Full wwPDB X-ray Structure Validation Report (i)

Oct 23, 2023 – 11:52 PM EDT

PDB ID	:	3AG1
Title	:	Bovine Heart Cytochrome c Oxidase in the Carbon Monoxide-bound Fully Reduced State at 280 K
Authors	:	Muramoto, K.; Ohta, K.; Shinzawa-Itoh, K.; Kanda, K.; Taniguchi, M.; Nabekura, H.; Yamashita, E.; Tsukihara, T.; Yoshikawa, S.
Deposited on	:	2010-03-19
Resolution	:	2.20 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 (i) 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 (i)) were used in the production of this report:

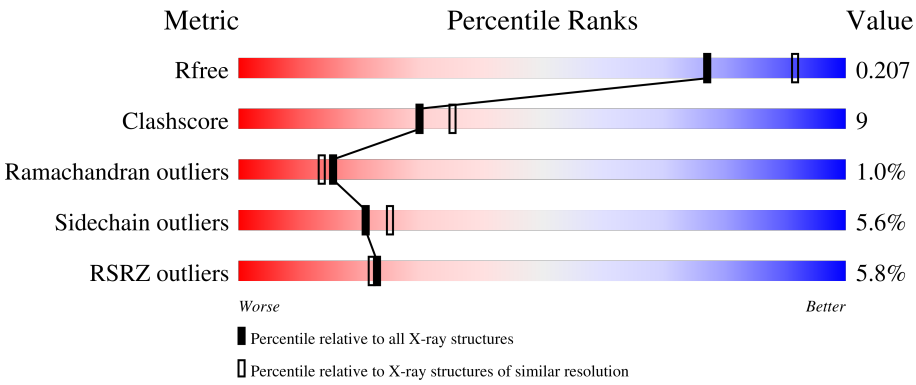
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	3% 85% 13% •
1	N	514	2% 85% 13% •
2	B	227	68% 27% • •
2	O	227	3% 75% 20% 5%

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Mol	Chain	Length	Quality of chain
3	C	261	8% 87% 10%
3	P	261	10% 87% 10%
4	D	147	% 84% 14%
4	Q	147	11% 80% 14%
5	E	109	83% 11%
5	R	109	8% 83% 11%
6	F	98	7% 80% 17%
6	S	98	7% 74% 21%
7	G	85	18% 71% 19% 8%
7	T	85	19% 62% 25% 11%
8	H	85	4% 75% 13% 7%
8	U	85	2% 75% 11% 5% 7%
9	I	73	8% 73% 19% 8%
9	V	73	16% 66% 25% 10%
10	J	59	7% 85% 10%
10	W	59	8% 69% 25%
11	K	56	71% 12% 12%
11	X	56	18% 73% 12% 12%
12	L	47	2% 77% 19%
12	Y	47	6% 74% 17% 6%
13	M	46	2% 72% 15% 7% 7%
13	Z	46	15% 70% 24% 7%

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
20	PGV	C	268	-	-	-	X
20	PGV	P	1268	-	-	-	X
23	CHD	B	1085	X	-	-	-
23	CHD	C	271	X	-	-	-
23	CHD	J	60	X	-	-	-
23	CHD	O	229	X	-	-	-
23	CHD	P	1271	X	-	-	-
23	CHD	W	1059	X	-	-	-
24	UNX	C	262	-	-	-	X
24	UNX	P	262	-	-	-	X
25	CDL	C	270	-	-	X	-
25	CDL	G	269	-	-	X	X
25	CDL	T	1269	-	-	X	X
26	DMU	C	272	X	-	-	-
26	DMU	M	526	X	-	-	-
26	DMU	T	1272	X	-	-	-
26	DMU	Z	1526	X	-	-	-
28	PEK	G	1263	-	-	-	X
28	PEK	T	263	-	-	-	X
7	TPO	G	11	-	-	-	X
7	TPO	T	11	-	-	-	X
9	SAC	I	1	-	-	-	X
9	SAC	V	1	-	X	-	X

2 Entry composition (i)

There are 29 unique types of molecules in this entry. The entry contains 32105 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
			Total	C	N	O	S			
1	A	514	4027	2691	623	678	35	0	0	0
1	N	514	4027	2691	623	678	35	0	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 10 is a protein called Cytochrome c oxidase polypeptide 7A1.

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

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

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

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

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

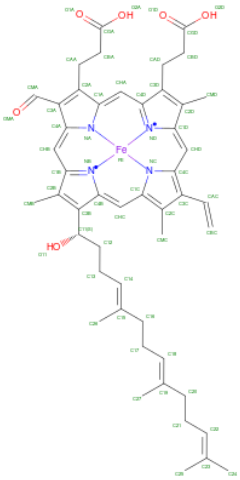
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	46	380	254	64	60	2	0	0	0
			Total	C	N	O	S			
12	Y	46	380	254	64	60	2	0	0	0

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

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

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

HEA



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

- Molecule 15 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).

CMO

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

- Molecule 16 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

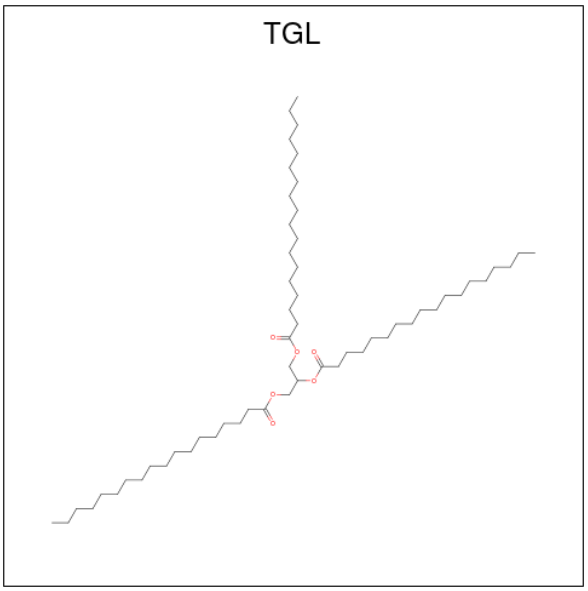
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 18 is SODIUM ION (three-letter code: NA) (formula: Na).

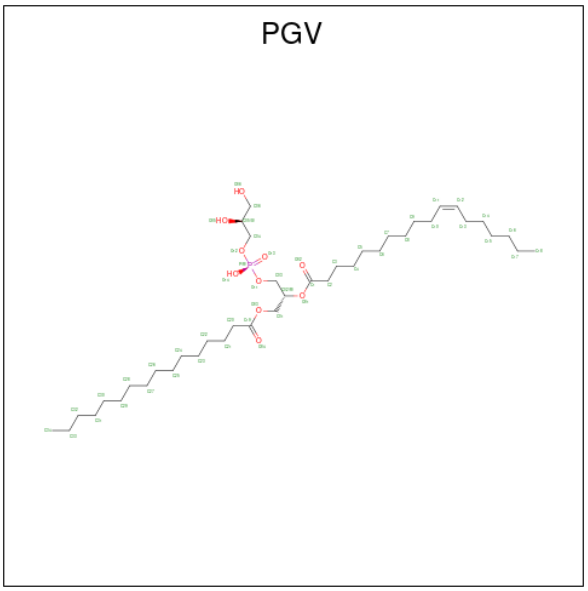
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
18	A	1	1	1	0	0
18	N	1	1	1	0	0

- Molecule 19 is TRISTEAROYLGLYCEROL (three-letter code: TGL) (formula: $C_{57}H_{110}O_6$).



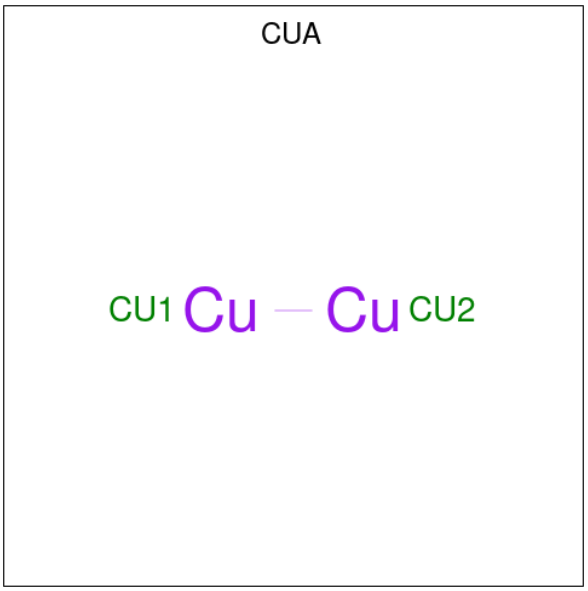
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
19	A	1	63	57	6	0	0
19	B	1	63	57	6	0	0
19	L	1	63	57	6	0	0
19	N	1	63	57	6	0	0
19	N	1	63	57	6	0	0
19	N	1	63	57	6	0	0

- Molecule 20 is (1R)-2-{[{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: $C_{40}H_{77}O_{10}P$).



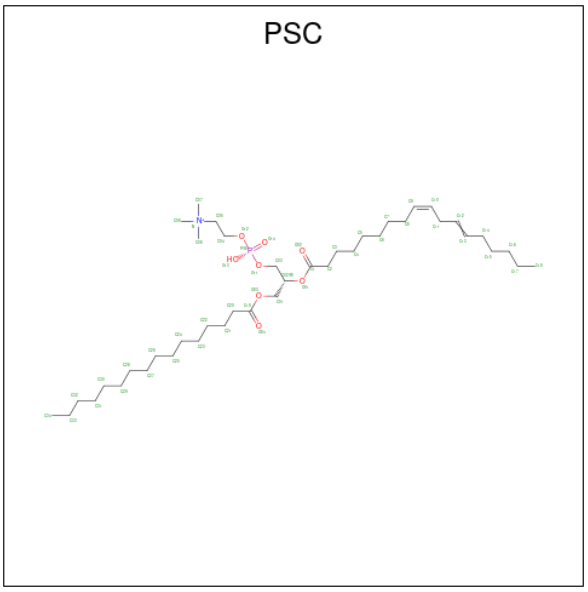
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
20	A	1	51	40	10	1	0	0
			Total	C	O	P		
20	A	1	51	40	10	1	0	0
			Total	C	O	P		
20	C	1	51	40	10	1	0	0
			Total	C	O	P		
20	C	1	51	40	10	1	0	0
			Total	C	O	P		
20	N	1	51	40	10	1	0	0
			Total	C	O	P		
20	N	1	51	40	10	1	0	0
			Total	C	O	P		
20	P	1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

- Molecule 21 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu_2).



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

- Molecule 22 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 (three-letter code: PSC) (formula: $C_{42}H_{81}NO_8P$).



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

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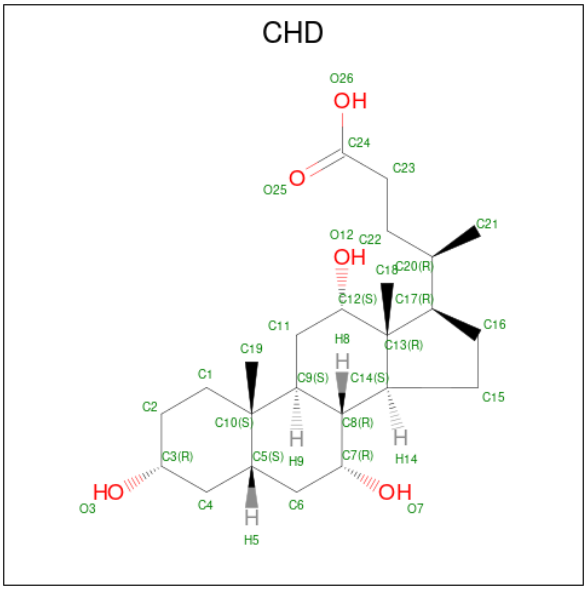
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
22	R	1	52	42	1	8	1	0	0

- Molecule 23 is CHOLIC ACID (three-letter code: CHD) (formula: $C_{24}H_{40}O_5$).

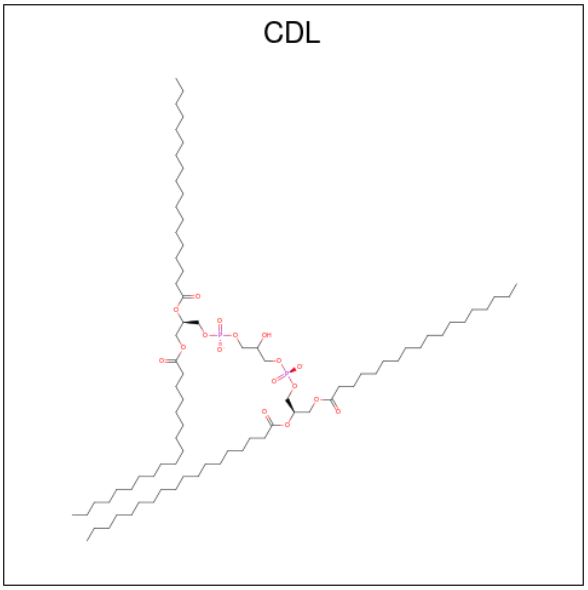


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
23	B	1	29	24	5	0	0
23	C	1	29	24	5	0	0
23	C	1	29	24	5	0	0
23	J	1	29	24	5	0	0
23	O	1	29	24	5	0	0
23	P	1	29	24	5	0	0
23	P	1	29	24	5	0	0
23	W	1	29	24	5	0	0

- Molecule 24 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

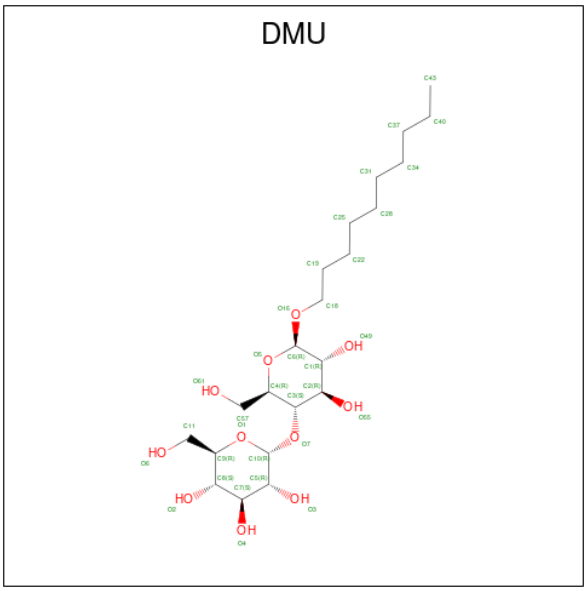
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	X		
24	C	1	1	1	0	0
			Total	X		
24	P	1	1	1	0	0

- Molecule 25 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



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

- Molecule 26 is DECYL-BETA-D-MALTOPYRANOSIDE (three-letter code: DMU) (formula: $C_{22}H_{42}O_{11}$).

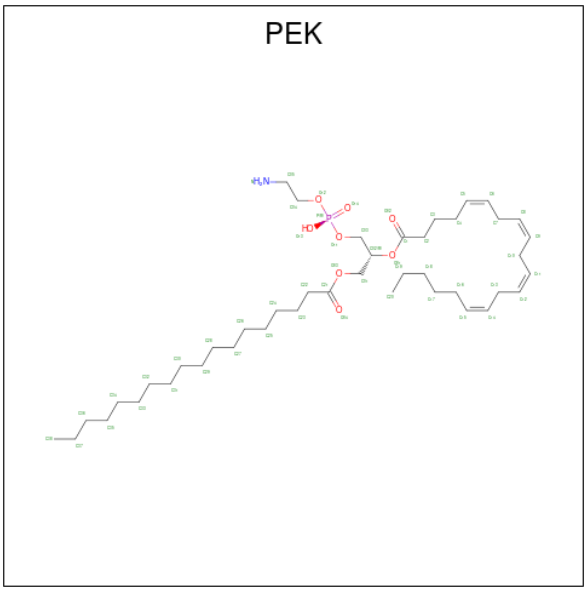


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
26	C	1	Total	C	O	0	0
			33	22	11		
26	M	1	Total	C	O	0	0
			33	22	11		
26	T	1	Total	C	O	0	0
			33	22	11		
26	Z	1	Total	C	O	0	0
			33	22	11		

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 28 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (three-letter code: PEK) (formula: $C_{43}H_{78}NO_8P$).



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

- Molecule 29 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
29	A	205	205	205	0	0
			Total	O		
29	B	121	121	121	0	0
			Total	O		
29	C	80	80	80	0	0
			Total	O		
29	D	75	75	75	0	0
			Total	O		
29	E	39	39	39	0	0
			Total	O		
29	F	70	70	70	0	0

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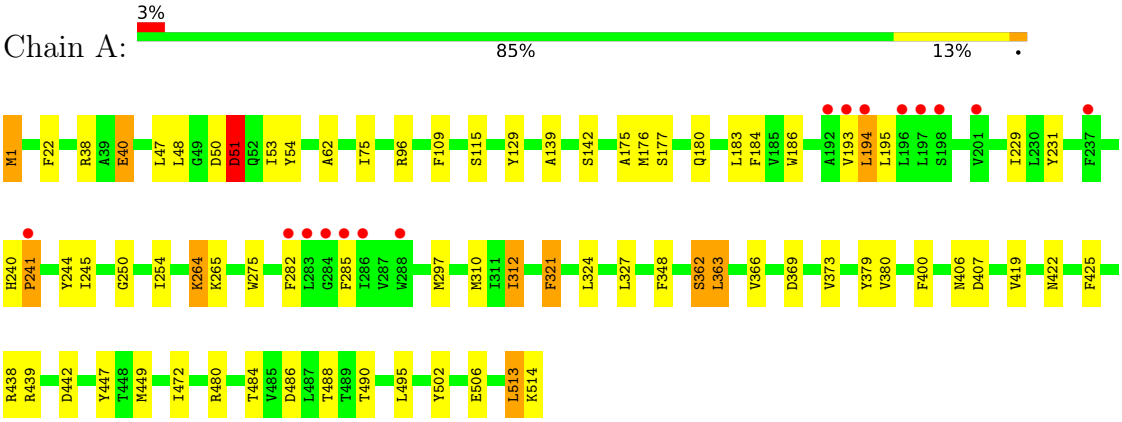
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
29	G	42	Total O 42 42	0	0
29	H	33	Total O 33 33	0	0
29	I	24	Total O 24 24	0	0
29	J	9	Total O 9 9	0	0
29	K	17	Total O 17 17	0	0
29	L	20	Total O 20 20	0	0
29	M	15	Total O 15 15	0	0
29	N	184	Total O 184 184	0	0
29	O	97	Total O 97 97	0	0
29	P	81	Total O 81 81	0	0
29	Q	47	Total O 47 47	0	0
29	R	27	Total O 27 27	0	0
29	S	52	Total O 52 52	0	0
29	T	37	Total O 37 37	0	0
29	U	28	Total O 28 28	0	0
29	V	17	Total O 17 17	0	0
29	W	12	Total O 12 12	0	0
29	X	12	Total O 12 12	0	0
29	Y	16	Total O 16 16	0	0
29	Z	9	Total O 9 9	0	0

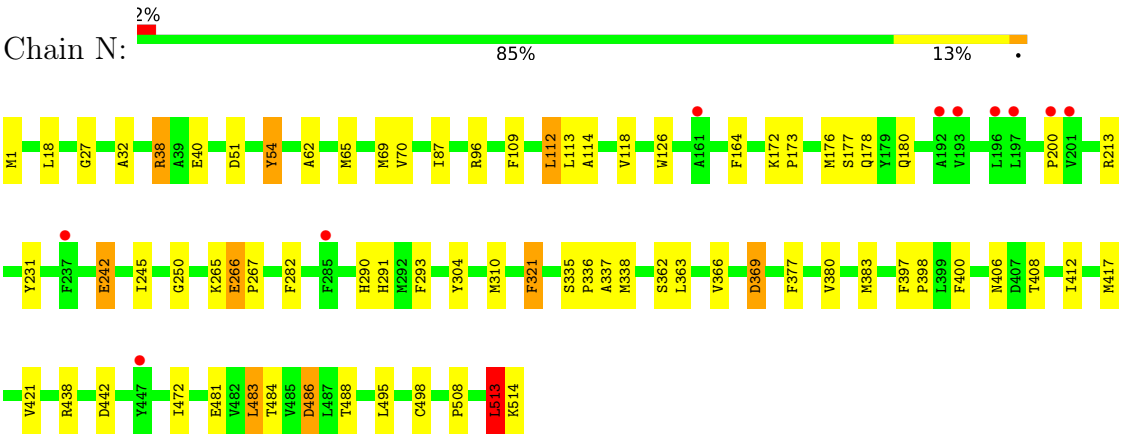
3 Residue-property plots (i)

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.

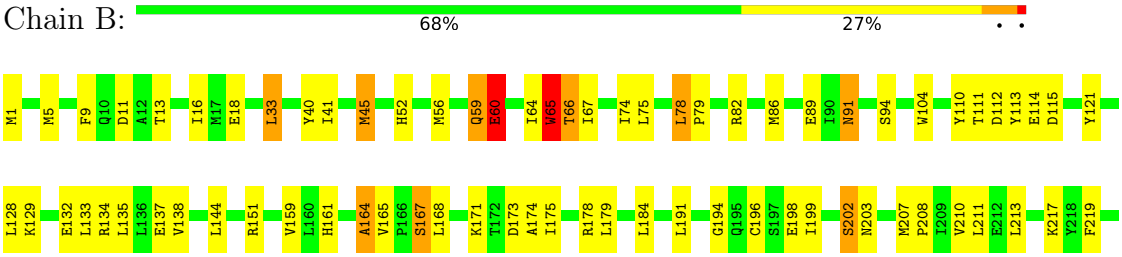
• Molecule 1: Cytochrome c oxidase subunit 1



• Molecule 1: Cytochrome c oxidase subunit 1



• Molecule 2: Cytochrome c oxidase subunit 2



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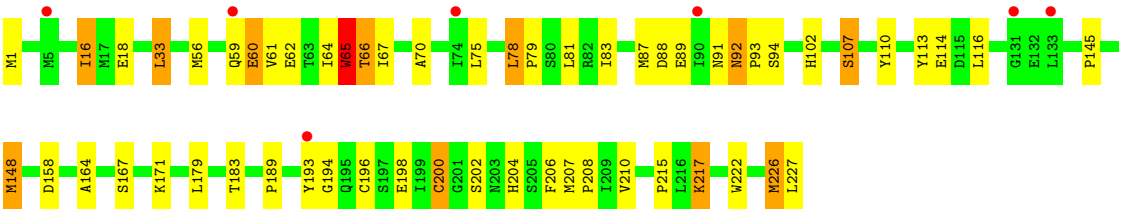
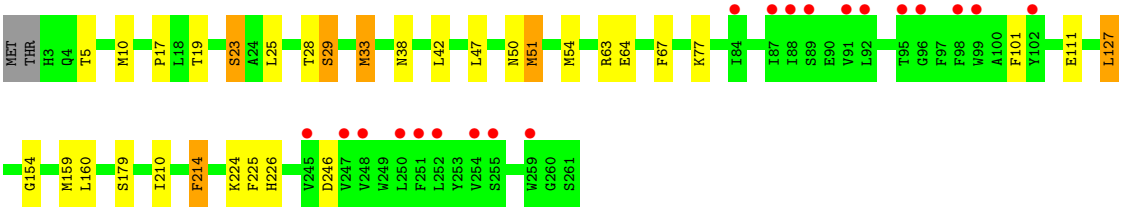
- Molecule 2: Cytochrome c oxidase subunit 2

Chain O:



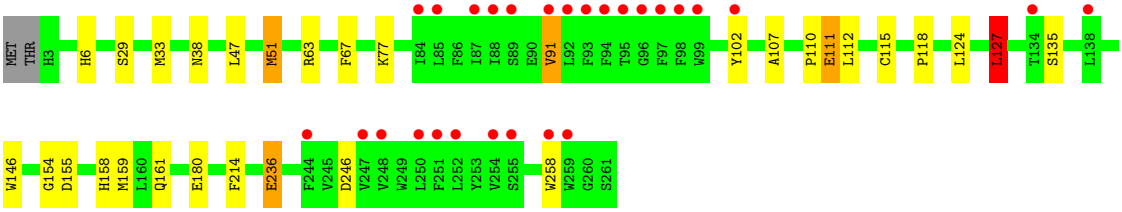
- Molecule 3: Cytochrome c oxidase subunit 3

Chain C:



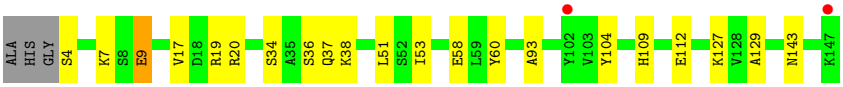
- Molecule 3: Cytochrome c oxidase subunit 3

Chain P:



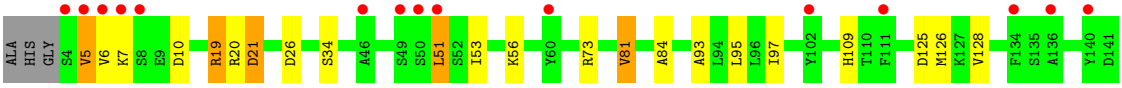
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain D:



- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain Q:

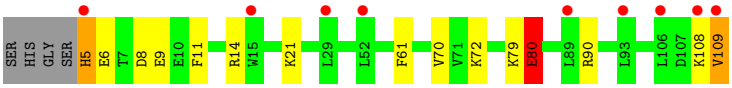


• Molecule 5: Cytochrome c oxidase subunit 5A

Chain E:

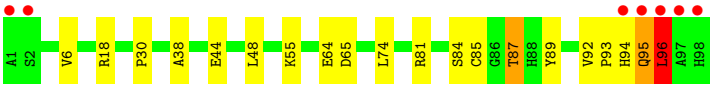
• Molecule 5: Cytochrome c oxidase subunit 5A

Chain R:



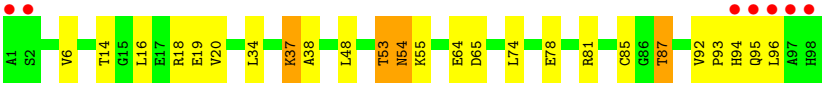
• Molecule 6: Cytochrome c oxidase subunit 5B

Chain F:



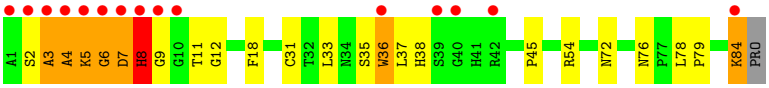
• Molecule 6: Cytochrome c oxidase subunit 5B

Chain S:



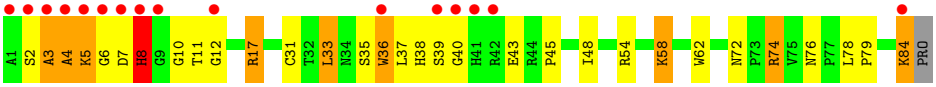
• Molecule 7: Cytochrome c oxidase subunit 6A2

Chain G:



• Molecule 7: Cytochrome c oxidase subunit 6A2

Chain T:

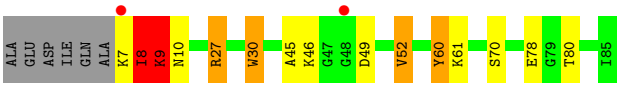


• Molecule 8: Cytochrome c oxidase subunit 6B1

Chain H:

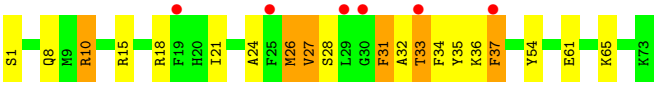
• Molecule 8: Cytochrome c oxidase subunit 6B1

Chain U:



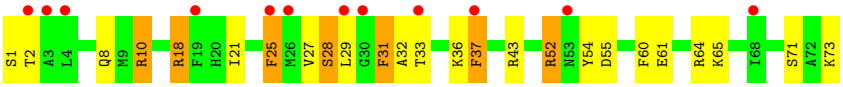
• Molecule 9: Cytochrome c oxidase subunit 6C

Chain I:



• Molecule 9: Cytochrome c oxidase subunit 6C

Chain V:

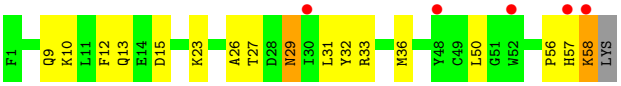


• Molecule 10: Cytochrome c oxidase polypeptide 7A1

Chain J:

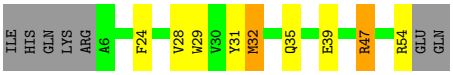
• Molecule 10: Cytochrome c oxidase polypeptide 7A1

Chain W:



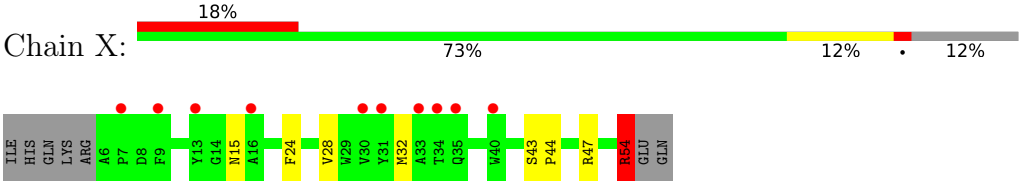
• Molecule 11: Cytochrome c oxidase subunit 7B

Chain K:



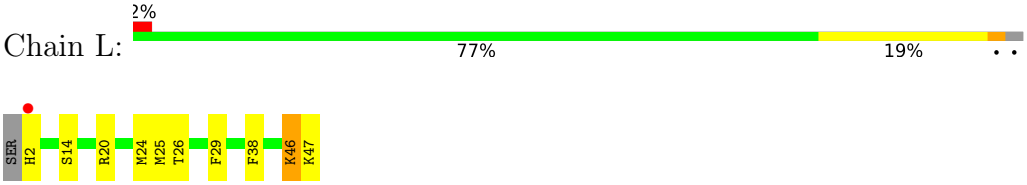
• Molecule 11: Cytochrome c oxidase subunit 7B

Chain X:



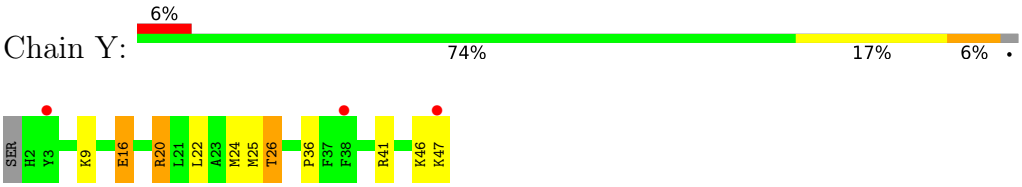
• Molecule 12: Cytochrome c oxidase subunit 7C

Chain L:



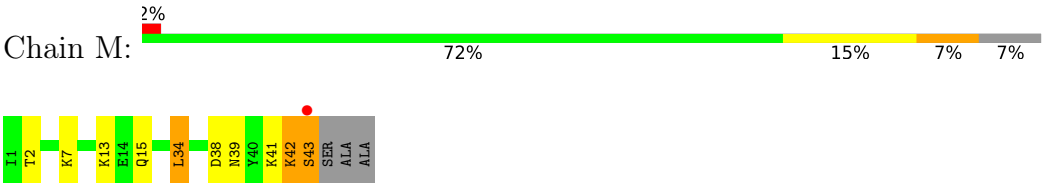
• Molecule 12: Cytochrome c oxidase subunit 7C

Chain Y:



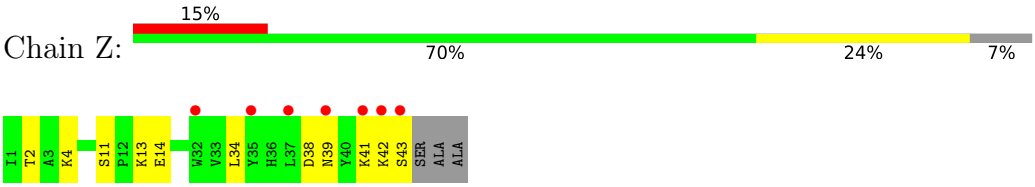
• Molecule 13: Cytochrome c oxidase subunit 8B

Chain M:



• Molecule 13: Cytochrome c oxidase subunit 8B

Chain Z:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	189.49Å 210.89Å 178.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.20 94.75 – 2.21	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.20) 99.2 (94.75-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.3	Depositor
R, R_{free}	0.162 , 0.192 0.180 , 0.207	Depositor DCC
R_{free} test set	17414 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	51.1	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 61.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	32105	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: TGL, CDL, FME, SAC, HEA, PGV, UNX, PSC, DMU, NA, MG, CHD, CMO, CUA, ZN, PEK, CU, 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	1.52	24/4156 (0.6%)	1.14	17/5678 (0.3%)
1	N	1.30	13/4156 (0.3%)	1.00	9/5678 (0.2%)
2	B	1.52	17/1860 (0.9%)	1.22	15/2534 (0.6%)
2	O	1.19	5/1860 (0.3%)	1.02	3/2534 (0.1%)
3	C	1.44	6/2197 (0.3%)	1.00	2/3005 (0.1%)
3	P	1.26	7/2197 (0.3%)	0.96	4/3005 (0.1%)
4	D	1.42	8/1229 (0.7%)	1.12	1/1658 (0.1%)
4	Q	1.10	2/1229 (0.2%)	0.98	6/1658 (0.4%)
5	E	1.26	2/871 (0.2%)	1.07	3/1182 (0.3%)
5	R	1.03	2/871 (0.2%)	0.93	1/1182 (0.1%)
6	F	1.47	3/765 (0.4%)	1.25	4/1038 (0.4%)
6	S	1.25	2/765 (0.3%)	1.09	3/1038 (0.3%)
7	G	1.38	2/690 (0.3%)	1.12	3/937 (0.3%)
7	T	1.43	4/690 (0.6%)	1.09	4/937 (0.4%)
8	H	1.29	1/682 (0.1%)	1.01	1/921 (0.1%)
8	U	1.09	1/682 (0.1%)	0.94	0/921
9	I	1.45	3/605 (0.5%)	1.13	3/802 (0.4%)
9	V	1.31	2/605 (0.3%)	1.10	4/802 (0.5%)
10	J	1.35	0/471	1.12	2/636 (0.3%)
10	W	1.10	1/471 (0.2%)	0.98	0/636
11	K	1.34	3/398 (0.8%)	1.16	2/546 (0.4%)
11	X	0.97	0/398	0.93	1/546 (0.2%)
12	L	1.49	1/393 (0.3%)	1.07	1/526 (0.2%)
12	Y	1.10	0/393	0.98	1/526 (0.2%)
13	M	1.20	0/345	1.15	2/470 (0.4%)
13	Z	0.98	0/345	0.97	0/470
All	All	1.33	109/29324 (0.4%)	1.06	92/39866 (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
6	F	0	1
6	S	0	1
10	J	0	1
10	W	0	1
All	All	0	4

All (109) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	36	TRP	CB-CG	12.12	1.72	1.50
7	G	36	TRP	CB-CG	10.31	1.68	1.50
7	T	58	LYS	CE-NZ	9.32	1.72	1.49
2	O	198	GLU	C-O	8.13	1.38	1.23
2	B	198	GLU	C-O	7.69	1.38	1.23
2	B	198	GLU	CG-CD	7.52	1.63	1.51
1	A	321	PHE	CE1-CZ	7.36	1.51	1.37
2	B	164	ALA	CA-CB	7.18	1.67	1.52
1	A	40	GLU	CG-CD	6.91	1.62	1.51
3	P	29	SER	CB-OG	-6.80	1.33	1.42
1	A	139	ALA	CA-CB	6.79	1.66	1.52
1	N	126	TRP	CZ3-CH2	6.73	1.50	1.40
9	V	37	PHE	CB-CG	6.71	1.62	1.51
7	T	17	ARG	CG-CD	-6.66	1.35	1.51
1	N	54	TYR	CD1-CE1	6.62	1.49	1.39
2	B	18	GLU	CD-OE2	6.60	1.32	1.25
1	A	129	TYR	CD1-CE1	-6.57	1.29	1.39
2	B	18	GLU	CD-OE1	6.50	1.32	1.25
4	D	17	VAL	CB-CG1	-6.46	1.39	1.52
6	F	89	TYR	CE2-CZ	6.40	1.46	1.38
7	G	5	LYS	CB-CG	6.39	1.69	1.52
8	U	30	TRP	CB-CG	6.33	1.61	1.50
1	N	231	TYR	CD2-CE2	6.33	1.48	1.39
1	A	348	PHE	CE1-CZ	6.31	1.49	1.37
2	B	121	TYR	CD1-CE1	6.26	1.48	1.39
5	R	9	GLU	CG-CD	6.25	1.61	1.51
11	K	39	GLU	CB-CG	6.25	1.64	1.52
3	C	214	PHE	CG-CD2	6.19	1.48	1.38
1	A	22	PHE	CD1-CE1	6.18	1.51	1.39
3	P	91	VAL	CB-CG1	6.16	1.65	1.52
1	A	231	TYR	CD1-CE1	6.16	1.48	1.39
3	C	29	SER	CB-OG	-6.14	1.34	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	214	PHE	CD1-CE1	6.13	1.51	1.39
10	W	26	ALA	CA-CB	6.10	1.65	1.52
1	A	480	ARG	CZ-NH2	6.08	1.41	1.33
2	B	115	ASP	CB-CG	6.06	1.64	1.51
1	A	373	VAL	CB-CG1	5.90	1.65	1.52
4	D	104	TYR	CD1-CE1	5.83	1.48	1.39
2	O	18	GLU	CD-OE1	5.79	1.32	1.25
1	A	175	ALA	CA-CB	5.76	1.64	1.52
3	P	258	TRP	CB-CG	-5.71	1.40	1.50
1	A	447	TYR	CD1-CE1	5.71	1.48	1.39
5	E	70	VAL	CB-CG1	-5.70	1.40	1.52
8	H	8	ILE	CA-CB	5.69	1.68	1.54
1	A	186	TRP	CE2-CZ2	5.67	1.49	1.39
1	A	275	TRP	CZ3-CH2	5.66	1.49	1.40
1	A	362	SER	CB-OG	-5.64	1.34	1.42
2	B	9	PHE	CE2-CZ	5.63	1.48	1.37
1	N	321	PHE	CE1-CZ	5.59	1.48	1.37
1	A	425	PHE	CE2-CZ	5.55	1.47	1.37
1	A	400	PHE	CB-CG	5.53	1.60	1.51
1	N	250	GLY	N-CA	5.52	1.54	1.46
5	R	80	GLU	CG-CD	5.50	1.60	1.51
1	N	242	GLU	CG-CD	5.49	1.60	1.51
1	A	506	GLU	CG-CD	5.46	1.60	1.51
1	A	193	VAL	CB-CG1	5.45	1.64	1.52
4	Q	5	VAL	CA-CB	5.44	1.66	1.54
2	B	167	SER	CB-OG	-5.43	1.35	1.42
2	B	138	VAL	CB-CG1	5.43	1.64	1.52
9	I	37	PHE	CB-CG	5.41	1.60	1.51
3	C	64	GLU	CB-CG	5.39	1.62	1.52
7	T	5	LYS	CB-CG	5.38	1.67	1.52
11	K	47	ARG	CG-CD	5.38	1.65	1.51
3	P	115	CYS	CB-SG	5.37	1.91	1.82
1	A	419	VAL	CB-CG2	5.37	1.64	1.52
6	S	19	GLU	CD-OE1	5.36	1.31	1.25
4	D	9	GLU	CG-CD	5.36	1.59	1.51
4	D	129	ALA	CA-CB	5.35	1.63	1.52
2	B	59	GLN	CG-CD	5.32	1.63	1.51
11	K	29	TRP	CB-CG	5.32	1.59	1.50
4	D	112	GLU	CD-OE1	5.32	1.31	1.25
1	A	184	PHE	CD1-CE1	5.31	1.49	1.39
2	O	65	TRP	CB-CG	-5.31	1.40	1.50
2	O	200	CYS	CB-SG	5.31	1.91	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	111	GLU	CD-OE1	5.28	1.31	1.25
1	N	293	PHE	CD1-CE1	5.25	1.49	1.39
1	A	366	VAL	CB-CG1	-5.25	1.41	1.52
9	I	36	LYS	CD-CE	5.23	1.64	1.51
1	A	379	TYR	CG-CD1	5.22	1.46	1.39
4	Q	81	VAL	CB-CG1	5.21	1.63	1.52
2	B	159	VAL	CB-CG2	5.21	1.63	1.52
1	A	310	MET	CG-SD	-5.19	1.67	1.81
2	B	199	ILE	C-O	5.19	1.33	1.23
1	A	438	ARG	CB-CG	-5.18	1.38	1.52
3	C	101	PHE	CE2-CZ	5.18	1.47	1.37
1	N	397	PHE	CE1-CZ	5.18	1.47	1.37
2	O	208	PRO	C-O	5.17	1.33	1.23
6	S	20	VAL	CB-CG2	5.15	1.63	1.52
6	F	89	TYR	CD1-CE1	5.15	1.47	1.39
1	N	164	PHE	CD1-CE1	5.15	1.49	1.39
3	P	161	GLN	CB-CG	-5.15	1.38	1.52
1	N	266	GLU	CD-OE2	5.14	1.31	1.25
12	L	38	PHE	CE1-CZ	5.13	1.47	1.37
4	D	104	TYR	CD2-CE2	5.13	1.47	1.39
6	F	44	GLU	CG-CD	5.12	1.59	1.51
2	B	65	TRP	CB-CG	-5.12	1.41	1.50
1	N	366	VAL	CB-CG1	-5.11	1.42	1.52
9	V	37	PHE	CD2-CE2	5.10	1.49	1.39
4	D	60	TYR	CD1-CE1	-5.09	1.31	1.39
9	I	54	TYR	CD2-CE2	5.09	1.47	1.39
2	B	219	PHE	CE1-CZ	5.08	1.47	1.37
2	B	210	VAL	CB-CG1	5.08	1.63	1.52
3	C	10	MET	CB-CG	5.07	1.67	1.51
2	B	202	SER	CB-OG	-5.05	1.35	1.42
4	D	58	GLU	CB-CG	-5.03	1.42	1.52
1	N	337	ALA	CA-CB	5.02	1.62	1.52
3	P	236	GLU	CB-CG	-5.02	1.42	1.52
5	E	70	VAL	CB-CG2	5.01	1.63	1.52
1	N	70	VAL	CB-CG1	5.01	1.63	1.52

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	K	32	MET	CG-SD-CE	8.85	114.36	100.20
6	F	18	ARG	NE-CZ-NH2	-8.74	115.93	120.30
4	D	20	ARG	NE-CZ-NH2	-8.70	115.95	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	176	MET	CG-SD-CE	-8.47	86.66	100.20
2	B	112	ASP	CB-CG-OD2	-8.21	110.91	118.30
1	A	96	ARG	NE-CZ-NH2	-8.10	116.25	120.30
6	F	81	ARG	NE-CZ-NH2	-8.03	116.28	120.30
4	Q	20	ARG	NE-CZ-NH2	-7.78	116.41	120.30
1	A	297	MET	CG-SD-CE	7.71	112.53	100.20
1	A	438	ARG	NE-CZ-NH2	-7.64	116.48	120.30
1	N	310	MET	CG-SD-CE	-7.52	88.17	100.20
2	B	45	MET	CG-SD-CE	7.46	112.13	100.20
1	N	310	MET	CA-CB-CG	-7.37	100.77	113.30
12	Y	41	ARG	NE-CZ-NH1	7.16	123.88	120.30
13	M	34	LEU	CB-CG-CD1	7.12	123.10	111.00
9	I	10	ARG	NE-CZ-NH1	6.97	123.78	120.30
1	N	213	ARG	NE-CZ-NH2	-6.95	116.83	120.30
4	Q	125	ASP	CB-CG-OD1	-6.93	112.07	118.30
7	T	8	HIS	N-CA-C	6.92	129.69	111.00
1	A	363	LEU	CB-CG-CD2	6.91	122.74	111.00
7	T	7	ASP	N-CA-C	6.80	129.35	111.00
2	B	167	SER	CB-CA-C	-6.71	97.36	110.10
4	Q	20	ARG	NE-CZ-NH1	6.64	123.62	120.30
7	T	6	GLY	N-CA-C	6.56	129.51	113.10
9	I	10	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	A	362	SER	N-CA-CB	-6.41	100.89	110.50
3	P	127	LEU	CA-CB-CG	6.32	129.84	115.30
6	S	18	ARG	NE-CZ-NH2	-6.29	117.16	120.30
5	E	90	ARG	NE-CZ-NH2	-6.28	117.16	120.30
1	A	96	ARG	NE-CZ-NH1	6.24	123.42	120.30
13	M	7	LYS	CD-CE-NZ	-6.20	97.44	111.70
1	A	442	ASP	CB-CG-OD2	6.20	123.88	118.30
2	B	11	ASP	CB-CG-OD2	6.19	123.87	118.30
2	B	178	ARG	NE-CZ-NH1	6.17	123.38	120.30
8	H	35	ASP	CB-CG-OD2	-6.15	112.76	118.30
11	X	54	ARG	NE-CZ-NH2	6.14	123.37	120.30
7	G	7	ASP	N-CA-C	6.04	127.31	111.00
1	N	366	VAL	CG1-CB-CG2	-5.99	101.31	110.90
1	A	373	VAL	CA-CB-CG2	-5.98	101.93	110.90
1	N	483	LEU	CB-CG-CD1	-5.97	100.85	111.00
1	A	312	ILE	CG1-CB-CG2	-5.94	98.33	111.40
1	A	380	VAL	CG1-CB-CG2	-5.90	101.46	110.90
2	B	151	ARG	NE-CZ-NH1	5.85	123.22	120.30
1	A	407	ASP	CB-CG-OD2	5.83	123.54	118.30
4	Q	51	LEU	CA-CB-CG	5.75	128.54	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	18	GLU	OE1-CD-OE2	5.73	130.18	123.30
9	V	55	ASP	CB-CG-OD1	5.72	123.45	118.30
5	R	72	LYS	CD-CE-NZ	-5.62	98.77	111.70
2	B	129	LYS	CD-CE-NZ	-5.60	98.83	111.70
1	A	244	TYR	CA-CB-CG	-5.57	102.81	113.40
2	B	173	ASP	CB-CG-OD1	5.53	123.28	118.30
2	B	33	LEU	CB-CG-CD2	-5.53	101.61	111.00
1	N	96	ARG	NE-CZ-NH2	-5.51	117.55	120.30
3	P	51	MET	CA-CB-CG	5.48	122.61	113.30
1	A	264	LYS	CD-CE-NZ	5.47	124.28	111.70
3	P	246	ASP	N-CA-CB	-5.47	100.75	110.60
9	V	43	ARG	NE-CZ-NH2	5.44	123.02	120.30
10	J	11	LEU	CB-CG-CD1	-5.44	101.75	111.00
5	E	70	VAL	CG1-CB-CG2	-5.43	102.21	110.90
1	N	442	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	439	ARG	NE-CZ-NH1	5.39	122.99	120.30
6	F	92	VAL	CG1-CB-CG2	-5.38	102.29	110.90
2	B	151	ARG	NE-CZ-NH2	-5.35	117.62	120.30
6	S	18	ARG	NE-CZ-NH1	5.35	122.98	120.30
2	O	92	ASN	CB-CA-C	5.34	121.08	110.40
10	J	57	HIS	CB-CA-C	5.34	121.07	110.40
7	T	5	LYS	CD-CE-NZ	5.32	123.93	111.70
2	B	112	ASP	CB-CG-OD1	5.31	123.08	118.30
1	N	176	MET	CG-SD-CE	-5.31	91.71	100.20
9	V	10	ARG	NE-CZ-NH1	5.29	122.94	120.30
2	O	158	ASP	CB-CG-OD1	5.25	123.03	118.30
2	O	179	LEU	CA-CB-CG	5.25	127.37	115.30
2	B	65	TRP	N-CA-C	5.24	125.15	111.00
12	L	24	MET	CA-CB-CG	5.23	122.19	113.30
2	B	184	LEU	CB-CG-CD1	-5.23	102.12	111.00
3	P	102	TYR	CB-CG-CD2	-5.21	117.87	121.00
5	E	72	LYS	CD-CE-NZ	-5.19	99.76	111.70
2	B	133	LEU	CB-CG-CD1	-5.15	102.25	111.00
9	I	36	LYS	CD-CE-NZ	5.15	123.54	111.70
1	A	194	LEU	CB-CG-CD2	5.14	119.74	111.00
4	Q	26	ASP	CB-CG-OD1	5.12	122.91	118.30
11	K	47	ARG	NE-CZ-NH2	5.12	122.86	120.30
1	A	51	ASP	CB-CG-OD1	-5.11	113.70	118.30
7	G	6	GLY	N-CA-C	5.11	125.88	113.10
3	C	25	LEU	CB-CG-CD2	-5.11	102.32	111.00
7	G	8	HIS	N-CA-C	5.10	124.77	111.00
3	C	51	MET	CA-CB-CG	5.09	121.95	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	N	513	LEU	CB-CG-CD1	-5.07	102.39	111.00
9	V	10	ARG	NE-CZ-NH2	-5.05	117.78	120.30
4	Q	21	ASP	CB-CG-OD1	5.04	122.84	118.30
6	F	18	ARG	NE-CZ-NH1	5.02	122.81	120.30
6	S	96	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	F	93	PRO	Peptide
10	J	57	HIS	Peptide
6	S	93	PRO	Peptide
10	W	57	HIS	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4027	0	4001	38	0
1	N	4027	0	4001	48	0
2	B	1824	0	1833	34	0
2	O	1824	0	1833	40	0
3	C	2110	0	2027	22	0
3	P	2110	0	2027	22	0
4	D	1195	0	1183	9	0
4	Q	1195	0	1183	15	0
5	E	852	0	845	11	0
5	R	852	0	845	9	0
6	F	748	0	728	10	0
6	S	748	0	728	14	0
7	G	675	0	643	26	0
7	T	675	0	644	41	0
8	H	662	0	623	8	0
8	U	662	0	623	12	0
9	I	601	0	613	22	0
9	V	601	0	613	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	460	0	459	5	0
10	W	460	0	459	12	0
11	K	384	0	366	3	0
11	X	384	0	366	6	0
12	L	380	0	380	14	0
12	Y	380	0	380	9	0
13	M	335	0	352	7	0
13	Z	335	0	352	4	0
14	A	120	0	108	4	0
14	N	120	0	108	7	0
15	A	2	0	0	0	0
15	N	2	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	1	0	0	0	0
18	N	1	0	0	0	0
19	A	63	0	110	3	0
19	B	63	0	109	9	0
19	L	63	0	110	19	0
19	N	189	0	330	21	0
20	A	102	0	152	13	0
20	C	102	0	152	7	0
20	N	102	0	152	9	0
20	P	102	0	152	7	0
21	B	2	0	0	0	0
21	O	2	0	0	0	0
22	B	52	0	80	17	0
22	R	52	0	80	16	0
23	B	29	0	37	3	0
23	C	58	0	71	3	0
23	J	29	0	36	2	0
23	O	29	0	37	1	0
23	P	58	0	72	4	0
23	W	29	0	36	3	0
24	C	1	0	0	0	0
24	P	1	0	0	0	0
25	C	100	0	156	22	0
25	G	100	0	156	24	0
25	P	100	0	156	16	0
25	T	100	0	156	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	C	33	0	38	2	0
26	M	33	0	38	0	0
26	T	33	0	39	6	0
26	Z	33	0	39	1	0
27	F	1	0	0	0	0
27	S	1	0	0	0	0
28	G	159	0	231	22	0
28	S	53	0	77	6	0
28	T	106	0	154	19	0
29	A	205	0	0	3	0
29	B	121	0	0	3	0
29	C	80	0	0	2	0
29	D	75	0	0	1	0
29	E	39	0	0	1	0
29	F	70	0	0	2	0
29	G	42	0	0	5	0
29	H	33	0	0	5	0
29	I	24	0	0	1	0
29	J	9	0	0	0	0
29	K	17	0	0	0	0
29	L	20	0	0	2	0
29	M	15	0	0	0	0
29	N	184	0	0	6	0
29	O	97	0	0	2	0
29	P	81	0	0	7	0
29	Q	47	0	0	2	0
29	R	27	0	0	0	0
29	S	52	0	0	1	0
29	T	37	0	0	8	0
29	U	28	0	0	4	0
29	V	17	0	0	4	0
29	W	12	0	0	2	0
29	X	12	0	0	1	0
29	Y	16	0	0	0	0
29	Z	9	0	0	0	0
All	All	32105	0	31279	581	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 9.

All (581) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ILE:CD1	1:A:75:ILE:CG1	1.76	1.62
28:G:265:PEK:C7	28:G:265:PEK:C6	1.81	1.53
7:T:58:LYS:CE	7:T:58:LYS:NZ	1.72	1.47
12:L:20:ARG:NH2	19:L:522:TGL:HC32	1.40	1.36
7:T:45:PRO:CD	29:T:3099:HOH:O	1.75	1.35
7:T:5:LYS:CD	28:T:263:PEK:H382	1.73	1.19
7:T:5:LYS:HD2	28:T:263:PEK:C38	1.74	1.17
28:G:265:PEK:H383	25:G:269:CDL:C27	1.74	1.17
7:T:84:LYS:HD2	7:T:84:LYS:N	1.60	1.16
19:A:523:TGL:HG12	19:A:523:TGL:HC21	1.29	1.12
7:G:45:PRO:HD2	29:G:2099:HOH:O	1.49	1.11
7:T:5:LYS:HD2	28:T:263:PEK:H382	1.28	1.08
7:T:84:LYS:H	7:T:84:LYS:CD	1.67	1.07
7:T:45:PRO:HD2	29:T:3099:HOH:O	1.34	1.06
25:G:269:CDL:H112	25:G:269:CDL:HA21	1.32	1.05
29:P:4533:HOH:O	28:S:1265:PEK:H71	1.56	1.05
20:P:1267:PGV:H182	25:P:1270:CDL:H662	1.08	1.04
28:G:265:PEK:C38	25:G:269:CDL:H273	1.86	1.04
28:G:265:PEK:H383	25:G:269:CDL:H273	1.06	1.04
20:C:267:PGV:C12	20:C:267:PGV:H161	1.89	1.03
12:L:20:ARG:HH22	19:L:522:TGL:HC62	1.23	1.00
20:C:267:PGV:H161	20:C:267:PGV:H12	1.42	1.00
8:H:9:LYS:O	8:H:10:ASN:HB2	1.57	0.99
20:P:1267:PGV:C18	25:P:1270:CDL:H662	1.92	0.99
20:P:1267:PGV:H182	25:P:1270:CDL:C66	1.93	0.98
1:A:321:PHE:CD2	22:B:229:PSC:H341	1.99	0.98
3:C:111:GLU:HG3	29:H:4073:HOH:O	1.62	0.97
22:B:229:PSC:H072	9:I:10:ARG:HH21	1.29	0.96
28:T:1264:PEK:H32	28:T:1264:PEK:H71	1.46	0.96
1:N:112:LEU:HD12	29:N:3701:HOH:O	1.64	0.95
8:U:8:ILE:HG21	29:U:4330:HOH:O	1.66	0.95
6:S:85:CYS:SG	6:S:87:THR:HG23	2.07	0.94
26:C:272:DMU:H29	26:C:272:DMU:O1	1.68	0.94
22:B:229:PSC:C07	9:I:10:ARG:HH21	1.80	0.93
5:R:8:ASP:OD1	22:R:1229:PSC:H081	1.69	0.93
25:G:269:CDL:H522	25:G:269:CDL:H231	1.51	0.92
7:T:45:PRO:HD3	29:T:3099:HOH:O	1.47	0.92
12:L:20:ARG:HH22	19:L:522:TGL:HC32	1.13	0.92
6:F:85:CYS:SG	6:F:87:THR:HG23	2.09	0.91
3:C:67:PHE:HE1	25:C:270:CDL:H1	1.35	0.91
7:G:5:LYS:HD2	28:G:1263:PEK:H383	1.50	0.91
1:N:321:PHE:CD2	22:R:1229:PSC:H341	2.05	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:T:1269:CDL:H541	25:T:1269:CDL:H231	1.51	0.90
25:T:1269:CDL:HA21	25:T:1269:CDL:H111	1.53	0.90
19:B:521:TGL:H281	19:B:521:TGL:H102	1.52	0.89
7:T:5:LYS:CD	28:T:263:PEK:C38	2.41	0.89
22:R:1229:PSC:C07	9:V:10:ARG:HH21	1.85	0.89
7:T:62:TRP:HB3	26:T:1272:DMU:H30	1.52	0.89
7:T:84:LYS:HD2	7:T:84:LYS:H	0.77	0.88
12:L:20:ARG:NH2	19:L:522:TGL:CC3	2.34	0.88
12:L:20:ARG:HH21	19:L:522:TGL:HC32	1.36	0.86
9:V:18:ARG:HG2	9:V:18:ARG:HH11	1.39	0.86
25:G:269:CDL:H873	29:G:4364:HOH:O	1.75	0.86
7:T:31:CYS:SG	25:T:1269:CDL:H532	2.17	0.85
7:G:72:ASN:H	7:G:76:ASN:HD22	1.22	0.85
8:H:9:LYS:O	8:H:10:ASN:CB	2.25	0.85
19:N:1521:TGL:C28	19:N:1521:TGL:H102	2.08	0.83
7:T:62:TRP:CB	26:T:1272:DMU:H30	2.07	0.83
3:P:67:PHE:HE1	25:P:1270:CDL:H1	1.43	0.83
9:V:36:LYS:HG3	29:V:4356:HOH:O	1.77	0.82
28:G:265:PEK:C7	28:G:265:PEK:C5	2.58	0.82
2:B:33:LEU:HD11	9:I:28:SER:HB3	1.59	0.82
20:C:267:PGV:H12	20:C:267:PGV:C16	2.07	0.82
25:T:1269:CDL:H511	25:T:1269:CDL:H181	1.61	0.81
4:Q:109:HIS:HD2	29:Q:3122:HOH:O	1.64	0.81
7:G:45:PRO:CD	29:G:2099:HOH:O	2.16	0.80
11:X:54:ARG:HH21	11:X:54:ARG:HG3	1.46	0.80
7:T:72:ASN:H	7:T:76:ASN:HD22	1.26	0.80
7:T:76:ASN:HD21	28:T:1264:PEK:HN2	1.26	0.79
25:P:1270:CDL:HB32	25:P:1270:CDL:HB21	1.65	0.79
9:V:31:PHE:C	9:V:31:PHE:CD1	2.55	0.79
4:D:34:SER:H	4:D:37:GLN:HE21	1.31	0.78
1:N:406:ASN:HD21	20:N:1524:PGV:H21	1.49	0.78
19:N:1521:TGL:H222	19:N:1521:TGL:HA81	1.65	0.78
19:A:523:TGL:HG12	19:A:523:TGL:CC2	2.13	0.77
14:N:515:HEA:HMC1	14:N:515:HEA:HBC1	1.67	0.77
25:P:1270:CDL:H611	25:P:1270:CDL:H652	1.67	0.77
19:B:521:TGL:H102	19:B:521:TGL:C28	2.14	0.77
25:C:270:CDL:H231	25:C:270:CDL:H642	1.68	0.76
25:G:269:CDL:HA21	25:G:269:CDL:C11	2.14	0.76
7:T:62:TRP:HB3	26:T:1272:DMU:C57	2.15	0.75
2:B:82:ARG:NH1	2:B:86:MET:HE1	2.01	0.75
28:S:1265:PEK:H383	25:T:1269:CDL:C27	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:522:TGL:HC51	19:L:522:TGL:OC1	1.86	0.74
22:R:1229:PSC:H072	9:V:10:ARG:HH21	1.51	0.74
22:B:229:PSC:H212	22:B:229:PSC:O01	1.87	0.74
19:N:1521:TGL:H102	19:N:1521:TGL:H281	1.69	0.73
8:H:27:ARG:NH1	29:H:2431:HOH:O	2.22	0.73
1:N:177:SER:H	1:N:180:GLN:HE21	1.36	0.73
2:O:226:MET:HE1	29:O:4398:HOH:O	1.89	0.73
28:G:265:PEK:C38	25:G:269:CDL:C27	2.57	0.72
28:G:265:PEK:C6	28:G:265:PEK:C8	2.67	0.72
1:A:50:ASP:HB3	1:A:53:ILE:HD12	1.71	0.72
20:A:524:PGV:H221	20:A:524:PGV:C01	2.19	0.72
9:I:31:PHE:CD1	9:I:31:PHE:C	2.63	0.72
22:R:1229:PSC:H071	9:V:10:ARG:HH21	1.55	0.72
14:N:516:HEA:HMC1	14:N:516:HEA:HBC1	1.71	0.71
3:P:111:GLU:OE1	29:P:3467:HOH:O	2.08	0.71
5:R:80:GLU:H	5:R:80:GLU:CD	1.93	0.71
7:G:5:LYS:CD	28:G:1263:PEK:H383	2.21	0.71
7:G:31:CYS:SG	25:G:269:CDL:H532	2.30	0.71
7:G:76:ASN:HD21	28:G:264:PEK:HN2	1.37	0.71
7:G:84:LYS:H	7:G:84:LYS:HD2	1.54	0.71
25:G:269:CDL:H792	25:G:269:CDL:H562	1.72	0.71
13:M:39:ASN:O	13:M:43:SER:HB2	1.91	0.70
1:N:514:LYS:HA	6:S:38:ALA:HB3	1.72	0.70
19:A:523:TGL:H281	29:B:4178:HOH:O	1.91	0.70
25:T:1269:CDL:H181	25:T:1269:CDL:C51	2.22	0.69
3:C:63:ARG:HE	25:C:270:CDL:HA22	1.58	0.69
6:F:64:GLU:O	6:F:65:ASP:HB2	1.92	0.69
25:G:269:CDL:H522	25:G:269:CDL:C23	2.21	0.69
3:P:107:ALA:HB2	20:P:1268:PGV:H031	1.73	0.69
3:C:67:PHE:CE1	25:C:270:CDL:H1	2.25	0.68
1:N:484:THR:HB	13:Z:2:THR:OG1	1.93	0.68
25:C:270:CDL:HB32	25:C:270:CDL:HB21	1.74	0.68
3:C:246:ASP:HB2	29:C:4122:HOH:O	1.94	0.68
1:N:514:LYS:HA	6:S:38:ALA:CB	2.23	0.68
11:X:54:ARG:HH21	11:X:54:ARG:CG	2.06	0.68
1:A:484:THR:HB	13:M:2:THR:OG1	1.94	0.68
19:B:521:TGL:HC72	29:B:4575:HOH:O	1.94	0.67
1:N:177:SER:H	1:N:180:GLN:NE2	1.92	0.67
22:R:1229:PSC:H071	9:V:10:ARG:NH2	2.09	0.67
25:P:1270:CDL:H122	25:P:1270:CDL:HA4	1.75	0.67
25:G:269:CDL:H231	25:G:269:CDL:C52	2.22	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:26:MET:O	9:I:27:VAL:C	2.33	0.67
20:C:267:PGV:H182	25:C:270:CDL:H671	1.76	0.67
22:B:229:PSC:C07	9:I:10:ARG:NH2	2.56	0.67
7:T:5:LYS:CG	28:T:263:PEK:H382	2.24	0.67
5:E:109:VAL:HG23	5:E:109:VAL:OXT	1.93	0.66
7:G:4:ALA:HB3	1:N:282:PHE:HA	1.76	0.66
3:P:33:MET:HG2	29:P:4161:HOH:O	1.95	0.66
28:S:1265:PEK:H383	25:T:1269:CDL:H272	1.77	0.66
25:T:1269:CDL:H181	25:T:1269:CDL:CB5	2.26	0.66
14:A:516:HEA:HBC1	14:A:516:HEA:HMC1	1.77	0.66
25:G:269:CDL:H792	25:G:269:CDL:C56	2.26	0.66
8:H:12:GLN:HG3	29:H:4563:HOH:O	1.95	0.66
20:A:524:PGV:H062	29:A:2126:HOH:O	1.95	0.65
1:A:75:ILE:CD1	1:A:75:ILE:CB	2.71	0.65
25:P:1270:CDL:HB21	25:P:1270:CDL:CB3	2.26	0.65
1:A:486:ASP:OD1	4:D:19:ARG:HD2	1.96	0.65
22:B:229:PSC:H342	22:B:229:PSC:H142	1.78	0.65
22:B:229:PSC:H142	22:B:229:PSC:C34	2.26	0.65
10:W:33:ARG:HG2	23:W:1059:CHD:C15	2.27	0.65
3:P:146:TRP:CZ2	7:T:17:ARG:HG3	2.33	0.64
4:Q:19:ARG:HB3	4:Q:19:ARG:HH21	1.61	0.64
20:N:1524:PGV:C01	20:N:1524:PGV:H221	2.28	0.64
2:O:89:GLU:O	2:O:91:ASN:ND2	2.31	0.64
23:P:1271:CHD:H162	23:P:1271:CHD:H232	1.78	0.64
25:C:270:CDL:PA1	25:C:270:CDL:HB22	2.38	0.64
19:N:1521:TGL:HA71	19:N:1521:TGL:H101	1.79	0.64
11:X:54:ARG:HG3	11:X:54:ARG:NH2	2.09	0.64
3:C:29:SER:HB3	3:C:42:LEU:HD13	1.80	0.63
1:N:488:THR:HB	1:N:495:LEU:HD13	1.81	0.63
2:B:33:LEU:HD11	9:I:28:SER:CB	2.26	0.63
10:W:33:ARG:HG2	23:W:1059:CHD:H152	1.81	0.63
7:G:5:LYS:HG3	28:G:1263:PEK:H382	1.81	0.63
23:P:1271:CHD:H232	23:P:1271:CHD:C16	2.29	0.63
2:B:59:GLN:O	2:B:60:GLU:HG3	1.99	0.63
7:G:8:HIS:ND1	28:G:1263:PEK:H332	2.13	0.63
7:G:72:ASN:H	7:G:76:ASN:ND2	1.97	0.62
8:H:57:ARG:HD2	29:H:4481:HOH:O	1.99	0.62
7:G:37:LEU:HD23	7:G:38:HIS:ND1	2.15	0.62
1:N:513:LEU:O	1:N:514:LYS:HB2	1.99	0.62
7:T:12:GLY:HA3	29:T:3372:HOH:O	1.99	0.62
20:A:524:PGV:C06	29:A:2126:HOH:O	2.46	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:61:VAL:HA	2:O:64:ILE:HD12	1.80	0.62
22:R:1229:PSC:C07	9:V:10:ARG:NH2	2.60	0.61
28:G:264:PEK:H71	28:G:264:PEK:H32	1.81	0.61
4:D:34:SER:H	4:D:37:GLN:NE2	1.98	0.61
7:T:36:TRP:HB3	29:T:4417:HOH:O	2.00	0.61
12:L:20:ARG:HH21	19:L:522:TGL:CC3	2.08	0.61
1:A:502:TYR:CD1	12:L:2:HIS:HE1	2.19	0.60
20:A:524:PGV:H221	20:A:524:PGV:H011	1.83	0.60
7:G:84:LYS:H	7:G:84:LYS:CD	2.13	0.60
4:Q:7:LYS:O	4:Q:10:ASP:HB2	2.01	0.60
9:V:18:ARG:HH11	9:V:18:ARG:CG	2.11	0.60
20:N:1524:PGV:H221	20:N:1524:PGV:H011	1.83	0.60
22:B:229:PSC:H081	5:E:8:ASP:OD1	2.01	0.59
3:P:67:PHE:CE1	25:P:1270:CDL:H1	2.31	0.59
7:T:3:ALA:O	7:T:4:ALA:HB2	2.03	0.59
9:I:31:PHE:CD1	9:I:32:ALA:N	2.71	0.59
28:S:1265:PEK:C38	25:T:1269:CDL:H273	2.32	0.59
7:G:3:ALA:O	7:G:4:ALA:HB2	2.02	0.59
3:P:127:LEU:HG	25:T:1269:CDL:OB3	2.03	0.58
4:Q:109:HIS:CD2	29:Q:3122:HOH:O	2.47	0.58
25:T:1269:CDL:H111	25:T:1269:CDL:CA2	2.31	0.58
19:N:1521:TGL:H281	19:N:1521:TGL:HB92	1.86	0.58
1:A:406:ASN:HD21	20:A:524:PGV:H21	1.69	0.58
5:E:31:LYS:HE3	29:F:4383:HOH:O	2.04	0.58
1:A:177:SER:H	1:A:180:GLN:NE2	2.02	0.58
19:N:1521:TGL:H102	19:N:1521:TGL:H283	1.86	0.58
7:G:4:ALA:CB	1:N:282:PHE:HA	2.34	0.57
8:U:49:ASP:O	8:U:52:VAL:HG22	2.04	0.57
1:A:47:LEU:O	13:M:41:LYS:HE3	2.04	0.57
6:F:85:CYS:SG	6:F:87:THR:CG2	2.89	0.57
7:G:5:LYS:HG3	28:G:1263:PEK:C38	2.33	0.57
5:R:8:ASP:HA	22:R:1229:PSC:H071	1.86	0.57
25:P:1270:CDL:H661	25:P:1270:CDL:H252	1.87	0.57
2:B:56:MET:HA	22:B:229:PSC:H202	1.85	0.57
7:T:5:LYS:HD3	28:T:263:PEK:H382	1.79	0.57
20:A:524:PGV:H222	13:M:15:GLN:HE22	1.70	0.56
26:C:272:DMU:H29	26:C:272:DMU:C10	2.35	0.56
9:I:31:PHE:O	9:I:34:PHE:N	2.32	0.56
4:Q:95:LEU:HD22	26:Z:1526:DMU:H13	1.86	0.56
3:C:19:THR:O	3:C:23:SER:HB3	2.06	0.56
20:A:524:PGV:H221	20:A:524:PGV:H012	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:C:270:CDL:HB32	25:C:270:CDL:CB2	2.35	0.56
25:P:1270:CDL:H431	29:W:4138:HOH:O	2.05	0.56
2:O:196:CYS:HB2	2:O:207:MET:HG3	1.87	0.56
13:Z:11:SER:OG	13:Z:14:GLU:HG3	2.06	0.56
25:C:270:CDL:H672	25:C:270:CDL:H261	1.88	0.56
10:J:52:TRP:O	10:J:57:HIS:HE1	1.87	0.56
25:P:1270:CDL:OB9	25:P:1270:CDL:H522	2.05	0.56
2:B:66:THR:HG22	2:B:67:ILE:N	2.20	0.56
25:C:270:CDL:HB21	25:C:270:CDL:CB3	2.36	0.56
23:B:1085:CHD:H12	23:B:1085:CHD:H212	1.87	0.56
1:A:513:LEU:O	1:A:514:LYS:HB2	2.06	0.56
4:Q:19:ARG:NH2	4:Q:21:ASP:OD1	2.39	0.55
28:G:264:PEK:H101	28:G:264:PEK:H161	1.88	0.55
25:C:270:CDL:H661	25:C:270:CDL:H242	1.88	0.55
10:J:50:LEU:HD22	10:J:50:LEU:O	2.06	0.55
25:T:1269:CDL:H522	25:T:1269:CDL:H202	1.87	0.55
1:N:508:PRO:HG3	3:P:6:HIS:HB3	1.89	0.55
19:N:1523:TGL:CC2	19:N:1523:TGL:HG11	2.37	0.55
25:T:1269:CDL:OA7	25:T:1269:CDL:H311	2.05	0.55
25:G:269:CDL:H371	2:O:81:LEU:HD12	1.88	0.55
7:T:62:TRP:HB2	26:T:1272:DMU:H30	1.89	0.55
13:Z:39:ASN:O	13:Z:43:SER:HB2	2.07	0.55
7:G:2:SER:OG	28:G:1263:PEK:H301	2.07	0.55
3:P:33:MET:CG	29:P:4161:HOH:O	2.53	0.55
22:R:1229:PSC:H231	22:R:1229:PSC:H42	1.89	0.55
19:B:521:TGL:HA91	19:B:521:TGL:H252	1.88	0.55
7:G:3:ALA:O	7:G:4:ALA:CB	2.55	0.54
5:R:6:GLU:OE1	5:R:14:ARG:NH2	2.39	0.54
3:C:226:HIS:CE1	25:C:270:CDL:HB31	2.42	0.54
3:C:54:MET:HE3	25:C:270:CDL:H601	1.89	0.54
2:O:116:LEU:HD11	2:O:226:MET:HG2	1.90	0.54
3:P:124:LEU:HD13	3:P:180:GLU:OE1	2.07	0.54
8:U:8:ILE:HG12	29:U:4330:HOH:O	2.08	0.54
19:L:522:TGL:H362	29:L:4269:HOH:O	2.08	0.54
7:T:5:LYS:HD3	28:T:263:PEK:C38	2.35	0.54
1:N:408:THR:O	1:N:412:ILE:HD12	2.08	0.54
9:V:61:GLU:OE1	9:V:64:ARG:NH2	2.40	0.54
11:X:24:PHE:O	11:X:28:VAL:HG12	2.08	0.53
10:J:9:GLN:O	10:J:13:GLN:HG3	2.09	0.53
4:Q:73:ARG:HB3	5:R:109:VAL:HG11	1.91	0.53
20:C:267:PGV:H182	25:C:270:CDL:C67	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B:521:TGL:H252	19:B:521:TGL:C20	2.39	0.53
14:A:515:HEA:HBC1	14:A:515:HEA:HMC1	1.91	0.53
3:C:226:HIS:HE1	25:C:270:CDL:HB31	1.74	0.53
10:W:29:ASN:HD22	10:W:29:ASN:H	1.54	0.53
2:B:13:THR:OG1	2:B:167:SER:HB3	2.09	0.53
12:L:25:MET:HG2	19:L:522:TGL:HA62	1.90	0.53
6:F:64:GLU:O	6:F:65:ASP:CB	2.57	0.53
25:C:270:CDL:HB22	25:C:270:CDL:OA5	2.08	0.52
1:N:112:LEU:CD1	29:N:3701:HOH:O	2.39	0.52
2:B:33:LEU:CD1	9:I:28:SER:HB3	2.36	0.52
19:N:1523:TGL:HB52	4:Q:81:VAL:HG11	1.92	0.52
3:C:210:ILE:HG23	20:C:267:PGV:H102	1.90	0.52
6:S:64:GLU:O	6:S:65:ASP:HB2	2.09	0.52
25:T:1269:CDL:H172	29:T:4505:HOH:O	2.09	0.52
25:G:269:CDL:H231	25:G:269:CDL:C53	2.39	0.52
1:N:38:ARG:HD2	14:N:515:HEA:OMA	2.09	0.52
1:N:51:ASP:OD1	2:O:206:PHE:HE1	1.93	0.52
29:P:4415:HOH:O	26:T:1272:DMU:H24	2.10	0.52
2:O:62:GLU:HB2	29:O:4150:HOH:O	2.10	0.51
25:P:1270:CDL:PA1	25:P:1270:CDL:HB22	2.51	0.51
9:V:31:PHE:CD1	9:V:32:ALA:N	2.78	0.51
3:C:224:LYS:O	3:C:225:PHE:HB2	2.11	0.51
4:Q:56:LYS:HG2	5:R:61:PHE:CZ	2.46	0.51
10:W:29:ASN:H	10:W:29:ASN:ND2	2.09	0.51
1:N:113:LEU:CD1	19:N:1522:TGL:H292	2.40	0.51
2:O:33:LEU:CD1	9:V:28:SER:HB3	2.40	0.51
2:O:116:LEU:HD11	2:O:226:MET:CG	2.40	0.51
1:A:240:HIS:HB3	1:A:241:PRO:HD3	1.92	0.51
7:G:5:LYS:HB2	28:G:1263:PEK:H361	1.91	0.51
25:G:269:CDL:H542	25:G:269:CDL:H251	1.92	0.51
2:B:89:GLU:O	2:B:91:ASN:OD1	2.29	0.51
1:N:62:ALA:HB2	14:N:515:HEA:HBD1	1.91	0.51
3:C:51:MET:HB2	25:C:270:CDL:H392	1.94	0.50
19:B:521:TGL:C28	19:B:521:TGL:C10	2.87	0.50
7:T:3:ALA:O	7:T:4:ALA:CB	2.59	0.50
2:O:78:LEU:CB	2:O:79:PRO:CD	2.89	0.50
2:O:226:MET:HA	2:O:226:MET:CE	2.41	0.50
20:A:524:PGV:H132	20:A:524:PGV:H302	1.93	0.50
25:G:269:CDL:H761	1:N:282:PHE:HZ	1.77	0.50
2:O:56:MET:HG2	22:R:1229:PSC:H211	1.94	0.50
1:A:422:ASN:HB3	19:B:521:TGL:H242	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:A:524:PGV:H322	20:A:524:PGV:H151	1.94	0.50
12:L:20:ARG:HH22	19:L:522:TGL:CC3	2.04	0.50
12:L:20:ARG:HH22	19:L:522:TGL:CC6	2.08	0.49
8:U:7:LYS:C	8:U:9:LYS:H	2.16	0.49
6:S:34:LEU:HD22	29:S:4590:HOH:O	2.12	0.49
1:N:481:GLU:HB2	13:Z:4:LYS:HE2	1.94	0.49
19:N:1523:TGL:H352	29:V:4468:HOH:O	2.12	0.49
2:O:66:THR:HG22	2:O:67:ILE:N	2.27	0.49
11:X:15:ASN:HB2	29:X:3609:HOH:O	2.11	0.49
1:A:62:ALA:HB2	14:A:515:HEA:HBD1	1.95	0.49
11:K:24:PHE:O	11:K:28:VAL:HG12	2.12	0.49
20:A:521:PGV:H182	3:C:28:THR:HG22	1.94	0.49
3:C:50:ASN:HD22	3:C:51:MET:HE2	1.78	0.49
9:I:31:PHE:CZ	9:I:35:TYR:HB2	2.48	0.49
2:O:78:LEU:HB3	2:O:79:PRO:HD3	1.95	0.49
2:O:62:GLU:O	2:O:66:THR:HB	2.13	0.48
3:P:112:LEU:HD13	3:P:118:PRO:HG3	1.94	0.48
2:B:132:GLU:HB3	2:B:137:GLU:HG3	1.95	0.48
4:D:93:ALA:HB3	11:K:28:VAL:HG22	1.95	0.48
12:L:20:ARG:NH2	19:L:522:TGL:HC62	2.08	0.48
19:N:1521:TGL:C28	19:N:1521:TGL:C10	2.88	0.48
10:W:9:GLN:O	10:W:13:GLN:HG3	2.12	0.48
4:D:34:SER:N	4:D:37:GLN:HE21	2.07	0.48
19:L:522:TGL:H351	29:L:4252:HOH:O	2.13	0.48
19:N:1521:TGL:H281	19:N:1521:TGL:C10	2.39	0.48
9:V:27:VAL:HG11	29:V:4562:HOH:O	2.13	0.48
3:C:63:ARG:HE	25:C:270:CDL:CA2	2.25	0.48
19:N:1523:TGL:H242	19:N:1523:TGL:HA91	1.95	0.48
2:O:59:GLN:O	2:O:59:GLN:HG3	2.13	0.48
2:O:102:HIS:HE2	2:O:107:SER:HG	1.61	0.48
4:Q:19:ARG:NH2	4:Q:21:ASP:CG	2.66	0.48
8:U:60:TYR:CD1	8:U:60:TYR:C	2.87	0.48
9:V:36:LYS:CG	29:V:4356:HOH:O	2.49	0.48
6:F:55:LYS:HA	6:F:74:LEU:O	2.13	0.48
1:N:172:LYS:NZ	1:N:178:GLN:HE22	2.11	0.48
1:N:400:PHE:HB3	19:N:1522:TGL:H282	1.94	0.48
3:P:236:GLU:HG2	29:P:4386:HOH:O	2.12	0.48
20:P:1267:PGV:H182	25:P:1270:CDL:C67	2.43	0.48
6:S:92:VAL:O	6:S:92:VAL:HG23	2.14	0.48
1:N:87:ILE:O	1:N:173:PRO:HD3	2.14	0.48
7:T:2:SER:O	28:T:263:PEK:H331	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:T:5:LYS:CD	28:T:263:PEK:H383	2.40	0.48
29:W:4565:HOH:O	12:Y:47:LYS:HG3	2.13	0.48
22:B:229:PSC:H072	9:I:10:ARG:NH2	2.13	0.48
1:N:417:MET:CE	29:N:3166:HOH:O	2.62	0.48
7:T:78:LEU:HB3	7:T:79:PRO:HD2	1.96	0.48
25:T:1269:CDL:H762	25:T:1269:CDL:H561	1.96	0.48
3:P:154:GLY:HA2	6:S:6:VAL:HB	1.95	0.47
23:P:1525:CHD:H112	23:P:1525:CHD:H12A	1.72	0.47
1:A:177:SER:H	1:A:180:GLN:HE21	1.62	0.47
20:N:1524:PGV:H221	20:N:1524:PGV:H012	1.95	0.47
13:M:42:LYS:HA	13:M:42:LYS:CE	2.43	0.47
23:B:1085:CHD:H212	23:B:1085:CHD:C12	2.44	0.47
1:N:417:MET:HE1	29:N:3166:HOH:O	2.13	0.47
12:Y:20:ARG:NH2	12:Y:24:MET:HG3	2.30	0.47
2:B:94:SER:HB2	29:B:4446:HOH:O	2.15	0.47
8:U:27:ARG:NH1	29:U:3431:HOH:O	2.46	0.47
2:B:217:LYS:HD2	2:B:217:LYS:HA	1.60	0.47
1:A:51:ASP:HB3	2:B:202:SER:O	2.15	0.46
1:A:514:LYS:HA	6:F:38:ALA:HB3	1.96	0.46
3:C:33:MET:CG	29:C:4096:HOH:O	2.63	0.46
7:G:78:LEU:HB3	7:G:79:PRO:HD2	1.96	0.46
1:N:472:ILE:HG21	19:N:1522:TGL:HA91	1.97	0.46
20:N:1524:PGV:H152	20:N:1524:PGV:H322	1.96	0.46
3:P:63:ARG:HE	25:P:1270:CDL:HA22	1.80	0.46
7:T:5:LYS:HD2	28:T:263:PEK:H383	1.83	0.46
13:M:39:ASN:O	13:M:43:SER:CB	2.61	0.46
2:O:78:LEU:CB	2:O:79:PRO:HD3	2.44	0.46
4:Q:19:ARG:HB3	4:Q:19:ARG:NH2	2.29	0.46
6:S:53:THR:HB	6:S:54:ASN:H	1.36	0.46
9:V:28:SER:O	9:V:32:ALA:N	2.41	0.46
19:L:522:TGL:H201	19:L:522:TGL:C24	2.46	0.46
3:P:146:TRP:CE2	7:T:17:ARG:HG3	2.50	0.46
28:S:1265:PEK:H381	25:T:1269:CDL:H273	1.97	0.46
10:W:31:LEU:HD12	10:W:31:LEU:HA	1.80	0.46
2:O:217:LYS:HA	2:O:217:LYS:HE2	1.95	0.46
20:P:1268:PGV:H21	20:P:1268:PGV:H51	1.36	0.46
1:A:229:ILE:HD11	2:B:175:ILE:HD13	1.98	0.46
1:A:282:PHE:HA	7:T:4:ALA:HB3	1.97	0.46
2:B:196:CYS:HB2	2:B:207:MET:HG3	1.96	0.46
2:O:33:LEU:HD11	9:V:28:SER:HB3	1.98	0.46
2:O:67:ILE:O	2:O:70:ALA:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:TYR:CE2	9:I:24:ALA:HB2	2.51	0.46
22:B:229:PSC:H142	22:B:229:PSC:H343	1.98	0.46
8:H:12:GLN:CG	29:H:4563:HOH:O	2.59	0.46
8:U:78:GLU:O	8:U:78:GLU:HG2	2.16	0.46
1:A:321:PHE:HB3	2:B:65:TRP:CE3	2.51	0.46
3:C:5:THR:HG22	6:F:96:LEU:HD22	1.97	0.46
25:C:270:CDL:H411	25:C:270:CDL:H382	1.83	0.46
10:W:56:PRO:HD3	12:Y:46:LYS:HG2	1.98	0.46
2:B:52:HIS:CE1	22:B:229:PSC:H211	2.51	0.46
23:B:1085:CHD:H112	23:B:1085:CHD:H12A	1.69	0.46
25:G:269:CDL:H552	25:G:269:CDL:H582	1.60	0.46
12:L:46:LYS:O	12:L:47:LYS:CB	2.64	0.46
2:B:165:VAL:HG11	2:B:168:LEU:HD12	1.98	0.46
28:G:1263:PEK:H282	28:G:1263:PEK:H312	1.85	0.46
7:G:9:GLY:HA3	29:N:4361:HOH:O	2.16	0.45
1:N:398:PRO:O	1:N:498:CYS:HB3	2.16	0.45
2:O:164:ALA:O	2:O:194:GLY:HA3	2.15	0.45
7:G:38:HIS:CE1	25:G:269:CDL:H111	2.51	0.45
7:T:8:HIS:CE1	28:T:263:PEK:H341	2.50	0.45
9:V:18:ARG:CG	9:V:18:ARG:NH1	2.77	0.45
2:O:200:CYS:SG	2:O:204:HIS:HA	2.57	0.45
28:T:1264:PEK:H32	28:T:1264:PEK:C7	2.31	0.45
1:A:50:ASP:CB	1:A:53:ILE:HD12	2.44	0.45
19:N:1521:TGL:H222	19:N:1521:TGL:CA8	2.42	0.45
5:R:8:ASP:HA	22:R:1229:PSC:C07	2.47	0.45
12:Y:9:LYS:HA	12:Y:9:LYS:HD3	1.61	0.45
1:A:514:LYS:HA	6:F:38:ALA:CB	2.47	0.45
3:C:47:LEU:O	3:C:51:MET:HG2	2.16	0.45
22:R:1229:PSC:H251	22:R:1229:PSC:H221	1.39	0.45
8:U:7:LYS:O	8:U:8:ILE:HG22	2.16	0.45
12:Y:16:GLU:OE1	12:Y:16:GLU:HA	2.17	0.45
5:E:48:ILE:HG21	5:E:89:LEU:HD11	1.99	0.45
5:E:82:TYR:HB3	5:E:83:PRO:HD3	1.97	0.45
7:T:10:GLY:CA	29:T:4407:HOH:O	2.64	0.45
25:G:269:CDL:C87	29:G:4364:HOH:O	2.50	0.45
1:N:290:HIS:CD2	1:N:291:HIS:CD2	3.05	0.45
1:N:514:LYS:HA	6:S:38:ALA:HB2	1.98	0.45
2:O:83:ILE:O	2:O:87:MET:HG3	2.17	0.45
28:T:263:PEK:H231	28:T:263:PEK:H052	1.99	0.45
3:C:127:LEU:HG	25:G:269:CDL:OB3	2.16	0.45
4:D:127:LYS:HD2	29:I:2618:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:63:ARG:HE	25:P:1270:CDL:CA2	2.29	0.44
5:E:31:LYS:CE	29:F:4383:HOH:O	2.63	0.44
25:G:269:CDL:HB32	1:N:304:TYR:HD1	1.82	0.44
8:H:58:ARG:HD2	8:H:58:ARG:HA	1.85	0.44
7:T:33:LEU:O	7:T:37:LEU:HB2	2.17	0.44
20:A:524:PGV:H011	20:A:524:PGV:H22	1.99	0.44
19:B:521:TGL:H281	19:B:521:TGL:C10	2.36	0.44
3:C:154:GLY:HA2	6:F:6:VAL:HB	1.99	0.44
8:H:60:TYR:CD1	8:H:60:TYR:C	2.90	0.44
4:Q:126:MET:HG3	4:Q:128:VAL:HG23	2.00	0.44
25:T:1269:CDL:H541	25:T:1269:CDL:C23	2.34	0.44
10:W:12:PHE:O	10:W:23:LYS:HE2	2.17	0.44
1:N:369:ASP:HA	1:N:438:ARG:HD3	2.00	0.44
11:X:43:SER:HA	11:X:44:PRO:HD3	1.84	0.44
1:A:50:ASP:OD1	29:A:2067:HOH:O	2.21	0.44
22:B:229:PSC:H201	22:B:229:PSC:H232	1.33	0.44
7:G:5:LYS:CG	28:G:1263:PEK:H383	2.48	0.44
7:G:12:GLY:HA3	29:G:2372:HOH:O	2.18	0.44
2:O:66:THR:CG2	2:O:67:ILE:N	2.80	0.44
1:A:513:LEU:O	1:A:514:LYS:CB	2.66	0.44
2:B:128:LEU:HD11	2:B:134:ARG:HA	1.99	0.44
6:F:30:PRO:O	6:F:96:LEU:HD21	2.18	0.44
23:J:60:CHD:H112	23:J:60:CHD:H12A	1.41	0.44
1:N:383:MET:HG2	1:N:421:VAL:HG21	1.99	0.44
5:E:24:ILE:HG23	5:E:24:ILE:O	2.17	0.44
1:A:321:PHE:CE2	22:B:229:PSC:H341	2.48	0.44
2:O:16:ILE:HD13	2:O:16:ILE:HA	1.53	0.44
3:P:110:PRO:HB3	8:U:30:TRP:CE3	2.53	0.43
3:P:155:ASP:OD2	3:P:158:HIS:ND1	2.38	0.43
6:S:14:THR:HG1	10:W:13:GLN:HE22	1.64	0.43
2:B:111:THR:HA	2:B:114:GLU:O	2.19	0.43
2:B:161:HIS:HB2	2:B:174:ALA:HB3	1.99	0.43
28:G:265:PEK:H383	25:G:269:CDL:H272	1.84	0.43
1:N:114:ALA:O	1:N:118:VAL:HG13	2.18	0.43
1:N:321:PHE:HB3	2:O:65:TRP:CE3	2.53	0.43
20:N:1524:PGV:C01	20:N:1524:PGV:C22	2.96	0.43
2:O:145:PRO:HB2	2:O:148:MET:HG3	1.99	0.43
1:A:40:GLU:HG2	1:A:54:TYR:CD2	2.52	0.43
1:N:40:GLU:HG2	1:N:54:TYR:CD2	2.52	0.43
1:A:265:LYS:HB2	1:A:490:THR:HG21	2.01	0.43
1:N:18:LEU:HD22	19:N:1522:TGL:HB32	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:1521:TGL:H281	19:N:1521:TGL:CB9	2.48	0.43
9:V:31:PHE:HD1	9:V:32:ALA:N	2.16	0.43
2:B:78:LEU:CB	2:B:79:PRO:CD	2.97	0.43
20:N:1524:PGV:H242	20:N:1524:PGV:H41	1.99	0.43
1:A:250:GLY:O	1:A:254:ILE:HG12	2.19	0.43
2:O:33:LEU:HA	2:O:33:LEU:HD13	1.32	0.43
9:I:31:PHE:O	9:I:32:ALA:C	2.56	0.43
1:N:200:PRO:HB3	20:N:1266:PGV:H341	2.01	0.43
1:N:513:LEU:HD23	1:N:513:LEU:HA	1.60	0.43
2:O:33:LEU:CD1	9:V:28:SER:CB	2.96	0.43
28:S:1265:PEK:C38	25:T:1269:CDL:C27	2.88	0.43
23:W:1059:CHD:H12A	23:W:1059:CHD:H112	1.40	0.43
22:B:229:PSC:H071	9:I:10:ARG:NH2	2.31	0.43
7:T:74:ARG:HB2	29:T:3608:HOH:O	2.19	0.43
12:Y:22:LEU:O	12:Y:26:THR:HB	2.19	0.43
2:B:13:THR:O	2:B:13:THR:HG22	2.18	0.43
2:O:114:GLU:HB3	2:O:227:LEU:HD21	2.01	0.43
23:O:229:CHD:H112	23:O:229:CHD:H12A	1.68	0.43
22:R:1229:PSC:H212	22:R:1229:PSC:O01	2.19	0.43
7:T:2:SER:O	28:T:263:PEK:H322	2.19	0.43
1:N:377:PHE:HA	1:N:380:VAL:HG22	2.01	0.42
14:N:515:HEA:HHC	14:N:515:HEA:H11	1.79	0.42
2:O:114:GLU:HG3	2:O:227:LEU:HD11	2.00	0.42
2:B:16:ILE:HD13	2:B:16:ILE:HA	1.85	0.42
2:O:33:LEU:HD11	9:V:28:SER:CB	2.49	0.42
3:P:47:LEU:O	3:P:51:MET:HG2	2.19	0.42
1:N:486:ASP:HB2	29:N:3142:HOH:O	2.18	0.42
22:R:1229:PSC:H212	22:R:1229:PSC:C02	2.49	0.42
20:C:267:PGV:H182	25:C:270:CDL:C66	2.49	0.42
2:O:215:PRO:HD3	9:V:60:PHE:CD2	2.54	0.42
6:S:16:LEU:HD12	6:S:16:LEU:HA	1.83	0.42
28:T:1264:PEK:H71	28:T:1264:PEK:C3	2.34	0.42
23:C:271:CHD:H112	23:C:271:CHD:H12A	1.62	0.42
1:N:172:LYS:HZ2	1:N:178:GLN:HE22	1.67	0.42
7:T:31:CYS:SG	25:T:1269:CDL:H551	2.60	0.42
1:A:48:LEU:C	1:A:50:ASP:H	2.21	0.42
1:A:472:ILE:HG21	19:L:522:TGL:HA92	2.02	0.42
9:I:26:MET:O	9:I:27:VAL:O	2.36	0.42
2:O:222:TRP:HB2	9:V:71:SER:HB2	2.01	0.42
6:S:37:LYS:HD3	6:S:37:LYS:HA	1.83	0.42
10:W:32:TYR:CE1	10:W:36:MET:HE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:78:LEU:HB3	7:G:79:PRO:CD	2.50	0.42
9:I:31:PHE:O	9:I:34:PHE:HB3	2.20	0.42
12:L:14:SER:H	19:L:522:TGL:HC31	1.85	0.42
1:N:412:ILE:HG12	4:Q:84:ALA:HB3	2.01	0.42
3:P:135:SER:HB3	25:T:1269:CDL:H572	2.02	0.42
1:A:115:SER:HB2	1:A:142:SER:O	2.19	0.42
9:I:31:PHE:HD1	9:I:32:ALA:N	2.15	0.42
19:L:522:TGL:H202	19:L:522:TGL:H231	1.72	0.42
1:N:242:GLU:HA	1:N:245:ILE:HD12	2.01	0.42
28:T:263:PEK:O04	28:T:263:PEK:H242	2.19	0.42
10:J:31:LEU:HD12	10:J:31:LEU:HA	1.75	0.42
14:N:515:HEA:HAC	14:N:515:HEA:HHD	1.91	0.42
20:P:1267:PGV:H331	29:P:4415:HOH:O	2.19	0.42
1:N:27:GLY:HA2	1:N:69:MET:HG3	2.02	0.42
9:I:61:GLU:HG3	9:I:65:LYS:HE3	2.02	0.41
9:V:25:PHE:CZ	9:V:29:LEU:HD22	2.54	0.41
12:Y:20:ARG:HH11	12:Y:20:ARG:HB3	1.85	0.41
1:A:194:LEU:HD22	1:A:285:PHE:HE2	1.84	0.41
3:C:160:LEU:HD13	23:C:271:CHD:H181	2.02	0.41
19:N:1522:TGL:HC32	19:N:1522:TGL:HC62	1.90	0.41
4:Q:144:GLU:OE1	4:Q:147:LYS:HE3	2.19	0.41
6:S:81:ARG:HA	6:S:87:THR:O	2.19	0.41
1:A:488:THR:HB	1:A:495:LEU:HD13	2.02	0.41
5:E:82:TYR:N	5:E:83:PRO:CD	2.83	0.41
1:N:266:GLU:HB2	1:N:267:PRO:HD2	2.02	0.41
10:W:58:LYS:HA	10:W:58:LYS:HD3	1.81	0.41
10:J:33:ARG:HG2	23:J:60:CHD:H151	2.01	0.41
3:P:67:PHE:HA	10:W:9:GLN:HG2	2.02	0.41
1:A:195:LEU:HD23	1:A:245:ILE:HD13	2.02	0.41
19:B:521:TGL:C24	19:B:521:TGL:H201	2.50	0.41
28:G:264:PEK:H161	28:G:264:PEK:C10	2.49	0.41
28:G:1263:PEK:H161	3:P:91:VAL:HG13	2.03	0.41
19:L:522:TGL:C24	19:L:522:TGL:C20	2.95	0.41
20:N:1524:PGV:H011	20:N:1524:PGV:C22	2.49	0.41
5:R:5:HIS:HB3	5:R:6:GLU:H	1.41	0.41
12:L:29:PHE:CZ	19:L:522:TGL:HA82	2.56	0.41
2:O:196:CYS:CB	2:O:207:MET:HG3	2.50	0.41
8:U:8:ILE:CG2	29:U:4330:HOH:O	2.44	0.41
25:C:270:CDL:HA4	25:C:270:CDL:H122	2.02	0.41
1:N:335:SER:HB2	1:N:336:PRO:HD2	2.02	0.41
2:O:92:ASN:HA	2:O:93:PRO:HD2	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:T:58:LYS:NZ	7:T:58:LYS:CD	2.72	0.41
1:A:324:LEU:O	1:A:327:LEU:HB2	2.21	0.41
1:A:1:FME:CE	1:A:1:FME:HA	2.49	0.41
25:C:270:CDL:H852	25:C:270:CDL:H812	2.03	0.41
25:G:269:CDL:OA7	25:G:269:CDL:H342	2.21	0.41
9:I:27:VAL:HG12	9:I:28:SER:N	2.36	0.41
6:S:55:LYS:HA	6:S:74:LEU:O	2.20	0.41
20:A:524:PGV:H242	13:M:15:GLN:NE2	2.35	0.41
2:B:33:LEU:HD11	9:I:28:SER:CA	2.51	0.41
2:B:41:ILE:O	2:B:45:MET:HG2	2.21	0.41
2:B:144:LEU:HB2	2:B:213:LEU:HD13	2.03	0.41
22:B:229:PSC:H212	22:B:229:PSC:C02	2.50	0.41
22:B:229:PSC:H071	5:E:8:ASP:HA	2.02	0.41
4:D:9:GLU:CD	4:D:9:GLU:H	2.24	0.41
5:R:11:PHE:HB3	22:R:1229:PSC:H073	2.02	0.41
7:T:62:TRP:HB3	26:T:1272:DMU:H29	2.01	0.41
14:A:515:HEA:HHC	14:A:515:HEA:H11	1.83	0.40
2:B:104:TRP:CD2	2:B:203:ASN:HB2	2.55	0.40
2:B:191:LEU:HA	2:B:211:LEU:O	2.21	0.40
23:C:525:CHD:H12A	23:C:525:CHD:H112	1.52	0.40
5:E:90:ARG:NH2	29:E:4208:HOH:O	2.54	0.40
2:O:193:TYR:CD1	2:O:210:VAL:HG22	2.56	0.40
25:T:1269:CDL:H821	25:T:1269:CDL:H791	1.70	0.40
8:U:78:GLU:HG2	8:U:80:THR:HG23	2.04	0.40
1:A:183:LEU:HD23	1:A:183:LEU:HA	1.98	0.40
20:A:524:PGV:H202	20:A:524:PGV:H231	1.95	0.40
5:E:108:LYS:O	5:E:108:LYS:HG2	2.20	0.40
9:I:21:ILE:HD13	9:I:21:ILE:HA	1.96	0.40
14:N:516:HEA:HHA	14:N:516:HEA:HAD2	1.83	0.40
23:P:1271:CHD:C16	23:P:1271:CHD:C23	2.96	0.40
22:R:1229:PSC:H063	22:R:1229:PSC:H042	1.84	0.40
2:B:135:LEU:O	2:B:208:PRO:HG3	2.22	0.40
2:B:164:ALA:O	2:B:194:GLY:HA3	2.20	0.40
11:K:31:TYR:CD2	11:K:35:GLN:HG3	2.56	0.40
1:N:32:ALA:HB3	12:Y:36:PRO:HG2	2.03	0.40
2:O:189:PRO:HD2	9:V:54:TYR:OH	2.21	0.40
4:Q:93:ALA:O	4:Q:97:ILE:HG13	2.20	0.40
8:U:9:LYS:O	8:U:10:ASN:CB	2.68	0.40
1:A:449:MET:SD	2:B:5:MET:HG2	2.61	0.40
2:B:74:ILE:HD11	25:T:1269:CDL:H461	2.04	0.40
4:D:109:HIS:HD2	29:D:2122:HOH:O	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:1523:TGL:HC22	19:N:1523:TGL:HC51	1.88	0.40
4:D:34:SER:O	4:D:38:LYS:HG3	2.21	0.40
19:N:1522:TGL:HA51	12:Y:25:MET:HG2	2.02	0.40
7:T:8:HIS:ND1	28:T:263:PEK:H321	2.37	0.40
25:T:1269:CDL:OA7	25:T:1269:CDL:H342	2.22	0.40
9:V:52:ARG:CZ	9:V:52:ARG:HB2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	512/514 (100%)	500 (98%)	12 (2%)	0	100	100
1	N	512/514 (100%)	495 (97%)	17 (3%)	0	100	100
2	B	225/227 (99%)	213 (95%)	11 (5%)	1 (0%)	34	37
2	O	225/227 (99%)	212 (94%)	12 (5%)	1 (0%)	34	37
3	C	257/261 (98%)	253 (98%)	3 (1%)	1 (0%)	34	37
3	P	257/261 (98%)	252 (98%)	4 (2%)	1 (0%)	34	37
4	D	142/147 (97%)	139 (98%)	3 (2%)	0	100	100
4	Q	142/147 (97%)	132 (93%)	9 (6%)	1 (1%)	22	22
5	E	103/109 (94%)	103 (100%)	0	0	100	100
5	R	103/109 (94%)	102 (99%)	1 (1%)	0	100	100
6	F	96/98 (98%)	88 (92%)	5 (5%)	3 (3%)	4	2
6	S	96/98 (98%)	91 (95%)	3 (3%)	2 (2%)	7	4
7	G	81/85 (95%)	67 (83%)	9 (11%)	5 (6%)	1	0
7	T	81/85 (95%)	65 (80%)	11 (14%)	5 (6%)	1	0
8	H	77/85 (91%)	66 (86%)	5 (6%)	6 (8%)	1	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	U	77/85 (91%)	69 (90%)	4 (5%)	4 (5%)	2	0
9	I	71/73 (97%)	63 (89%)	6 (8%)	2 (3%)	5	2
9	V	71/73 (97%)	64 (90%)	4 (6%)	3 (4%)	3	1
10	J	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
10	W	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
11	K	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
11	X	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
12	L	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
12	Y	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
13	M	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
13	Z	41/46 (89%)	39 (95%)	1 (2%)	1 (2%)	6	3
All	All	3504/3614 (97%)	3339 (95%)	129 (4%)	36 (1%)	15	14

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	94	HIS
7	G	3	ALA
7	G	4	ALA
7	G	7	ASP
7	G	8	HIS
8	H	8	ILE
8	H	46	LYS
6	S	94	HIS
7	T	4	ALA
7	T	8	HIS
8	U	8	ILE
8	U	45	ALA
2	B	60	GLU
3	C	38	ASN
8	H	47	GLY
9	I	27	VAL
9	I	33	THR
2	O	60	GLU
3	P	38	ASN
7	T	3	ALA
7	T	40	GLY
6	F	95	GLN

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Mol	Chain	Res	Type
8	H	10	ASN
8	H	45	ALA
7	T	39	SER
8	U	46	LYS
6	F	96	LEU
8	H	9	LYS
8	U	9	LYS
9	V	28	SER
9	V	33	THR
9	V	37	PHE
4	Q	142	LYS
6	S	95	GLN
13	Z	41	LYS
7	G	6	GLY

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	426/426 (100%)	416 (98%)	10 (2%)	50	63
1	N	426/426 (100%)	414 (97%)	12 (3%)	43	56
2	B	210/210 (100%)	199 (95%)	11 (5%)	23	28
2	O	210/210 (100%)	191 (91%)	19 (9%)	9	9
3	C	224/226 (99%)	216 (96%)	8 (4%)	35	45
3	P	224/226 (99%)	220 (98%)	4 (2%)	59	72
4	D	128/129 (99%)	122 (95%)	6 (5%)	26	33
4	Q	128/129 (99%)	121 (94%)	7 (6%)	21	26
5	E	92/95 (97%)	89 (97%)	3 (3%)	38	49
5	R	92/95 (97%)	84 (91%)	8 (9%)	10	10
6	F	81/81 (100%)	76 (94%)	5 (6%)	18	21
6	S	81/81 (100%)	75 (93%)	6 (7%)	13	14
7	G	67/68 (98%)	60 (90%)	7 (10%)	7	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	T	67/68 (98%)	59 (88%)	8 (12%)	5	4
8	H	71/75 (95%)	66 (93%)	5 (7%)	15	16
8	U	71/75 (95%)	64 (90%)	7 (10%)	8	7
9	I	57/57 (100%)	50 (88%)	7 (12%)	4	4
9	V	57/57 (100%)	48 (84%)	9 (16%)	2	2
10	J	49/50 (98%)	48 (98%)	1 (2%)	55	69
10	W	49/50 (98%)	43 (88%)	6 (12%)	5	4
11	K	39/46 (85%)	36 (92%)	3 (8%)	13	13
11	X	39/46 (85%)	36 (92%)	3 (8%)	13	13
12	L	39/40 (98%)	37 (95%)	2 (5%)	24	29
12	Y	39/40 (98%)	36 (92%)	3 (8%)	13	13
13	M	37/38 (97%)	32 (86%)	5 (14%)	4	3
13	Z	37/38 (97%)	33 (89%)	4 (11%)	6	6
All	All	3040/3082 (99%)	2871 (94%)	169 (6%)	21	25

All (169) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ARG
1	A	51	ASP
1	A	109	PHE
1	A	241	PRO
1	A	264	LYS
1	A	312	ILE
1	A	362	SER
1	A	363	LEU
1	A	369	ASP
1	A	513	LEU
2	B	60	GLU
2	B	64	ILE
2	B	65	TRP
2	B	66	THR
2	B	75	LEU
2	B	78	LEU
2	B	91	ASN
2	B	110	TYR
2	B	113	TYR

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Mol	Chain	Res	Type
2	B	171	LYS
2	B	179	LEU
3	C	17	PRO
3	C	23	SER
3	C	33	MET
3	C	77	LYS
3	C	127	LEU
3	C	159	MET
3	C	179	SER
3	C	214	PHE
4	D	4	SER
4	D	7	LYS
4	D	36	SER
4	D	51	LEU
4	D	53	ILE
4	D	143	ASN
5	E	5	HIS
5	E	7	THR
5	E	70	VAL
6	F	48	LEU
6	F	84	SER
6	F	87	THR
6	F	95	GLN
6	F	96	LEU
7	G	8	HIS
7	G	18	PHE
7	G	33	LEU
7	G	35	SER
7	G	36	TRP
7	G	54	ARG
7	G	84	LYS
8	H	7	LYS
8	H	9	LYS
8	H	51	SER
8	H	60	TYR
8	H	61	LYS
9	I	8	GLN
9	I	15	ARG
9	I	18	ARG
9	I	26	MET
9	I	31	PHE
9	I	33	THR

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Mol	Chain	Res	Type
9	I	37	PHE
10	J	50	LEU
11	K	32	MET
11	K	47	ARG
11	K	54	ARG
12	L	26	THR
12	L	46	LYS
13	M	13	LYS
13	M	34	LEU
13	M	38	ASP
13	M	42	LYS
13	M	43	SER
1	N	38	ARG
1	N	65	MET
1	N	109	PHE
1	N	112	LEU
1	N	265	LYS
1	N	338	MET
1	N	362	SER
1	N	363	LEU
1	N	369	ASP
1	N	483	LEU
1	N	486	ASP
1	N	513	LEU
2	O	16	ILE
2	O	33	LEU
2	O	60	GLU
2	O	65	TRP
2	O	66	THR
2	O	75	LEU
2	O	78	LEU
2	O	88	ASP
2	O	94	SER
2	O	107	SER
2	O	110	TYR
2	O	113	TYR
2	O	148	MET
2	O	167	SER
2	O	171	LYS
2	O	183	THR
2	O	202	SER
2	O	217	LYS

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Mol	Chain	Res	Type
2	O	226	MET
3	P	77	LYS
3	P	127	LEU
3	P	159	MET
3	P	214	PHE
4	Q	5	VAL
4	Q	6	VAL
4	Q	19	ARG
4	Q	34	SER
4	Q	51	LEU
4	Q	53	ILE
4	Q	143	ASN
5	R	5	HIS
5	R	21	LYS
5	R	70	VAL
5	R	79	LYS
5	R	80	GLU
5	R	90	ARG
5	R	108	LYS
5	R	109	VAL
6	S	37	LYS
6	S	48	LEU
6	S	53	THR
6	S	54	ASN
6	S	78	GLU
6	S	87	THR
7	T	33	LEU
7	T	35	SER
7	T	38	HIS
7	T	43	GLU
7	T	48	ILE
7	T	54	ARG
7	T	74	ARG
7	T	84	LYS
8	U	8	ILE
8	U	9	LYS
8	U	27	ARG
8	U	52	VAL
8	U	60	TYR
8	U	61	LYS
8	U	70	SER
9	V	2	THR

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Mol	Chain	Res	Type
9	V	8	GLN
9	V	18	ARG
9	V	21	ILE
9	V	25	PHE
9	V	31	PHE
9	V	52	ARG
9	V	65	LYS
9	V	73	LYS
10	W	10	LYS
10	W	15	ASP
10	W	27	THR
10	W	29	ASN
10	W	50	LEU
10	W	58	LYS
11	X	32	MET
11	X	47	ARG
11	X	54	ARG
12	Y	16	GLU
12	Y	20	ARG
12	Y	26	THR
13	Z	13	LYS
13	Z	34	LEU
13	Z	38	ASP
13	Z	42	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	178	GLN
1	A	180	GLN
1	A	512	ASN
2	B	10	GLN
2	B	52	HIS
2	B	181	GLN
3	C	50	ASN
3	C	68	GLN
3	C	70	HIS
3	C	149	HIS
4	D	37	GLN
5	E	94	ASN
7	G	76	ASN
10	J	57	HIS

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Mol	Chain	Res	Type
12	L	2	HIS
13	M	15	GLN
1	N	178	GLN
1	N	180	GLN
1	N	512	ASN
2	O	10	GLN
2	O	91	ASN
2	O	181	GLN
3	P	50	ASN
3	P	68	GLN
3	P	161	GLN
4	Q	37	GLN
4	Q	101	HIS
5	R	94	ASN
7	T	76	ASN
8	U	22	ASN
9	V	8	GLN
10	W	29	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	$\#\|Z\| > 2$
1	FME	A	1	1	8,9,10	0.80	0	7,9,11	5.34	3 (42%)
2	FME	B	1	2	8,9,10	1.40	1 (12%)	7,9,11	6.53	3 (42%)
9	SAC	I	1	9	7,8,9	3.80	2 (28%)	8,9,11	5.05	4 (50%)
7	TPO	T	11	7	8,10,11	2.60	5 (62%)	10,14,16	2.20	3 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
9	SAC	V	1	9	7,8,9	3.80	3 (42%)	8,9,11	3.63	5 (62%)
7	TPO	G	11	7	8,10,11	2.47	5 (62%)	10,14,16	2.14	3 (30%)
1	FME	N	1	1	8,9,10	0.92	0	7,9,11	4.46	3 (42%)
2	FME	O	1	2	8,9,10	0.92	0	7,9,11	4.00	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
1	FME	A	1	1	-	3/7/9/11	-
2	FME	B	1	2	-	1/7/9/11	-
9	SAC	I	1	9	-	3/7/8/10	-
7	TPO	T	11	7	-	3/9/11/13	-
9	SAC	V	1	9	-	3/7/8/10	-
7	TPO	G	11	7	-	3/9/11/13	-
1	FME	N	1	1	-	4/7/9/11	-
2	FME	O	1	2	-	1/7/9/11	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	V	1	SAC	CA-N	7.65	1.57	1.46
9	I	1	SAC	CA-N	7.03	1.56	1.46
9	I	1	SAC	OAC-C1A	6.45	1.37	1.23
9	V	1	SAC	OAC-C1A	5.49	1.35	1.23
7	T	11	TPO	P-OG1	4.26	1.67	1.59
7	G	11	TPO	P-O1P	3.86	1.63	1.50
7	T	11	TPO	P-O1P	3.65	1.62	1.50
7	G	11	TPO	P-OG1	3.42	1.65	1.59
2	B	1	FME	O1-CN	-3.35	1.12	1.22
7	G	11	TPO	CG2-CB	2.51	1.57	1.51
9	V	1	SAC	CB-CA	2.47	1.58	1.53
7	T	11	TPO	P-O3P	2.41	1.64	1.54
7	T	11	TPO	CG2-CB	2.35	1.57	1.51
7	T	11	TPO	O-C	2.27	1.29	1.19
7	G	11	TPO	O-C	2.20	1.28	1.19
7	G	11	TPO	P-O2P	2.13	1.63	1.54

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	FME	CA-N-CN	-16.81	96.98	122.82
1	A	1	FME	CA-N-CN	-12.33	103.86	122.82
1	N	1	FME	CA-N-CN	-10.28	107.00	122.82
9	I	1	SAC	C-CA-N	9.43	126.74	109.73
2	O	1	FME	CA-N-CN	-9.32	108.49	122.82
9	V	1	SAC	CA-N-C1A	7.98	137.86	123.15
9	I	1	SAC	CB-CA-N	-7.47	93.78	110.55
9	I	1	SAC	CA-N-C1A	6.90	135.88	123.15
1	A	1	FME	CE-SD-CG	5.59	119.60	100.40
7	G	11	TPO	CG2-CB-CA	5.57	124.15	113.16
1	N	1	FME	CE-SD-CG	4.90	117.22	100.40
7	T	11	TPO	CG2-CB-CA	4.86	122.75	113.16
9	V	1	SAC	C2A-C1A-N	4.20	123.22	116.10
9	V	1	SAC	C-CA-N	3.01	115.16	109.73
1	A	1	FME	CG-CB-CA	-2.92	104.84	112.95
7	T	11	TPO	O-C-CA	-2.83	117.37	124.78
9	V	1	SAC	OAC-C1A-C2A	-2.72	117.01	122.06
2	O	1	FME	O1-CN-N	-2.70	118.17	125.27
2	B	1	FME	O-C-CA	-2.59	118.00	124.78
7	T	11	TPO	O3P-P-OG1	2.54	117.38	105.99
2	O	1	FME	C-CA-N	2.52	114.28	109.73
7	G	11	TPO	O2P-P-OG1	2.50	117.21	105.99
2	O	1	FME	O-C-CA	-2.28	118.80	124.78
7	G	11	TPO	O-C-CA	-2.25	118.88	124.78
9	I	1	SAC	OAC-C1A-N	2.25	126.08	121.95
2	B	1	FME	O1-CN-N	-2.24	119.36	125.27
9	V	1	SAC	OG-CB-CA	2.12	116.38	110.97
1	N	1	FME	O1-CN-N	2.04	130.63	125.27

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	O1-CN-N-CA
1	A	1	FME	N-CA-CB-CG
2	B	1	FME	O1-CN-N-CA
7	G	11	TPO	N-CA-CB-CG2
7	G	11	TPO	N-CA-CB-OG1
7	G	11	TPO	C-CA-CB-CG2
9	I	1	SAC	C-CA-N-C1A
9	I	1	SAC	O-C-CA-CB

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Mol	Chain	Res	Type	Atoms
1	N	1	FME	O1-CN-N-CA
1	N	1	FME	N-CA-CB-CG
2	O	1	FME	O1-CN-N-CA
7	T	11	TPO	N-CA-CB-CG2
7	T	11	TPO	N-CA-CB-OG1
7	T	11	TPO	C-CA-CB-CG2
9	V	1	SAC	C2A-C1A-N-CA
9	V	1	SAC	OAC-C1A-N-CA
1	N	1	FME	CB-CG-SD-CE
1	A	1	FME	C-CA-CB-CG
1	N	1	FME	C-CA-CB-CG
9	I	1	SAC	N-CA-CB-OG
9	V	1	SAC	C-CA-N-C1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	FME	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 56 ligands modelled in this entry, 8 are monoatomic and 2 are unknown - leaving 46 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	$\#\|Z\| > 2$
19	TGL	N	1521	-	62,62,62	1.43	9 (14%)	65,65,65	2.20	15 (23%)
23	CHD	C	525	-	32,32,32	1.42	4 (12%)	51,51,51	5.00	39 (76%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
19	TGL	N	1522	-	62,62,62	1.65	7 (11%)	65,65,65	1.79	16 (24%)
23	CHD	P	1525	-	32,32,32	1.08	2 (6%)	51,51,51	5.40	38 (74%)
19	TGL	A	523	-	62,62,62	1.43	6 (9%)	65,65,65	1.69	12 (18%)
25	CDL	G	269	-	99,99,99	1.46	13 (13%)	105,111,111	1.43	17 (16%)
20	PGV	C	268	-	50,50,50	1.47	3 (6%)	53,56,56	1.70	7 (13%)
23	CHD	P	1271	-	32,32,32	0.88	1 (3%)	51,51,51	5.18	35 (68%)
23	CHD	B	1085	-	32,32,32	1.59	4 (12%)	51,51,51	5.54	37 (72%)
14	HEA	N	515	1	57,67,67	1.69	15 (26%)	61,103,103	2.00	19 (31%)
26	DMU	T	1272	-	34,34,34	1.37	3 (8%)	45,45,45	3.12	22 (48%)
20	PGV	C	267	-	50,50,50	0.90	2 (4%)	53,56,56	1.20	5 (9%)
26	DMU	Z	1526	-	34,34,34	1.01	3 (8%)	45,45,45	3.11	21 (46%)
14	HEA	A	515	1	57,67,67	1.67	11 (19%)	61,103,103	2.51	20 (32%)
25	CDL	T	1269	-	99,99,99	1.52	13 (13%)	105,111,111	1.49	13 (12%)
22	PSC	R	1229	-	51,51,51	1.36	3 (5%)	57,59,59	1.26	5 (8%)
28	PEK	S	1265	-	52,52,52	1.29	3 (5%)	55,57,57	1.31	5 (9%)
20	PGV	P	1268	-	50,50,50	1.43	2 (4%)	53,56,56	1.60	8 (15%)
23	CHD	J	60	-	32,32,32	1.10	2 (6%)	51,51,51	5.30	37 (72%)
19	TGL	N	1523	-	62,62,62	1.45	7 (11%)	65,65,65	1.43	10 (15%)
28	PEK	G	1263	-	52,52,52	1.41	6 (11%)	55,57,57	1.48	7 (12%)
23	CHD	C	271	-	32,32,32	0.92	3 (9%)	51,51,51	5.00	34 (66%)
25	CDL	P	1270	-	99,99,99	1.47	13 (13%)	105,111,111	1.42	12 (11%)
20	PGV	A	521	-	50,50,50	0.82	2 (4%)	53,56,56	1.73	7 (13%)
25	CDL	C	270	-	99,99,99	1.45	15 (15%)	105,111,111	1.46	15 (14%)
20	PGV	N	1524	-	50,50,50	1.26	2 (4%)	53,56,56	1.21	6 (11%)
23	CHD	W	1059	-	32,32,32	0.78	1 (3%)	51,51,51	5.06	34 (66%)
14	HEA	A	516	1	57,67,67	1.61	11 (19%)	61,103,103	2.42	23 (37%)
20	PGV	N	1266	-	50,50,50	0.85	3 (6%)	53,56,56	1.37	5 (9%)
21	CUA	B	228	2	0,1,1	-	-	-		
23	CHD	O	229	-	32,32,32	1.51	6 (18%)	51,51,51	5.47	37 (72%)
19	TGL	L	522	-	62,62,62	1.72	9 (14%)	65,65,65	1.99	16 (24%)
22	PSC	B	229	-	51,51,51	1.40	3 (5%)	57,59,59	1.29	7 (12%)
28	PEK	T	1264	-	52,52,52	0.90	4 (7%)	55,57,57	1.44	9 (16%)
15	CMO	A	520	-	0,1,1	-	-	-		
19	TGL	B	521	-	62,62,62	1.49	8 (12%)	65,65,65	2.47	18 (27%)
20	PGV	P	1267	-	50,50,50	1.02	2 (4%)	53,56,56	1.01	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
26	DMU	C	272	-	34,34,34	1.34	5 (14%)	45,45,45	3.33	21 (46%)
15	CMO	N	520	14	0,1,1	-	-	-		
20	PGV	A	524	-	50,50,50	1.33	3 (6%)	53,56,56	1.40	8 (15%)
14	HEA	N	516	15,1	57,67,67	1.68	12 (21%)	61,103,103	2.28	20 (32%)
28	PEK	G	265	-	52,52,52	1.62	6 (11%)	55,57,57	1.52	11 (20%)
28	PEK	G	264	-	52,52,52	1.04	5 (9%)	55,57,57	1.58	10 (18%)
26	DMU	M	526	-	34,34,34	1.28	2 (5%)	45,45,45	3.40	22 (48%)
21	CUA	O	228	2	0,1,1	-	-	-		
28	PEK	T	263	-	52,52,52	1.42	4 (7%)	55,57,57	1.20	5 (9%)

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
19	TGL	N	1521	-	-	36/65/65/65	-
23	CHD	C	525	-	-	1/9/74/74	0/4/4/4
19	TGL	N	1522	-	-	34/65/65/65	-
23	CHD	P	1525	-	-	4/9/74/74	0/4/4/4
19	TGL	A	523	-	-	34/65/65/65	-
25	CDL	G	269	-	-	59/110/110/110	-
20	PGV	C	268	-	-	30/55/55/55	-
23	CHD	P	1271	-	1/1/12/12	6/9/74/74	0/4/4/4
23	CHD	B	1085	-	1/1/12/12	2/9/74/74	0/4/4/4
14	HEA	N	515	1	-	4/32/76/76	-
26	DMU	T	1272	-	6/6/10/10	12/19/59/59	0/2/2/2
20	PGV	C	267	-	-	13/55/55/55	-
26	DMU	Z	1526	-	5/5/10/10	10/19/59/59	0/2/2/2
14	HEA	A	515	1	-	4/32/76/76	-
25	CDL	T	1269	-	-	59/110/110/110	-
22	PSC	R	1229	-	-	28/55/55/55	-
28	PEK	S	1265	-	-	27/56/56/56	-
23	CHD	J	60	-	1/1/12/12	7/9/74/74	0/4/4/4
20	PGV	P	1268	-	-	36/55/55/55	-
19	TGL	N	1523	-	-	34/65/65/65	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	PEK	G	1263	-	-	32/56/56/56	-
23	CHD	C	271	-	1/1/12/12	7/9/74/74	0/4/4/4
25	CDL	P	1270	-	-	78/110/110/110	-
20	PGV	A	521	-	-	14/55/55/55	-
25	CDL	C	270	-	-	68/110/110/110	-
23	CHD	W	1059	-	2/2/12/12	6/9/74/74	0/4/4/4
20	PGV	N	1524	-	-	30/55/55/55	-
14	HEA	A	516	1	-	4/32/76/76	-
20	PGV	N	1266	-	-	14/55/55/55	-
23	CHD	O	229	-	1/1/12/12	5/9/74/74	0/4/4/4
19	TGL	L	522	-	-	42/65/65/65	-
22	PSC	B	229	-	-	32/55/55/55	-
28	PEK	T	1264	-	-	22/56/56/56	-
19	TGL	B	521	-	-	35/65/65/65	-
26	DMU	C	272	-	5/5/10/10	12/19/59/59	0/2/2/2
20	PGV	P	1267	-	-	15/55/55/55	-
20	PGV	A	524	-	-	33/55/55/55	-
14	HEA	N	516	15,1	-	6/32/76/76	-
28	PEK	G	265	-	-	24/56/56/56	-
28	PEK	G	264	-	-	23/56/56/56	-
26	DMU	M	526	-	5/5/10/10	8/19/59/59	0/2/2/2
28	PEK	T	263	-	-	26/56/56/56	-

All (238) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	L	522	TGL	OG2-CB1	7.64	1.55	1.34
19	N	1522	TGL	OG2-CB1	7.48	1.55	1.34
20	C	268	PGV	O01-C1	7.21	1.54	1.34
20	P	1268	PGV	O01-C1	7.10	1.54	1.34
28	G	1263	PEK	O03-C21	6.42	1.52	1.33
28	T	263	PEK	O03-C21	6.35	1.51	1.33
19	A	523	TGL	OG2-CB1	5.98	1.51	1.34
19	N	1523	TGL	OG2-CB1	5.95	1.51	1.34
20	A	524	PGV	O03-C19	5.76	1.50	1.33
22	B	229	PSC	O01-C1	5.59	1.50	1.34
25	G	269	CDL	OB6-CB5	5.58	1.50	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	L	522	TGL	OG1-CA1	5.48	1.49	1.33
25	T	1269	CDL	OB8-CB7	5.44	1.49	1.33
28	S	1265	PEK	O01-C1	5.38	1.49	1.34
28	T	263	PEK	O01-C1	5.37	1.49	1.34
28	G	265	PEK	O01-C1	5.35	1.49	1.34
25	T	1269	CDL	OA6-CA5	5.33	1.49	1.34
25	T	1269	CDL	OB6-CB5	5.33	1.49	1.34
25	C	270	CDL	OA6-CA5	5.32	1.49	1.34
19	L	522	TGL	OG3-CC1	5.32	1.48	1.33
25	P	1270	CDL	OA6-CA5	5.31	1.49	1.34
19	N	1522	TGL	OG3-CC1	5.30	1.48	1.33
26	T	1272	DMU	O16-C6	5.29	1.49	1.40
22	R	1229	PSC	O01-C1	5.26	1.49	1.34
25	G	269	CDL	OA6-CA5	5.25	1.49	1.34
19	N	1522	TGL	OG1-CA1	5.21	1.48	1.33
25	P	1270	CDL	OA8-CA7	5.20	1.48	1.33
20	N	1524	PGV	O03-C19	5.17	1.48	1.33
28	S	1265	PEK	O03-C21	5.15	1.48	1.33
19	N	1523	TGL	OG3-CC1	5.10	1.48	1.33
19	A	523	TGL	OG3-CC1	5.03	1.48	1.33
19	B	521	TGL	OG1-CA1	5.03	1.48	1.33
25	T	1269	CDL	OA8-CA7	5.02	1.48	1.33
19	N	1521	TGL	OG1-CA1	5.00	1.47	1.33
20	C	268	PGV	O03-C19	4.97	1.47	1.33
20	N	1524	PGV	O01-C1	4.97	1.48	1.34
23	C	525	CHD	C18-C13	4.94	1.62	1.54
28	G	1263	PEK	O01-C1	4.90	1.48	1.34
14	A	515	HEA	CHD-C1D	4.83	1.47	1.35
28	G	265	PEK	C17-C16	4.80	1.71	1.52
25	G	269	CDL	OB8-CB7	4.78	1.47	1.33
25	P	1270	CDL	OB6-CB5	4.76	1.47	1.34
19	B	521	TGL	OG2-CB1	4.73	1.47	1.34
25	P	1270	CDL	OB8-CB7	4.72	1.47	1.33
22	R	1229	PSC	O03-C19	4.72	1.47	1.33
26	C	272	DMU	O16-C6	4.68	1.48	1.40
19	B	521	TGL	OC1-CC1	-4.64	1.08	1.22
22	B	229	PSC	O03-C19	4.60	1.46	1.33
20	P	1268	PGV	O03-C19	4.49	1.46	1.33
19	N	1521	TGL	OG2-CB1	4.49	1.47	1.34
23	B	1085	CHD	C18-C13	4.45	1.61	1.54
25	G	269	CDL	OA8-CA7	4.41	1.46	1.33
25	C	270	CDL	OB8-CB7	4.40	1.46	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	A	524	PGV	O01-C1	4.39	1.46	1.34
14	A	516	HEA	CHC-C4B	4.32	1.46	1.35
25	C	270	CDL	OB6-CB5	4.32	1.46	1.34
28	G	265	PEK	C7-C6	4.27	1.81	1.51
19	A	523	TGL	OG1-CA1	4.27	1.45	1.33
19	N	1521	TGL	OG3-CC1	4.20	1.45	1.33
22	B	229	PSC	C13-C12	4.19	1.56	1.31
22	R	1229	PSC	C13-C12	4.18	1.56	1.31
19	N	1523	TGL	OG1-CA1	4.13	1.45	1.33
25	C	270	CDL	OA8-CA7	4.11	1.45	1.33
14	N	515	HEA	CHD-C1D	4.05	1.45	1.35
14	A	515	HEA	CHC-C4B	3.99	1.45	1.35
26	M	526	DMU	C3-C4	-3.98	1.42	1.52
20	P	1267	PGV	O03-C19	3.96	1.44	1.33
26	M	526	DMU	O16-C6	3.93	1.46	1.40
28	G	265	PEK	O03-C21	3.85	1.44	1.33
14	A	516	HEA	C1D-C2D	-3.77	1.37	1.44
23	O	229	CHD	C13-C14	-3.73	1.49	1.55
28	G	264	PEK	O01-C1	3.72	1.44	1.34
14	N	515	HEA	FE-ND	3.64	2.14	1.96
25	T	1269	CDL	C59-C58	-3.64	1.31	1.51
20	N	1266	PGV	O01-C1	3.61	1.44	1.34
14	N	516	HEA	C1D-ND	-3.59	1.34	1.40
14	A	516	HEA	C4B-C3B	-3.53	1.38	1.44
14	N	516	HEA	C4D-ND	-3.52	1.31	1.38
25	P	1270	CDL	C59-C58	-3.48	1.32	1.51
14	A	515	HEA	C13-C14	3.44	1.61	1.50
25	C	270	CDL	C40-C39	3.43	1.70	1.51
19	B	521	TGL	C10-CB9	-3.42	1.32	1.51
20	A	521	PGV	O03-C19	3.42	1.43	1.33
28	G	265	PEK	C6-C5	3.42	1.51	1.31
14	N	516	HEA	CHC-C4B	3.40	1.43	1.35
14	N	516	HEA	C3A-C2A	-3.40	1.35	1.40
14	A	516	HEA	CHD-C1D	3.38	1.43	1.35
28	T	1264	PEK	O01-C1	3.38	1.43	1.34
14	N	516	HEA	CHD-C1D	3.37	1.43	1.35
26	Z	1526	DMU	O16-C6	3.37	1.45	1.40
19	L	522	TGL	C20-CA9	-3.34	1.32	1.51
25	C	270	CDL	C59-C58	-3.33	1.32	1.51
25	G	269	CDL	C59-C58	-3.32	1.33	1.51
19	N	1521	TGL	C10-CB9	-3.30	1.33	1.51
25	T	1269	CDL	C62-C61	-3.29	1.33	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	B	521	TGL	OG3-CC1	3.27	1.42	1.33
14	A	515	HEA	CMB-C2B	3.27	1.57	1.50
20	P	1267	PGV	O01-C1	3.26	1.43	1.34
14	A	516	HEA	C3A-C2A	-3.24	1.35	1.40
14	N	515	HEA	C4B-C3B	-3.24	1.39	1.44
25	G	269	CDL	C62-C61	-3.22	1.33	1.51
14	N	515	HEA	C4B-NB	-3.20	1.34	1.40
14	N	516	HEA	C18-C19	3.18	1.40	1.33
25	T	1269	CDL	C42-C41	-3.18	1.33	1.51
19	N	1522	TGL	C20-CA9	-3.18	1.33	1.51
19	N	1522	TGL	C10-CB9	-3.16	1.33	1.51
19	N	1523	TGL	C10-CB9	-3.16	1.33	1.51
23	P	1271	CHD	C20-C17	3.15	1.59	1.54
20	C	267	PGV	O01-C1	3.10	1.43	1.34
25	P	1270	CDL	C62-C61	-3.10	1.34	1.51
25	T	1269	CDL	C19-C18	-3.07	1.34	1.51
25	P	1270	CDL	C79-C78	-3.04	1.34	1.51
14	N	515	HEA	C4D-C3D	-3.03	1.39	1.45
19	B	521	TGL	C20-CA9	-3.02	1.34	1.51
25	C	270	CDL	C62-C61	-3.02	1.34	1.51
25	C	270	CDL	C37-C36	2.98	1.68	1.51
28	G	264	PEK	O03-C01	-2.98	1.38	1.45
14	N	515	HEA	C1D-ND	-2.96	1.35	1.40
25	P	1270	CDL	C39-C38	-2.94	1.35	1.51
14	A	515	HEA	C4B-NB	-2.93	1.35	1.40
25	C	270	CDL	C82-C81	-2.93	1.35	1.51
25	P	1270	CDL	C22-C21	-2.92	1.35	1.51
14	A	515	HEA	C1D-ND	-2.92	1.35	1.40
19	A	523	TGL	C10-CB9	-2.91	1.35	1.51
26	C	272	DMU	O1-C10	2.91	1.49	1.41
25	C	270	CDL	C22-C21	-2.90	1.35	1.51
23	B	1085	CHD	C13-C14	-2.89	1.50	1.55
19	A	523	TGL	C20-CA9	-2.88	1.35	1.51
25	P	1270	CDL	C82-C81	-2.88	1.35	1.51
23	B	1085	CHD	C10-C5	-2.88	1.50	1.55
14	A	516	HEA	C1B-NB	-2.88	1.32	1.38
26	Z	1526	DMU	C3-C4	-2.87	1.45	1.52
19	N	1521	TGL	C20-CA9	-2.87	1.35	1.51
14	A	515	HEA	C20-C19	2.85	1.57	1.51
19	L	522	TGL	C10-CB9	-2.85	1.35	1.51
25	C	270	CDL	C19-C18	-2.84	1.35	1.51
25	T	1269	CDL	C39-C38	-2.84	1.35	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	J	60	CHD	C23-C24	2.83	1.57	1.50
14	N	516	HEA	C4B-NB	-2.82	1.35	1.40
25	P	1270	CDL	C19-C18	-2.81	1.35	1.51
23	B	1085	CHD	C4-C3	2.80	1.57	1.51
25	T	1269	CDL	C79-C78	-2.79	1.35	1.51
19	A	523	TGL	C15-CC9	-2.74	1.36	1.51
20	C	267	PGV	O03-C19	2.70	1.41	1.33
19	L	522	TGL	CC2-CC1	2.68	1.58	1.50
25	G	269	CDL	C79-C78	-2.67	1.36	1.51
19	N	1523	TGL	C20-CA9	-2.67	1.36	1.51
25	T	1269	CDL	C22-C21	-2.66	1.36	1.51
26	C	272	DMU	C8-C7	2.66	1.59	1.52
23	O	229	CHD	C4-C3	2.66	1.56	1.51
19	N	1523	TGL	C17-C16	2.65	1.66	1.51
20	N	1266	PGV	O03-C19	2.65	1.41	1.33
25	G	269	CDL	C22-C21	-2.65	1.36	1.51
14	N	515	HEA	C3C-C2C	-2.65	1.36	1.40
14	N	516	HEA	C1D-C2D	-2.63	1.39	1.44
28	G	1263	PEK	C01-C02	2.63	1.58	1.50
28	T	263	PEK	C01-C02	2.63	1.58	1.50
25	T	1269	CDL	C82-C81	-2.62	1.36	1.51
19	N	1521	TGL	C17-C16	2.61	1.66	1.51
14	N	515	HEA	CHA-C4D	2.59	1.48	1.41
28	T	1264	PEK	O01-C02	-2.59	1.40	1.46
25	P	1270	CDL	C42-C41	-2.58	1.37	1.51
14	A	516	HEA	C4D-C3D	-2.54	1.40	1.45
25	G	269	CDL	C19-C18	-2.54	1.37	1.51
28	G	264	PEK	O03-C21	2.54	1.40	1.33
14	N	515	HEA	CHC-C4B	2.54	1.41	1.35
23	P	1525	CHD	C13-C14	-2.53	1.51	1.55
25	G	269	CDL	C39-C38	-2.52	1.37	1.51
28	G	264	PEK	O01-C02	-2.51	1.40	1.46
14	A	516	HEA	C3D-C2D	2.51	1.42	1.36
28	T	1264	PEK	O03-C01	-2.50	1.39	1.45
19	L	522	TGL	C15-CC9	-2.49	1.37	1.51
19	N	1523	TGL	C15-CC9	-2.48	1.37	1.51
25	G	269	CDL	C82-C81	-2.48	1.37	1.51
14	N	516	HEA	O11-C11	2.47	1.48	1.42
14	N	516	HEA	C1B-C2B	-2.45	1.39	1.44
19	L	522	TGL	CG3-CG2	2.45	1.58	1.50
20	A	521	PGV	O03-C01	2.44	1.50	1.45
28	G	1263	PEK	P-O12	2.43	1.69	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	N	1521	TGL	OG1-CG1	-2.42	1.39	1.45
25	C	270	CDL	OB6-CB4	-2.41	1.40	1.46
14	N	516	HEA	C4B-C3B	-2.40	1.40	1.44
14	N	515	HEA	C3B-C2B	2.40	1.40	1.34
25	G	269	CDL	C42-C41	-2.38	1.38	1.51
14	N	516	HEA	C4D-C3D	-2.38	1.40	1.45
19	N	1522	TGL	C15-CC9	-2.38	1.38	1.51
14	N	515	HEA	C1B-C2B	-2.38	1.40	1.44
26	T	1272	DMU	O5-C6	2.36	1.47	1.41
14	N	515	HEA	CMD-C2D	2.36	1.55	1.50
19	N	1522	TGL	CG3-CG2	2.35	1.57	1.50
23	C	525	CHD	O26-C24	-2.34	1.22	1.30
23	O	229	CHD	C11-C9	2.33	1.57	1.53
19	N	1521	TGL	OC1-CC1	-2.32	1.15	1.22
14	A	515	HEA	O11-C11	2.32	1.47	1.42
25	C	270	CDL	CB2-C1	2.31	1.59	1.51
23	C	271	CHD	C10-C9	-2.29	1.51	1.56
14	A	515	HEA	C3A-C2A	2.29	1.43	1.40
20	A	524	PGV	P-O11	2.27	1.68	1.59
25	C	270	CDL	PB2-OB2	2.27	1.68	1.59
28	G	265	PEK	P-O12	2.27	1.68	1.59
28	T	263	PEK	C03-C02	2.26	1.57	1.50
26	T	1272	DMU	O1-C10	2.24	1.47	1.41
23	P	1525	CHD	C11-C9	2.23	1.57	1.53
23	C	525	CHD	C19-C10	2.22	1.58	1.54
25	P	1270	CDL	CB2-C1	2.21	1.59	1.51
19	B	521	TGL	OG1-CG1	-2.21	1.40	1.45
19	B	521	TGL	C15-CC9	-2.21	1.39	1.51
14	A	516	HEA	C14-C15	2.19	1.38	1.33
14	A	516	HEA	C22-C23	2.19	1.38	1.32
28	T	1264	PEK	O03-C21	2.17	1.39	1.33
14	A	515	HEA	C4D-C3D	-2.16	1.41	1.45
23	C	271	CHD	O26-C24	-2.15	1.23	1.30
19	N	1521	TGL	C18-C17	2.15	1.63	1.51
23	J	60	CHD	C20-C17	2.14	1.58	1.54
20	C	268	PGV	P-O11	2.13	1.67	1.59
14	N	515	HEA	C4C-CHD	2.13	1.46	1.41
14	A	516	HEA	O2D-CGD	-2.12	1.23	1.30
26	C	272	DMU	O5-C6	2.10	1.47	1.41
23	O	229	CHD	C13-C17	-2.09	1.51	1.55
14	N	515	HEA	C3D-C2D	2.09	1.41	1.36
26	C	272	DMU	C3-C4	-2.08	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	L	522	TGL	OG2-CG2	2.08	1.51	1.46
28	S	1265	PEK	P-O12	2.08	1.67	1.59
25	G	269	CDL	CB3-CB4	2.08	1.57	1.50
23	O	229	CHD	C21-C20	2.08	1.58	1.53
28	G	1263	PEK	P-O11	2.07	1.67	1.59
23	W	1059	CHD	C23-C24	2.06	1.55	1.50
25	T	1269	CDL	CB3-CB4	2.06	1.57	1.50
14	N	515	HEA	C3C-CAC	2.05	1.52	1.47
23	C	271	CHD	C20-C17	2.05	1.58	1.54
23	O	229	CHD	C8-C14	-2.05	1.49	1.53
23	C	525	CHD	C13-C14	-2.05	1.52	1.55
20	N	1266	PGV	O01-C02	-2.04	1.41	1.46
26	Z	1526	DMU	O1-C10	2.04	1.47	1.41
28	G	264	PEK	C2-C1	2.04	1.56	1.50
28	G	1263	PEK	C03-C02	2.02	1.56	1.50
14	A	515	HEA	CBD-CGD	2.01	1.55	1.50
25	C	270	CDL	C80-C79	2.00	1.62	1.51

All (711) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	P	1525	CHD	C6-C5-C10	14.76	128.34	112.66
23	J	60	CHD	C10-C9-C8	13.98	126.83	111.82
23	C	271	CHD	C10-C9-C8	13.67	126.50	111.82
23	B	1085	CHD	C6-C5-C10	13.41	126.90	112.66
23	P	1271	CHD	C10-C9-C8	12.93	125.70	111.82
23	W	1059	CHD	C10-C9-C8	12.90	125.67	111.82
23	P	1525	CHD	C1-C10-C5	12.59	126.39	107.77
23	P	1525	CHD	C4-C3-C2	12.16	125.07	110.55
23	O	229	CHD	C6-C5-C10	12.02	125.42	112.66
23	O	229	CHD	C14-C13-C12	11.90	118.48	107.40
23	O	229	CHD	C1-C10-C5	11.65	125.00	107.77
23	B	1085	CHD	C18-C13-C12	-11.54	97.32	109.07
23	O	229	CHD	C18-C13-C12	-11.54	97.32	109.07
23	C	525	CHD	C10-C9-C8	10.77	123.39	111.82
23	B	1085	CHD	C1-C10-C5	10.75	123.67	107.77
23	O	229	CHD	C19-C10-C9	-10.55	96.65	111.18
23	B	1085	CHD	C14-C13-C12	10.50	117.17	107.40
23	C	525	CHD	C6-C5-C10	10.36	123.66	112.66
23	B	1085	CHD	C10-C9-C8	10.16	122.73	111.82
23	C	525	CHD	C1-C10-C5	9.99	122.55	107.77
23	J	60	CHD	C18-C13-C12	-9.82	99.07	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	O	229	CHD	C10-C9-C8	9.81	122.36	111.82
23	P	1525	CHD	C19-C10-C9	-9.47	98.13	111.18
23	C	271	CHD	C1-C2-C3	9.46	122.61	110.47
23	B	1085	CHD	C5-C4-C3	9.33	126.46	112.76
23	P	1525	CHD	C17-C13-C12	9.31	126.16	117.67
23	P	1271	CHD	C6-C7-C8	9.28	121.39	111.48
23	J	60	CHD	C17-C13-C12	9.07	125.94	117.67
19	N	1521	TGL	CG2-OG2-CB1	8.96	139.85	117.79
23	J	60	CHD	C6-C7-C8	8.96	121.04	111.48
23	C	525	CHD	O12-C12-C13	-8.93	95.93	111.03
23	B	1085	CHD	C17-C13-C14	8.86	109.03	100.09
23	O	229	CHD	C17-C13-C12	8.81	125.71	117.67
19	B	521	TGL	CG2-OG2-CB1	8.81	139.47	117.79
23	C	525	CHD	C14-C13-C12	8.66	115.47	107.40
23	J	60	CHD	C6-C5-C10	8.63	121.83	112.66
23	P	1271	CHD	C16-C17-C20	8.63	125.50	112.15
23	P	1525	CHD	C14-C13-C12	8.59	115.40	107.40
23	J	60	CHD	C13-C17-C20	8.57	129.73	119.50
23	W	1059	CHD	C6-C7-C8	8.50	120.55	111.48
23	B	1085	CHD	C1-C2-C3	8.35	121.19	110.47
23	P	1271	CHD	C18-C13-C12	-8.33	100.58	109.07
23	W	1059	CHD	C4-C3-C2	8.32	120.49	110.55
23	C	271	CHD	C4-C5-C10	8.31	121.48	112.66
23	C	525	CHD	C18-C13-C12	-8.31	100.61	109.07
23	C	525	CHD	C4-C3-C2	8.30	120.46	110.55
23	O	229	CHD	C15-C14-C13	8.17	111.56	103.55
14	N	515	HEA	C13-C12-C11	-8.13	102.14	114.35
23	C	271	CHD	C15-C14-C8	8.09	129.65	118.33
23	P	1271	CHD	C14-C13-C12	8.03	114.88	107.40
23	W	1059	CHD	C13-C17-C20	7.97	129.01	119.50
26	M	526	DMU	O1-C9-C8	7.94	124.12	109.69
19	A	523	TGL	OG2-CB1-CB2	7.93	128.60	111.50
23	C	271	CHD	C6-C7-C8	7.93	119.95	111.48
23	P	1525	CHD	C10-C9-C8	7.90	120.30	111.82
23	W	1059	CHD	C6-C5-C4	-7.89	102.11	111.19
23	P	1525	CHD	C15-C14-C13	7.82	111.22	103.55
23	P	1271	CHD	C17-C13-C12	7.73	124.72	117.67
26	C	272	DMU	O16-C6-C1	7.73	120.36	108.30
23	B	1085	CHD	C17-C13-C12	7.71	124.70	117.67
23	O	229	CHD	C4-C3-C2	7.67	119.71	110.55
26	C	272	DMU	O1-C10-C5	7.61	126.45	110.35
23	B	1085	CHD	C16-C17-C20	7.59	123.90	112.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	J	60	CHD	C1-C10-C5	7.56	118.95	107.77
23	C	271	CHD	C6-C5-C10	7.52	120.65	112.66
23	J	60	CHD	C5-C4-C3	7.52	123.80	112.76
23	W	1059	CHD	C1-C10-C5	7.50	118.86	107.77
23	P	1525	CHD	C18-C13-C14	-7.40	99.63	111.21
23	W	1059	CHD	C1-C10-C9	-7.34	99.81	111.35
23	C	525	CHD	C11-C12-C13	7.34	118.78	111.24
19	N	1521	TGL	OG2-CB1-CB2	7.32	127.27	111.50
23	W	1059	CHD	C16-C17-C13	7.31	110.73	103.55
23	C	271	CHD	C16-C17-C20	7.29	123.43	112.15
23	C	271	CHD	C16-C17-C13	7.25	110.67	103.55
23	J	60	CHD	C6-C5-C4	-7.23	102.86	111.19
23	P	1271	CHD	C1-C2-C3	7.19	119.69	110.47
23	P	1271	CHD	C4-C3-C2	7.17	119.11	110.55
23	P	1525	CHD	C11-C12-C13	7.11	118.54	111.24
23	P	1271	CHD	C15-C14-C8	7.05	128.19	118.33
23	P	1271	CHD	C18-C13-C17	-7.04	100.20	111.21
14	N	516	HEA	CHB-C1B-NB	7.02	132.06	124.43
23	W	1059	CHD	C15-C14-C13	7.01	110.43	103.55
19	B	521	TGL	CG3-OG3-CC1	7.01	143.07	117.12
25	P	1270	CDL	OA6-CA5-C11	7.01	126.60	111.50
23	P	1271	CHD	C4-C5-C10	6.99	120.08	112.66
23	B	1085	CHD	C6-C5-C4	-6.97	103.17	111.19
23	C	271	CHD	C18-C13-C12	-6.96	101.98	109.07
23	W	1059	CHD	C6-C5-C10	6.92	120.01	112.66
23	O	229	CHD	C6-C5-C4	-6.92	103.23	111.19
23	P	1271	CHD	C11-C9-C8	6.91	121.00	110.88
26	T	1272	DMU	O1-C10-C5	6.91	124.98	110.35
23	C	525	CHD	C19-C10-C9	-6.90	101.68	111.18
23	J	60	CHD	C11-C12-C13	6.87	118.30	111.24
23	B	1085	CHD	C19-C10-C9	-6.84	101.75	111.18
23	C	525	CHD	C17-C13-C12	6.81	123.88	117.67
23	C	271	CHD	C11-C12-C13	6.80	118.23	111.24
23	W	1059	CHD	C14-C13-C12	6.77	113.71	107.40
23	C	271	CHD	C19-C10-C9	-6.77	101.86	111.18
23	O	229	CHD	O12-C12-C13	-6.72	99.67	111.03
26	M	526	DMU	O1-C10-C5	6.69	124.51	110.35
23	O	229	CHD	C16-C17-C20	6.69	122.50	112.15
23	O	229	CHD	C5-C4-C3	6.68	122.58	112.76
23	O	229	CHD	C18-C13-C17	-6.66	100.79	111.21
26	T	1272	DMU	O1-C9-C8	6.65	121.78	109.69
26	Z	1526	DMU	O1-C9-C8	6.63	121.73	109.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	J	60	CHD	C4-C3-C2	6.63	118.47	110.55
23	C	271	CHD	C15-C14-C13	6.62	110.04	103.55
20	C	268	PGV	O01-C1-C2	6.58	125.68	111.50
20	A	521	PGV	O03-C19-O04	-6.53	107.10	123.59
26	M	526	DMU	O16-C6-C1	6.52	118.48	108.30
23	C	271	CHD	C5-C6-C7	6.51	121.65	114.46
23	W	1059	CHD	C5-C4-C3	6.51	122.32	112.76
23	B	1085	CHD	O12-C12-C13	-6.49	100.05	111.03
23	B	1085	CHD	C18-C13-C14	-6.47	101.08	111.21
26	Z	1526	DMU	O1-C10-C5	6.46	124.03	110.35
23	P	1271	CHD	C5-C6-C7	6.46	121.59	114.46
23	P	1525	CHD	C6-C7-C8	6.42	118.33	111.48
26	M	526	DMU	O5-C4-C57	6.41	122.39	106.44
23	C	271	CHD	C11-C9-C8	6.41	120.25	110.88
25	C	270	CDL	OA6-CA5-C11	6.40	125.29	111.50
26	Z	1526	DMU	O5-C4-C3	6.38	123.20	109.75
25	T	1269	CDL	OB6-CB5-C51	6.36	125.21	111.50
26	Z	1526	DMU	O16-C6-C1	6.31	118.15	108.30
23	P	1271	CHD	C1-C10-C5	6.30	117.09	107.77
26	C	272	DMU	O5-C4-C57	6.29	122.08	106.44
23	W	1059	CHD	C14-C8-C7	6.27	120.13	111.81
23	J	60	CHD	C14-C13-C12	6.22	113.20	107.40
23	W	1059	CHD	C2-C1-C10	6.22	123.45	112.78
23	J	60	CHD	O7-C7-C6	-6.17	94.64	109.94
23	C	525	CHD	C6-C7-C8	6.17	118.06	111.48
23	B	1085	CHD	C11-C9-C10	6.15	120.07	113.73
23	W	1059	CHD	C15-C14-C8	6.15	126.93	118.33
23	J	60	CHD	C2-C1-C10	6.14	123.32	112.78
23	P	1271	CHD	C19-C10-C9	-6.13	102.73	111.18
23	P	1271	CHD	O7-C7-C6	-6.11	94.80	109.94
20	P	1268	PGV	O03-C19-C20	6.07	130.94	111.91
23	W	1059	CHD	C5-C6-C7	6.06	121.15	114.46
23	C	271	CHD	C5-C4-C3	6.05	121.64	112.76
23	B	1085	CHD	C14-C8-C9	6.05	118.01	109.71
20	A	521	PGV	O03-C19-C20	6.00	130.74	111.91
26	Z	1526	DMU	O5-C6-C1	5.98	123.02	110.35
26	T	1272	DMU	O16-C6-C1	5.96	117.60	108.30
23	W	1059	CHD	C11-C9-C8	5.94	119.58	110.88
25	T	1269	CDL	OA6-CA5-C11	5.91	124.24	111.50
23	J	60	CHD	C1-C2-C3	5.89	118.03	110.47
23	J	60	CHD	C15-C14-C8	5.88	126.56	118.33
23	P	1271	CHD	C6-C5-C10	5.88	118.90	112.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	P	1271	CHD	C5-C4-C3	5.87	121.38	112.76
23	J	60	CHD	C9-C11-C12	5.86	122.03	114.30
23	C	525	CHD	C15-C14-C8	5.83	126.48	118.33
23	B	1085	CHD	C18-C13-C17	-5.82	102.11	111.21
23	B	1085	CHD	C6-C7-C8	5.81	117.68	111.48
26	M	526	DMU	O1-C9-C11	5.79	120.83	106.44
26	M	526	DMU	O5-C4-C3	5.76	121.89	109.75
23	C	525	CHD	C5-C4-C3	5.75	121.20	112.76
23	C	271	CHD	O7-C7-C6	-5.74	95.71	109.94
23	C	525	CHD	C17-C13-C14	5.71	105.85	100.09
26	C	272	DMU	O1-C9-C11	5.70	120.60	106.44
19	L	522	TGL	CG2-OG2-CB1	5.69	131.81	117.79
26	C	272	DMU	O1-C9-C8	5.69	120.03	109.69
23	P	1271	CHD	C17-C13-C14	5.69	105.83	100.09
14	A	515	HEA	CAA-CBA-CGA	-5.68	97.85	113.76
26	C	272	DMU	C8-C7-C5	5.67	120.72	110.82
23	P	1525	CHD	C18-C13-C12	-5.66	103.31	109.07
23	P	1525	CHD	C6-C5-C4	-5.65	104.68	111.19
23	P	1525	CHD	C9-C8-C7	5.65	118.63	111.88
19	B	521	TGL	OG3-CG3-CG2	-5.64	92.01	108.43
23	P	1271	CHD	C2-C1-C10	5.63	122.43	112.78
19	B	521	TGL	OG2-CG2-CG3	5.59	128.65	108.40
14	A	515	HEA	C13-C12-C11	-5.58	105.96	114.35
14	A	516	HEA	CHB-C1B-NB	5.54	130.45	124.43
23	J	60	CHD	C5-C6-C7	5.53	120.56	114.46
14	N	516	HEA	CHB-C1B-C2B	-5.53	116.34	124.98
23	C	271	CHD	C1-C10-C5	5.51	115.92	107.77
14	A	516	HEA	CHA-C4D-ND	5.48	130.39	124.43
20	C	268	PGV	O03-C19-C20	5.48	129.09	111.91
26	T	1272	DMU	O5-C4-C3	5.47	121.28	109.75
20	P	1268	PGV	O01-C1-C2	5.46	123.28	111.50
25	G	269	CDL	OB6-CB5-C51	5.43	123.20	111.50
23	O	229	CHD	C1-C2-C3	5.43	117.43	110.47
23	P	1525	CHD	C11-C9-C10	5.42	119.31	113.73
26	T	1272	DMU	C8-C7-C5	5.39	120.23	110.82
23	P	1525	CHD	C11-C9-C8	5.39	118.76	110.88
23	J	60	CHD	C16-C17-C20	5.32	120.38	112.15
28	S	1265	PEK	O03-C21-C22	5.32	128.59	111.91
23	W	1059	CHD	C11-C12-C13	5.31	116.70	111.24
23	P	1525	CHD	O12-C12-C13	-5.30	102.06	111.03
14	A	516	HEA	CAD-CBD-CGD	-5.30	102.20	113.60
19	B	521	TGL	OG1-CA1-CA2	5.25	128.39	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	W	1059	CHD	C17-C13-C12	5.25	122.46	117.67
14	A	515	HEA	C4A-CHB-C1B	5.24	129.47	122.56
23	W	1059	CHD	O12-C12-C11	-5.24	98.46	109.12
23	C	525	CHD	C11-C9-C8	5.21	118.50	110.88
23	W	1059	CHD	C1-C2-C3	5.20	117.14	110.47
23	J	60	CHD	C14-C8-C7	5.20	118.70	111.81
26	C	272	DMU	O5-C6-C1	5.18	121.32	110.35
19	N	1522	TGL	CG2-OG2-CB1	5.18	130.55	117.79
26	M	526	DMU	O5-C6-C1	5.18	121.31	110.35
23	C	271	CHD	C14-C13-C12	5.17	112.21	107.40
23	C	271	CHD	C2-C1-C10	5.16	121.63	112.78
26	M	526	DMU	C8-C7-C5	5.16	119.83	110.82
28	G	264	PEK	O03-C01-C02	-5.11	93.56	108.43
23	W	1059	CHD	C9-C11-C12	5.10	121.04	114.30
23	J	60	CHD	C15-C14-C13	5.10	108.55	103.55
14	A	515	HEA	CHA-C4D-C3D	-5.06	117.41	124.84
28	G	1263	PEK	O01-C1-C2	5.05	122.39	111.50
23	P	1271	CHD	C14-C8-C7	5.05	118.50	111.81
14	A	516	HEA	CMD-C2D-C1D	5.04	132.72	125.04
19	N	1521	TGL	CG3-OG3-CC1	5.04	135.78	117.12
26	Z	1526	DMU	O1-C9-C11	5.03	118.93	106.44
28	G	265	PEK	O03-C21-C22	5.01	127.63	111.91
23	B	1085	CHD	C15-C14-C13	5.01	108.47	103.55
23	C	525	CHD	C2-C1-C10	5.00	121.36	112.78
26	C	272	DMU	C2-C3-C4	4.99	122.37	110.93
23	O	229	CHD	C14-C8-C9	4.99	116.56	109.71
23	P	1525	CHD	C14-C8-C9	4.98	116.55	109.71
19	L	522	TGL	OG2-CB1-CB2	4.96	122.19	111.50
23	O	229	CHD	C11-C9-C8	4.95	118.11	110.88
23	O	229	CHD	C9-C8-C7	4.93	117.77	111.88
20	N	1266	PGV	O03-C19-O04	-4.92	111.17	123.59
23	P	1271	CHD	C16-C17-C13	4.90	108.36	103.55
26	C	272	DMU	C7-C8-C9	4.88	118.95	110.24
19	L	522	TGL	OG3-CC1-OC1	-4.87	111.30	123.59
19	N	1521	TGL	OG1-CA1-CA2	4.87	127.19	111.91
26	M	526	DMU	C2-C3-C4	4.87	122.08	110.93
23	C	525	CHD	C6-C5-C4	-4.86	105.60	111.19
26	Z	1526	DMU	C8-C7-C5	4.86	119.30	110.82
23	J	60	CHD	C1-C10-C9	-4.85	103.74	111.35
23	B	1085	CHD	C9-C11-C12	4.84	120.69	114.30
23	P	1271	CHD	C21-C20-C17	4.81	120.29	112.92
23	C	271	CHD	C4-C3-C2	4.78	116.26	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	G	1263	PEK	O03-C01-C02	4.78	122.36	108.43
23	C	525	CHD	C18-C13-C17	-4.76	103.75	111.21
14	A	515	HEA	C16-C15-C14	4.76	130.75	121.12
14	A	516	HEA	C20-C21-C22	4.76	127.51	111.88
26	Z	1526	DMU	O5-C4-C57	4.74	118.23	106.44
23	P	1271	CHD	C11-C12-C13	4.74	116.11	111.24
23	C	271	CHD	C17-C13-C12	4.74	121.99	117.67
19	B	521	TGL	OG1-CA1-OA1	-4.73	111.65	123.59
19	N	1523	TGL	OG2-CB1-CB2	4.71	121.66	111.50
23	W	1059	CHD	C4-C5-C10	4.69	117.64	112.66
28	T	1264	PEK	O03-C01-C02	-4.67	94.83	108.43
26	Z	1526	DMU	C7-C8-C9	4.67	118.56	110.24
23	W	1059	CHD	O7-C7-C6	-4.67	98.37	109.94
23	W	1059	CHD	C22-C20-C17	4.64	119.87	110.28
14	N	516	HEA	C20-C21-C22	4.64	127.12	111.88
26	M	526	DMU	O7-C10-C5	-4.62	96.13	108.10
23	J	60	CHD	C11-C9-C8	4.61	117.62	110.88
19	N	1522	TGL	OG2-CB1-CB2	4.58	121.37	111.50
14	N	516	HEA	C1D-C2D-C3D	-4.57	102.15	106.96
28	G	1263	PEK	O03-C21-C22	4.56	126.21	111.91
23	P	1271	CHD	C9-C10-C5	4.55	114.97	108.58
23	J	60	CHD	C16-C17-C13	4.53	108.00	103.55
23	O	229	CHD	C5-C6-C7	4.52	119.45	114.46
23	W	1059	CHD	C18-C13-C14	-4.52	104.14	111.21
23	C	525	CHD	C15-C14-C13	4.51	107.98	103.55
23	W	1059	CHD	C18-C13-C12	-4.51	104.48	109.07
23	C	271	CHD	C14-C8-C7	4.50	117.77	111.81
14	A	515	HEA	CHA-C4D-ND	4.49	129.31	124.43
28	G	265	PEK	O01-C1-C2	4.49	121.19	111.50
23	P	1525	CHD	C16-C17-C13	4.48	107.95	103.55
20	N	1266	PGV	O03-C19-C20	4.47	125.92	111.91
23	P	1525	CHD	O7-C7-C6	-4.47	98.86	109.94
14	N	515	HEA	C26-C15-C16	4.46	122.78	115.27
23	C	271	CHD	C6-C5-C4	-4.46	106.06	111.19
19	B	521	TGL	OG2-CB1-CB2	4.45	121.10	111.50
23	O	229	CHD	C11-C9-C10	4.44	118.30	113.73
26	T	1272	DMU	O1-C9-C11	4.42	117.44	106.44
26	C	272	DMU	O5-C4-C3	4.42	119.06	109.75
23	C	525	CHD	C5-C6-C7	4.42	119.33	114.46
23	O	229	CHD	C17-C13-C14	4.40	104.53	100.09
23	J	60	CHD	O12-C12-C11	-4.40	100.17	109.12
23	W	1059	CHD	C9-C10-C5	4.38	114.73	108.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	J	60	CHD	C18-C13-C14	-4.37	104.37	111.21
26	T	1272	DMU	O5-C6-C1	4.37	119.60	110.35
26	T	1272	DMU	C6-C1-C2	4.37	119.09	110.00
23	P	1271	CHD	C15-C14-C13	4.36	107.83	103.55
23	C	525	CHD	O7-C7-C6	-4.36	99.13	109.94
23	P	1525	CHD	C15-C14-C8	4.31	124.36	118.33
14	A	515	HEA	O1A-CGA-CBA	-4.31	109.25	123.08
14	A	516	HEA	O1A-CGA-CBA	-4.29	109.29	123.08
23	C	525	CHD	C13-C17-C20	4.29	124.62	119.50
26	T	1272	DMU	O5-C4-C57	4.29	117.09	106.44
23	C	525	CHD	C14-C8-C9	4.28	115.58	109.71
23	P	1271	CHD	C9-C11-C12	4.26	119.93	114.30
26	T	1272	DMU	C7-C8-C9	4.26	117.83	110.24
23	W	1059	CHD	C16-C17-C20	4.25	118.73	112.15
23	P	1271	CHD	C6-C5-C4	-4.23	106.31	111.19
23	J	60	CHD	C17-C13-C14	4.23	104.36	100.09
14	A	515	HEA	O2A-CGA-CBA	4.23	127.62	114.03
14	N	516	HEA	CHC-C4B-NB	4.21	129.59	124.38
19	N	1522	TGL	OG3-CC1-OC1	-4.21	112.97	123.59
19	N	1521	TGL	OG2-CG2-CG3	4.19	123.58	108.40
23	O	229	CHD	C1-C10-C9	-4.18	104.78	111.35
23	P	1525	CHD	O12-C12-C11	-4.18	100.61	109.12
22	R	1229	PSC	O01-C1-C2	4.15	120.44	111.50
23	J	60	CHD	C4-C5-C10	4.14	117.06	112.66
23	J	60	CHD	C22-C20-C17	4.14	118.84	110.28
25	G	269	CDL	OA6-CA5-C11	4.10	120.34	111.50
26	M	526	DMU	O16-C18-C19	4.09	123.91	109.56
26	T	1272	DMU	O7-C10-C5	4.09	118.69	108.10
23	C	525	CHD	C18-C13-C14	-4.09	104.82	111.21
23	C	525	CHD	C1-C2-C3	4.08	115.70	110.47
26	M	526	DMU	O5-C6-O16	4.07	119.61	109.97
14	A	516	HEA	CAA-CBA-CGA	-4.03	102.46	113.76
23	P	1525	CHD	C18-C13-C17	-4.03	104.91	111.21
23	C	525	CHD	C22-C20-C17	-4.01	102.00	110.28
19	L	522	TGL	CC3-CC2-CC1	4.01	128.20	113.62
20	A	524	PGV	O03-C19-C20	3.99	124.44	111.91
26	T	1272	DMU	C1-C2-C3	3.99	118.80	109.68
20	A	524	PGV	C4-C3-C2	-3.98	98.87	113.19
22	B	229	PSC	O01-C1-C2	3.97	120.06	111.50
14	A	516	HEA	C20-C19-C18	-3.97	113.08	121.12
26	C	272	DMU	C6-O5-C4	3.96	121.46	113.69
14	A	515	HEA	CHB-C1B-NB	-3.95	120.14	124.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	O	229	CHD	O7-C7-C6	-3.95	100.14	109.94
19	L	522	TGL	OG3-CC1-CC2	3.93	124.25	111.91
26	T	1272	DMU	C6-O5-C4	3.93	121.39	113.69
26	M	526	DMU	O7-C3-C2	3.92	117.71	107.28
26	T	1272	DMU	C18-O16-C6	3.92	120.34	113.84
23	P	1271	CHD	O12-C12-C11	-3.90	101.18	109.12
14	N	516	HEA	CMC-C2C-C3C	3.88	131.93	124.68
19	B	521	TGL	OG1-CG1-CG2	3.86	119.66	108.43
28	S	1265	PEK	O01-C1-C2	3.85	119.79	111.50
23	B	1085	CHD	C19-C10-C5	-3.84	103.84	110.36
26	M	526	DMU	C22-C19-C18	-3.84	96.47	113.49
26	C	272	DMU	C6-C1-C2	3.84	117.99	110.00
28	G	264	PEK	O01-C1-O02	-3.81	114.49	123.70
26	T	1272	DMU	C2-C3-C4	3.81	119.66	110.93
23	J	60	CHD	C19-C10-C5	-3.81	103.91	110.36
23	C	271	CHD	C9-C11-C12	3.80	119.33	114.30
23	B	1085	CHD	C23-C22-C20	-3.79	107.59	114.52
23	C	271	CHD	C18-C13-C17	-3.79	105.28	111.21
23	B	1085	CHD	C9-C8-C7	3.79	116.40	111.88
23	P	1525	CHD	C5-C4-C3	3.78	118.31	112.76
19	B	521	TGL	OG2-CG2-CG1	3.78	122.08	108.40
26	M	526	DMU	C6-C1-C2	3.78	117.86	110.00
28	T	263	PEK	O03-C21-C22	3.78	123.75	111.91
14	A	516	HEA	CMC-C2C-C3C	3.77	131.74	124.68
26	Z	1526	DMU	C2-C3-C4	3.75	119.53	110.93
14	A	516	HEA	CHC-C4B-NB	3.73	129.00	124.38
26	Z	1526	DMU	O5-C6-O16	3.73	118.80	109.97
23	O	229	CHD	C9-C11-C12	3.73	119.22	114.30
26	Z	1526	DMU	C6-C1-C2	3.72	117.74	110.00
22	R	1229	PSC	O03-C19-C20	3.72	123.57	111.91
23	C	525	CHD	C23-C22-C20	-3.70	107.75	114.52
19	B	521	TGL	CG3-CG2-CG1	-3.70	103.03	111.79
19	N	1522	TGL	OG3-CC1-CC2	3.70	123.53	111.91
28	T	263	PEK	O03-C01-C02	3.70	119.21	108.43
19	A	523	TGL	OG3-CC1-CC2	3.67	123.42	111.91
23	P	1525	CHD	C17-C13-C14	3.67	103.79	100.09
23	O	229	CHD	C22-C20-C17	-3.66	102.72	110.28
14	A	515	HEA	C13-C14-C15	-3.66	118.85	127.66
20	C	267	PGV	C22-C21-C20	-3.65	100.06	113.19
23	P	1525	CHD	C13-C17-C20	3.65	123.85	119.50
23	J	60	CHD	C13-C14-C8	3.65	119.40	114.74
19	B	521	TGL	OG3-CC1-CC2	3.64	123.34	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
14	N	515	HEA	CBA-CAA-C2A	3.63	118.72	112.60
23	C	271	CHD	O12-C12-C13	-3.62	104.91	111.03
25	C	270	CDL	C52-C51-CB5	-3.61	100.49	113.62
23	O	229	CHD	C16-C17-C13	3.60	107.08	103.55
25	T	1269	CDL	OA8-CA7-C31	3.60	123.20	111.91
26	M	526	DMU	C7-C8-C9	3.60	116.66	110.24
14	A	515	HEA	CHD-C1D-ND	3.58	128.80	124.38
25	C	270	CDL	OA8-CA7-C31	3.57	123.11	111.91
23	C	525	CHD	O3-C3-C4	3.57	116.95	109.85
25	P	1270	CDL	OB8-CB7-C71	3.56	123.09	111.91
14	A	515	HEA	C1B-C2B-C3B	-3.55	102.56	106.80
23	B	1085	CHD	C1-C10-C9	-3.53	105.80	111.35
23	P	1525	CHD	C16-C17-C20	3.53	117.61	112.15
14	N	516	HEA	CHA-C4D-ND	3.53	128.26	124.43
23	B	1085	CHD	C11-C12-C13	3.52	114.86	111.24
23	P	1271	CHD	C23-C22-C20	-3.51	108.10	114.52
23	P	1525	CHD	C1-C10-C9	-3.48	105.88	111.35
26	M	526	DMU	C10-C5-C7	3.48	117.25	110.00
23	B	1085	CHD	C11-C9-C8	3.48	115.97	110.88
26	C	272	DMU	C1-C2-C3	3.46	117.59	109.68
26	M	526	DMU	C6-O5-C4	3.45	120.45	113.69
14	A	516	HEA	O2A-CGA-CBA	3.45	125.10	114.03
23	C	525	CHD	C21-C20-C22	-3.44	104.97	110.36
25	C	270	CDL	OB8-CB7-OB9	-3.43	114.92	123.59
14	N	516	HEA	OMA-CMA-C3A	-3.42	117.45	124.91
23	C	271	CHD	C17-C13-C14	3.42	103.54	100.09
19	B	521	TGL	OG3-CC1-OC1	-3.42	114.97	123.59
20	N	1524	PGV	C02-O01-C1	3.39	126.14	117.79
26	C	272	DMU	O5-C6-O16	3.39	118.00	109.97
23	C	525	CHD	C1-C10-C9	-3.38	106.03	111.35
19	N	1521	TGL	OG1-CA1-OA1	-3.37	115.08	123.59
28	G	265	PEK	O03-C21-O04	-3.36	115.11	123.59
28	T	1264	PEK	O01-C1-O02	-3.35	115.60	123.70
19	L	522	TGL	CG3-OG3-CC1	3.34	129.50	117.12
23	C	271	CHD	C21-C20-C17	3.32	118.00	112.92
25	C	270	CDL	OA8-CA7-OA9	-3.32	115.22	123.59
14	N	516	HEA	CMC-C2C-C1C	-3.30	123.39	128.46
26	T	1272	DMU	C11-C9-C8	3.30	120.73	113.00
26	Z	1526	DMU	C1-C2-C3	3.30	117.21	109.68
14	A	515	HEA	C4D-CHA-C1A	-3.29	118.21	122.56
23	C	271	CHD	C19-C10-C1	-3.29	102.96	108.26
20	P	1267	PGV	O03-C19-O04	-3.29	115.29	123.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	C	272	DMU	O61-C57-C4	3.28	122.55	111.29
25	C	270	CDL	CB4-OB6-CB5	-3.28	109.72	117.79
23	B	1085	CHD	C2-C1-C10	3.28	118.40	112.78
19	L	522	TGL	OB1-CB1-CB2	-3.27	110.96	123.73
23	O	229	CHD	C11-C12-C13	3.26	114.59	111.24
19	N	1523	TGL	OG1-CA1-CA2	3.25	122.12	111.91
19	L	522	TGL	OG2-CG2-CG3	3.25	120.17	108.40
14	A	515	HEA	C27-C19-C18	-3.25	115.34	123.68
26	C	272	DMU	O7-C3-C4	3.24	118.33	109.45
26	C	272	DMU	C10-O1-C9	3.24	120.05	113.69
23	C	271	CHD	C23-C22-C20	-3.23	108.62	114.52
20	P	1268	PGV	O04-C19-C20	-3.23	111.14	123.73
26	T	1272	DMU	C10-O1-C9	3.22	120.02	113.69
23	B	1085	CHD	C15-C16-C17	3.22	111.52	105.13
20	C	268	PGV	O04-C19-C20	-3.22	111.17	123.73
28	G	264	PEK	C24-C23-C22	-3.22	101.62	113.19
14	A	515	HEA	C26-C15-C16	-3.21	109.86	115.27
20	C	268	PGV	O03-C01-C02	3.21	117.78	108.43
23	P	1271	CHD	C13-C17-C20	3.21	123.33	119.50
23	P	1525	CHD	C1-C2-C3	3.20	114.58	110.47
19	N	1523	TGL	OG1-CA1-OA1	-3.20	115.53	123.59
25	C	270	CDL	OB8-CB7-C71	3.19	121.93	111.91
28	T	1264	PEK	C2-C3-C4	3.19	118.91	113.23
14	N	516	HEA	O1A-CGA-CBA	-3.18	112.85	123.08
25	P	1270	CDL	OA6-CA5-OA7	-3.18	116.02	123.70
20	C	267	PGV	C27-C26-C25	-3.18	98.29	114.42
28	T	1264	PEK	C32-C31-C30	-3.18	98.29	114.42
23	C	525	CHD	C9-C8-C7	3.17	115.67	111.88
20	A	524	PGV	C02-O01-C1	3.16	125.58	117.79
23	B	1085	CHD	C22-C20-C17	3.16	116.82	110.28
19	N	1522	TGL	OB1-CB1-CB2	-3.16	111.40	123.73
14	A	516	HEA	CHA-C4D-C3D	-3.16	120.19	124.84
19	N	1521	TGL	CG1-OG1-CA1	-3.15	105.44	117.12
26	Z	1526	DMU	C10-C5-C7	3.15	116.56	110.00
23	B	1085	CHD	C21-C20-C17	-3.15	108.10	112.92
19	N	1521	TGL	OG2-CB1-OB1	-3.15	116.10	123.70
14	A	516	HEA	CMC-C2C-C1C	-3.14	123.64	128.46
25	T	1269	CDL	CB2-C1-CA2	-3.14	103.55	112.79
14	N	515	HEA	O2A-CGA-CBA	3.14	124.11	114.03
23	O	229	CHD	C2-C1-C10	3.12	118.13	112.78
20	A	521	PGV	C02-O01-C1	-3.12	110.11	117.79
23	B	1085	CHD	O26-C24-C23	3.11	124.02	114.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
19	B	521	TGL	C15-CC9-CC8	3.11	130.19	114.42
19	N	1522	TGL	CC3-CC2-CC1	3.10	124.91	113.62
23	C	525	CHD	C19-C10-C5	-3.10	105.10	110.36
14	N	516	HEA	O2A-CGA-CBA	3.10	123.97	114.03
20	N	1524	PGV	O03-C19-C20	3.09	121.62	111.91
26	C	272	DMU	C18-O16-C6	3.08	118.95	113.84
19	N	1521	TGL	OG3-CC1-CC2	3.08	121.57	111.91
23	C	525	CHD	C14-C8-C7	3.07	115.88	111.81
26	Z	1526	DMU	C10-O1-C9	3.07	119.72	113.69
23	O	229	CHD	C18-C13-C14	-3.07	106.41	111.21
19	N	1523	TGL	OG3-CC1-CC2	3.06	121.51	111.91
28	S	1265	PEK	O03-C21-O04	-3.06	115.87	123.59
23	O	229	CHD	C21-C20-C17	3.06	117.60	112.92
23	W	1059	CHD	C19-C10-C9	-3.06	106.97	111.18
23	B	1085	CHD	O7-C7-C8	-3.05	102.60	109.43
19	L	522	TGL	CA5-CA4-CA3	-3.05	98.93	114.42
23	J	60	CHD	C14-C8-C9	3.05	113.90	109.71
14	A	516	HEA	C1D-C2D-C3D	-3.05	103.75	106.96
20	C	268	PGV	O02-C1-C2	-3.04	111.86	123.73
14	N	515	HEA	C2B-C1B-NB	3.04	113.52	109.88
28	T	263	PEK	O01-C1-C2	3.03	118.03	111.50
14	A	516	HEA	C4B-NB-C1B	3.03	108.20	105.07
20	N	1266	PGV	O03-C01-C02	3.02	117.22	108.43
28	G	1263	PEK	C01-O03-C21	3.01	128.28	117.12
20	A	524	PGV	O03-C01-C02	3.01	117.19	108.43
28	G	264	PEK	O01-C02-C03	-3.01	97.52	108.40
23	J	60	CHD	C22-C23-C24	3.00	120.48	112.51
25	T	1269	CDL	CB6-OB8-CB7	2.97	128.13	117.12
23	C	271	CHD	O12-C12-C11	-2.97	103.07	109.12
14	A	515	HEA	C3C-C4C-NC	2.96	113.04	109.21
23	C	271	CHD	C9-C10-C5	2.96	112.74	108.58
23	C	525	CHD	C9-C11-C12	2.95	118.20	114.30
25	P	1270	CDL	OA8-CA7-C31	2.94	121.12	111.91
23	C	525	CHD	C16-C17-C13	2.93	106.43	103.55
14	N	516	HEA	C20-C19-C18	-2.93	115.19	121.12
20	N	1266	PGV	O01-C1-O02	-2.92	116.64	123.70
26	Z	1526	DMU	O16-C18-C19	2.92	119.80	109.56
23	C	271	CHD	C13-C17-C20	2.92	122.98	119.50
26	M	526	DMU	C1-C2-C3	2.91	116.33	109.68
26	C	272	DMU	O7-C3-C2	2.90	115.01	107.28
19	L	522	TGL	OG1-CA1-CA2	2.90	121.02	111.91
19	N	1522	TGL	CA4-CA3-CA2	-2.90	102.76	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	G	264	PEK	C27-C26-C25	-2.90	99.70	114.42
14	A	515	HEA	C2B-C1B-NB	2.87	113.33	109.88
26	C	272	DMU	O16-C18-C19	2.87	119.64	109.56
23	C	525	CHD	O12-C12-C11	-2.85	103.31	109.12
26	T	1272	DMU	C57-C4-C3	2.85	121.62	113.33
20	N	1524	PGV	O01-C1-C2	2.85	117.64	111.50
23	P	1271	CHD	C1-C10-C9	-2.85	106.88	111.35
28	G	264	PEK	O01-C02-C01	-2.85	98.10	108.40
14	N	516	HEA	CAD-C3D-C4D	-2.84	119.69	124.66
14	N	515	HEA	CAD-CBD-CGD	-2.84	107.49	113.60
19	B	521	TGL	CG1-OG1-CA1	-2.84	106.60	117.12
14	N	515	HEA	C1D-C2D-C3D	-2.84	103.97	106.96
25	G	269	CDL	C22-C21-C20	2.84	128.83	114.42
23	P	1525	CHD	C19-C10-C5	-2.84	105.55	110.36
22	R	1229	PSC	C32-C31-C30	-2.83	100.08	114.42
25	G	269	CDL	C42-C41-C40	2.82	128.73	114.42
14	N	515	HEA	O1A-CGA-CBA	-2.82	114.03	123.08
25	G	269	CDL	C80-C79-C78	2.82	128.72	114.42
19	N	1523	TGL	CG3-OG3-CC1	2.81	127.53	117.12
19	A	523	TGL	OG1-CA1-CA2	2.81	120.72	111.91
20	A	521	PGV	O01-C1-O02	-2.80	116.94	123.70
26	T	1272	DMU	O5-C6-O16	2.80	116.60	109.97
20	P	1268	PGV	C03-C02-C01	-2.79	105.18	111.79
19	N	1522	TGL	C16-C15-CC9	2.79	128.60	114.42
14	N	516	HEA	C2D-C1D-ND	2.79	113.14	109.84
28	G	265	PEK	O01-C1-O02	-2.79	116.97	123.70
20	C	267	PGV	O03-C19-O04	-2.79	116.56	123.59
25	P	1270	CDL	CA4-OA6-CA5	2.78	124.64	117.79
14	N	515	HEA	C26-C15-C14	-2.78	116.56	123.68
23	O	229	CHD	C6-C7-C8	2.78	114.44	111.48
19	A	523	TGL	CG3-OG3-CC1	2.77	127.39	117.12
25	G	269	CDL	C83-C82-C81	2.77	128.49	114.42
26	Z	1526	DMU	C6-O5-C4	2.77	119.12	113.69
23	B	1085	CHD	C15-C14-C8	2.76	122.20	118.33
22	B	229	PSC	C32-C31-C30	-2.75	100.44	114.42
20	A	524	PGV	C01-O03-C19	2.75	127.31	117.12
28	G	264	PEK	C3-C2-C1	-2.75	103.62	113.62
19	A	523	TGL	OB1-CB1-CB2	-2.75	113.00	123.73
23	P	1271	CHD	O12-C12-C13	-2.75	106.39	111.03
19	L	522	TGL	CA8-CA7-CA6	-2.75	100.49	114.42
14	N	515	HEA	C4A-CHB-C1B	2.74	126.18	122.56
14	A	516	HEA	CHD-C1D-ND	2.74	127.77	124.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	M	526	DMU	O2-C8-C7	-2.74	104.02	110.35
25	P	1270	CDL	C58-C57-C56	-2.73	100.57	114.42
20	A	524	PGV	O03-C19-O04	-2.73	116.70	123.59
23	B	1085	CHD	O7-C7-C6	-2.73	103.18	109.94
19	N	1523	TGL	CG3-CG2-CG1	-2.72	105.35	111.79
25	T	1269	CDL	C83-C82-C81	2.72	128.23	114.42
26	C	272	DMU	C11-C9-C8	2.71	119.36	113.00
14	A	515	HEA	C27-C19-C20	2.71	119.83	115.27
22	B	229	PSC	C02-O01-C1	2.71	124.46	117.79
23	B	1085	CHD	C19-C10-C1	2.71	112.63	108.26
23	B	1085	CHD	C4-C3-C2	2.70	113.78	110.55
26	Z	1526	DMU	C11-C9-C8	2.70	119.33	113.00
14	A	516	HEA	O2D-CGD-CBD	2.69	122.69	114.03
14	A	516	HEA	CHD-C1D-C2D	-2.69	119.28	126.72
19	A	523	TGL	CG3-CG2-CG1	-2.69	105.42	111.79
14	N	515	HEA	C20-C19-C18	2.69	126.56	121.12
19	L	522	TGL	C16-C15-CC9	2.69	128.06	114.42
28	S	1265	PEK	C03-C02-C01	-2.68	105.46	111.79
25	C	270	CDL	C42-C41-C40	2.66	127.95	114.42
25	P	1270	CDL	C54-C53-C52	-2.66	100.92	114.42
19	A	523	TGL	CG1-OG1-CA1	2.65	126.94	117.12
19	N	1521	TGL	OG1-CG1-CG2	2.65	116.15	108.43
28	G	265	PEK	C7-C6-C5	-2.64	101.25	123.57
25	T	1269	CDL	OA6-CA4-CA6	2.64	117.97	108.40
25	G	269	CDL	C43-C42-C41	2.63	127.80	114.42
28	G	264	PEK	C25-C24-C23	-2.62	101.11	114.42
25	T	1269	CDL	OA6-CA5-OA7	-2.62	117.37	123.70
14	A	516	HEA	C2D-C1D-ND	2.62	112.94	109.84
28	G	264	PEK	O01-C1-C2	2.62	117.15	111.50
22	B	229	PSC	O03-C01-C02	2.62	116.06	108.43
20	P	1268	PGV	C02-O01-C1	2.61	124.21	117.79
14	A	515	HEA	CHD-C1D-C2D	-2.60	119.54	126.72
23	P	1525	CHD	O3-C3-C4	2.59	115.01	109.85
23	W	1059	CHD	O3-C3-C2	-2.59	103.58	110.16
20	N	1524	PGV	O03-C01-C02	2.58	115.94	108.43
26	T	1272	DMU	O61-C57-C4	2.57	120.12	111.29
14	N	515	HEA	C3B-C4B-NB	2.57	112.89	109.84
20	N	1524	PGV	O01-C02-C03	2.56	117.67	108.40
26	T	1272	DMU	O7-C3-C4	2.55	116.45	109.45
20	A	524	PGV	O01-C02-C03	2.54	117.60	108.40
14	N	516	HEA	CHC-C4B-C3B	-2.54	119.26	125.80
20	A	521	PGV	C4-C3-C2	-2.54	104.08	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	P	1525	CHD	C2-C1-C10	2.53	117.11	112.78
19	N	1522	TGL	C26-C25-C24	-2.51	101.66	114.42
22	B	229	PSC	C03-C02-C01	-2.51	105.84	111.79
26	M	526	DMU	O3-C5-C7	2.51	116.16	110.35
19	N	1522	TGL	C15-CC9-CC8	2.51	127.16	114.42
19	N	1522	TGL	OG1-CG1-CG2	2.50	115.72	108.43
28	G	1263	PEK	O04-C21-C22	-2.49	114.01	123.73
25	C	270	CDL	OA6-CA5-OA7	-2.48	117.71	123.70
23	B	1085	CHD	C5-C6-C7	2.48	117.19	114.46
25	P	1270	CDL	OB8-CB7-OB9	-2.48	117.34	123.59
25	G	269	CDL	CB6-OB8-CB7	2.47	126.28	117.12
25	T	1269	CDL	C80-C79-C78	2.47	126.95	114.42
28	G	265	PEK	C2-C3-C4	-2.47	108.83	113.23
25	C	270	CDL	C38-C37-C36	-2.46	101.94	114.42
20	P	1267	PGV	C27-C26-C25	-2.46	101.94	114.42
19	B	521	TGL	OB1-CB1-CB2	-2.46	114.14	123.73
25	G	269	CDL	C40-C39-C38	2.46	126.90	114.42
25	G	269	CDL	C19-C18-C17	2.46	126.90	114.42
25	G	269	CDL	C23-C22-C21	2.45	126.86	114.42
23	J	60	CHD	C9-C10-C5	2.44	112.00	108.58
19	N	1523	TGL	C20-CA9-CA8	2.43	126.78	114.42
19	A	523	TGL	OG1-CA1-OA1	-2.43	117.45	123.59
26	M	526	DMU	C31-C28-C25	-2.43	102.09	114.42
23	O	229	CHD	O26-C24-C23	2.43	121.83	114.03
23	O	229	CHD	C21-C20-C22	2.43	114.17	110.36
20	P	1268	PGV	O02-C1-C2	-2.42	114.28	123.73
23	P	1525	CHD	O26-C24-C23	2.41	121.78	114.03
23	P	1271	CHD	C22-C23-C24	-2.41	106.12	112.51
20	C	268	PGV	C03-C02-C01	-2.41	106.10	111.79
25	C	270	CDL	O1-C1-CB2	2.41	117.99	109.56
23	C	271	CHD	C22-C23-C24	-2.40	106.13	112.51
25	C	270	CDL	C53-C52-C51	-2.40	104.55	113.19
25	P	1270	CDL	C56-C55-C54	-2.40	102.24	114.42
23	W	1059	CHD	O7-C7-C8	-2.39	104.07	109.43
19	N	1521	TGL	OG2-CG2-CG1	2.39	117.07	108.40
23	J	60	CHD	C19-C10-C9	-2.39	107.89	111.18
20	A	521	PGV	O03-C01-C02	2.39	115.39	108.43
19	A	523	TGL	CB4-CB3-CB2	2.39	121.77	113.19
14	A	515	HEA	CMD-C2D-C1D	2.38	128.66	125.04
19	N	1522	TGL	OG1-CA1-CA2	2.38	119.37	111.91
20	N	1524	PGV	C3-C2-C1	-2.38	104.97	113.62
19	L	522	TGL	CA4-CA3-CA2	-2.37	104.66	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	G	265	PEK	C03-C02-C01	-2.37	106.18	111.79
19	N	1522	TGL	OG3-CG3-CG2	2.37	115.32	108.43
14	N	515	HEA	CHB-C1B-C2B	-2.36	121.29	124.98
28	G	265	PEK	C23-C22-C21	-2.36	105.04	113.62
25	P	1270	CDL	OA8-CA7-OA9	-2.35	117.65	123.59
26	T	1272	DMU	C10-C5-C7	2.35	114.90	110.00
23	O	229	CHD	C15-C14-C8	2.35	121.61	118.33
14	N	516	HEA	C26-C15-C14	-2.33	117.71	123.68
14	N	516	HEA	C27-C19-C18	2.33	129.64	123.68
14	N	515	HEA	C1B-C2B-C3B	-2.32	104.03	106.80
14	A	516	HEA	CHB-C1B-C2B	-2.32	121.36	124.98
28	T	1264	PEK	C30-C29-C28	-2.32	102.67	114.42
19	L	522	TGL	C15-CC9-CC8	2.31	126.14	114.42
20	C	267	PGV	C8-C9-C10	-2.30	103.76	113.79
22	B	229	PSC	C29-C28-C27	-2.30	102.74	114.42
28	T	263	PEK	O04-C21-C22	-2.30	114.75	123.73
14	A	516	HEA	C13-C14-C15	-2.30	122.12	127.66
23	J	60	CHD	O26-C24-O25	-2.30	117.58	123.30
19	N	1522	TGL	OG2-CG2-CG3	2.29	116.69	108.40
25	G	269	CDL	OA6-CA4-CA6	2.29	116.68	108.40
28	T	1264	PEK	C24-C23-C22	-2.29	104.97	113.19
14	A	516	HEA	O11-C11-C12	2.28	115.80	109.42
23	P	1525	CHD	C23-C22-C20	-2.28	110.35	114.52
23	P	1525	CHD	O7-C7-C8	-2.28	104.33	109.43
20	A	521	PGV	C25-C24-C23	-2.27	102.89	114.42
23	C	525	CHD	C11-C9-C10	2.27	116.07	113.73
28	G	1263	PEK	O01-C1-O02	-2.27	118.22	123.70
19	B	521	TGL	C16-C15-CC9	2.27	125.94	114.42
14	N	515	HEA	CMD-C2D-C3D	2.27	132.27	126.12
23	W	1059	CHD	O3-C3-C4	-2.26	105.36	109.85
25	P	1270	CDL	CA6-OA8-CA7	2.26	125.48	117.12
19	N	1522	TGL	CA8-CA7-CA6	-2.25	102.99	114.42
20	P	1268	PGV	O03-C19-O04	-2.25	117.91	123.59
28	T	263	PEK	C01-O03-C21	2.25	125.44	117.12
26	Z	1526	DMU	O3-C5-C7	2.24	115.52	110.35
23	W	1059	CHD	C13-C14-C8	2.23	117.59	114.74
19	L	522	TGL	CA3-CA2-CA1	-2.23	105.51	113.62
25	G	269	CDL	C82-C81-C80	2.23	125.75	114.42
25	C	270	CDL	C39-C38-C37	2.23	125.74	114.42
19	L	522	TGL	OG1-CG1-CG2	2.22	114.91	108.43
25	T	1269	CDL	OB6-CB5-OB7	-2.22	118.33	123.70
25	P	1270	CDL	C42-C41-C40	2.22	125.70	114.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
20	N	1266	PGV	C15-C14-C13	-2.22	104.12	113.79
28	G	264	PEK	C29-C28-C27	-2.22	103.15	114.42
14	N	515	HEA	CHC-C4B-C3B	-2.22	120.09	125.80
25	C	270	CDL	OA4-PA1-OA3	2.21	123.19	112.24
19	A	523	TGL	OG2-CB1-OB1	-2.21	118.36	123.70
14	N	516	HEA	CAD-C3D-C2D	2.20	131.98	127.88
14	N	515	HEA	C13-C14-C15	-2.20	122.37	127.66
28	G	265	PEK	C8-C7-C6	-2.20	101.21	112.02
20	C	268	PGV	C01-O03-C19	2.18	125.20	117.12
25	T	1269	CDL	C82-C81-C80	2.17	125.44	114.42
25	G	269	CDL	OA6-CA5-OA7	-2.16	118.47	123.70
25	T	1269	CDL	OB5-PB2-OB3	-2.16	100.62	109.07
19	N	1521	TGL	CC3-CC2-CC1	2.16	121.48	113.62
19	A	523	TGL	OG3-CC1-OC1	-2.16	118.14	123.59
23	J	60	CHD	C18-C13-C17	-2.16	107.84	111.21
19	N	1522	TGL	CG3-OG3-CC1	2.16	125.11	117.12
25	G	269	CDL	C79-C78-C77	2.15	125.36	114.42
20	P	1268	PGV	O14-P-O13	2.15	122.87	112.24
26	Z	1526	DMU	O49-C1-C6	-2.15	104.83	110.05
23	C	525	CHD	O26-C24-O25	-2.15	117.95	123.30
23	O	229	CHD	C22-C23-C24	2.13	118.15	112.51
23	P	1525	CHD	C4-C5-C10	-2.12	110.40	112.66
28	T	1264	PEK	O01-C02-C01	-2.12	100.71	108.40
25	G	269	CDL	C39-C38-C37	2.12	125.18	114.42
23	P	1271	CHD	O7-C7-C8	-2.11	104.70	109.43
20	P	1267	PGV	O03-C19-C20	2.11	118.54	111.91
14	N	515	HEA	C21-C20-C19	-2.11	106.04	112.98
19	N	1521	TGL	C21-C20-CA9	2.10	125.10	114.42
23	P	1525	CHD	C9-C11-C12	2.10	117.08	114.30
23	P	1525	CHD	C22-C23-C24	-2.10	106.93	112.51
26	Z	1526	DMU	O2-C8-C7	-2.10	105.49	110.35
28	S	1265	PEK	O04-C21-C22	-2.10	115.54	123.73
25	C	270	CDL	C20-C19-C18	2.09	125.06	114.42
28	T	1264	PEK	O01-C1-C2	2.09	116.00	111.50
20	C	267	PGV	O01-C1-C2	2.08	115.99	111.50
28	G	265	PEK	O12-C04-C05	2.08	116.89	109.10
19	N	1523	TGL	CB3-CB2-CB1	-2.08	106.05	113.62
23	O	229	CHD	C4-C5-C10	-2.08	110.45	112.66
19	N	1523	TGL	C21-C20-CA9	2.08	124.97	114.42
23	C	525	CHD	C16-C17-C20	2.08	115.36	112.15
14	N	516	HEA	CMD-C2D-C1D	2.08	128.20	125.04
25	G	269	CDL	OB5-PB2-OB3	-2.08	100.95	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	R	1229	PSC	C29-C28-C27	-2.08	103.88	114.42
28	G	265	PEK	P-O12-C04	2.07	131.79	121.59
19	N	1521	TGL	C16-C15-CC9	2.07	124.93	114.42
25	T	1269	CDL	OB8-CB6-CB4	2.06	114.44	108.43
23	O	229	CHD	O7-C7-C8	-2.06	104.82	109.43
14	N	515	HEA	CHC-C4B-NB	2.06	126.92	124.38
19	N	1523	TGL	OG2-CG2-CG3	2.05	115.84	108.40
28	T	1264	PEK	C28-C27-C26	-2.05	104.00	114.42
14	A	516	HEA	C27-C19-C18	2.04	128.92	123.68
19	A	523	TGL	OG2-CG2-CG3	2.04	115.80	108.40
19	N	1521	TGL	OB1-CB1-CB2	-2.04	115.77	123.73
14	N	516	HEA	C12-C13-C14	-2.04	106.86	112.23
28	G	1263	PEK	O01-C02-C01	2.03	115.76	108.40
20	A	524	PGV	C3-C2-C1	-2.02	106.28	113.62
19	B	521	TGL	CA5-CA4-CA3	-2.01	104.20	114.42
19	B	521	TGL	C21-C20-CA9	2.01	124.64	114.42
22	B	229	PSC	O03-C19-C20	2.01	118.20	111.91
22	R	1229	PSC	O03-C19-O04	-2.00	118.53	123.59

All (28) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	B	1085	CHD	C9
23	C	271	CHD	C9
23	J	60	CHD	C9
23	O	229	CHD	C9
23	P	1271	CHD	C9
23	W	1059	CHD	C17
23	W	1059	CHD	C9
26	C	272	DMU	C4
26	C	272	DMU	C9
26	C	272	DMU	C2
26	C	272	DMU	C6
26	C	272	DMU	C5
26	M	526	DMU	C4
26	M	526	DMU	C9
26	M	526	DMU	C2
26	M	526	DMU	C6
26	M	526	DMU	C5
26	T	1272	DMU	C4
26	T	1272	DMU	C6
26	T	1272	DMU	C10

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Mol	Chain	Res	Type	Atom
26	T	1272	DMU	C9
26	T	1272	DMU	C2
26	T	1272	DMU	C5
26	Z	1526	DMU	C4
26	Z	1526	DMU	C9
26	Z	1526	DMU	C2
26	Z	1526	DMU	C6
26	Z	1526	DMU	C5

All (976) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	A	523	TGL	CC2-CC1-OG3-CG3
19	A	523	TGL	OC1-CC1-OG3-CG3
19	N	1521	TGL	CB2-CB1-OG2-CG2
20	A	524	PGV	C03-O11-P-O13
20	A	524	PGV	C04-O12-P-O11
20	A	524	PGV	C04-O12-P-O14
20	A	524	PGV	C02-C03-O11-P
20	A	524	PGV	C05-C04-O12-P
20	A	524	PGV	C04-C05-C06-O06
20	A	524	PGV	O02-C1-O01-C02
20	C	267	PGV	C04-O12-P-O14
20	C	268	PGV	O01-C02-C03-O11
20	C	268	PGV	C2-C1-O01-C02
20	N	1524	PGV	C04-O12-P-O13
20	N	1524	PGV	C04-O12-P-O14
20	N	1524	PGV	C02-C03-O11-P
20	N	1524	PGV	O12-C04-C05-C06
20	N	1524	PGV	O02-C1-O01-C02
20	N	1524	PGV	C10-C11-C12-C13
20	P	1268	PGV	C03-O11-P-O13
20	P	1268	PGV	C04-O12-P-O13
20	P	1268	PGV	C2-C1-O01-C02
22	B	229	PSC	C04-O12-P-O13
22	B	229	PSC	C04-O12-P-O14
22	B	229	PSC	C11-C10-C9-C8
22	R	1229	PSC	O12-C04-C05-N
22	R	1229	PSC	C05-C04-O12-P
23	J	60	CHD	C16-C17-C20-C22
23	W	1059	CHD	C16-C17-C20-C21
25	C	270	CDL	CA2-C1-CB2-OB2

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Mol	Chain	Res	Type	Atoms
25	C	270	CDL	CA2-OA2-PA1-OA3
25	C	270	CDL	CA2-OA2-PA1-OA4
25	C	270	CDL	CA2-OA2-PA1-OA5
25	C	270	CDL	OA7-CA5-OA6-CA4
25	C	270	CDL	CB2-OB2-PB2-OB3
25	G	269	CDL	C1-CB2-OB2-PB2
25	G	269	CDL	CB3-OB5-PB2-OB3
25	G	269	CDL	CB3-OB5-PB2-OB4
25	G	269	CDL	OB6-CB4-CB6-OB8
25	P	1270	CDL	CA2-OA2-PA1-OA3
25	P	1270	CDL	CA2-OA2-PA1-OA4
25	P	1270	CDL	CA2-OA2-PA1-OA5
25	P	1270	CDL	OA7-CA5-OA6-CA4
25	P	1270	CDL	CB2-OB2-PB2-OB3
25	P	1270	CDL	CB2-OB2-PB2-OB4
25	P	1270	CDL	CB2-OB2-PB2-OB5
25	T	1269	CDL	O1-C1-CA2-OA2
25	T	1269	CDL	C1-CB2-OB2-PB2
25	T	1269	CDL	CB2-OB2-PB2-OB5
25	T	1269	CDL	CB3-OB5-PB2-OB3
26	C	272	DMU	C1-C6-O16-C18
26	C	272	DMU	O5-C6-O16-C18
26	M	526	DMU	O5-C6-O16-C18
26	T	1272	DMU	C1-C6-O16-C18
26	Z	1526	DMU	O5-C6-O16-C18
28	G	264	PEK	C11-C12-C13-C14
28	G	264	PEK	C12-C13-C14-C15
28	G	265	PEK	C03-O11-P-O13
28	G	265	PEK	C04-O12-P-O11
28	G	265	PEK	C04-O12-P-O13
28	G	265	PEK	C04-O12-P-O14
28	G	265	PEK	C7-C8-C9-C10
28	G	265	PEK	C10-C11-C12-C13
28	G	1263	PEK	C03-O11-P-O13
28	G	1263	PEK	C03-O11-P-O14
28	G	1263	PEK	O12-C04-C05-N
28	G	1263	PEK	C11-C10-C9-C8
28	S	1265	PEK	C04-O12-P-O13
28	S	1265	PEK	C04-O12-P-O14
28	S	1265	PEK	C7-C8-C9-C10
28	T	263	PEK	C03-O11-P-O14
28	T	263	PEK	O03-C01-C02-O01

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Mol	Chain	Res	Type	Atoms
28	T	263	PEK	O12-C04-C05-N
28	T	263	PEK	C6-C7-C8-C9
28	T	263	PEK	C13-C14-C15-C16
28	T	1264	PEK	C10-C11-C12-C13
28	T	1264	PEK	C12-C13-C14-C15
20	N	1524	PGV	O04-C19-O03-C01
25	T	1269	CDL	OA9-CA7-OA8-CA6
20	N	1524	PGV	C20-C19-O03-C01
25	T	1269	CDL	C31-CA7-OA8-CA6
23	O	229	CHD	C21-C20-C22-C23
19	N	1523	TGL	OC1-CC1-OG3-CG3
20	A	524	PGV	O04-C19-O03-C01
23	W	1059	CHD	C16-C17-C20-C22
19	B	521	TGL	OB1-CB1-OG2-CG2
20	A	524	PGV	C20-C19-O03-C01
22	R	1229	PSC	C20-C19-O03-C01
19	B	521	TGL	CB2-CB1-OG2-CG2
20	A	524	PGV	C2-C1-O01-C02
20	N	1524	PGV	C2-C1-O01-C02
25	C	270	CDL	C11-CA5-OA6-CA4
25	P	1270	CDL	C11-CA5-OA6-CA4
19	N	1521	TGL	OA1-CA1-OG1-CG1
19	N	1522	TGL	OA1-CA1-OG1-CG1
26	Z	1526	DMU	O5-C4-C57-O61
19	B	521	TGL	C22-C23-C24-C25
20	C	267	PGV	C28-C29-C30-C31
19	N	1521	TGL	CA2-CA1-OG1-CG1
19	N	1522	TGL	CA2-CA1-OG1-CG1
19	N	1523	TGL	CC2-CC1-OG3-CG3
26	M	526	DMU	O6-C11-C9-O1
19	L	522	TGL	CC1-CC2-CC3-CC4
20	A	521	PGV	C10-C11-C12-C13
20	C	267	PGV	C10-C11-C12-C13
20	P	1267	PGV	C10-C11-C12-C13
20	P	1268	PGV	C10-C11-C12-C13
22	R	1229	PSC	C11-C10-C9-C8
22	R	1229	PSC	C11-C12-C13-C14
28	G	264	PEK	C13-C14-C15-C16
28	G	1263	PEK	C4-C5-C6-C7
28	G	1263	PEK	C10-C11-C12-C13
28	S	1265	PEK	C13-C14-C15-C16
28	T	1264	PEK	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
19	N	1521	TGL	C11-C10-CB9-CB8
19	N	1521	TGL	CC5-CC6-CC7-CC8
19	N	1521	TGL	OB1-CB1-OG2-CG2
20	C	268	PGV	O02-C1-O01-C02
20	P	1268	PGV	O02-C1-O01-C02
19	L	522	TGL	OA1-CA1-OG1-CG1
25	C	270	CDL	C38-C39-C40-C41
26	C	272	DMU	O6-C11-C9-O1
20	N	1524	PGV	O12-C04-C05-O05
25	C	270	CDL	O1-C1-CB2-OB2
19	B	521	TGL	CA2-CA1-OG1-CG1
19	B	521	TGL	CC2-CC1-OG3-CG3
22	B	229	PSC	C20-C19-O03-C01
19	B	521	TGL	C20-C21-C22-C23
19	B	521	TGL	OC1-CC1-OG3-CG3
22	R	1229	PSC	O04-C19-O03-C01
20	P	1268	PGV	C2-C3-C4-C5
22	R	1229	PSC	C20-C21-C22-C23
25	T	1269	CDL	C31-C32-C33-C34
26	C	272	DMU	C28-C31-C34-C37
19	B	521	TGL	CB6-CB7-CB8-CB9
20	N	1524	PGV	C20-C21-C22-C23
25	G	269	CDL	C73-C74-C75-C76
25	G	269	CDL	C80-C81-C82-C83
25	T	1269	CDL	C79-C80-C81-C82
28	T	263	PEK	C29-C30-C31-C32
22	B	229	PSC	C20-C21-C22-C23
19	L	522	TGL	CA2-CA1-OG1-CG1
26	T	1272	DMU	O6-C11-C9-O1
19	A	523	TGL	C11-C10-CB9-CB8
25	P	1270	CDL	C38-C39-C40-C41
19	B	521	TGL	C11-C10-CB9-CB8
25	T	1269	CDL	C22-C23-C24-C25
23	W	1059	CHD	C21-C20-C22-C23
26	M	526	DMU	C3-C4-C57-O61
19	N	1522	TGL	CC1-CC2-CC3-CC4
23	C	271	CHD	C17-C20-C22-C23
23	W	1059	CHD	C17-C20-C22-C23
22	B	229	PSC	O04-C19-O03-C01
25	C	270	CDL	CB2-C1-CA2-OA2
25	G	269	CDL	CA2-C1-CB2-OB2
25	P	1270	CDL	CB2-C1-CA2-OA2

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Mol	Chain	Res	Type	Atoms
26	Z	1526	DMU	O6-C11-C9-O1
25	T	1269	CDL	C71-CB7-OB8-CB6
19	N	1522	TGL	CC3-CC4-CC5-CC6
23	O	229	CHD	C17-C20-C22-C23
19	N	1523	TGL	CB1-CB2-CB3-CB4
25	G	269	CDL	CA7-C31-C32-C33
19	B	521	TGL	OA1-CA1-OG1-CG1
23	J	60	CHD	C16-C17-C20-C21
23	J	60	CHD	C13-C17-C20-C21
25	C	270	CDL	C19-C20-C21-C22
23	W	1059	CHD	C13-C17-C20-C22
19	N	1521	TGL	CB1-CB2-CB3-CB4
25	G	269	CDL	CB7-C71-C72-C73
25	P	1270	CDL	CB7-C71-C72-C73
25	T	1269	CDL	CB5-C51-C52-C53
25	T	1269	CDL	CB7-C71-C72-C73
23	C	271	CHD	C21-C20-C22-C23
25	C	270	CDL	CB7-C71-C72-C73
26	T	1272	DMU	C5-C10-O7-C3
28	G	1263	PEK	C13-C14-C15-C16
28	T	263	PEK	C7-C8-C9-C10
19	L	522	TGL	CB1-CB2-CB3-CB4
20	P	1268	PGV	C1-C2-C3-C4
22	B	229	PSC	C19-C20-C21-C22
22	R	1229	PSC	C1-C2-C3-C4
25	C	270	CDL	CA5-C11-C12-C13
28	G	264	PEK	C1-C2-C3-C4
28	T	263	PEK	C34-C35-C36-C37
19	L	522	TGL	CC3-CC4-CC5-CC6
25	T	1269	CDL	OB9-CB7-OB8-CB6
23	C	271	CHD	C16-C17-C20-C22
23	J	60	CHD	C13-C17-C20-C22
19	N	1521	TGL	C21-C20-CA9-CA8
22	B	229	PSC	C1-C2-C3-C4
25	P	1270	CDL	CB5-C51-C52-C53
20	C	268	PGV	O12-C04-C05-O05
25	G	269	CDL	O1-C1-CB2-OB2
25	P	1270	CDL	O1-C1-CB2-OB2
23	C	271	CHD	C16-C17-C20-C21
25	G	269	CDL	C15-C16-C17-C18
26	C	272	DMU	O16-C18-C19-C22
20	C	267	PGV	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
20	P	1267	PGV	C12-C13-C14-C15
19	B	521	TGL	CB1-CB2-CB3-CB4
28	G	264	PEK	C10-C11-C12-C13
28	S	1265	PEK	C4-C5-C6-C7
25	T	1269	CDL	C11-CA5-OA6-CA4
19	N	1521	TGL	C16-C15-CC9-CC8
20	N	1524	PGV	C04-O12-P-O11
22	B	229	PSC	C04-O12-P-O11
25	C	270	CDL	CA3-OA5-PA1-OA2
25	C	270	CDL	CB2-OB2-PB2-OB5
25	G	269	CDL	CB3-OB5-PB2-OB2
25	P	1270	CDL	CA3-OA5-PA1-OA2
25	T	1269	CDL	CB3-OB5-PB2-OB2
28	G	265	PEK	C03-O11-P-O12
28	G	1263	PEK	C03-O11-P-O12
28	S	1265	PEK	C04-O12-P-O11
28	T	263	PEK	C03-O11-P-O12
26	C	272	DMU	C3-C4-C57-O61
23	W	1059	CHD	C13-C17-C20-C21
25	G	269	CDL	CA5-C11-C12-C13
25	P	1270	CDL	CA2-C1-CB2-OB2
25	G	269	CDL	OA7-CA5-OA6-CA4
25	T	1269	CDL	OA7-CA5-OA6-CA4
19	L	522	TGL	C20-C21-C22-C23
22	R	1229	PSC	C04-C05-N-C06
22	R	1229	PSC	C04-C05-N-C08
26	T	1272	DMU	O5-C4-C57-O61
26	C	272	DMU	O5-C4-C57-O61
28	T	1264	PEK	C1-C2-C3-C4
19	L	522	TGL	C22-C23-C24-C25
20	A	524	PGV	C14-C15-C16-C17
22	R	1229	PSC	C26-C27-C28-C29
25	C	270	CDL	C13-C14-C15-C16
25	C	270	CDL	C41-C42-C43-C44
26	Z	1526	DMU	C25-C28-C31-C34
28	S	1265	PEK	C28-C29-C30-C31
25	G	269	CDL	C11-CA5-OA6-CA4
19	A	523	TGL	CB3-CB4-CB5-CB6
19	L	522	TGL	CB5-CB6-CB7-CB8
19	L	522	TGL	C10-C11-C12-C13
20	P	1268	PGV	C24-C25-C26-C27
25	G	269	CDL	C43-C44-C45-C46

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Mol	Chain	Res	Type	Atoms
25	P	1270	CDL	C72-C73-C74-C75
28	S	1265	PEK	C27-C28-C29-C30
14	N	516	HEA	C2D-C3D-CAD-CBD
19	L	522	TGL	C16-C17-C18-C19
19	L	522	TGL	C17-C18-C19-C33
19	N	1521	TGL	CB6-CB7-CB8-CB9
19	N	1522	TGL	CA2-CA3-CA4-CA5
19	N	1522	TGL	C16-C17-C18-C19
19	N	1523	TGL	CA6-CA7-CA8-CA9
19	N	1523	TGL	C21-C20-CA9-CA8
20	C	268	PGV	C6-C7-C8-C9
25	C	270	CDL	C11-C12-C13-C14
25	P	1270	CDL	C73-C74-C75-C76
25	G	269	CDL	CB5-C51-C52-C53
19	N	1523	TGL	CB2-CB3-CB4-CB5
22	B	229	PSC	C4-C5-C6-C7
25	P	1270	CDL	C19-C20-C21-C22
25	P	1270	CDL	C74-C75-C76-C77
20	A	524	PGV	C10-C11-C12-C13
20	C	268	PGV	C10-C11-C12-C13
22	B	229	PSC	C11-C12-C13-C14
19	L	522	TGL	C19-C33-C34-C35
19	N	1521	TGL	CC6-CC7-CC8-CC9
19	N	1522	TGL	C12-C13-C14-C29
19	N	1523	TGL	C16-C15-CC9-CC8
20	C	268	PGV	C23-C24-C25-C26
20	P	1267	PGV	C7-C8-C9-C10
20	P	1268	PGV	C29-C30-C31-C32
25	G	269	CDL	C62-C63-C64-C65
25	T	1269	CDL	C33-C34-C35-C36
25	T	1269	CDL	C34-C35-C36-C37
14	N	516	HEA	C4D-C3D-CAD-CBD
25	C	270	CDL	O1-C1-CA2-OA2
25	P	1270	CDL	O1-C1-CA2-OA2
19	N	1522	TGL	CB5-CB6-CB7-CB8
25	C	270	CDL	C16-C17-C18-C19
25	C	270	CDL	C22-C23-C24-C25
25	G	269	CDL	C79-C80-C81-C82
28	G	264	PEK	C25-C26-C27-C28
25	P	1270	CDL	CA5-C11-C12-C13
28	G	1263	PEK	O03-C01-C02-O01
20	C	268	PGV	C20-C19-O03-C01

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Mol	Chain	Res	Type	Atoms
19	N	1522	TGL	CB3-CB4-CB5-CB6
19	N	1522	TGL	CA9-C20-C21-C22
19	N	1523	TGL	CC5-CC6-CC7-CC8
25	C	270	CDL	C73-C74-C75-C76
25	G	269	CDL	C59-C60-C61-C62
19	N	1522	TGL	C10-C11-C12-C13
19	N	1523	TGL	C20-C21-C22-C23
20	A	524	PGV	C21-C22-C23-C24
20	A	521	PGV	C4-C5-C6-C7
20	C	267	PGV	C30-C31-C32-C33
20	P	1268	PGV	C23-C24-C25-C26
22	R	1229	PSC	C24-C25-C26-C27
25	C	270	CDL	C42-C43-C44-C45
25	T	1269	CDL	C37-C38-C39-C40
19	L	522	TGL	CA5-CA6-CA7-CA8
20	A	521	PGV	C5-C6-C7-C8
20	C	268	PGV	C24-C25-C26-C27
22	R	1229	PSC	C21-C22-C23-C24
25	G	269	CDL	C52-C53-C54-C55
25	P	1270	CDL	C40-C41-C42-C43
25	T	1269	CDL	C41-C42-C43-C44
25	T	1269	CDL	C62-C63-C64-C65
25	T	1269	CDL	C80-C81-C82-C83
26	M	526	DMU	C19-C22-C25-C28
28	T	1264	PEK	C26-C27-C28-C29
19	L	522	TGL	C23-C24-C25-C26
20	A	521	PGV	C27-C28-C29-C30
20	C	268	PGV	C28-C29-C30-C31
20	N	1266	PGV	C5-C6-C7-C8
20	N	1266	PGV	C7-C8-C9-C10
20	P	1268	PGV	C22-C23-C24-C25
20	N	1524	PGV	C04-C05-C06-O06
19	L	522	TGL	C24-C25-C26-C27
19	N	1522	TGL	C22-C23-C24-C25
19	N	1523	TGL	CC4-CC5-CC6-CC7
20	C	268	PGV	C25-C26-C27-C28
25	P	1270	CDL	C54-C55-C56-C57
28	G	264	PEK	C31-C32-C33-C34
28	T	263	PEK	C24-C25-C26-C27
28	T	1264	PEK	C23-C24-C25-C26
28	G	1263	PEK	C15-C16-C17-C18
19	A	523	TGL	CB7-CB8-CB9-C10

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Mol	Chain	Res	Type	Atoms
19	A	523	TGL	C15-C16-C17-C18
19	B	521	TGL	CC5-CC6-CC7-CC8
19	N	1522	TGL	C21-C22-C23-C24
22	R	1229	PSC	C27-C28-C29-C30
25	P	1270	CDL	C14-C15-C16-C17
25	P	1270	CDL	C22-C23-C24-C25
28	G	264	PEK	C27-C28-C29-C30
22	R	1229	PSC	C04-C05-N-C07
22	B	229	PSC	C02-C01-O03-C19
19	B	521	TGL	CA4-CA5-CA6-CA7
19	N	1521	TGL	C17-C18-C19-C33
19	N	1523	TGL	CA2-CA3-CA4-CA5
19	N	1523	TGL	C24-C25-C26-C27
20	C	268	PGV	C22-C23-C24-C25
22	R	1229	PSC	C3-C4-C5-C6
25	C	270	CDL	C83-C84-C85-C86
25	G	269	CDL	C31-C32-C33-C34
25	T	1269	CDL	C20-C21-C22-C23
19	A	523	TGL	CB6-CB7-CB8-CB9
19	B	521	TGL	CC4-CC5-CC6-CC7
20	A	524	PGV	C4-C5-C6-C7
25	G	269	CDL	C58-C59-C60-C61
28	G	265	PEK	C24-C25-C26-C27
28	G	1263	PEK	C33-C34-C35-C36
19	A	523	TGL	CB5-CB6-CB7-CB8
19	L	522	TGL	CC6-CC7-CC8-CC9
20	N	1266	PGV	C23-C24-C25-C26
22	R	1229	PSC	C22-C23-C24-C25
25	P	1270	CDL	C13-C14-C15-C16
28	G	1263	PEK	C32-C33-C34-C35
25	C	270	CDL	C31-CA7-OA8-CA6
25	G	269	CDL	C71-CB7-OB8-CB6
25	P	1270	CDL	C31-CA7-OA8-CA6
19	N	1522	TGL	CB4-CB5-CB6-CB7
20	C	268	PGV	C27-C28-C29-C30
20	P	1267	PGV	C14-C15-C16-C17
25	G	269	CDL	C76-C77-C78-C79
19	N	1522	TGL	C23-C24-C25-C26
20	C	268	PGV	C13-C14-C15-C16
22	B	229	PSC	C26-C27-C28-C29
25	P	1270	CDL	C11-C12-C13-C14
25	P	1270	CDL	C41-C42-C43-C44

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Mol	Chain	Res	Type	Atoms
25	P	1270	CDL	C79-C80-C81-C82
25	T	1269	CDL	C52-C53-C54-C55
19	A	523	TGL	CB9-C10-C11-C12
25	C	270	CDL	C57-C58-C59-C60
25	T	1269	CDL	C56-C57-C58-C59
19	L	522	TGL	C21-C22-C23-C24
20	P	1268	PGV	C3-C4-C5-C6
28	G	1263	PEK	C22-C21-O03-C01
19	L	522	TGL	CB2-CB1-OG2-CG2
19	N	1523	TGL	CG2-CG3-OG3-CC1
25	P	1270	CDL	C42-C43-C44-C45
25	P	1270	CDL	C71-C72-C73-C74
20	A	524	PGV	O05-C05-C06-O06
20	N	1524	PGV	O05-C05-C06-O06
19	A	523	TGL	C22-C23-C24-C25
20	A	524	PGV	C29-C30-C31-C32
20	A	521	PGV	C7-C8-C9-C10
20	P	1268	PGV	C12-C13-C14-C15
22	B	229	PSC	C13-C14-C15-C16
20	C	268	PGV	O04-C19-O03-C01
25	G	269	CDL	C13-C14-C15-C16
20	P	1268	PGV	C14-C15-C16-C17
19	N	1521	TGL	CA5-CA6-CA7-CA8
20	C	267	PGV	C25-C26-C27-C28
28	S	1265	PEK	C24-C25-C26-C27
25	G	269	CDL	OB9-CB7-OB8-CB6
25	C	270	CDL	CA7-C31-C32-C33
19	B	521	TGL	CA5-CA6-CA7-CA8
19	N	1521	TGL	C10-C11-C12-C13
19	N	1522	TGL	C16-C15-CC9-CC8
25	G	269	CDL	C74-C75-C76-C77
19	L	522	TGL	OB1-CB1-OG2-CG2
22	B	229	PSC	C24-C25-C26-C27
19	A	523	TGL	CA6-CA7-CA8-CA9
20	N	1524	PGV	C29-C30-C31-C32
20	P	1267	PGV	C25-C26-C27-C28
19	A	523	TGL	C13-C14-C29-C30
19	N	1521	TGL	CC4-CC5-CC6-CC7
20	A	521	PGV	C24-C25-C26-C27
20	C	267	PGV	C7-C8-C9-C10
25	C	270	CDL	C43-C44-C45-C46
25	P	1270	CDL	C59-C60-C61-C62

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Mol	Chain	Res	Type	Atoms
25	G	269	CDL	C57-C58-C59-C60
28	G	264	PEK	C24-C25-C26-C27
28	G	1263	PEK	O04-C21-O03-C01
19	N	1521	TGL	C22-C23-C24-C25
28	G	1263	PEK	C25-C26-C27-C28
20	N	1524	PGV	C23-C24-C25-C26
26	Z	1526	DMU	C28-C31-C34-C37
28	T	263	PEK	C10-C11-C12-C13
28	T	1264	PEK	C13-C14-C15-C16
19	N	1523	TGL	C17-C18-C19-C33
25	C	270	CDL	C14-C15-C16-C17
28	S	1265	PEK	C15-C16-C17-C18
19	N	1522	TGL	CA1-CA2-CA3-CA4
19	N	1522	TGL	CC4-CC5-CC6-CC7
20	P	1267	PGV	C13-C14-C15-C16
25	G	269	CDL	C37-C38-C39-C40
19	A	523	TGL	C21-C20-CA9-CA8
19	N	1522	TGL	CA3-CA4-CA5-CA6
25	P	1270	CDL	C31-C32-C33-C34
25	P	1270	CDL	C63-C64-C65-C66
19	N	1522	TGL	C24-C25-C26-C27
20	A	524	PGV	C26-C27-C28-C29
25	G	269	CDL	C41-C42-C43-C44
25	C	270	CDL	CB5-C51-C52-C53
25	T	1269	CDL	CA7-C31-C32-C33
23	P	1271	CHD	C21-C20-C22-C23
25	C	270	CDL	C81-C82-C83-C84
26	Z	1526	DMU	C22-C25-C28-C31
28	S	1265	PEK	C22-C23-C24-C25
20	P	1268	PGV	C20-C19-O03-C01
19	N	1523	TGL	CB9-C10-C11-C12
25	C	270	CDL	C72-C73-C74-C75
25	P	1270	CDL	C52-C53-C54-C55
25	P	1270	CDL	C83-C84-C85-C86
28	T	263	PEK	C32-C33-C34-C35
25	P	1270	CDL	C51-CB5-OB6-CB4
19	N	1523	TGL	C12-C13-C14-C29
26	M	526	DMU	C25-C28-C31-C34
28	T	1264	PEK	C3-C4-C5-C6
28	G	265	PEK	O02-C1-O01-C02
26	T	1272	DMU	C3-C4-C57-O61
28	G	265	PEK	C21-C22-C23-C24

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Mol	Chain	Res	Type	Atoms
19	N	1522	TGL	C17-C18-C19-C33
20	N	1266	PGV	C26-C27-C28-C29
19	A	523	TGL	OG1-CG1-CG2-OG2
25	T	1269	CDL	OB6-CB4-CB6-OB8
25	C	270	CDL	C79-C80-C81-C82
25	T	1269	CDL	C61-C62-C63-C64
25	P	1270	CDL	OA9-CA7-OA8-CA6
25	G	269	CDL	C78-C79-C80-C81
19	N	1521	TGL	C14-C29-C30-C31
20	A	524	PGV	C2-C3-C4-C5
25	C	270	CDL	C71-C72-C73-C74
25	T	1269	CDL	C15-C16-C17-C18
19	B	521	TGL	CA9-C20-C21-C22
19	L	522	TGL	C12-C13-C14-C29
28	G	265	PEK	C29-C30-C31-C32
19	B	521	TGL	C15-C16-C17-C18
22	B	229	PSC	C29-C30-C31-C32
26	T	1272	DMU	C18-C19-C22-C25
25	C	270	CDL	OA9-CA7-OA8-CA6
19	N	1522	TGL	OB1-CB1-OG2-CG2
28	G	265	PEK	C2-C1-O01-C02
19	N	1521	TGL	CB4-CB5-CB6-CB7
19	N	1521	TGL	C15-C16-C17-C18
25	C	270	CDL	C53-C54-C55-C56
25	C	270	CDL	C59-C60-C61-C62
25	P	1270	CDL	C36-C37-C38-C39
25	P	1270	CDL	C55-C56-C57-C58
28	T	263	PEK	C16-C17-C18-C19
19	A	523	TGL	CC6-CC7-CC8-CC9
22	B	229	PSC	C27-C28-C29-C30
20	A	521	PGV	C19-C20-C21-C22
20	P	1267	PGV	C28-C29-C30-C31
26	M	526	DMU	O16-C18-C19-C22
20	C	268	PGV	C01-C02-C03-O11
25	P	1270	CDL	OB5-CB3-CB4-CB6
25	P	1270	CDL	C81-C82-C83-C84
19	B	521	TGL	C16-C17-C18-C19
25	G	269	CDL	C32-C33-C34-C35
19	B	521	TGL	CC7-CC8-CC9-C15
28	G	1263	PEK	C26-C27-C28-C29
22	B	229	PSC	C6-C7-C8-C9
26	T	1272	DMU	C31-C34-C37-C40

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Mol	Chain	Res	Type	Atoms
20	C	268	PGV	O12-C04-C05-C06
25	T	1269	CDL	CB2-C1-CA2-OA2
28	G	1263	PEK	C16-C17-C18-C19
19	N	1521	TGL	C13-C14-C29-C30
28	G	1263	PEK	C29-C30-C31-C32
19	N	1522	TGL	CC5-CC6-CC7-CC8
20	C	268	PGV	C14-C15-C16-C17
19	A	523	TGL	OG1-CG1-CG2-CG3
19	B	521	TGL	OG1-CG1-CG2-CG3
20	A	524	PGV	O03-C01-C02-C03
25	C	270	CDL	CA3-CA4-CA6-OA8
25	G	269	CDL	C21-C22-C23-C24
25	G	269	CDL	C24-C25-C26-C27
25	G	269	CDL	CB3-CB4-CB6-OB8
25	G	269	CDL	C64-C65-C66-C67
25	T	1269	CDL	CB3-CB4-CB6-OB8
28	G	1263	PEK	O03-C01-C02-C03
25	G	269	CDL	C23-C24-C25-C26
19	A	523	TGL	C29-C30-C31-C32
19	N	1521	TGL	CB3-CB4-CB5-CB6
25	G	269	CDL	C40-C41-C42-C43
25	T	1269	CDL	C44-C45-C46-C47
26	Z	1526	DMU	C34-C37-C40-C43
20	N	1524	PGV	C2-C3-C4-C5
25	P	1270	CDL	C62-C63-C64-C65
25	T	1269	CDL	C18-C19-C20-C21
26	M	526	DMU	C34-C37-C40-C43
19	N	1521	TGL	CA1-CA2-CA3-CA4
22	R	1229	PSC	C19-C20-C21-C22
19	N	1522	TGL	CC6-CC7-CC8-CC9
19	L	522	TGL	C16-C15-CC9-CC8
19	L	522	TGL	C33-C34-C35-C36
20	P	1268	PGV	C30-C31-C32-C33
20	P	1268	PGV	C31-C32-C33-C34
26	T	1272	DMU	C34-C37-C40-C43
19	L	522	TGL	CB4-CB5-CB6-CB7
19	N	1522	TGL	C29-C30-C31-C32
25	G	269	CDL	C44-C45-C46-C47
25	P	1270	CDL	C82-C83-C84-C85
28	G	264	PEK	C17-C18-C19-C20
20	A	524	PGV	C11-C10-C9-C8
19	N	1522	TGL	C25-C26-C27-C28

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Mol	Chain	Res	Type	Atoms
20	C	268	PGV	C5-C6-C7-C8
25	C	270	CDL	C15-C16-C17-C18
28	G	1263	PEK	C2-C1-O01-C02
28	T	1264	PEK	C33-C34-C35-C36
19	B	521	TGL	C25-C26-C27-C28
25	C	270	CDL	C32-C33-C34-C35
25	P	1270	CDL	C35-C36-C37-C38
25	P	1270	CDL	C44-C45-C46-C47
19	N	1523	TGL	C29-C30-C31-C32
20	N	1266	PGV	C31-C32-C33-C34
20	N	1524	PGV	C03-C02-O01-C1
19	N	1523	TGL	C33-C34-C35-C36
28	T	263	PEK	C14-C15-C16-C17
20	P	1268	PGV	C4-C5-C6-C7
25	P	1270	CDL	C76-C77-C78-C79
25	T	1269	CDL	C16-C17-C18-C19
25	P	1270	CDL	OA5-CA3-CA4-OA6
28	T	1264	PEK	C4-C5-C6-C7
19	N	1521	TGL	C16-C17-C18-C19
25	C	270	CDL	C37-C38-C39-C40
20	P	1268	PGV	O04-C19-O03-C01
25	T	1269	CDL	C53-C54-C55-C56
25	T	1269	CDL	C81-C82-C83-C84
25	P	1270	CDL	OA6-CA4-CA6-OA8
20	C	268	PGV	C31-C32-C33-C34
28	G	265	PEK	C27-C28-C29-C30
25	P	1270	CDL	OB7-CB5-OB6-CB4
19	N	1521	TGL	C21-C22-C23-C24
25	T	1269	CDL	C63-C64-C65-C66
25	T	1269	CDL	C84-C85-C86-C87
20	P	1268	PGV	C9-C10-C11-C12
20	A	521	PGV	C6-C7-C8-C9
25	P	1270	CDL	C18-C19-C20-C21
25	T	1269	CDL	C36-C37-C38-C39
19	N	1521	TGL	CB7-CB8-CB9-C10
19	N	1523	TGL	C13-C14-C29-C30
28	T	263	PEK	C28-C29-C30-C31
20	P	1268	PGV	C15-C16-C17-C18
25	T	1269	CDL	C57-C58-C59-C60
19	N	1522	TGL	CB2-CB1-OG2-CG2
19	L	522	TGL	C15-C16-C17-C18
19	N	1521	TGL	C24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
19	A	523	TGL	CA2-CA3-CA4-CA5
20	N	1266	PGV	C6-C7-C8-C9
28	G	264	PEK	C4-C5-C6-C7
25	P	1270	CDL	C61-C62-C63-C64
28	G	264	PEK	C33-C34-C35-C36
20	N	1524	PGV	C01-C02-C03-O11
25	C	270	CDL	OA5-CA3-CA4-CA6
25	P	1270	CDL	OA5-CA3-CA4-CA6
25	G	269	CDL	C36-C37-C38-C39
25	G	269	CDL	O1-C1-CA2-OA2
26	C	272	DMU	C18-C19-C22-C25
19	L	522	TGL	CC5-CC6-CC7-CC8
23	J	60	CHD	C17-C20-C22-C23
25	T	1269	CDL	CB4-CB3-OB5-PB2
20	P	1268	PGV	C11-C12-C13-C14
20	P	1268	PGV	C13-C14-C15-C16
28	G	1263	PEK	C30-C31-C32-C33
28	T	263	PEK	C25-C26-C27-C28
26	Z	1526	DMU	C19-C18-O16-C6
19	A	523	TGL	CB2-CB3-CB4-CB5
19	N	1521	TGL	C25-C26-C27-C28
19	N	1522	TGL	C19-C33-C34-C35
20	A	521	PGV	C26-C27-C28-C29
20	N	1524	PGV	C14-C15-C16-C17
28	G	264	PEK	C35-C36-C37-C38
28	S	1265	PEK	C23-C24-C25-C26
19	A	523	TGL	C10-C11-C12-C13
28	S	1265	PEK	C16-C17-C18-C19
28	S	1265	PEK	C22-C21-O03-C01
20	P	1268	PGV	C26-C27-C28-C29
25	G	269	CDL	C19-C20-C21-C22
25	C	270	CDL	CB3-CB4-CB6-OB8
25	T	1269	CDL	CA3-CA4-CA6-OA8
19	A	523	TGL	C16-C15-CC9-CC8
28	G	264	PEK	C22-C23-C24-C25
28	G	264	PEK	C7-C8-C9-C10
28	G	265	PEK	C4-C5-C6-C7
19	L	522	TGL	CC4-CC5-CC6-CC7
28	T	1264	PEK	C28-C29-C30-C31
20	A	524	PGV	O03-C19-C20-C21
20	A	524	PGV	C22-C23-C24-C25
25	T	1269	CDL	C39-C40-C41-C42

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Mol	Chain	Res	Type	Atoms
22	B	229	PSC	C9-C10-C11-C12
22	B	229	PSC	C10-C11-C12-C13
22	R	1229	PSC	C9-C10-C11-C12
28	G	265	PEK	C11-C10-C9-C8
28	G	265	PEK	C9-C10-C11-C12
28	G	265	PEK	C12-C13-C14-C15
28	G	1263	PEK	C6-C7-C8-C9
28	G	1263	PEK	C9-C10-C11-C12
28	S	1265	PEK	C5-C6-C7-C8
28	S	1265	PEK	C9-C10-C11-C12
28	S	1265	PEK	C11-C12-C13-C14
28	T	263	PEK	C5-C6-C7-C8
28	T	263	PEK	C9-C10-C11-C12
28	T	1264	PEK	C9-C10-C11-C12
25	C	270	CDL	C36-C37-C38-C39
28	S	1265	PEK	C34-C35-C36-C37
20	P	1268	PGV	O01-C02-C03-O11
28	G	1263	PEK	O01-C02-C03-O11
28	T	263	PEK	O01-C02-C03-O11
25	C	270	CDL	C31-C32-C33-C34
20	P	1268	PGV	C25-C26-C27-C28
22	R	1229	PSC	C5-C6-C7-C8
25	P	1270	CDL	C43-C44-C45-C46
28	T	1264	PEK	C17-C18-C19-C20
28	T	1264	PEK	C25-C26-C27-C28
28	G	264	PEK	C23-C24-C25-C26
19	B	521	TGL	C13-C14-C29-C30
20	A	524	PGV	C25-C26-C27-C28
20	N	1266	PGV	C15-C16-C17-C18
20	N	1266	PGV	C19-C20-C21-C22
25	P	1270	CDL	C80-C81-C82-C83
22	B	229	PSC	C28-C29-C30-C31
26	T	1272	DMU	C25-C28-C31-C34
19	B	521	TGL	C24-C25-C26-C27
28	T	1264	PEK	C34-C35-C36-C37
20	N	1524	PGV	C05-C04-O12-P
25	P	1270	CDL	CA4-CA3-OA5-PA1
26	M	526	DMU	C22-C25-C28-C31
19	N	1523	TGL	CC1-CC2-CC3-CC4
20	N	1266	PGV	C24-C25-C26-C27
25	G	269	CDL	C61-C62-C63-C64
19	N	1522	TGL	C11-C10-CB9-CB8

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Mol	Chain	Res	Type	Atoms
20	P	1267	PGV	C31-C32-C33-C34
19	L	522	TGL	CA7-CA8-CA9-C20
25	T	1269	CDL	OB5-CB3-CB4-CB6
20	A	521	PGV	C23-C24-C25-C26
25	C	270	CDL	C21-C22-C23-C24
20	P	1267	PGV	C24-C25-C26-C27
28	G	265	PEK	C16-C17-C18-C19
20	C	268	PGV	C12-C13-C14-C15
25	G	269	CDL	C53-C54-C55-C56
28	G	1263	PEK	C28-C29-C30-C31
25	G	269	CDL	C34-C35-C36-C37
25	G	269	CDL	C22-C23-C24-C25
25	P	1270	CDL	C56-C57-C58-C59
25	C	270	CDL	C34-C35-C36-C37
20	A	524	PGV	C03-C02-O01-C1
22	B	229	PSC	C03-C02-O01-C1
19	N	1521	TGL	CA3-CA4-CA5-CA6
28	S	1265	PEK	C26-C27-C28-C29
20	C	268	PGV	C05-C04-O12-P
20	N	1524	PGV	O03-C01-C02-C03
20	P	1267	PGV	C02-C03-O11-P
25	C	270	CDL	C1-CA2-OA2-PA1
25	G	269	CDL	CB4-CB3-OB5-PB2
25	P	1270	CDL	CB3-CB4-CB6-OB8
25	T	1269	CDL	C1-CA2-OA2-PA1
28	T	263	PEK	O03-C01-C02-C03
28	T	263	PEK	C02-C03-O11-P
19	A	523	TGL	C19-C33-C34-C35
22	B	229	PSC	O01-C02-C03-O11
25	C	270	CDL	OA5-CA3-CA4-OA6
25	C	270	CDL	OB5-CB3-CB4-OB6
23	C	271	CHD	C20-C22-C23-C24
20	C	267	PGV	C29-C30-C31-C32
25	C	270	CDL	C20-C21-C22-C23
28	G	1263	PEK	O02-C1-O01-C02
28	S	1265	PEK	O04-C21-O03-C01
19	B	521	TGL	OG1-CG1-CG2-OG2
19	B	521	TGL	OG2-CG2-CG3-OG3
20	A	524	PGV	O03-C01-C02-O01
25	C	270	CDL	OA6-CA4-CA6-OA8
25	C	270	CDL	OB6-CB4-CB6-OB8
20	P	1267	PGV	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
22	B	229	PSC	C23-C24-C25-C26
28	G	265	PEK	C26-C27-C28-C29
28	G	1263	PEK	C24-C25-C26-C27
19	B	521	TGL	CA3-CA4-CA5-CA6
19	L	522	TGL	C11-C10-CB9-CB8
19	N	1523	TGL	CB6-CB7-CB8-CB9
20	P	1268	PGV	C21-C22-C23-C24
19	N	1523	TGL	CB3-CB4-CB5-CB6
20	N	1266	PGV	C10-C11-C12-C13
25	C	270	CDL	C58-C59-C60-C61
26	C	272	DMU	C31-C34-C37-C40
19	N	1523	TGL	C16-C17-C18-C19
19	L	522	TGL	C25-C26-C27-C28
20	A	524	PGV	C20-C21-C22-C23
20	A	524	PGV	C03-O11-P-O12
22	R	1229	PSC	C04-O12-P-O11
25	G	269	CDL	CB2-OB2-PB2-OB5
25	T	1269	CDL	C43-C44-C45-C46
26	C	272	DMU	C4-C3-O7-C10
19	L	522	TGL	CA3-CA4-CA5-CA6
19	N	1522	TGL	C11-C12-C13-C14
20	C	267	PGV	C02-C03-O11-P
20	C	267	PGV	C05-C04-O12-P
20	P	1268	PGV	C02-C03-O11-P
25	C	270	CDL	CA4-CA3-OA5-PA1
25	P	1270	CDL	C1-CA2-OA2-PA1
20	A	524	PGV	C04-O12-P-O13
20	P	1268	PGV	C03-O11-P-O14
22	B	229	PSC	C04-C05-N-C08
25	C	270	CDL	CA3-OA5-PA1-OA3
25	C	270	CDL	CB2-OB2-PB2-OB4
25	P	1270	CDL	CA3-OA5-PA1-OA3
25	T	1269	CDL	CB3-OB5-PB2-OB4
28	G	265	PEK	C03-O11-P-O14
28	T	263	PEK	C03-O11-P-O13
19	N	1522	TGL	CB6-CB7-CB8-CB9
19	N	1523	TGL	CA5-CA6-CA7-CA8
22	B	229	PSC	C01-C02-C03-O11
28	T	263	PEK	C01-C02-C03-O11
23	P	1271	CHD	C16-C17-C20-C22
25	T	1269	CDL	C73-C74-C75-C76
25	P	1270	CDL	C24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
26	C	272	DMU	C19-C22-C25-C28
20	P	1267	PGV	C1-C2-C3-C4
28	G	264	PEK	C34-C35-C36-C37
28	T	1264	PEK	C24-C25-C26-C27
19	B	521	TGL	CA1-CA2-CA3-CA4
25	P	1270	CDL	C37-C38-C39-C40
25	T	1269	CDL	C71-C72-C73-C74
22	R	1229	PSC	O01-C02-C03-O11
25	P	1270	CDL	OB5-CB3-CB4-OB6
20	C	268	PGV	C21-C22-C23-C24
25	C	270	CDL	C80-C81-C82-C83
19	N	1523	TGL	C18-C19-C33-C34
19	B	521	TGL	CB9-C10-C11-C12
19	N	1523	TGL	C22-C23-C24-C25
19	L	522	TGL	CG1-CG2-CG3-OG3
19	N	1521	TGL	OG1-CG1-CG2-CG3
25	P	1270	CDL	CA3-CA4-CA6-OA8
20	N	1524	PGV	O03-C01-C02-O01
25	P	1270	CDL	OB6-CB4-CB6-OB8
25	P	1270	CDL	C57-C58-C59-C60
20	N	1266	PGV	C4-C5-C6-C7
20	P	1268	PGV	C20-C21-C22-C23
19	N	1521	TGL	CA7-CA8-CA9-C20
22	B	229	PSC	O01-C1-C2-C3
26	T	1272	DMU	O16-C18-C19-C22
25	G	269	CDL	C55-C56-C57-C58
19	N	1522	TGL	CB2-CB3-CB4-CB5
26	T	1272	DMU	C22-C25-C28-C31
20	A	524	PGV	C31-C32-C33-C34
20	P	1267	PGV	C30-C31-C32-C33
25	C	270	CDL	C60-C61-C62-C63
22	R	1229	PSC	O03-C19-C20-C21
19	L	522	TGL	C13-C14-C29-C30
28	G	264	PEK	C16-C17-C18-C19
19	A	523	TGL	C17-C18-C19-C33
19	N	1523	TGL	CG1-CG2-OG2-CB1
22	R	1229	PSC	C01-C02-C03-O11
28	G	1263	PEK	C01-C02-C03-O11
23	P	1271	CHD	C20-C22-C23-C24
25	P	1270	CDL	C33-C34-C35-C36
19	A	523	TGL	CA9-C20-C21-C22
20	A	521	PGV	O03-C19-C20-C21

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Mol	Chain	Res	Type	Atoms
19	A	523	TGL	C16-C17-C18-C19
20	N	1524	PGV	C7-C8-C9-C10
25	C	270	CDL	C40-C41-C42-C43
19	A	523	TGL	CA4-CA5-CA6-CA7
20	N	1524	PGV	O01-C02-C03-O11
25	T	1269	CDL	OB5-CB3-CB4-OB6
20	A	524	PGV	C24-C25-C26-C27
20	N	1524	PGV	C22-C23-C24-C25
20	A	524	PGV	C11-C12-C13-C14
19	A	523	TGL	C33-C34-C35-C36
23	P	1525	CHD	C13-C17-C20-C21
25	T	1269	CDL	OA6-CA4-CA6-OA8
20	C	268	PGV	C04-O12-P-O11
20	N	1524	PGV	C03-O11-P-O12
20	P	1268	PGV	C03-O11-P-O12
20	P	1268	PGV	C04-O12-P-O11
20	N	1524	PGV	C30-C31-C32-C33
22	R	1229	PSC	C31-C32-C33-C34
25	C	270	CDL	C63-C64-C65-C66
25	P	1270	CDL	C12-C11-CA5-OA6
19	N	1523	TGL	CB4-CB5-CB6-CB7
20	P	1268	PGV	C7-C8-C9-C10
20	P	1267	PGV	C05-C04-O12-P
25	G	269	CDL	CA4-CA3-OA5-PA1
28	S	1265	PEK	C32-C33-C34-C35
25	P	1270	CDL	C21-C22-C23-C24
20	N	1524	PGV	C31-C32-C33-C34
25	T	1269	CDL	C40-C41-C42-C43
20	P	1268	PGV	C01-C02-C03-O11
25	G	269	CDL	OB5-CB3-CB4-CB6
19	L	522	TGL	OG2-CB1-CB2-CB3
28	G	264	PEK	C26-C27-C28-C29
19	L	522	TGL	CB6-CB7-CB8-CB9
20	A	521	PGV	C12-C13-C14-C15
20	C	267	PGV	C11-C10-C9-C8
28	G	264	PEK	C3-C4-C5-C6
14	A	515	HEA	CAD-CBD-CGD-O1D
19	L	522	TGL	C11-C12-C13-C14
19	B	521	TGL	C11-C12-C13-C14
23	P	1525	CHD	C13-C17-C20-C22
19	N	1523	TGL	OG1-CG1-CG2-OG2
28	T	263	PEK	C31-C32-C33-C34

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Mol	Chain	Res	Type	Atoms
14	N	516	HEA	CAA-CBA-CGA-O1A
19	N	1523	TGL	OG1-CA1-CA2-CA3
20	N	1266	PGV	O03-C19-C20-C21
20	C	268	PGV	C11-C10-C9-C8
19	N	1521	TGL	CC1-CC2-CC3-CC4
25	C	270	CDL	C52-C53-C54-C55
20	C	267	PGV	C24-C25-C26-C27
23	O	229	CHD	C16-C17-C20-C22
26	Z	1526	DMU	O6-C11-C9-C8
28	G	1263	PEK	C17-C18-C19-C20
19	A	523	TGL	CG3-CG2-OG2-CB1
19	N	1521	TGL	CG1-CG2-OG2-CB1
22	R	1229	PSC	C01-C02-O01-C1
22	R	1229	PSC	C03-C02-O01-C1
28	G	1263	PEK	C14-C15-C16-C17
28	G	265	PEK	C5-C6-C7-C8
28	G	265	PEK	C6-C7-C8-C9
28	G	1263	PEK	C12-C13-C14-C15
28	S	1265	PEK	C6-C7-C8-C9
28	S	1265	PEK	C11-C10-C9-C8
28	T	1264	PEK	C11-C10-C9-C8
28	T	1264	PEK	C11-C12-C13-C14
19	N	1523	TGL	CC9-C15-C16-C17
22	B	229	PSC	C2-C3-C4-C5
14	N	515	HEA	CAD-CBD-CGD-O1D
20	P	1268	PGV	C11-C10-C9-C8
25	T	1269	CDL	O1-C1-CB2-OB2
14	A	516	HEA	CAD-CBD-CGD-O1D
19	A	523	TGL	OG2-CG2-CG3-OG3
28	G	264	PEK	O03-C01-C02-O01
14	A	515	HEA	CAD-CBD-CGD-O2D
23	O	229	CHD	C22-C23-C24-O25
28	T	263	PEK	C02-C01-O03-C21
19	L	522	TGL	CB3-CB4-CB5-CB6
25	P	1270	CDL	C75-C76-C77-C78
26	Z	1526	DMU	C19-C22-C25-C28
25	C	270	CDL	C12-C13-C14-C15
25	T	1269	CDL	C13-C14-C15-C16
22	B	229	PSC	C04-C05-N-C07
28	S	1265	PEK	C25-C26-C27-C28
28	S	1265	PEK	C29-C30-C31-C32
23	C	271	CHD	C22-C23-C24-O26

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Mol	Chain	Res	Type	Atoms
20	A	524	PGV	O04-C19-C20-C21
28	T	263	PEK	C4-C5-C6-C7
23	P	1271	CHD	C16-C17-C20-C21
14	N	516	HEA	CAD-CBD-CGD-O2D
20	N	1266	PGV	C14-C15-C16-C17
14	A	516	HEA	CAD-CBD-CGD-O2D
14	N	516	HEA	CAD-CBD-CGD-O1D
23	O	229	CHD	C22-C23-C24-O26
22	B	229	PSC	C04-C05-N-C06
25	C	270	CDL	OB5-CB3-CB4-CB6
25	G	269	CDL	C38-C39-C40-C41
20	C	267	PGV	C15-C16-C17-C18
25	T	1269	CDL	C75-C76-C77-C78
25	G	269	CDL	C33-C34-C35-C36
19	L	522	TGL	OG2-CG2-CG3-OG3
22	B	229	PSC	C12-C13-C14-C15
19	N	1521	TGL	OG3-CC1-CC2-CC3
25	P	1270	CDL	C20-C21-C22-C23
23	B	1085	CHD	C22-C23-C24-O25
20	A	521	PGV	C9-C10-C11-C12
22	R	1229	PSC	C12-C13-C14-C15
19	N	1523	TGL	CB5-CB6-CB7-CB8
22	B	229	PSC	O02-C1-O01-C02
19	B	521	TGL	C14-C29-C30-C31
25	P	1270	CDL	C32-C31-CA7-OA8
28	G	264	PEK	O01-C1-C2-C3
23	P	1525	CHD	C22-C23-C24-O25
23	P	1271	CHD	C22-C23-C24-O26
25	P	1270	CDL	C39-C40-C41-C42
23	C	271	CHD	C22-C23-C24-O25
23	P	1525	CHD	C22-C23-C24-O26
19	A	523	TGL	OG1-CA1-CA2-CA3
19	B	521	TGL	OG3-CC1-CC2-CC3
28	S	1265	PEK	O01-C1-C2-C3
19	N	1521	TGL	CC2-CC3-CC4-CC5
20	C	268	PGV	C1-C2-C3-C4
14	N	515	HEA	CAA-CBA-CGA-O1A
20	C	268	PGV	O01-C1-C2-C3
23	J	60	CHD	C22-C23-C24-O25
23	J	60	CHD	C22-C23-C24-O26
23	P	1271	CHD	C22-C23-C24-O25
19	L	522	TGL	CA4-CA5-CA6-CA7

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Mol	Chain	Res	Type	Atoms
14	A	516	HEA	CAA-CBA-CGA-O2A
14	N	516	HEA	CAA-CBA-CGA-O2A
26	T	1272	DMU	C19-C22-C25-C28
20	N	1524	PGV	O03-C19-C20-C21
25	C	270	CDL	C32-C31-CA7-OA8
28	G	265	PEK	O01-C1-C2-C3
28	T	1264	PEK	O03-C01-C02-O01
14	N	515	HEA	CAA-CBA-CGA-O2A
25	G	269	CDL	C11-C12-C13-C14
14	N	515	HEA	CAD-CBD-CGD-O2D
23	B	1085	CHD	C22-C23-C24-O26
25	G	269	CDL	C71-C72-C73-C74
25	G	269	CDL	C52-C51-CB5-OB6
20	A	524	PGV	C23-C24-C25-C26
20	C	268	PGV	C02-C03-O11-P
19	L	522	TGL	CA2-CA3-CA4-CA5
20	N	1266	PGV	C9-C10-C11-C12
25	T	1269	CDL	C11-C12-C13-C14
25	P	1270	CDL	C60-C61-C62-C63
19	A	523	TGL	OA1-CA1-CA2-CA3
19	A	523	TGL	OG2-CB1-CB2-CB3
28	G	1263	PEK	O01-C1-C2-C3
28	G	265	PEK	C33-C34-C35-C36
25	P	1270	CDL	C32-C31-CA7-OA9
28	S	1265	PEK	O02-C1-C2-C3
19	A	523	TGL	CA3-CA4-CA5-CA6
20	C	268	PGV	C30-C31-C32-C33
20	A	521	PGV	C11-C12-C13-C14
28	G	264	PEK	O02-C1-C2-C3
19	L	522	TGL	CB2-CB3-CB4-CB5
28	T	1264	PEK	O01-C1-C2-C3
28	T	1264	PEK	C30-C31-C32-C33
19	B	521	TGL	CB3-CB4-CB5-CB6
25	P	1270	CDL	C17-C18-C19-C20
25	G	269	CDL	OB7-CB5-OB6-CB4
25	C	270	CDL	C32-C31-CA7-OA9
25	C	270	CDL	CB3-OB5-PB2-OB3
25	T	1269	CDL	CA2-OA2-PA1-OA4
19	B	521	TGL	OC1-CC1-CC2-CC3
20	C	268	PGV	O02-C1-C2-C3
20	P	1268	PGV	C6-C7-C8-C9
19	N	1521	TGL	C18-C19-C33-C34

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Mol	Chain	Res	Type	Atoms
14	A	515	HEA	CAA-CBA-CGA-O2A
19	L	522	TGL	OG1-CA1-CA2-CA3
25	P	1270	CDL	C52-C51-CB5-OB6
19	N	1522	TGL	CC7-CC8-CC9-C15
19	B	521	TGL	CA7-CA8-CA9-C20
19	B	521	TGL	CG1-CG2-OG2-CB1
19	N	1521	TGL	CA4-CA5-CA6-CA7
23	C	525	CHD	C21-C20-C22-C23
14	A	515	HEA	CAA-CBA-CGA-O1A
19	N	1522	TGL	CB1-CB2-CB3-CB4
19	N	1523	TGL	OG3-CC1-CC2-CC3
25	T	1269	CDL	C54-C55-C56-C57
14	A	516	HEA	CAA-CBA-CGA-O1A
19	L	522	TGL	C21-C20-CA9-CA8
25	C	270	CDL	C12-C11-CA5-OA6
25	G	269	CDL	C16-C17-C18-C19
25	T	1269	CDL	C78-C79-C80-C81
19	A	523	TGL	OB1-CB1-CB2-CB3
19	N	1523	TGL	OC1-CC1-CC2-CC3
28	T	1264	PEK	O02-C1-C2-C3
20	P	1267	PGV	C22-C23-C24-C25
26	C	272	DMU	C34-C37-C40-C43

There are no ring outliers.

40 monomers are involved in 272 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	N	1521	TGL	10	0
23	C	525	CHD	1	0
19	N	1522	TGL	6	0
23	P	1525	CHD	1	0
19	A	523	TGL	3	0
25	G	269	CDL	24	0
23	P	1271	CHD	3	0
23	B	1085	CHD	3	0
14	N	515	HEA	5	0
26	T	1272	DMU	6	0
20	C	267	PGV	7	0
26	Z	1526	DMU	1	0
14	A	515	HEA	3	0
25	T	1269	CDL	23	0
22	R	1229	PSC	16	0

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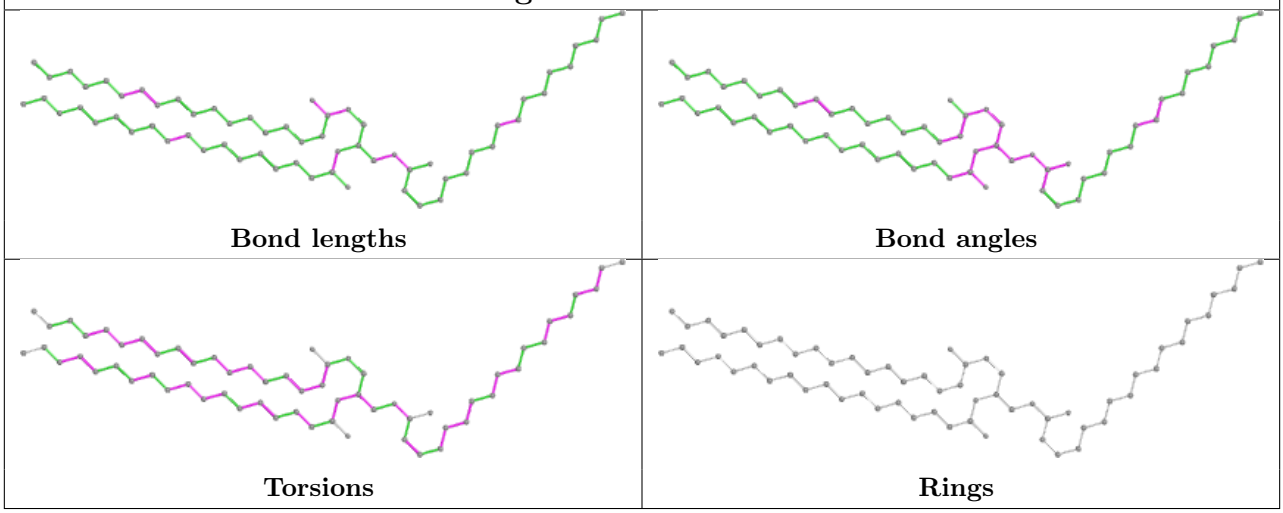
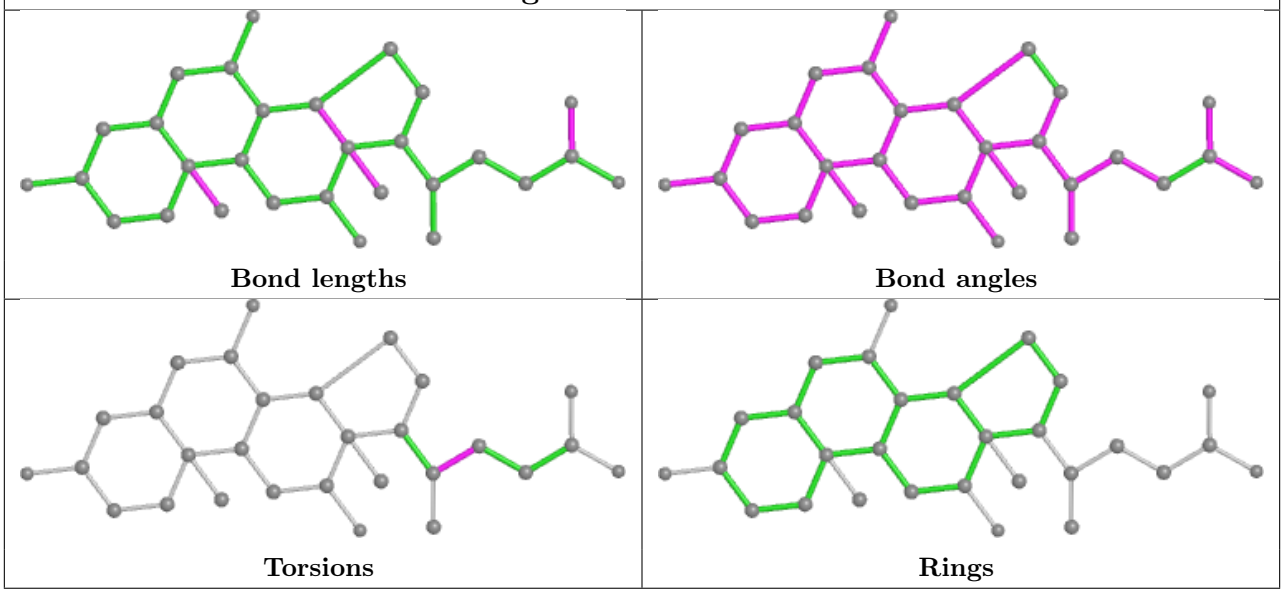
Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	S	1265	PEK	6	0
20	P	1268	PGV	2	0
23	J	60	CHD	2	0
19	N	1523	TGL	5	0
28	G	1263	PEK	10	0
23	C	271	CHD	2	0
25	P	1270	CDL	16	0
20	A	521	PGV	1	0
25	C	270	CDL	22	0
20	N	1524	PGV	8	0
23	W	1059	CHD	3	0
14	A	516	HEA	1	0
20	N	1266	PGV	1	0
23	O	229	CHD	1	0
19	L	522	TGL	19	0
22	B	229	PSC	17	0
28	T	1264	PEK	4	0
19	B	521	TGL	9	0
20	P	1267	PGV	5	0
26	C	272	DMU	2	0
20	A	524	PGV	12	0
14	N	516	HEA	2	0
28	G	265	PEK	8	0
28	G	264	PEK	4	0
28	T	263	PEK	15	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 then 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 TGL N 1521



Ligand CHD C 525



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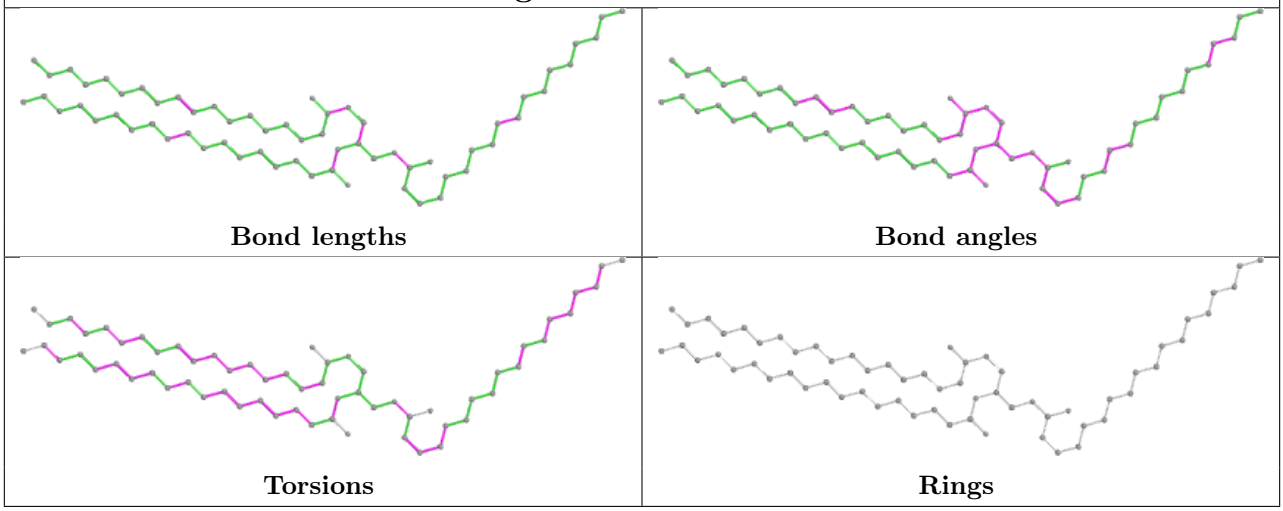
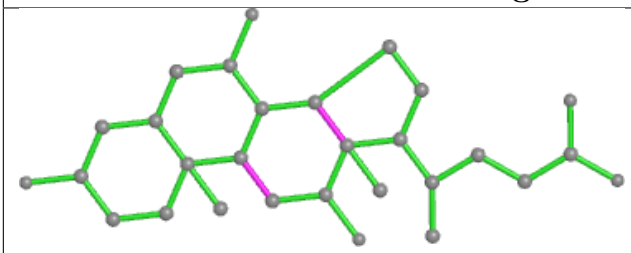
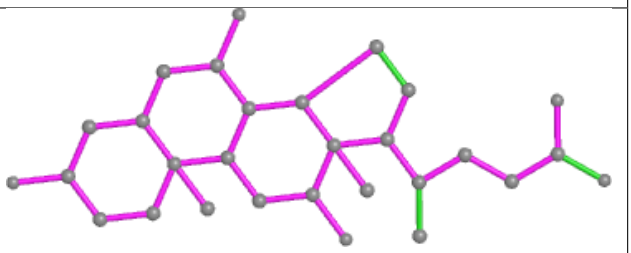


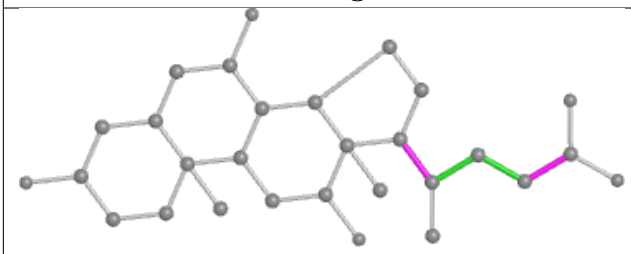
Ligand CHD P 1525



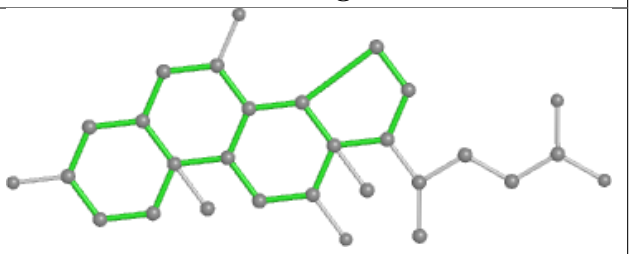
Bond lengths



Bond angles

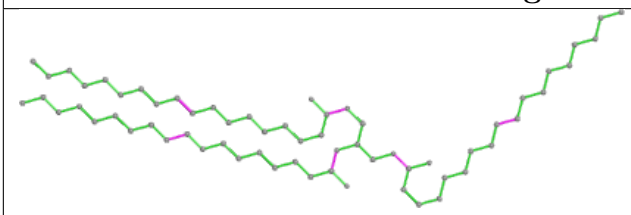


Torsions

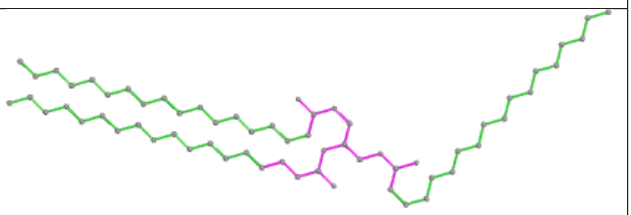


Rings

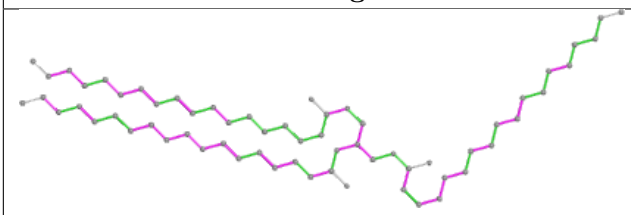
Ligand TGL A 523



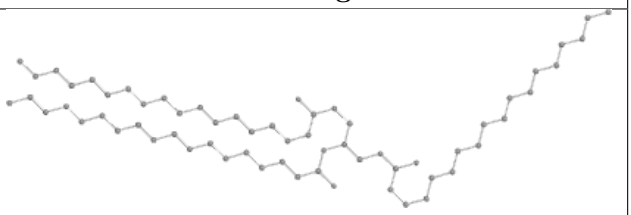
Bond lengths



Bond angles

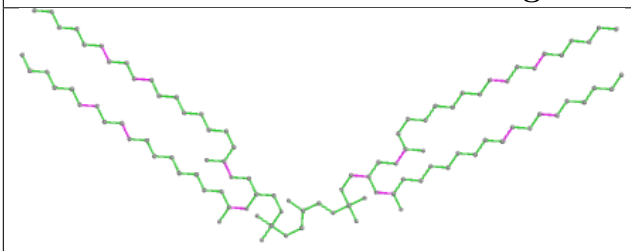


Torsions

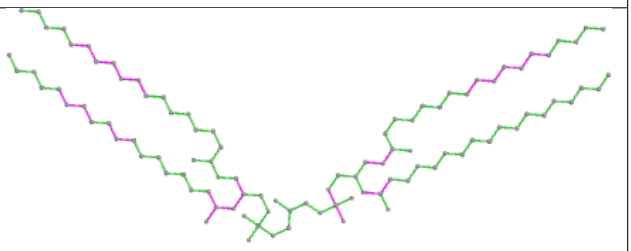


Rings

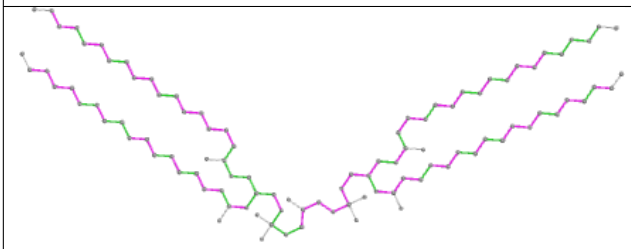
Ligand CDL G 269



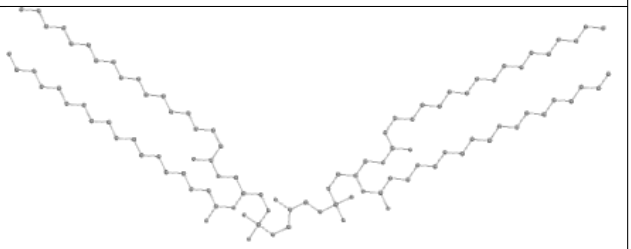
Bond lengths



Bond angles

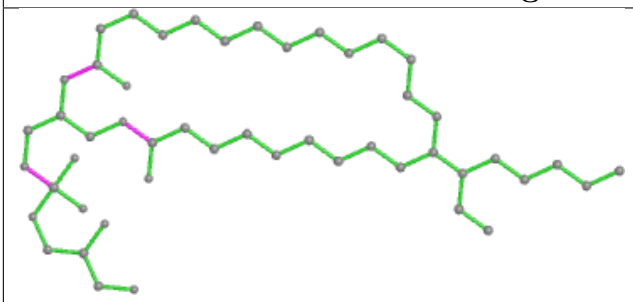


Torsions



Rings

Ligand PGV C 268



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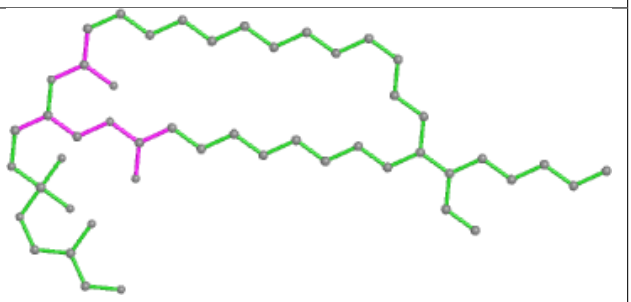
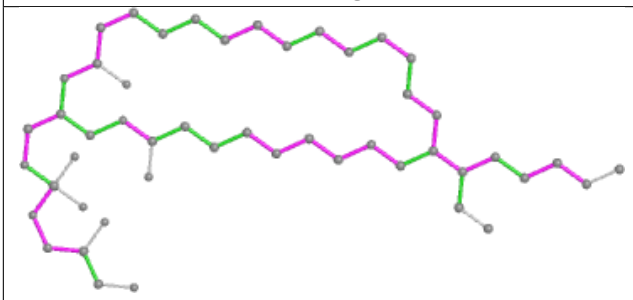
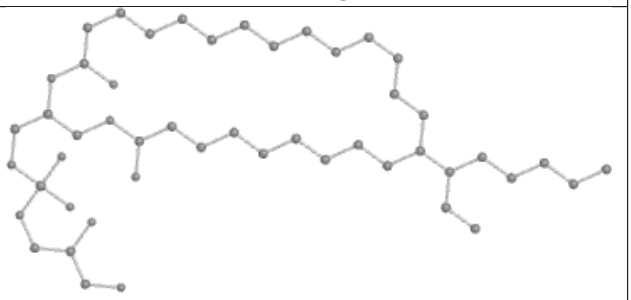


Bond angles

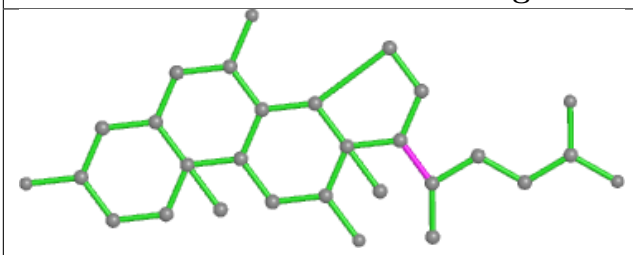


Torsions



Rings

Ligand CHD P 1271



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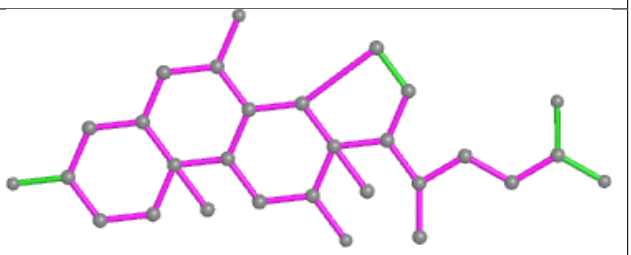
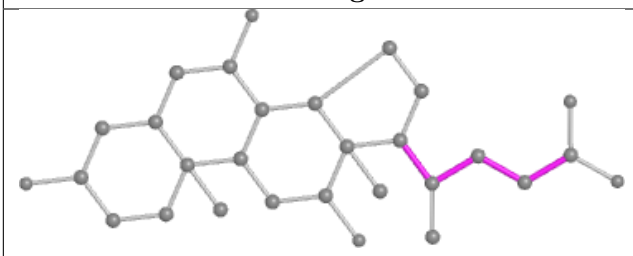


Bond angles



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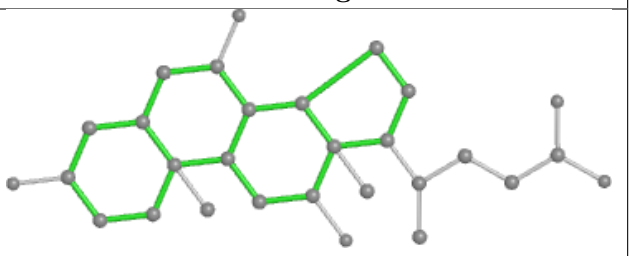
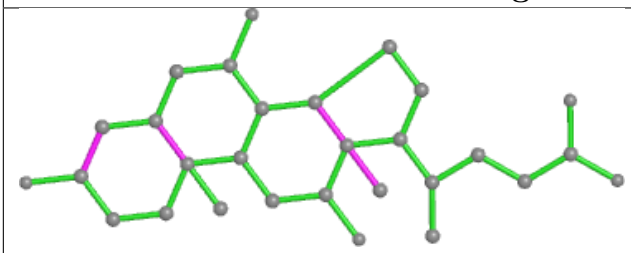


Rings

Ligand CHD B 1085



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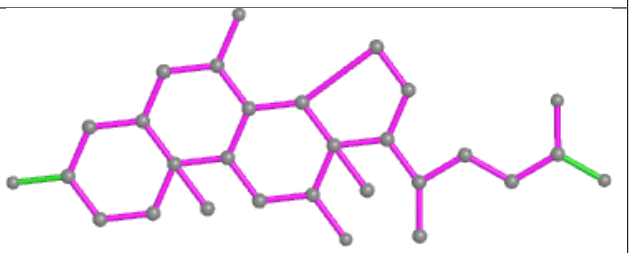
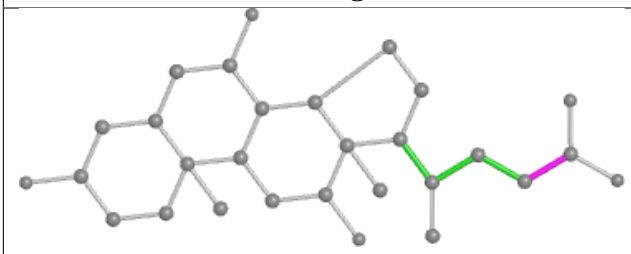


Bond angles



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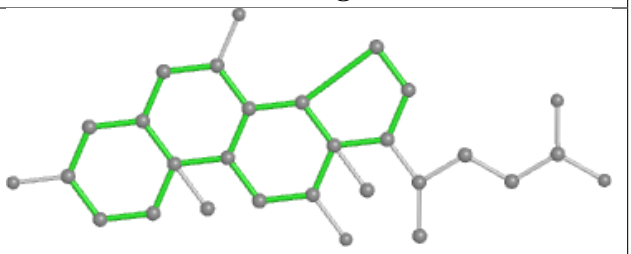
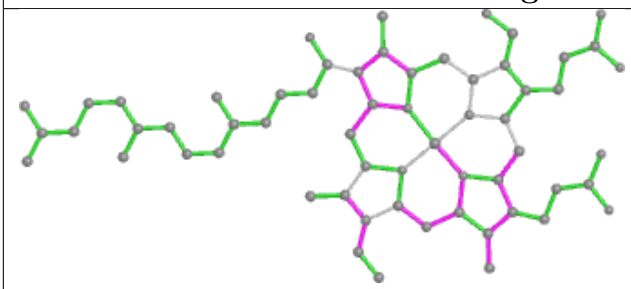


Rings

Ligand HEA N 515



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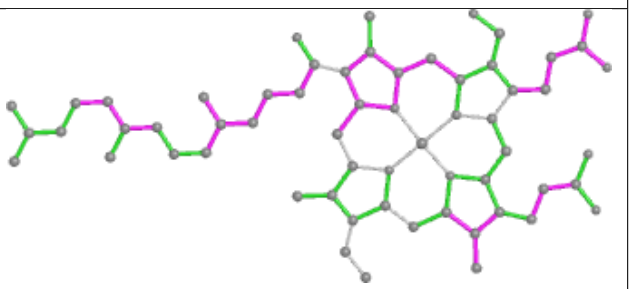
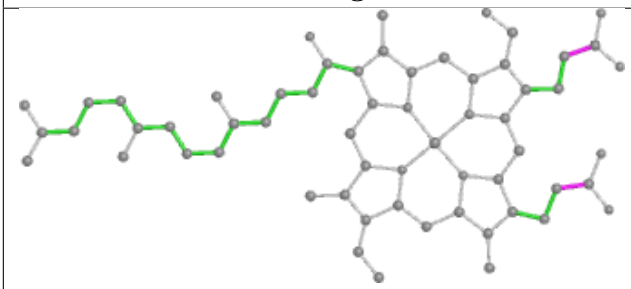
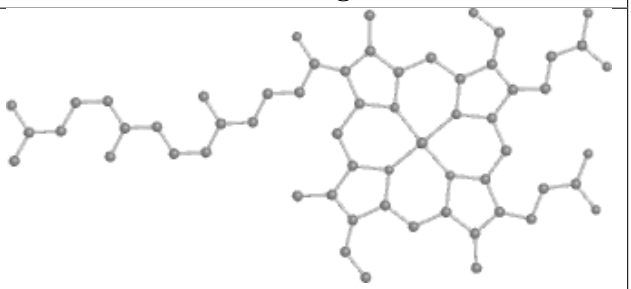


Bond angles

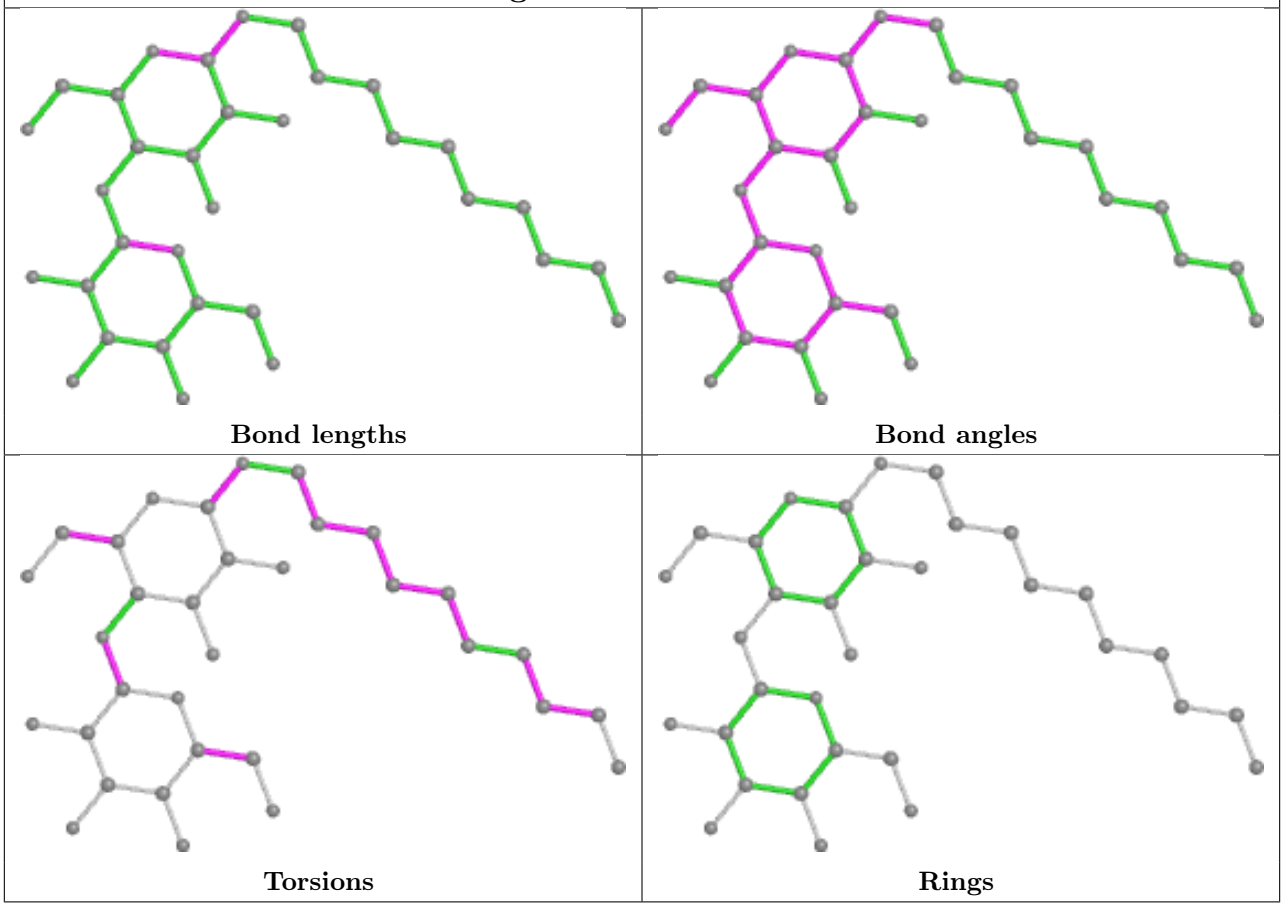


Torsions

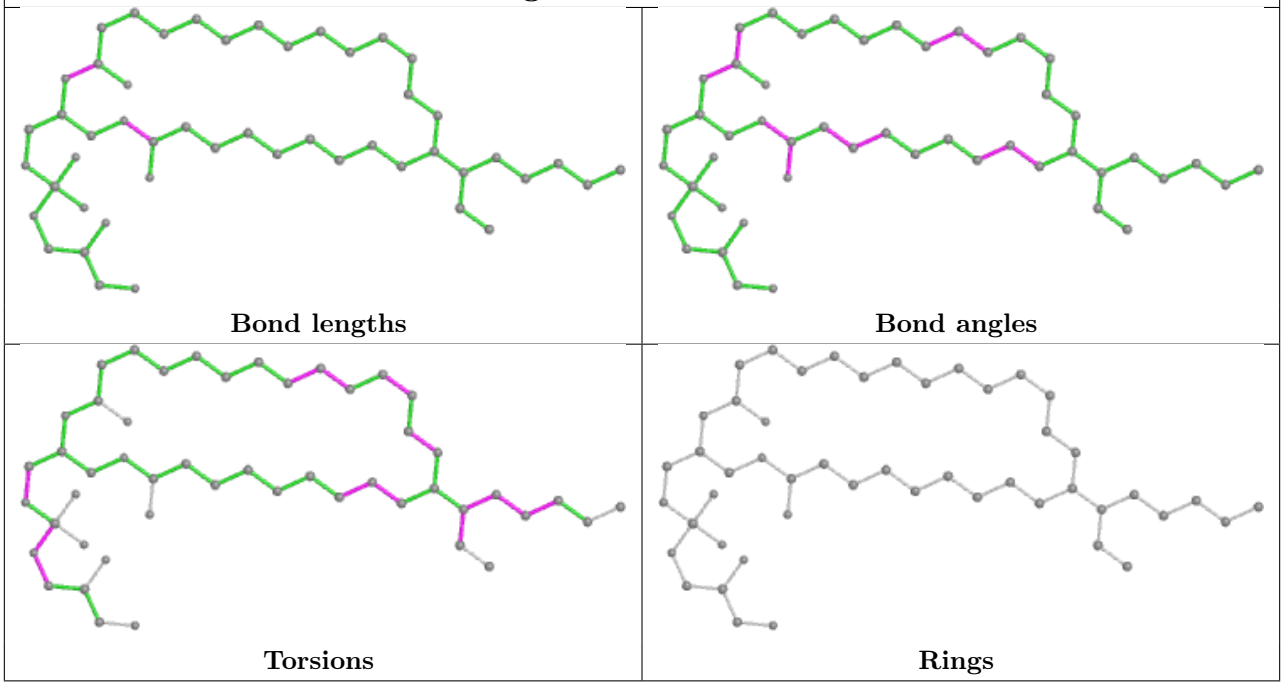


Rings

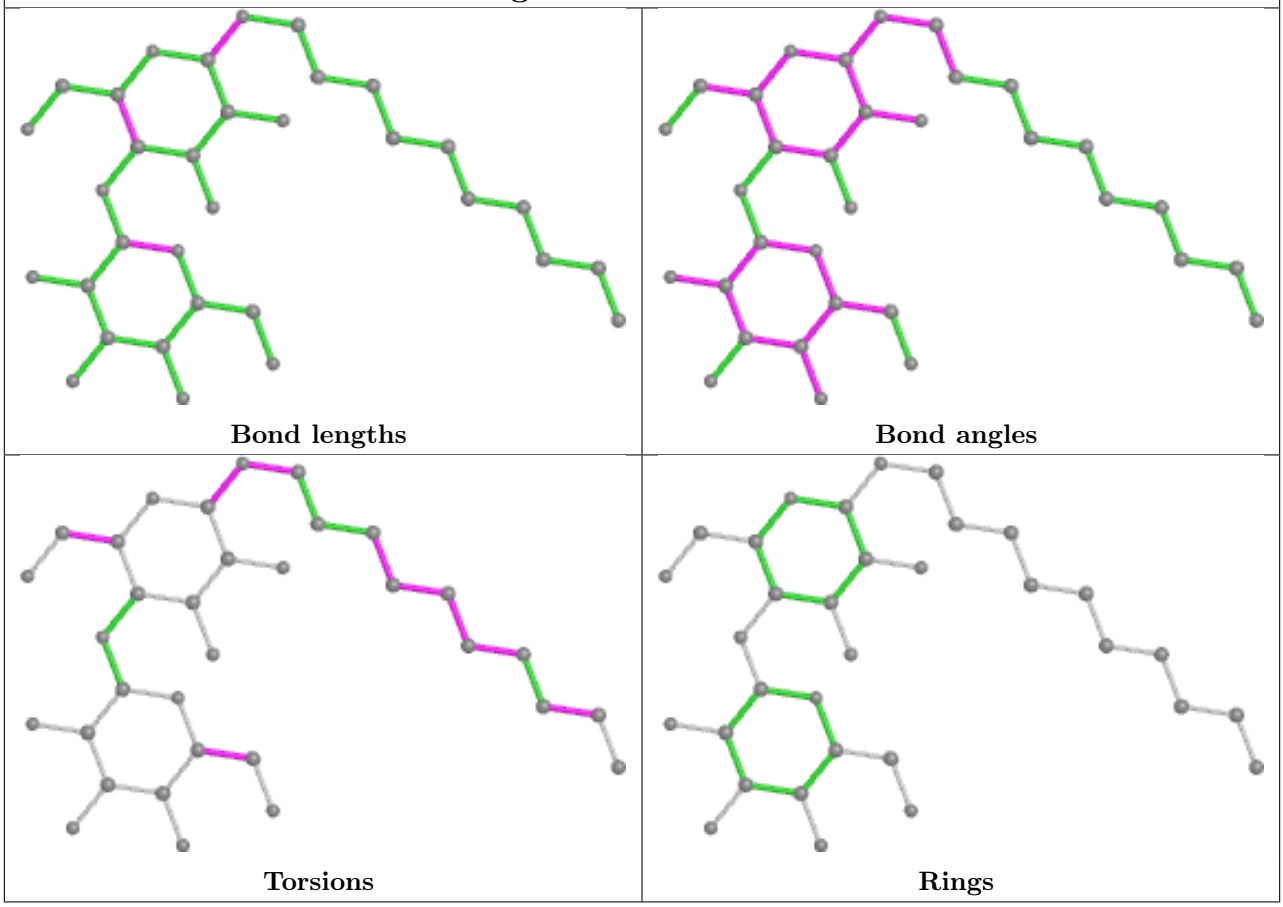
Ligand DMU T 1272



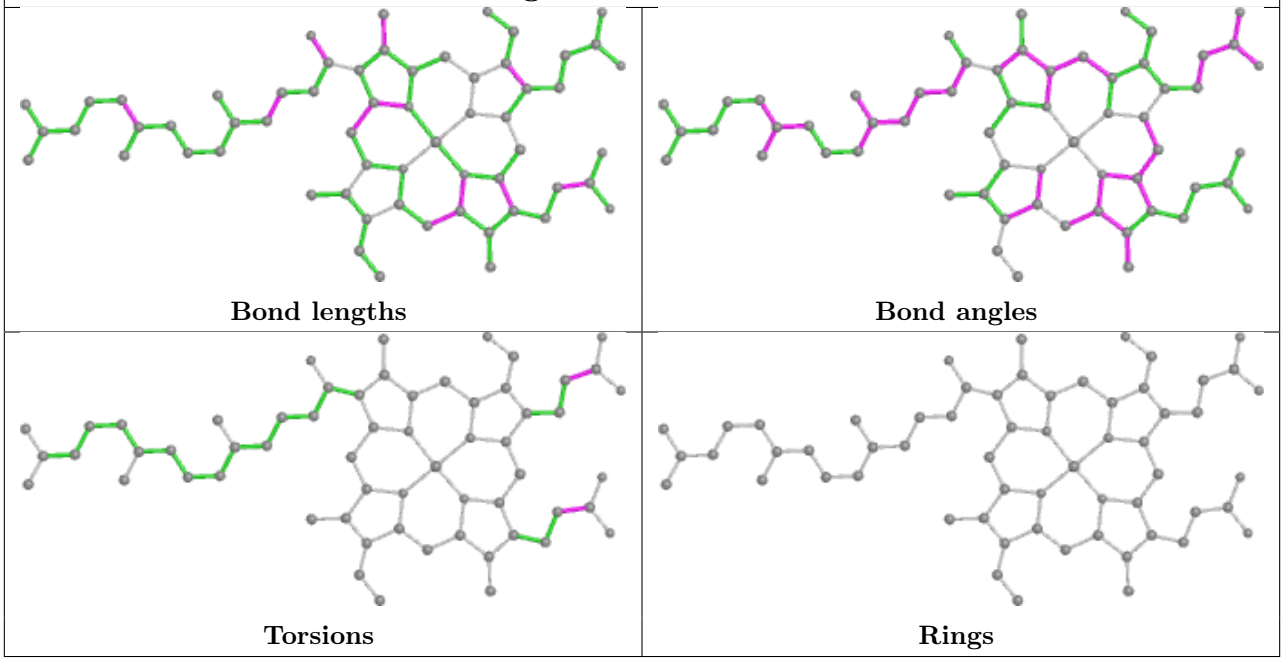
Ligand PGV C 267



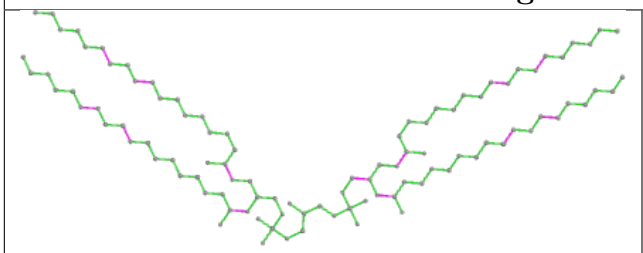
Ligand DMU Z 1526



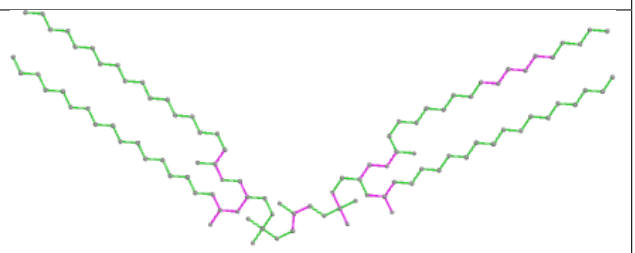
Ligand HEA A 515



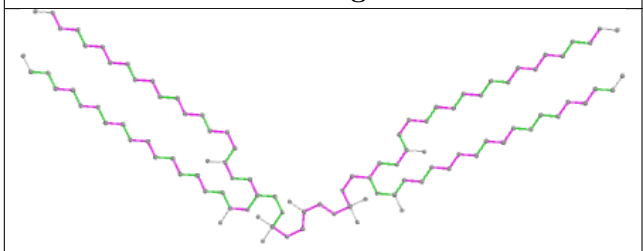
Ligand CDL T 1269



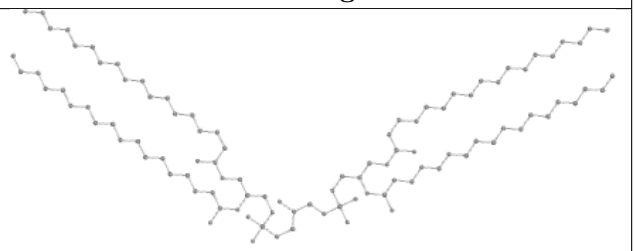
Bond lengths



Bond angles

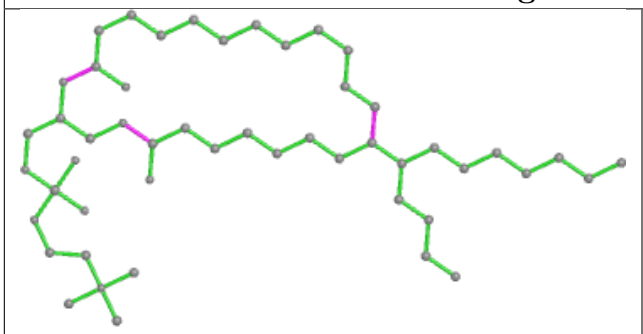


Torsions



Rings

Ligand PSC R 1229



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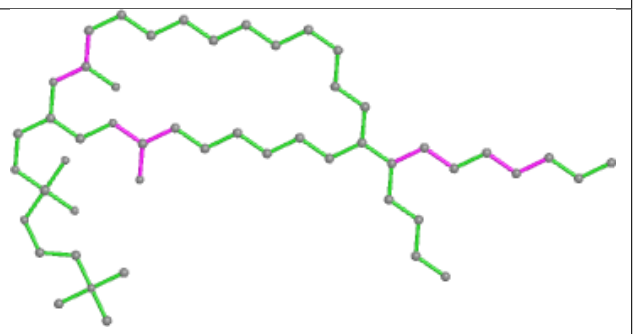
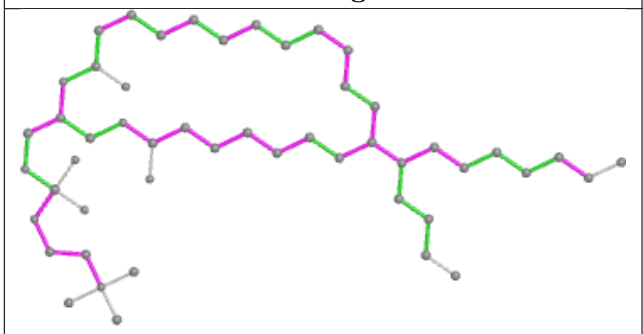
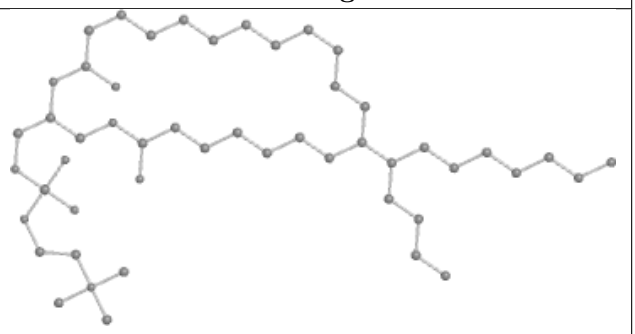


Bond angles

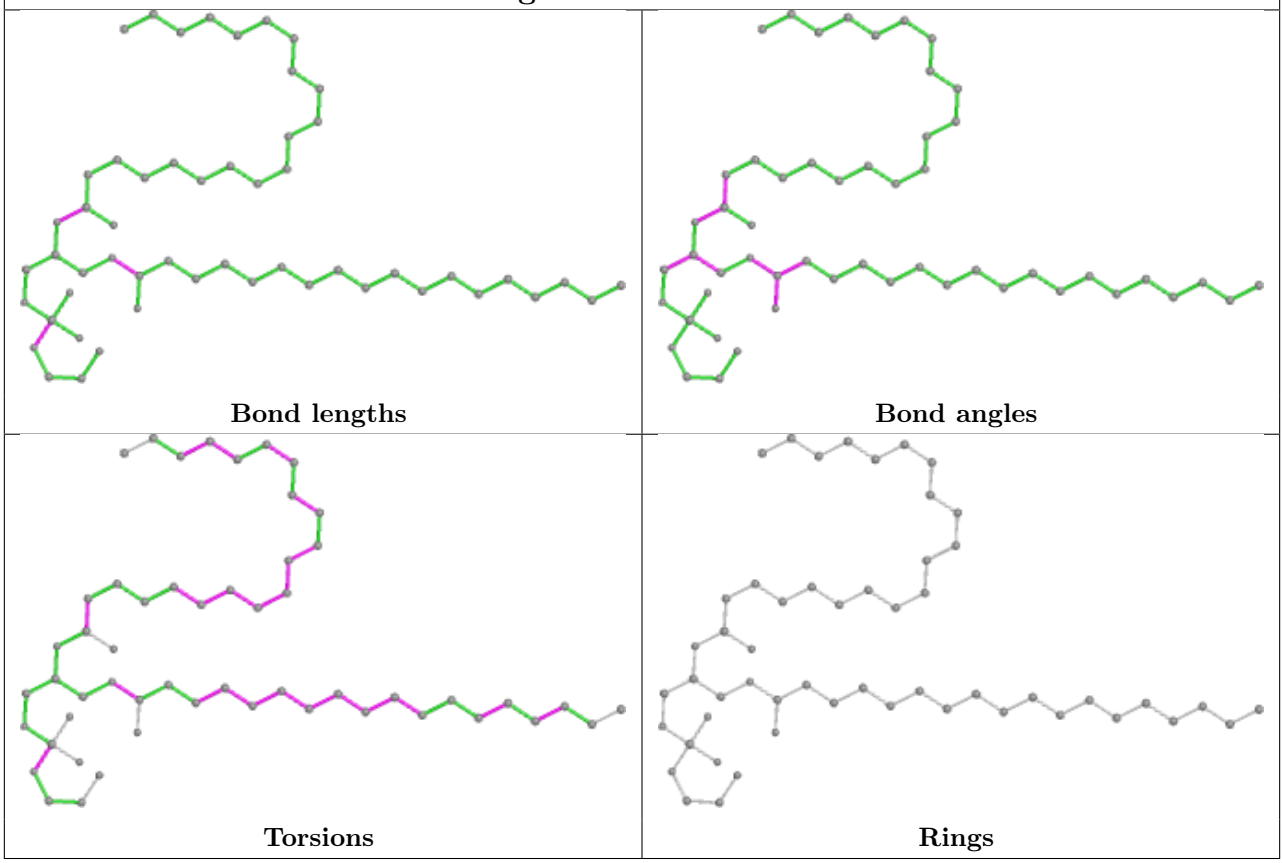


Torsions

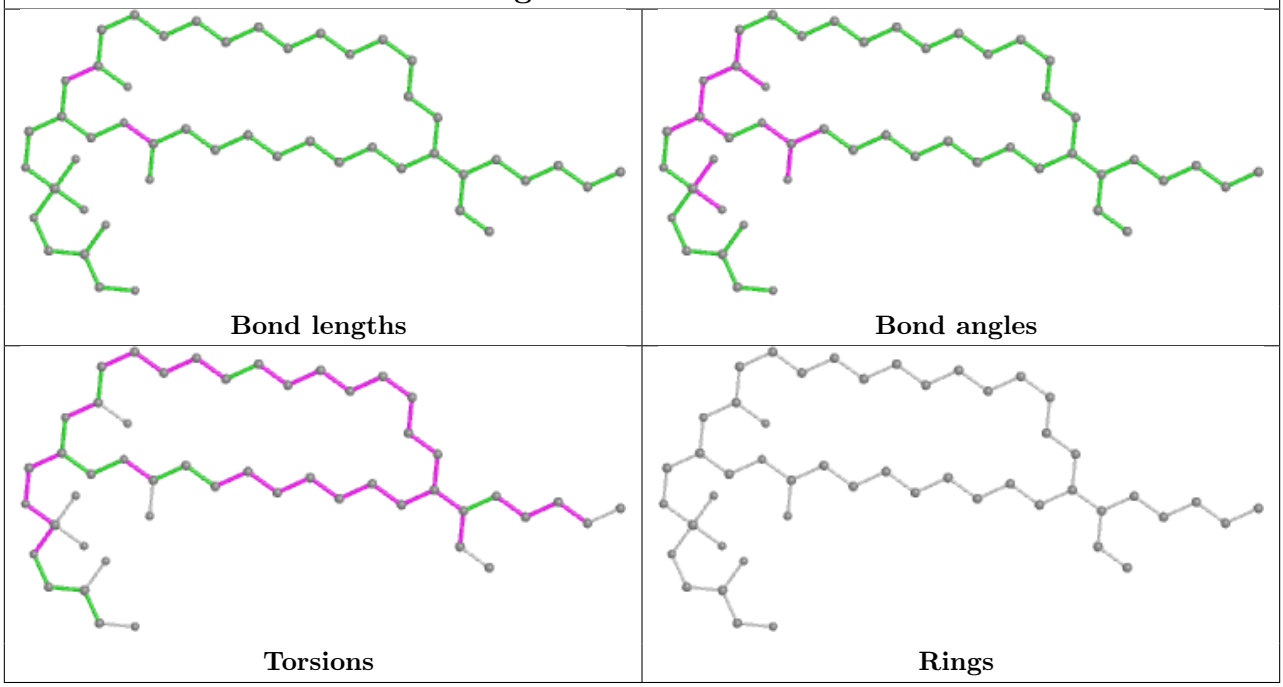


Rings

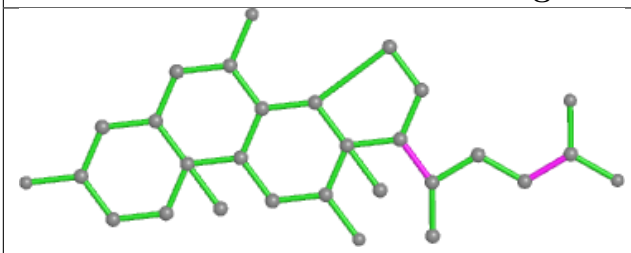
Ligand PEK S 1265



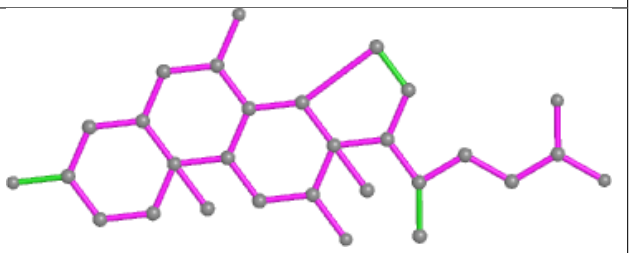
Ligand PGV P 1268



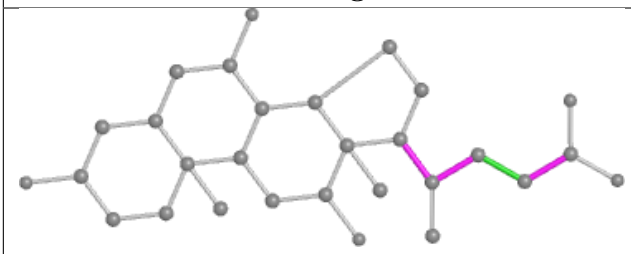
Ligand CHD J 60



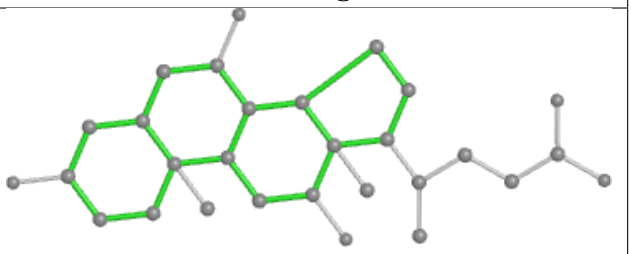
Bond lengths



Bond angles

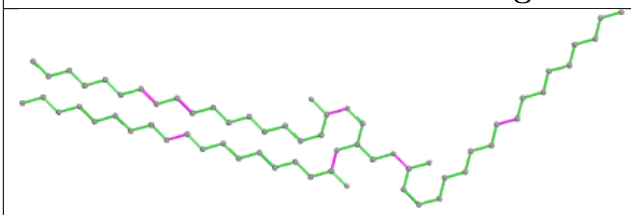


Torsions

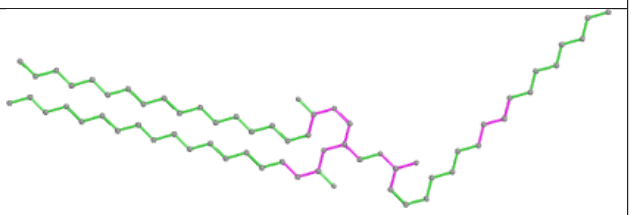


Rings

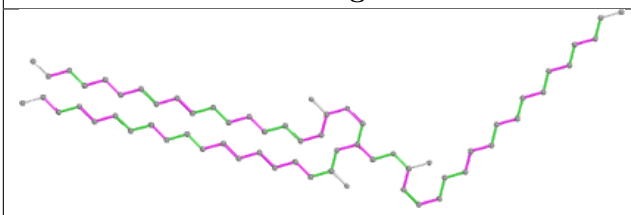
Ligand TGL N 1523



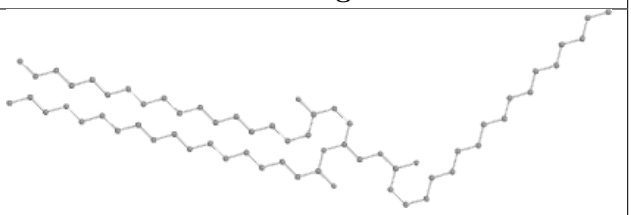
Bond lengths



Bond angles

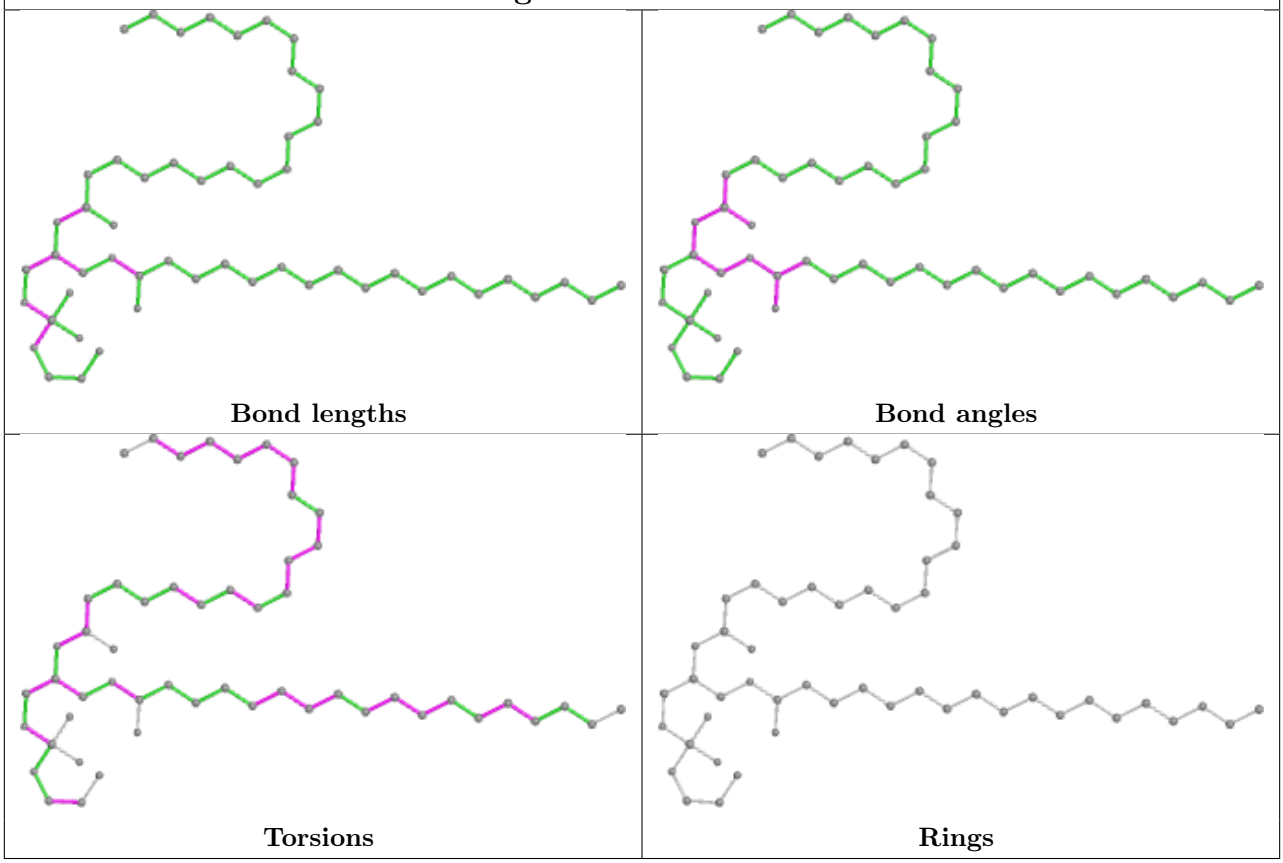


Torsions

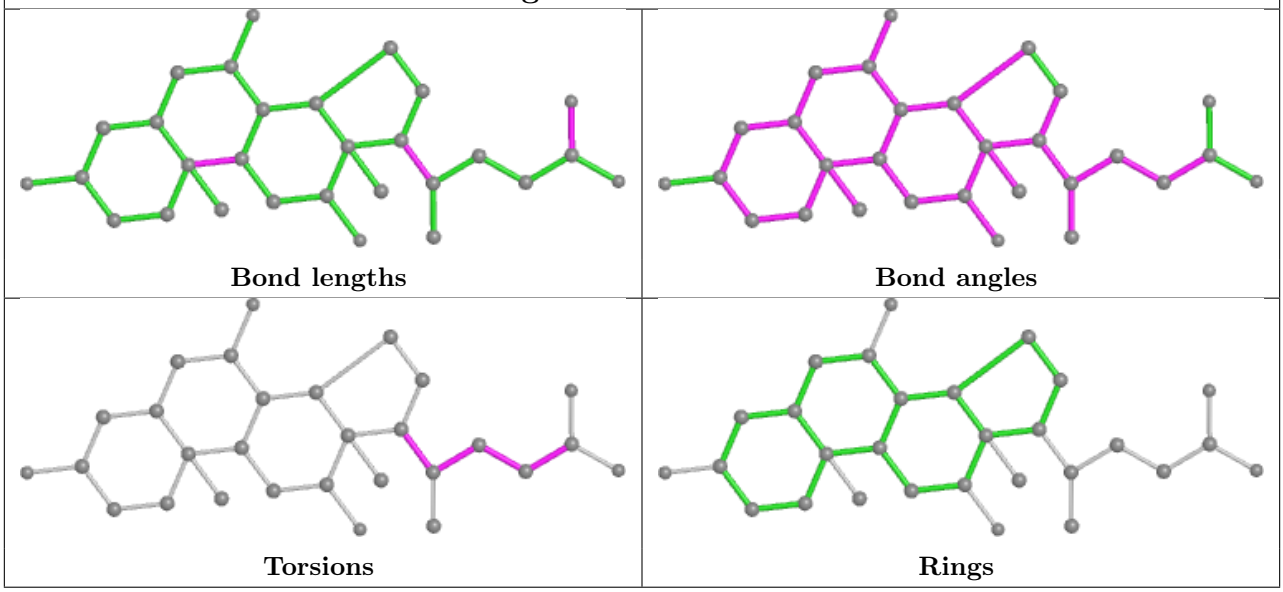


Rings

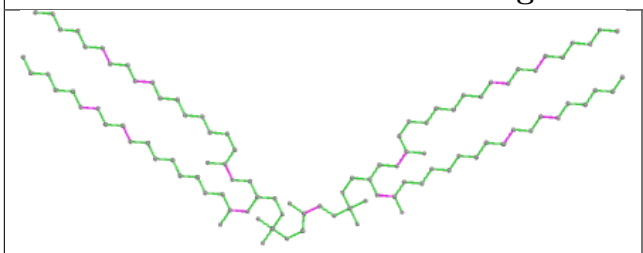
Ligand PEK G 1263



Ligand CHD C 271



Ligand CDL P 1270



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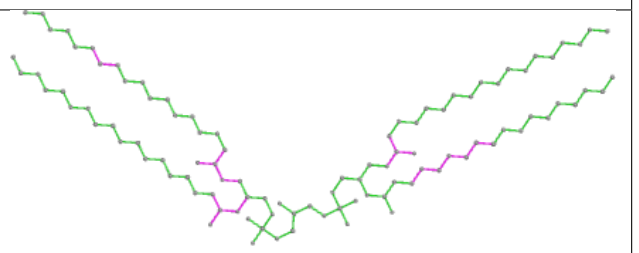
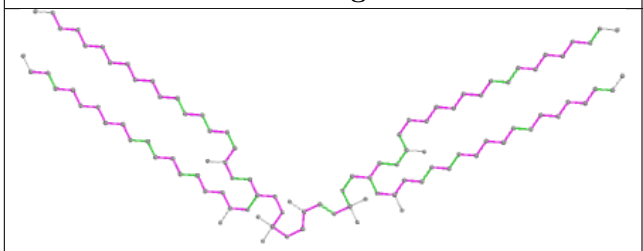
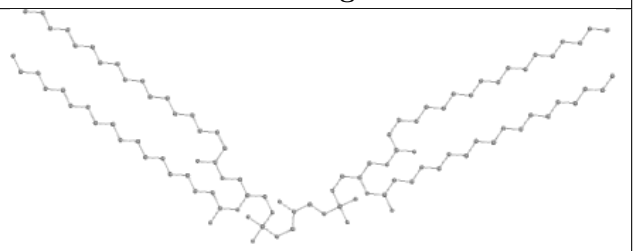


Bond angles

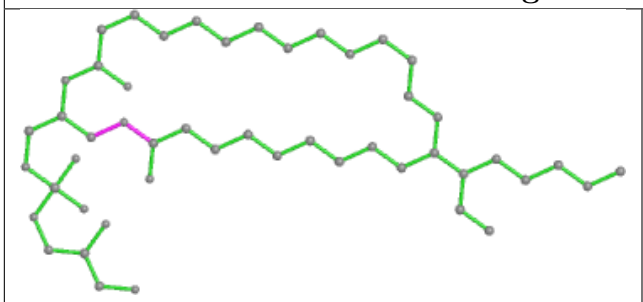


Torsions



Rings

Ligand PGV A 521



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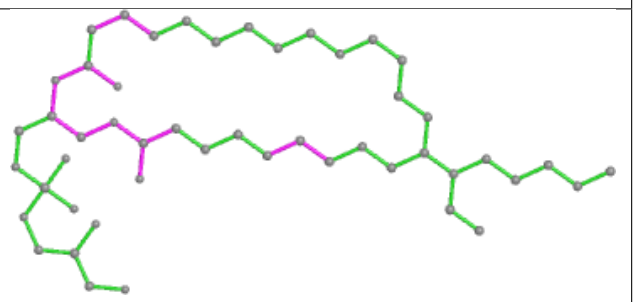
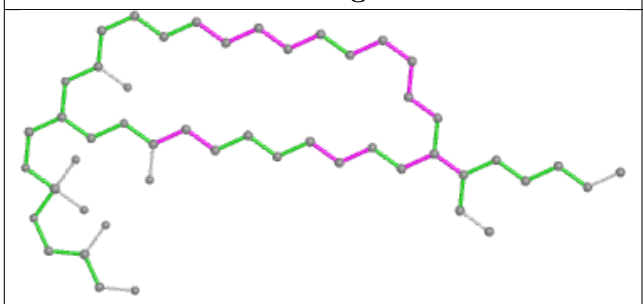


Bond angles



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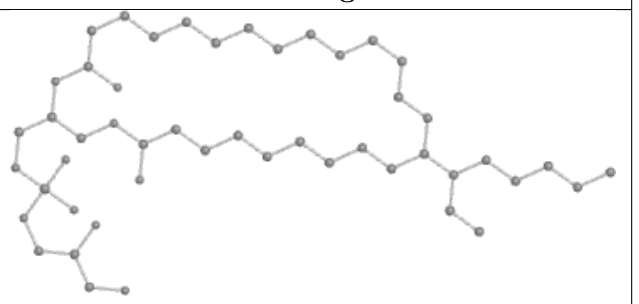
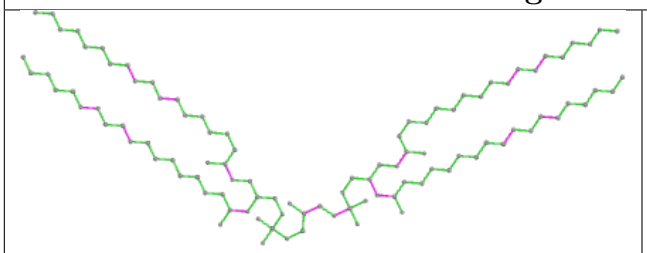


Rings

Ligand CDL C 270



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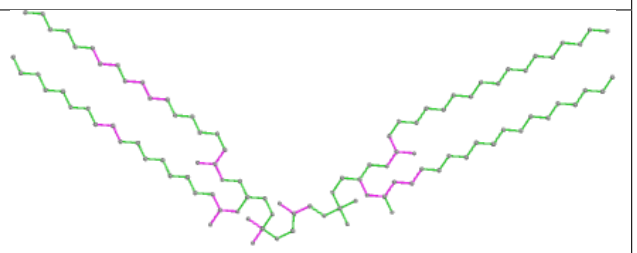
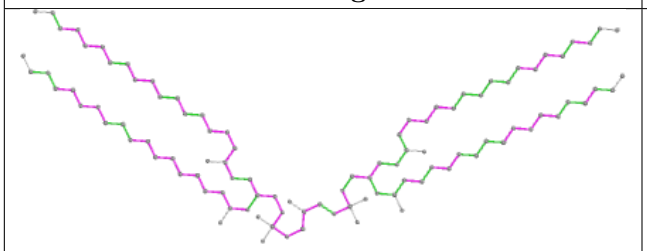


Bond angles



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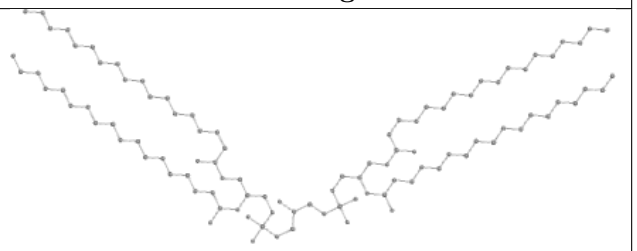
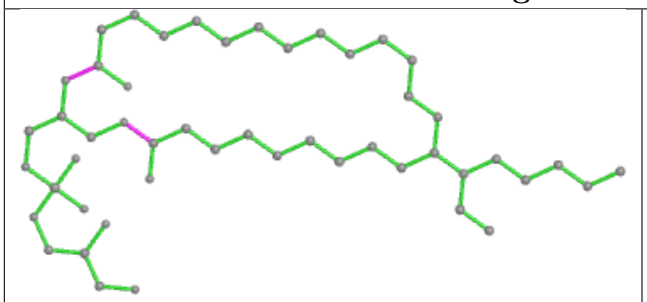


Rings

Ligand PGV N 1524



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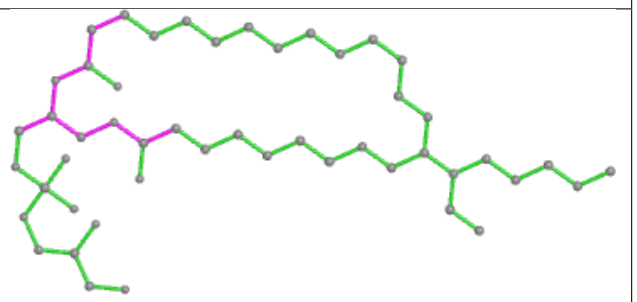
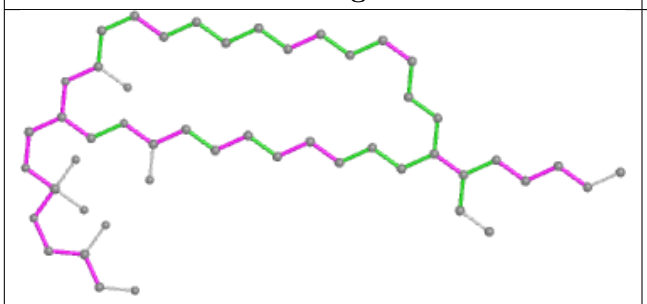


Bond angles



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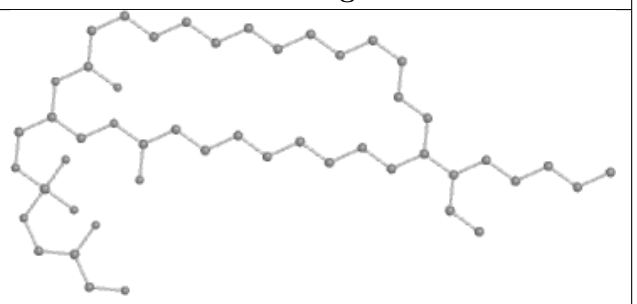
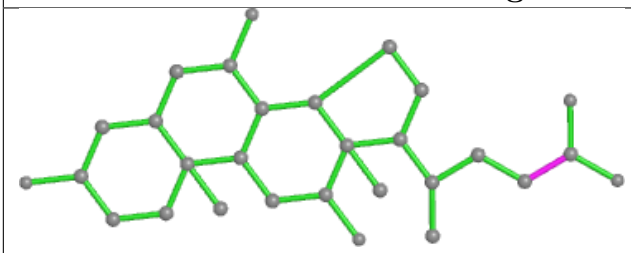
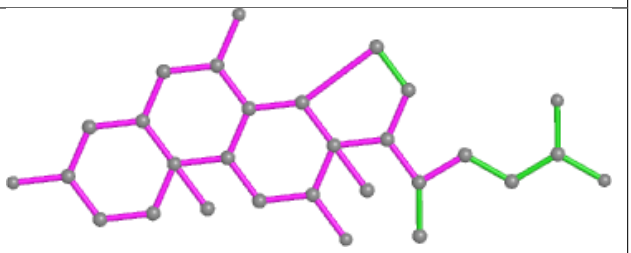


Rings

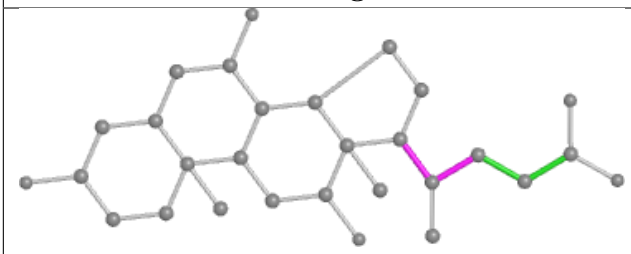
Ligand CHD W 1059



Bond lengths



Bond angles



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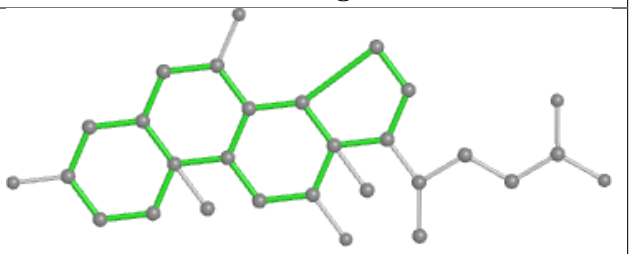
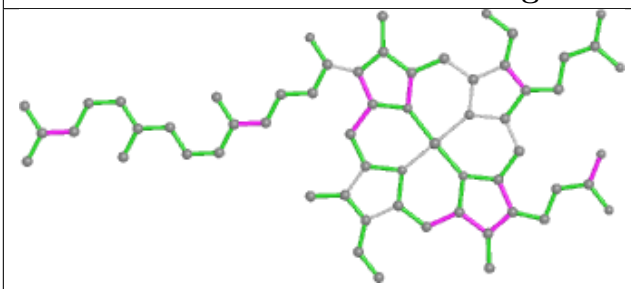


Rings

Ligand HEA A 516



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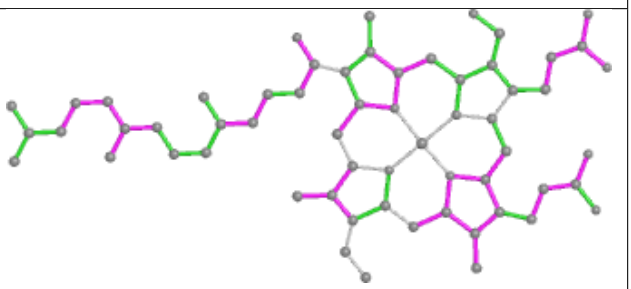
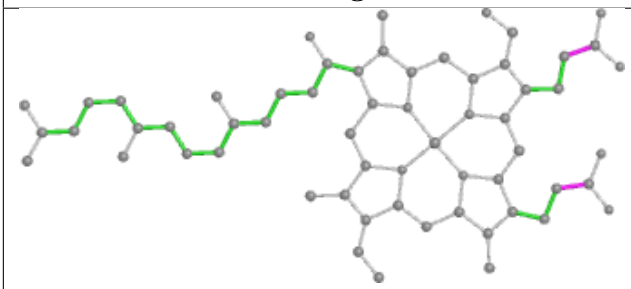


Bond angles



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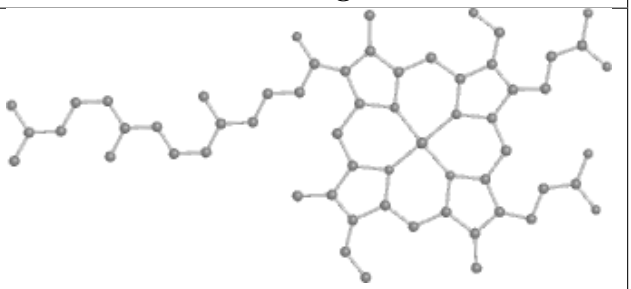
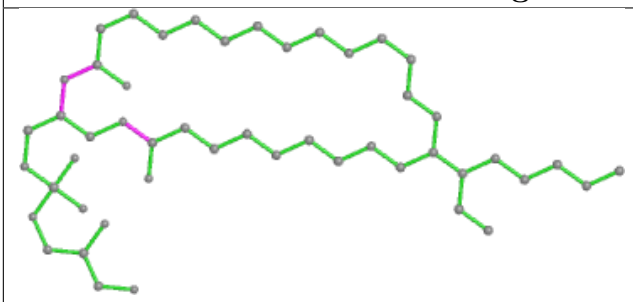


Rings

Ligand PGV N 1266



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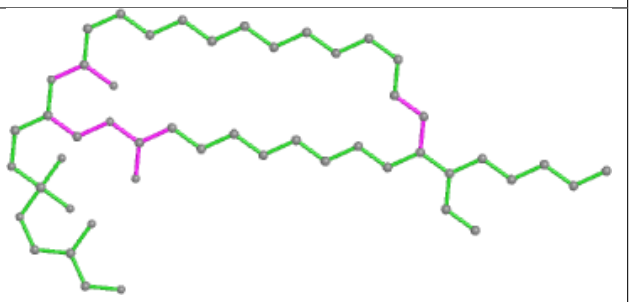
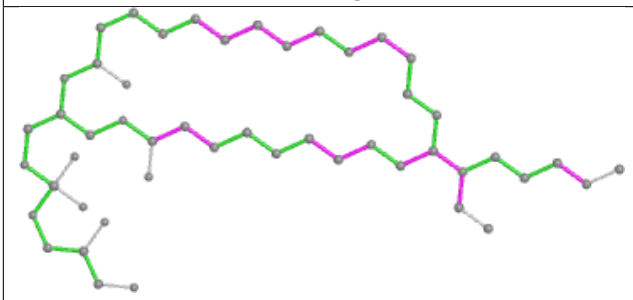
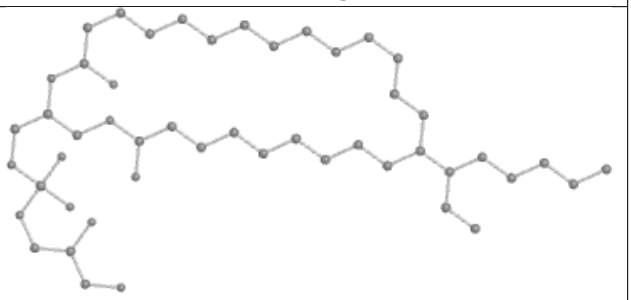


Bond angles

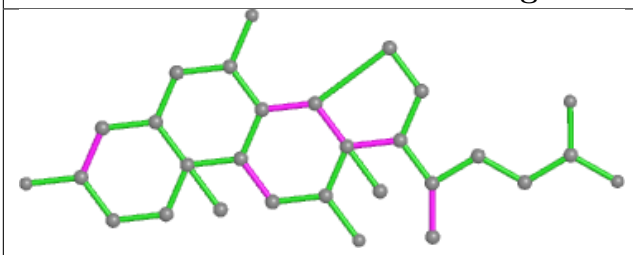


Torsions



Rings

Ligand CHD O 229



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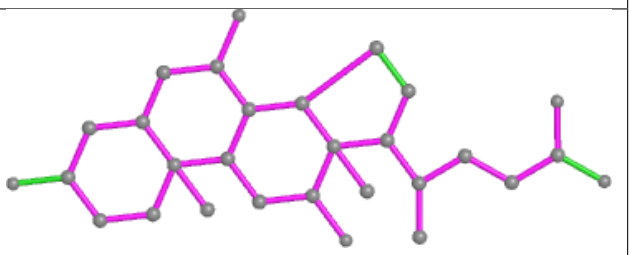
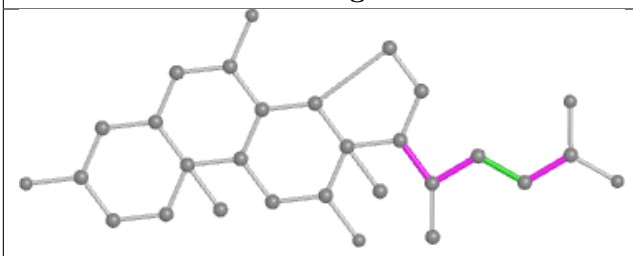
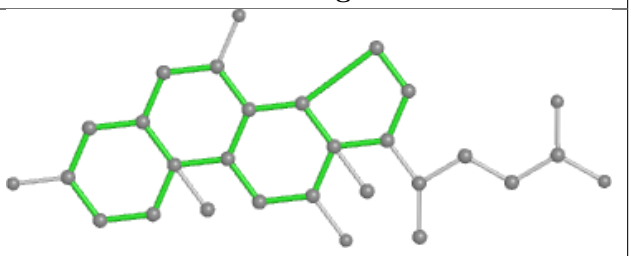


Bond angles

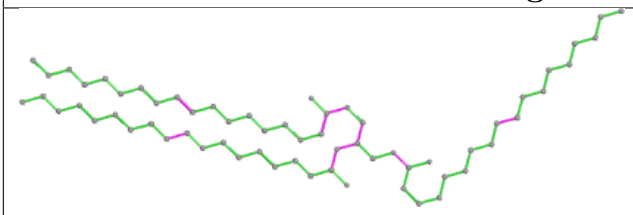


Torsions



Rings

Ligand TGL L 522



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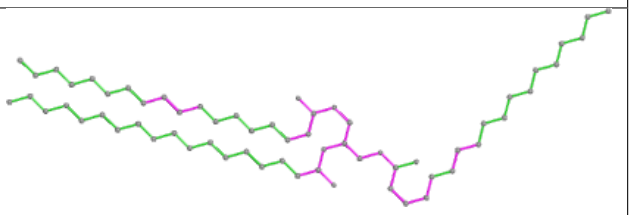
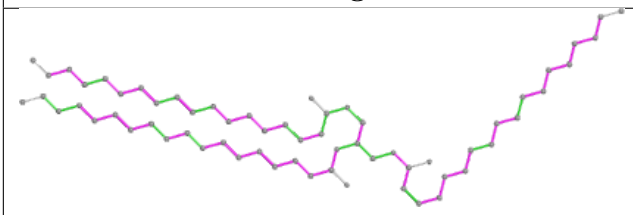


Bond angles



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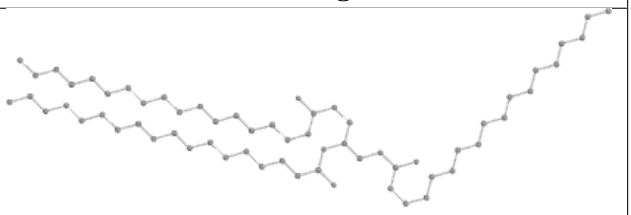
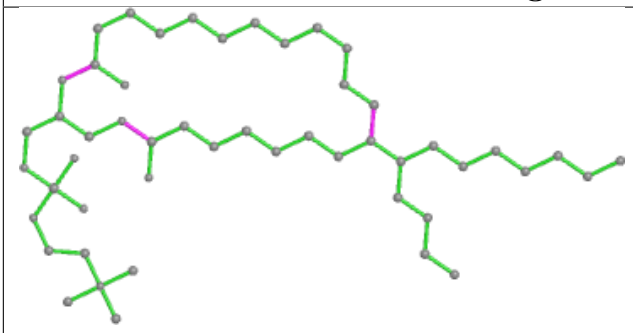


Rings

Ligand PSC B 229



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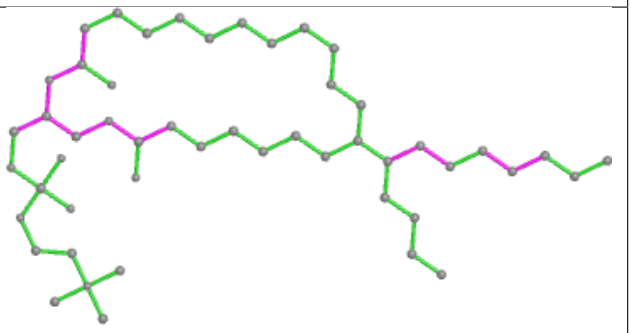
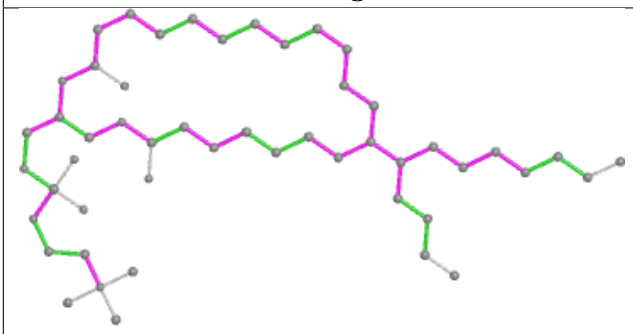
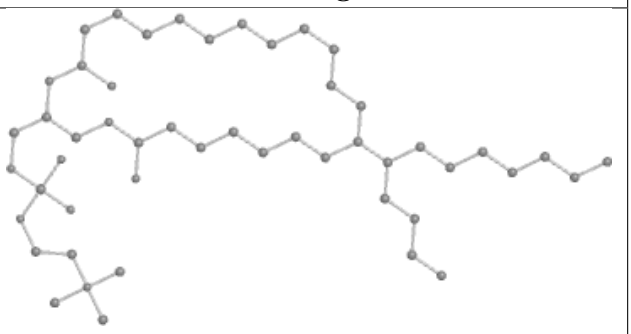


Bond angles

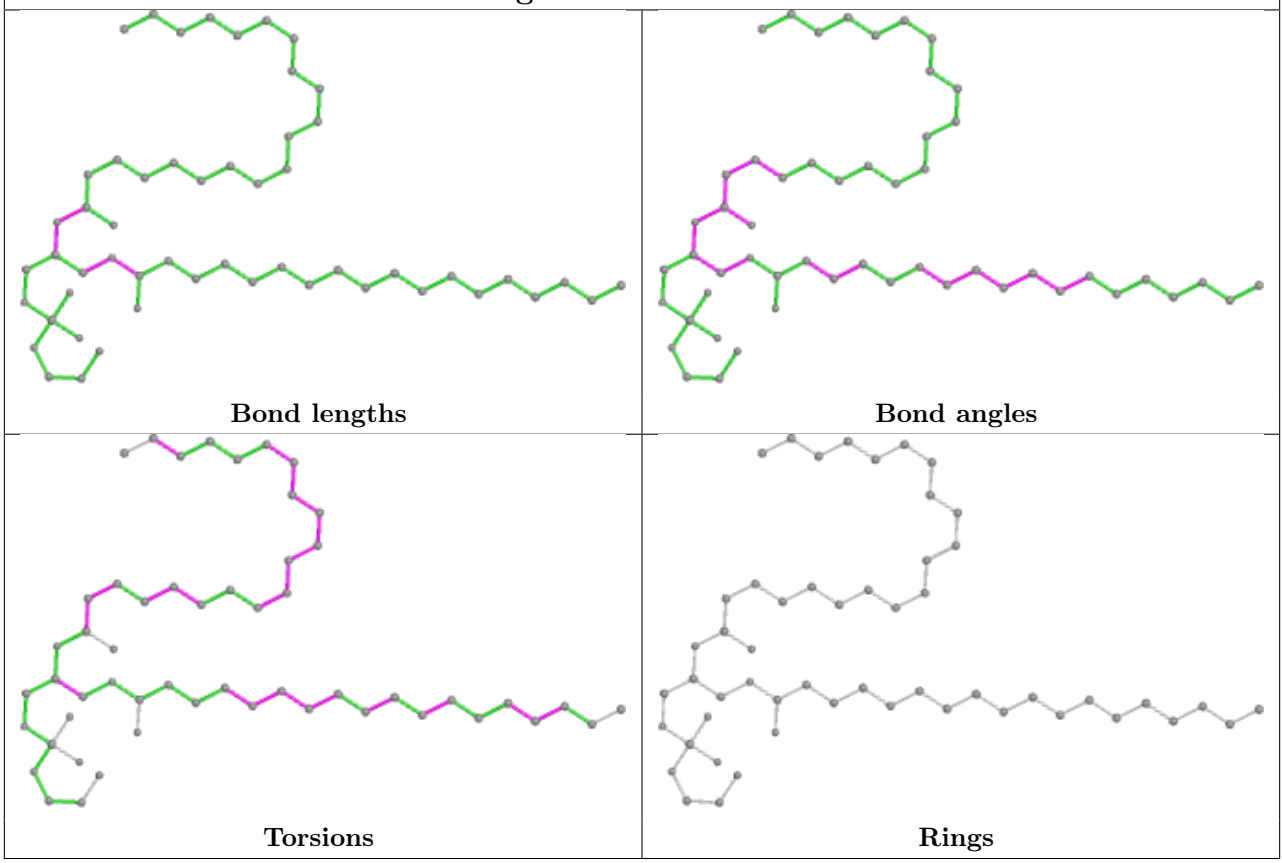


Torsions

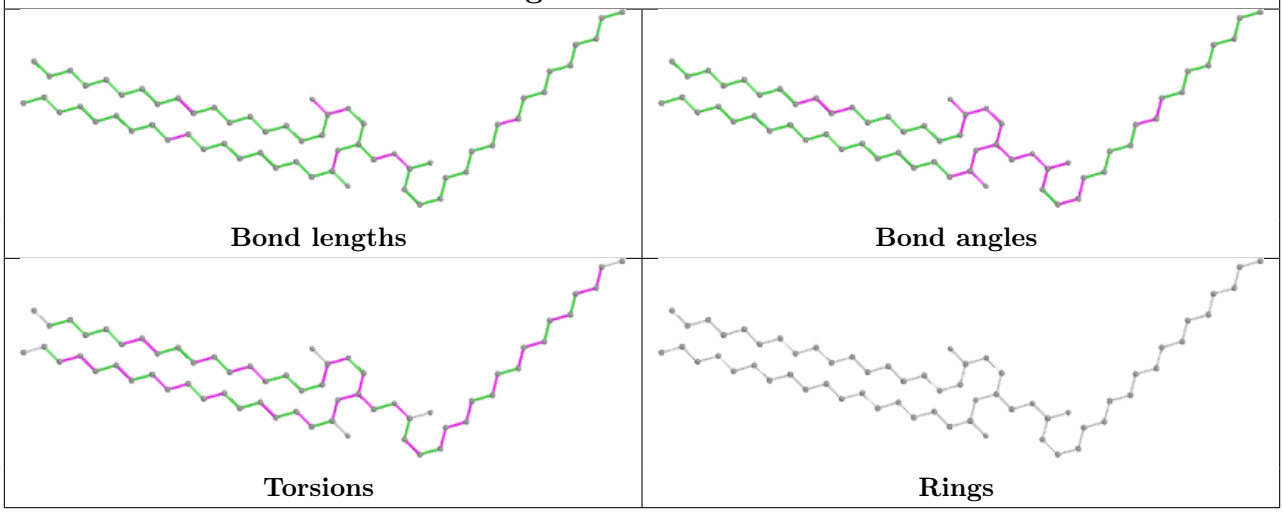


Rings

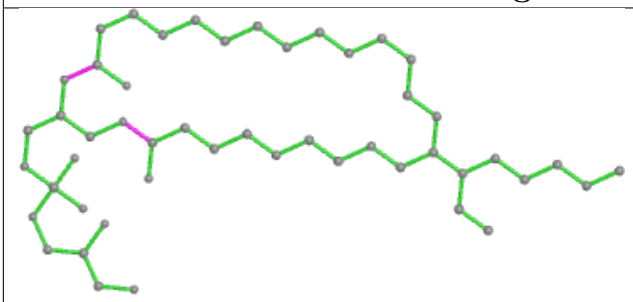
Ligand PEK T 1264



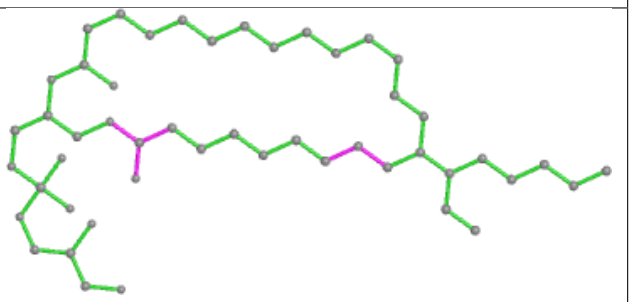
Ligand TGL B 521



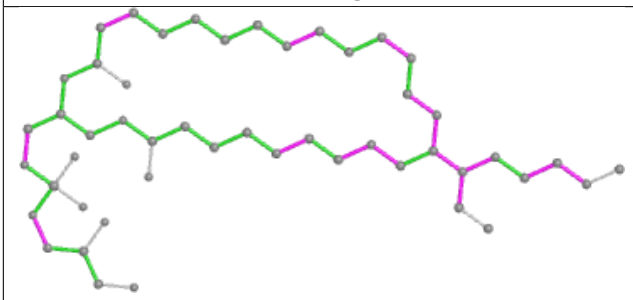
Ligand PGV P 1267



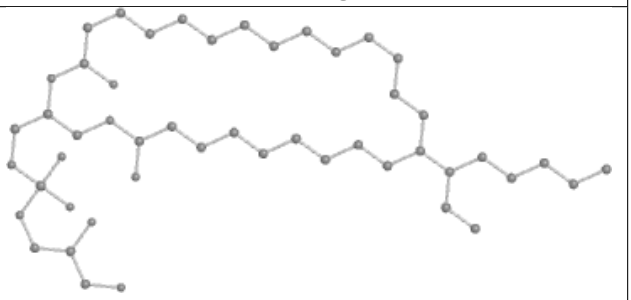
Bond lengths



Bond angles

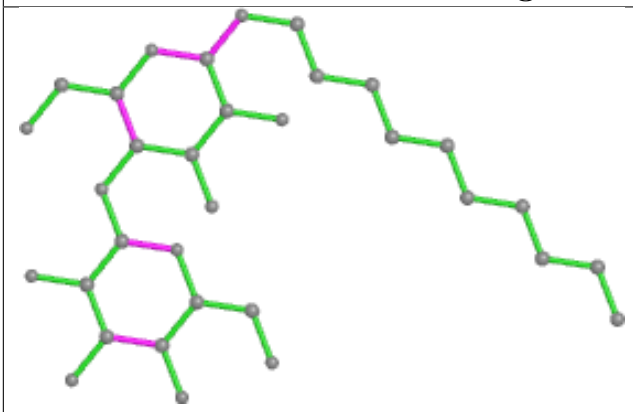


Torsions

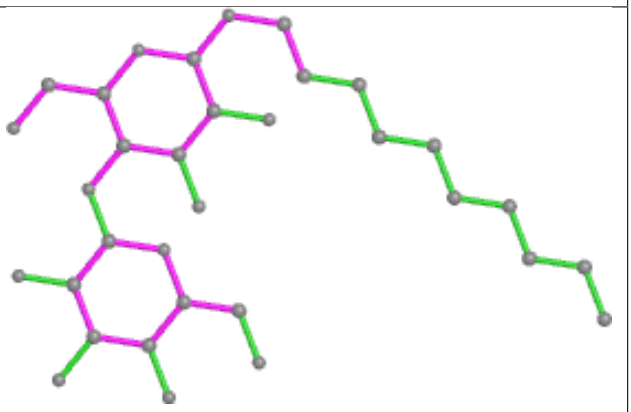


Rings

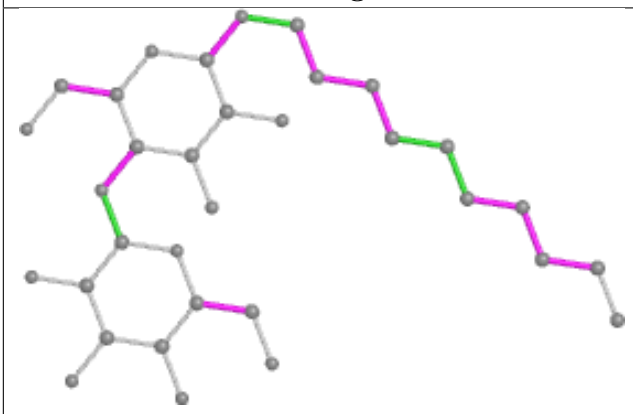
Ligand DMU C 272



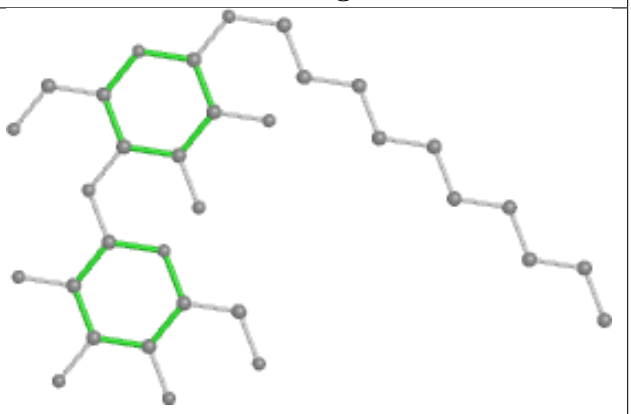
Bond lengths



Bond angles

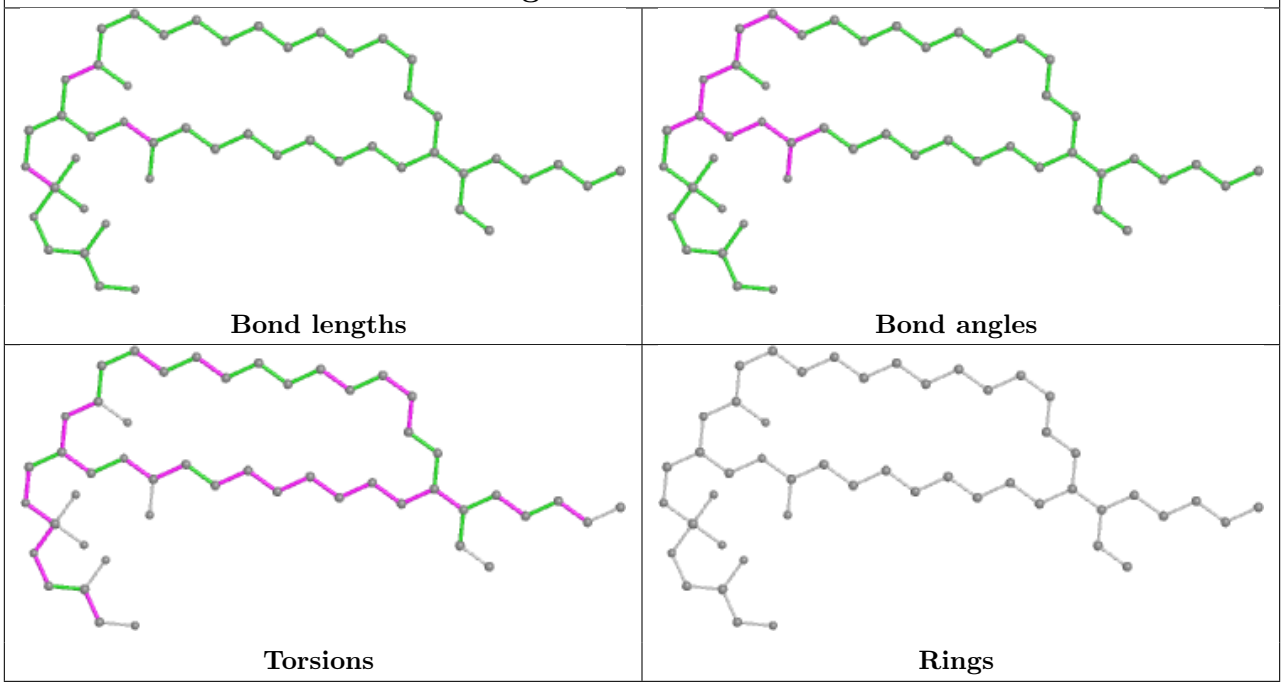


Torsions

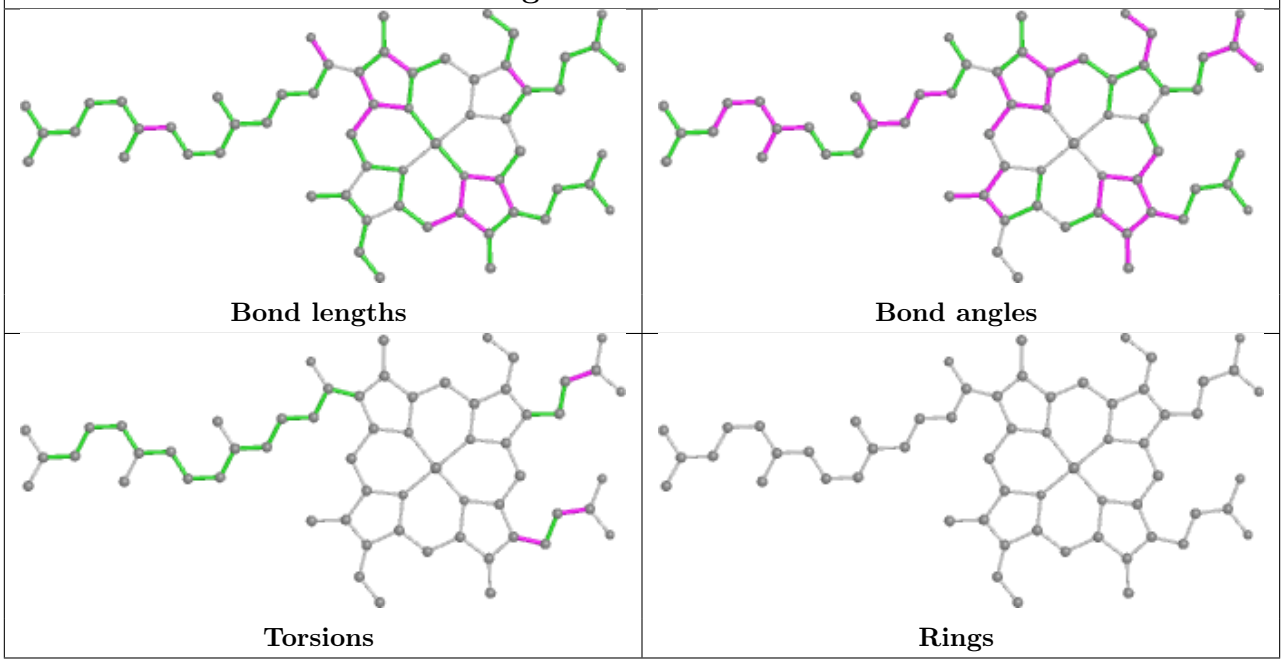


Rings

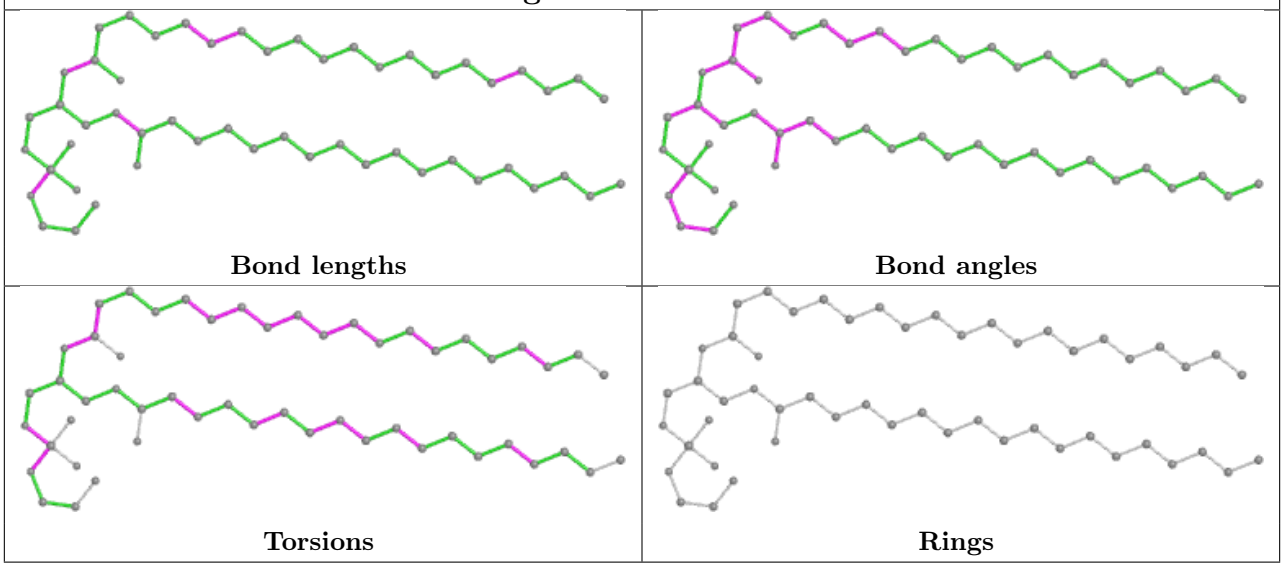
Ligand PGV A 524



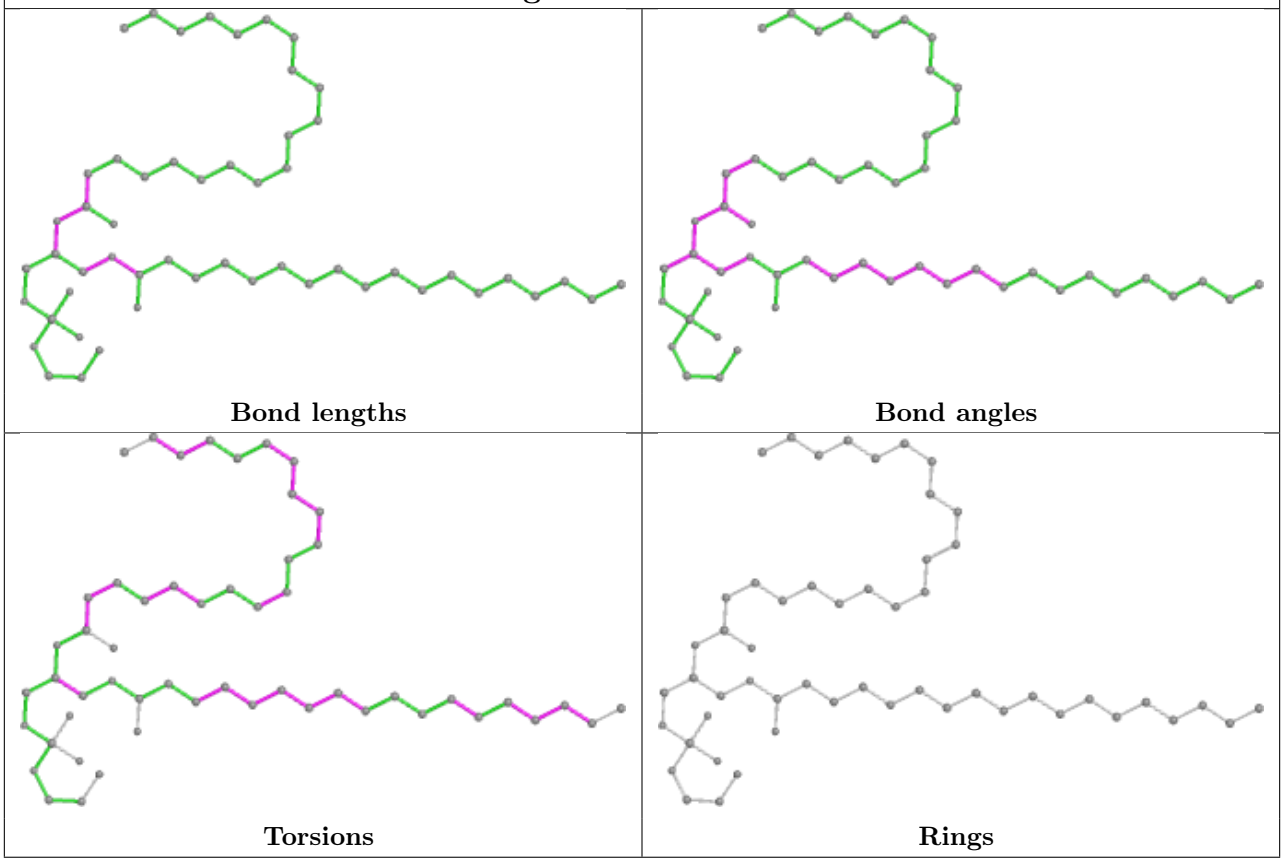
Ligand HEA N 516



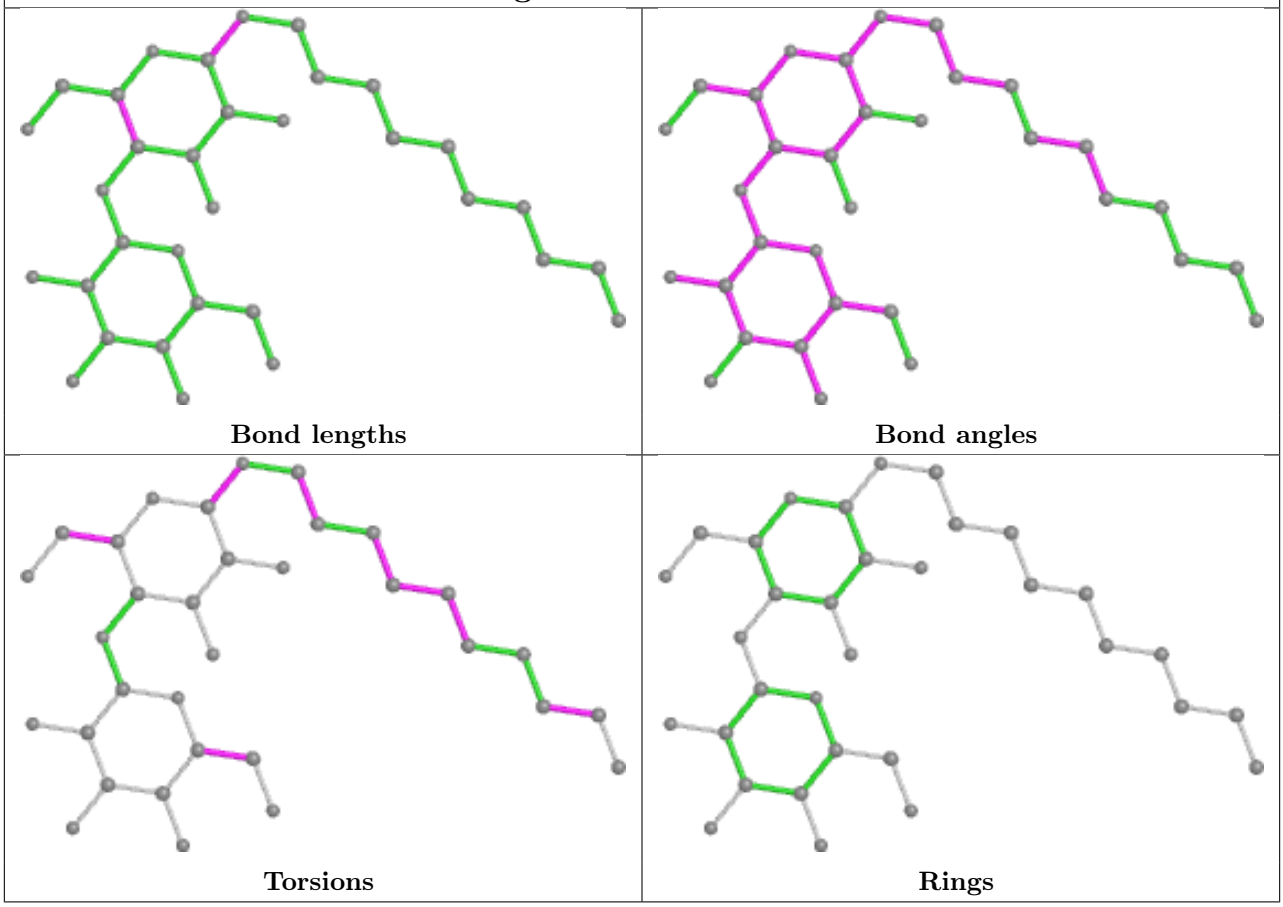
Ligand PEK G 265



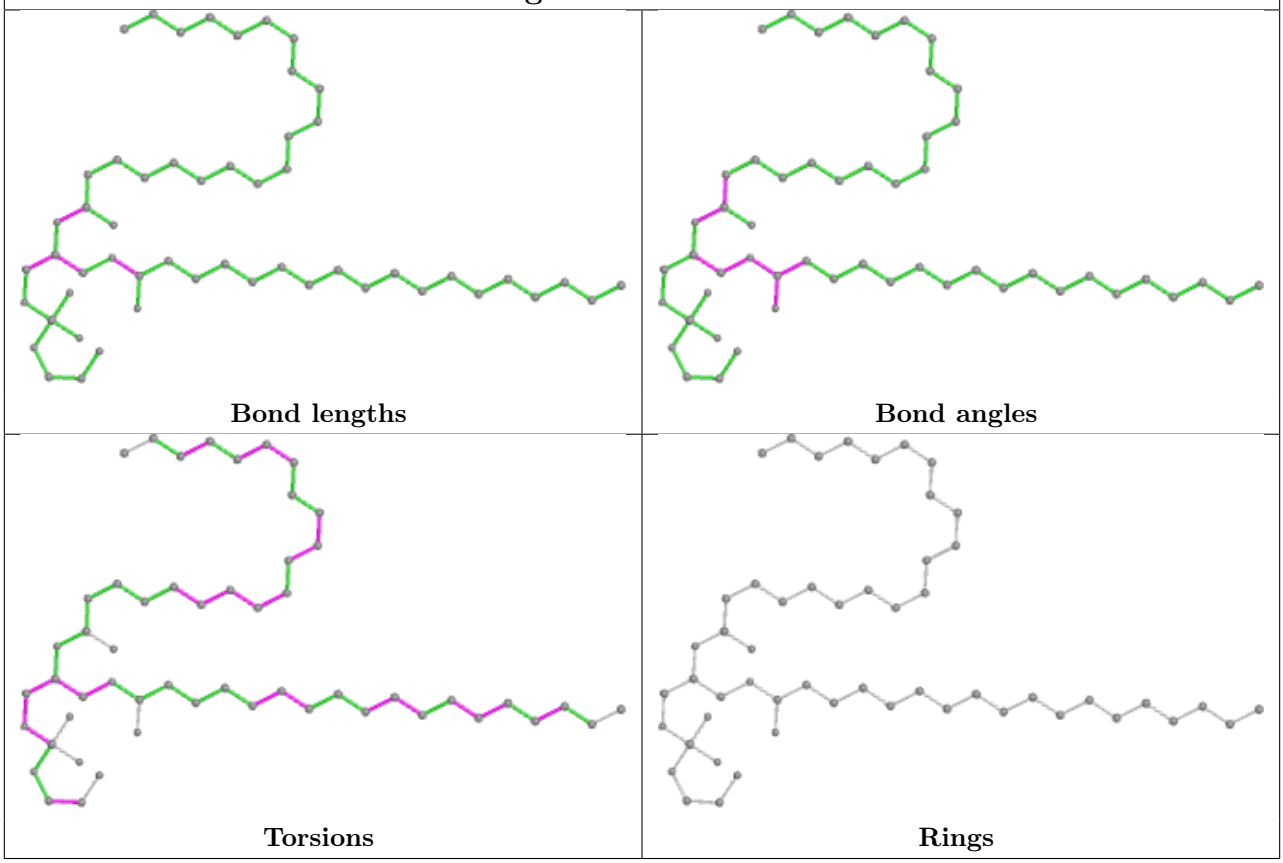
Ligand PEK G 264



Ligand DMU M 526



Ligand PEK T 263



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 (i)

6.1 Protein, DNA and RNA chains (i)

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%)	-0.09	15 (2%)	51	49	36, 42, 52, 84	0
1	N	513/514 (99%)	-0.17	10 (1%)	66	65	43, 51, 63, 92	0
2	B	226/227 (99%)	-0.45	0	100	100	36, 48, 78, 111	0
2	O	226/227 (99%)	-0.11	7 (3%)	49	47	49, 61, 93, 120	0
3	C	259/261 (99%)	0.04	20 (7%)	13	12	38, 45, 59, 86	0
3	P	259/261 (99%)	0.36	27 (10%)	6	5	44, 51, 68, 88	0
4	D	144/147 (97%)	-0.58	2 (1%)	75	73	43, 51, 75, 91	0
4	Q	144/147 (97%)	0.70	16 (11%)	5	4	55, 69, 96, 132	0
5	E	105/109 (96%)	-0.35	0	100	100	43, 51, 83, 118	0
5	R	105/109 (96%)	0.71	9 (8%)	10	9	51, 63, 92, 123	0
6	F	98/98 (100%)	-0.16	7 (7%)	16	14	40, 53, 112, 143	0
6	S	98/98 (100%)	-0.20	7 (7%)	16	14	49, 61, 113, 144	0
7	G	83/85 (97%)	0.47	15 (18%)	1	1	42, 55, 123, 129	0
7	T	83/85 (97%)	0.67	16 (19%)	1	1	46, 62, 121, 133	0
8	H	79/85 (92%)	-0.02	3 (3%)	40	38	46, 58, 119, 129	0
8	U	79/85 (92%)	-0.35	2 (2%)	57	55	54, 69, 120, 127	0
9	I	72/73 (98%)	0.20	6 (8%)	11	10	48, 60, 105, 112	0
9	V	72/73 (98%)	0.93	12 (16%)	1	1	52, 74, 109, 112	0
10	J	58/59 (98%)	0.14	4 (6%)	16	15	45, 58, 86, 119	0
10	W	58/59 (98%)	0.41	5 (8%)	10	9	54, 66, 88, 120	0
11	K	49/56 (87%)	-0.42	0	100	100	45, 57, 75, 83	0
11	X	49/56 (87%)	0.84	10 (20%)	1	1	62, 69, 85, 99	0
12	L	46/47 (97%)	-0.38	1 (2%)	62	59	43, 48, 70, 100	0
12	Y	46/47 (97%)	-0.14	3 (6%)	18	17	53, 61, 82, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	M	43/46 (93%)	-0.33	1 (2%) 60 58	44, 51, 88, 120	0
13	Z	43/46 (93%)	0.44	7 (16%) 1 1	57, 65, 96, 121	0
All	All	3550/3614 (98%)	0.01	205 (5%) 23 22	36, 53, 92, 144	0

All (205) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	Q	6	VAL	14.6
4	Q	5	VAL	11.0
7	T	1	ALA	10.7
6	F	1	ALA	10.3
4	Q	7	LYS	10.1
7	G	1	ALA	9.7
4	Q	8	SER	9.4
7	G	8	HIS	9.2
10	J	58	LYS	8.0
6	S	1	ALA	7.7
7	T	3	ALA	7.7
9	V	30	GLY	7.6
9	I	30	GLY	7.5
13	Z	43	SER	7.1
10	W	58	LYS	7.1
6	F	96	LEU	6.7
6	S	2	SER	6.6
8	H	46	LYS	6.3
6	F	97	ALA	6.2
6	S	96	LEU	6.2
7	G	2	SER	6.0
7	T	40	GLY	5.9
4	Q	4	SER	5.9
9	I	29	LEU	5.9
7	T	8	HIS	5.8
6	F	98	HIS	5.6
6	S	97	ALA	5.6
10	W	52	TRP	5.5
7	G	40	GLY	5.4
7	G	5	LYS	5.3
6	F	2	SER	5.3
12	L	2	HIS	5.3
9	V	29	LEU	5.1
7	T	4	ALA	5.1

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Mol	Chain	Res	Type	RSRZ
5	R	109	VAL	4.9
7	G	9	GLY	4.8
9	I	37	PHE	4.7
10	J	1	PHE	4.6
6	S	98	HIS	4.5
7	T	5	LYS	4.5
3	P	247	VAL	4.5
13	M	43	SER	4.5
4	Q	147	LYS	4.5
13	Z	42	LYS	4.4
11	X	13	TYR	4.4
9	V	25	PHE	4.3
3	P	92	LEU	4.3
10	W	48	TYR	4.2
9	V	37	PHE	4.1
7	G	3	ALA	4.1
3	P	91	VAL	4.1
10	W	57	HIS	4.0
7	G	36	TRP	4.0
7	G	84	LYS	4.0
7	T	36	TRP	4.0
3	P	259	TRP	3.8
3	P	254	VAL	3.8
1	A	285	PHE	3.8
3	P	248	VAL	3.8
5	R	108	LYS	3.8
11	X	31	TYR	3.7
3	P	258	TRP	3.7
5	R	5	HIS	3.7
3	P	251	PHE	3.7
11	X	7	PRO	3.6
3	C	92	LEU	3.6
7	T	41	HIS	3.6
1	N	196	LEU	3.6
6	S	95	GLN	3.5
3	P	98	PHE	3.5
7	T	2	SER	3.5
8	H	45	ALA	3.5
4	Q	51	LEU	3.5
1	A	197	LEU	3.4
7	T	84	LYS	3.4
8	U	7	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
3	P	252	LEU	3.4
7	G	39	SER	3.4
1	N	197	LEU	3.4
3	P	84	ILE	3.4
3	P	95	THR	3.4
1	A	193	VAL	3.4
3	C	88	ILE	3.4
3	P	88	ILE	3.4
1	N	201	VAL	3.3
9	V	2	THR	3.3
4	Q	111	PHE	3.3
9	V	19	PHE	3.3
11	X	9	PHE	3.3
10	J	57	HIS	3.3
2	O	5	MET	3.2
3	C	91	VAL	3.2
1	A	237	PHE	3.2
9	V	33	THR	3.2
7	T	39	SER	3.2
3	C	251	PHE	3.1
2	O	131	GLY	3.1
3	C	95	THR	3.1
13	Z	32	TRP	3.1
9	V	26	MET	3.1
3	P	244	PHE	3.1
2	O	90	ILE	3.0
8	U	48	GLY	3.0
5	R	106	LEU	3.0
3	P	94	PHE	3.0
7	G	6	GLY	3.0
3	P	99	TRP	3.0
9	I	25	PHE	3.0
1	A	201	VAL	2.9
9	I	33	THR	2.9
1	A	194	LEU	2.9
3	P	87	ILE	2.9
3	P	96	GLY	2.9
7	G	42	ARG	2.9
1	N	200	PRO	2.9
4	Q	140	TYR	2.8
1	A	286	ILE	2.8
9	V	68	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
3	P	138	LEU	2.8
1	A	282	PHE	2.8
1	N	285	PHE	2.8
3	C	254	VAL	2.8
2	O	74	ILE	2.8
3	C	248	VAL	2.7
4	Q	136	ALA	2.7
3	P	250	LEU	2.7
3	C	102	TYR	2.7
13	Z	35	TYR	2.7
3	C	250	LEU	2.7
13	Z	39	ASN	2.7
2	O	59	GLN	2.7
6	F	95	GLN	2.6
11	X	34	THR	2.6
3	C	87	ILE	2.6
2	O	133	LEU	2.6
3	C	255	SER	2.6
4	Q	102	TYR	2.6
7	T	6	GLY	2.6
1	N	237	PHE	2.6
3	P	102	TYR	2.6
1	A	284	GLY	2.6
7	T	12	GLY	2.5
9	V	3	ALA	2.5
11	X	35	GLN	2.5
7	G	10	GLY	2.5
4	Q	60	TYR	2.5
6	S	94	HIS	2.5
7	G	4	ALA	2.5
1	A	241	PRO	2.5
1	A	288	TRP	2.4
1	N	447	TYR	2.4
3	P	134	THR	2.4
7	T	7	ASP	2.4
2	O	193	TYR	2.4
4	Q	49	SER	2.4
7	T	42	ARG	2.4
4	Q	46	ALA	2.4
4	Q	50	SER	2.4
4	D	147	LYS	2.3
3	C	259	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	N	193	VAL	2.3
11	X	30	VAL	2.3
6	F	94	HIS	2.3
11	X	33	ALA	2.3
3	P	93	PHE	2.3
10	W	30	ILE	2.3
3	C	252	LEU	2.3
3	P	89	SER	2.3
4	D	102	TYR	2.3
9	I	19	PHE	2.3
5	R	93	LEU	2.2
3	C	98	PHE	2.2
4	Q	134	PHE	2.2
3	C	99	TRP	2.2
5	R	15	TRP	2.2
11	X	16	ALA	2.2
1	A	283	LEU	2.2
3	C	245	VAL	2.2
3	P	97	PHE	2.2
12	Y	47	LYS	2.2
3	P	255	SER	2.2
8	H	44	THR	2.2
13	Z	37	LEU	2.2
10	J	4	ARG	2.2
9	V	53	ASN	2.2
11	X	40	TRP	2.2
13	Z	41	LYS	2.2
3	P	85	LEU	2.2
3	C	96	GLY	2.2
7	G	7	ASP	2.1
3	C	89	SER	2.1
3	C	84	ILE	2.1
5	R	89	LEU	2.1
7	T	9	GLY	2.1
1	A	196	LEU	2.1
3	C	247	VAL	2.1
5	R	29	LEU	2.1
9	V	4	LEU	2.1
5	R	52	LEU	2.0
1	A	192	ALA	2.0
1	N	192	ALA	2.0
12	Y	38	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
12	Y	3	TYR	2.0
1	A	198	SER	2.0
1	N	161	ALA	2.0

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
7	TPO	T	11	11/12	0.34	0.41	97,105,129,130	0
9	SAC	V	1	9/10	0.50	0.62	110,112,114,115	0
7	TPO	G	11	11/12	0.51	0.45	93,102,125,127	0
9	SAC	I	1	9/10	0.58	0.54	99,103,106,106	0
1	FME	N	1	10/11	0.87	0.46	77,82,105,107	0
1	FME	A	1	10/11	0.94	0.21	63,70,93,102	0
2	FME	O	1	10/11	0.94	0.25	59,59,64,64	0
2	FME	B	1	10/11	0.98	0.10	46,48,51,61	0

6.3 Carbohydrates (i)

There are no monosaccharides 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
24	UNX	C	262	1/1	0.39	0.65	75,75,75,75	0
28	PEK	G	1263	53/53	0.41	0.68	83,126,150,150	0
22	PSC	R	1229	52/52	0.55	0.35	73,120,150,150	0
28	PEK	T	263	53/53	0.55	0.51	78,123,145,149	0
25	CDL	T	1269	100/100	0.58	0.45	92,117,138,143	0
25	CDL	G	269	100/100	0.60	0.40	89,118,138,141	0
26	DMU	T	1272	33/33	0.60	0.37	111,140,141,141	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
26	DMU	C	272	33/33	0.62	0.28	96,129,132,134	0
22	PSC	B	229	52/52	0.62	0.32	70,117,150,150	0
20	PGV	C	268	51/51	0.64	0.66	78,103,119,120	0
19	TGL	N	1522	63/63	0.65	0.30	72,95,111,112	0
24	UNX	P	262	1/1	0.69	0.68	75,75,75,75	0
28	PEK	S	1265	53/53	0.71	0.26	75,112,133,136	0
20	PGV	P	1268	51/51	0.73	0.57	78,108,125,126	0
20	PGV	N	1524	51/51	0.73	0.39	67,106,139,140	0
28	PEK	G	265	53/53	0.74	0.23	70,109,135,138	0
25	CDL	P	1270	100/100	0.76	0.38	69,119,136,137	0
23	CHD	W	1059	29/29	0.77	0.37	110,117,120,122	0
19	TGL	N	1523	63/63	0.77	0.34	84,111,131,133	0
19	TGL	L	522	63/63	0.77	0.25	57,89,109,113	0
20	PGV	A	524	51/51	0.78	0.27	62,101,132,135	0
19	TGL	A	523	63/63	0.78	0.21	78,102,131,132	0
25	CDL	C	270	100/100	0.83	0.34	56,112,137,139	0
23	CHD	J	60	29/29	0.85	0.34	103,112,119,120	0
19	TGL	B	521	63/63	0.86	0.18	54,96,118,120	0
18	NA	N	519	1/1	0.87	0.24	58,58,58,58	0
19	TGL	N	1521	63/63	0.88	0.21	69,101,120,123	0
26	DMU	Z	1526	33/33	0.90	0.28	73,80,94,96	0
17	MG	N	518	1/1	0.92	0.11	50,50,50,50	0
23	CHD	C	271	29/29	0.94	0.19	86,97,99,99	0
23	CHD	P	1271	29/29	0.94	0.13	98,101,103,104	0
26	DMU	M	526	33/33	0.94	0.14	52,63,87,91	0
17	MG	A	518	1/1	0.95	0.17	40,40,40,40	0
28	PEK	T	1264	53/53	0.95	0.17	49,70,109,111	0
23	CHD	P	1525	29/29	0.96	0.27	48,54,57,59	0
28	PEK	G	264	53/53	0.96	0.14	44,65,107,109	0
20	PGV	P	1267	51/51	0.96	0.19	45,56,102,106	0
23	CHD	C	525	29/29	0.96	0.29	38,50,57,65	0
18	NA	A	519	1/1	0.96	0.06	47,47,47,47	0
20	PGV	N	1266	51/51	0.96	0.15	45,60,81,84	0
23	CHD	O	229	29/29	0.96	0.13	45,49,56,62	0
23	CHD	B	1085	29/29	0.97	0.14	46,50,53,59	0
20	PGV	C	267	51/51	0.97	0.14	38,52,95,97	0
20	PGV	A	521	51/51	0.97	0.15	36,53,77,79	0
14	HEA	N	515	60/60	0.98	0.12	47,52,65,66	0
21	CUA	O	228	2/2	0.98	0.11	52,52,52,54	0
15	CMO	A	520	2/2	0.99	0.15	39,39,39,41	0
14	HEA	A	516	60/60	0.99	0.14	32,40,56,64	0
14	HEA	A	515	60/60	0.99	0.12	33,40,54,68	0

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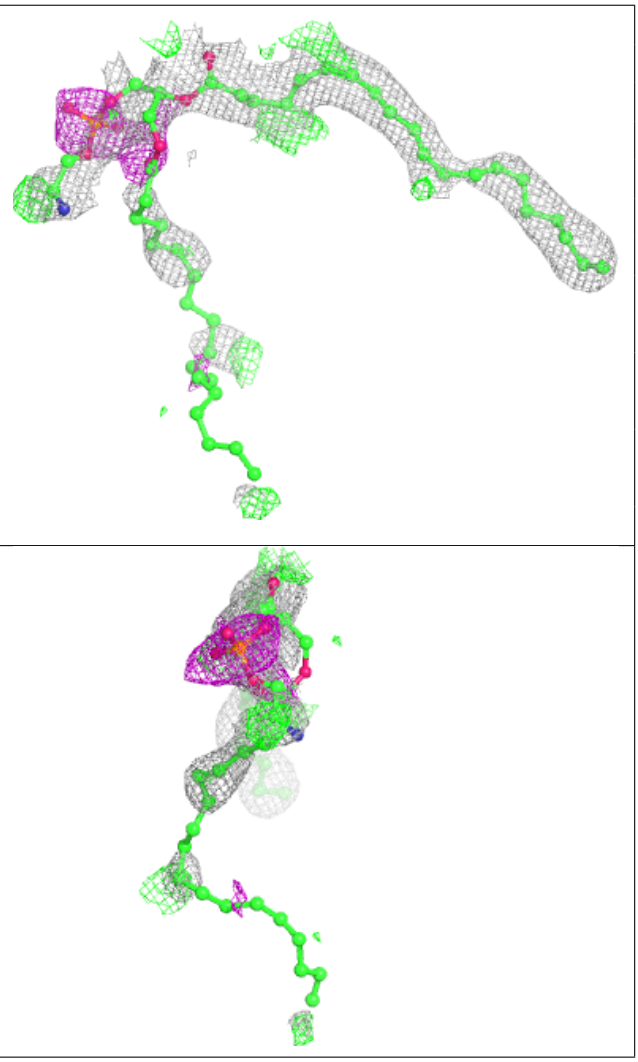
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
21	CUA	B	228	2/2	0.99	0.15	41,41,41,42	0
14	HEA	N	516	60/60	0.99	0.14	42,48,69,74	0
27	ZN	F	99	1/1	0.99	0.15	48,48,48,48	0
16	CU	A	517	1/1	1.00	0.20	40,40,40,40	0
27	ZN	S	99	1/1	1.00	0.11	56,56,56,56	0
16	CU	N	517	1/1	1.00	0.18	49,49,49,49	0
15	CMO	N	520	2/2	1.00	0.14	47,47,47,48	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.

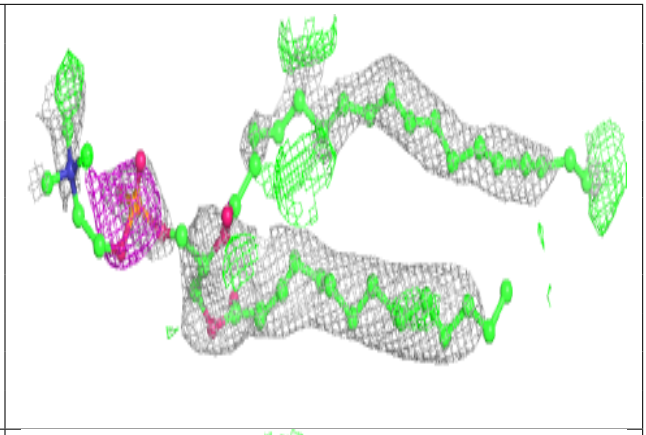
Electron density around PEK G 1263:

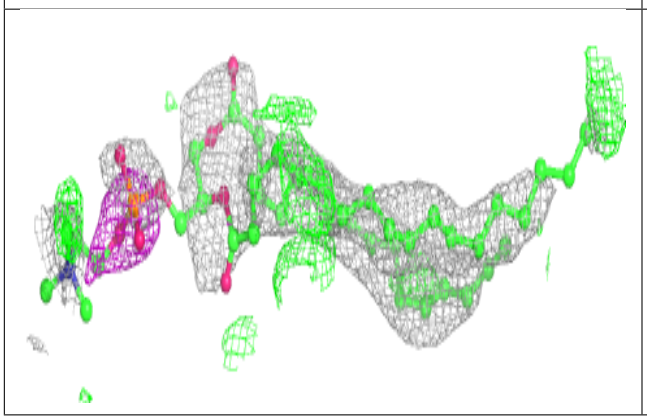
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

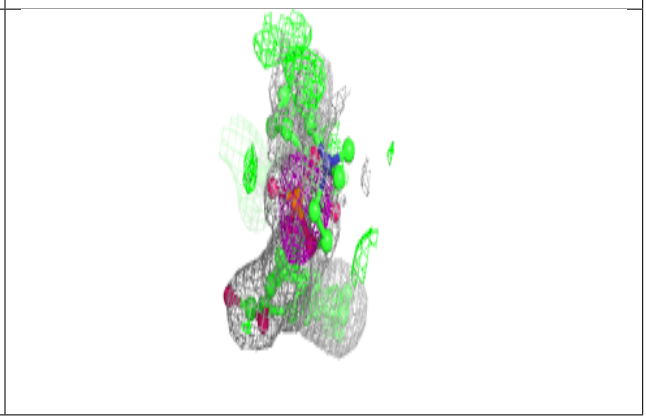


Electron density around PSC R 1229:

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

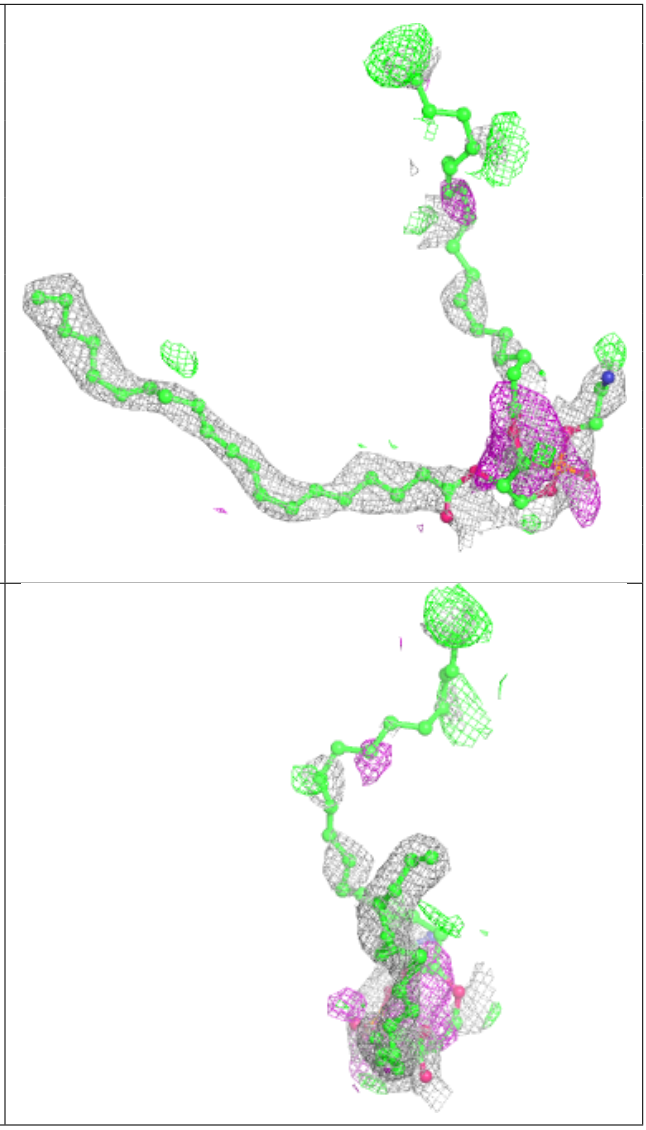






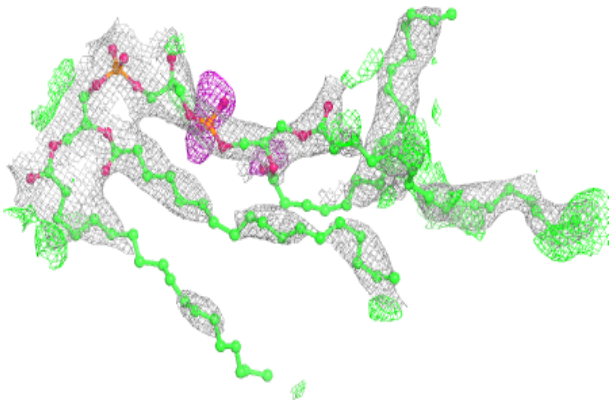
Electron density around PEK T 263:

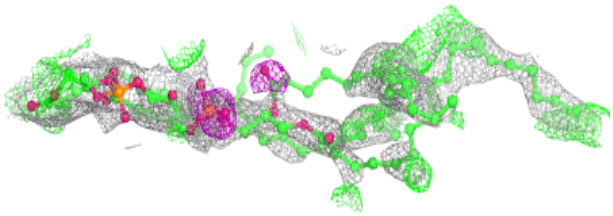
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

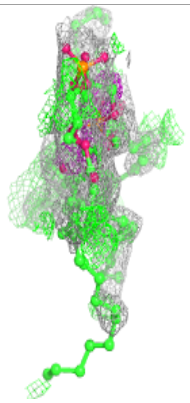


Electron density around CDL T 1269:

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

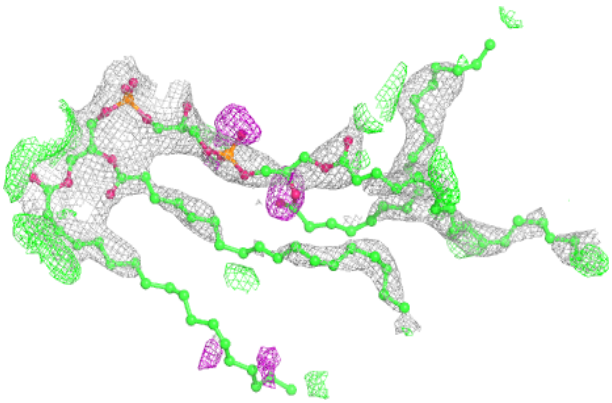


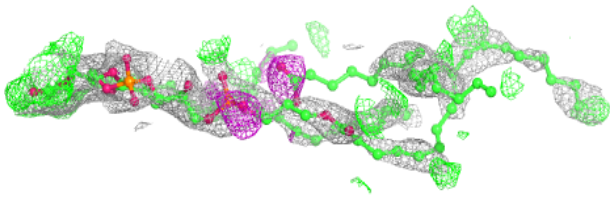


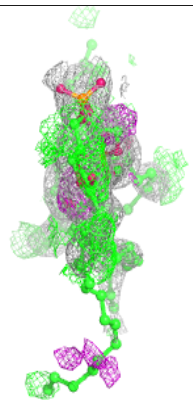


Electron density around CDL G 269:

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

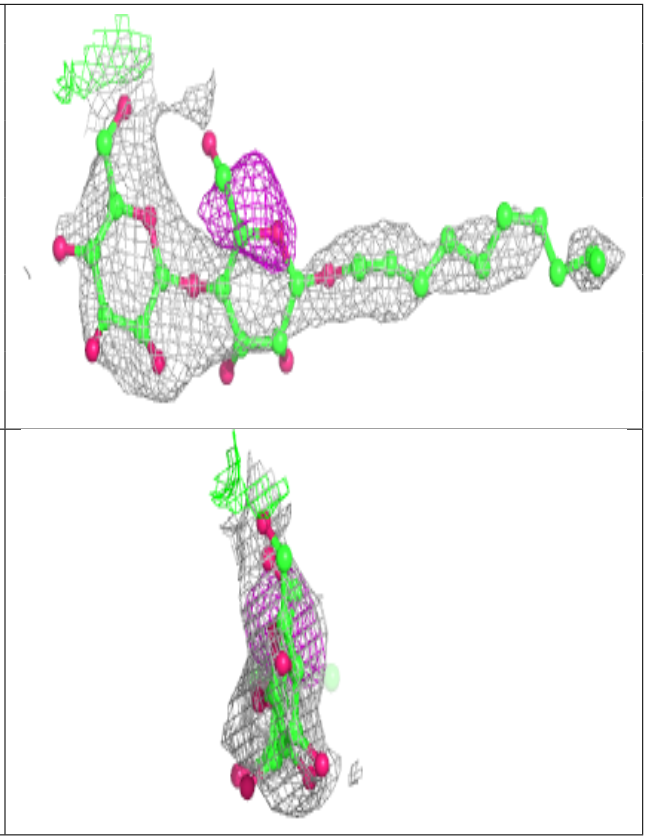






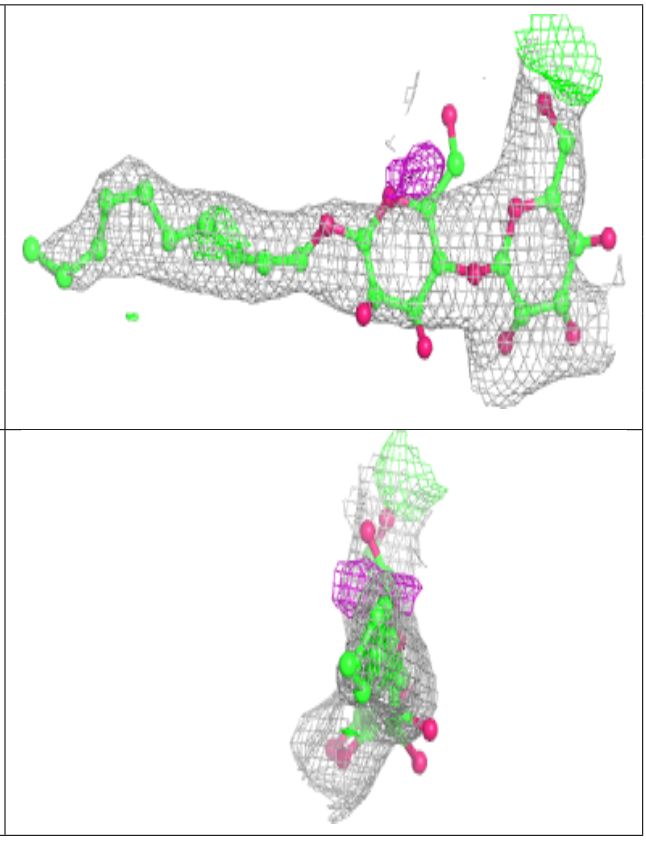
Electron density around DMU T 1272:

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



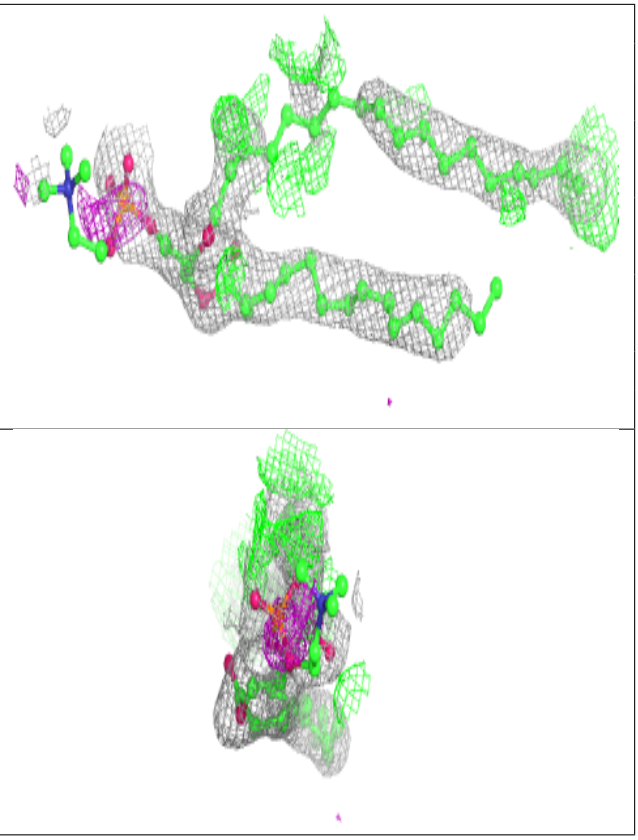
Electron density around DMU C 272:

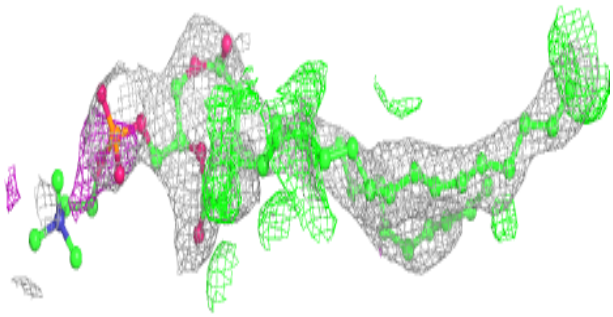
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PSC B 229:

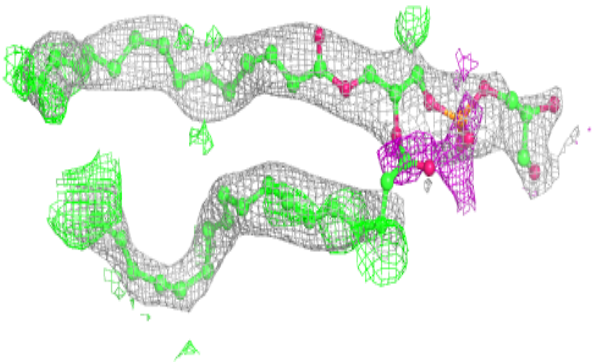
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

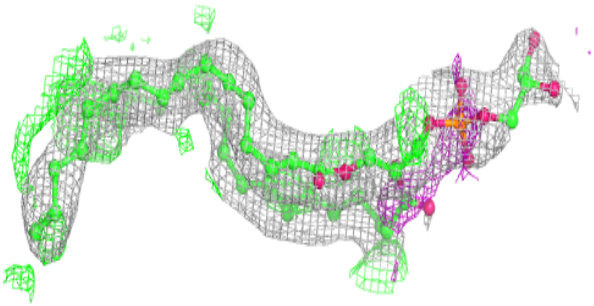




Electron density around PGV C 268:

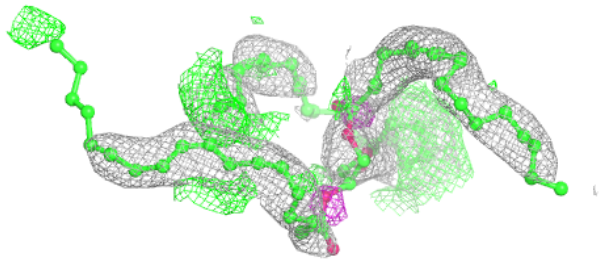
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

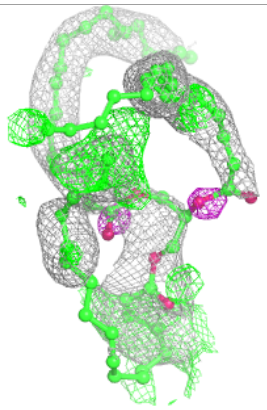




Electron density around TGL N 1522:

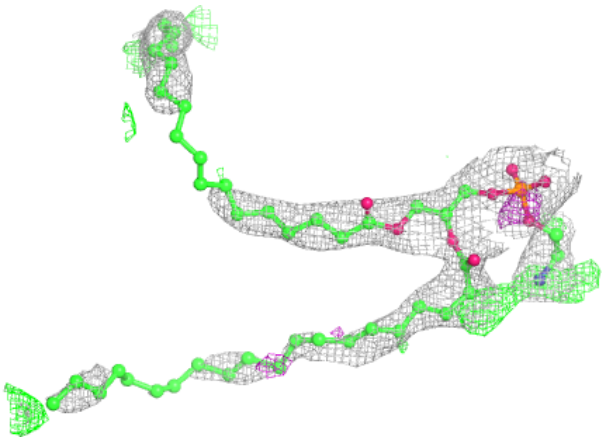
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

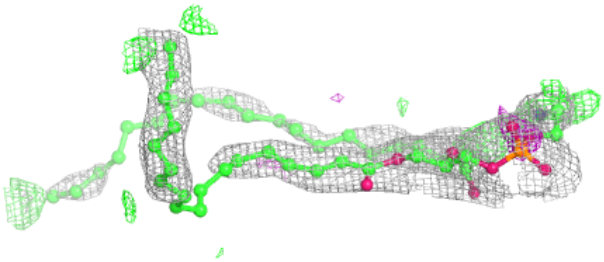


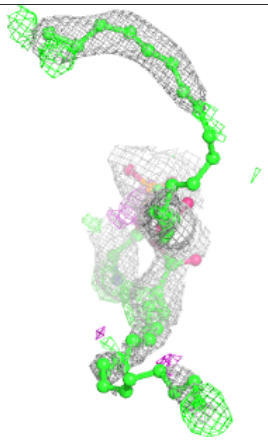


Electron density around PEK S 1265:

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

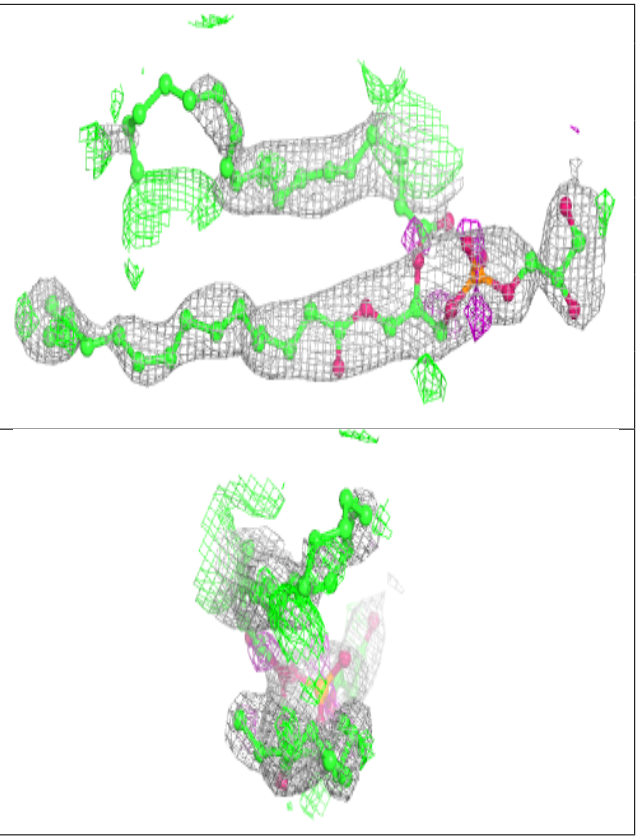






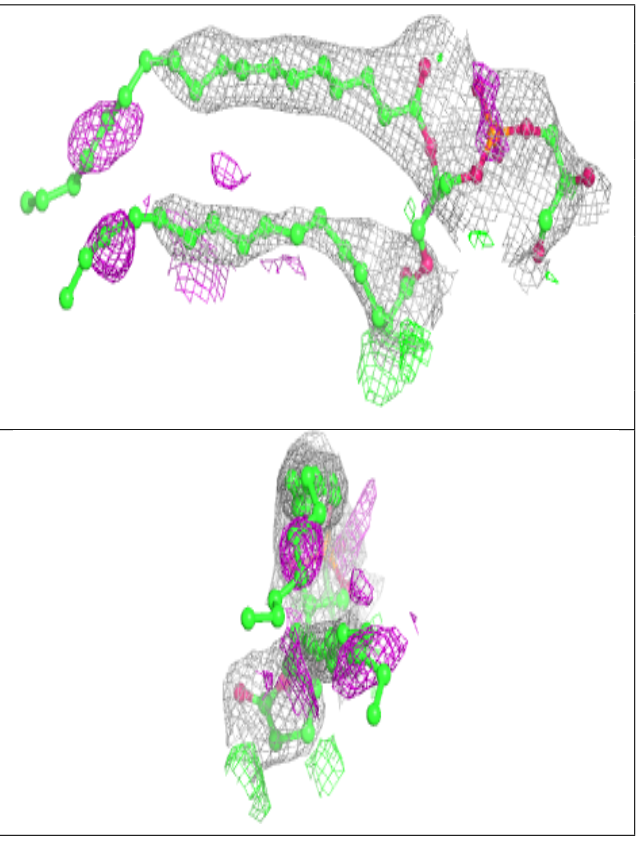
Electron density around PGV P 1268:

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



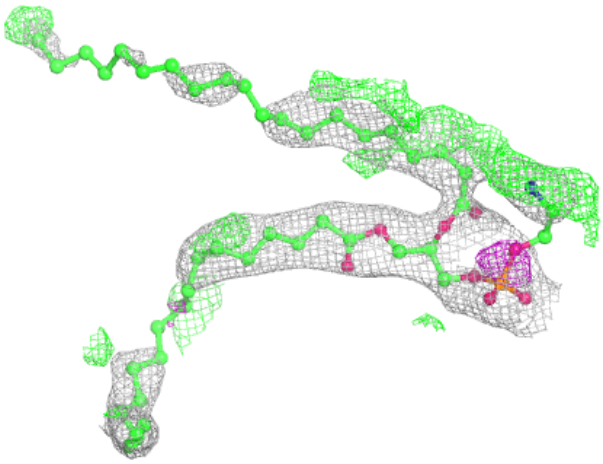
Electron density around PGV N 1524:

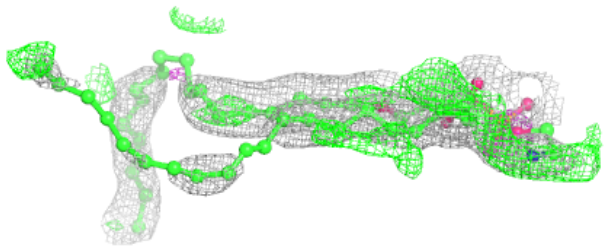
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

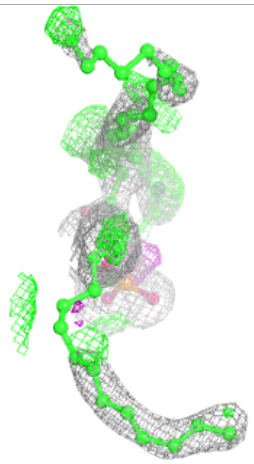


Electron density around PEK G 265:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

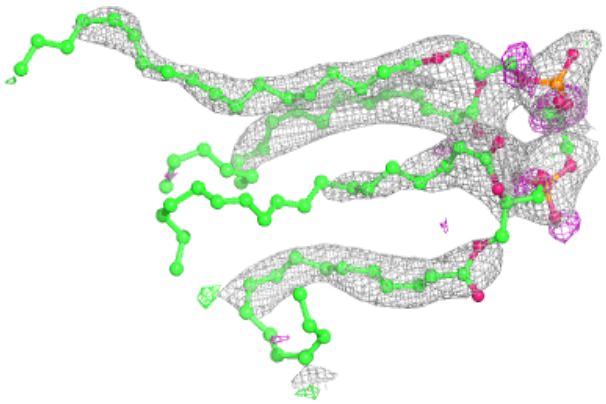


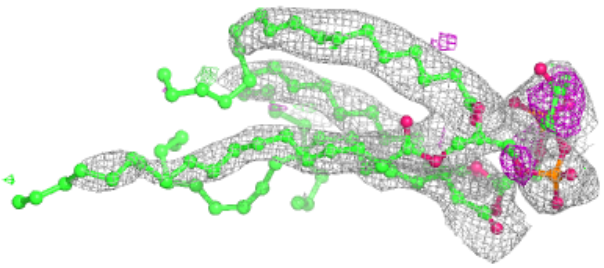


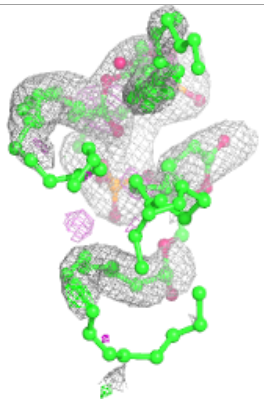


Electron density around CDL P 1270:

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

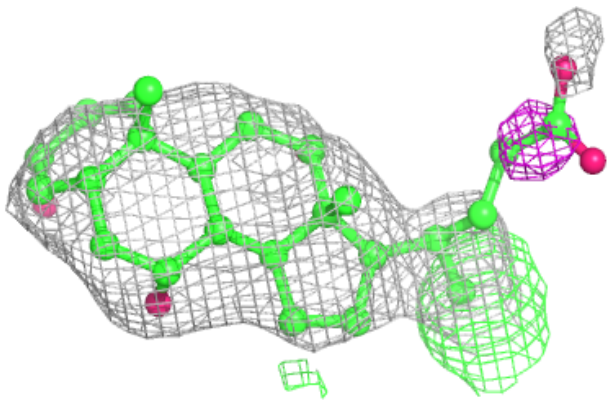


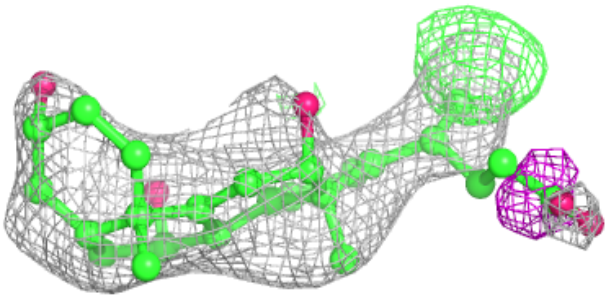


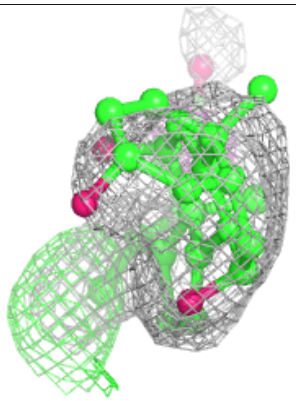


Electron density around CHD W 1059:

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

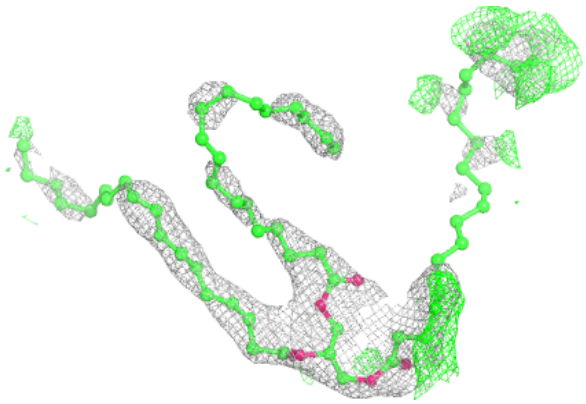


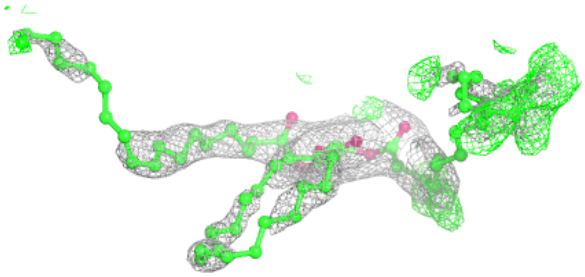


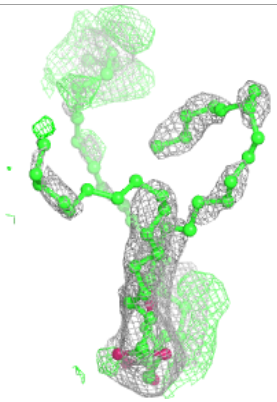


Electron density around TGL N 1523:

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

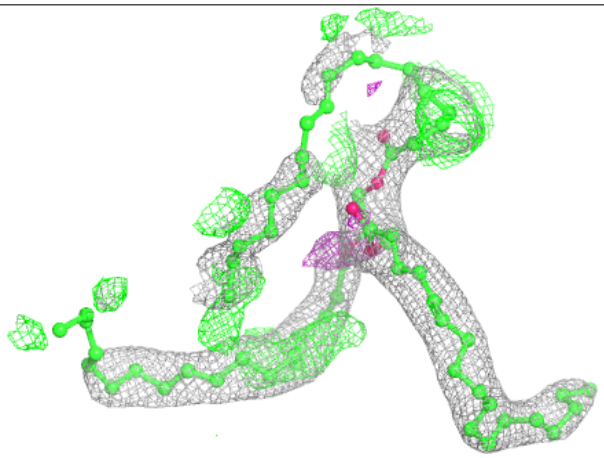


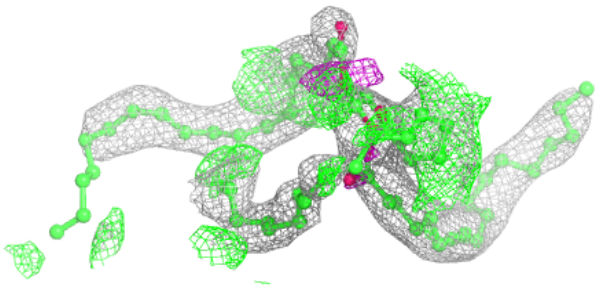


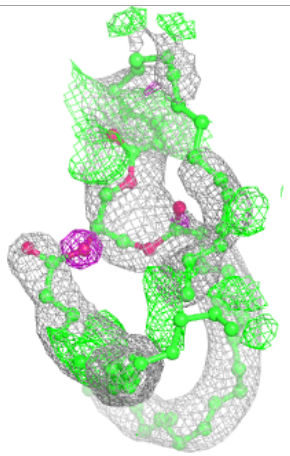


Electron density around TGL L 522:

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

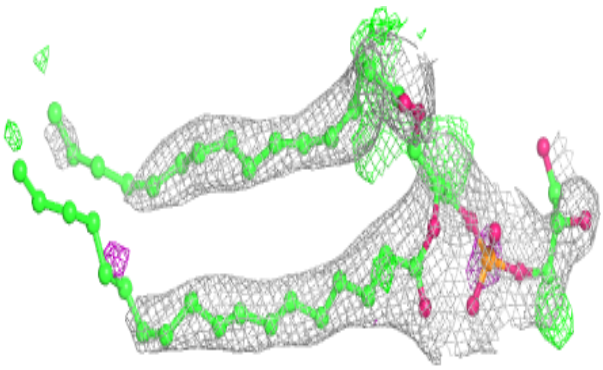


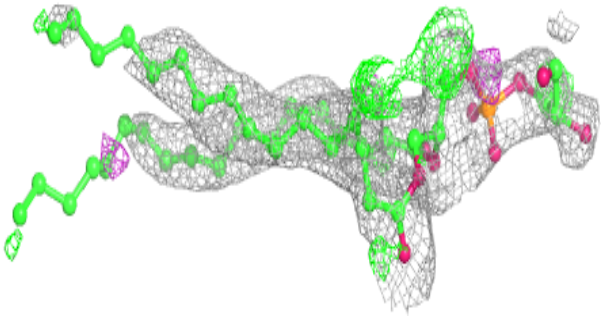


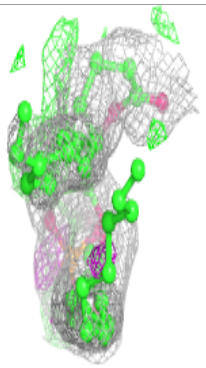


Electron density around PGV A 524:

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

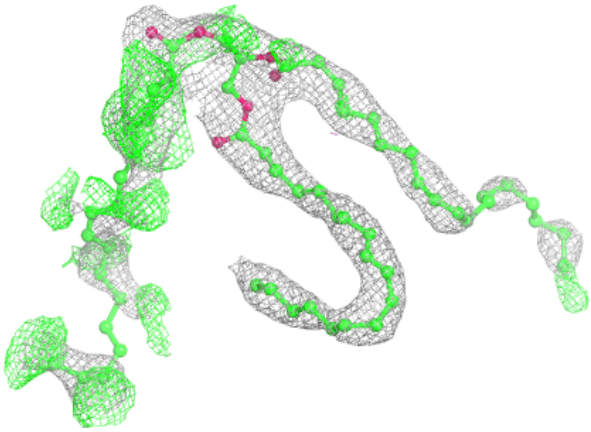


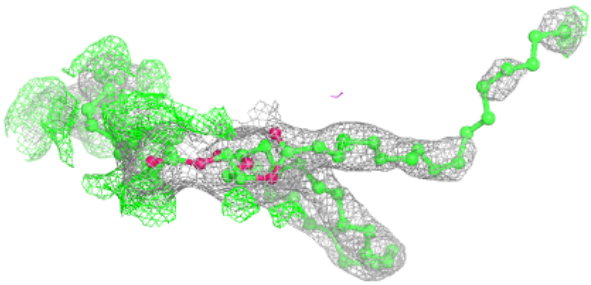


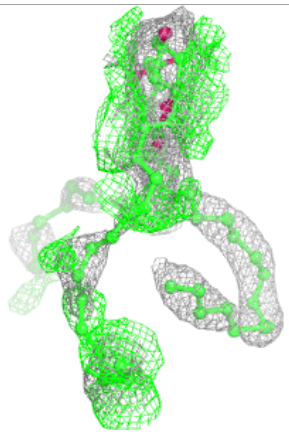


Electron density around TGL A 523:

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

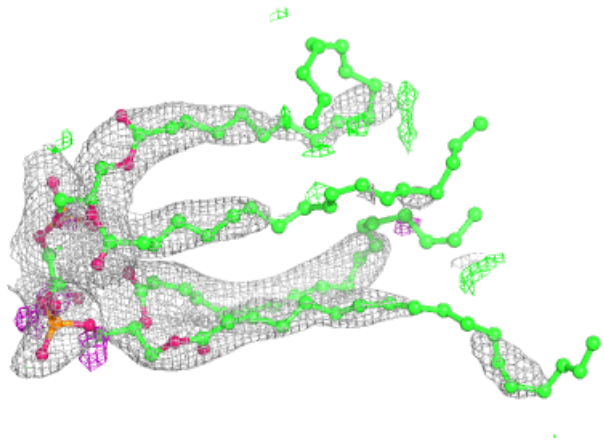


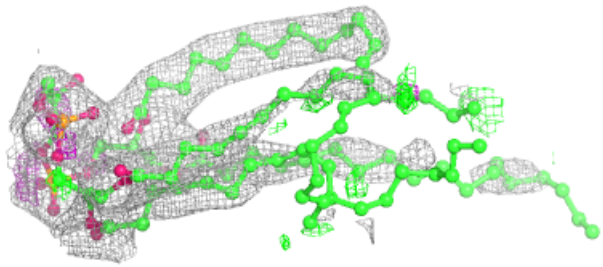


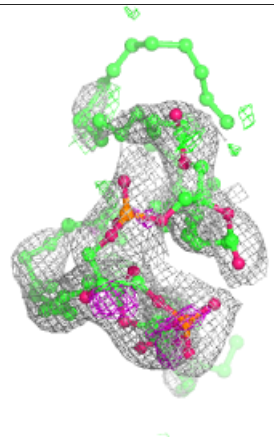


Electron density around CDL C 270:

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

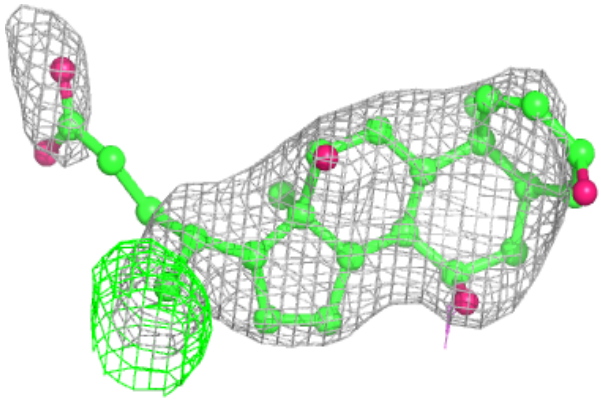


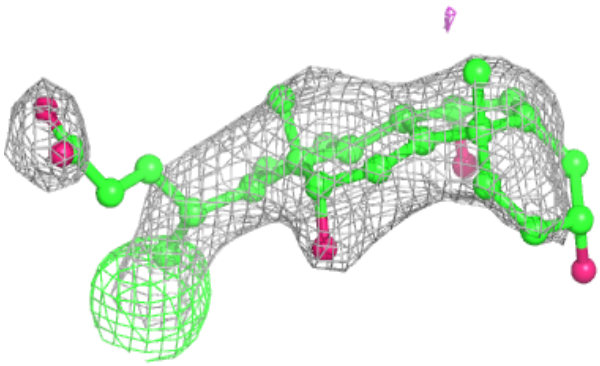


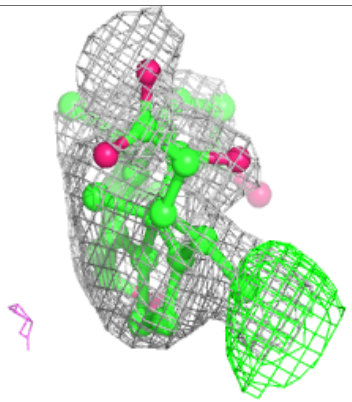


Electron density around CHD J 60:

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

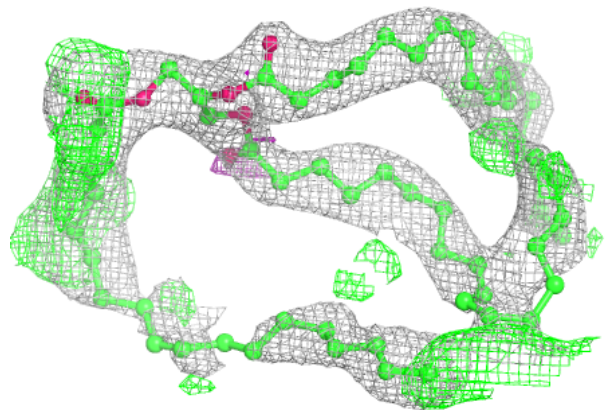


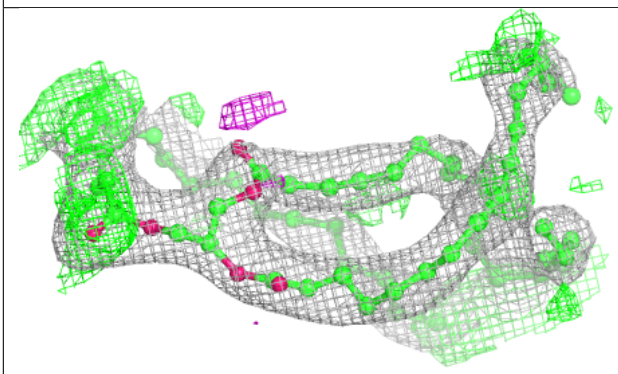


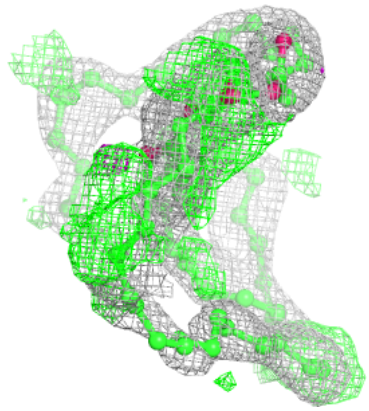


Electron density around TGL B 521:

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

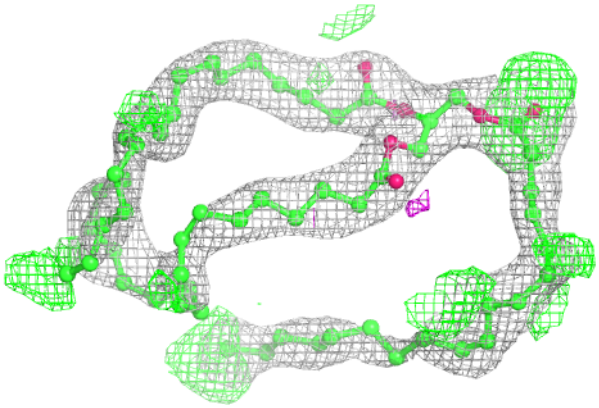


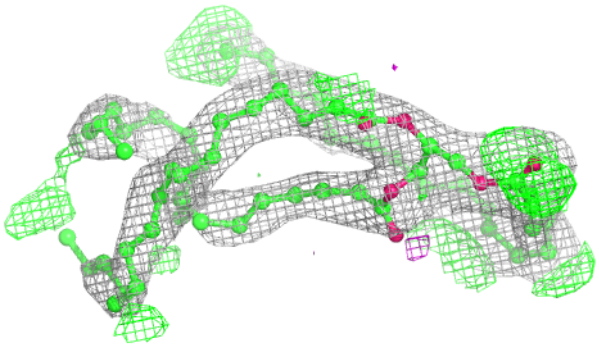


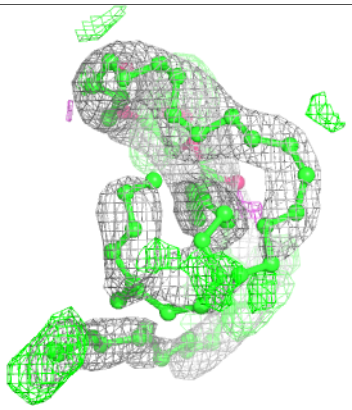


Electron density around TGL N 1521:

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

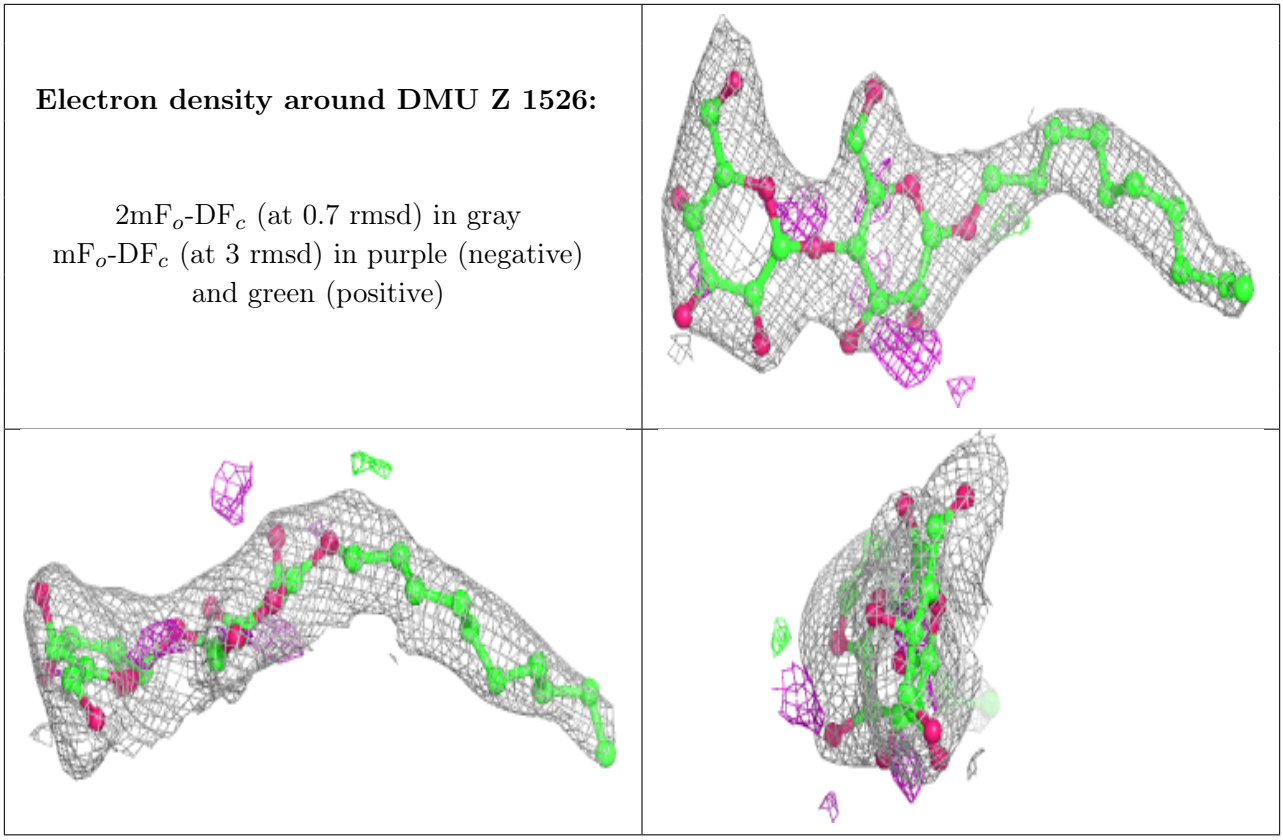






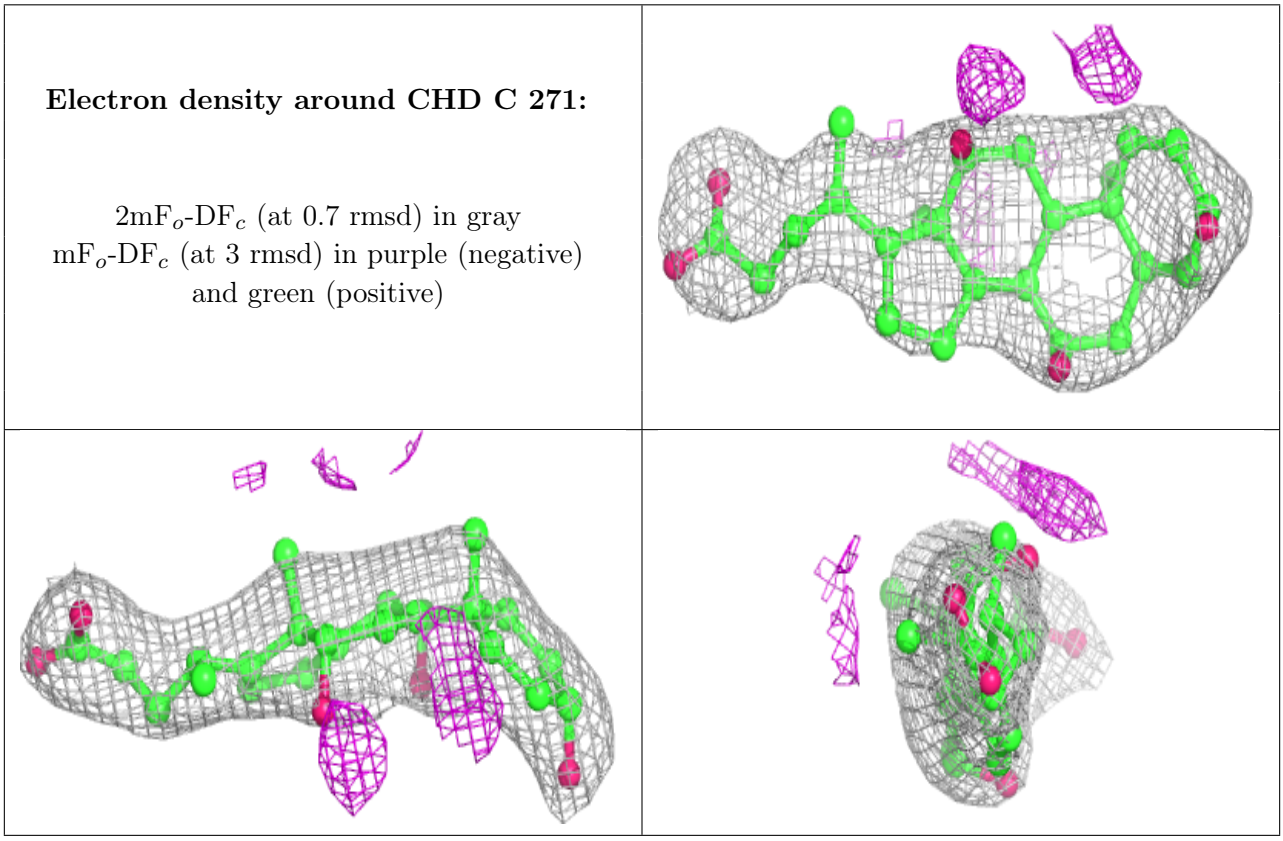
Electron density around DMU Z 1526:

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



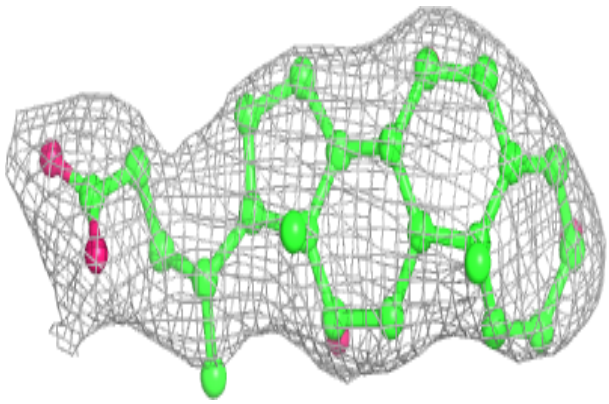
Electron density around CHD C 271:

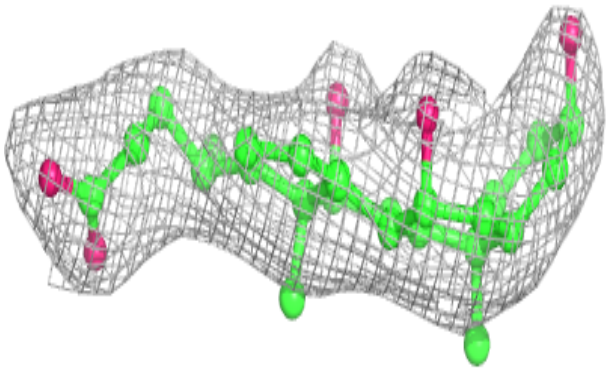
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

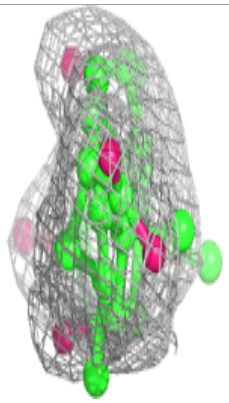


Electron density around CHD P 1271:

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

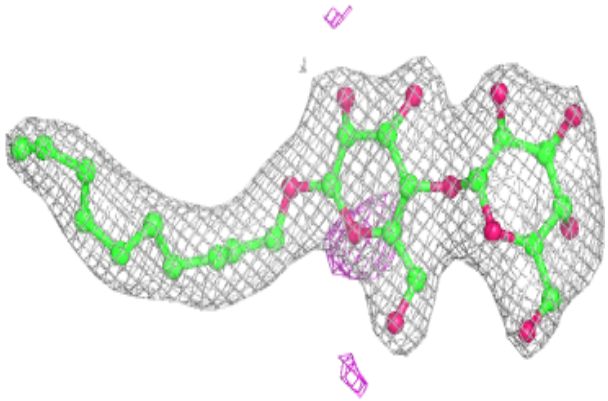


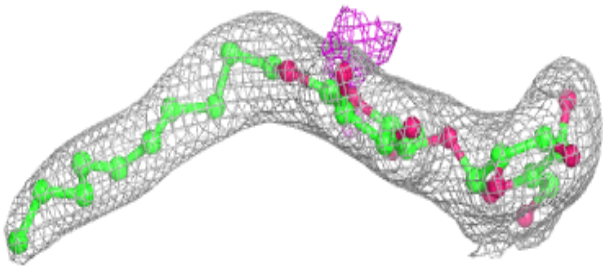


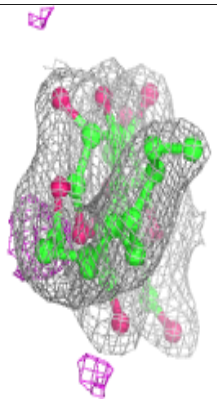


Electron density around DMU M 526:

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

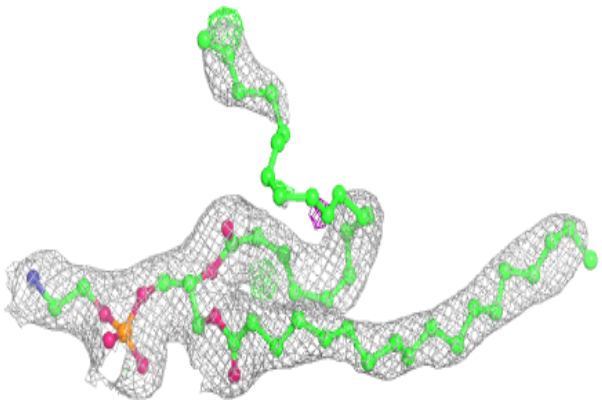


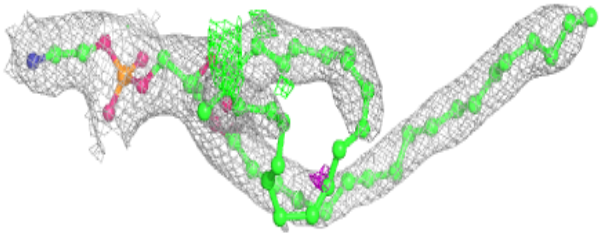


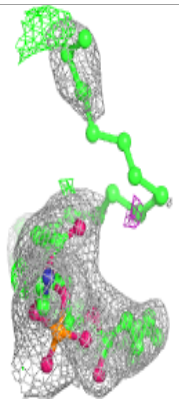


Electron density around PEK T 1264:

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

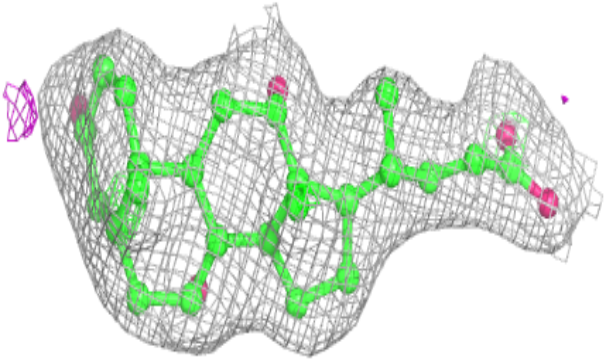


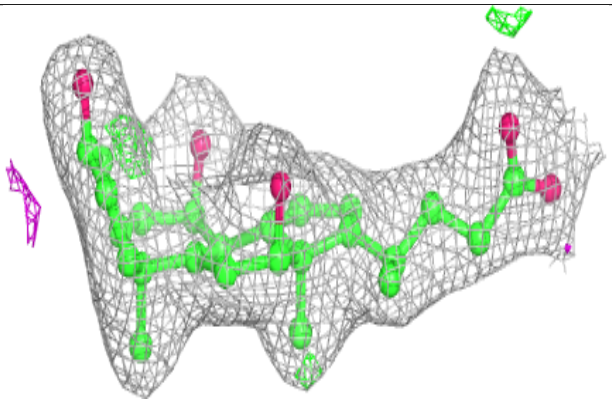


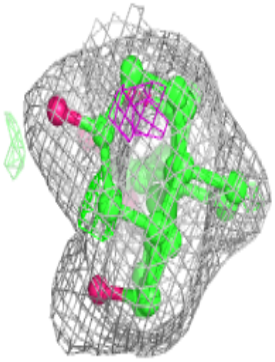


Electron density around CHD P 1525:

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

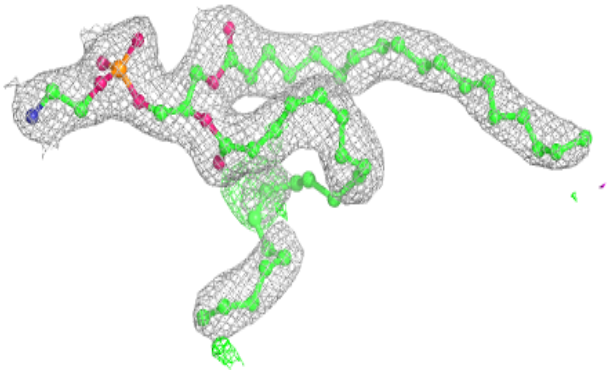


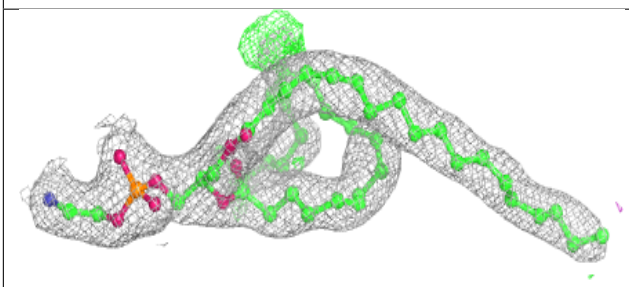


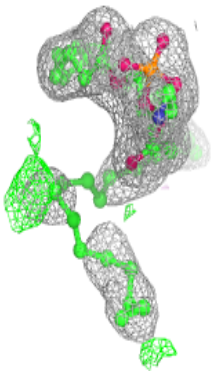


Electron density around PEK G 264:

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

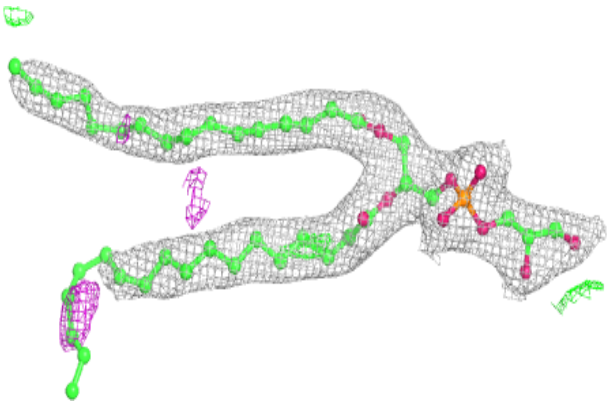


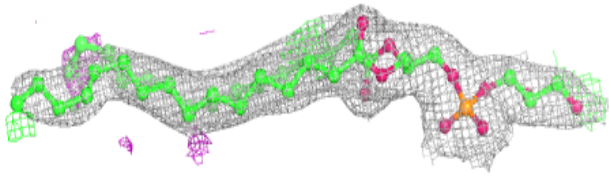


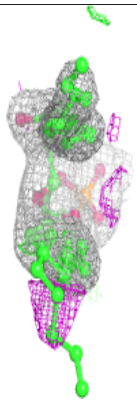


Electron density around PGV P 1267:

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

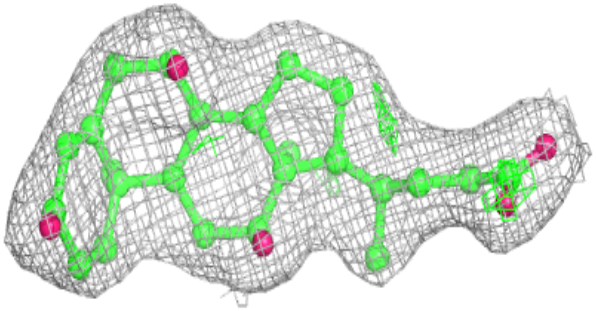


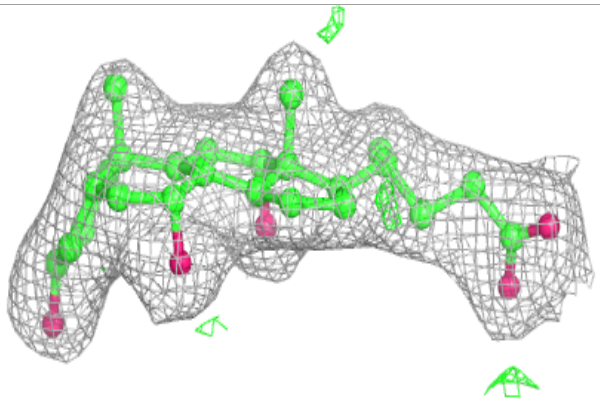


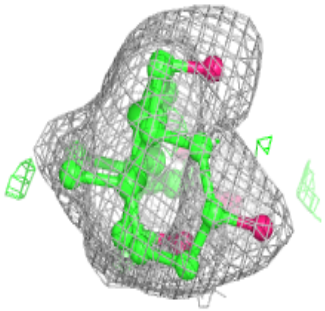


Electron density around CHD C 525:

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

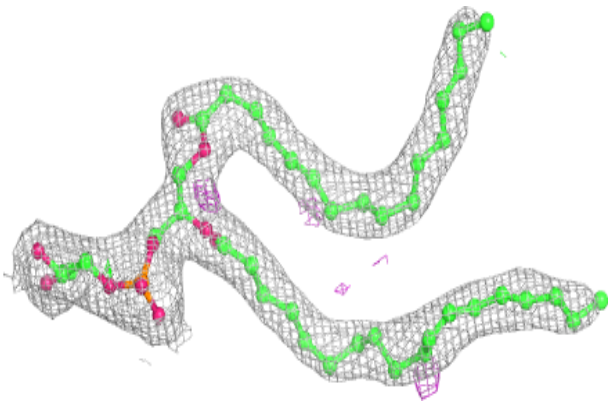


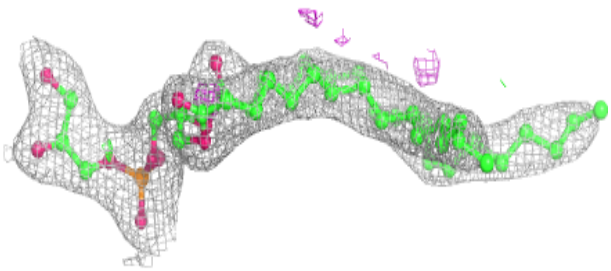


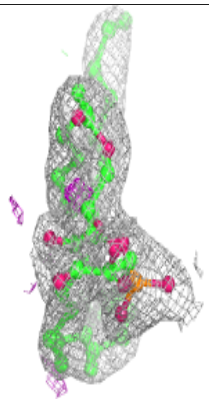


Electron density around PGV N 1266:

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

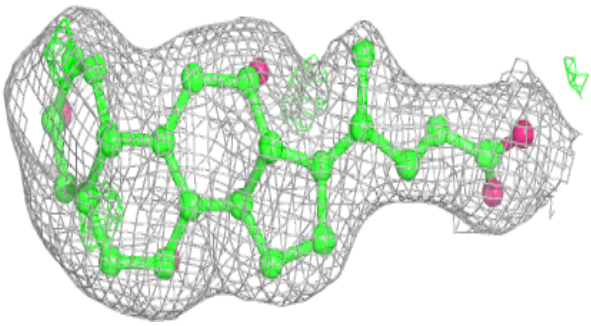


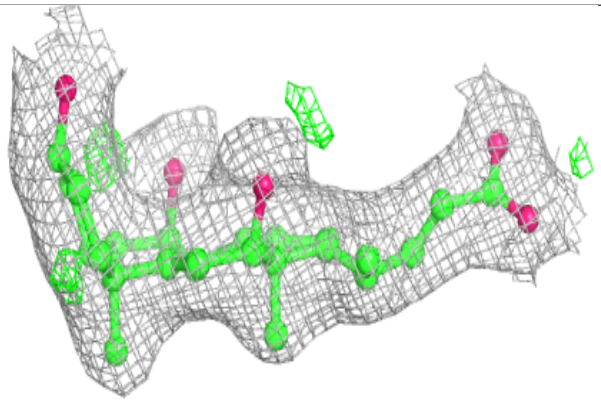


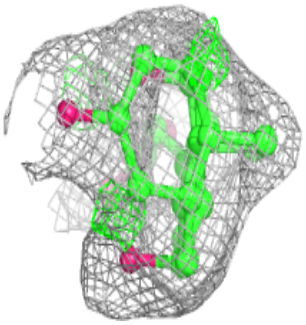


Electron density around CHD O 229:

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

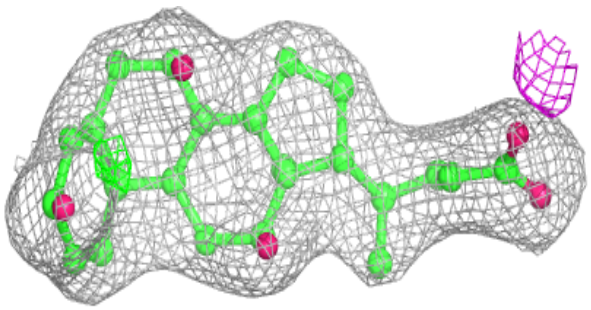


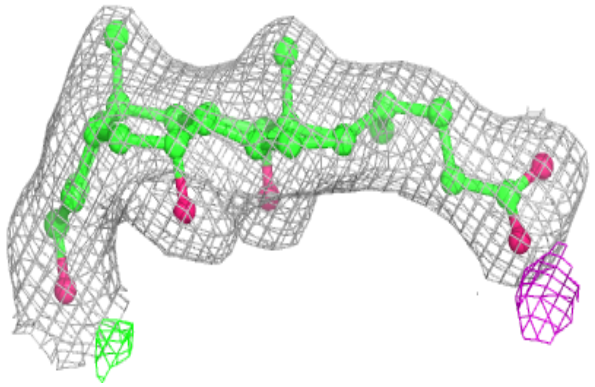


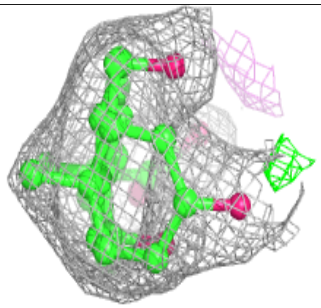


Electron density around CHD B 1085:

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

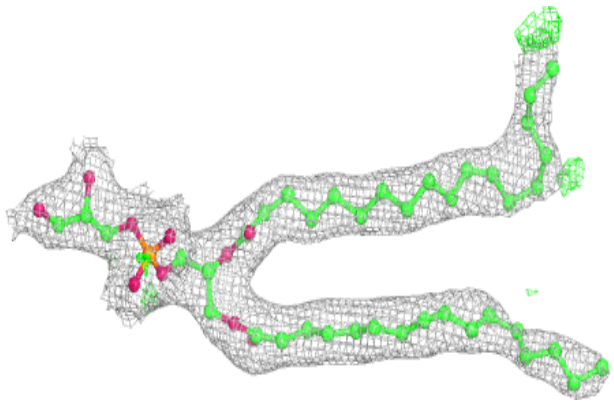


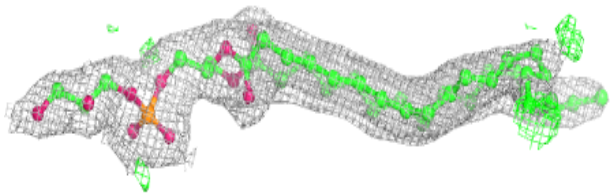


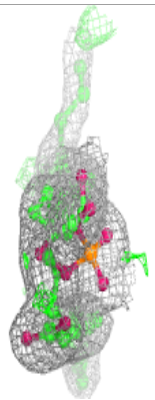


Electron density around PGV C 267:

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

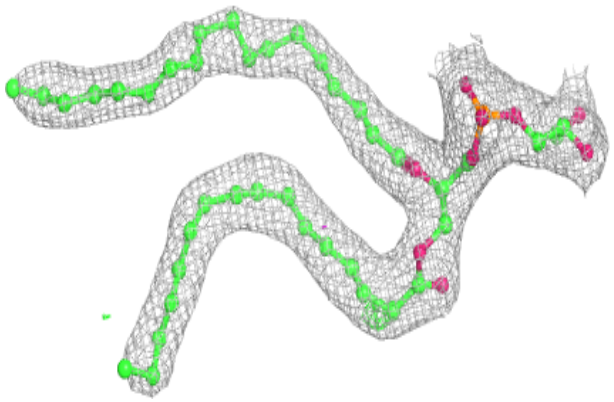


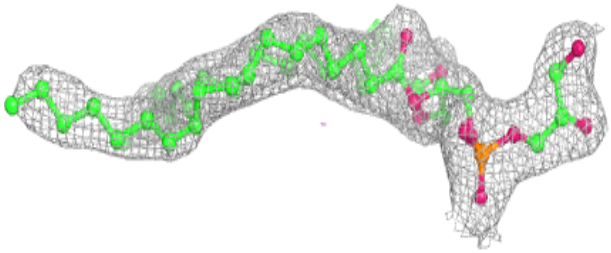


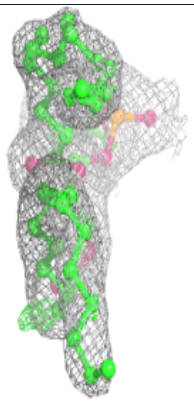


Electron density around PGV A 521:

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

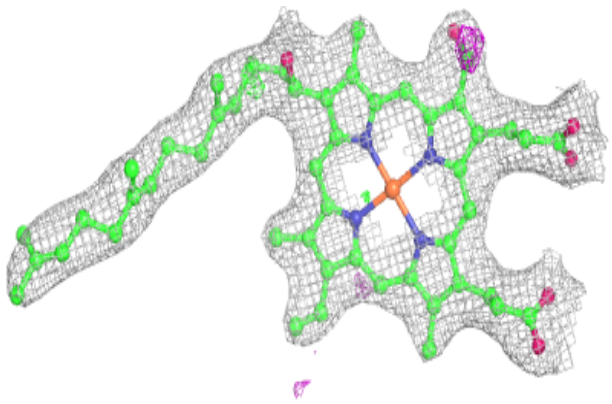


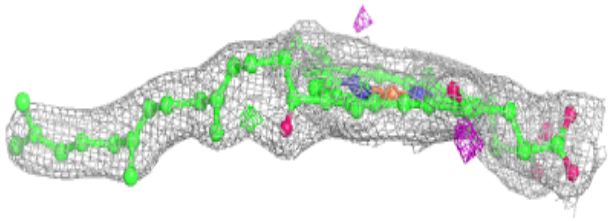


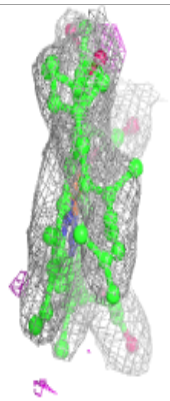


Electron density around HEA N 515:

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

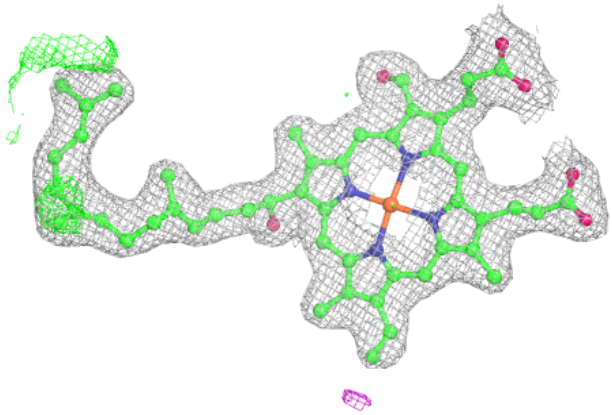


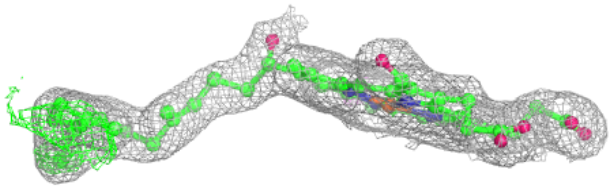


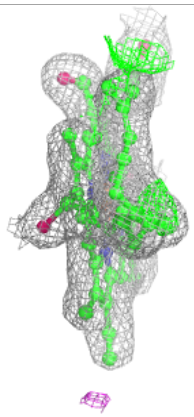


Electron density around HEA A 516:

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

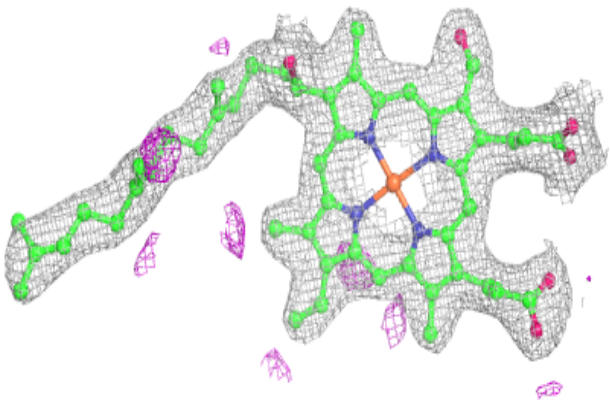


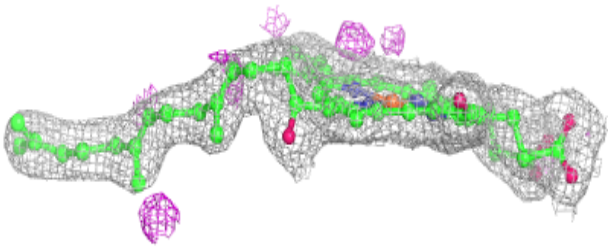


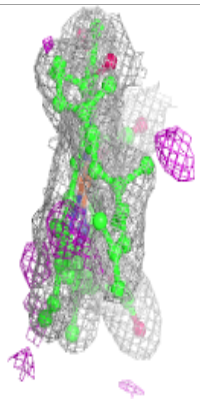


Electron density around HEA A 515:

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

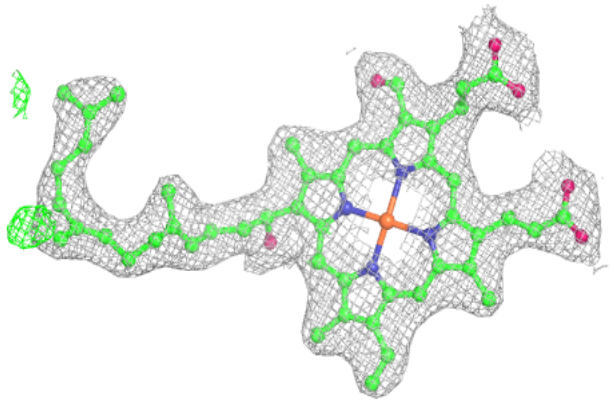


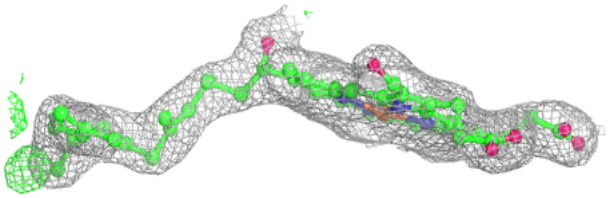


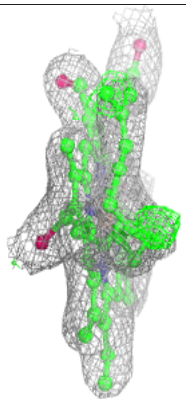


Electron density around HEA N 516:

$2mF_o$-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.