:LEU:C	2.60	0.45
3:C:110:PRO:HB3	8:H:30:TRP:CE3	2.51	0.45
7:G:2:SER:O	7:G:3:ALA:HB2	2.16	0.45
1:N:71:MET:HB2	1:N:72:PRO:HD3	1.99	0.45
3:P:37:PHE:O	3:P:38:ASN:C	2.59	0.45
4:Q:29:HIS:CD2	4:Q:30:VAL:HG23	2.51	0.45
4:Q:147:LYS:HA	30:Q:220:HOH:O	2.16	0.45
1:N:51:ASP:HB2	2:O:202:SER:O	2.16	0.45
27:C:306:PEK:H42	27:C:306:PEK:H221	1.99	0.45
1:N:68:PHE:C	1:N:72:PRO:HG2	2.41	0.45
2:B:58:ALA:O	2:B:59:GLN:C	2.58	0.45
2:B:145:PRO:HA	2:B:214:VAL:O	2.16	0.45
1:N:412:ILE:HD13	4:Q:84:ALA:HB3	1.99	0.45
2:O:111:THR:HG22	2:O:115:ASP:HA	1.97	0.45
2:O:226:MET:HA	2:O:226:MET:CE	2.47	0.45
2:O:128:LEU:HD22	2:O:132:GLU:HB3	1.99	0.45
2:B:74:ILE:HG22	2:B:78:LEU:HD22	1.98	0.45
7:G:77:PRO:HD3	7:G:82:TYR:CE1	2.52	0.45
1:N:399:LEU:HB2	1:N:494:TRP:CZ3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:207:MET:HE3	2:O:207:MET:HB2	1.89	0.45
4:Q:118:LYS:HA	11:X:51:LYS:O	2.17	0.45
9:V:57:MET:O	9:V:58:LYS:C	2.60	0.45
19:N:610:TGL:HG12	19:N:610:TGL:HC42	1.98	0.44
8:U:43:MET:O	8:U:44:THR:C	2.59	0.44
9:I:58:LYS:O	9:I:62:GLU:HG3	2.17	0.44
1:N:240:HIS:CD2	1:N:240:HIS:C	2.95	0.44
19:N:611:TGL:OC1	19:N:611:TGL:CC4	2.58	0.44
3:P:51:MET:HE2	26:P:304:CDL:H381	1.99	0.44
2:B:40:TYR:CD1	2:B:40:TYR:C	2.95	0.44
2:B:86:MET:C	2:B:88:ASP:H	2.25	0.44
4:D:130:PRO:O	4:D:136:ALA:HB2	2.18	0.44
1:A:28:MET:HG3	12:L:29:PHE:HD1	1.82	0.44
3:C:197:PHE:CD1	3:C:197:PHE:C	2.95	0.44
27:G:101:PEK:H361	27:G:101:PEK:H331	1.71	0.44
2:O:68:LEU:HA	2:O:68:LEU:HD12	1.78	0.44
5:R:67:ILE:O	5:R:71:VAL:HG23	2.18	0.44
7:T:25:LEU:HD23	7:T:25:LEU:HA	1.85	0.44
9:V:19:PHE:HB2	30:V:118:HOH:O	2.18	0.44
13:Z:40:TYR:C	13:Z:42:LYS:H	2.25	0.44
23:B:302:CHD:H212	23:B:302:CHD:H12	1.98	0.44
6:F:62:CYS:HB3	6:F:85:CYS:HB3	2.00	0.44
2:B:179:LEU:HD11	8:H:65:PRO:HD3	2.00	0.44
1:A:172:LYS:HZ2	1:A:178:GLN:HE22	1.64	0.44
7:G:25:LEU:HA	7:G:25:LEU:HD23	1.68	0.44
1:N:343:GLY:O	1:N:344:PHE:C	2.60	0.44
14:N:601:HEA:CBC	14:N:601:HEA:HMC3	2.48	0.44
1:N:230:LEU:HD21	3:P:100:ALA:HA	1.99	0.44
1:A:127:THR:HB	1:A:129:TYR:CE1	2.52	0.44
2:B:181:GLN:O	8:H:23:GLN:HG2	2.17	0.44
30:L:210:HOH:O	13:M:32:TRP:HH2	2.00	0.44
23:P:305:CHD:O7	23:P:305:CHD:H41	2.18	0.44
7:T:7:ASP:O	7:T:9:GLY:N	2.51	0.44
8:U:17:ASP:OD2	8:U:19:ARG:NH2	2.51	0.44
1:A:390:MET:O	1:A:394:VAL:HG13	2.18	0.43
24:B:303:PSC:H272	24:B:303:PSC:C20	2.40	0.43
1:N:74:MET:HE3	1:N:389:ILE:CD1	2.47	0.43
1:A:156:SER:HA	30:A:788:HOH:O	2.17	0.43
1:N:34:SER:HB2	14:N:601:HEA:C2B	2.48	0.43
19:N:610:TGL:H351	9:V:16:ARG:HH21	1.84	0.43
3:P:121:ILE:HB	30:P:403:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:53:THR:HB	6:S:54:ASN:HD22	1.83	0.43
1:A:32:ALA:HB3	12:L:36:PRO:HG2	2.00	0.43
1:A:43:GLN:OE1	4:D:104:TYR:HB3	2.18	0.43
14:A:601:HEA:H11	14:A:601:HEA:HHC	1.81	0.43
3:C:14:SER:HA	3:C:15:PRO:HD3	1.87	0.43
3:P:195:SER:O	3:P:199:VAL:HG23	2.18	0.43
5:R:102:GLU:HA	5:R:107:ASP:OD1	2.19	0.43
9:V:67:GLY:HA2	30:V:102:HOH:O	2.17	0.43
26:C:307:CDL:H131	26:C:307:CDL:H1	1.99	0.43
10:J:50:LEU:HB2	30:J:215:HOH:O	2.18	0.43
13:M:10:THR:HA	13:M:14:GLU:OE2	2.19	0.43
6:S:58:VAL:O	6:S:71:TRP:HA	2.18	0.43
2:O:217:LYS:H	2:O:217:LYS:HZ2	1.67	0.43
3:P:30:GLY:HA2	3:P:42:LEU:HB3	2.00	0.43
6:S:53:THR:HB	6:S:54:ASN:H	1.44	0.43
2:B:49:LYS:O	4:D:20:ARG:NH2	2.41	0.43
24:B:303:PSC:H012	24:B:303:PSC:H221	2.00	0.43
1:N:412:ILE:HD13	4:Q:84:ALA:CB	2.49	0.43
2:O:215:PRO:HB2	2:O:217:LYS:HE2	2.01	0.43
4:Q:108:PRO:N	30:Q:202:HOH:O	2.52	0.43
30:A:779:HOH:O	3:C:111:GLU:HB3	2.18	0.43
12:L:21:LEU:O	12:L:24:MET:HB2	2.19	0.43
3:P:42:LEU:O	3:P:43:LEU:C	2.62	0.43
6:S:94:HIS:O	6:S:96:LEU:HD13	2.19	0.43
7:T:33:LEU:HD22	7:T:33:LEU:HA	1.75	0.43
1:A:106:PRO:N	1:A:107:PRO:HD2	2.33	0.43
1:A:316:THR:HG21	14:A:602:HEA:C14	2.49	0.43
1:A:459:PHE:CE1	21:A:614:EDO:H11	2.54	0.43
2:B:70:ALA:O	2:B:74:ILE:HG13	2.18	0.43
3:C:179:SER:O	3:C:183:GLU:HG2	2.19	0.43
1:N:365:ILE:O	2:O:171:LYS:HD2	2.18	0.43
3:P:90:GLU:O	3:P:93:PHE:HB3	2.19	0.43
3:C:92:LEU:O	3:C:95:THR:HB	2.19	0.43
1:N:194:LEU:CD2	1:N:285:PHE:HE2	2.30	0.43
1:N:298:ASP:OD1	1:N:298:ASP:N	2.46	0.43
2:O:208:PRO:C	2:O:209:ILE:HG13	2.43	0.43
4:Q:118:LYS:HB3	11:X:53:TRP:HB3	2.01	0.43
26:T:103:CDL:H762	26:T:103:CDL:H561	2.00	0.43
1:A:174:PRO:HB2	6:F:35:ALA:HB2	2.01	0.43
1:A:274:VAL:O	1:A:275:TRP:C	2.61	0.43
3:C:108:PRO:HA	30:C:446:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:120:THR:HG21	30:K:207:HOH:O	2.18	0.43
7:G:15:THR:O	7:G:18:PHE:HB3	2.18	0.43
1:N:199:LEU:HD23	1:N:199:LEU:HA	1.78	0.43
1:A:278:MET:HE2	21:T:104:EDO:O1	2.18	0.42
1:N:498:CYS:HA	1:N:499:PRO:HA	1.93	0.42
3:P:55:TYR:HA	26:P:304:CDL:H552	2.01	0.42
4:Q:145:TRP:CD1	11:X:46:GLY:HA2	2.54	0.42
7:G:74:ARG:HD2	7:G:75:VAL:HG13	2.01	0.42
3:P:63:ARG:HE	26:P:304:CDL:CA2	2.32	0.42
5:R:24:ILE:HG13	5:R:28:GLU:HB2	2.01	0.42
1:A:268:PHE:CD1	1:A:268:PHE:C	2.97	0.42
12:L:47:LYS:HA	30:L:212:HOH:O	2.18	0.42
19:N:609:TGL:H283	19:N:609:TGL:H102	2.01	0.42
2:O:59:GLN:C	2:O:60:GLU:HG3	2.44	0.42
8:U:49:ASP:O	8:U:52:VAL:HG23	2.19	0.42
13:Z:40:TYR:O	13:Z:42:LYS:N	2.52	0.42
1:A:407:ASP:O	1:A:411:LYS:HG3	2.19	0.42
1:N:89:ALA:HA	1:N:90:PRO:HD3	1.83	0.42
8:U:9:LYS:HD3	8:U:9:LYS:HA	1.82	0.42
1:A:227:ASP:HA	1:A:228:PRO:HD3	1.74	0.42
1:A:380:VAL:HG21	14:A:602:HEA:C4C	2.50	0.42
3:C:42:LEU:HD23	3:C:42:LEU:HA	1.73	0.42
3:C:76:GLN:O	3:C:80:ARG:HG3	2.20	0.42
1:N:36:LEU:HD21	12:Y:37:PHE:CE1	2.54	0.42
1:N:351:GLY:HA3	1:N:380:VAL:HG13	2.01	0.42
3:P:92:LEU:HD13	3:P:92:LEU:HA	1.85	0.42
4:Q:90:GLY:O	4:Q:93:ALA:HB3	2.19	0.42
23:C:304:CHD:H112	23:C:304:CHD:H12A	1.86	0.42
7:G:30:LEU:HD23	7:G:30:LEU:HA	1.83	0.42
3:P:204:HIS:CE1	3:P:249:TRP:HB2	2.55	0.42
6:S:93:PRO:O	6:S:94:HIS:C	2.62	0.42
1:A:324:LEU:HD21	2:B:42:ILE:HG12	2.02	0.42
2:B:86:MET:HE3	2:B:86:MET:HB2	1.74	0.42
26:C:303:CDL:H112	26:C:303:CDL:HA4	1.89	0.42
10:J:30:ILE:O	10:J:34:VAL:HG23	2.19	0.42
1:N:366:VAL:HB	30:N:704:HOH:O	2.19	0.42
2:O:78:LEU:N	2:O:79:PRO:HD2	2.35	0.42
1:A:9:SER:HA	21:A:612:EDO:H11	2.02	0.42
20:A:609:PGV:O02	20:A:609:PGV:O14	2.37	0.42
5:E:96:LEU:HD23	5:E:96:LEU:HA	1.77	0.42
7:G:1:ALA:H2	20:G:103:PGV:C31	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:2:ALA:HB3	30:O:458:HOH:O	2.19	0.42
2:O:103:GLN:HA	2:O:104:TRP:HA	1.81	0.42
2:O:144:LEU:HA	2:O:145:PRO:HD3	1.83	0.42
23:O:302:CHD:H161	23:O:302:CHD:H221	1.73	0.42
26:P:304:CDL:PA1	26:P:304:CDL:HB21	2.60	0.42
30:A:720:HOH:O	3:C:93:PHE:HA	2.20	0.42
2:B:132:GLU:HB3	2:B:137:GLU:HG3	2.01	0.42
6:F:60:CYS:SG	6:F:89:TYR:OH	2.73	0.42
6:S:8:THR:OG1	6:S:11:GLU:HG3	2.19	0.42
7:T:33:LEU:O	7:T:34:ASN:C	2.62	0.42
13:Z:21:VAL:O	13:Z:22:THR:C	2.63	0.42
24:B:303:PSC:H202	24:B:303:PSC:H242	2.02	0.42
27:C:306:PEK:O14	7:G:17:ARG:NH2	2.52	0.42
4:D:52:SER:OG	4:D:55:GLU:HG3	2.20	0.42
2:O:68:LEU:HB3	2:O:69:PRO:HD3	2.01	0.42
12:Y:45:LEU:C	12:Y:47:LYS:N	2.77	0.42
1:A:377:PHE:HA	1:A:380:VAL:HG22	2.01	0.41
12:L:13:PHE:HA	19:L:101:TGL:HC21	2.01	0.41
1:N:176:MET:HB2	1:N:176:MET:HE3	1.67	0.41
4:Q:129:ALA:HB3	4:Q:134:PHE:CB	2.50	0.41
30:A:825:HOH:O	19:L:101:TGL:H101	2.19	0.41
6:F:30:PRO:O	6:F:96:LEU:HD23	2.20	0.41
2:O:23:PHE:O	2:O:26:HIS:HB3	2.20	0.41
4:Q:91:PHE:O	4:Q:94:LEU:HB2	2.20	0.41
5:R:78:HIS:HB2	5:R:81:ILE:HD12	2.01	0.41
7:G:69:PHE:HD2	7:G:70:PHE:CE1	2.37	0.41
1:N:280:ILE:HG12	1:N:312:ILE:CD1	2.48	0.41
3:P:116:TRP:CE3	3:P:118:PRO:HD3	2.55	0.41
4:Q:82:VAL:O	4:Q:86:MET:HG3	2.20	0.41
27:T:101:PEK:H241	27:T:101:PEK:H271	1.83	0.41
3:C:177:GLN:HA	30:C:402:HOH:O	2.21	0.41
12:L:41:ARG:O	12:L:42:HIS:C	2.63	0.41
7:T:53:LEU:HD23	7:T:53:LEU:HA	1.83	0.41
1:A:404:THR:OG1	1:A:480:ARG:HB2	2.20	0.41
2:B:68:LEU:HD12	2:B:68:LEU:HA	1.65	0.41
3:C:83:MET:O	3:C:84:ILE:C	2.62	0.41
9:I:20:HIS:O	9:I:21:ILE:C	2.64	0.41
4:Q:78:TRP:CE2	4:Q:79:LYS:HG3	2.56	0.41
4:Q:98:TRP:HE1	29:Z:101:DMU:H29	1.86	0.41
26:T:103:CDL:H372	26:T:103:CDL:H111	2.03	0.41
1:A:261:TYR:OH	21:A:610:EDO:H12	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:ASN:OD1	1:A:406:ASN:C	2.63	0.41
6:F:49:VAL:HA	6:F:50:PRO:HD2	1.87	0.41
1:N:28:MET:HE1	1:N:465:VAL:HG13	2.02	0.41
2:B:100:MET:CE	2:B:157:GLU:HG3	2.50	0.41
1:N:188:VAL:O	1:N:189:MET:C	2.64	0.41
3:P:51:MET:HG2	26:P:304:CDL:H602	2.02	0.41
7:T:44:ARG:HD2	7:T:82:TYR:CE1	2.55	0.41
7:T:44:ARG:HD3	7:T:74:ARG:O	2.19	0.41
4:D:29:HIS:CE1	4:D:65:LYS:HG3	2.56	0.41
10:J:46:SER:O	10:J:47:LEU:C	2.63	0.41
1:N:119:GLU:HB2	1:N:120:ALA:H	1.71	0.41
1:N:289:ALA:HB3	1:N:305:PHE:CD2	2.55	0.41
4:Q:16:TYR:CE1	4:Q:25:PRO:HG2	2.56	0.41
9:V:31:PHE:CE1	9:V:32:ALA:O	2.74	0.41
11:X:32:MET:HE3	11:X:32:MET:HB3	1.99	0.41
1:A:71:MET:HE3	1:A:245:ILE:HG21	2.02	0.41
14:A:602:HEA:H243	2:B:69:PRO:HB3	2.03	0.41
2:B:16:ILE:HD13	2:B:16:ILE:HA	1.84	0.41
24:B:303:PSC:H272	24:B:303:PSC:H242	1.82	0.41
7:G:42:ARG:O	7:G:43:GLU:C	2.64	0.41
8:H:18:SER:HB2	30:H:115:HOH:O	2.21	0.41
1:N:3:ILE:N	1:N:3:ILE:HD12	2.35	0.41
1:N:65:MET:HG3	14:N:601:HEA:C2C	2.51	0.41
1:N:165:ILE:O	1:N:169:ILE:HG12	2.20	0.41
1:N:212:ASP:HA	1:N:217:THR:OG1	2.21	0.41
1:N:406:ASN:HD21	20:N:607:PGV:H032	1.82	0.41
2:O:99:THR:HB	2:O:108:TYR:CE1	2.56	0.41
3:P:99:TRP:CD1	3:P:99:TRP:C	2.97	0.41
3:P:151:LEU:HD21	3:P:232:HIS:CG	2.56	0.41
5:R:31:LYS:HA	5:R:31:LYS:HD2	1.96	0.41
7:T:25:LEU:N	7:T:26:PRO:CD	2.83	0.41
12:Y:25:MET:HE2	12:Y:25:MET:HB3	1.96	0.41
13:Z:40:TYR:C	13:Z:42:LYS:N	2.79	0.41
3:P:210:ILE:HG23	20:P:303:PGV:H91	2.03	0.41
5:E:66:ARG:O	5:E:70:VAL:HG12	2.21	0.40
13:M:11:SER:HB2	13:M:12:PRO:HD2	2.01	0.40
2:O:121:TYR:O	2:O:138:VAL:HA	2.21	0.40
2:O:149:THR:HG22	30:O:448:HOH:O	2.21	0.40
3:P:109:THR:HB	3:P:110:PRO:CD	2.52	0.40
26:T:103:CDL:H402	26:T:103:CDL:H161	2.03	0.40
1:A:266:GLU:HB2	1:A:267:PRO:HD2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:B:303:PSC:H202	24:B:303:PSC:C24	2.52	0.40
19:D:201:TGL:HG31	19:D:201:TGL:HC21	1.92	0.40
1:N:403:TYR:HA	1:N:480:ARG:O	2.21	0.40
3:P:109:THR:HB	3:P:110:PRO:HD2	2.02	0.40
3:P:121:ILE:HG13	30:P:403:HOH:O	2.20	0.40
5:R:19:PHE:HB2	30:R:303:HOH:O	2.21	0.40
6:S:64:GLU:O	6:S:65:ASP:HB2	2.22	0.40
1:N:377:PHE:CE1	1:N:378:HIS:CE1	3.09	0.40
1:N:452:THR:CG2	1:N:456:MET:HE3	2.51	0.40
11:X:28:VAL:O	11:X:31:TYR:HB3	2.22	0.40
20:A:609:PGV:H271	20:A:609:PGV:H12	2.03	0.40
24:B:303:PSC:H221	24:B:303:PSC:H251	1.88	0.40
3:C:40:MET:O	3:C:44:MET:HG2	2.22	0.40
10:J:26:ALA:N	30:J:201:HOH:O	2.54	0.40
1:N:71:MET:N	1:N:72:PRO:CD	2.85	0.40
1:N:363:LEU:HD23	1:N:363:LEU:HA	1.94	0.40
3:P:193:TYR:CD1	3:P:193:TYR:C	3.00	0.40
8:U:34:LEU:O	8:U:35:ASP:C	2.64	0.40
13:Z:37:LEU:O	13:Z:38:ASP:C	2.64	0.40
1:A:65:MET:HB3	14:A:601:HEA:CBC	2.52	0.40
1:A:342:LEU:HA	1:A:342:LEU:HD23	1.87	0.40
30:B:404:HOH:O	9:I:20:HIS:HA	2.21	0.40
3:C:187:THR:OG1	30:C:401:HOH:O	2.22	0.40
4:D:33:LEU:HA	4:D:37:GLN:NE2	2.37	0.40
5:E:44:GLU:HB3	30:E:202:HOH:O	2.22	0.40
9:I:43:ARG:HH11	9:I:43:ARG:HD3	1.74	0.40
10:J:44:LEU:HD23	10:J:44:LEU:HA	1.85	0.40
7:T:38:HIS:CE1	26:T:103:CDL:H142	2.56	0.40
7:T:79:PRO:CD	30:T:201:HOH:O	2.53	0.40
26:T:103:CDL:H312	30:T:205:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	513/514 (100%)	494 (96%)	19 (4%)	0	100	100
1	N	512/514 (100%)	488 (95%)	23 (4%)	1 (0%)	43	58
2	B	225/227 (99%)	213 (95%)	11 (5%)	1 (0%)	30	43
2	O	225/227 (99%)	211 (94%)	12 (5%)	2 (1%)	14	22
3	C	257/261 (98%)	250 (97%)	7 (3%)	0	100	100
3	P	257/261 (98%)	248 (96%)	6 (2%)	3 (1%)	10	16
4	D	142/147 (97%)	133 (94%)	9 (6%)	0	100	100
4	Q	142/147 (97%)	130 (92%)	9 (6%)	3 (2%)	5	7
5	E	103/109 (94%)	98 (95%)	4 (4%)	1 (1%)	12	20
5	R	103/109 (94%)	99 (96%)	3 (3%)	1 (1%)	12	20
6	F	96/98 (98%)	87 (91%)	7 (7%)	2 (2%)	5	7
6	S	96/98 (98%)	90 (94%)	5 (5%)	1 (1%)	12	20
7	G	81/85 (95%)	69 (85%)	8 (10%)	4 (5%)	1	1
7	T	81/85 (95%)	68 (84%)	5 (6%)	8 (10%)	0	0
8	H	77/85 (91%)	67 (87%)	9 (12%)	1 (1%)	9	14
8	U	77/85 (91%)	69 (90%)	4 (5%)	4 (5%)	1	1
9	I	71/73 (97%)	66 (93%)	5 (7%)	0	100	100
9	V	71/73 (97%)	64 (90%)	6 (8%)	1 (1%)	9	13
10	J	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
10	W	56/59 (95%)	53 (95%)	2 (4%)	1 (2%)	6	9
11	K	47/56 (84%)	47 (100%)	0	0	100	100
11	X	47/56 (84%)	41 (87%)	5 (11%)	1 (2%)	5	7
12	L	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
12	Y	44/47 (94%)	40 (91%)	4 (9%)	0	100	100
13	M	41/46 (89%)	40 (98%)	0	1 (2%)	4	5
13	Z	41/46 (89%)	38 (93%)	2 (5%)	1 (2%)	4	5
All	All	3505/3614 (97%)	3301 (94%)	167 (5%)	37 (1%)	11	18

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	97	ALA
7	G	3	ALA
7	G	4	ALA
7	G	8	HIS
8	H	8	ILE
2	O	59	GLN
7	T	4	ALA
7	T	8	HIS
9	V	32	ALA
7	G	43	GLU
2	O	60	GLU
3	P	37	PHE
3	P	38	ASN
4	Q	5	VAL
4	Q	65	LYS
6	S	94	HIS
7	T	2	SER
7	T	37	LEU
13	Z	41	LYS
13	M	42	LYS
1	N	119	GLU
7	T	6	GLY
7	T	7	ASP
8	U	8	ILE
8	U	51	SER
2	B	59	GLN
5	E	8	ASP
6	F	94	HIS
3	P	232	HIS
4	Q	47	SER
5	R	101	PRO
8	U	48	GLY
10	W	57	HIS
11	X	7	PRO
7	T	3	ALA
7	T	5	LYS
8	U	9	LYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	427/426 (100%)	406 (95%)	21 (5%)	22	39
1	N	426/426 (100%)	403 (95%)	23 (5%)	20	35
2	B	210/210 (100%)	198 (94%)	12 (6%)	18	33
2	O	210/210 (100%)	197 (94%)	13 (6%)	16	29
3	C	224/226 (99%)	221 (99%)	3 (1%)	61	80
3	P	224/226 (99%)	217 (97%)	7 (3%)	35	57
4	D	128/129 (99%)	124 (97%)	4 (3%)	35	57
4	Q	128/129 (99%)	118 (92%)	10 (8%)	11	20
5	E	92/95 (97%)	87 (95%)	5 (5%)	20	35
5	R	92/95 (97%)	86 (94%)	6 (6%)	15	27
6	F	81/81 (100%)	74 (91%)	7 (9%)	10	16
6	S	81/81 (100%)	71 (88%)	10 (12%)	4	6
7	G	67/68 (98%)	63 (94%)	4 (6%)	17	31
7	T	67/68 (98%)	64 (96%)	3 (4%)	24	42
8	H	71/75 (95%)	64 (90%)	7 (10%)	7	11
8	U	71/75 (95%)	65 (92%)	6 (8%)	10	16
9	I	57/57 (100%)	54 (95%)	3 (5%)	20	36
9	V	57/57 (100%)	50 (88%)	7 (12%)	4	6
10	J	49/50 (98%)	43 (88%)	6 (12%)	5	7
10	W	49/50 (98%)	44 (90%)	5 (10%)	7	11
11	K	39/46 (85%)	35 (90%)	4 (10%)	7	11
11	X	39/46 (85%)	36 (92%)	3 (8%)	12	20
12	L	39/40 (98%)	37 (95%)	2 (5%)	21	37
12	Y	39/40 (98%)	37 (95%)	2 (5%)	21	37
13	M	37/38 (97%)	34 (92%)	3 (8%)	11	18
13	Z	37/38 (97%)	32 (86%)	5 (14%)	4	5
All	All	3041/3082 (99%)	2860 (94%)	181 (6%)	17	31

All (181) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	SER
1	A	118	VAL
1	A	128	VAL
1	A	136	LEU
1	A	138	HIS
1	A	172	LYS
1	A	177	SER
1	A	178	GLN
1	A	180	GLN
1	A	189	MET
1	A	245	ILE
1	A	264	LYS
1	A	312	ILE
1	A	361	SER
1	A	366	VAL
1	A	369	ASP
1	A	382	SER
1	A	394	VAL
1	A	495	LEU
1	A	504	THR
1	A	513	LEU
2	B	7	LEU
2	B	55	THR
2	B	60	GLU
2	B	68	LEU
2	B	71	ILE
2	B	75	LEU
2	B	78	LEU
2	B	92	ASN
2	B	94	SER
2	B	117	SER
2	B	217	LYS
2	B	223	SER
3	C	159	MET
3	C	179	SER
3	C	230	ASN
4	D	45	LYS
4	D	51	LEU
4	D	121	LYS
4	D	143	ASN
5	E	6	GLU
5	E	9	GLU
5	E	70	VAL

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Mol	Chain	Res	Type
5	E	79	LYS
5	E	108	LYS
6	F	10	GLU
6	F	33	ILE
6	F	43	LYS
6	F	53	THR
6	F	54	ASN
6	F	90	LYS
6	F	95	GLN
7	G	33	LEU
7	G	36	TRP
7	G	37	LEU
7	G	74	ARG
8	H	8	ILE
8	H	9	LYS
8	H	23	GLN
8	H	27	ARG
8	H	46	LYS
8	H	49	ASP
8	H	52	VAL
9	I	18	ARG
9	I	21	ILE
9	I	29	LEU
10	J	2	GLU
10	J	14	GLU
10	J	29	ASN
10	J	37	THR
10	J	50	LEU
10	J	58	LYS
11	K	12	LYS
11	K	20	SER
11	K	28	VAL
11	K	54	ARG
12	L	5	GLU
12	L	26	THR
13	M	19	LEU
13	M	34	LEU
13	M	38	ASP
1	N	38	ARG
1	N	127	THR
1	N	128	VAL
1	N	138	HIS

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Mol	Chain	Res	Type
1	N	152	LEU
1	N	178	GLN
1	N	180	GLN
1	N	189	MET
1	N	190	ILE
1	N	245	ILE
1	N	273	MET
1	N	295	VAL
1	N	298	ASP
1	N	312	ILE
1	N	361	SER
1	N	366	VAL
1	N	369	ASP
1	N	389	ILE
1	N	394	VAL
1	N	484	THR
1	N	485	VAL
1	N	486	ASP
1	N	514	LYS
2	O	33	LEU
2	O	47	THR
2	O	48	THR
2	O	60	GLU
2	O	65	TRP
2	O	75	LEU
2	O	88	ASP
2	O	91	ASN
2	O	183	THR
2	O	185	MET
2	O	217	LYS
2	O	226	MET
2	O	227	LEU
3	P	44	MET
3	P	77	LYS
3	P	80	ARG
3	P	105	SER
3	P	127	LEU
3	P	128	GLU
3	P	179	SER
4	Q	5	VAL
4	Q	6	VAL
4	Q	15	SER

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Mol	Chain	Res	Type
4	Q	26	ASP
4	Q	33	LEU
4	Q	51	LEU
4	Q	58	GLU
4	Q	59	LEU
4	Q	126	MET
4	Q	144	GLU
5	R	21	LYS
5	R	36	LEU
5	R	70	VAL
5	R	79	LYS
5	R	80	GLU
5	R	92	THR
6	S	14	THR
6	S	25	ARG
6	S	33	ILE
6	S	37	LYS
6	S	53	THR
6	S	54	ASN
6	S	87	THR
6	S	90	LYS
6	S	95	GLN
6	S	96	LEU
7	T	17	ARG
7	T	33	LEU
7	T	35	SER
8	U	8	ILE
8	U	27	ARG
8	U	52	VAL
8	U	60	TYR
8	U	61	LYS
8	U	84	LYS
9	V	2	THR
9	V	4	LEU
9	V	19	PHE
9	V	27	VAL
9	V	31	PHE
9	V	62	GLU
9	V	68	ILE
10	W	10	LYS
10	W	14	GLU
10	W	27	THR

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Mol	Chain	Res	Type
10	W	29	ASN
10	W	50	LEU
11	X	38	ILE
11	X	52	GLU
11	X	54	ARG
12	Y	27	LEU
12	Y	47	LYS
13	Z	1	ILE
13	Z	19	LEU
13	Z	20	SER
13	Z	34	LEU
13	Z	42	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (58) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	178	GLN
1	A	180	GLN
1	A	413	HIS
1	A	422	ASN
1	A	512	ASN
2	B	10	GLN
2	B	52	HIS
2	B	181	GLN
2	B	203	ASN
3	C	68	GLN
4	D	29	HIS
4	D	37	GLN
4	D	72	ASN
5	E	78	HIS
5	E	94	ASN
6	F	88	HIS
7	G	8	HIS
7	G	71	HIS
7	G	76	ASN
8	H	12	GLN
8	H	23	GLN
8	H	28	ASN
8	H	31	GLN
8	H	32	ASN
10	J	57	HIS

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Mol	Chain	Res	Type
11	K	35	GLN
1	N	4	ASN
1	N	178	GLN
1	N	214	ASN
1	N	291	HIS
1	N	413	HIS
1	N	422	ASN
1	N	428	GLN
1	N	503	HIS
1	N	512	ASN
2	O	10	GLN
2	O	59	GLN
2	O	91	ASN
2	O	181	GLN
3	P	50	ASN
3	P	68	GLN
3	P	70	HIS
3	P	161	GLN
4	Q	37	GLN
4	Q	109	HIS
4	Q	119	GLN
4	Q	143	ASN
5	R	94	ASN
6	S	54	ASN
7	T	8	HIS
7	T	34	ASN
7	T	71	HIS
7	T	76	ASN
8	U	23	GLN
9	V	8	GLN
10	W	29	ASN
13	Z	15	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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$
9	SAC	I	1	9	7,8,9	1.30	1 (14%)	8,9,11	0.99	0
7	TPO	T	11	7	8,10,11	1.73	2 (25%)	10,14,16	1.02	1 (10%)
9	SAC	V	1	9	7,8,9	1.70	1 (14%)	8,9,11	1.82	2 (25%)
2	FME	B	1	2	8,9,10	0.97	0	7,9,11	1.45	3 (42%)
1	FME	N	1	1	8,9,10	0.45	0	7,9,11	1.59	2 (28%)
2	FME	O	1	2	8,9,10	0.85	0	7,9,11	1.63	1 (14%)
7	TPO	G	11	7	8,10,11	1.45	1 (12%)	10,14,16	0.92	1 (10%)
1	FME	A	1	1	8,9,10	0.44	0	7,9,11	1.97	4 (57%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	SAC	I	1	9	-	4/7/8/10	-
7	TPO	T	11	7	-	2/9/11/13	-
9	SAC	V	1	9	-	4/7/8/10	-
2	FME	B	1	2	-	1/7/9/11	-
1	FME	N	1	1	-	2/7/9/11	-
2	FME	O	1	2	-	0/7/9/11	-
7	TPO	G	11	7	-	2/9/11/13	-
1	FME	A	1	1	-	3/7/9/11	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	V	1	SAC	CA-N	4.27	1.52	1.46
9	I	1	SAC	CA-N	3.22	1.50	1.46
7	T	11	TPO	P-O1P	2.85	1.59	1.50
7	G	11	TPO	P-O1P	2.83	1.59	1.50
7	T	11	TPO	P-OG1	2.33	1.63	1.59

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	V	1	SAC	C-CA-N	3.75	116.49	109.73
2	O	1	FME	CA-N-CN	3.70	128.51	122.82
1	N	1	FME	C-CA-N	2.76	114.71	109.73
1	A	1	FME	C-CA-N	2.75	114.69	109.73
1	A	1	FME	CE-SD-CG	2.60	109.33	100.40
1	A	1	FME	CG-CB-CA	-2.48	106.06	112.95
1	N	1	FME	O-C-CA	-2.38	118.55	124.78
7	G	11	TPO	CB-CA-N	-2.28	99.43	114.41
7	T	11	TPO	CB-CA-N	-2.23	99.75	114.41
2	B	1	FME	CG-CB-CA	-2.22	106.77	112.95
9	V	1	SAC	CA-N-C1A	2.21	127.22	123.15
1	A	1	FME	O-C-CA	-2.13	119.19	124.78
2	B	1	FME	O-C-CA	-2.01	119.50	124.78
2	B	1	FME	CA-N-CN	2.01	125.92	122.82

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	N-CA-CB-CG
1	A	1	FME	C-CA-CB-CG
7	G	11	TPO	N-CA-CB-OG1
9	I	1	SAC	C2A-C1A-N-CA
9	I	1	SAC	OAC-C1A-N-CA
9	I	1	SAC	C-CA-N-C1A
9	I	1	SAC	CB-CA-N-C1A
1	N	1	FME	CA-CB-CG-SD
7	T	11	TPO	N-CA-CB-OG1
9	V	1	SAC	C2A-C1A-N-CA
9	V	1	SAC	OAC-C1A-N-CA
9	V	1	SAC	C-CA-CB-OG
1	A	1	FME	CB-CG-SD-CE
1	N	1	FME	CB-CG-SD-CE
9	V	1	SAC	N-CA-CB-OG
2	B	1	FME	CB-CG-SD-CE
7	T	11	TPO	CB-OG1-P-O3P
7	G	11	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 72 ligands modelled in this entry, 8 are monoatomic and 2 are unknown - leaving 62 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
29	DMU	Z	101	-	34,34,34	0.53	0	45,45,45	1.13	4 (8%)
21	EDO	B	304	-	3,3,3	0.40	0	2,2,2	0.60	0
20	PGV	C	302	-	50,50,50	0.92	2 (4%)	53,56,56	0.93	4 (7%)
14	HEA	N	602	1	66,67,67	2.18	22 (33%)	78,103,103	1.53	17 (21%)
19	TGL	L	101	-	62,62,62	1.19	3 (4%)	65,65,65	1.25	5 (7%)
20	PGV	C	308	-	50,50,50	1.21	2 (4%)	53,56,56	1.01	3 (5%)
18	CMO	N	606	-	0,1,1	-	-	-	-	-
19	TGL	D	201	-	62,62,62	1.13	3 (4%)	65,65,65	0.99	5 (7%)
23	CHD	W	101	-	32,32,32	0.91	1 (3%)	51,51,51	2.11	17 (33%)
21	EDO	A	612	-	3,3,3	0.52	0	2,2,2	0.10	0
23	CHD	O	302	-	32,32,32	1.04	2 (6%)	51,51,51	1.46	8 (15%)
27	PEK	P	302	-	52,52,52	0.87	2 (3%)	55,57,57	1.35	5 (9%)
27	PEK	T	102	-	52,52,52	1.19	2 (3%)	55,57,57	1.13	4 (7%)
21	EDO	B	305	-	3,3,3	0.39	0	2,2,2	0.49	0
21	EDO	C	310	-	3,3,3	0.53	0	2,2,2	0.33	0
26	CDL	T	103	-	99,99,99	1.37	12 (12%)	105,111,111	1.31	11 (10%)
23	CHD	C	305	-	32,32,32	0.99	1 (3%)	51,51,51	1.25	7 (13%)
20	PGV	A	609	-	50,50,50	1.10	2 (4%)	53,56,56	1.08	5 (9%)
14	HEA	A	602	1	66,67,67	2.20	21 (31%)	78,103,103	1.53	17 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	PEK	G	102	-	52,52,52	1.21	2 (3%)	55,57,57	1.06	5 (9%)
21	EDO	A	614	-	3,3,3	0.59	0	2,2,2	0.11	0
21	EDO	F	102	-	3,3,3	0.57	0	2,2,2	0.06	0
21	EDO	G	104	-	3,3,3	0.40	0	2,2,2	0.56	0
20	PGV	A	608	-	50,50,50	0.79	2 (4%)	53,56,56	1.44	5 (9%)
19	TGL	N	609	-	62,62,62	1.12	3 (4%)	65,65,65	1.29	8 (12%)
21	EDO	A	613	-	3,3,3	0.54	0	2,2,2	0.24	0
20	PGV	P	303	-	50,50,50	0.93	2 (4%)	53,56,56	1.08	5 (9%)
21	EDO	K	103	-	3,3,3	0.56	0	2,2,2	0.11	0
19	TGL	A	607	-	62,62,62	1.23	4 (6%)	65,65,65	1.38	10 (15%)
21	EDO	A	610	-	3,3,3	0.52	0	2,2,2	0.57	0
21	EDO	T	104	-	3,3,3	0.45	0	2,2,2	0.26	0
23	CHD	C	304	-	32,32,32	0.62	0	51,51,51	1.97	16 (31%)
23	CHD	P	305	-	32,32,32	0.59	0	51,51,51	1.81	13 (25%)
20	PGV	N	607	-	50,50,50	1.09	2 (4%)	53,56,56	1.07	4 (7%)
20	PGV	N	608	-	50,50,50	0.90	3 (6%)	53,56,56	1.17	4 (7%)
19	TGL	N	610	-	62,62,62	1.13	3 (4%)	65,65,65	1.13	6 (9%)
20	PGV	G	103	-	50,50,50	1.07	2 (4%)	53,56,56	0.95	2 (3%)
27	PEK	C	306	-	52,52,52	1.03	2 (3%)	55,57,57	0.90	3 (5%)
21	EDO	K	101	-	3,3,3	0.47	0	2,2,2	0.33	0
23	CHD	B	302	-	32,32,32	0.81	0	51,51,51	1.26	4 (7%)
14	HEA	A	601	1	66,67,67	1.86	19 (28%)	78,103,103	2.34	33 (42%)
23	CHD	P	306	-	32,32,32	0.74	1 (3%)	51,51,51	1.53	12 (23%)
29	DMU	M	101	-	34,34,34	0.53	0	45,45,45	1.14	4 (8%)
19	TGL	N	611	-	62,62,62	1.18	3 (4%)	65,65,65	1.24	7 (10%)
21	EDO	L	102	-	3,3,3	0.46	0	2,2,2	0.40	0
26	CDL	P	304	-	99,99,99	1.39	12 (12%)	105,111,111	1.16	7 (6%)
21	EDO	N	612	-	3,3,3	0.56	0	2,2,2	0.16	0
14	HEA	N	601	1	66,67,67	1.88	21 (31%)	78,103,103	1.52	13 (16%)
26	CDL	C	303	-	99,99,99	1.39	12 (12%)	105,111,111	1.22	7 (6%)
21	EDO	C	311	-	3,3,3	0.53	0	2,2,2	0.30	0
21	EDO	K	102	-	3,3,3	0.50	0	2,2,2	0.26	0
24	PSC	R	201	-	51,51,51	1.22	3 (5%)	57,59,59	0.99	4 (7%)
26	CDL	C	307	-	99,99,99	1.43	13 (13%)	105,111,111	1.23	8 (7%)
22	CUA	O	301	2	0,1,1	-	-	-	-	-
23	CHD	J	101	-	32,32,32	0.66	0	51,51,51	1.54	10 (19%)
27	PEK	G	101	-	52,52,52	0.94	2 (3%)	55,57,57	1.23	4 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	CMO	A	606	15	0,1,1	-	-	-		
21	EDO	A	611	-	3,3,3	0.37	0	2,2,2	0.61	0
24	PSC	B	303	-	51,51,51	1.28	3 (5%)	57,59,59	1.07	5 (8%)
21	EDO	C	309	-	3,3,3	0.38	0	2,2,2	0.68	0
27	PEK	T	101	-	52,52,52	1.16	2 (3%)	55,57,57	1.06	4 (7%)
22	CUA	B	301	2	0,1,1	-	-	-		

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
29	DMU	Z	101	-	-	9/19/59/59	0/2/2/2
21	EDO	B	304	-	-	1/1/1/1	-
20	PGV	C	302	-	-	15/55/55/55	-
14	HEA	N	602	1	-	8/36/76/76	-
19	TGL	L	101	-	-	35/65/65/65	-
20	PGV	C	308	-	-	32/55/55/55	-
19	TGL	D	201	-	-	38/65/65/65	-
23	CHD	W	101	-	-	6/9/74/74	0/4/4/4
21	EDO	A	612	-	-	1/1/1/1	-
23	CHD	O	302	-	-	4/9/74/74	0/4/4/4
27	PEK	P	302	-	-	17/56/56/56	-
27	PEK	T	102	-	-	29/56/56/56	-
21	EDO	B	305	-	-	0/1/1/1	-
21	EDO	C	310	-	-	1/1/1/1	-
26	CDL	T	103	-	-	63/110/110/110	-
23	CHD	C	305	-	-	2/9/74/74	0/4/4/4
20	PGV	A	609	-	-	31/55/55/55	-
14	HEA	A	602	1	-	5/36/76/76	-
27	PEK	G	102	-	-	35/56/56/56	-
21	EDO	A	614	-	-	0/1/1/1	-
21	EDO	F	102	-	-	0/1/1/1	-
21	EDO	G	104	-	-	0/1/1/1	-
20	PGV	A	608	-	-	11/55/55/55	-
19	TGL	N	609	-	-	37/65/65/65	-
21	EDO	A	613	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
20	PGV	P	303	-	-	21/55/55/55	-
21	EDO	K	103	-	-	0/1/1/1	-
19	TGL	A	607	-	-	36/65/65/65	-
21	EDO	A	610	-	-	1/1/1/1	-
21	EDO	T	104	-	-	1/1/1/1	-
23	CHD	C	304	-	-	5/9/74/74	0/4/4/4
23	CHD	P	305	-	-	9/9/74/74	0/4/4/4
20	PGV	N	607	-	-	33/55/55/55	-
20	PGV	N	608	-	-	22/55/55/55	-
19	TGL	N	610	-	-	42/65/65/65	-
20	PGV	G	103	-	-	33/55/55/55	-
27	PEK	C	306	-	-	30/56/56/56	-
21	EDO	K	101	-	-	1/1/1/1	-
23	CHD	B	302	-	-	2/9/74/74	0/4/4/4
14	HEA	A	601	1	-	10/36/76/76	-
23	CHD	P	306	-	-	3/9/74/74	0/4/4/4
29	DMU	M	101	-	-	5/19/59/59	0/2/2/2
19	TGL	N	611	-	-	34/65/65/65	-
21	EDO	L	102	-	-	1/1/1/1	-
26	CDL	P	304	-	-	66/110/110/110	-
21	EDO	N	612	-	-	0/1/1/1	-
14	HEA	N	601	1	-	7/36/76/76	-
26	CDL	C	303	-	-	65/110/110/110	-
21	EDO	C	311	-	-	0/1/1/1	-
21	EDO	K	102	-	-	1/1/1/1	-
24	PSC	R	201	-	-	29/55/55/55	-
26	CDL	C	307	-	-	64/110/110/110	-
23	CHD	J	101	-	-	9/9/74/74	0/4/4/4
27	PEK	G	101	-	-	21/56/56/56	-
21	EDO	A	611	-	-	1/1/1/1	-
24	PSC	B	303	-	-	30/55/55/55	-
21	EDO	C	309	-	-	1/1/1/1	-
27	PEK	T	101	-	-	22/56/56/56	-

All (191) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	602	HEA	FE-ND	7.22	2.17	1.94
14	N	602	HEA	FE-NB	6.39	2.14	1.94
14	N	602	HEA	FE-ND	5.64	2.12	1.94
19	L	101	TGL	OG2-CB1	5.59	1.50	1.34
19	A	607	TGL	OG1-CA1	5.58	1.49	1.33
27	T	102	PEK	O01-C1	5.50	1.49	1.34
19	A	607	TGL	OG2-CB1	5.44	1.49	1.34
20	C	308	PGV	O01-C1	5.43	1.49	1.34
19	N	609	TGL	OG2-CB1	5.35	1.49	1.34
27	G	102	PEK	O01-C1	5.32	1.49	1.34
19	N	611	TGL	OG2-CB1	5.29	1.49	1.34
27	G	102	PEK	O03-C21	5.27	1.48	1.33
26	C	307	CDL	OB8-CB7	5.25	1.48	1.33
19	N	611	TGL	OG3-CC1	5.19	1.48	1.33
24	B	303	PSC	O03-C19	5.14	1.48	1.33
26	T	103	CDL	OB8-CB7	5.12	1.48	1.33
26	C	303	CDL	OB8-CB7	5.12	1.48	1.33
20	A	609	PGV	O01-C1	5.10	1.48	1.34
26	C	303	CDL	OB6-CB5	5.10	1.48	1.34
19	L	101	TGL	OG3-CC1	5.09	1.48	1.33
26	P	304	CDL	OB8-CB7	5.06	1.48	1.33
20	C	308	PGV	O03-C19	5.06	1.48	1.33
14	A	602	HEA	FE-NB	5.04	2.10	1.94
27	T	101	PEK	O01-C1	5.01	1.48	1.34
27	T	101	PEK	O03-C21	5.00	1.47	1.33
20	N	607	PGV	O01-C1	4.98	1.48	1.34
19	N	610	TGL	OG2-CB1	4.97	1.48	1.34
24	B	303	PSC	O01-C1	4.96	1.48	1.34
26	P	304	CDL	OA6-CA5	4.93	1.48	1.34
26	P	304	CDL	OA8-CA7	4.93	1.47	1.33
26	C	307	CDL	OB6-CB5	4.91	1.48	1.34
27	T	102	PEK	O03-C21	4.90	1.47	1.33
19	D	201	TGL	OG1-CA1	4.90	1.47	1.33
24	R	201	PSC	O01-C1	4.86	1.48	1.34
26	C	303	CDL	OA6-CA5	4.85	1.48	1.34
20	G	103	PGV	O01-C1	4.83	1.47	1.34
14	N	602	HEA	C4B-NB	-4.80	1.32	1.40
20	N	607	PGV	O03-C19	4.77	1.47	1.33
20	G	103	PGV	O03-C19	4.74	1.47	1.33
26	C	307	CDL	OA8-CA7	4.73	1.47	1.33
14	A	602	HEA	FE-NC	4.72	2.11	1.95
26	T	103	CDL	OA6-CA5	4.68	1.47	1.34
26	C	303	CDL	OA8-CA7	4.66	1.47	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	C	307	CDL	OA6-CA5	4.65	1.47	1.34
26	T	103	CDL	OB6-CB5	4.65	1.47	1.34
14	A	601	HEA	C1D-ND	-4.64	1.32	1.40
19	N	609	TGL	OG1-CA1	4.63	1.46	1.33
19	N	610	TGL	OG3-CC1	4.63	1.46	1.33
27	C	306	PEK	O01-C1	4.63	1.47	1.34
14	A	602	HEA	CHA-C1A	4.59	1.47	1.38
26	P	304	CDL	OB6-CB5	4.57	1.47	1.34
20	A	609	PGV	O03-C19	4.57	1.46	1.33
24	R	201	PSC	O03-C19	4.55	1.46	1.33
19	D	201	TGL	OG3-CC1	4.55	1.46	1.33
27	C	306	PEK	O03-C21	4.54	1.46	1.33
20	P	303	PGV	O03-C19	4.52	1.46	1.33
14	A	602	HEA	C4B-NB	-4.52	1.32	1.40
19	N	610	TGL	OG1-CA1	4.44	1.46	1.33
19	N	611	TGL	OG1-CA1	4.40	1.46	1.33
14	A	601	HEA	C4B-C3B	-4.39	1.37	1.44
19	D	201	TGL	OG2-CB1	4.37	1.46	1.34
19	L	101	TGL	OG1-CA1	4.34	1.46	1.33
20	C	302	PGV	O03-C19	4.18	1.45	1.33
26	T	103	CDL	OA8-CA7	4.14	1.45	1.33
14	N	602	HEA	CHB-C4A	4.12	1.46	1.38
27	G	101	PEK	O03-C21	4.09	1.45	1.33
20	N	608	PGV	O03-C19	4.02	1.45	1.33
27	G	101	PEK	O01-C1	3.98	1.45	1.34
14	A	601	HEA	CHB-C4A	3.98	1.46	1.38
19	N	609	TGL	OG3-CC1	3.94	1.44	1.33
20	A	608	PGV	O03-C19	3.90	1.44	1.33
27	P	302	PEK	O01-C1	3.89	1.45	1.34
24	B	303	PSC	C13-C12	3.83	1.54	1.31
14	N	602	HEA	C1D-ND	-3.81	1.33	1.40
14	A	601	HEA	FE-ND	3.79	2.06	1.94
14	N	601	HEA	FE-ND	3.75	2.06	1.94
14	N	601	HEA	CHA-C1A	3.74	1.45	1.38
14	N	601	HEA	C4B-C3B	-3.74	1.38	1.44
24	R	201	PSC	C13-C12	3.72	1.53	1.31
14	N	601	HEA	C1B-NB	-3.71	1.31	1.38
27	P	302	PEK	O03-C21	3.69	1.44	1.33
14	N	601	HEA	C1D-ND	-3.67	1.34	1.40
20	P	303	PGV	O01-C1	3.60	1.44	1.34
14	A	601	HEA	C4B-NB	-3.58	1.34	1.40
14	N	602	HEA	FE-NA	3.54	2.07	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	602	HEA	C3A-C4A	-3.53	1.39	1.46
14	A	602	HEA	C1B-C2B	-3.41	1.38	1.44
14	N	602	HEA	C1B-C2B	-3.41	1.38	1.44
20	N	608	PGV	O01-C1	3.40	1.43	1.34
14	N	601	HEA	C1B-C2B	-3.38	1.38	1.44
14	A	602	HEA	CHB-C4A	3.37	1.44	1.38
14	A	601	HEA	FE-NB	3.36	2.05	1.94
14	N	602	HEA	C3A-C4A	-3.36	1.40	1.46
14	A	601	HEA	CHA-C1A	3.35	1.44	1.38
20	C	302	PGV	O01-C1	3.34	1.43	1.34
14	A	602	HEA	CHC-C4B	3.28	1.45	1.38
14	N	601	HEA	CMA-C3A	3.18	1.51	1.45
14	N	602	HEA	C1A-C2A	-3.18	1.39	1.45
19	A	607	TGL	OG3-CC1	3.17	1.42	1.33
26	C	307	CDL	C19-C18	-3.17	1.33	1.51
14	A	602	HEA	CHD-C4C	3.16	1.46	1.39
14	N	601	HEA	FE-NC	3.14	2.05	1.95
26	T	103	CDL	C19-C18	-3.12	1.34	1.51
26	C	303	CDL	C59-C58	-3.12	1.34	1.51
26	C	307	CDL	C59-C58	-3.11	1.34	1.51
14	N	602	HEA	C4B-C3B	-3.09	1.39	1.44
26	P	304	CDL	C22-C21	-3.09	1.34	1.51
26	T	103	CDL	C62-C61	-3.08	1.34	1.51
26	C	303	CDL	C79-C78	-3.07	1.34	1.51
14	A	601	HEA	C3A-C4A	-3.07	1.40	1.46
26	C	303	CDL	C22-C21	-3.07	1.34	1.51
26	T	103	CDL	C42-C41	-3.06	1.34	1.51
26	C	303	CDL	C19-C18	-3.05	1.34	1.51
26	P	304	CDL	C79-C78	-3.04	1.34	1.51
26	P	304	CDL	C82-C81	-3.04	1.34	1.51
26	P	304	CDL	C39-C38	-3.04	1.34	1.51
14	N	601	HEA	CHD-C1D	3.03	1.44	1.38
26	T	103	CDL	C79-C78	-3.03	1.34	1.51
26	C	307	CDL	C39-C38	-3.01	1.34	1.51
26	T	103	CDL	C39-C38	-3.01	1.34	1.51
26	P	304	CDL	C59-C58	-3.01	1.34	1.51
26	P	304	CDL	C19-C18	-3.00	1.34	1.51
26	C	307	CDL	C79-C78	-3.00	1.34	1.51
26	T	103	CDL	C59-C58	-2.99	1.34	1.51
26	P	304	CDL	C42-C41	-2.99	1.34	1.51
26	C	303	CDL	C39-C38	-2.98	1.34	1.51
26	C	307	CDL	C42-C41	-2.96	1.35	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	602	HEA	C4C-NC	-2.95	1.34	1.39
26	C	303	CDL	C42-C41	-2.95	1.35	1.51
14	N	601	HEA	C4A-NA	-2.95	1.34	1.39
26	C	307	CDL	C62-C61	-2.93	1.35	1.51
14	N	601	HEA	CHC-C4B	2.93	1.44	1.38
26	C	303	CDL	C62-C61	-2.92	1.35	1.51
26	T	103	CDL	C22-C21	-2.92	1.35	1.51
20	A	608	PGV	O01-C1	2.91	1.42	1.34
26	P	304	CDL	C62-C61	-2.90	1.35	1.51
26	C	303	CDL	C82-C81	-2.90	1.35	1.51
14	A	602	HEA	CMA-C3A	2.90	1.51	1.45
14	N	602	HEA	CHA-C1A	2.85	1.43	1.38
26	T	103	CDL	C82-C81	-2.84	1.35	1.51
26	C	307	CDL	C22-C21	-2.84	1.35	1.51
26	C	307	CDL	C82-C81	-2.80	1.35	1.51
14	A	601	HEA	C1C-NC	-2.78	1.34	1.39
14	A	601	HEA	C1A-C2A	-2.76	1.40	1.45
14	A	602	HEA	CHD-C1D	2.71	1.44	1.38
14	A	602	HEA	C4A-NA	-2.70	1.34	1.39
14	A	601	HEA	O11-C11	2.69	1.48	1.42
14	N	601	HEA	C4B-NB	-2.67	1.35	1.40
14	A	601	HEA	C4C-NC	-2.67	1.34	1.39
14	N	601	HEA	C3A-C4A	-2.61	1.41	1.46
14	N	602	HEA	CHD-C1D	2.60	1.43	1.38
14	N	601	HEA	C1C-NC	-2.59	1.34	1.39
14	N	602	HEA	CMA-C3A	2.59	1.50	1.45
14	N	601	HEA	FE-NB	2.57	2.02	1.94
14	N	602	HEA	C4D-ND	-2.56	1.33	1.38
14	N	602	HEA	C1C-NC	-2.55	1.34	1.39
14	N	602	HEA	CHA-C4D	2.55	1.45	1.39
14	N	601	HEA	C4D-C3D	-2.52	1.40	1.45
14	A	602	HEA	C4B-C3B	-2.51	1.40	1.44
14	A	601	HEA	CMA-C3A	2.50	1.50	1.45
14	A	602	HEA	C1A-C2A	-2.49	1.40	1.45
14	N	601	HEA	CHD-C4C	2.48	1.45	1.39
14	A	601	HEA	CHB-C1B	2.47	1.44	1.39
14	N	601	HEA	CHA-C4D	2.46	1.44	1.39
14	N	602	HEA	CHD-C4C	2.46	1.44	1.39
14	N	602	HEA	C4D-C3D	-2.43	1.40	1.45
14	A	602	HEA	C4D-ND	-2.42	1.33	1.38
14	A	602	HEA	C1C-NC	-2.36	1.35	1.39
14	A	601	HEA	CHC-C4B	2.34	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	601	HEA	C3A-C2A	2.34	1.41	1.36
14	A	602	HEA	C1B-NB	-2.33	1.34	1.38
14	N	602	HEA	C1D-C2D	-2.32	1.40	1.44
14	N	602	HEA	C3A-C2A	2.31	1.41	1.36
14	N	602	HEA	CHB-C1B	2.29	1.44	1.39
14	A	602	HEA	C4C-NC	-2.28	1.35	1.39
14	A	602	HEA	C1D-ND	-2.25	1.36	1.40
14	A	601	HEA	CHD-C1D	2.22	1.43	1.38
26	C	307	CDL	CB3-CB4	2.21	1.57	1.50
14	A	601	HEA	CHD-C4C	2.21	1.44	1.39
20	N	608	PGV	O01-C02	-2.20	1.41	1.46
14	A	601	HEA	C1B-C2B	-2.20	1.40	1.44
23	C	305	CHD	C19-C10	-2.18	1.50	1.54
14	N	601	HEA	CHC-C1C	2.17	1.44	1.39
14	A	601	HEA	O1A-CGA	2.15	1.29	1.22
14	A	602	HEA	O2A-CGA	-2.14	1.23	1.30
23	W	101	CHD	C20-C17	2.12	1.58	1.54
23	P	306	CHD	C13-C14	-2.10	1.51	1.55
19	A	607	TGL	OC1-CC1	-2.07	1.16	1.22
23	O	302	CHD	C13-C17	-2.05	1.52	1.55
14	N	601	HEA	C4C-NC	-2.04	1.35	1.39
23	O	302	CHD	O26-C24	-2.01	1.24	1.30

All (315) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601	HEA	C3C-C4C-NC	7.18	114.66	110.25
14	A	601	HEA	C3D-C4D-ND	6.48	116.63	110.36
23	W	101	CHD	C13-C17-C20	5.97	126.63	119.50
19	N	611	TGL	OG2-CB1-CB2	5.80	124.01	111.50
19	N	609	TGL	OG2-CB1-CB2	5.64	123.66	111.50
26	T	103	CDL	OB6-CB5-C51	5.53	123.42	111.50
26	C	303	CDL	OA6-CA5-C11	5.44	123.22	111.50
27	G	101	PEK	O01-C1-C2	5.30	122.93	111.50
26	T	103	CDL	OA6-CA5-C11	5.15	122.60	111.50
19	N	610	TGL	OG2-CB1-CB2	5.12	122.54	111.50
19	A	607	TGL	CG3-CG2-CG1	-5.12	99.69	111.79
26	C	307	CDL	OB6-CB5-C51	5.09	122.48	111.50
23	C	304	CHD	C10-C9-C8	5.08	117.27	111.82
27	T	102	PEK	O01-C1-C2	5.06	122.40	111.50
23	O	302	CHD	C15-C14-C13	5.04	108.50	103.55
27	P	302	PEK	O01-C1-C2	4.97	122.22	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	608	PGV	O03-C19-C20	4.97	127.51	111.91
19	L	101	TGL	OG2-CB1-CB2	4.96	122.20	111.50
26	P	304	CDL	OA6-CA5-C11	4.90	122.06	111.50
23	P	305	CHD	C6-C5-C4	-4.86	105.60	111.19
14	A	601	HEA	C26-C15-C16	4.71	123.20	115.27
23	W	101	CHD	C9-C10-C5	4.69	115.17	108.58
19	A	607	TGL	OG2-CB1-CB2	4.64	121.51	111.50
27	P	302	PEK	O03-C21-C22	4.62	126.42	111.91
23	W	101	CHD	C6-C5-C10	4.61	117.55	112.66
23	W	101	CHD	C22-C20-C17	4.54	119.66	110.28
14	A	601	HEA	C27-C19-C20	4.44	122.75	115.27
14	A	602	HEA	CAD-CBD-CGD	-4.38	104.18	113.60
26	C	303	CDL	OB6-CB5-C51	4.37	120.93	111.50
14	A	601	HEA	C1D-ND-C4D	-4.37	100.56	105.07
26	C	307	CDL	OA6-CA5-C11	4.26	120.68	111.50
20	A	608	PGV	O03-C19-O04	-4.25	112.86	123.59
20	A	608	PGV	O01-C1-C2	4.21	120.58	111.50
27	C	306	PEK	O01-C1-C2	4.18	120.50	111.50
23	C	304	CHD	C15-C14-C8	4.12	124.10	118.33
23	C	304	CHD	C16-C17-C20	4.12	118.53	112.15
24	B	303	PSC	O01-C1-C2	4.00	120.12	111.50
14	A	601	HEA	C2D-C1D-ND	3.99	114.56	109.84
20	P	303	PGV	O01-C1-C2	3.95	120.01	111.50
23	P	305	CHD	C4-C5-C10	3.94	116.85	112.66
23	C	304	CHD	C6-C5-C4	-3.89	106.72	111.19
14	N	601	HEA	C3C-C4C-NC	3.88	112.64	110.25
20	A	609	PGV	O01-C1-C2	3.88	119.87	111.50
20	N	608	PGV	O03-C19-C20	3.80	123.83	111.91
19	N	609	TGL	OG1-CA1-CA2	3.78	123.77	111.91
23	P	305	CHD	C9-C10-C5	3.78	113.89	108.58
20	N	608	PGV	O01-C1-C2	3.76	119.61	111.50
26	P	304	CDL	OB6-CB5-C51	3.76	119.61	111.50
27	P	302	PEK	O03-C21-O04	-3.75	114.12	123.59
23	B	302	CHD	C1-C2-C3	3.74	115.27	110.47
14	A	601	HEA	C4D-C3D-C2D	-3.73	101.46	106.90
19	A	607	TGL	OG3-CC1-CC2	3.72	123.59	111.91
14	N	602	HEA	CAD-CBD-CGD	-3.71	105.61	113.60
20	G	103	PGV	O01-C1-C2	3.71	119.49	111.50
19	L	101	TGL	OG3-CC1-CC2	3.68	123.46	111.91
27	T	101	PEK	O01-C1-C2	3.68	119.43	111.50
14	N	601	HEA	C13-C12-C11	-3.67	108.83	114.35
14	N	602	HEA	C27-C19-C20	3.64	121.39	115.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	P	305	CHD	C15-C14-C13	3.63	107.12	103.55
24	B	303	PSC	O03-C19-C20	3.63	123.30	111.91
14	A	601	HEA	CHA-C1A-NA	3.59	128.32	124.44
23	W	101	CHD	C10-C9-C8	3.56	115.64	111.82
20	N	607	PGV	O01-C1-C2	3.54	119.14	111.50
19	A	607	TGL	OG3-CC1-OC1	-3.53	114.69	123.59
20	G	103	PGV	O03-C19-C20	3.51	122.92	111.91
29	M	101	DMU	C6-O5-C4	3.51	120.57	113.69
27	T	101	PEK	O03-C01-C02	3.50	118.61	108.43
24	R	201	PSC	O03-C19-C20	3.49	122.87	111.91
23	J	101	CHD	C21-C20-C22	-3.49	104.90	110.36
23	J	101	CHD	C1-C2-C3	3.49	114.94	110.47
27	G	102	PEK	O01-C1-C2	3.42	118.88	111.50
20	N	607	PGV	O03-C19-C20	3.41	122.61	111.91
27	G	102	PEK	O03-C01-C02	3.40	118.32	108.43
20	C	308	PGV	O03-C19-C20	3.39	122.56	111.91
24	R	201	PSC	O01-C1-C2	3.39	118.81	111.50
14	N	602	HEA	CHC-C1C-C2C	-3.39	117.66	127.24
14	A	601	HEA	C4C-NC-C1C	-3.39	102.03	105.35
23	W	101	CHD	C17-C13-C12	3.36	120.74	117.67
14	N	602	HEA	C3A-C2A-C1A	-3.36	103.87	107.08
19	N	611	TGL	OG3-CC1-CC2	3.36	122.45	111.91
26	C	307	CDL	OA8-CA7-C31	3.36	122.44	111.91
26	C	303	CDL	OB8-CB7-C71	3.35	122.43	111.91
14	N	601	HEA	CHB-C4A-C3A	-3.33	119.55	125.26
14	A	602	HEA	CHA-C4D-ND	-3.33	120.80	124.42
23	B	302	CHD	C13-C17-C20	-3.32	115.54	119.50
23	C	304	CHD	C4-C5-C10	3.30	116.16	112.66
14	A	601	HEA	C1C-CHC-C4B	-3.30	118.52	126.34
14	N	602	HEA	CBD-CAD-C3D	3.27	121.72	112.63
14	A	601	HEA	C13-C12-C11	-3.27	109.44	114.35
23	P	306	CHD	C13-C17-C20	-3.24	115.63	119.50
19	N	611	TGL	OG2-CB1-OB1	-3.23	115.89	123.70
27	P	302	PEK	O01-C1-O02	-3.23	115.89	123.70
19	A	607	TGL	OG1-CA1-CA2	3.21	121.99	111.91
14	A	602	HEA	C27-C19-C20	3.21	120.67	115.27
23	C	304	CHD	C23-C22-C20	-3.21	108.66	114.52
14	N	602	HEA	CHC-C1C-NC	3.21	129.75	123.85
14	N	601	HEA	C4A-C3A-C2A	-3.20	104.13	106.75
23	C	305	CHD	C6-C7-C8	3.20	114.89	111.48
20	C	308	PGV	O01-C1-C2	3.19	118.39	111.50
14	A	601	HEA	CHA-C1A-C2A	-3.18	119.78	124.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601	HEA	CHA-C4D-C3D	-3.18	120.16	124.84
27	T	102	PEK	O03-C21-C22	3.18	121.89	111.91
19	N	609	TGL	CG3-CG2-CG1	-3.18	104.27	111.79
20	A	609	PGV	O03-C19-C20	3.18	121.88	111.91
23	O	302	CHD	C14-C8-C9	-3.17	105.35	109.71
27	G	101	PEK	O01-C1-O02	-3.17	116.05	123.70
19	N	610	TGL	OG3-CC1-CC2	3.15	121.80	111.91
14	A	601	HEA	CHD-C1D-ND	-3.15	120.49	124.37
27	G	102	PEK	O03-C21-C22	3.13	121.75	111.91
23	C	304	CHD	C15-C14-C13	3.13	106.62	103.55
20	A	608	PGV	O01-C1-O02	-3.12	116.16	123.70
19	N	610	TGL	OG2-CB1-OB1	-3.09	116.24	123.70
14	A	601	HEA	CAD-C3D-C4D	3.09	130.05	124.66
14	A	601	HEA	C1A-CHA-C4D	-3.08	119.41	126.06
19	N	610	TGL	OG1-CA1-CA2	3.06	121.52	111.91
26	T	103	CDL	OB8-CB7-C71	3.02	121.39	111.91
23	W	101	CHD	C6-C5-C4	-3.02	107.71	111.19
23	J	101	CHD	C6-C7-C8	3.02	114.70	111.48
20	A	608	PGV	C02-O01-C1	-3.01	110.37	117.79
19	N	609	TGL	OG3-CC1-CC2	3.01	121.34	111.91
29	M	101	DMU	O2-C8-C7	-2.99	103.43	110.35
20	N	608	PGV	O03-C19-O04	-2.99	116.05	123.59
20	P	303	PGV	O03-C19-C20	2.97	121.24	111.91
14	A	601	HEA	CHB-C4A-C3A	-2.97	120.18	125.26
19	D	201	TGL	OG3-CC1-CC2	2.96	121.21	111.91
23	P	305	CHD	C16-C17-C13	2.95	106.44	103.55
14	N	602	HEA	C1C-CHC-C4B	-2.94	119.36	126.34
27	G	101	PEK	O03-C01-C02	-2.93	99.90	108.43
20	P	303	PGV	O01-C1-O02	-2.92	116.65	123.70
23	P	306	CHD	O12-C12-C11	-2.91	103.19	109.12
14	A	601	HEA	C27-C19-C18	-2.91	116.22	123.68
23	C	304	CHD	C1-C10-C5	2.89	112.04	107.77
19	N	611	TGL	OG3-CG3-CG2	2.87	116.79	108.43
20	C	308	PGV	C01-O03-C19	2.87	127.74	117.12
14	A	602	HEA	C1D-C2D-C3D	-2.86	103.95	106.96
19	D	201	TGL	OG1-CA1-CA2	2.86	120.89	111.91
23	C	304	CHD	C9-C11-C12	-2.86	110.52	114.30
23	P	305	CHD	C11-C12-C13	2.83	114.15	111.24
27	G	102	PEK	C02-O01-C1	2.83	124.76	117.79
14	A	601	HEA	CHB-C4A-NA	2.83	127.50	124.44
19	D	201	TGL	OG2-CB1-CB2	2.82	117.57	111.50
19	D	201	TGL	CG2-OG2-CB1	-2.81	110.87	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	P	306	CHD	C16-C15-C14	-2.81	99.56	105.13
23	W	101	CHD	C1-C2-C3	2.80	114.06	110.47
23	P	305	CHD	C10-C9-C8	2.78	114.80	111.82
23	O	302	CHD	C1-C10-C5	2.77	111.87	107.77
26	P	304	CDL	OB8-CB7-C71	2.76	120.58	111.91
14	N	601	HEA	C2A-C1A-NA	2.76	113.01	110.32
23	P	305	CHD	C19-C10-C1	-2.76	103.82	108.26
26	C	307	CDL	OB8-CB7-C71	2.73	120.49	111.91
14	A	601	HEA	C2C-C1C-NC	2.73	114.24	110.08
14	N	602	HEA	C20-C19-C18	-2.73	115.59	121.12
19	L	101	TGL	OG3-CG3-CG2	2.73	116.38	108.43
20	N	607	PGV	O03-C19-O04	-2.71	116.76	123.59
14	A	601	HEA	CAA-C2A-C1A	-2.70	119.81	124.89
14	A	601	HEA	O11-C11-C12	2.70	116.96	109.42
23	J	101	CHD	C21-C20-C17	2.67	117.01	112.92
14	A	602	HEA	C3A-C2A-C1A	-2.67	104.53	107.08
26	P	304	CDL	OA8-CA7-C31	2.66	120.25	111.91
26	T	103	CDL	OA8-CA7-C31	2.65	120.24	111.91
20	A	609	PGV	C02-O01-C1	2.65	124.32	117.79
23	P	306	CHD	C18-C13-C14	-2.65	107.06	111.21
14	N	601	HEA	C3A-C2A-C1A	-2.63	104.56	107.08
26	T	103	CDL	OB6-CB5-OB7	-2.62	117.36	123.70
14	A	602	HEA	O2A-CGA-O1A	-2.62	116.77	123.30
14	A	602	HEA	CHB-C4A-C3A	-2.61	120.79	125.26
26	C	303	CDL	OA6-CA5-OA7	-2.61	117.39	123.70
23	B	302	CHD	C6-C5-C4	-2.60	108.20	111.19
19	N	610	TGL	OG3-CC1-OC1	-2.58	117.07	123.59
29	Z	101	DMU	C10-O1-C9	2.58	118.74	113.69
14	A	601	HEA	CHC-C1C-C2C	-2.57	119.97	127.24
29	M	101	DMU	O1-C9-C11	2.57	112.83	106.44
14	N	601	HEA	C4A-NA-C1A	-2.54	102.86	105.35
23	J	101	CHD	C5-C4-C3	2.54	116.49	112.76
23	P	306	CHD	C14-C13-C12	2.53	109.75	107.40
26	C	307	CDL	CB6-OB8-CB7	2.52	126.45	117.12
14	N	602	HEA	CMD-C2D-C1D	2.52	128.87	125.04
23	O	302	CHD	C6-C5-C4	-2.52	108.29	111.19
23	P	306	CHD	C9-C11-C12	-2.52	110.98	114.30
19	N	609	TGL	OG1-CA1-OA1	-2.51	117.26	123.59
23	C	305	CHD	C9-C10-C5	2.51	112.11	108.58
23	C	305	CHD	O26-C24-C23	2.50	122.06	114.03
14	A	602	HEA	C20-C19-C18	-2.50	116.06	121.12
20	C	302	PGV	O03-C19-C20	2.50	119.74	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	602	HEA	CBA-CAA-C2A	2.49	119.56	112.63
23	P	305	CHD	C1-C10-C5	2.49	111.44	107.77
26	C	307	CDL	OB6-CB5-OB7	-2.48	117.70	123.70
19	L	101	TGL	OG3-CC1-OC1	-2.48	117.33	123.59
26	T	103	CDL	CB6-OB8-CB7	2.48	126.30	117.12
26	P	304	CDL	OB8-CB7-OB9	-2.47	117.35	123.59
27	T	101	PEK	O03-C21-C22	2.47	119.67	111.91
27	P	302	PEK	C03-C02-C01	-2.47	105.94	111.79
27	T	102	PEK	O03-C01-C02	2.47	115.62	108.43
14	N	602	HEA	C2A-C1A-NA	2.45	112.70	110.32
23	P	306	CHD	O12-C12-C13	2.44	115.15	111.03
23	J	101	CHD	C10-C9-C8	2.43	114.43	111.82
14	A	602	HEA	CMC-C2C-C1C	2.43	129.07	125.37
19	N	611	TGL	OG1-CA1-CA2	2.43	119.53	111.91
23	C	305	CHD	C19-C10-C1	-2.43	104.35	108.26
24	R	201	PSC	O03-C19-O04	-2.42	117.48	123.59
29	M	101	DMU	C18-O16-C6	-2.42	109.83	113.84
14	A	601	HEA	O2A-CGA-O1A	2.41	129.31	123.30
19	N	609	TGL	OG3-CC1-OC1	-2.41	117.52	123.59
26	C	303	CDL	OA8-CA7-C31	2.40	119.43	111.91
26	C	307	CDL	OA8-CA6-CA4	2.39	115.39	108.43
19	N	611	TGL	CG2-OG2-CB1	2.39	123.67	117.79
23	J	101	CHD	C4-C3-C2	2.39	113.40	110.55
14	N	602	HEA	C2D-C1D-ND	2.39	112.67	109.84
19	D	201	TGL	OG3-CC1-OC1	-2.39	117.57	123.59
20	C	302	PGV	O01-C1-C2	2.39	116.64	111.50
20	N	607	PGV	O03-C01-C02	2.38	115.36	108.43
23	W	101	CHD	C18-C13-C14	-2.38	107.49	111.21
14	N	601	HEA	CBA-CAA-C2A	2.38	119.23	112.63
23	O	302	CHD	C22-C20-C17	-2.38	105.38	110.28
26	T	103	CDL	CA6-CA4-CA3	-2.38	106.17	111.79
26	T	103	CDL	OA6-CA5-OA7	-2.38	117.96	123.70
23	P	305	CHD	C15-C14-C8	2.36	121.64	118.33
23	W	101	CHD	C4-C5-C10	2.36	115.16	112.66
23	P	306	CHD	C18-C13-C12	2.36	111.47	109.07
20	C	302	PGV	C03-C02-C01	-2.35	106.22	111.79
23	W	101	CHD	C22-C23-C24	2.35	118.75	112.51
14	A	601	HEA	CHC-C4B-NB	2.34	127.26	124.37
14	A	602	HEA	C2D-C1D-ND	2.34	112.61	109.84
23	W	101	CHD	C19-C10-C9	-2.33	107.97	111.18
29	Z	101	DMU	O1-C9-C11	2.33	112.22	106.44
14	N	602	HEA	C3C-C2C-C1C	-2.32	104.36	107.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	609	PGV	O03-C19-O04	-2.31	117.75	123.59
14	A	601	HEA	C3B-C4B-NB	2.31	112.57	109.84
23	W	101	CHD	C4-C3-C2	2.30	113.30	110.55
27	C	306	PEK	C01-O03-C21	2.30	125.64	117.12
23	W	101	CHD	O26-C24-C23	2.30	121.42	114.03
23	C	305	CHD	C6-C5-C4	-2.30	108.54	111.19
29	Z	101	DMU	C18-O16-C6	-2.29	110.04	113.84
27	G	102	PEK	C01-O03-C21	2.29	125.59	117.12
24	B	303	PSC	O03-C01-C02	2.29	115.09	108.43
14	N	601	HEA	O2A-CGA-CBA	2.28	121.37	114.03
19	A	607	TGL	CG2-OG2-CB1	2.28	123.41	117.79
23	W	101	CHD	C16-C17-C20	2.28	115.67	112.15
23	W	101	CHD	C18-C13-C12	-2.27	106.76	109.07
14	A	601	HEA	C4A-C3A-C2A	-2.26	104.90	106.75
19	N	610	TGL	OG1-CA1-OA1	-2.26	117.89	123.59
23	C	304	CHD	C19-C10-C1	-2.26	104.62	108.26
20	P	303	PGV	O03-C19-O04	-2.25	117.92	123.59
23	C	304	CHD	C11-C9-C10	-2.25	111.41	113.73
23	C	304	CHD	C14-C13-C12	2.25	109.50	107.40
14	N	601	HEA	C2B-C1B-NB	2.24	112.57	109.88
23	P	305	CHD	C14-C8-C9	-2.24	106.63	109.71
14	A	601	HEA	CHD-C4C-C3C	-2.22	117.85	127.71
14	A	602	HEA	C26-C15-C16	2.21	118.99	115.27
14	N	602	HEA	C3D-C4D-ND	2.21	112.49	110.36
27	T	102	PEK	O03-C21-O04	-2.20	118.03	123.59
14	N	601	HEA	C3D-C4D-ND	2.20	112.48	110.36
23	O	302	CHD	C21-C20-C22	2.20	113.81	110.36
14	A	601	HEA	CHC-C4B-C3B	-2.19	120.15	125.80
23	P	305	CHD	C5-C4-C3	2.19	115.98	112.76
14	A	602	HEA	CHB-C4A-NA	2.19	126.81	124.44
23	P	306	CHD	C6-C7-C8	2.18	113.81	111.48
19	A	607	TGL	OB1-CB1-CB2	-2.18	115.23	123.73
26	T	103	CDL	C83-C82-C81	2.18	125.48	114.42
14	N	602	HEA	CHD-C4C-NC	2.16	127.82	123.85
23	C	304	CHD	C1-C2-C3	2.16	113.24	110.47
14	N	602	HEA	CMC-C2C-C3C	2.16	131.81	126.59
23	B	302	CHD	C22-C20-C17	2.15	114.74	110.28
23	C	304	CHD	O25-C24-C23	-2.15	116.17	123.08
24	B	303	PSC	C01-O03-C19	2.15	125.07	117.12
23	W	101	CHD	C14-C8-C7	2.14	114.65	111.81
23	P	306	CHD	O26-C24-C23	2.14	120.91	114.03
29	Z	101	DMU	C6-O5-C4	-2.14	109.48	113.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	T	101	PEK	O01-C02-C01	2.14	116.15	108.40
20	N	608	PGV	O01-C1-O02	-2.14	118.53	123.70
14	A	602	HEA	C3C-C2C-C1C	-2.14	104.58	107.16
14	A	602	HEA	C4A-CHB-C1B	-2.14	121.45	126.06
14	A	601	HEA	CMB-C2B-C1B	2.13	128.29	125.04
19	N	609	TGL	OB1-CB1-CB2	-2.13	115.42	123.73
14	N	601	HEA	CMD-C2D-C1D	2.13	128.28	125.04
14	A	602	HEA	CMB-C2B-C1B	2.12	128.26	125.04
23	P	305	CHD	C13-C17-C20	-2.11	116.98	119.50
23	C	305	CHD	C4-C3-C2	2.11	113.07	110.55
14	A	602	HEA	CBD-CAD-C3D	2.10	118.47	112.63
19	A	607	TGL	OG1-CA1-OA1	-2.10	118.29	123.59
19	A	607	TGL	OG1-CG1-CG2	2.10	114.55	108.43
14	A	601	HEA	C26-C15-C14	-2.10	118.29	123.68
27	C	306	PEK	O03-C21-C22	2.10	118.49	111.91
14	N	601	HEA	CAA-C2A-C1A	2.09	128.84	124.89
23	J	101	CHD	C19-C10-C1	-2.09	104.89	108.26
26	C	307	CDL	OA6-CA5-OA7	-2.09	118.66	123.70
23	C	304	CHD	C9-C10-C5	2.09	111.51	108.58
23	J	101	CHD	C22-C23-C24	-2.08	106.98	112.51
20	P	303	PGV	C03-C02-C01	-2.08	106.87	111.79
19	A	607	TGL	CG1-OG1-CA1	2.08	124.81	117.12
23	P	306	CHD	C11-C12-C13	2.07	113.37	111.24
14	A	601	HEA	CMB-C2B-C3B	-2.07	126.39	130.34
26	C	303	CDL	CA6-CA4-CA3	-2.07	106.90	111.79
23	O	302	CHD	C9-C10-C5	2.07	111.48	108.58
23	J	101	CHD	C13-C17-C20	2.06	121.95	119.50
19	N	611	TGL	OG3-CC1-OC1	-2.06	118.39	123.59
26	P	304	CDL	CA6-OA8-CA7	2.06	124.75	117.12
19	N	609	TGL	OG3-CG3-CG2	2.05	114.41	108.43
26	T	103	CDL	OA8-CA7-OA9	-2.05	118.41	123.59
27	G	101	PEK	C02-O01-C1	-2.05	112.74	117.79
14	N	602	HEA	C3C-C4C-NC	2.05	111.51	110.25
26	T	103	CDL	OB8-CB7-OB9	-2.05	118.42	123.59
19	L	101	TGL	CG3-CG2-CG1	-2.05	106.95	111.79
23	P	306	CHD	C21-C20-C17	-2.05	109.79	112.92
26	C	303	CDL	OA8-CA7-OA9	-2.05	118.43	123.59
24	B	303	PSC	O01-C1-O02	-2.04	118.77	123.70
14	N	602	HEA	CBC-CAC-C3C	-2.04	117.48	127.62
26	P	304	CDL	OA6-CA5-OA7	-2.03	118.80	123.70
23	C	305	CHD	C18-C13-C14	-2.01	108.06	111.21
14	A	601	HEA	O1A-CGA-CBA	-2.01	116.61	123.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	R	201	PSC	C08-N-C06	-2.01	103.81	108.97
20	A	609	PGV	O03-C01-C02	2.01	114.27	108.43
23	O	302	CHD	C1-C10-C9	-2.00	108.20	111.35
20	C	302	PGV	O03-C19-O04	-2.00	118.54	123.59
23	C	304	CHD	C2-C1-C10	2.00	116.21	112.78

There are no chirality outliers.

All (986) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	601	HEA	C1A-C2A-CAA-CBA
14	A	601	HEA	C3A-C2A-CAA-CBA
14	A	602	HEA	C2A-C3A-CMA-OMA
14	A	602	HEA	C4A-C3A-CMA-OMA
14	N	601	HEA	C2A-C3A-CMA-OMA
14	N	601	HEA	C4A-C3A-CMA-OMA
14	N	602	HEA	C2A-C3A-CMA-OMA
19	D	201	TGL	CC2-CC1-OG3-CG3
19	D	201	TGL	OC1-CC1-OG3-CG3
19	L	101	TGL	CB2-CB1-OG2-CG2
19	L	101	TGL	OB1-CB1-OG2-CG2
19	N	610	TGL	OB1-CB1-OG2-CG2
19	N	611	TGL	CB2-CB1-OG2-CG2
19	N	611	TGL	OB1-CB1-OG2-CG2
20	A	609	PGV	C03-O11-P-O12
20	A	609	PGV	C03-O11-P-O13
20	A	609	PGV	C03-O11-P-O14
20	A	609	PGV	C04-C05-C06-O06
20	A	609	PGV	C2-C1-O01-C02
20	C	308	PGV	C03-O11-P-O12
20	C	308	PGV	C03-O11-P-O13
20	C	308	PGV	C03-O11-P-O14
20	C	308	PGV	C04-O12-P-O11
20	C	308	PGV	O12-C04-C05-C06
20	G	103	PGV	C03-O11-P-O13
20	G	103	PGV	C04-O12-P-O11
20	G	103	PGV	C04-O12-P-O13
20	G	103	PGV	C04-O12-P-O14
20	G	103	PGV	O03-C01-C02-O01
20	G	103	PGV	O12-C04-C05-C06
20	N	607	PGV	C03-O11-P-O14
20	N	607	PGV	C04-C05-C06-O06

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Mol	Chain	Res	Type	Atoms
20	N	607	PGV	C20-C19-O03-C01
20	N	608	PGV	C10-C11-C12-C13
23	W	101	CHD	C13-C17-C20-C22
23	W	101	CHD	C16-C17-C20-C22
24	B	303	PSC	O12-C04-C05-N
24	B	303	PSC	C2-C1-O01-C02
24	B	303	PSC	O04-C19-O03-C01
24	B	303	PSC	C11-C10-C9-C8
24	R	201	PSC	C03-O11-P-O12
24	R	201	PSC	C03-O11-P-O13
24	R	201	PSC	C03-O11-P-O14
24	R	201	PSC	C04-O12-P-O14
26	C	303	CDL	CA2-C1-CB2-OB2
26	C	303	CDL	C1-CA2-OA2-PA1
26	C	303	CDL	CA2-OA2-PA1-OA3
26	C	303	CDL	CA2-OA2-PA1-OA4
26	C	303	CDL	CA2-OA2-PA1-OA5
26	C	303	CDL	CA3-OA5-PA1-OA2
26	C	303	CDL	CA3-OA5-PA1-OA3
26	C	303	CDL	OA7-CA5-OA6-CA4
26	C	303	CDL	C11-CA5-OA6-CA4
26	C	303	CDL	CB2-OB2-PB2-OB3
26	C	307	CDL	CB2-C1-CA2-OA2
26	C	307	CDL	C11-CA5-OA6-CA4
26	C	307	CDL	CB2-OB2-PB2-OB3
26	C	307	CDL	CB2-OB2-PB2-OB4
26	C	307	CDL	CB3-OB5-PB2-OB3
26	C	307	CDL	CB3-OB5-PB2-OB4
26	C	307	CDL	OB5-CB3-CB4-OB6
26	C	307	CDL	C51-CB5-OB6-CB4
26	P	304	CDL	CA2-OA2-PA1-OA4
26	P	304	CDL	CA3-OA5-PA1-OA3
26	P	304	CDL	CA3-OA5-PA1-OA4
26	P	304	CDL	OA7-CA5-OA6-CA4
26	P	304	CDL	CB3-OB5-PB2-OB3
26	T	103	CDL	CB2-C1-CA2-OA2
26	T	103	CDL	CA2-OA2-PA1-OA3
26	T	103	CDL	CA2-OA2-PA1-OA4
26	T	103	CDL	CA3-OA5-PA1-OA3
26	T	103	CDL	OA6-CA4-CA6-OA8
26	T	103	CDL	C11-CA5-OA6-CA4
27	C	306	PEK	C03-O11-P-O13

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Mol	Chain	Res	Type	Atoms
27	C	306	PEK	C03-O11-P-O14
27	C	306	PEK	O12-C04-C05-N
27	G	102	PEK	C03-O11-P-O13
27	T	101	PEK	C04-O12-P-O14
27	T	101	PEK	O12-C04-C05-N
27	T	102	PEK	C04-O12-P-O13
27	T	102	PEK	C2-C1-O01-C02
19	L	101	TGL	OA1-CA1-OG1-CG1
19	N	610	TGL	OC1-CC1-OG3-CG3
20	N	607	PGV	O04-C19-O03-C01
26	P	304	CDL	OB9-CB7-OB8-CB6
19	N	610	TGL	CC2-CC1-OG3-CG3
26	P	304	CDL	C71-CB7-OB8-CB6
20	A	609	PGV	O04-C19-O03-C01
20	A	609	PGV	O02-C1-O01-C02
26	C	307	CDL	OA7-CA5-OA6-CA4
26	C	307	CDL	OB7-CB5-OB6-CB4
26	T	103	CDL	OA7-CA5-OA6-CA4
19	L	101	TGL	CA2-CA1-OG1-CG1
19	L	101	TGL	CC2-CC1-OG3-CG3
20	A	609	PGV	C20-C19-O03-C01
19	N	610	TGL	CB2-CB1-OG2-CG2
26	P	304	CDL	C11-CA5-OA6-CA4
23	O	302	CHD	C21-C20-C22-C23
19	N	609	TGL	OC1-CC1-OG3-CG3
19	N	609	TGL	CC2-CC1-OG3-CG3
19	N	611	TGL	CA2-CA1-OG1-CG1
24	B	303	PSC	C20-C19-O03-C01
27	G	102	PEK	C22-C21-O03-C01
27	C	306	PEK	C4-C5-C6-C7
27	G	101	PEK	C4-C5-C6-C7
27	G	101	PEK	C13-C14-C15-C16
27	P	302	PEK	C4-C5-C6-C7
27	P	302	PEK	C10-C11-C12-C13
27	P	302	PEK	C13-C14-C15-C16
24	B	303	PSC	C24-C25-C26-C27
24	B	303	PSC	O02-C1-O01-C02
26	P	304	CDL	OB7-CB5-OB6-CB4
27	T	102	PEK	O02-C1-O01-C02
19	A	607	TGL	OC1-CC1-OG3-CG3
27	G	102	PEK	O04-C21-O03-C01
23	J	101	CHD	C13-C17-C20-C21

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Mol	Chain	Res	Type	Atoms
29	M	101	DMU	O6-C11-C9-O1
20	C	308	PGV	O12-C04-C05-O05
26	C	303	CDL	O1-C1-CB2-OB2
26	C	307	CDL	O1-C1-CA2-OA2
26	P	304	CDL	O1-C1-CA2-OA2
26	T	103	CDL	O1-C1-CA2-OA2
19	A	607	TGL	CC2-CC1-OG3-CG3
26	T	103	CDL	C31-CA7-OA8-CA6
27	C	306	PEK	C22-C21-O03-C01
19	L	101	TGL	OC1-CC1-OG3-CG3
29	Z	101	DMU	O5-C4-C57-O61
29	Z	101	DMU	C3-C4-C57-O61
26	P	304	CDL	C51-CB5-OB6-CB4
27	T	101	PEK	C2-C1-O01-C02
27	T	101	PEK	C24-C25-C26-C27
19	N	611	TGL	CC1-CC2-CC3-CC4
24	R	201	PSC	C20-C19-O03-C01
14	N	602	HEA	C2D-C3D-CAD-CBD
19	N	611	TGL	OA1-CA1-OG1-CG1
26	T	103	CDL	OA9-CA7-OA8-CA6
20	A	608	PGV	C26-C27-C28-C29
23	C	304	CHD	C21-C20-C22-C23
24	R	201	PSC	O04-C19-O03-C01
27	C	306	PEK	O04-C21-O03-C01
23	J	101	CHD	C16-C17-C20-C22
23	C	304	CHD	C17-C20-C22-C23
23	P	305	CHD	C17-C20-C22-C23
14	N	602	HEA	C4D-C3D-CAD-CBD
20	C	302	PGV	C27-C28-C29-C30
26	P	304	CDL	CB2-C1-CA2-OA2
27	T	101	PEK	O02-C1-O01-C02
29	M	101	DMU	O6-C11-C9-C8
19	N	609	TGL	CA2-CA1-OG1-CG1
20	C	308	PGV	C20-C19-O03-C01
26	C	303	CDL	C71-CB7-OB8-CB6
19	A	607	TGL	CB1-CB2-CB3-CB4
19	L	101	TGL	CA1-CA2-CA3-CA4
20	G	103	PGV	C1-C2-C3-C4
27	G	102	PEK	C1-C2-C3-C4
27	G	101	PEK	C33-C34-C35-C36
23	J	101	CHD	C17-C20-C22-C23
20	G	103	PGV	O12-C04-C05-O05

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Mol	Chain	Res	Type	Atoms
20	N	608	PGV	O12-C04-C05-O05
23	P	306	CHD	C21-C20-C22-C23
26	C	303	CDL	OB9-CB7-OB8-CB6
23	C	304	CHD	C20-C22-C23-C24
23	W	101	CHD	C16-C17-C20-C21
19	D	201	TGL	CB2-CB1-OG2-CG2
27	G	102	PEK	C2-C1-O01-C02
20	A	609	PGV	C19-C20-C21-C22
26	C	303	CDL	CA7-C31-C32-C33
26	C	307	CDL	CB5-C51-C52-C53
19	N	609	TGL	OA1-CA1-OG1-CG1
23	O	302	CHD	C17-C20-C22-C23
23	P	305	CHD	C21-C20-C22-C23
26	C	303	CDL	CA5-C11-C12-C13
26	T	103	CDL	CB7-C71-C72-C73
20	A	608	PGV	C10-C11-C12-C13
20	C	308	PGV	C10-C11-C12-C13
20	C	302	PGV	C1-C2-C3-C4
20	P	303	PGV	C1-C2-C3-C4
19	D	201	TGL	OB1-CB1-OG2-CG2
27	G	102	PEK	O02-C1-O01-C02
23	J	101	CHD	C21-C20-C22-C23
26	C	303	CDL	CA4-CA3-OA5-PA1
19	N	609	TGL	CA1-CA2-CA3-CA4
19	N	610	TGL	CA1-CA2-CA3-CA4
19	N	611	TGL	CA1-CA2-CA3-CA4
20	P	303	PGV	C19-C20-C21-C22
26	P	304	CDL	CA5-C11-C12-C13
21	B	304	EDO	O1-C1-C2-O2
23	J	101	CHD	C20-C22-C23-C24
20	C	308	PGV	O04-C19-O03-C01
14	A	601	HEA	C19-C20-C21-C22
19	D	201	TGL	CB1-CB2-CB3-CB4
20	G	103	PGV	C10-C11-C12-C13
20	P	303	PGV	C10-C11-C12-C13
29	Z	101	DMU	O6-C11-C9-C8
19	N	609	TGL	CB2-CB1-OG2-CG2
20	A	609	PGV	C04-O12-P-O11
20	N	607	PGV	C03-O11-P-O12
20	N	608	PGV	C04-O12-P-O11
24	R	201	PSC	C04-O12-P-O11
26	C	303	CDL	CB2-OB2-PB2-OB5

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Mol	Chain	Res	Type	Atoms
26	C	307	CDL	CB2-OB2-PB2-OB5
26	C	307	CDL	CB3-OB5-PB2-OB2
26	P	304	CDL	CA2-OA2-PA1-OA5
26	P	304	CDL	CA3-OA5-PA1-OA2
26	T	103	CDL	CA2-OA2-PA1-OA5
26	T	103	CDL	CB3-OB5-PB2-OB2
27	C	306	PEK	C03-O11-P-O12
27	G	102	PEK	C03-O11-P-O12
27	T	102	PEK	C04-O12-P-O11
20	C	308	PGV	C19-C20-C21-C22
23	W	101	CHD	C13-C17-C20-C21
20	N	608	PGV	O12-C04-C05-C06
19	N	609	TGL	OB1-CB1-OG2-CG2
26	T	103	CDL	C79-C80-C81-C82
27	T	102	PEK	C22-C21-O03-C01
19	L	101	TGL	C21-C22-C23-C24
19	N	610	TGL	C11-C10-CB9-CB8
20	C	308	PGV	C26-C27-C28-C29
26	C	303	CDL	C35-C36-C37-C38
26	C	303	CDL	C63-C64-C65-C66
26	C	307	CDL	C71-C72-C73-C74
27	G	102	PEK	C30-C31-C32-C33
27	P	302	PEK	C26-C27-C28-C29
26	T	103	CDL	C51-CB5-OB6-CB4
19	A	607	TGL	C11-C12-C13-C14
19	D	201	TGL	C14-C29-C30-C31
19	N	609	TGL	CA2-CA3-CA4-CA5
19	N	609	TGL	CB9-C10-C11-C12
19	N	609	TGL	C24-C25-C26-C27
19	N	611	TGL	C24-C25-C26-C27
20	C	308	PGV	C4-C5-C6-C7
26	C	307	CDL	C57-C58-C59-C60
26	T	103	CDL	C36-C37-C38-C39
27	G	101	PEK	C29-C30-C31-C32
19	N	609	TGL	CA5-CA6-CA7-CA8
19	N	609	TGL	CC6-CC7-CC8-CC9
19	N	610	TGL	C16-C15-CC9-CC8
20	A	609	PGV	C20-C21-C22-C23
20	G	103	PGV	C6-C7-C8-C9
20	N	608	PGV	C2-C3-C4-C5
20	N	608	PGV	C13-C14-C15-C16
26	T	103	CDL	C54-C55-C56-C57

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Mol	Chain	Res	Type	Atoms
27	G	101	PEK	C26-C27-C28-C29
27	T	102	PEK	C29-C30-C31-C32
29	Z	101	DMU	C25-C28-C31-C34
20	C	308	PGV	O02-C1-O01-C02
26	T	103	CDL	OB7-CB5-OB6-CB4
19	A	607	TGL	CC2-CC3-CC4-CC5
19	L	101	TGL	CB5-CB6-CB7-CB8
20	A	609	PGV	C21-C22-C23-C24
20	P	303	PGV	C20-C21-C22-C23
24	B	303	PSC	C28-C29-C30-C31
24	R	201	PSC	C20-C21-C22-C23
26	C	307	CDL	C17-C18-C19-C20
26	P	304	CDL	C20-C21-C22-C23
26	T	103	CDL	C42-C43-C44-C45
27	C	306	PEK	C16-C17-C18-C19
19	D	201	TGL	CC6-CC7-CC8-CC9
19	N	610	TGL	CA2-CA3-CA4-CA5
20	C	308	PGV	C7-C8-C9-C10
26	C	303	CDL	C12-C13-C14-C15
26	P	304	CDL	C81-C82-C83-C84
26	T	103	CDL	C12-C13-C14-C15
26	T	103	CDL	C57-C58-C59-C60
29	Z	101	DMU	C28-C31-C34-C37
20	N	607	PGV	O12-C04-C05-O05
19	L	101	TGL	C12-C13-C14-C29
19	N	610	TGL	C18-C19-C33-C34
19	N	610	TGL	C19-C33-C34-C35
20	C	308	PGV	C23-C24-C25-C26
20	P	303	PGV	C7-C8-C9-C10
24	R	201	PSC	C3-C4-C5-C6
26	C	303	CDL	C33-C34-C35-C36
26	C	307	CDL	C33-C34-C35-C36
27	G	102	PEK	C23-C24-C25-C26
19	L	101	TGL	CA6-CA7-CA8-CA9
19	N	611	TGL	CB5-CB6-CB7-CB8
20	G	103	PGV	C22-C23-C24-C25
26	C	303	CDL	C80-C81-C82-C83
26	C	307	CDL	C22-C23-C24-C25
26	T	103	CDL	C52-C53-C54-C55
27	P	302	PEK	C28-C29-C30-C31
19	D	201	TGL	C10-C11-C12-C13
19	D	201	TGL	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
19	L	101	TGL	C16-C17-C18-C19
20	N	607	PGV	C29-C30-C31-C32
20	N	608	PGV	C23-C24-C25-C26
26	C	307	CDL	C35-C36-C37-C38
19	D	201	TGL	C12-C13-C14-C29
19	L	101	TGL	CA2-CA3-CA4-CA5
19	L	101	TGL	C21-C20-CA9-CA8
19	N	610	TGL	CA3-CA4-CA5-CA6
20	A	608	PGV	C22-C23-C24-C25
24	R	201	PSC	C4-C5-C6-C7
26	C	307	CDL	C58-C59-C60-C61
26	C	307	CDL	C61-C62-C63-C64
26	P	304	CDL	C43-C44-C45-C46
26	T	103	CDL	C40-C41-C42-C43
27	C	306	PEK	C34-C35-C36-C37
27	T	101	PEK	C28-C29-C30-C31
19	N	610	TGL	C17-C18-C19-C33
20	C	308	PGV	C6-C7-C8-C9
24	R	201	PSC	C5-C6-C7-C8
26	C	303	CDL	C20-C21-C22-C23
26	T	103	CDL	C41-C42-C43-C44
27	G	102	PEK	C31-C32-C33-C34
20	C	308	PGV	C2-C1-O01-C02
19	A	607	TGL	C14-C29-C30-C31
19	D	201	TGL	C18-C19-C33-C34
19	L	101	TGL	CB3-CB4-CB5-CB6
19	L	101	TGL	C20-C21-C22-C23
19	N	609	TGL	CA4-CA5-CA6-CA7
19	N	611	TGL	CA7-CA8-CA9-C20
20	P	303	PGV	C25-C26-C27-C28
27	G	102	PEK	C15-C16-C17-C18
19	N	610	TGL	CB1-CB2-CB3-CB4
19	A	607	TGL	C24-C25-C26-C27
19	N	609	TGL	C21-C20-CA9-CA8
19	N	609	TGL	CB2-CB3-CB4-CB5
19	N	611	TGL	CB3-CB4-CB5-CB6
20	A	609	PGV	C30-C31-C32-C33
20	C	308	PGV	C3-C4-C5-C6
20	G	103	PGV	C4-C5-C6-C7
20	G	103	PGV	C24-C25-C26-C27
20	P	303	PGV	C29-C30-C31-C32
26	C	303	CDL	C81-C82-C83-C84

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Mol	Chain	Res	Type	Atoms
26	C	307	CDL	C62-C63-C64-C65
26	P	304	CDL	C31-C32-C33-C34
26	P	304	CDL	C37-C38-C39-C40
26	T	103	CDL	C18-C19-C20-C21
26	T	103	CDL	C59-C60-C61-C62
27	G	101	PEK	C30-C31-C32-C33
19	A	607	TGL	CA3-CA4-CA5-CA6
19	A	607	TGL	CC3-CC4-CC5-CC6
19	D	201	TGL	CA3-CA4-CA5-CA6
19	N	611	TGL	C17-C18-C19-C33
24	R	201	PSC	C21-C22-C23-C24
26	C	307	CDL	C23-C24-C25-C26
26	P	304	CDL	C35-C36-C37-C38
26	P	304	CDL	C56-C57-C58-C59
27	G	102	PEK	C32-C33-C34-C35
27	T	102	PEK	C26-C27-C28-C29
19	A	607	TGL	C17-C18-C19-C33
19	L	101	TGL	CC2-CC3-CC4-CC5
19	L	101	TGL	CC7-CC8-CC9-C15
19	N	609	TGL	CC2-CC3-CC4-CC5
24	B	303	PSC	C27-C28-C29-C30
26	P	304	CDL	C36-C37-C38-C39
26	T	103	CDL	C73-C74-C75-C76
27	C	306	PEK	C25-C26-C27-C28
27	G	101	PEK	C31-C32-C33-C34
20	N	608	PGV	C19-C20-C21-C22
27	T	102	PEK	O04-C21-O03-C01
19	N	609	TGL	CB4-CB5-CB6-CB7
19	N	610	TGL	CC5-CC6-CC7-CC8
20	C	302	PGV	C30-C31-C32-C33
26	C	303	CDL	C42-C43-C44-C45
19	A	607	TGL	CA5-CA6-CA7-CA8
19	N	609	TGL	C21-C22-C23-C24
19	N	610	TGL	C21-C20-CA9-CA8
20	C	308	PGV	C2-C3-C4-C5
26	C	303	CDL	C77-C78-C79-C80
27	P	302	PEK	C25-C26-C27-C28
23	J	101	CHD	C13-C17-C20-C22
19	A	607	TGL	CA9-C20-C21-C22
19	L	101	TGL	C18-C19-C33-C34
19	N	610	TGL	C20-C21-C22-C23
19	N	611	TGL	CC5-CC6-CC7-CC8

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Mol	Chain	Res	Type	Atoms
20	G	103	PGV	C23-C24-C25-C26
24	B	303	PSC	C1-C2-C3-C4
19	A	607	TGL	CB9-C10-C11-C12
19	A	607	TGL	CC9-C15-C16-C17
19	A	607	TGL	C21-C22-C23-C24
26	C	307	CDL	C14-C15-C16-C17
26	C	307	CDL	C16-C17-C18-C19
26	P	304	CDL	C38-C39-C40-C41
24	R	201	PSC	C11-C12-C13-C14
27	C	306	PEK	C10-C11-C12-C13
27	G	101	PEK	C7-C8-C9-C10
19	L	101	TGL	CA4-CA5-CA6-CA7
19	N	610	TGL	C12-C13-C14-C29
19	N	611	TGL	C21-C22-C23-C24
20	G	103	PGV	C13-C14-C15-C16
20	G	103	PGV	C26-C27-C28-C29
27	C	306	PEK	C29-C30-C31-C32
19	D	201	TGL	C21-C20-CA9-CA8
20	G	103	PGV	C3-C4-C5-C6
26	C	303	CDL	C19-C20-C21-C22
19	N	609	TGL	CC4-CC5-CC6-CC7
26	C	303	CDL	C62-C63-C64-C65
27	G	101	PEK	C28-C29-C30-C31
20	A	609	PGV	O05-C05-C06-O06
19	D	201	TGL	CA9-C20-C21-C22
19	N	610	TGL	C15-C16-C17-C18
20	P	303	PGV	C21-C22-C23-C24
27	P	302	PEK	C22-C23-C24-C25
26	C	303	CDL	C37-C38-C39-C40
26	T	103	CDL	C22-C23-C24-C25
26	T	103	CDL	CA7-C31-C32-C33
20	N	607	PGV	O12-C04-C05-C06
19	L	101	TGL	CA7-CA8-CA9-C20
26	C	307	CDL	C54-C55-C56-C57
26	C	307	CDL	C59-C60-C61-C62
24	R	201	PSC	O02-C1-O01-C02
26	P	304	CDL	C1-CA2-OA2-PA1
26	T	103	CDL	C1-CA2-OA2-PA1
24	B	303	PSC	C14-C15-C16-C17
26	P	304	CDL	C21-C22-C23-C24
24	B	303	PSC	C19-C20-C21-C22
21	A	612	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
21	A	613	EDO	O1-C1-C2-O2
21	L	102	EDO	O1-C1-C2-O2
21	T	104	EDO	O1-C1-C2-O2
19	A	607	TGL	CB4-CB5-CB6-CB7
19	D	201	TGL	CB9-C10-C11-C12
19	N	609	TGL	C14-C29-C30-C31
24	R	201	PSC	C2-C1-O01-C02
19	N	609	TGL	CC5-CC6-CC7-CC8
20	A	608	PGV	C15-C16-C17-C18
19	L	101	TGL	CC1-CC2-CC3-CC4
27	C	306	PEK	C1-C2-C3-C4
27	T	102	PEK	C1-C2-C3-C4
26	C	303	CDL	C58-C59-C60-C61
26	P	304	CDL	C52-C53-C54-C55
24	R	201	PSC	C11-C10-C9-C8
27	G	102	PEK	C13-C14-C15-C16
27	T	101	PEK	C7-C8-C9-C10
19	D	201	TGL	CC7-CC8-CC9-C15
20	C	308	PGV	C24-C25-C26-C27
26	C	303	CDL	C16-C17-C18-C19
27	C	306	PEK	C32-C33-C34-C35
26	C	307	CDL	C78-C79-C80-C81
27	G	102	PEK	C34-C35-C36-C37
19	D	201	TGL	CA1-CA2-CA3-CA4
27	G	101	PEK	C21-C22-C23-C24
19	D	201	TGL	C21-C22-C23-C24
26	C	307	CDL	C52-C53-C54-C55
27	G	101	PEK	C23-C24-C25-C26
27	G	102	PEK	C16-C17-C18-C19
26	P	304	CDL	C16-C17-C18-C19
26	P	304	CDL	C19-C20-C21-C22
26	T	103	CDL	C11-C12-C13-C14
26	T	103	CDL	C55-C56-C57-C58
27	T	102	PEK	C30-C31-C32-C33
19	A	607	TGL	CB2-CB1-OG2-CG2
19	L	101	TGL	CB2-CB3-CB4-CB5
20	N	607	PGV	C25-C26-C27-C28
20	A	608	PGV	C20-C21-C22-C23
19	N	610	TGL	CA9-C20-C21-C22
20	N	608	PGV	C6-C7-C8-C9
26	P	304	CDL	C42-C43-C44-C45
26	T	103	CDL	C43-C44-C45-C46

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Mol	Chain	Res	Type	Atoms
20	A	608	PGV	C11-C10-C9-C8
20	P	303	PGV	C11-C10-C9-C8
24	B	303	PSC	C6-C7-C8-C9
27	G	101	PEK	C15-C16-C17-C18
27	P	302	PEK	C2-C3-C4-C5
14	A	601	HEA	C27-C19-C20-C21
20	A	609	PGV	C5-C6-C7-C8
19	D	201	TGL	C23-C24-C25-C26
19	N	610	TGL	CC2-CC3-CC4-CC5
26	C	307	CDL	C56-C57-C58-C59
26	T	103	CDL	C60-C61-C62-C63
19	N	609	TGL	C20-C21-C22-C23
20	N	607	PGV	C7-C8-C9-C10
19	N	610	TGL	CB7-CB8-CB9-C10
19	N	611	TGL	C11-C12-C13-C14
26	C	303	CDL	C36-C37-C38-C39
27	P	302	PEK	C16-C17-C18-C19
19	N	610	TGL	CA6-CA7-CA8-CA9
27	T	102	PEK	C03-O11-P-O12
20	G	103	PGV	C2-C3-C4-C5
26	P	304	CDL	OA5-CA3-CA4-CA6
26	P	304	CDL	OB5-CB3-CB4-CB6
26	T	103	CDL	OA5-CA3-CA4-CA6
26	T	103	CDL	OB5-CB3-CB4-CB6
19	N	610	TGL	CA5-CA6-CA7-CA8
20	C	308	PGV	C25-C26-C27-C28
27	P	302	PEK	C1-C2-C3-C4
19	D	201	TGL	C16-C17-C18-C19
20	N	607	PGV	C3-C4-C5-C6
26	C	303	CDL	C83-C84-C85-C86
27	P	302	PEK	C27-C28-C29-C30
19	A	607	TGL	C22-C23-C24-C25
26	C	307	CDL	C32-C33-C34-C35
20	N	607	PGV	C12-C13-C14-C15
19	N	610	TGL	CB6-CB7-CB8-CB9
27	T	101	PEK	C29-C30-C31-C32
19	A	607	TGL	OB1-CB1-OG2-CG2
19	A	607	TGL	C19-C33-C34-C35
19	L	101	TGL	CC6-CC7-CC8-CC9
20	G	103	PGV	C25-C26-C27-C28
24	B	303	PSC	C23-C24-C25-C26
26	C	307	CDL	C76-C77-C78-C79

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Mol	Chain	Res	Type	Atoms
19	D	201	TGL	C11-C10-CB9-CB8
19	D	201	TGL	CC2-CC3-CC4-CC5
19	N	609	TGL	CC3-CC4-CC5-CC6
26	T	103	CDL	C77-C78-C79-C80
19	N	611	TGL	OG1-CG1-CG2-CG3
20	G	103	PGV	O03-C01-C02-C03
26	C	303	CDL	CB3-CB4-CB6-OB8
26	C	307	CDL	CA3-CA4-CA6-OA8
27	G	101	PEK	O03-C01-C02-C03
19	D	201	TGL	C20-C21-C22-C23
19	L	101	TGL	CA9-C20-C21-C22
27	G	101	PEK	C35-C36-C37-C38
19	L	101	TGL	CB9-C10-C11-C12
26	P	304	CDL	C64-C65-C66-C67
20	N	608	PGV	O03-C19-C20-C21
19	A	607	TGL	C10-C11-C12-C13
27	C	306	PEK	C17-C18-C19-C20
27	G	101	PEK	C17-C18-C19-C20
20	N	608	PGV	C31-C32-C33-C34
24	R	201	PSC	C30-C31-C32-C33
20	N	607	PGV	O05-C05-C06-O06
27	T	102	PEK	C23-C24-C25-C26
27	C	306	PEK	C2-C3-C4-C5
19	N	609	TGL	C12-C13-C14-C29
19	D	201	TGL	CA7-CA8-CA9-C20
19	L	101	TGL	CC4-CC5-CC6-CC7
19	L	101	TGL	C22-C23-C24-C25
24	R	201	PSC	C29-C30-C31-C32
26	T	103	CDL	C71-CB7-OB8-CB6
20	A	609	PGV	C03-C02-O01-C1
26	P	304	CDL	C58-C59-C60-C61
26	T	103	CDL	C58-C59-C60-C61
27	G	102	PEK	C27-C28-C29-C30
19	A	607	TGL	C12-C13-C14-C29
20	N	607	PGV	C5-C6-C7-C8
26	C	303	CDL	C31-C32-C33-C34
26	C	307	CDL	C21-C22-C23-C24
26	P	304	CDL	C18-C19-C20-C21
26	P	304	CDL	C73-C74-C75-C76
26	T	103	CDL	C81-C82-C83-C84
20	C	308	PGV	C05-C04-O12-P
20	G	103	PGV	C05-C04-O12-P

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Mol	Chain	Res	Type	Atoms
26	P	304	CDL	C23-C24-C25-C26
26	P	304	CDL	C61-C62-C63-C64
19	N	610	TGL	CA2-CA1-OG1-CG1
29	Z	101	DMU	O6-C11-C9-O1
27	G	102	PEK	C4-C5-C6-C7
20	G	103	PGV	C19-C20-C21-C22
19	D	201	TGL	CA2-CA3-CA4-CA5
26	C	303	CDL	C73-C74-C75-C76
26	C	307	CDL	C53-C54-C55-C56
20	C	302	PGV	C31-C32-C33-C34
26	T	103	CDL	C38-C39-C40-C41
27	T	101	PEK	C30-C31-C32-C33
27	G	102	PEK	C35-C36-C37-C38
20	A	609	PGV	C22-C23-C24-C25
19	D	201	TGL	CB7-CB8-CB9-C10
20	G	103	PGV	C31-C32-C33-C34
26	T	103	CDL	C32-C33-C34-C35
20	N	607	PGV	C15-C16-C17-C18
26	P	304	CDL	C33-C34-C35-C36
24	R	201	PSC	C1-C2-C3-C4
26	C	307	CDL	CA7-C31-C32-C33
26	P	304	CDL	C63-C64-C65-C66
20	A	608	PGV	C20-C19-O03-C01
20	N	608	PGV	C7-C8-C9-C10
19	N	609	TGL	C29-C30-C31-C32
19	N	609	TGL	C19-C33-C34-C35
26	T	103	CDL	C71-C72-C73-C74
19	N	609	TGL	CA9-C20-C21-C22
20	P	303	PGV	C24-C25-C26-C27
26	C	303	CDL	C38-C39-C40-C41
24	B	303	PSC	C4-C5-C6-C7
29	M	101	DMU	C3-C4-C57-O61
20	A	609	PGV	C14-C15-C16-C17
24	R	201	PSC	C13-C14-C15-C16
26	C	303	CDL	C57-C58-C59-C60
26	C	303	CDL	C78-C79-C80-C81
19	L	101	TGL	CA5-CA6-CA7-CA8
20	A	609	PGV	C01-C02-C03-O11
20	G	103	PGV	C01-C02-C03-O11
26	C	303	CDL	OB5-CB3-CB4-CB6
26	C	307	CDL	OB5-CB3-CB4-CB6
27	C	306	PEK	C01-C02-C03-O11

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Mol	Chain	Res	Type	Atoms
20	A	609	PGV	C2-C3-C4-C5
23	P	305	CHD	C16-C17-C20-C21
26	C	303	CDL	C56-C57-C58-C59
26	C	307	CDL	C74-C75-C76-C77
19	N	611	TGL	CB2-CB3-CB4-CB5
26	C	307	CDL	C37-C38-C39-C40
26	T	103	CDL	OB9-CB7-OB8-CB6
26	P	304	CDL	C80-C81-C82-C83
20	A	608	PGV	C24-C25-C26-C27
19	N	611	TGL	CC2-CC1-OG3-CG3
26	T	103	CDL	C39-C40-C41-C42
26	C	307	CDL	C1-CB2-OB2-PB2
20	P	303	PGV	C31-C32-C33-C34
26	C	303	CDL	C53-C54-C55-C56
19	N	609	TGL	CB5-CB6-CB7-CB8
24	B	303	PSC	C29-C30-C31-C32
26	T	103	CDL	C75-C76-C77-C78
19	A	607	TGL	CG1-CG2-CG3-OG3
20	N	607	PGV	O03-C01-C02-C03
26	C	303	CDL	CA3-CA4-CA6-OA8
27	T	101	PEK	O03-C01-C02-C03
27	G	102	PEK	C17-C18-C19-C20
26	P	304	CDL	CB5-C51-C52-C53
27	C	306	PEK	C13-C14-C15-C16
19	A	607	TGL	CB5-CB6-CB7-CB8
20	P	303	PGV	C26-C27-C28-C29
24	B	303	PSC	C3-C4-C5-C6
19	L	101	TGL	C24-C25-C26-C27
20	A	609	PGV	C3-C4-C5-C6
14	A	601	HEA	C2A-C3A-CMA-OMA
24	B	303	PSC	C9-C10-C11-C12
24	B	303	PSC	C10-C11-C12-C13
24	R	201	PSC	C9-C10-C11-C12
24	R	201	PSC	C10-C11-C12-C13
27	C	306	PEK	C6-C7-C8-C9
27	C	306	PEK	C9-C10-C11-C12
27	G	102	PEK	C5-C6-C7-C8
27	G	102	PEK	C11-C10-C9-C8
27	P	302	PEK	C5-C6-C7-C8
27	T	101	PEK	C12-C13-C14-C15
27	T	102	PEK	C5-C6-C7-C8
27	T	102	PEK	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
27	T	102	PEK	C11-C10-C9-C8
27	T	102	PEK	C9-C10-C11-C12
19	N	610	TGL	C33-C34-C35-C36
27	T	102	PEK	C34-C35-C36-C37
20	C	308	PGV	O01-C02-C03-O11
26	T	103	CDL	OB5-CB3-CB4-OB6
23	P	305	CHD	C16-C17-C20-C22
20	G	103	PGV	C11-C10-C9-C8
19	N	610	TGL	OA1-CA1-OG1-CG1
19	D	201	TGL	C13-C14-C29-C30
20	P	303	PGV	C13-C14-C15-C16
19	D	201	TGL	CA6-CA7-CA8-CA9
19	D	201	TGL	C25-C26-C27-C28
19	N	609	TGL	CA3-CA4-CA5-CA6
20	G	103	PGV	C20-C21-C22-C23
19	L	101	TGL	CC5-CC6-CC7-CC8
26	C	303	CDL	C18-C19-C20-C21
20	A	609	PGV	O03-C01-C02-O01
20	C	308	PGV	O03-C01-C02-O01
20	N	607	PGV	O03-C01-C02-O01
27	T	101	PEK	O03-C01-C02-O01
19	N	611	TGL	C29-C30-C31-C32
26	C	307	CDL	C77-C78-C79-C80
26	C	303	CDL	C64-C65-C66-C67
20	C	302	PGV	C26-C27-C28-C29
20	C	308	PGV	C27-C28-C29-C30
27	G	101	PEK	C34-C35-C36-C37
26	P	304	CDL	C11-C12-C13-C14
26	P	304	CDL	C54-C55-C56-C57
20	A	609	PGV	C02-C03-O11-P
20	C	302	PGV	C12-C13-C14-C15
19	N	610	TGL	C22-C23-C24-C25
21	A	610	EDO	O1-C1-C2-O2
27	G	102	PEK	C24-C25-C26-C27
19	N	609	TGL	CC9-C15-C16-C17
20	C	308	PGV	C30-C31-C32-C33
20	P	303	PGV	C27-C28-C29-C30
26	P	304	CDL	C82-C83-C84-C85
26	T	103	CDL	C78-C79-C80-C81
27	G	102	PEK	C2-C3-C4-C5
19	N	610	TGL	CB3-CB4-CB5-CB6
20	N	607	PGV	C22-C23-C24-C25

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Mol	Chain	Res	Type	Atoms
26	T	103	CDL	C16-C17-C18-C19
20	N	607	PGV	C02-C01-O03-C19
27	P	302	PEK	C34-C35-C36-C37
20	P	303	PGV	C20-C19-O03-C01
27	G	102	PEK	C33-C34-C35-C36
19	N	609	TGL	C16-C15-CC9-CC8
20	C	308	PGV	C22-C23-C24-C25
19	D	201	TGL	C16-C15-CC9-CC8
19	N	611	TGL	CC3-CC4-CC5-CC6
19	N	609	TGL	C25-C26-C27-C28
19	N	610	TGL	CC1-CC2-CC3-CC4
19	D	201	TGL	C24-C25-C26-C27
19	A	607	TGL	OG1-CG1-CG2-CG3
20	A	609	PGV	O03-C01-C02-C03
20	P	303	PGV	O03-C01-C02-C03
24	B	303	PSC	O03-C01-C02-C03
26	P	304	CDL	CA3-CA4-CA6-OA8
26	T	103	CDL	CB3-CB4-CB6-OB8
27	G	102	PEK	O03-C01-C02-C03
26	C	303	CDL	OB5-CB3-CB4-OB6
27	C	306	PEK	O01-C02-C03-O11
27	T	101	PEK	O01-C02-C03-O11
24	R	201	PSC	O03-C19-C20-C21
19	A	607	TGL	CC6-CC7-CC8-CC9
27	C	306	PEK	C27-C28-C29-C30
19	N	611	TGL	C25-C26-C27-C28
19	N	611	TGL	OC1-CC1-OG3-CG3
20	A	608	PGV	O04-C19-O03-C01
20	P	303	PGV	O04-C19-O03-C01
26	C	303	CDL	C84-C85-C86-C87
26	C	307	CDL	C72-C73-C74-C75
19	A	607	TGL	OG2-CG2-CG3-OG3
19	L	101	TGL	OG1-CG1-CG2-OG2
20	P	303	PGV	O03-C01-C02-O01
26	C	303	CDL	OA6-CA4-CA6-OA8
26	C	303	CDL	OB6-CB4-CB6-OB8
26	T	103	CDL	OB6-CB4-CB6-OB8
23	J	101	CHD	C16-C17-C20-C21
26	C	307	CDL	C24-C25-C26-C27
26	P	304	CDL	C78-C79-C80-C81
27	P	302	PEK	C30-C31-C32-C33
20	C	302	PGV	O05-C05-C06-O06

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Mol	Chain	Res	Type	Atoms
19	N	610	TGL	C13-C14-C29-C30
27	C	306	PEK	C22-C23-C24-C25
26	T	103	CDL	C56-C57-C58-C59
19	N	609	TGL	C16-C17-C18-C19
27	T	102	PEK	C25-C26-C27-C28
20	C	302	PGV	C04-C05-C06-O06
20	N	607	PGV	C20-C21-C22-C23
27	T	101	PEK	C25-C26-C27-C28
19	N	610	TGL	C29-C30-C31-C32
26	P	304	CDL	C74-C75-C76-C77
20	G	103	PGV	C03-O11-P-O12
24	B	303	PSC	C03-O11-P-O12
24	B	303	PSC	C04-O12-P-O11
26	T	103	CDL	CA3-OA5-PA1-OA2
19	A	607	TGL	C25-C26-C27-C28
27	P	302	PEK	C17-C18-C19-C20
20	C	302	PGV	C02-C03-O11-P
20	C	302	PGV	C05-C04-O12-P
20	P	303	PGV	C02-C03-O11-P
26	P	304	CDL	CA4-CA3-OA5-PA1
26	T	103	CDL	C1-CB2-OB2-PB2
19	N	609	TGL	CB7-CB8-CB9-C10
20	A	609	PGV	C04-O12-P-O13
20	A	609	PGV	C04-O12-P-O14
20	C	308	PGV	C04-O12-P-O14
20	N	607	PGV	C03-O11-P-O13
20	N	608	PGV	C04-O12-P-O13
20	N	608	PGV	C04-O12-P-O14
24	R	201	PSC	C04-O12-P-O13
26	C	303	CDL	CB2-OB2-PB2-OB4
26	T	103	CDL	CB3-OB5-PB2-OB3
27	T	102	PEK	C03-O11-P-O13
27	T	102	PEK	C03-O11-P-O14
27	T	102	PEK	C04-O12-P-O14
27	T	101	PEK	C01-C02-C03-O11
21	C	309	EDO	O1-C1-C2-O2
14	A	601	HEA	O11-C11-C12-C13
26	C	303	CDL	C54-C55-C56-C57
26	C	303	CDL	C21-C22-C23-C24
27	T	102	PEK	C33-C34-C35-C36
26	C	307	CDL	C81-C82-C83-C84
19	A	607	TGL	CB2-CB3-CB4-CB5

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Mol	Chain	Res	Type	Atoms
20	C	308	PGV	C31-C32-C33-C34
20	N	608	PGV	C4-C5-C6-C7
26	P	304	CDL	C60-C61-C62-C63
26	T	103	CDL	C17-C18-C19-C20
27	G	102	PEK	C26-C27-C28-C29
20	A	609	PGV	O01-C02-C03-O11
20	G	103	PGV	O01-C02-C03-O11
26	P	304	CDL	OA5-CA3-CA4-OA6
26	T	103	CDL	OA5-CA3-CA4-OA6
20	A	609	PGV	C9-C10-C11-C12
20	N	607	PGV	C23-C24-C25-C26
26	C	307	CDL	C73-C74-C75-C76
19	A	607	TGL	CA4-CA5-CA6-CA7
26	C	303	CDL	O1-C1-CA2-OA2
19	N	611	TGL	CA2-CA3-CA4-CA5
26	C	307	CDL	C12-C13-C14-C15
14	A	601	HEA	C4A-C3A-CMA-OMA
14	N	602	HEA	C4A-C3A-CMA-OMA
24	R	201	PSC	O12-C04-C05-N
26	T	103	CDL	CA3-CA4-CA6-OA8
19	N	611	TGL	OG1-CG1-CG2-OG2
24	B	303	PSC	O03-C01-C02-O01
26	P	304	CDL	OA6-CA4-CA6-OA8
27	G	102	PEK	O03-C01-C02-O01
29	Z	101	DMU	C22-C25-C28-C31
27	P	302	PEK	C7-C8-C9-C10
19	D	201	TGL	CC4-CC5-CC6-CC7
20	A	609	PGV	C26-C27-C28-C29
27	G	102	PEK	C28-C29-C30-C31
23	P	305	CHD	C13-C17-C20-C22
19	N	611	TGL	CA4-CA5-CA6-CA7
26	P	304	CDL	C40-C41-C42-C43
23	P	305	CHD	C13-C17-C20-C21
27	C	306	PEK	C28-C29-C30-C31
20	G	103	PGV	C27-C28-C29-C30
19	N	610	TGL	CB4-CB5-CB6-CB7
26	P	304	CDL	C13-C14-C15-C16
26	C	303	CDL	C14-C15-C16-C17
26	T	103	CDL	C33-C34-C35-C36
29	M	101	DMU	C34-C37-C40-C43
24	R	201	PSC	C28-C29-C30-C31
26	C	307	CDL	C39-C40-C41-C42

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Mol	Chain	Res	Type	Atoms
27	T	101	PEK	C35-C36-C37-C38
23	P	305	CHD	C20-C22-C23-C24
26	C	303	CDL	OB7-CB5-OB6-CB4
27	G	101	PEK	C1-C2-C3-C4
20	G	103	PGV	C14-C15-C16-C17
26	C	303	CDL	C1-CB2-OB2-PB2
26	P	304	CDL	OB5-CB3-CB4-OB6
20	P	303	PGV	C23-C24-C25-C26
21	K	102	EDO	O1-C1-C2-O2
26	C	303	CDL	OA9-CA7-OA8-CA6
19	A	607	TGL	OG1-CG1-CG2-OG2
27	G	101	PEK	O03-C01-C02-O01
20	G	103	PGV	C7-C8-C9-C10
26	C	303	CDL	C31-CA7-OA8-CA6
26	C	307	CDL	CA3-OA5-PA1-OA2
26	P	304	CDL	CB3-OB5-PB2-OB2
27	T	101	PEK	C04-O12-P-O11
29	Z	101	DMU	O16-C18-C19-C22
27	G	102	PEK	C21-C22-C23-C24
19	L	101	TGL	OG1-CG1-CG2-CG3
19	N	611	TGL	C19-C33-C34-C35
20	N	608	PGV	C5-C6-C7-C8
27	C	306	PEK	O02-C1-O01-C02
19	N	611	TGL	CA6-CA7-CA8-CA9
14	N	601	HEA	CAA-CBA-CGA-O1A
26	C	307	CDL	C75-C76-C77-C78
19	N	610	TGL	C21-C22-C23-C24
24	R	201	PSC	C23-C24-C25-C26
19	N	609	TGL	C11-C12-C13-C14
27	G	101	PEK	C2-C3-C4-C5
14	A	601	HEA	CAD-CBD-CGD-O2D
26	P	304	CDL	C62-C63-C64-C65
20	A	608	PGV	C9-C10-C11-C12
20	C	302	PGV	C24-C25-C26-C27
24	B	303	PSC	C22-C23-C24-C25
26	C	303	CDL	OA5-CA3-CA4-CA6
27	T	102	PEK	O01-C02-C03-O11
27	T	102	PEK	O01-C1-C2-C3
26	C	303	CDL	C59-C60-C61-C62
20	N	608	PGV	C27-C28-C29-C30
29	M	101	DMU	C19-C22-C25-C28
20	N	608	PGV	O04-C19-C20-C21

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Mol	Chain	Res	Type	Atoms
14	A	601	HEA	CAD-CBD-CGD-O1D
23	B	302	CHD	C22-C23-C24-O25
19	N	610	TGL	CC3-CC4-CC5-CC6
19	N	611	TGL	CC7-CC8-CC9-C15
26	T	103	CDL	C37-C38-C39-C40
23	C	304	CHD	C22-C23-C24-O25
24	B	303	PSC	C12-C13-C14-C15
19	A	607	TGL	CB7-CB8-CB9-C10
26	P	304	CDL	C22-C23-C24-C25
19	N	611	TGL	C23-C24-C25-C26
24	R	201	PSC	C19-C20-C21-C22
24	B	303	PSC	C03-C02-O01-C1
27	G	101	PEK	C27-C28-C29-C30
27	T	102	PEK	C3-C4-C5-C6
14	N	601	HEA	CAD-CBD-CGD-O1D
26	C	303	CDL	C13-C14-C15-C16
27	C	306	PEK	C26-C27-C28-C29
27	C	306	PEK	C12-C13-C14-C15
27	G	102	PEK	C9-C10-C11-C12
27	G	102	PEK	C11-C12-C13-C14
27	T	101	PEK	C9-C10-C11-C12
27	T	102	PEK	C11-C12-C13-C14
27	T	102	PEK	C12-C13-C14-C15
19	N	611	TGL	C33-C34-C35-C36
19	A	607	TGL	CA6-CA7-CA8-CA9
23	P	306	CHD	C22-C23-C24-O26
20	C	302	PGV	C20-C21-C22-C23
23	B	302	CHD	C22-C23-C24-O26
20	C	302	PGV	C13-C14-C15-C16
14	N	601	HEA	CAA-CBA-CGA-O2A
26	C	307	CDL	C83-C84-C85-C86
26	C	307	CDL	OA6-CA4-CA6-OA8
26	T	103	CDL	C61-C62-C63-C64
19	N	611	TGL	CC4-CC5-CC6-CC7
23	P	306	CHD	C22-C23-C24-O25
27	T	102	PEK	C02-C03-O11-P
26	P	304	CDL	C55-C56-C57-C58
19	D	201	TGL	OG1-CG1-CG2-CG3
29	Z	101	DMU	C19-C22-C25-C28
14	N	602	HEA	CAD-CBD-CGD-O2D
19	N	611	TGL	CA9-C20-C21-C22
20	N	607	PGV	O01-C02-C03-O11

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Mol	Chain	Res	Type	Atoms
20	N	607	PGV	C31-C32-C33-C34
19	N	610	TGL	CA4-CA5-CA6-CA7
20	N	608	PGV	C15-C16-C17-C18
26	T	103	CDL	C13-C14-C15-C16
26	C	303	CDL	C51-CB5-OB6-CB4
26	C	307	CDL	C18-C19-C20-C21
14	A	602	HEA	CAD-CBD-CGD-O1D
14	N	602	HEA	CAA-CBA-CGA-O1A
19	L	101	TGL	C15-C16-C17-C18
20	N	607	PGV	O01-C1-C2-C3
23	W	101	CHD	C22-C23-C24-O25
24	B	303	PSC	C20-C21-C22-C23
20	N	607	PGV	C9-C10-C11-C12
20	N	607	PGV	C04-O12-P-O11
14	A	601	HEA	C18-C19-C20-C21
20	N	607	PGV	O03-C19-C20-C21
26	C	307	CDL	C12-C11-CA5-OA6
14	N	602	HEA	CAD-CBD-CGD-O1D
23	C	304	CHD	C22-C23-C24-O26
20	C	302	PGV	C9-C10-C11-C12
20	N	608	PGV	C11-C12-C13-C14
27	G	102	PEK	C14-C15-C16-C17
23	C	305	CHD	C22-C23-C24-O26
23	O	302	CHD	C22-C23-C24-O26
24	B	303	PSC	C01-C02-O01-C1
26	P	304	CDL	CB3-CB4-OB6-CB5
26	P	304	CDL	CB6-CB4-OB6-CB5
20	A	609	PGV	C24-C25-C26-C27
19	N	610	TGL	C10-C11-C12-C13
20	A	609	PGV	C7-C8-C9-C10
20	C	308	PGV	C14-C15-C16-C17
26	C	307	CDL	C13-C14-C15-C16
19	L	101	TGL	OG1-CA1-CA2-CA3
27	T	101	PEK	O03-C21-C22-C23
19	N	611	TGL	CC2-CC3-CC4-CC5
26	P	304	CDL	C14-C15-C16-C17
14	N	601	HEA	C26-C15-C16-C17
23	P	305	CHD	C22-C23-C24-O26
26	P	304	CDL	C12-C11-CA5-OA6
27	G	102	PEK	O01-C1-C2-C3
26	P	304	CDL	C77-C78-C79-C80
20	P	303	PGV	C9-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
20	C	302	PGV	C11-C10-C9-C8
23	J	101	CHD	C22-C23-C24-O25
23	J	101	CHD	C22-C23-C24-O26
23	O	302	CHD	C22-C23-C24-O25
26	C	303	CDL	C22-C23-C24-C25
20	N	607	PGV	C14-C15-C16-C17
19	D	201	TGL	OG1-CA1-CA2-CA3
19	N	610	TGL	OG1-CA1-CA2-CA3
21	A	611	EDO	O1-C1-C2-O2
21	C	310	EDO	O1-C1-C2-O2
21	K	101	EDO	O1-C1-C2-O2
14	A	602	HEA	CAD-CBD-CGD-O2D
23	P	305	CHD	C22-C23-C24-O25
14	A	602	HEA	C26-C15-C16-C17
20	C	308	PGV	C11-C10-C9-C8
20	N	607	PGV	C01-C02-C03-O11
23	C	305	CHD	C22-C23-C24-O25
26	C	307	CDL	C64-C65-C66-C67
19	A	607	TGL	OG3-CC1-CC2-CC3
27	C	306	PEK	C3-C4-C5-C6
20	G	103	PGV	O01-C1-C2-C3
24	B	303	PSC	O03-C19-C20-C21
26	C	307	CDL	C32-C31-CA7-OA8
14	N	601	HEA	CAD-CBD-CGD-O2D
14	N	602	HEA	CAA-CBA-CGA-O2A
19	A	607	TGL	C20-C21-C22-C23
20	A	608	PGV	C21-C22-C23-C24
20	C	308	PGV	C9-C10-C11-C12
27	G	102	PEK	C3-C4-C5-C6
23	W	101	CHD	C22-C23-C24-O26
27	C	306	PEK	C2-C1-O01-C02
19	N	611	TGL	C14-C29-C30-C31
26	P	304	CDL	C59-C60-C61-C62
20	N	607	PGV	O02-C1-C2-C3
19	N	610	TGL	CB5-CB6-CB7-CB8
26	C	307	CDL	C31-C32-C33-C34
27	T	101	PEK	C13-C14-C15-C16
19	D	201	TGL	OA1-CA1-CA2-CA3
26	C	307	CDL	C12-C11-CA5-OA7
27	T	101	PEK	O04-C21-C22-C23
20	N	608	PGV	O02-C1-O01-C02
20	N	607	PGV	O04-C19-C20-C21

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Mol	Chain	Res	Type	Atoms
27	G	102	PEK	O02-C1-C2-C3
19	N	611	TGL	C13-C14-C29-C30
19	N	609	TGL	CA7-CA8-CA9-C20
20	N	607	PGV	C04-O12-P-O13
26	C	307	CDL	CA2-OA2-PA1-OA3
19	N	610	TGL	OA1-CA1-CA2-CA3
27	P	302	PEK	O12-C04-C05-N
27	T	102	PEK	O12-C04-C05-N
24	B	303	PSC	O04-C19-C20-C21
26	C	307	CDL	C32-C31-CA7-OA9
19	D	201	TGL	C19-C33-C34-C35
27	T	101	PEK	C31-C32-C33-C34
27	C	306	PEK	C05-C04-O12-P
27	G	101	PEK	C05-C04-O12-P
24	R	201	PSC	O04-C19-C20-C21
26	P	304	CDL	C12-C11-CA5-OA7
20	G	103	PGV	O02-C1-C2-C3
19	D	201	TGL	C11-C12-C13-C14
26	C	307	CDL	C52-C51-CB5-OB6
19	N	610	TGL	CB9-C10-C11-C12
20	N	608	PGV	C26-C27-C28-C29
19	D	201	TGL	OG3-CC1-CC2-CC3
26	C	307	CDL	C72-C71-CB7-OB8
26	C	303	CDL	CB2-C1-CA2-OA2
19	A	607	TGL	OC1-CC1-CC2-CC3
19	N	609	TGL	CA6-CA7-CA8-CA9
26	C	303	CDL	C12-C11-CA5-OA6
26	C	307	CDL	C72-C71-CB7-OB9
19	N	610	TGL	CB2-CB3-CB4-CB5
26	T	103	CDL	C32-C31-CA7-OA8

There are no ring outliers.

46 monomers are involved in 157 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	Z	101	DMU	1	0
14	N	602	HEA	3	0
19	L	101	TGL	4	0
19	D	201	TGL	1	0
23	W	101	CHD	1	0
21	A	612	EDO	2	0
23	O	302	CHD	1	0

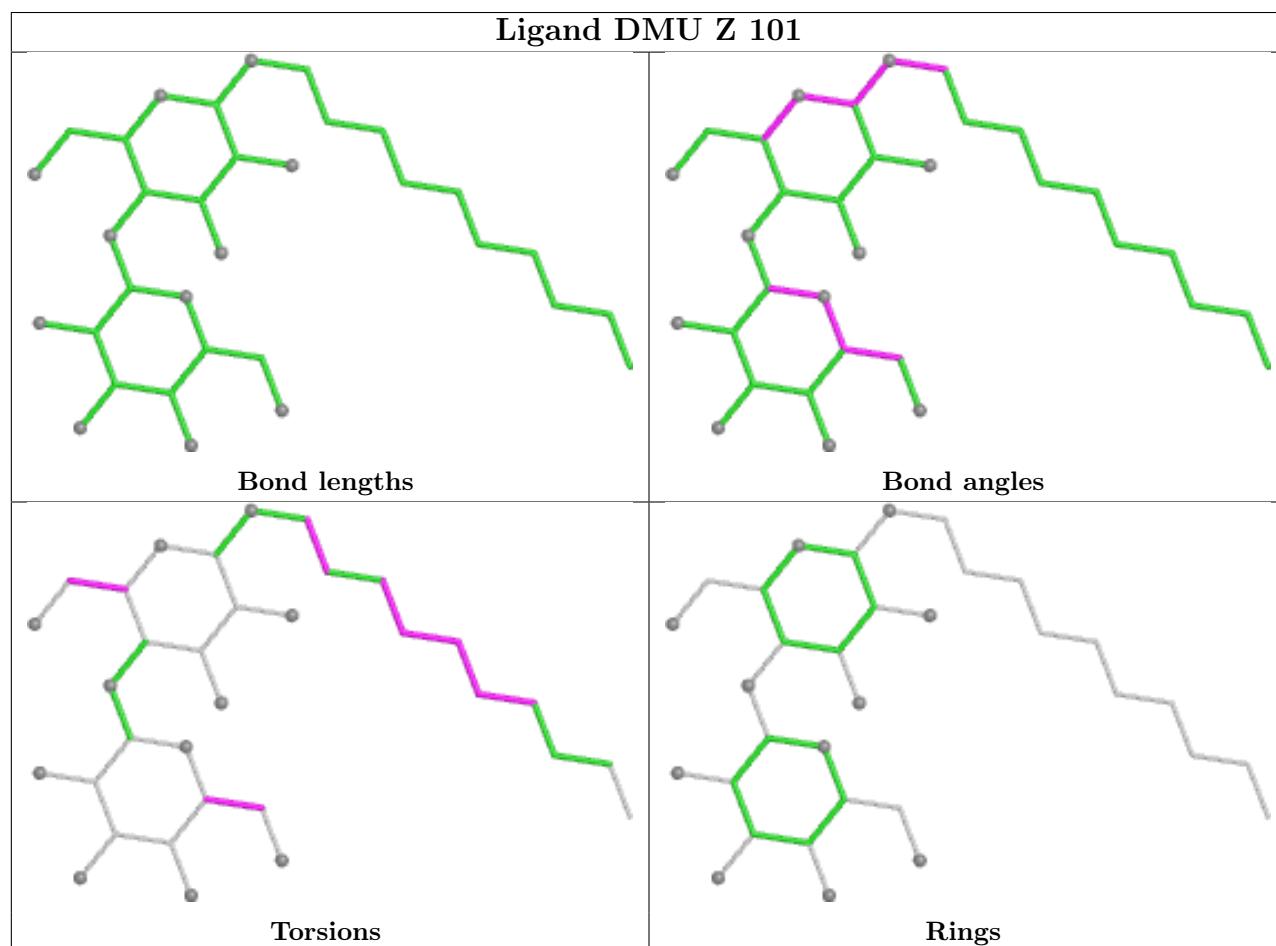
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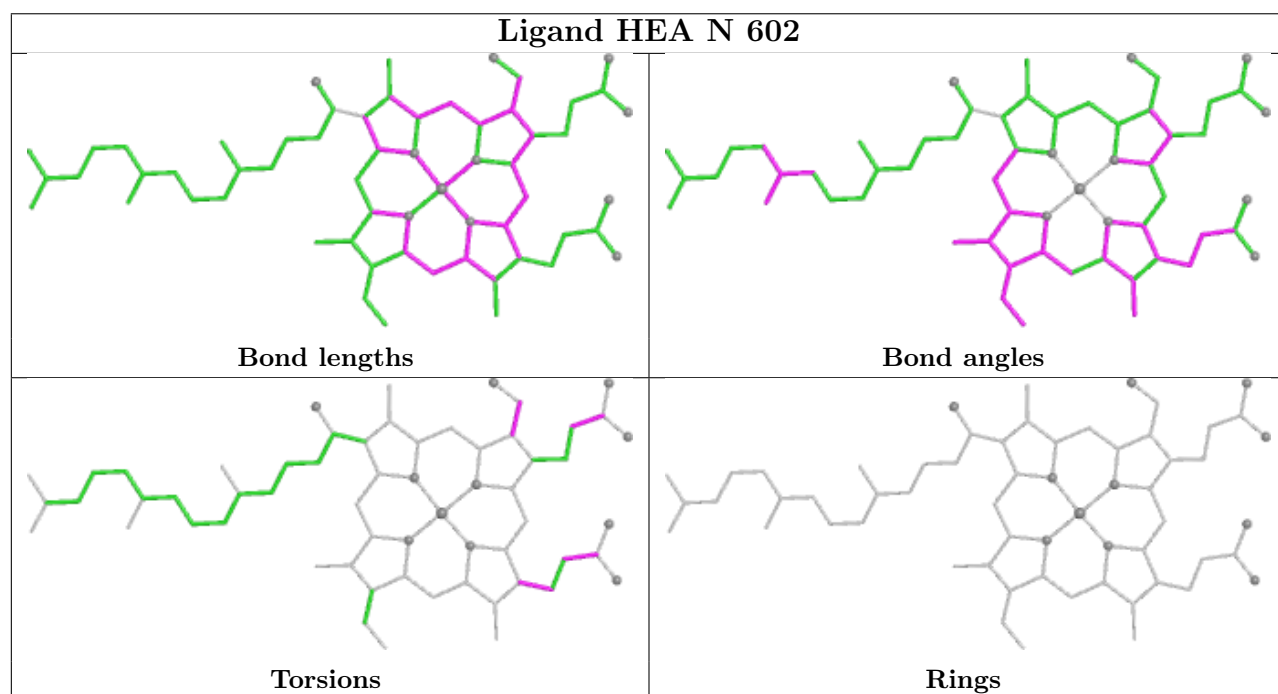
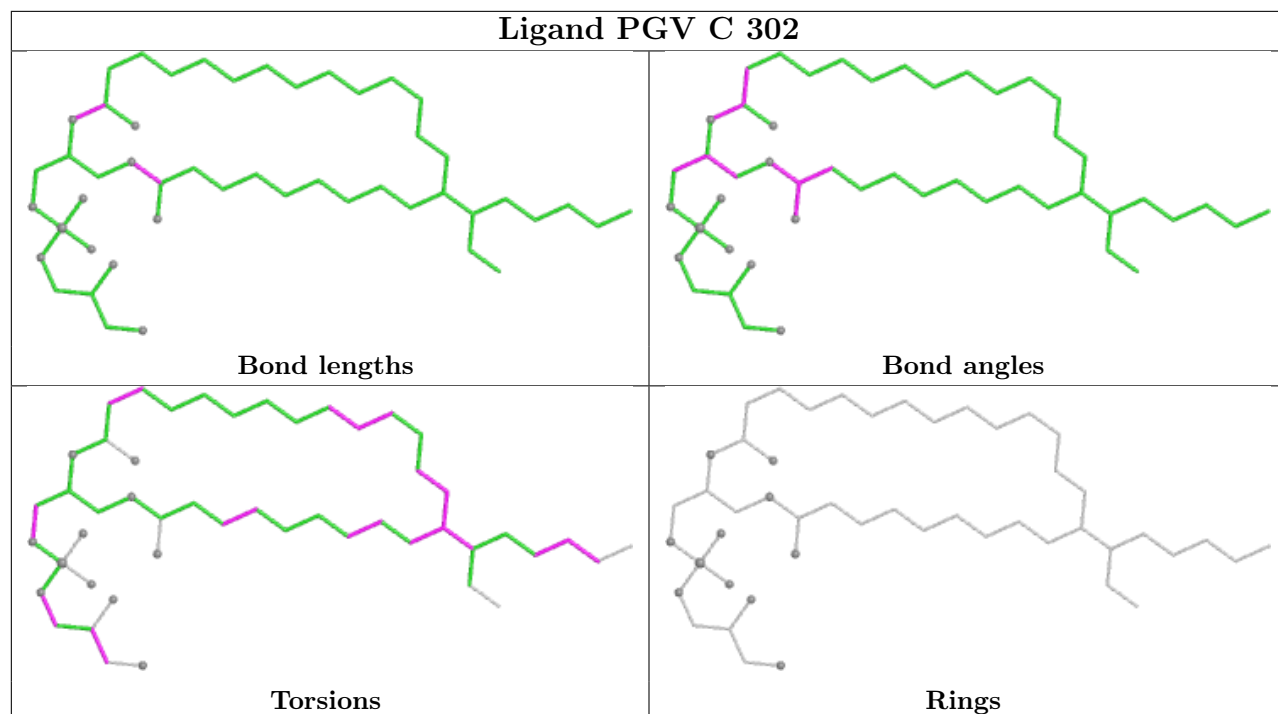
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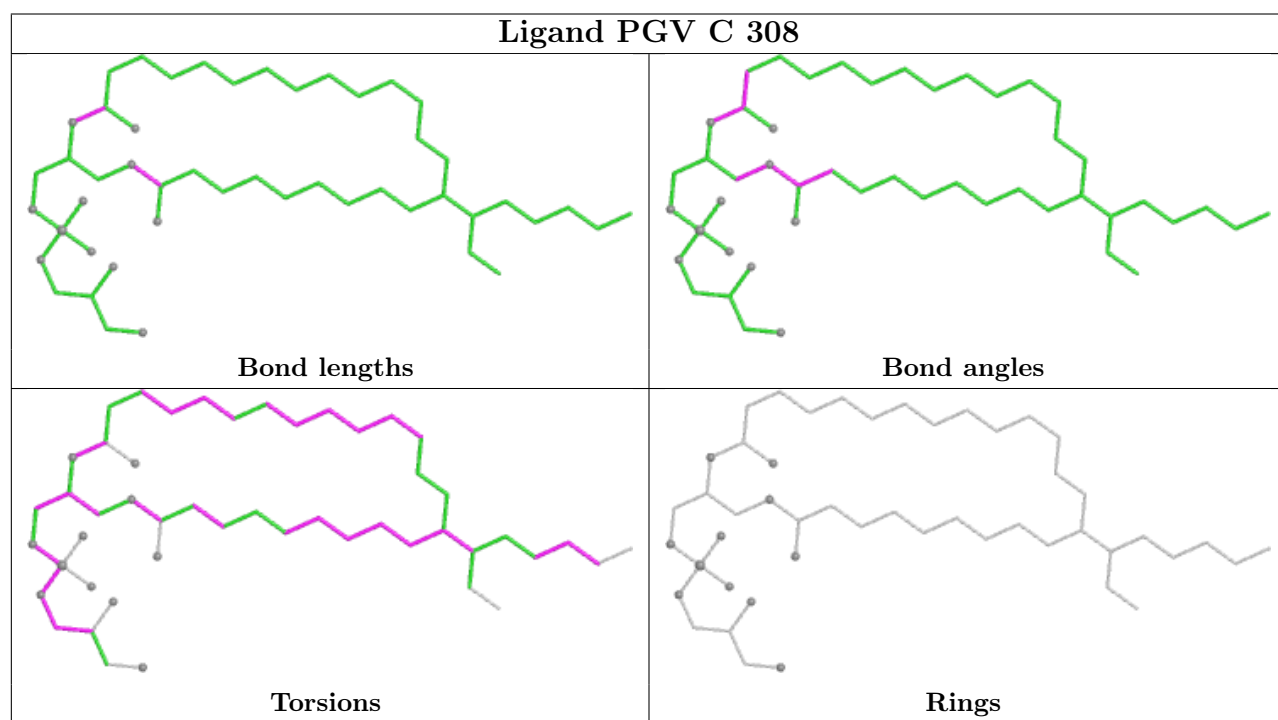
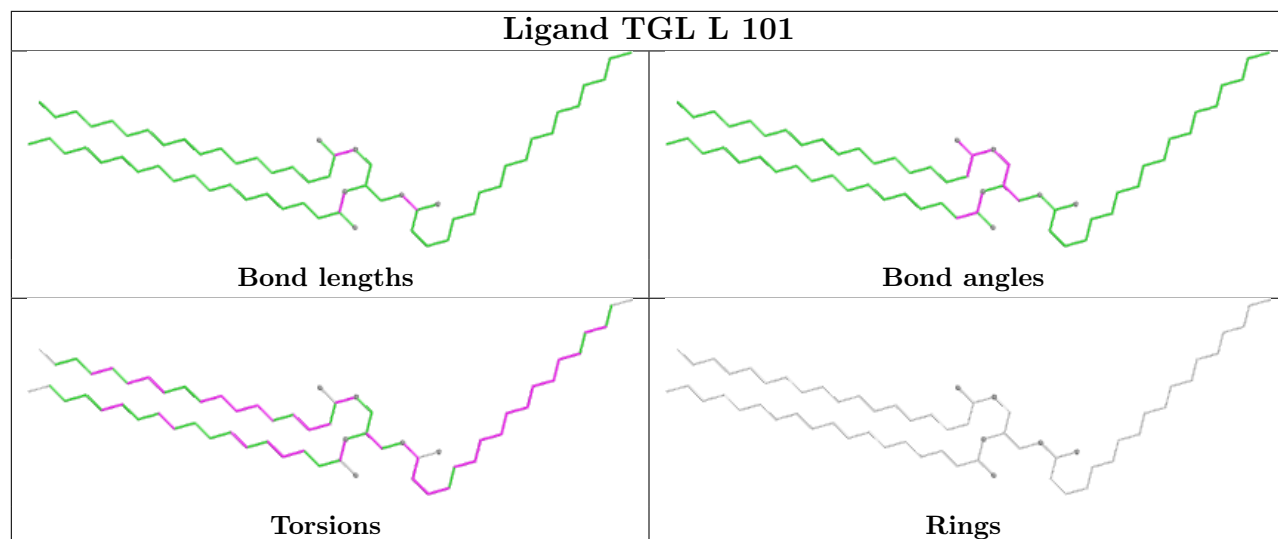
Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	P	302	PEK	4	0
27	T	102	PEK	1	0
21	B	305	EDO	1	0
26	T	103	CDL	13	0
23	C	305	CHD	1	0
20	A	609	PGV	2	0
14	A	602	HEA	6	0
27	G	102	PEK	6	0
21	A	614	EDO	4	0
20	A	608	PGV	1	0
19	N	609	TGL	5	0
21	A	613	EDO	2	0
20	P	303	PGV	3	0
19	A	607	TGL	3	0
21	A	610	EDO	1	0
21	T	104	EDO	2	0
23	C	304	CHD	2	0
23	P	305	CHD	1	0
20	N	607	PGV	6	0
20	N	608	PGV	2	0
19	N	610	TGL	3	0
20	G	103	PGV	2	0
27	C	306	PEK	3	0
23	B	302	CHD	1	0
14	A	601	HEA	6	0
23	P	306	CHD	1	0
29	M	101	DMU	1	0
19	N	611	TGL	4	0
26	P	304	CDL	8	0
21	N	612	EDO	1	0
14	N	601	HEA	10	0
26	C	303	CDL	2	0
24	R	201	PSC	6	0
26	C	307	CDL	13	0
23	J	101	CHD	1	0
27	G	101	PEK	4	0
18	A	606	CMO	1	0
24	B	303	PSC	12	0
27	T	101	PEK	3	0

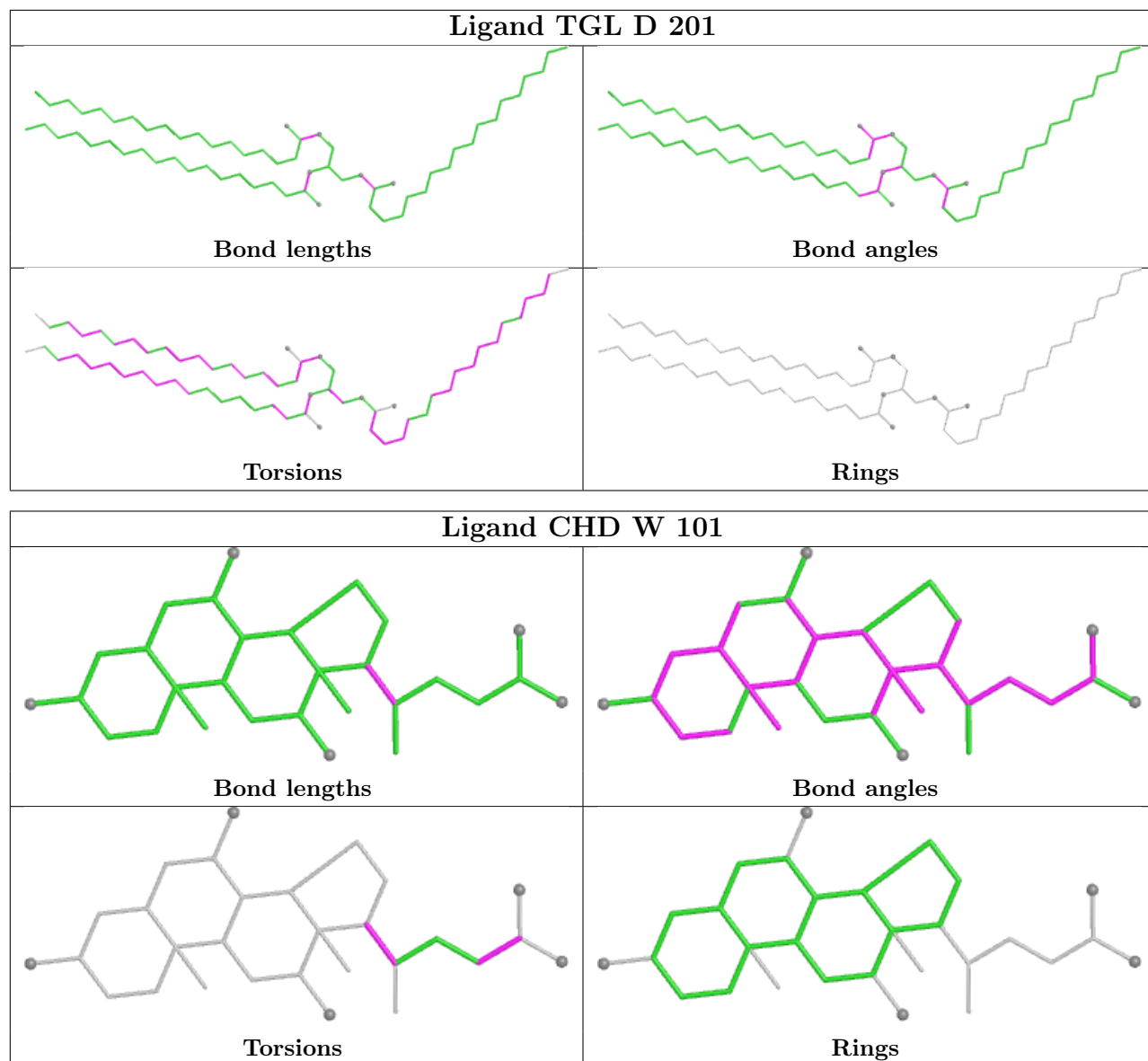
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

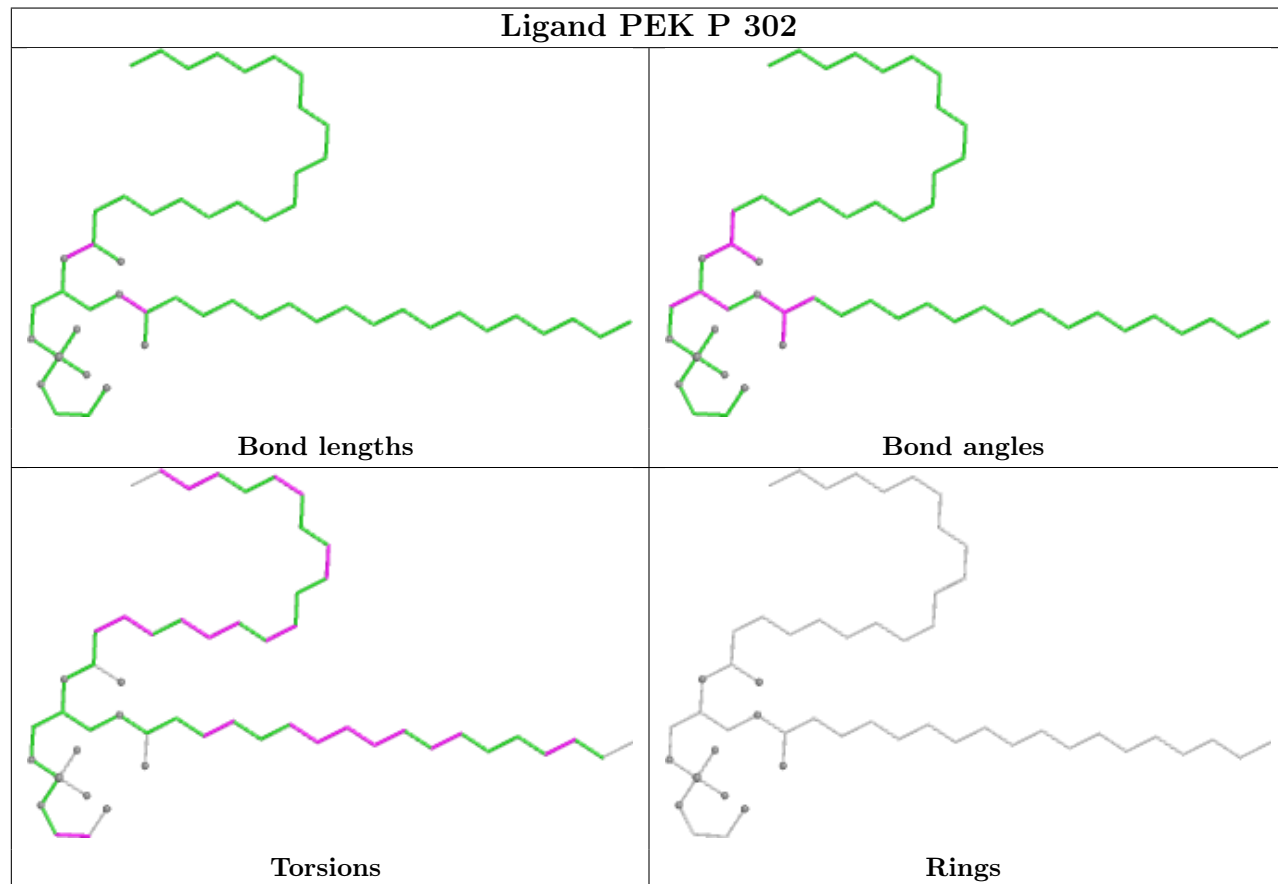
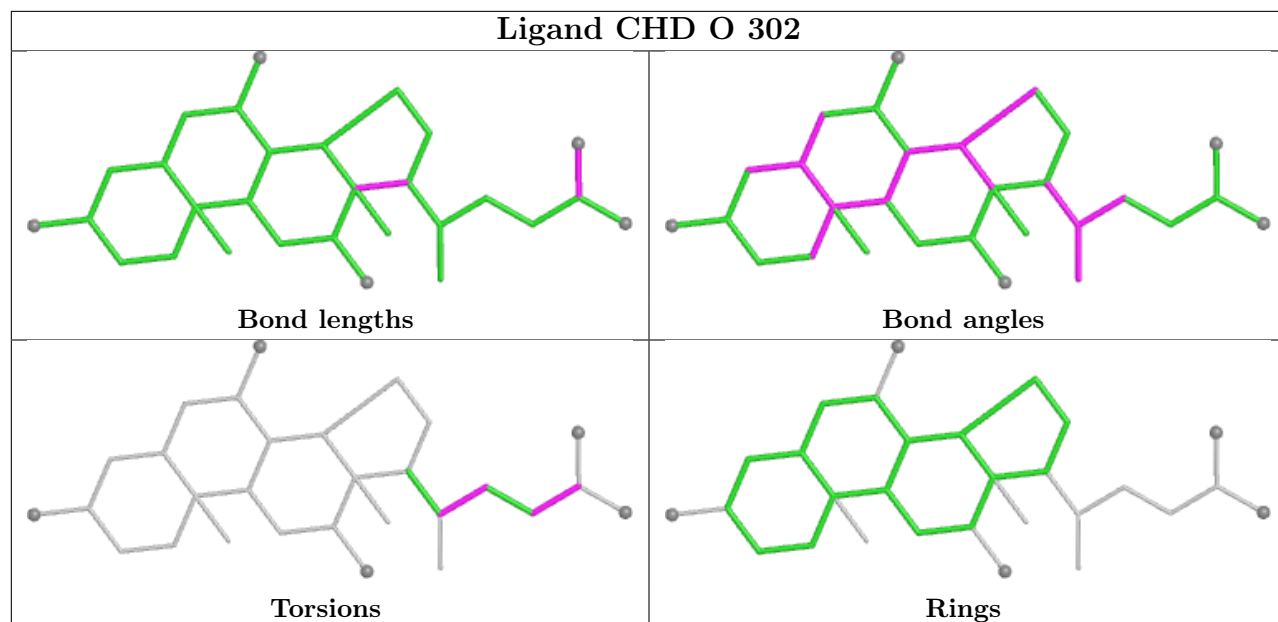
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

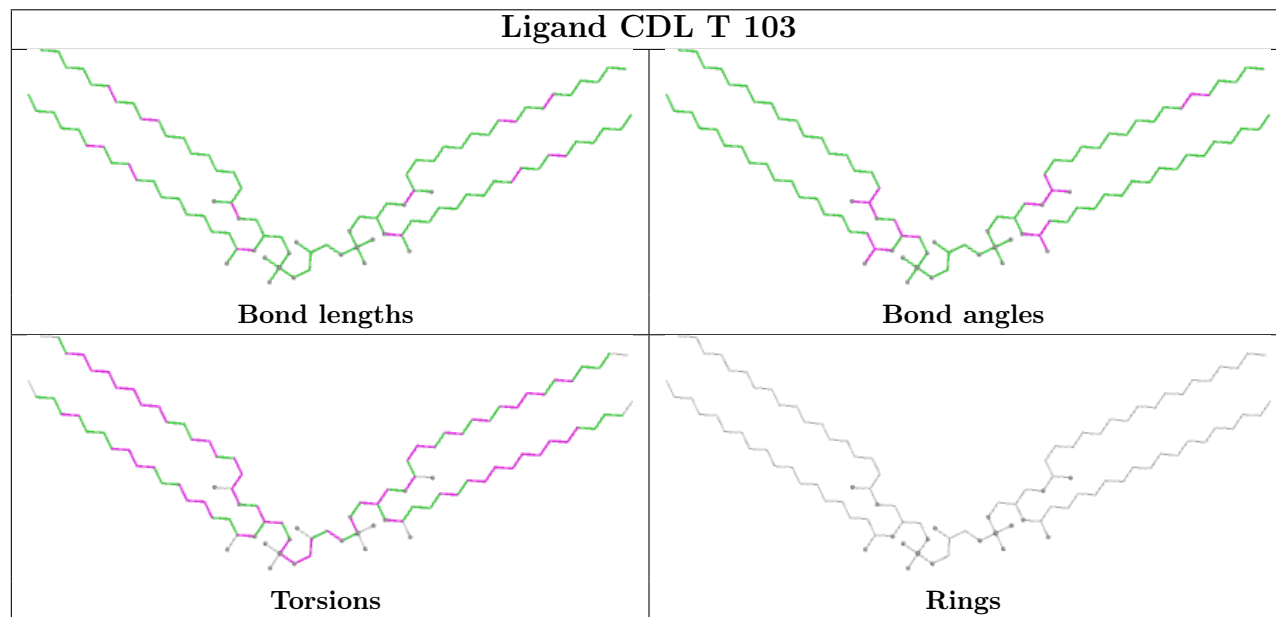
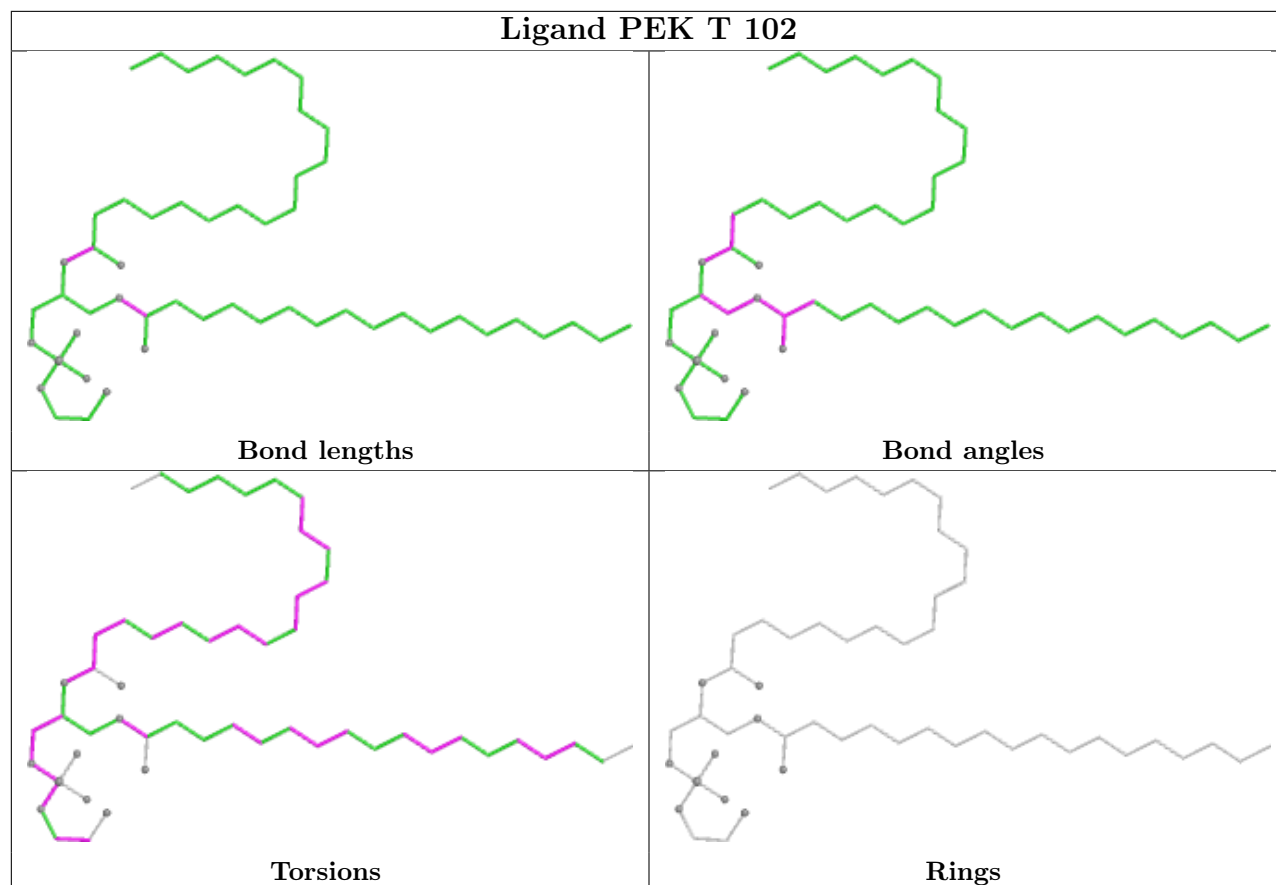


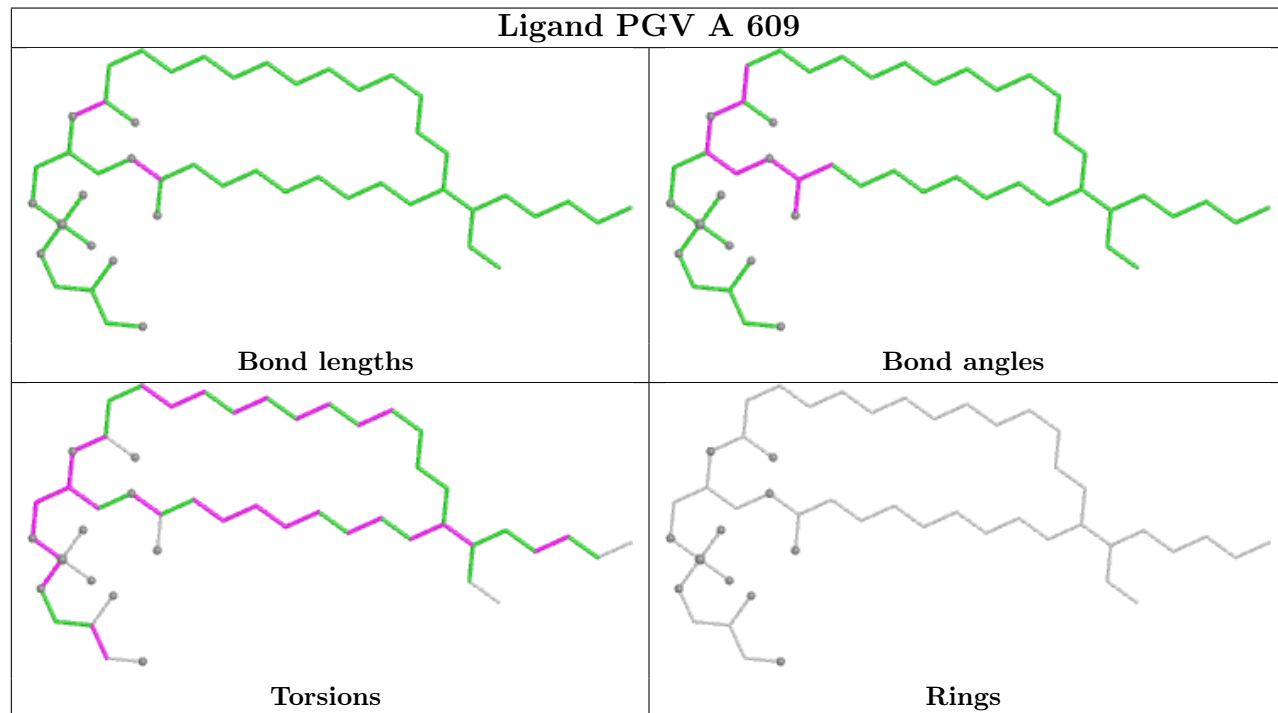
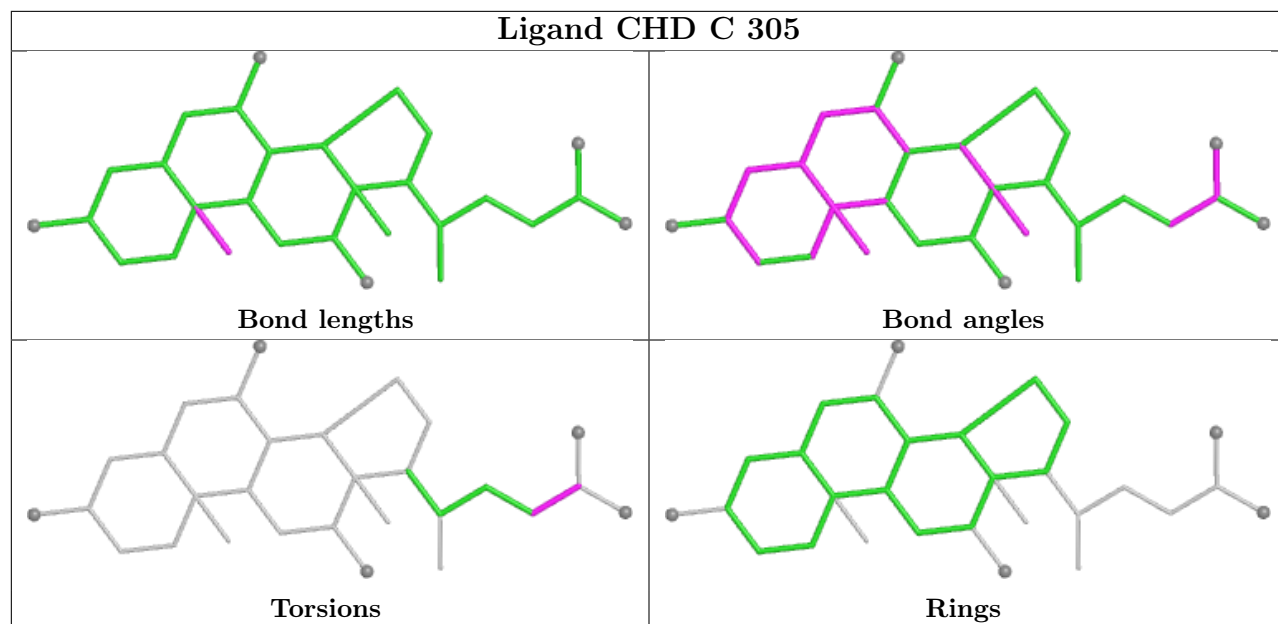


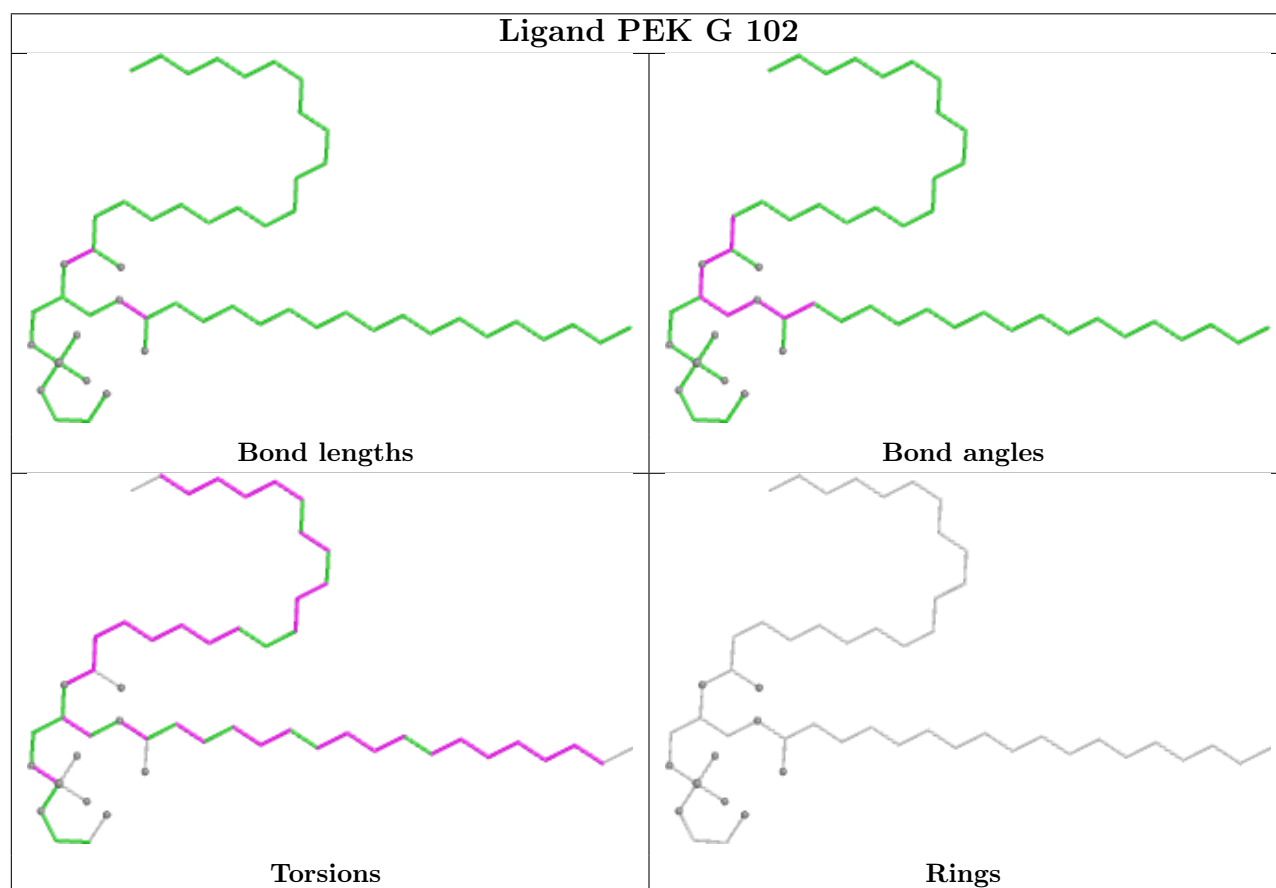
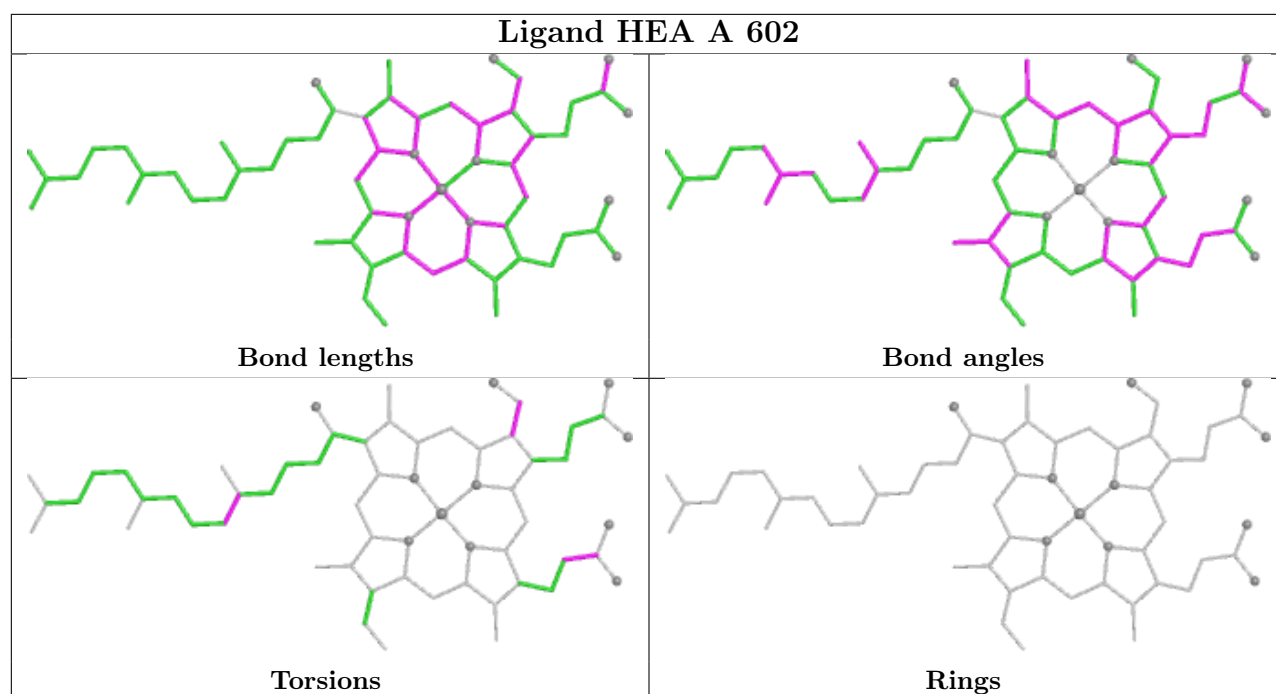


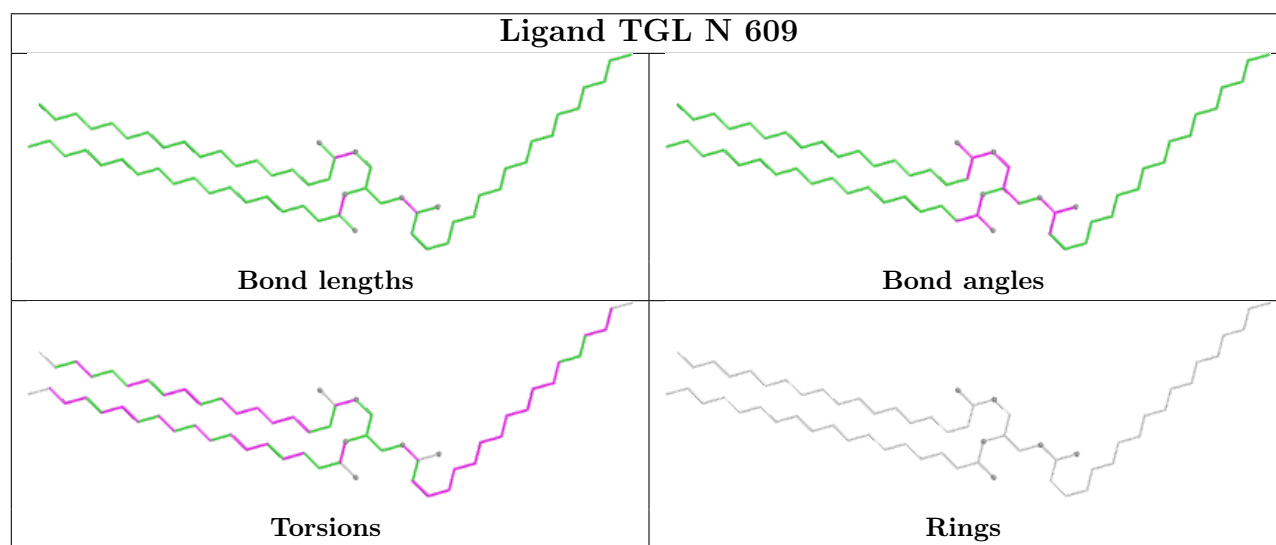
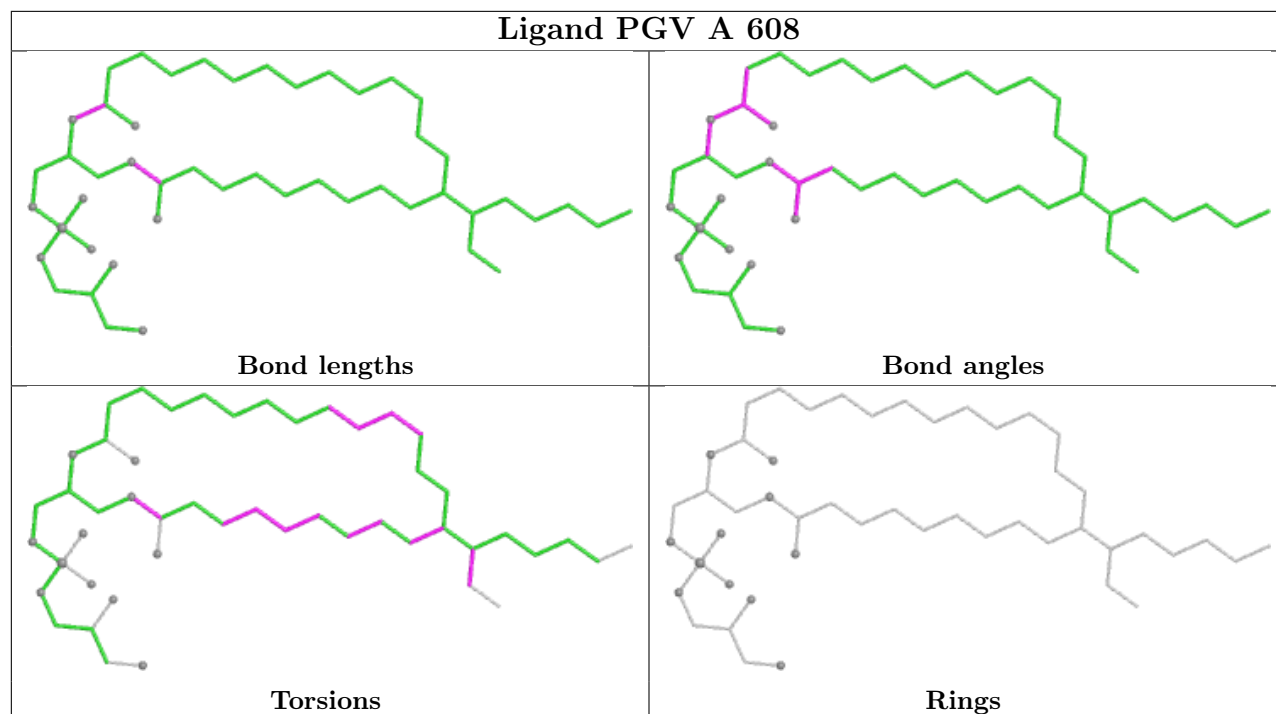


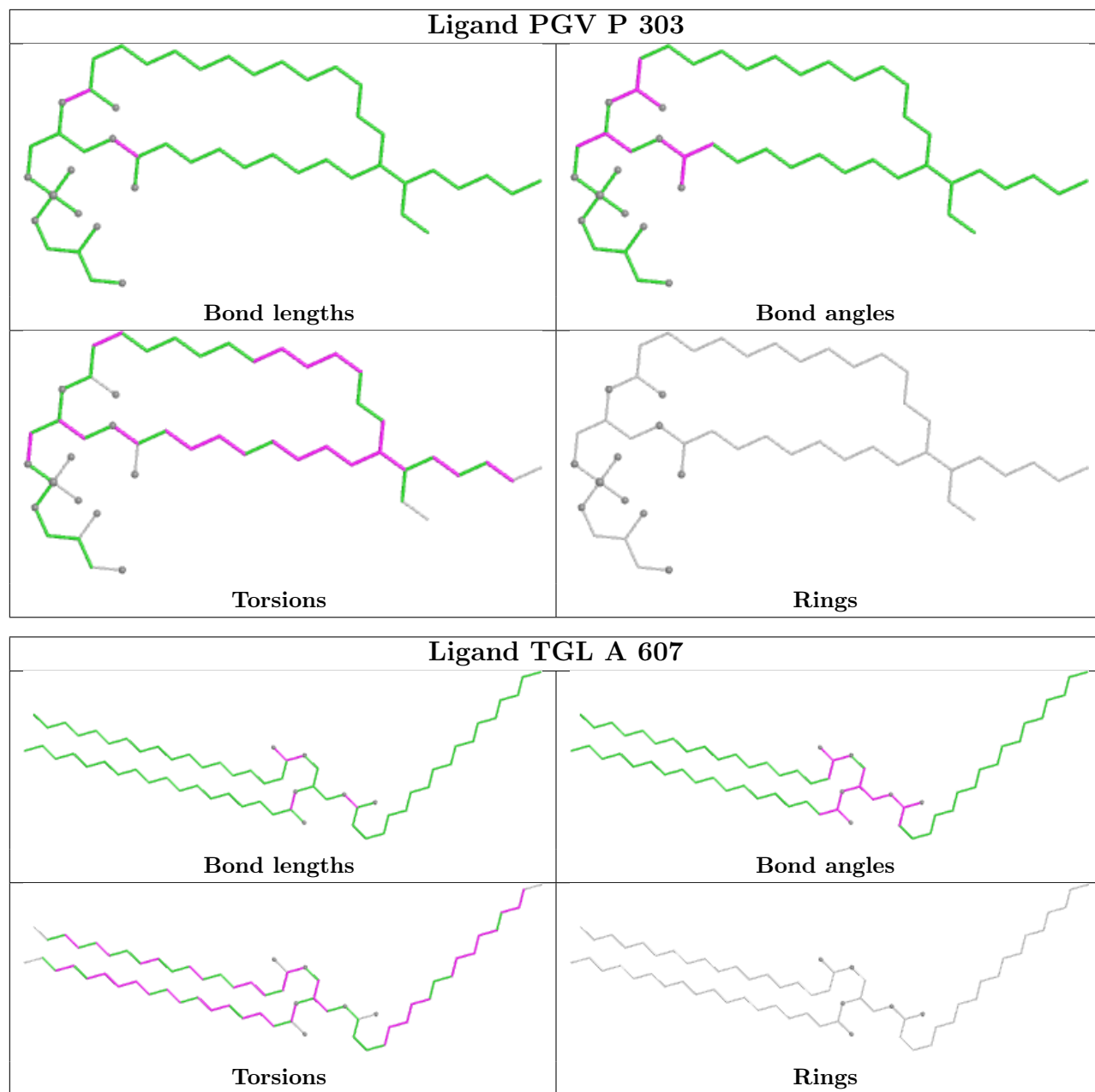


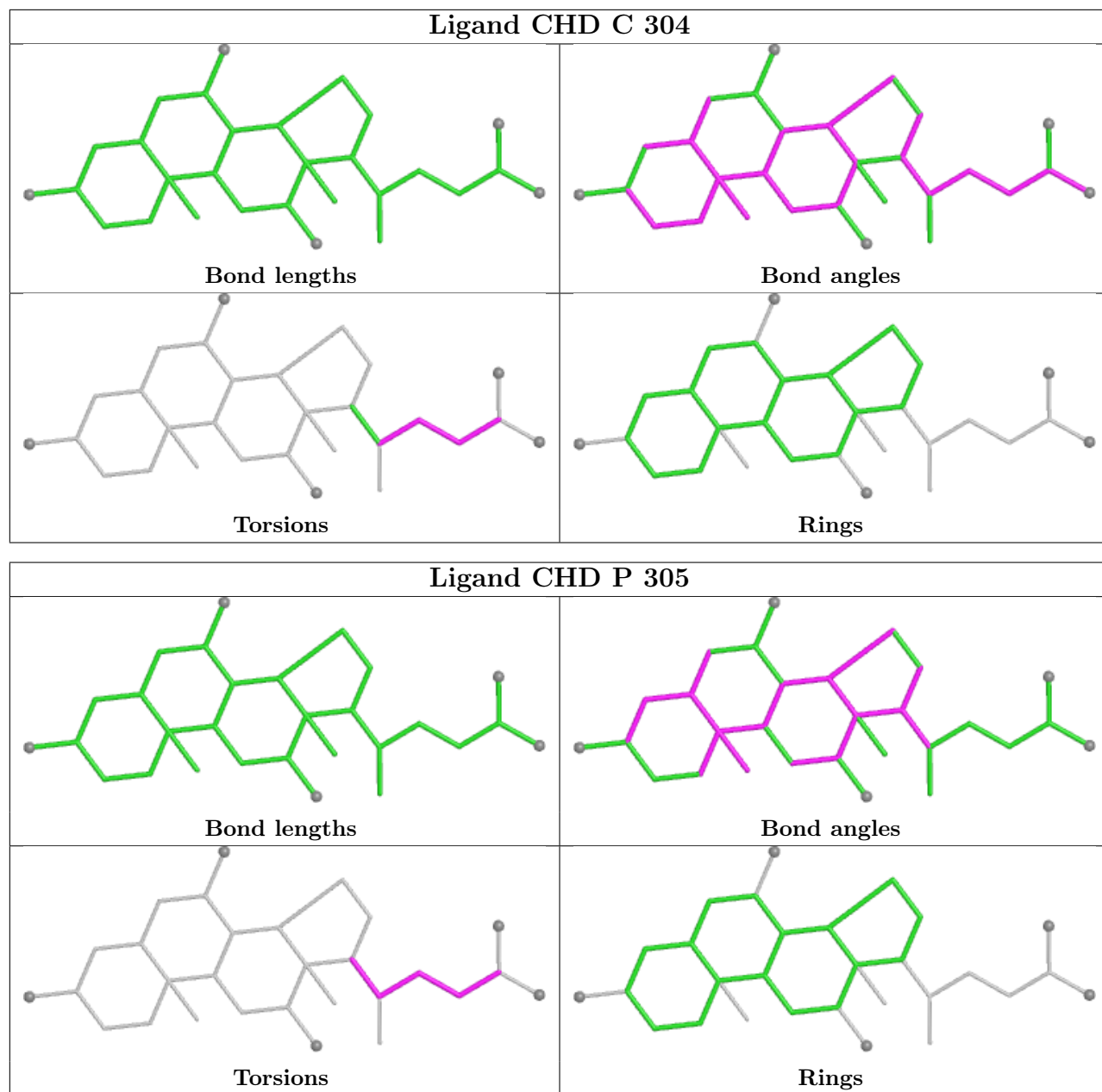


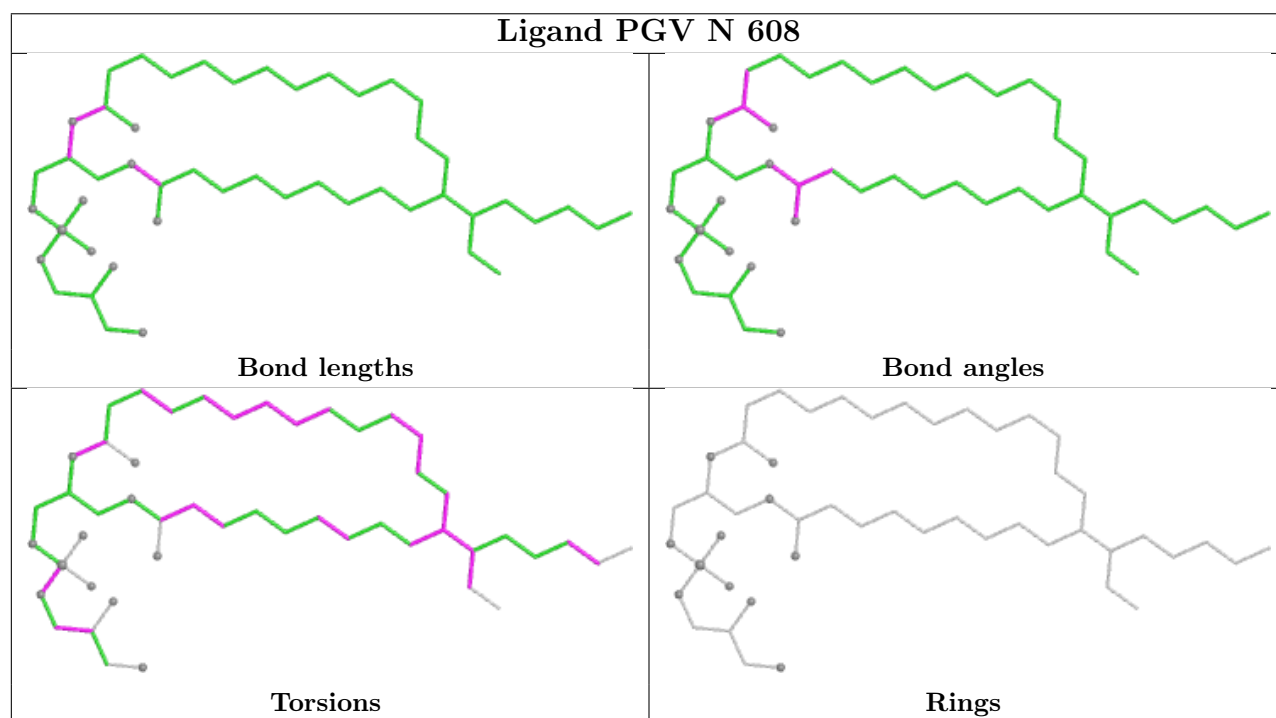
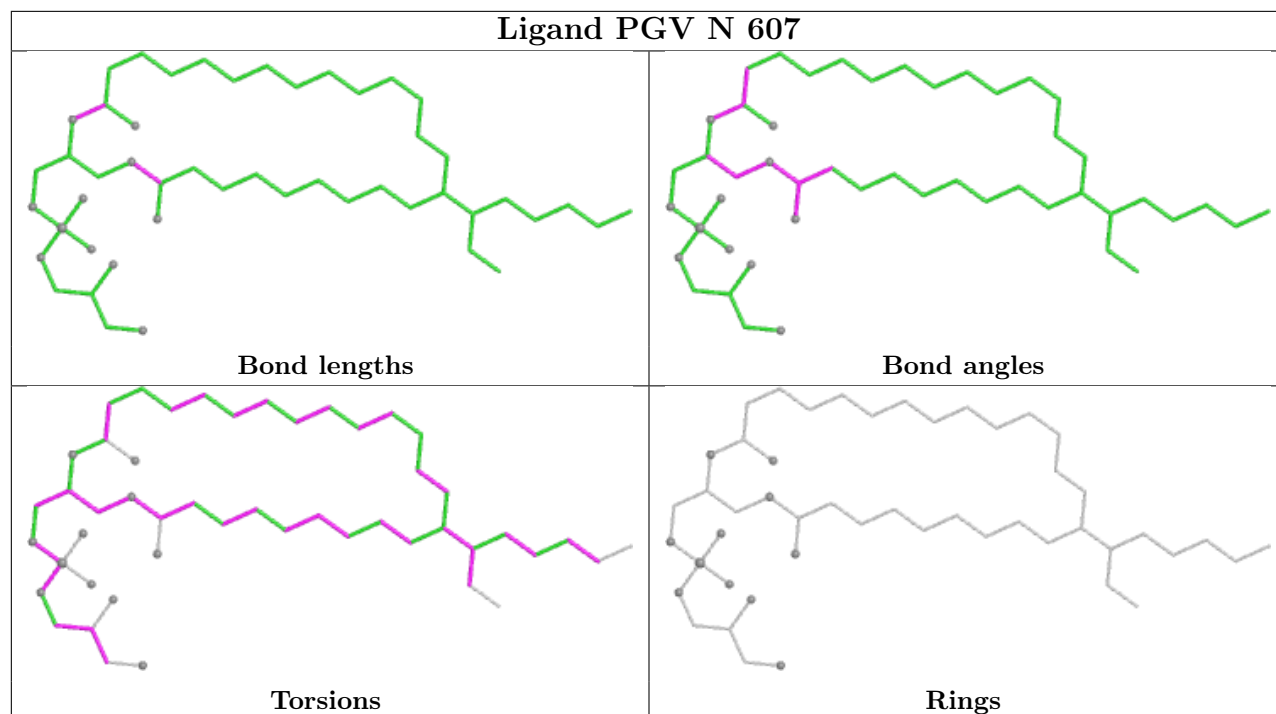


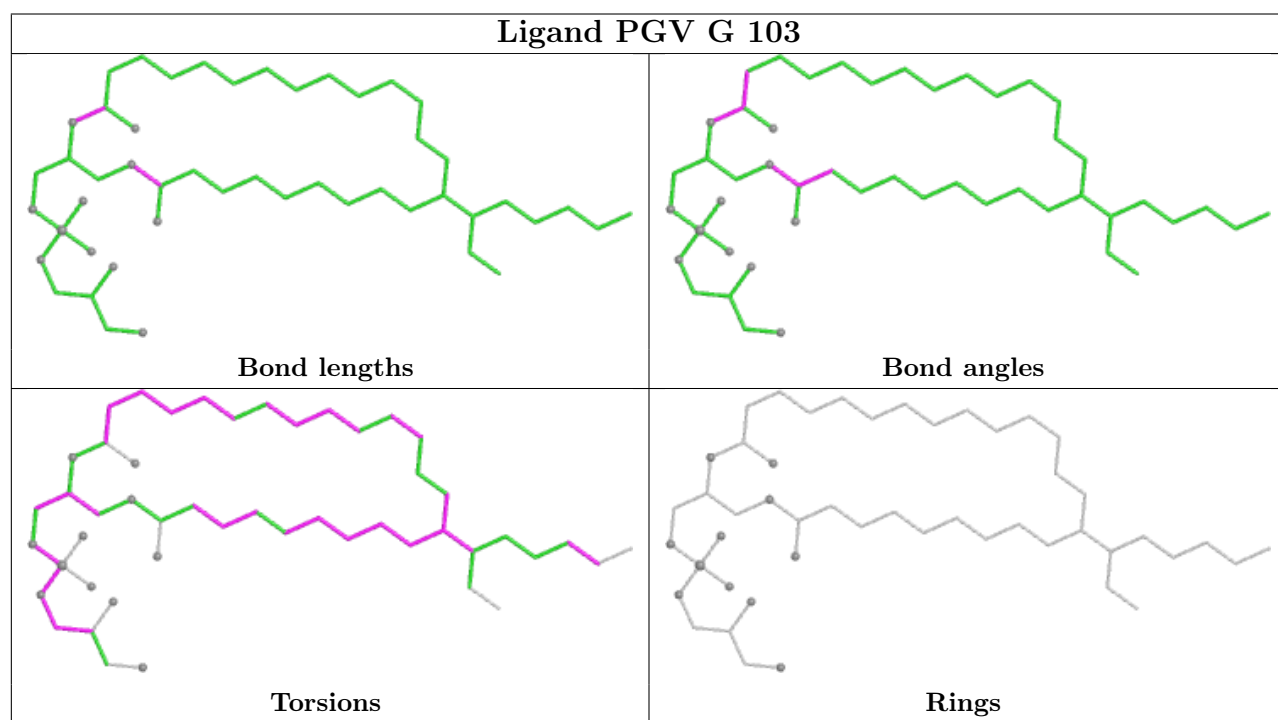
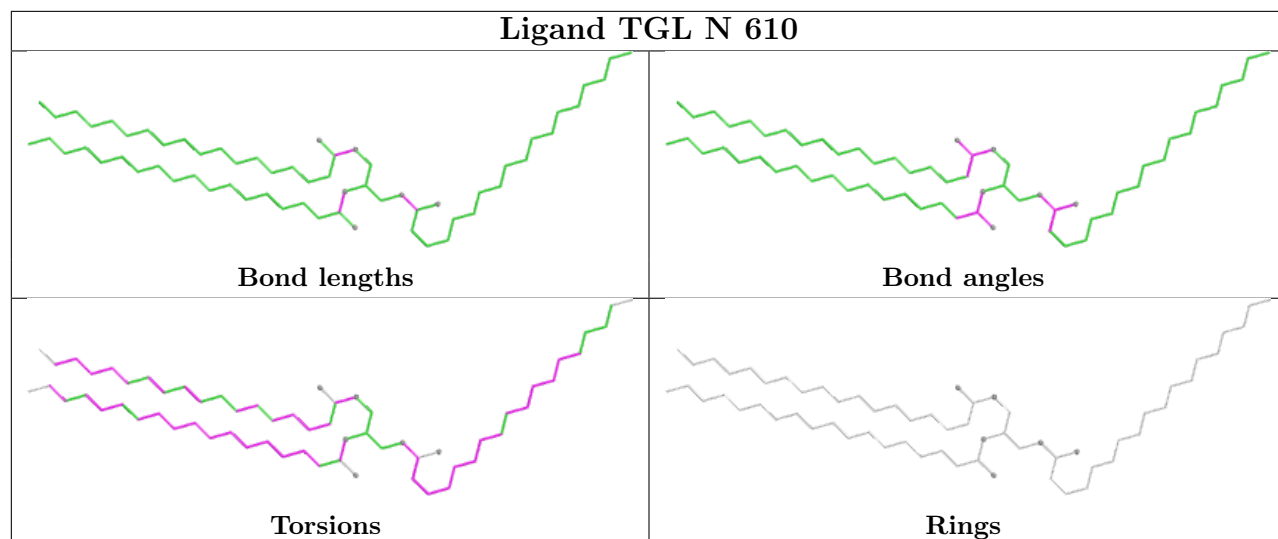




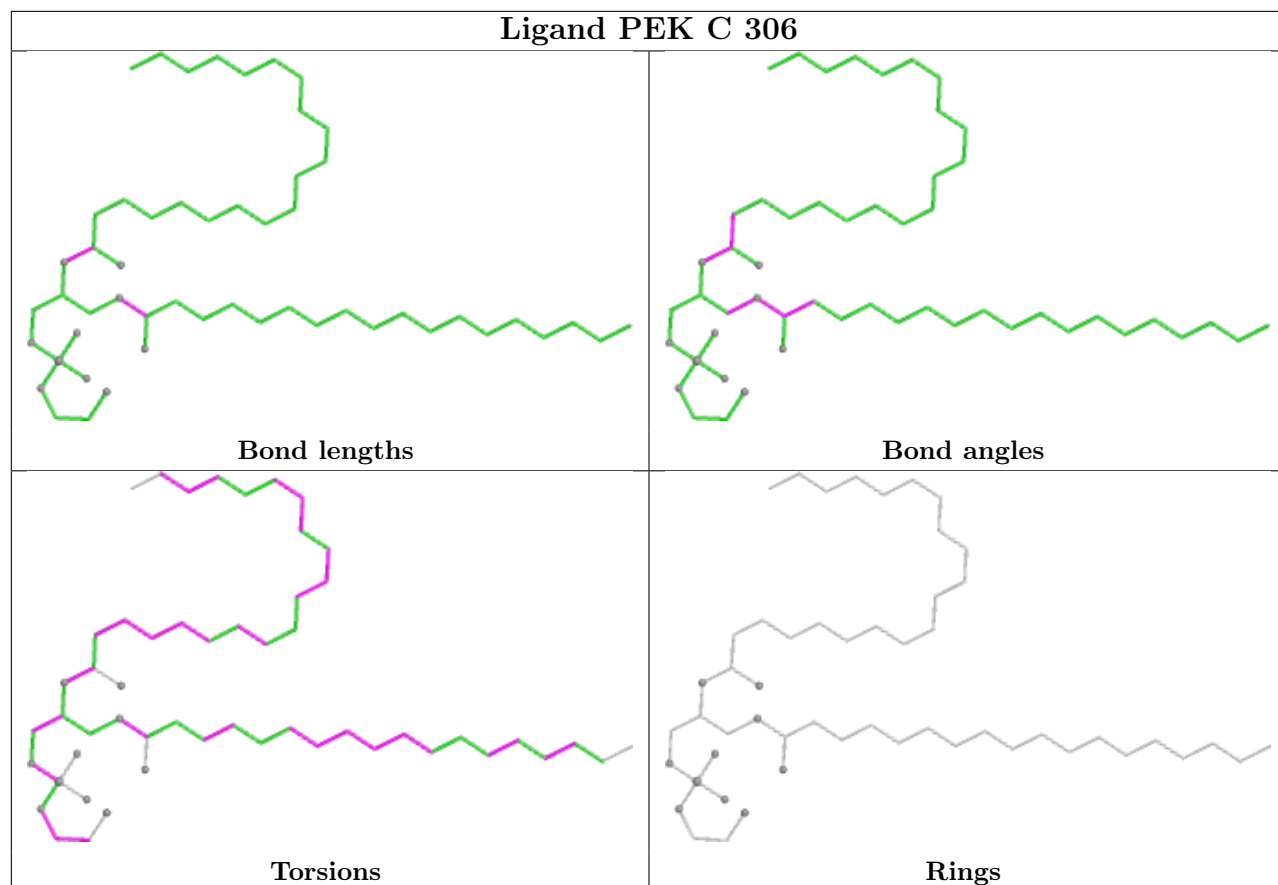




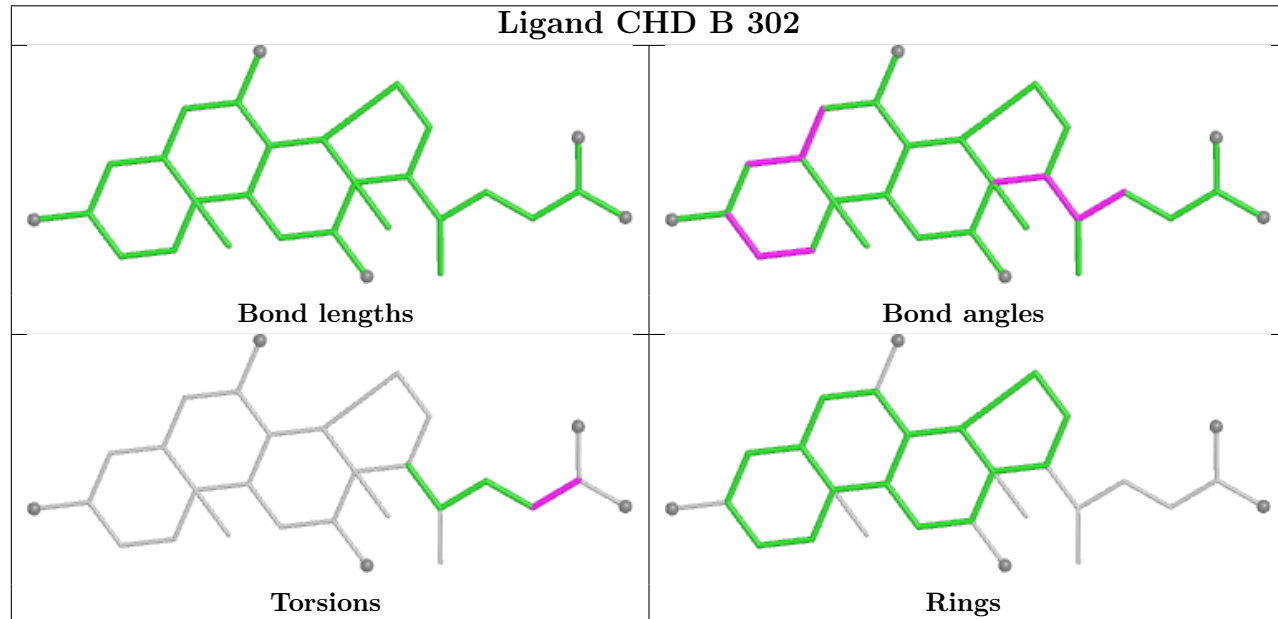


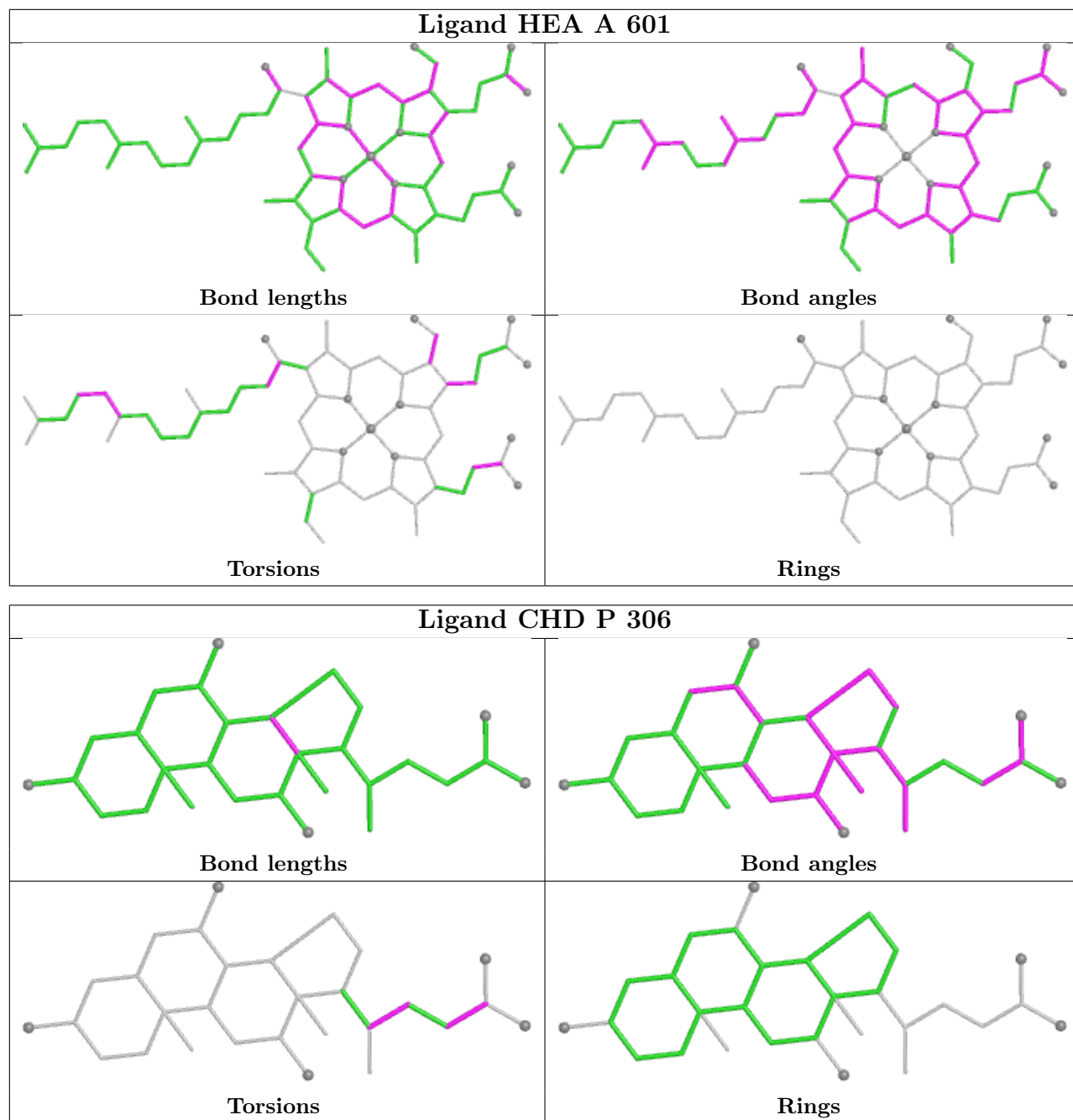


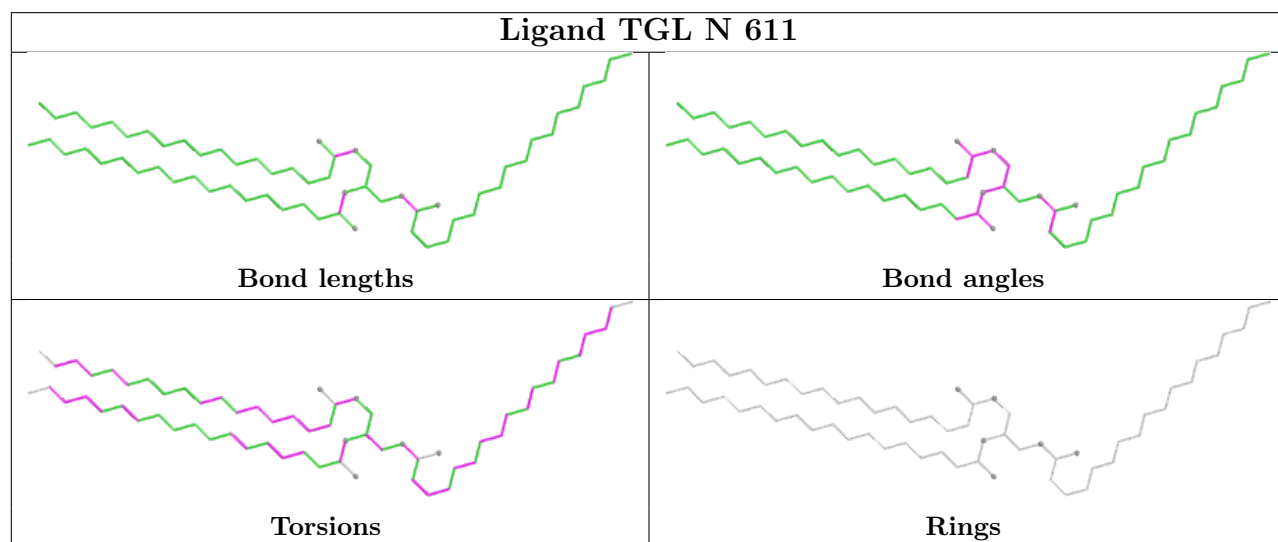
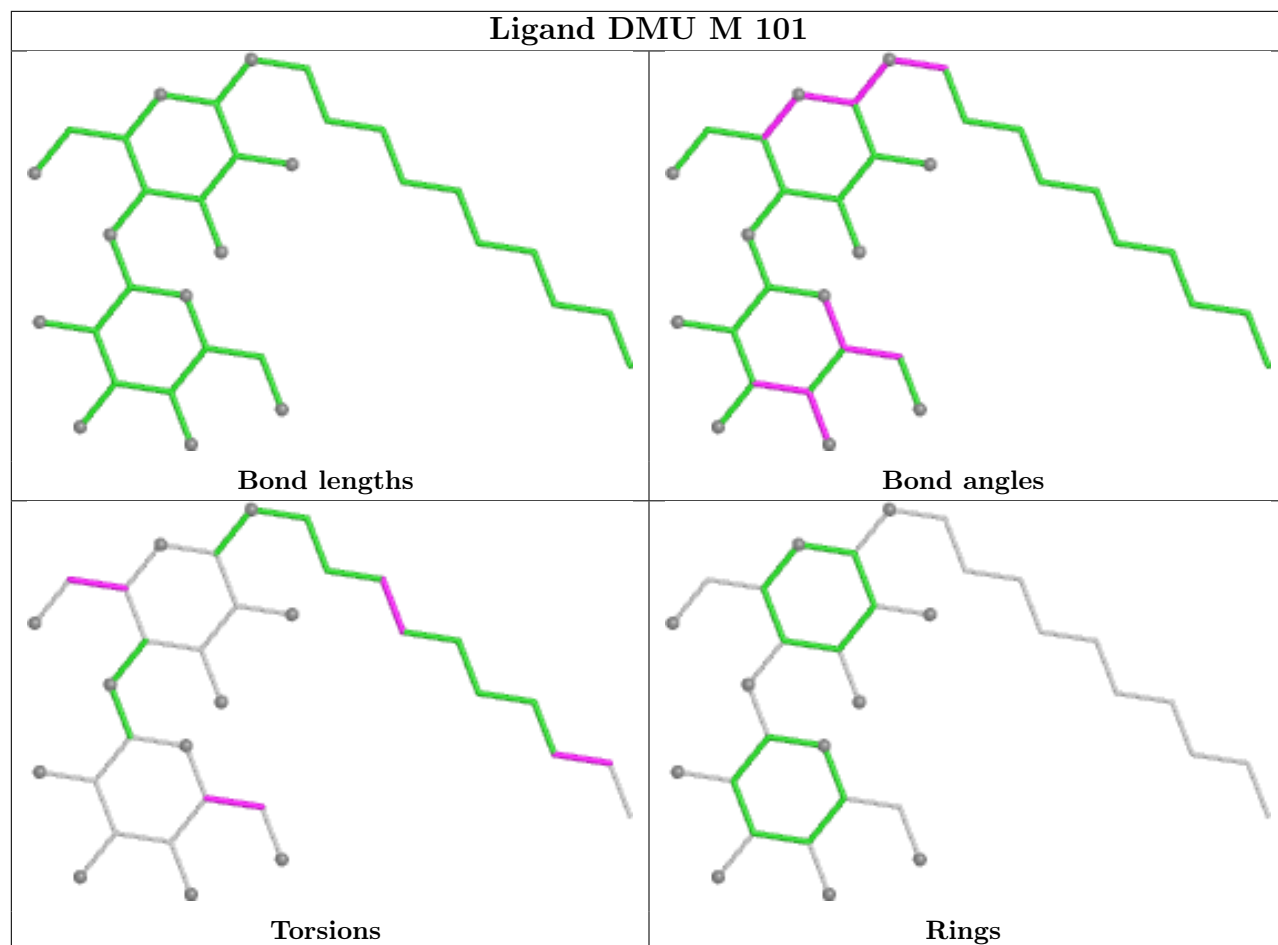
Ligand PEK C 306

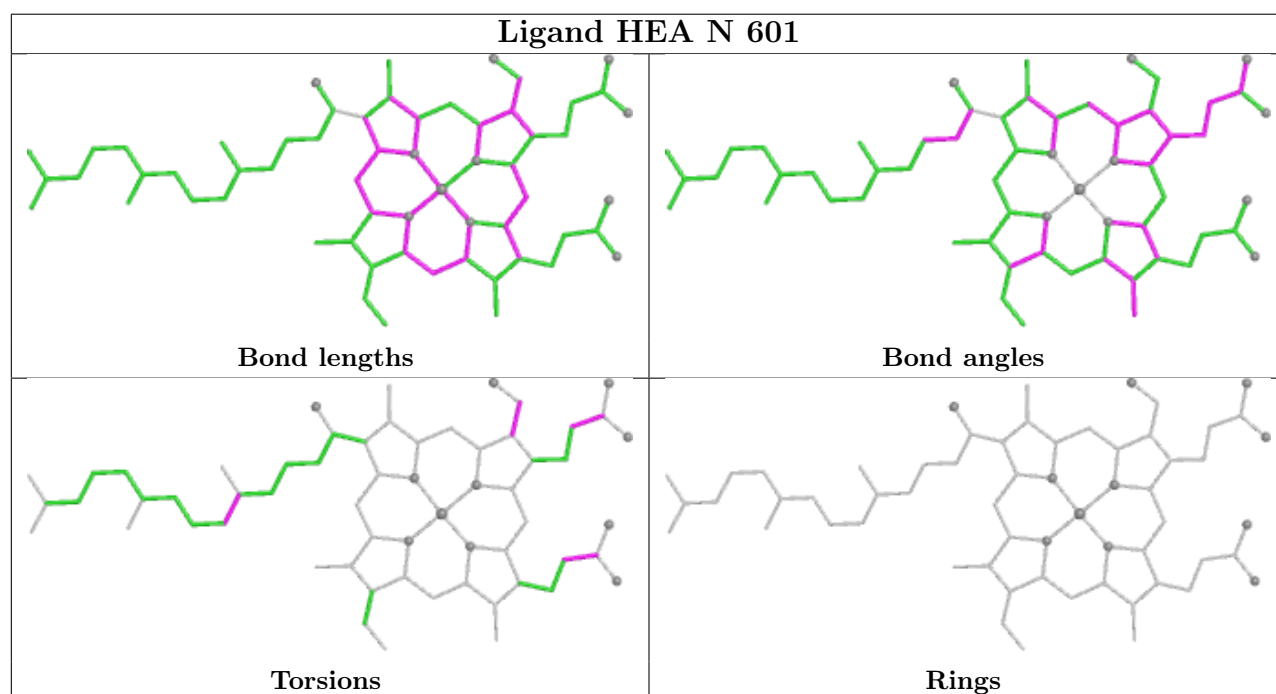
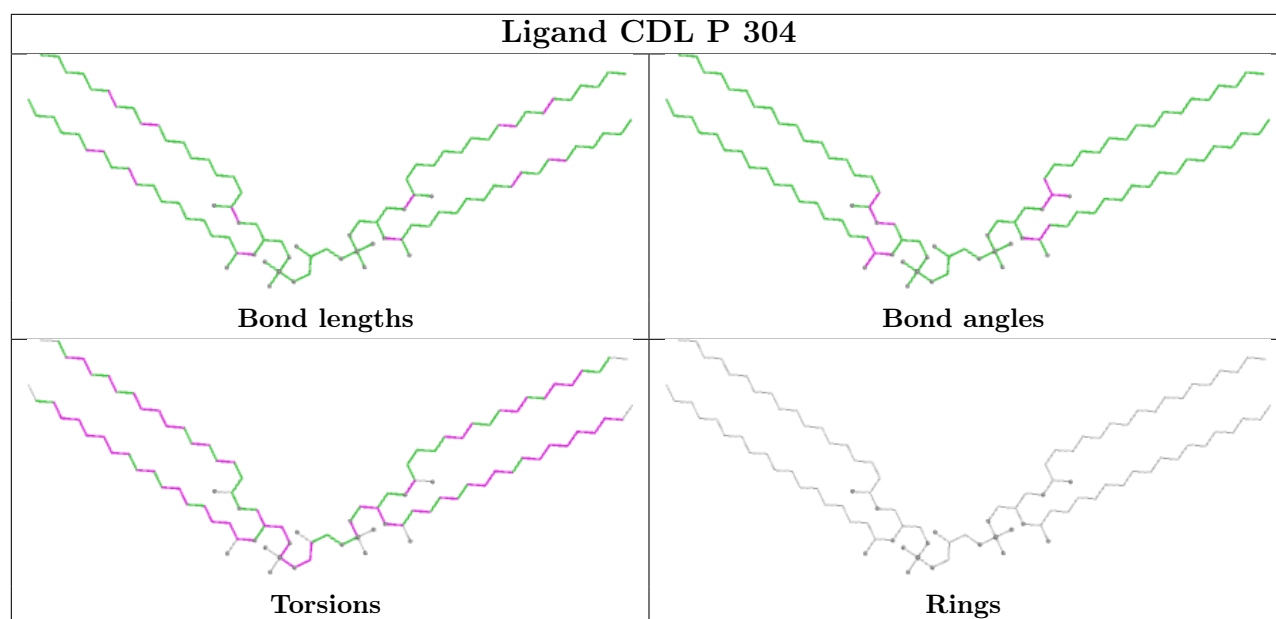


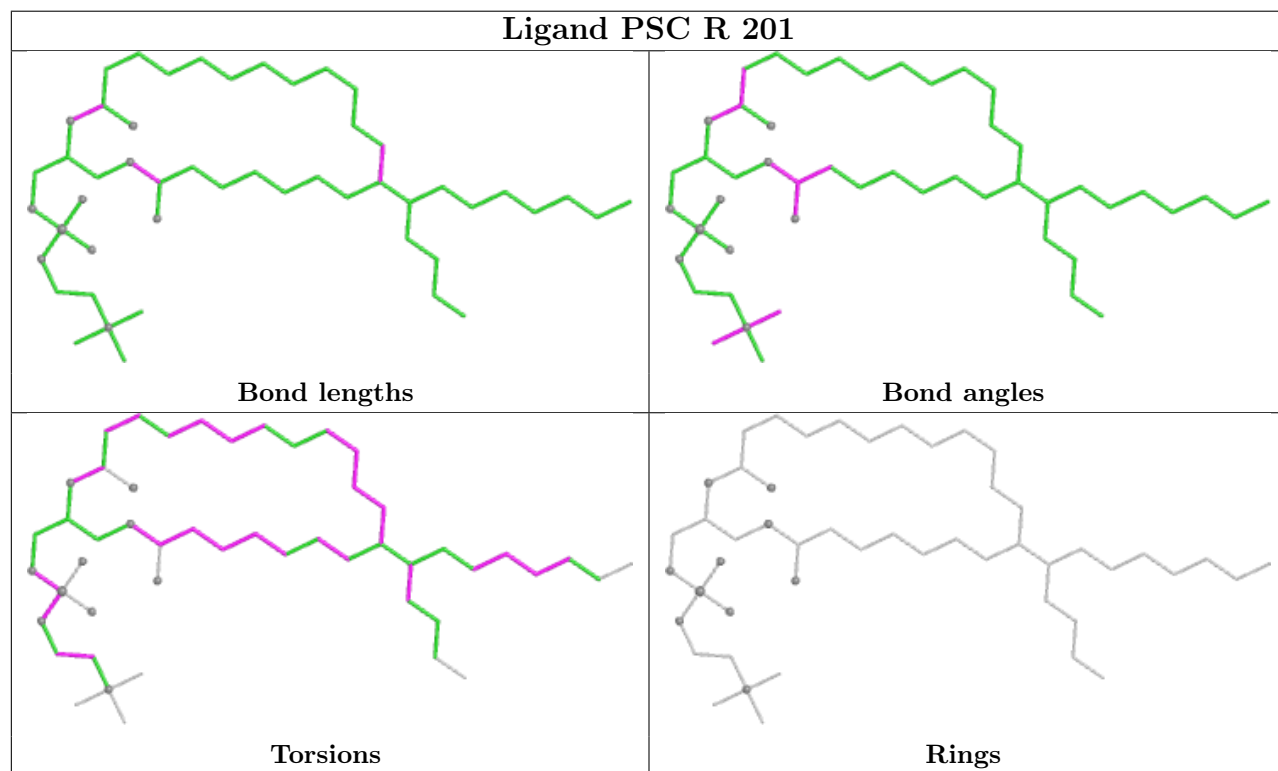
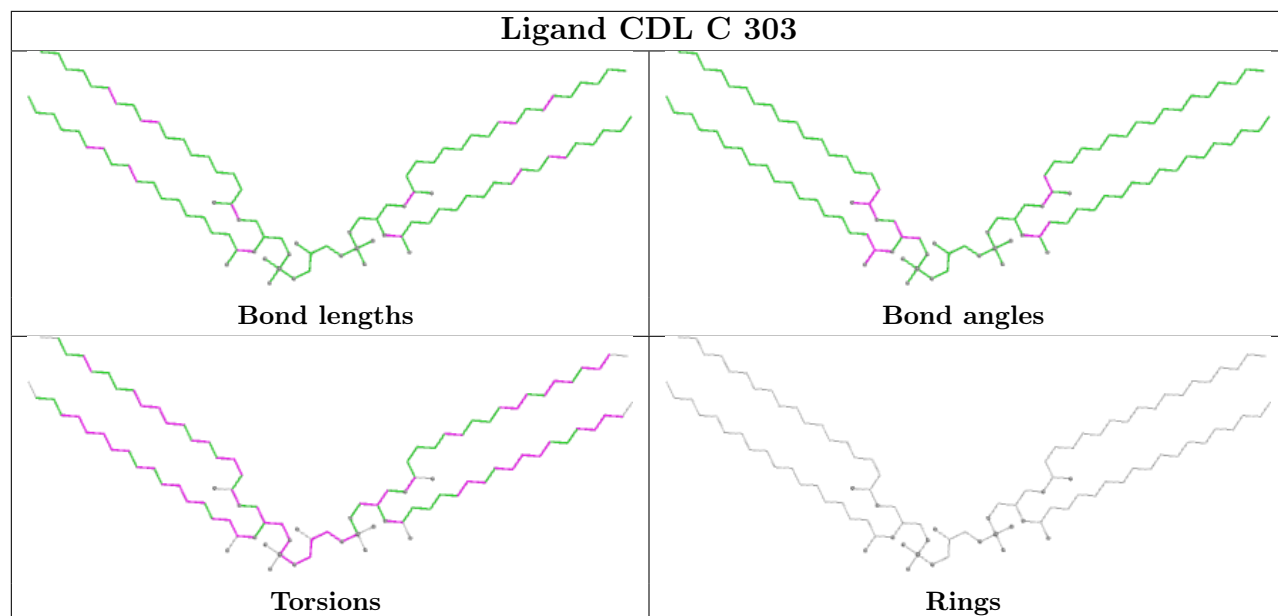
Ligand CHD B 302

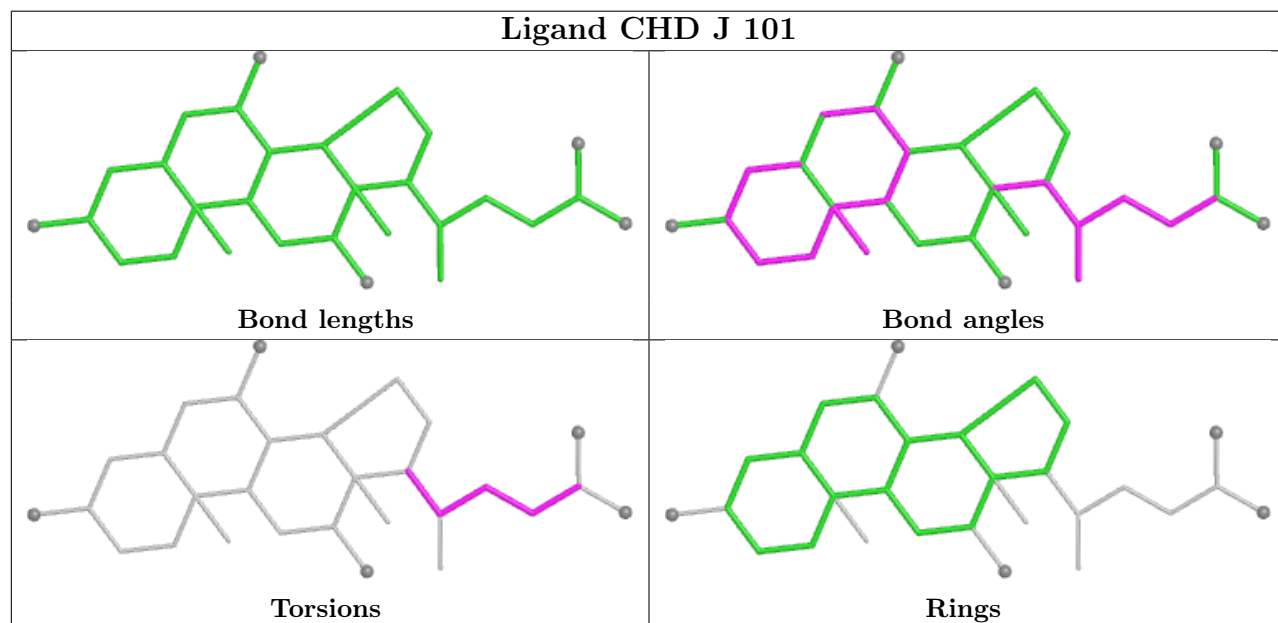
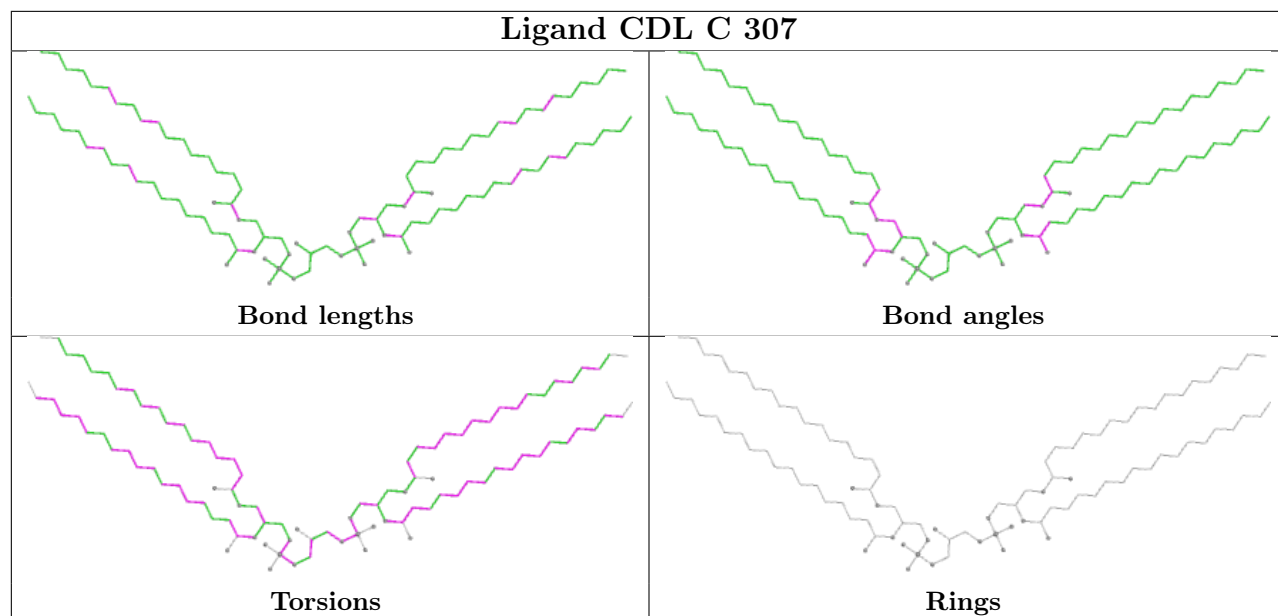


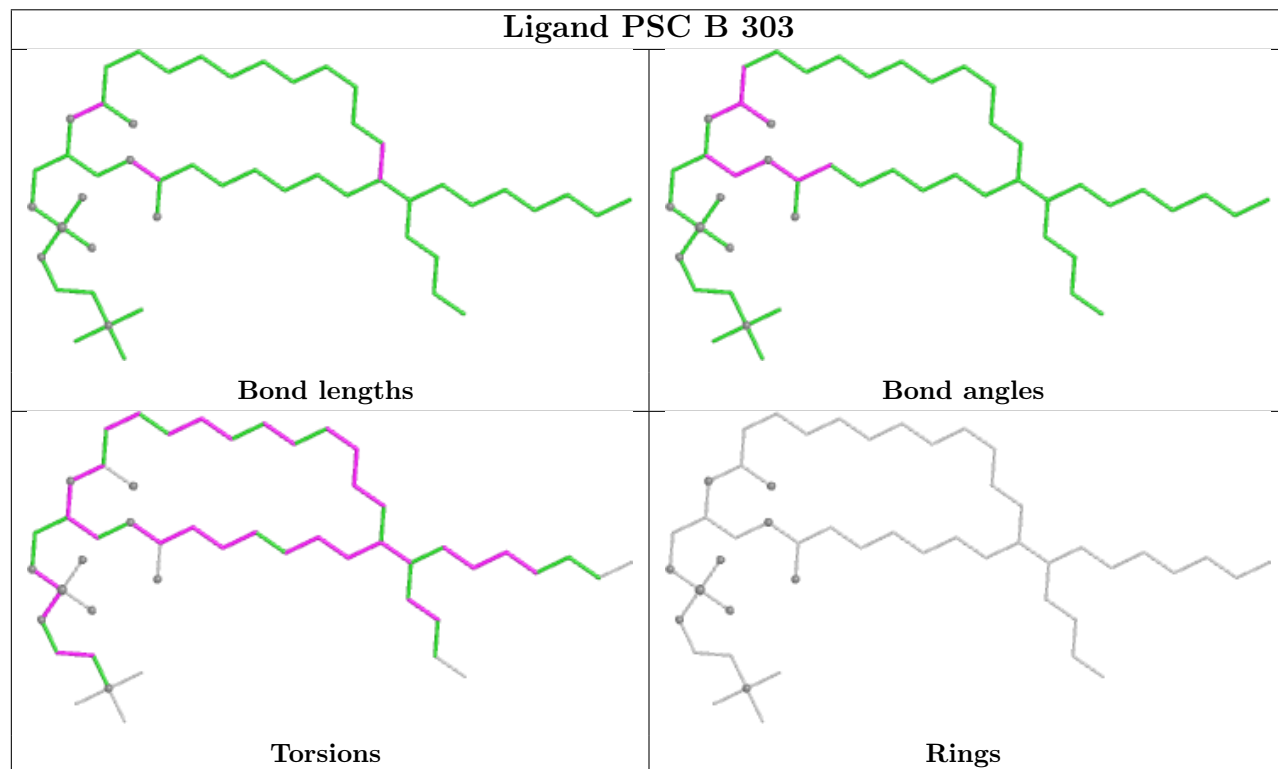
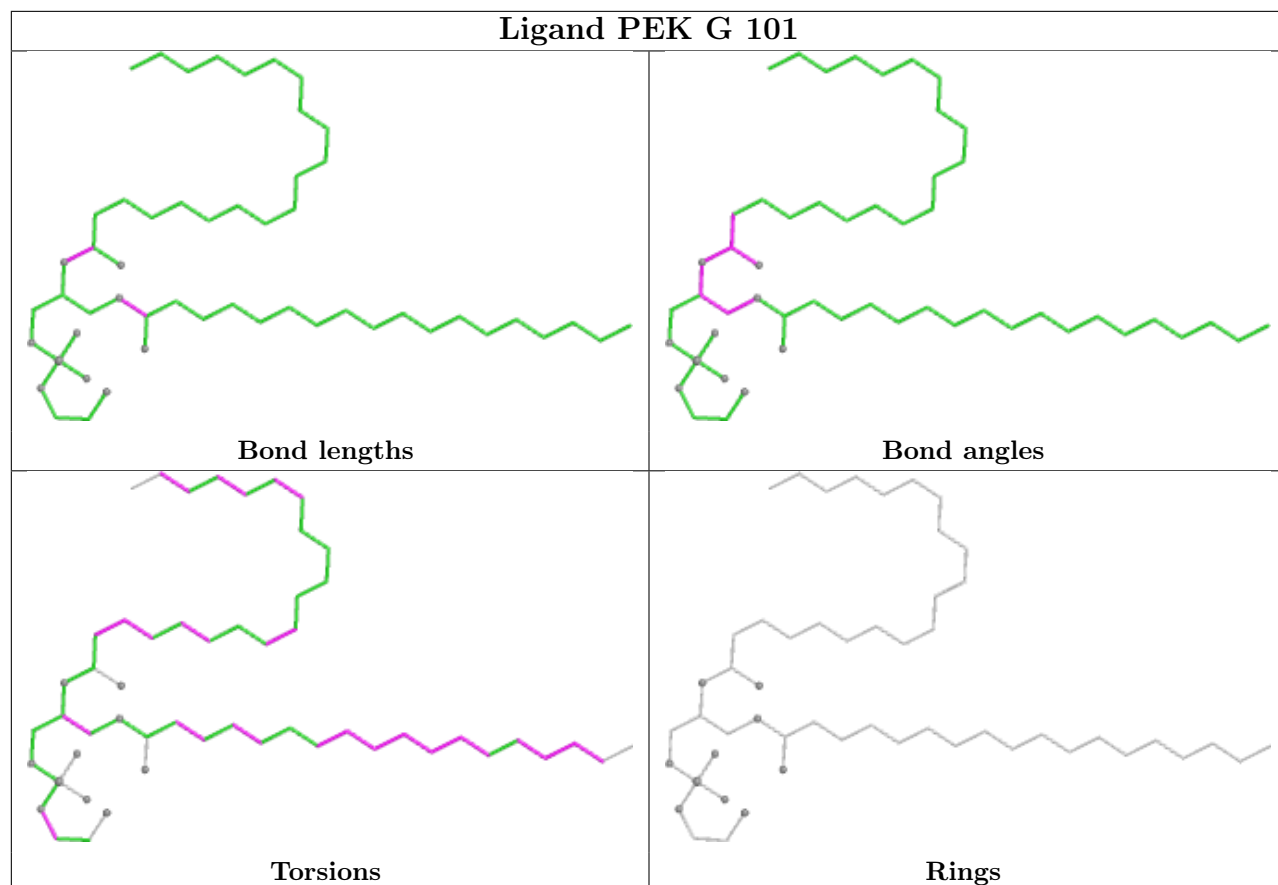


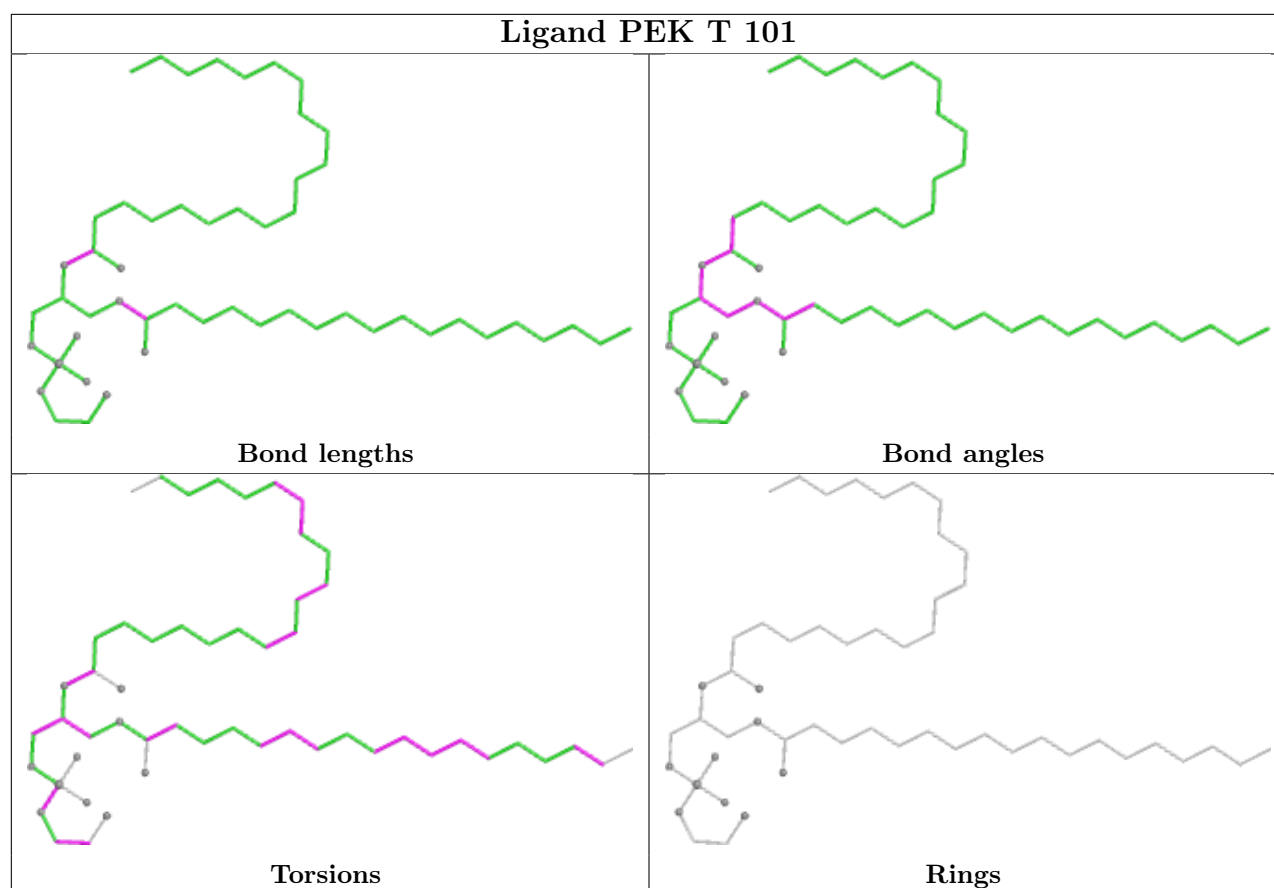












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	513/514 (99%)	-1.16	0 100 100	39, 53, 66, 101	1 (0%)
1	N	513/514 (99%)	-1.09	0 100 100	43, 60, 76, 104	0
2	B	226/227 (99%)	-1.07	0 100 100	46, 59, 91, 128	0
2	O	226/227 (99%)	-0.97	1 (0%) 88 86	54, 69, 104, 150	0
3	C	259/261 (99%)	-1.09	0 100 100	46, 57, 75, 115	0
3	P	259/261 (99%)	-1.02	0 100 100	46, 62, 81, 121	0
4	D	144/147 (97%)	-1.08	0 100 100	52, 66, 89, 117	0
4	Q	144/147 (97%)	-0.78	1 (0%) 84 81	64, 83, 125, 160	0
5	E	105/109 (96%)	-1.19	0 100 100	50, 65, 92, 147	0
5	R	105/109 (96%)	-1.04	0 100 100	62, 79, 105, 154	0
6	F	98/98 (100%)	-0.94	0 100 100	52, 66, 134, 154	0
6	S	98/98 (100%)	-0.84	1 (1%) 79 76	58, 74, 145, 162	0
7	G	83/85 (97%)	-0.72	1 (1%) 76 73	55, 66, 143, 159	0
7	T	83/85 (97%)	-0.65	0 100 100	53, 73, 147, 158	0
8	H	79/85 (92%)	-0.89	0 100 100	54, 69, 141, 156	0
8	U	79/85 (92%)	-0.82	1 (1%) 75 71	61, 80, 139, 153	0
9	I	72/73 (98%)	-0.85	0 100 100	58, 73, 101, 114	0
9	V	72/73 (98%)	-0.79	0 100 100	59, 84, 114, 142	0
10	J	58/59 (98%)	-1.01	0 100 100	57, 70, 111, 144	0
10	W	58/59 (98%)	-0.94	0 100 100	66, 82, 123, 158	0
11	K	49/56 (87%)	-0.89	0 100 100	59, 72, 93, 119	0
11	X	49/56 (87%)	-0.81	0 100 100	70, 84, 119, 127	0
12	L	46/47 (97%)	-1.08	0 100 100	49, 60, 80, 122	0
12	Y	46/47 (97%)	-0.88	0 100 100	60, 75, 102, 119	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	M	43/46 (93%)	-0.92	0	100 100	50, 63, 99, 147	0
13	Z	43/46 (93%)	-0.74	0	100 100	70, 79, 121, 164	0
All	All	3550/3614 (98%)	-1.00	5 (0%)	92 90	39, 64, 107, 164	1 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	Q	6	VAL	3.0
2	O	90	ILE	2.9
6	S	96	LEU	2.5
7	G	5	LYS	2.4
8	U	8	ILE	2.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	SAC	V	1	9/10	0.63	0.09	138,151,167,167	0
7	TPO	T	11	11/12	0.68	0.15	101,147,160,160	0
7	TPO	G	11	11/12	0.80	0.10	102,140,157,157	0
9	SAC	I	1	9/10	0.84	0.07	116,134,157,165	0
1	FME	N	1	10/11	0.91	0.10	80,86,125,151	0
1	FME	A	1	10/11	0.95	0.11	74,86,128,147	0
2	FME	O	1	10/11	0.97	0.06	64,71,76,79	0
2	FME	B	1	10/11	0.98	0.04	58,65,72,72	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	CHD	W	101	29/29	0.75	0.12	107,145,150,150	0
27	PEK	G	102	53/53	0.76	0.15	100,135,150,150	0
24	PSC	B	303	52/52	0.77	0.15	75,147,150,150	0
27	PEK	T	101	53/53	0.78	0.15	79,136,150,150	0
20	PGV	N	607	51/51	0.79	0.12	99,137,150,150	0
24	PSC	R	201	52/52	0.79	0.15	76,137,150,150	0
21	EDO	C	310	4/4	0.82	0.18	94,105,106,112	0
20	PGV	A	609	51/51	0.82	0.11	69,115,159,161	0
19	TGL	N	611	63/63	0.82	0.15	90,126,148,150	0
27	PEK	T	102	53/53	0.82	0.14	78,133,150,150	0
26	CDL	P	304	100/100	0.83	0.12	71,140,150,150	0
26	CDL	T	103	100/100	0.83	0.15	76,140,150,150	0
19	TGL	A	607	63/63	0.83	0.12	54,97,122,132	0
25	UNX	P	301	1/1	0.83	0.39	15,15,15,15	1
26	CDL	C	307	100/100	0.83	0.15	89,138,150,150	0
19	TGL	L	101	63/63	0.84	0.17	67,113,143,150	0
20	PGV	C	308	51/51	0.84	0.11	75,125,150,150	0
19	TGL	N	610	63/63	0.85	0.13	90,134,149,150	0
25	UNX	C	301	1/1	0.86	0.33	26,26,26,26	1
21	EDO	A	614	4/4	0.87	0.30	133,137,141,148	0
19	TGL	D	201	63/63	0.87	0.13	87,126,147,150	0
27	PEK	C	306	53/53	0.87	0.12	71,132,149,150	0
29	DMU	Z	101	33/33	0.87	0.12	80,128,149,150	0
26	CDL	C	303	100/100	0.88	0.10	66,123,153,155	0
19	TGL	N	609	63/63	0.88	0.10	60,120,149,150	0
20	PGV	G	103	51/51	0.88	0.10	96,127,150,150	0
21	EDO	C	309	4/4	0.90	0.09	76,86,100,122	0
21	EDO	C	311	4/4	0.91	0.10	80,95,109,118	0
23	CHD	C	304	29/29	0.91	0.08	93,117,125,127	0
21	EDO	B	305	4/4	0.92	0.12	105,110,115,123	0
23	CHD	P	305	29/29	0.92	0.09	120,135,145,147	0
21	EDO	K	103	4/4	0.92	0.08	90,92,99,101	0
21	EDO	T	104	4/4	0.92	0.16	124,129,131,132	0
23	CHD	J	101	29/29	0.93	0.07	123,142,150,150	0
21	EDO	L	102	4/4	0.93	0.12	83,84,84,90	0
21	EDO	K	102	4/4	0.93	0.15	101,108,112,116	0
21	EDO	K	101	4/4	0.93	0.14	86,107,118,131	0
21	EDO	A	613	4/4	0.94	0.22	112,112,121,122	0
29	DMU	M	101	33/33	0.94	0.08	70,102,129,136	0
21	EDO	A	610	4/4	0.94	0.08	75,75,78,81	0
21	EDO	N	612	4/4	0.95	0.10	79,80,82,84	0

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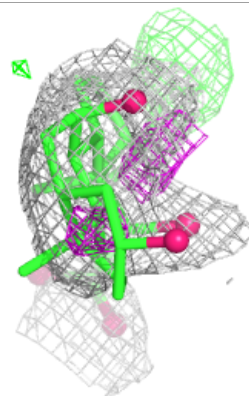
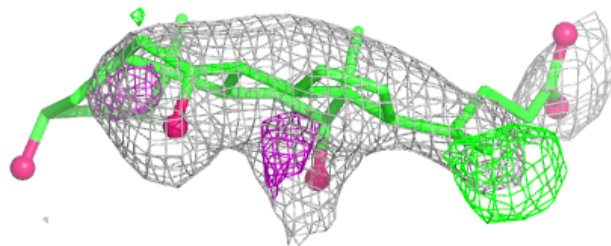
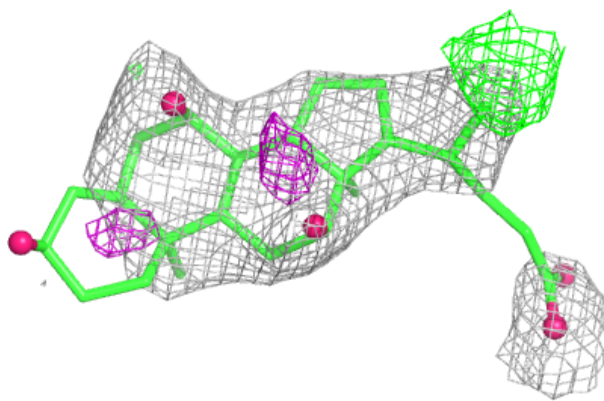
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
21	EDO	A	612	4/4	0.95	0.21	88,115,122,127	0
21	EDO	F	102	4/4	0.96	0.06	80,88,96,96	0
27	PEK	P	302	53/53	0.96	0.07	59,91,150,150	0
27	PEK	G	101	53/53	0.97	0.05	57,72,126,136	0
23	CHD	B	302	29/29	0.97	0.05	48,64,74,77	0
23	CHD	P	306	29/29	0.97	0.04	57,65,72,73	0
21	EDO	A	611	4/4	0.97	0.07	86,94,107,113	0
23	CHD	C	305	29/29	0.97	0.05	47,61,71,81	0
21	EDO	G	104	4/4	0.97	0.10	97,101,102,105	0
23	CHD	O	302	29/29	0.97	0.05	50,57,67,72	0
17	NA	A	605	1/1	0.98	0.05	59,59,59,59	0
20	PGV	N	608	51/51	0.98	0.06	47,76,117,142	0
20	PGV	P	303	51/51	0.98	0.05	51,72,132,148	0
20	PGV	A	608	51/51	0.98	0.05	51,66,79,86	0
18	CMO	A	606	2/2	0.98	0.13	55,55,55,55	0
20	PGV	C	302	51/51	0.98	0.05	49,58,90,99	0
18	CMO	N	606	2/2	0.98	0.14	77,77,77,80	0
14	HEA	N	602	60/60	0.98	0.06	47,57,69,75	0
21	EDO	B	304	4/4	0.98	0.07	71,75,75,75	0
14	HEA	A	602	60/60	0.99	0.05	45,51,60,62	0
17	NA	N	605	1/1	0.99	0.02	70,70,70,70	0
14	HEA	N	601	60/60	0.99	0.05	47,56,78,84	0
28	ZN	F	101	1/1	0.99	0.02	64,64,64,64	0
14	HEA	A	601	60/60	0.99	0.05	34,46,65,70	0
16	MG	N	604	1/1	0.99	0.03	57,57,57,57	0
15	CU	N	603	1/1	1.00	0.01	55,55,55,55	0
16	MG	A	604	1/1	1.00	0.01	51,51,51,51	0
15	CU	A	603	1/1	1.00	0.02	55,55,55,55	0
28	ZN	S	101	1/1	1.00	0.03	70,70,70,70	0
22	CUA	B	301	2/2	1.00	0.03	54,54,54,58	0
22	CUA	O	301	2/2	1.00	0.02	66,66,66,67	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

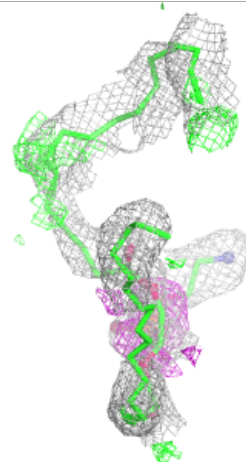
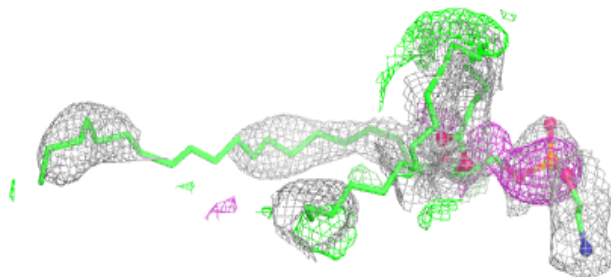
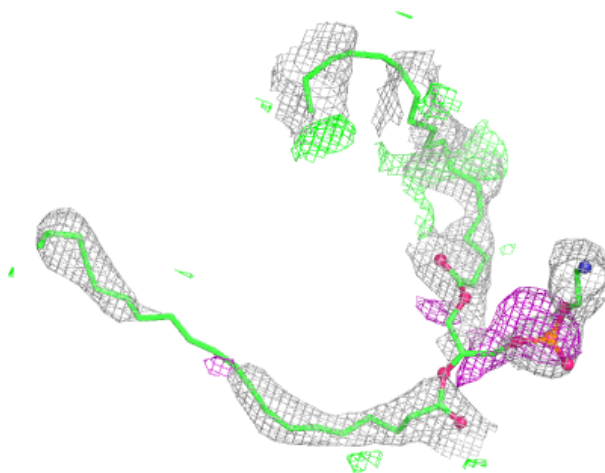
Electron density around CHD W 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



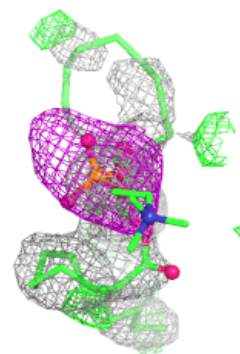
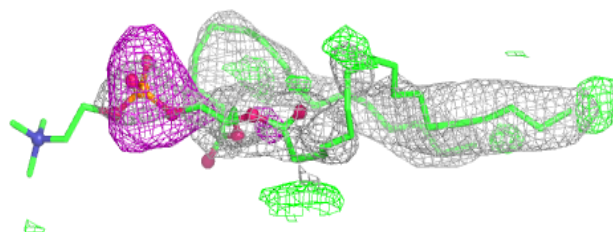
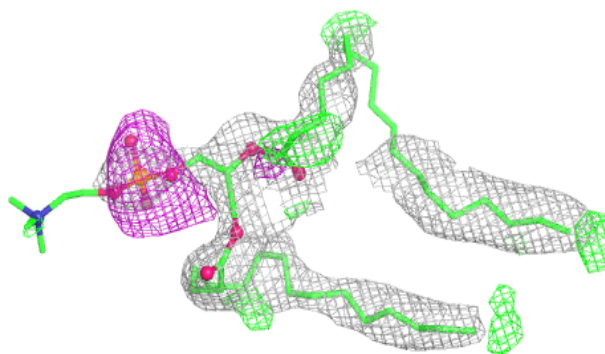
Electron density around PEK G 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

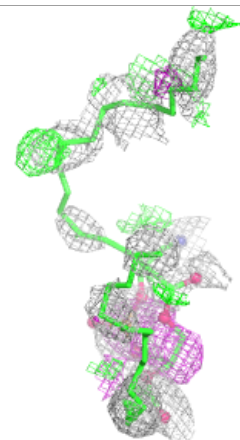
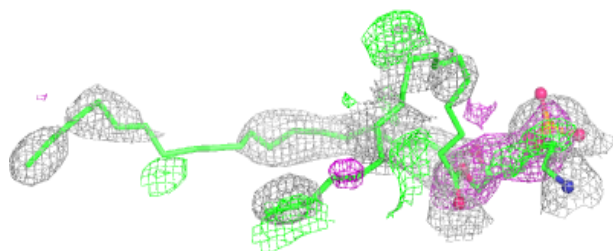
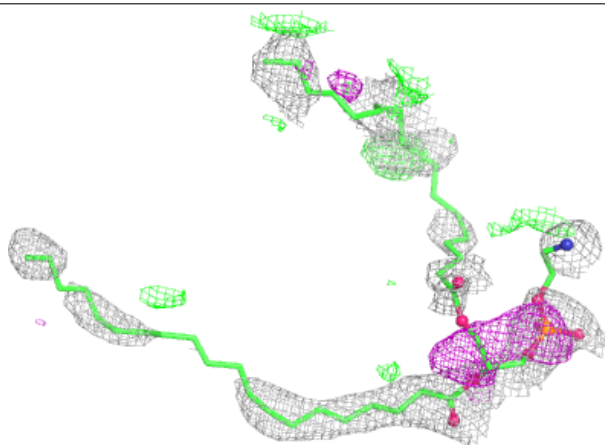


Electron density around PSC B 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

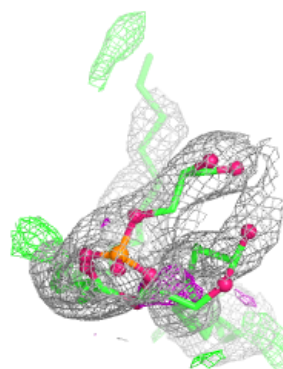
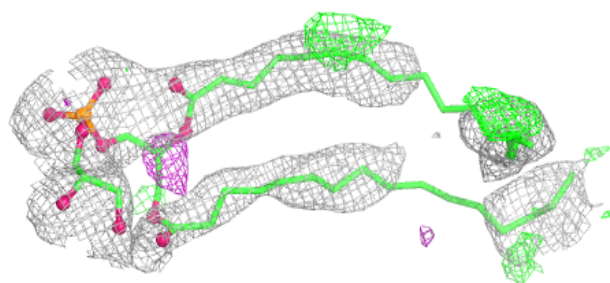
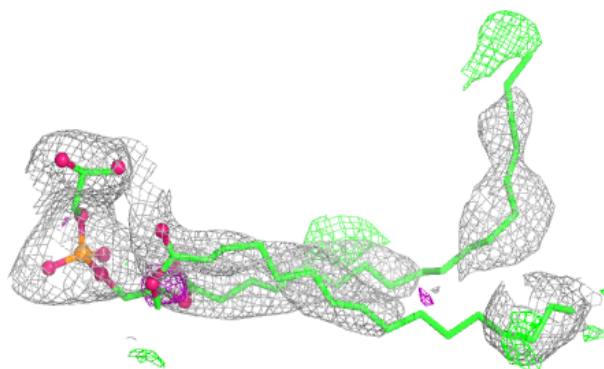
**Electron density around PEK T 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

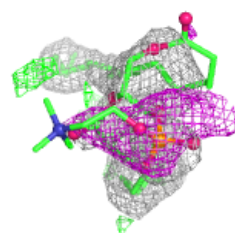
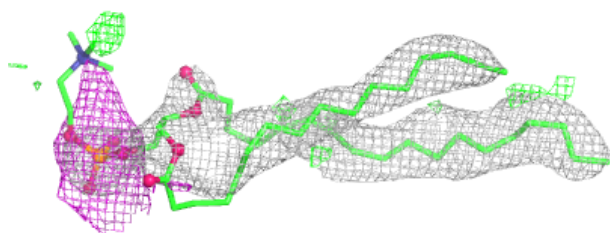
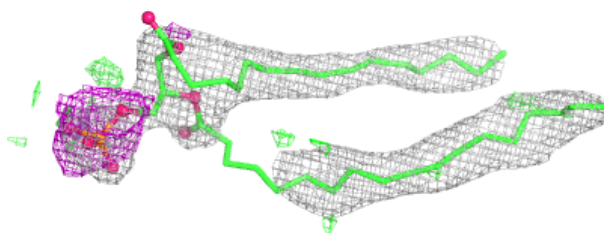


Electron density around PGV N 607:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

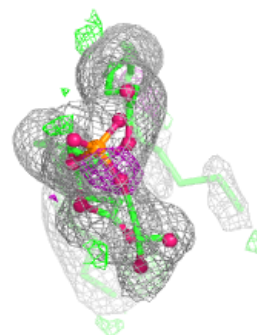
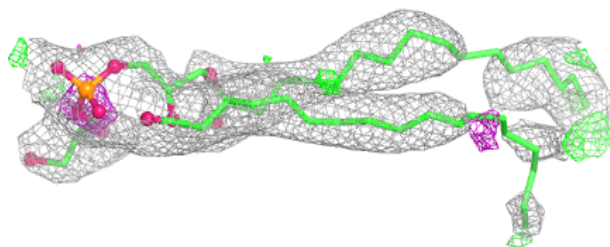
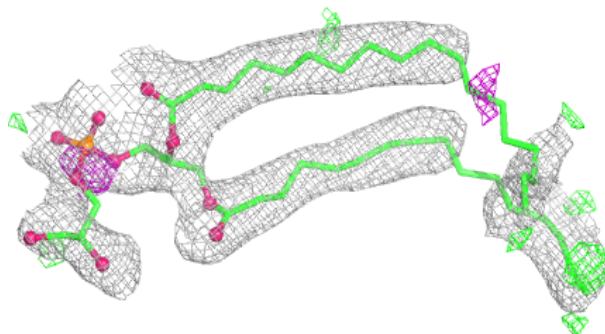
**Electron density around PSC R 201:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



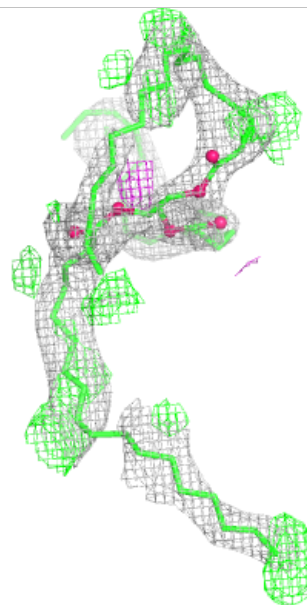
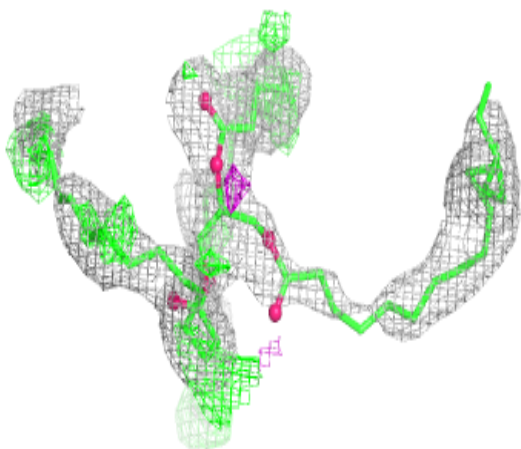
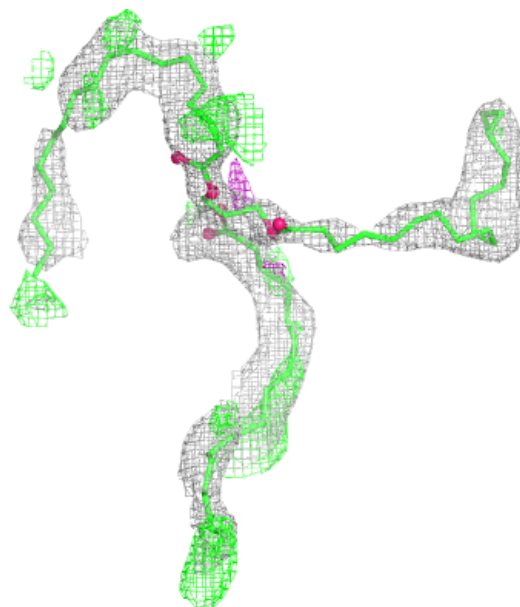
Electron density around PGV A 609:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



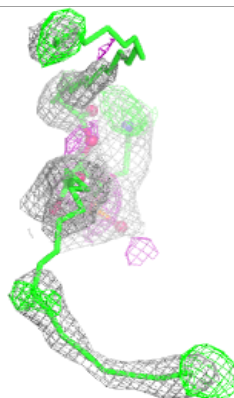
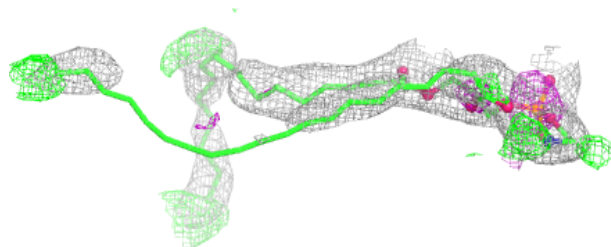
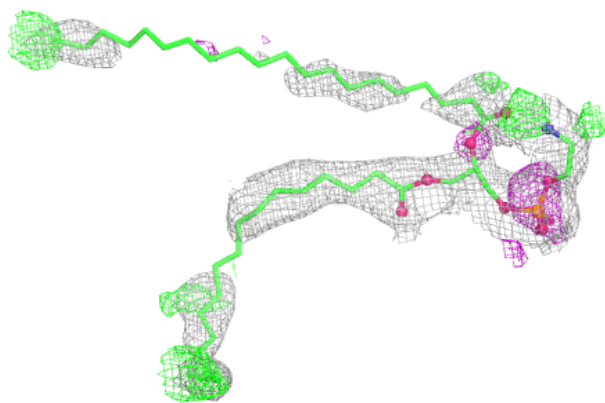
Electron density around TGL N 611:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

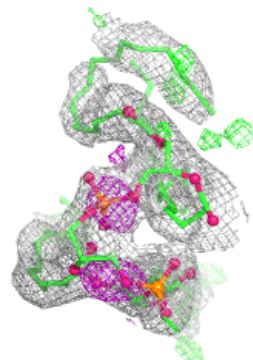
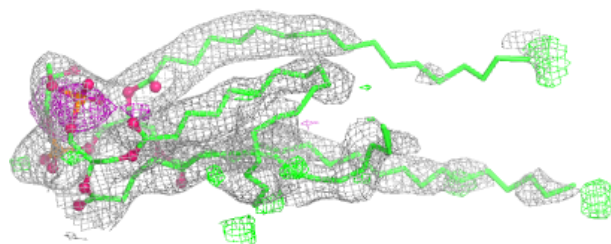
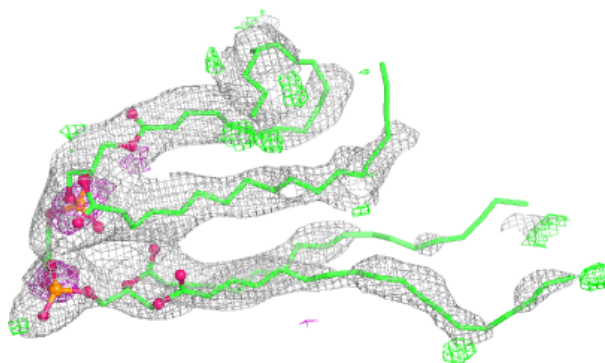


Electron density around PEK T 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

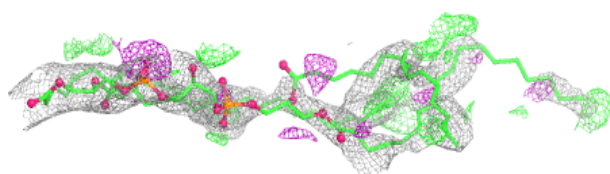
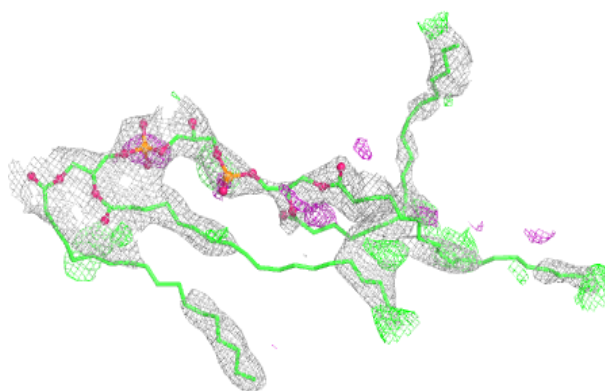
**Electron density around CDL P 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

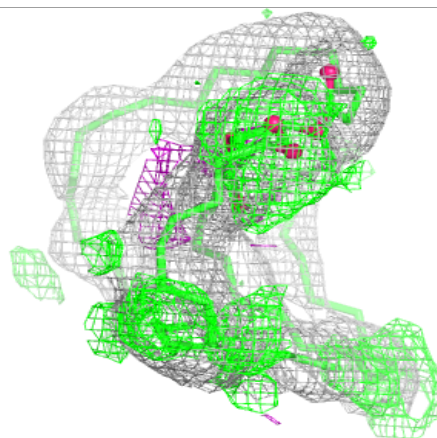
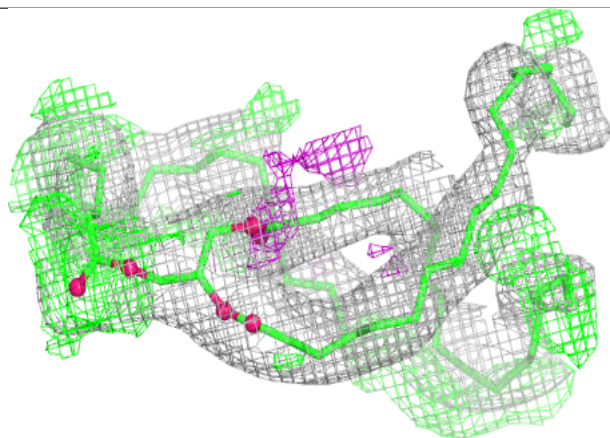
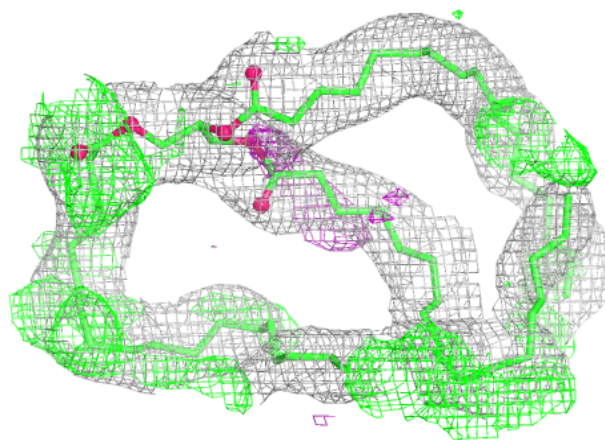


Electron density around CDL T 103:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

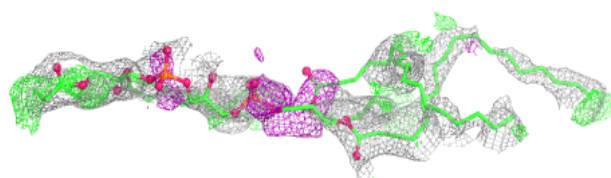
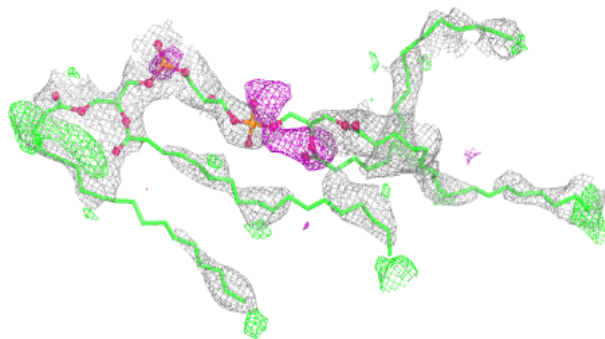
**Electron density around TGL A 607:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



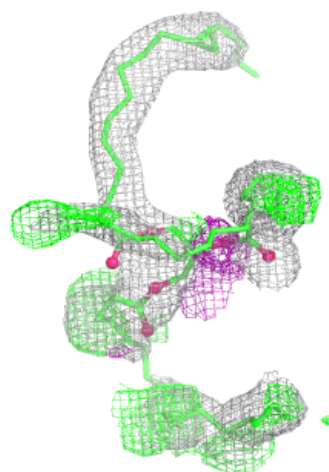
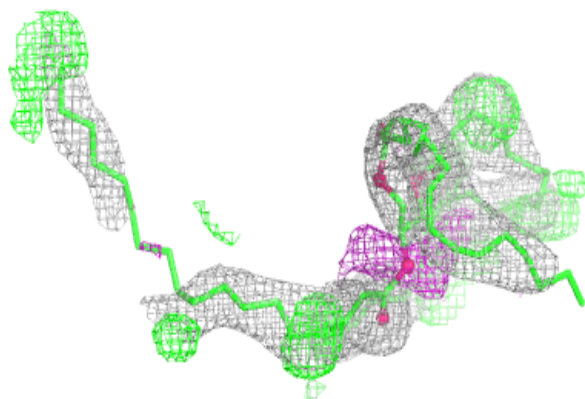
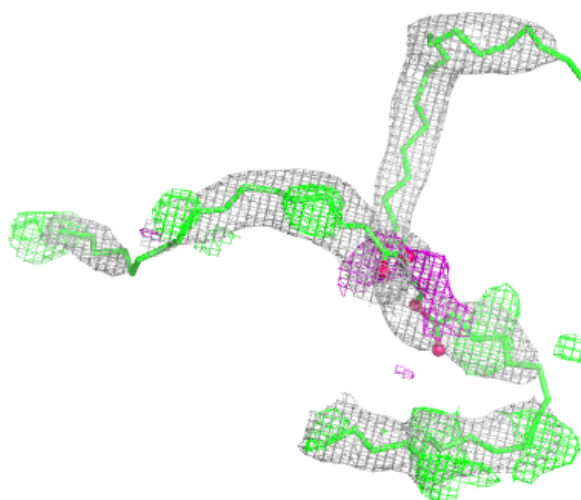
Electron density around CDL C 307:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



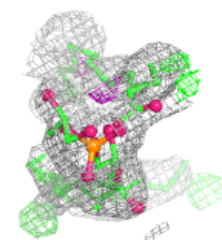
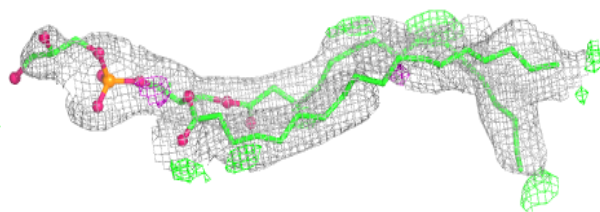
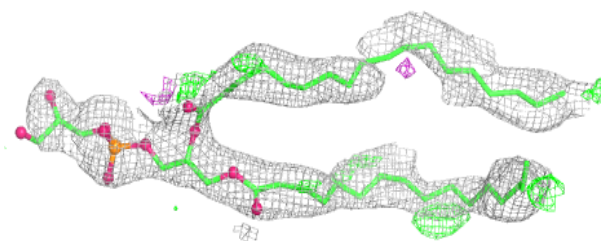
Electron density around TGL L 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

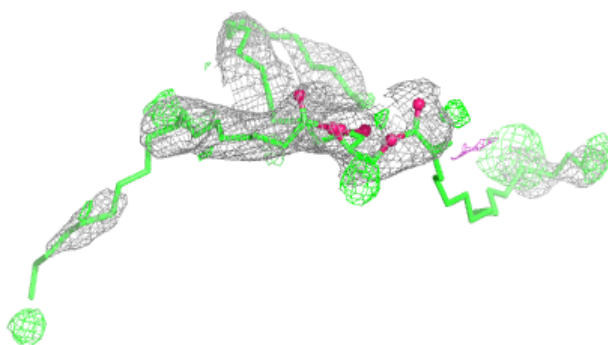
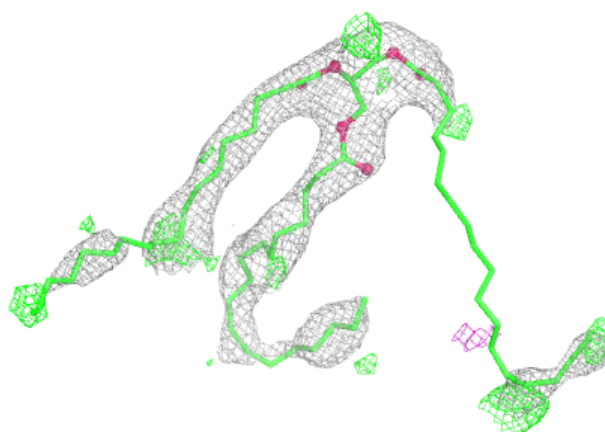


Electron density around PGV C 308:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

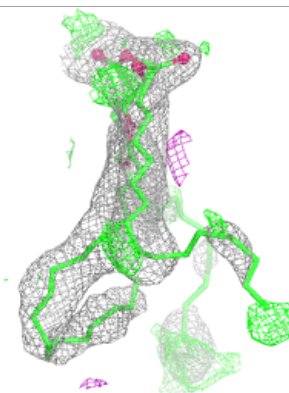
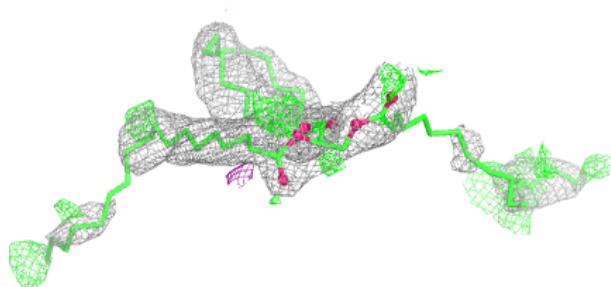
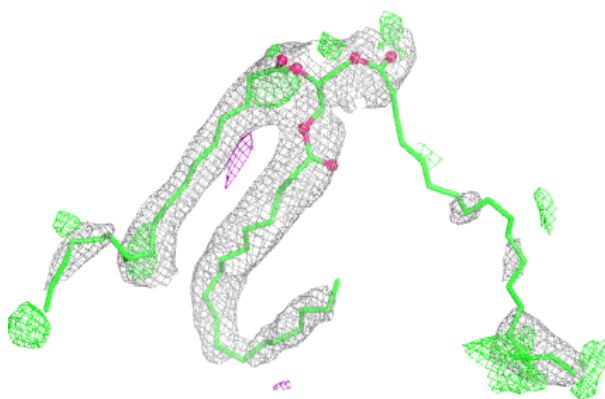
**Electron density around TGL N 610:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

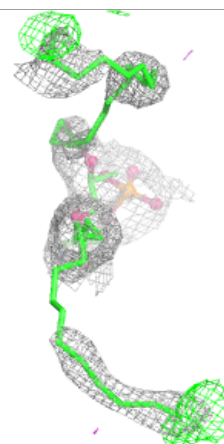
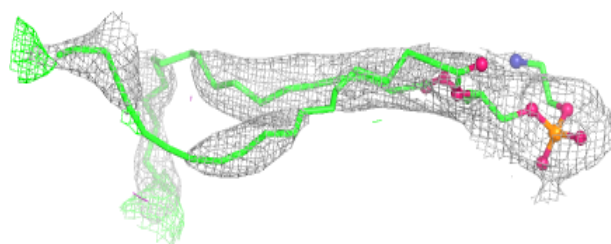
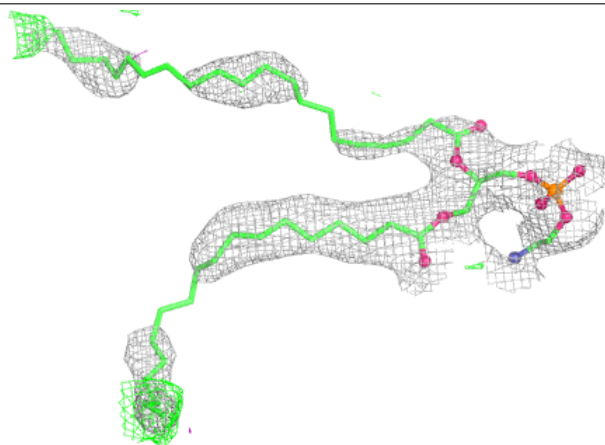


Electron density around TGL D 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

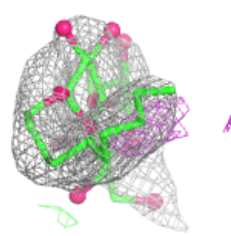
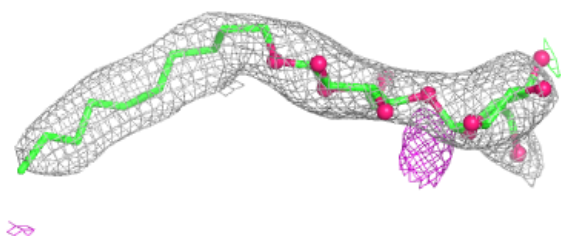
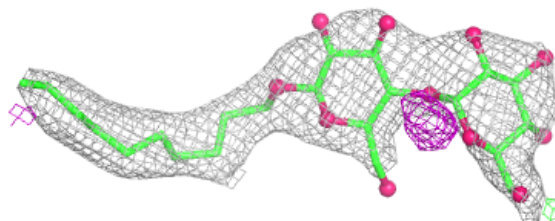
**Electron density around PEK C 306:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

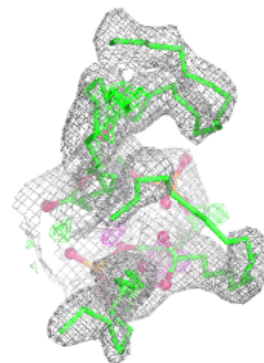
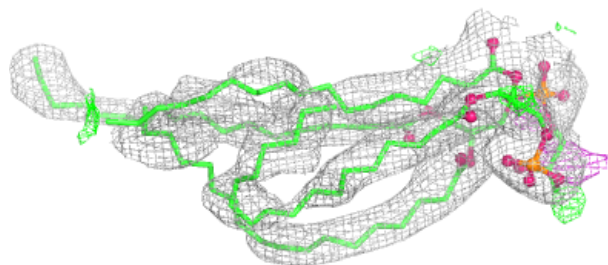
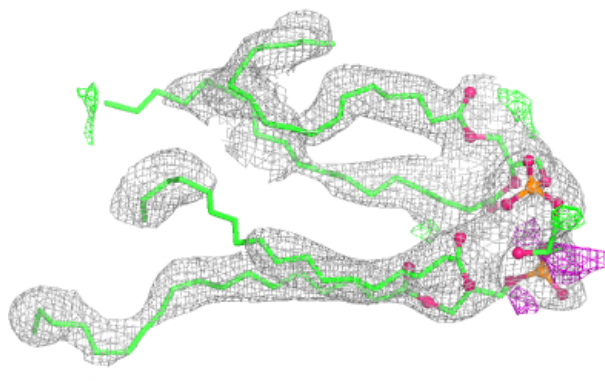


Electron density around DMU Z 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

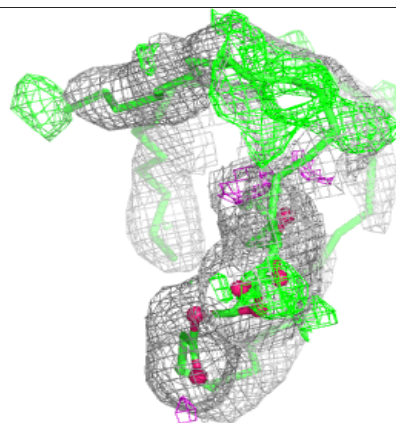
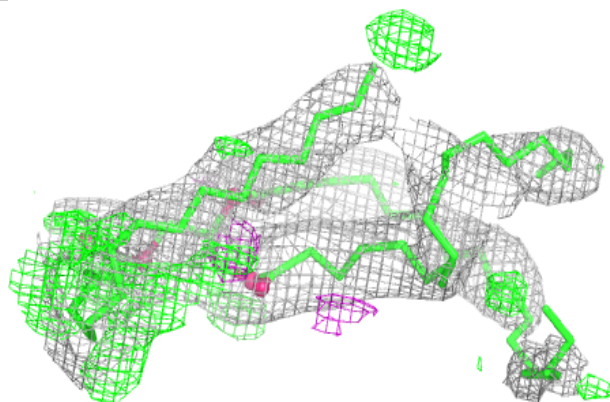
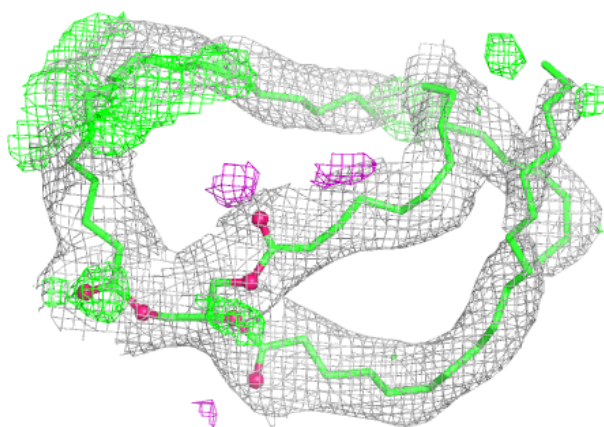
**Electron density around CDL C 303:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

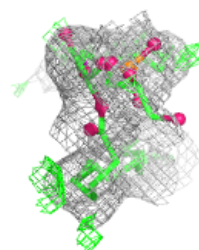
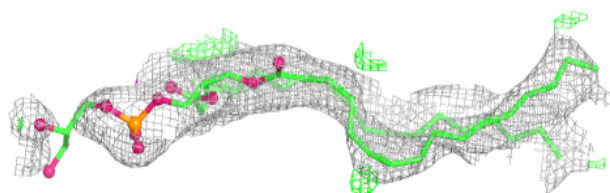
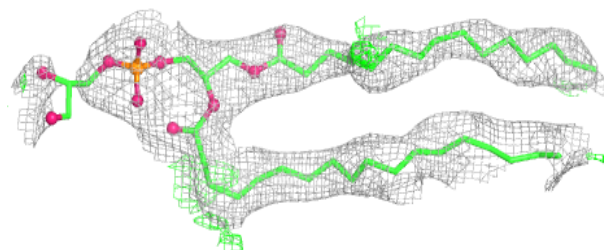


Electron density around TGL N 609:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

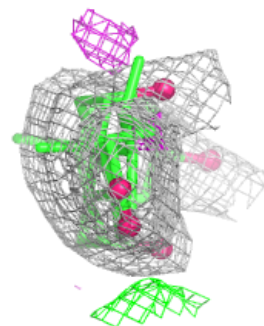
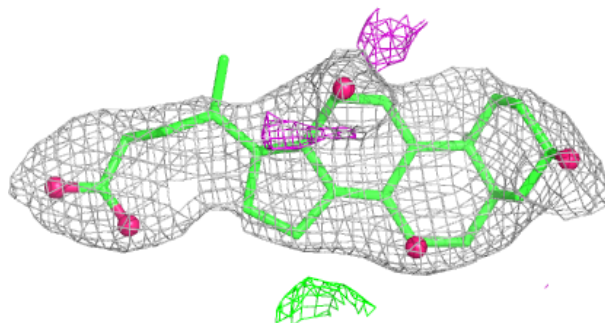
**Electron density around PGV G 103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

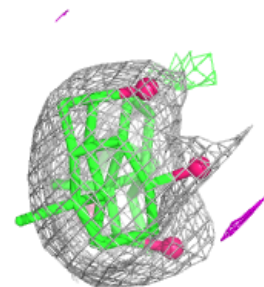
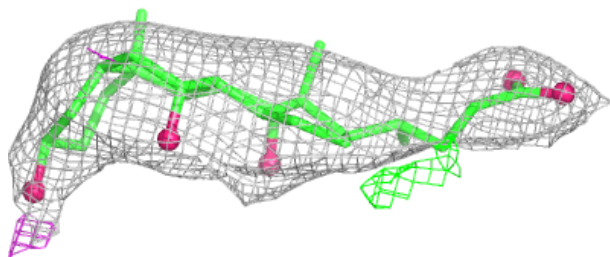
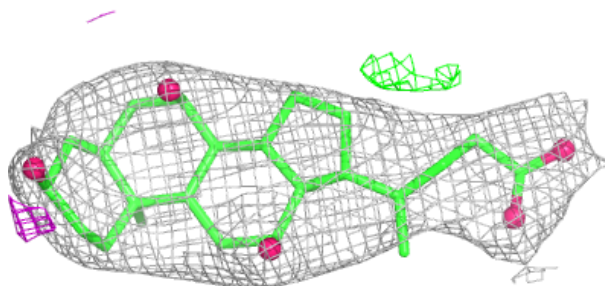


Electron density around CHD C 304:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

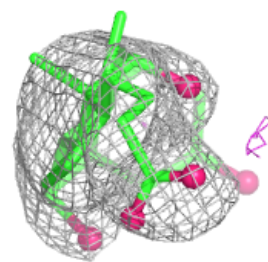
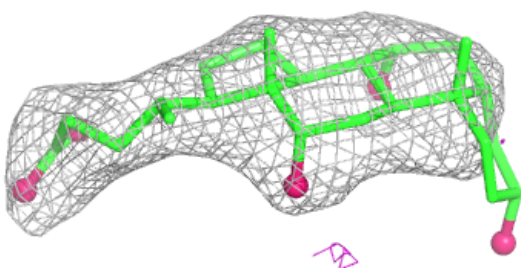
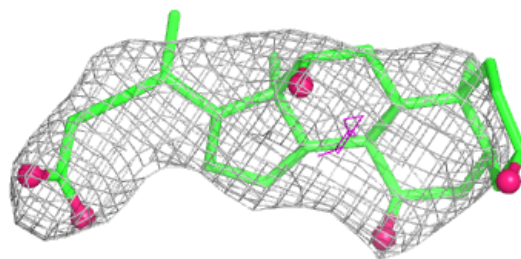
**Electron density around CHD P 305:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

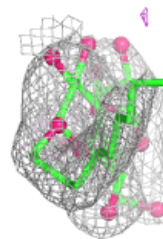
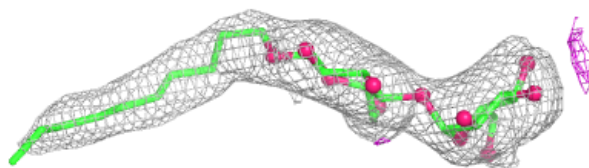


Electron density around CHD J 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

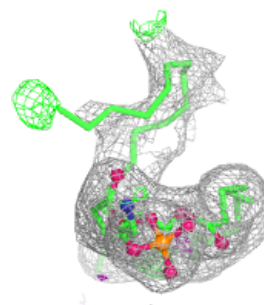
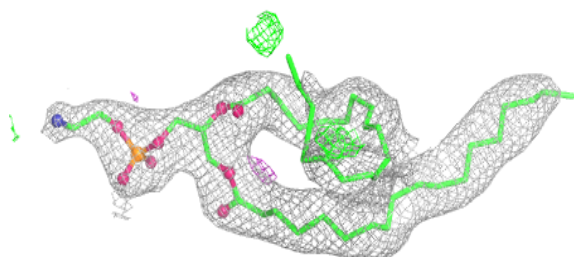
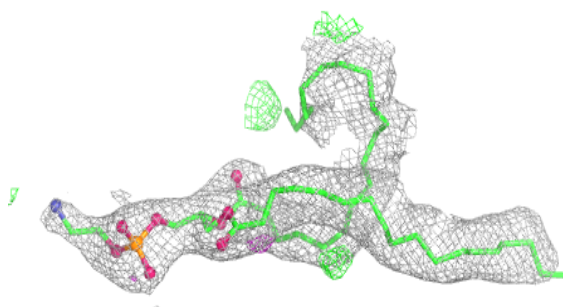
**Electron density around DMU M 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

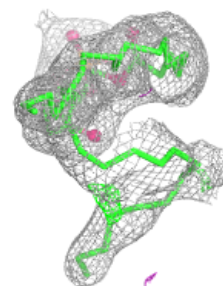
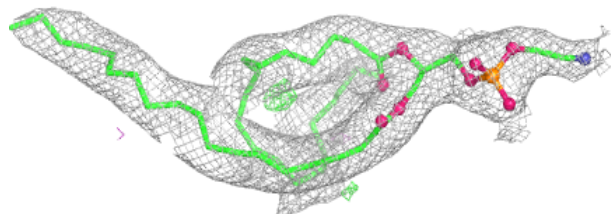
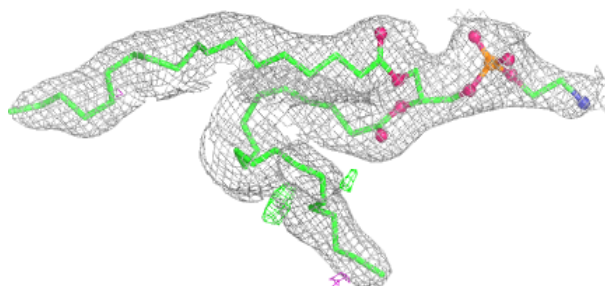


Electron density around PEK P 302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

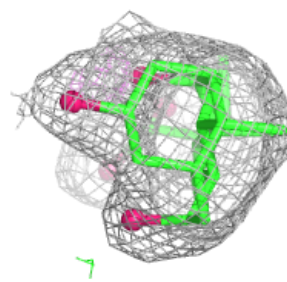
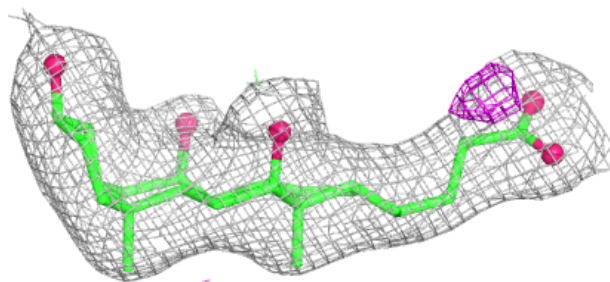
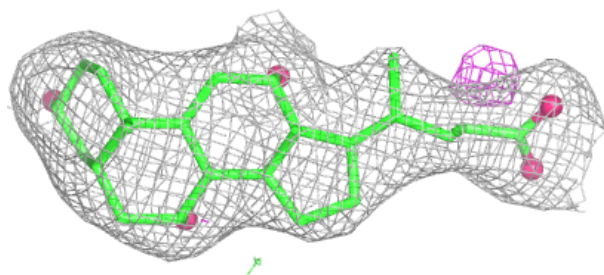
**Electron density around PEK G 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

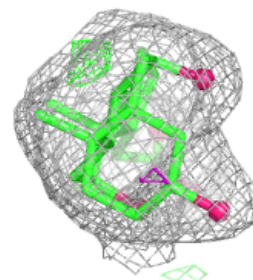
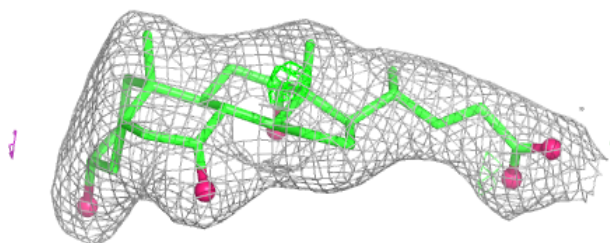
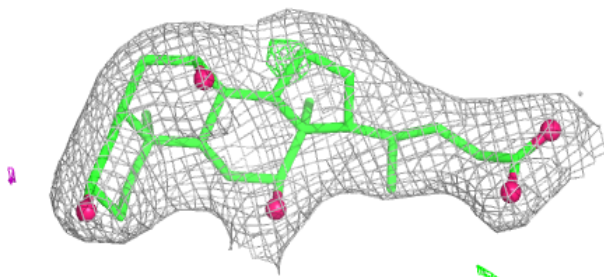


Electron density around CHD B 302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

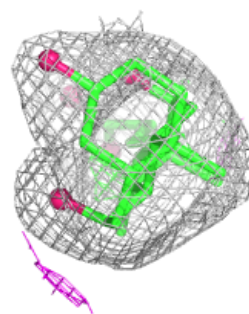
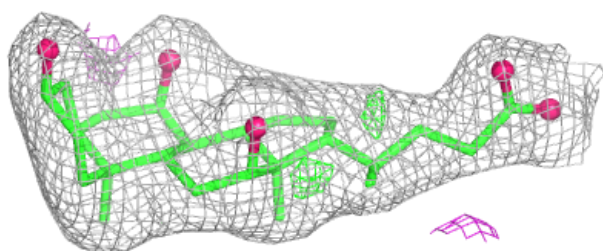
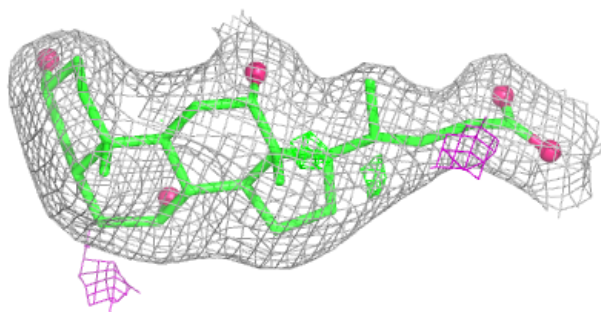
**Electron density around CHD P 306:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

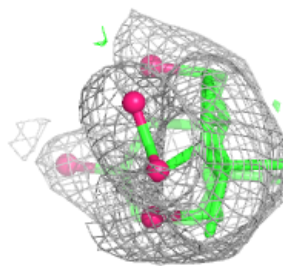
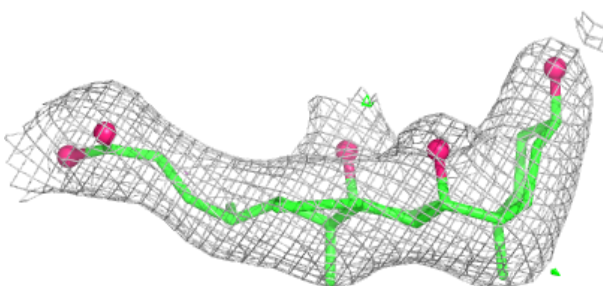
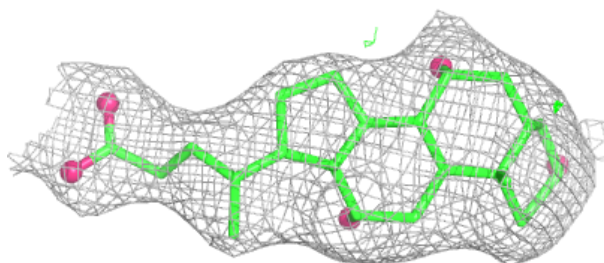


Electron density around CHD C 305:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

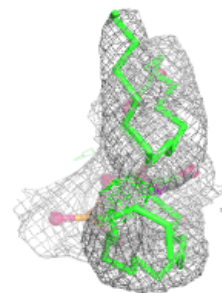
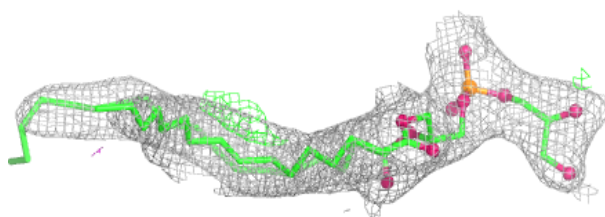
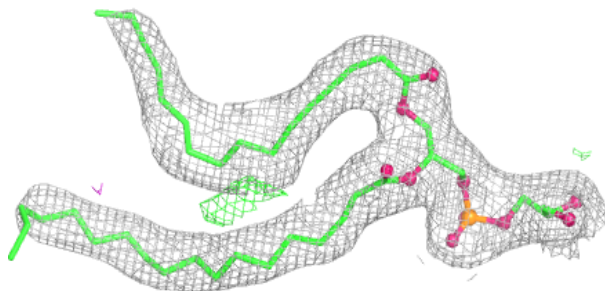
**Electron density around CHD O 302:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

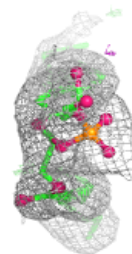
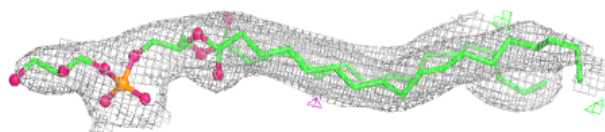
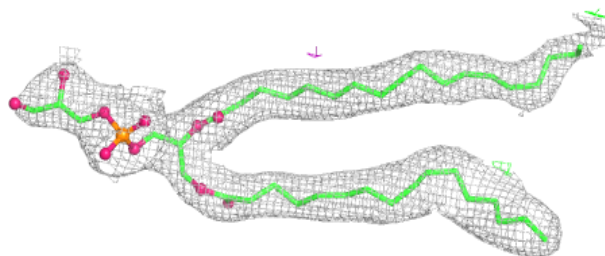


Electron density around PGV N 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

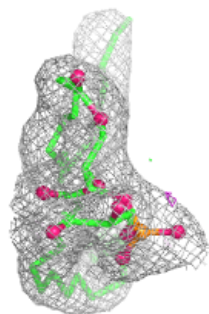
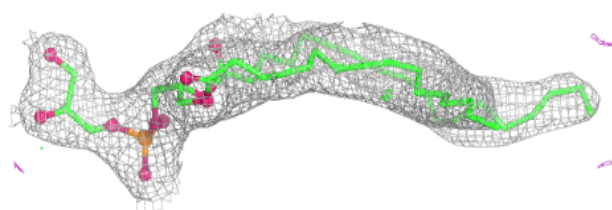
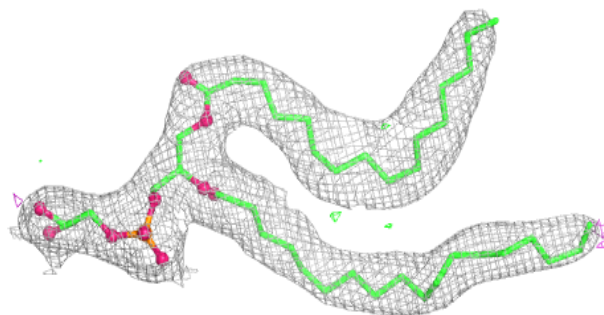
**Electron density around PGV P 303:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

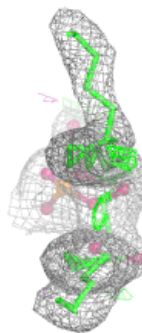
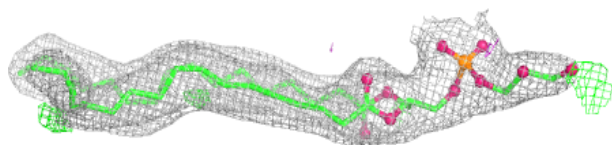
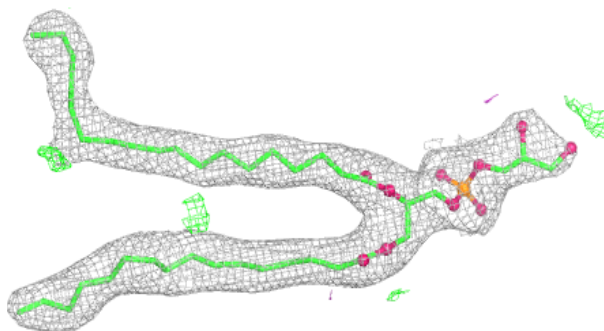


Electron density around PGV A 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

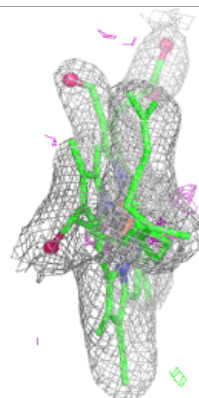
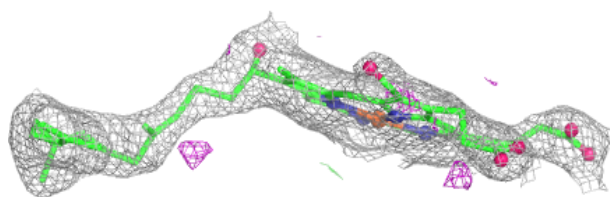
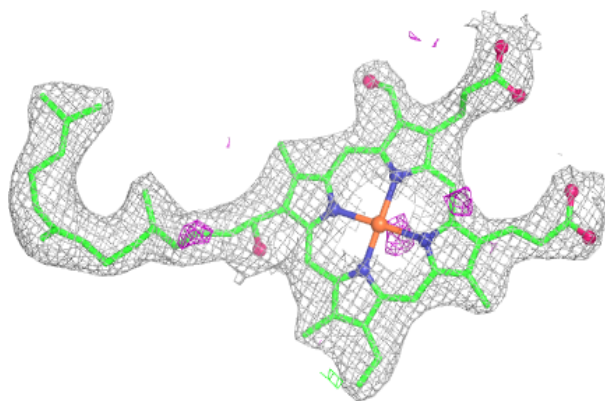
**Electron density around PGV C 302:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

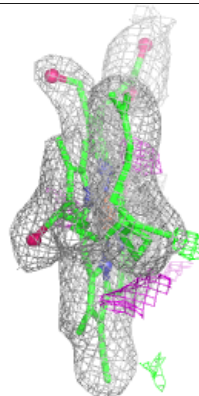
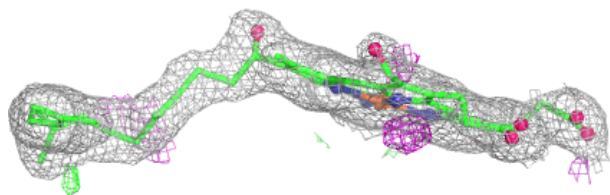
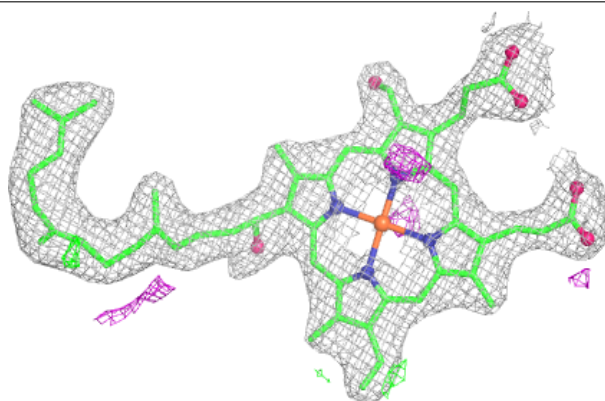


Electron density around HEA N 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

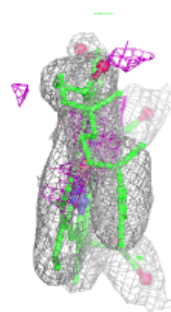
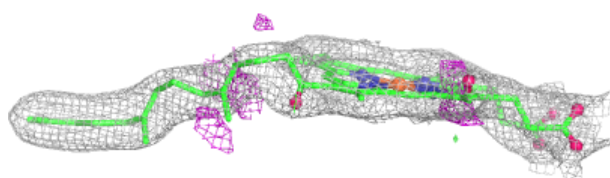
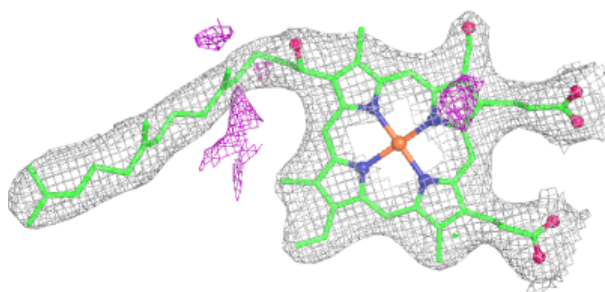
**Electron density around HEA A 602:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

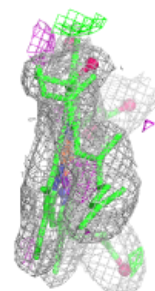
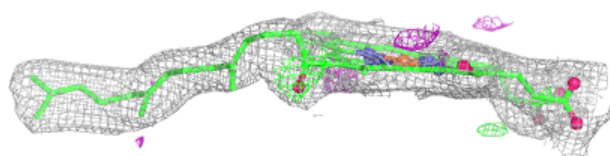
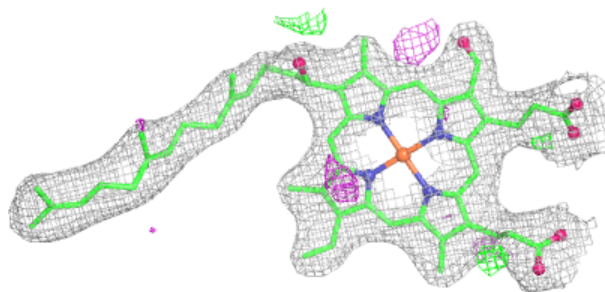


Electron density around HEA N 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around HEA A 601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.