



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 09:09 PM EDT

PDB ID : 3WGV / pdb_00003wgv
Title : Crystal structure of a Na⁺-bound Na⁺,K⁺-ATPase preceding the E1P state with oligomycin
Authors : Kanai, R.; Ogawa, H.; Vilsen, B.; Cornelius, F.; Toyoshima, C.
Deposited on : 2013-08-09
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

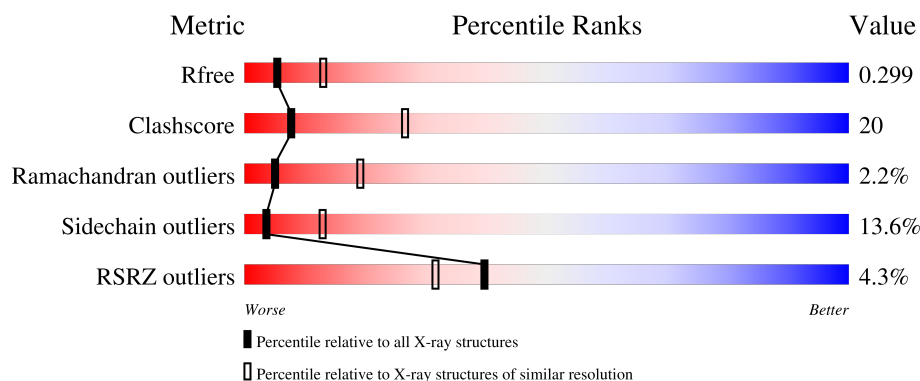
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



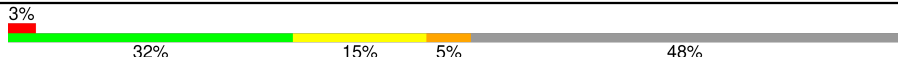
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	1016	0% 53% 36% 8% .
1	C	1016	3% 57% 34% 6% .
2	B	303	10% 52% 39% 9%
2	D	303	14% 53% 37% 9% .
3	E	65	2% 20% 28% 5% . 46%

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Mol	Chain	Length	Quality of chain
3	G	65	

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
5	ALF	C	2002	-	-	X	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 21909 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 Sodium/potassium-transporting ATPase subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	994	Total	C	N	O	S	0	0	0
			7714	4918	1300	1449	47			
1	C	994	Total	C	N	O	S	0	0	0
			7714	4918	1300	1449	47			

- Molecule 2 is a protein called Sodium/potassium-transporting ATPase subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	303	Total	C	N	O	S	0	0	0
			2479	1603	408	454	14			
2	D	303	Total	C	N	O	S	0	0	0
			2479	1603	408	454	14			

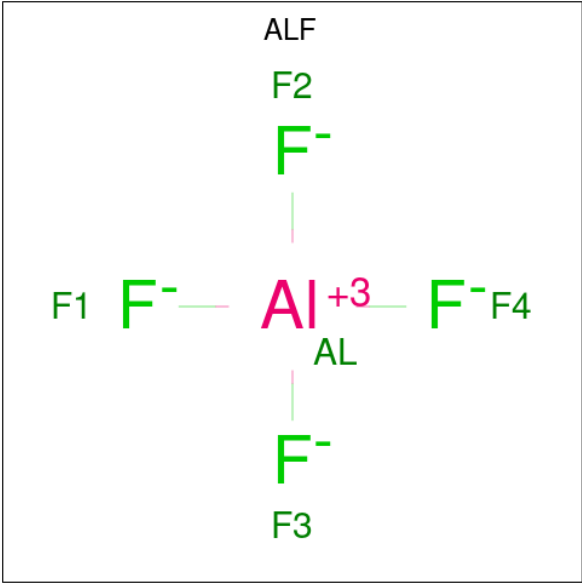
- Molecule 3 is a protein called Na⁺/K⁺ ATPase gamma subunit transcript variant a.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	34	Total	C	N	O	0	0	0
			270	183	39	48			
3	E	35	Total	C	N	O	0	0	0
			281	189	43	49			

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

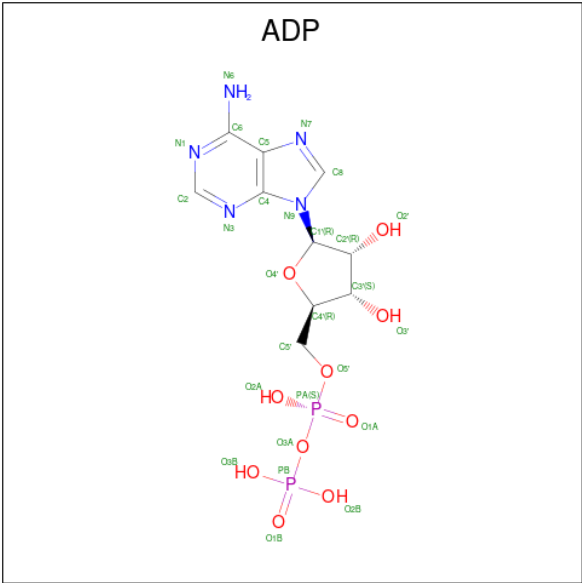
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	C	2	Total	Mg	0	0
			2	2		

- Molecule 5 is TETRAFLUOROALUMINATE ION (CCD ID: ALF) (formula: AlF₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Al	F	0	0
			5	1	4		
5	C	1	Total	Al	F	0	0
			5	1	4		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

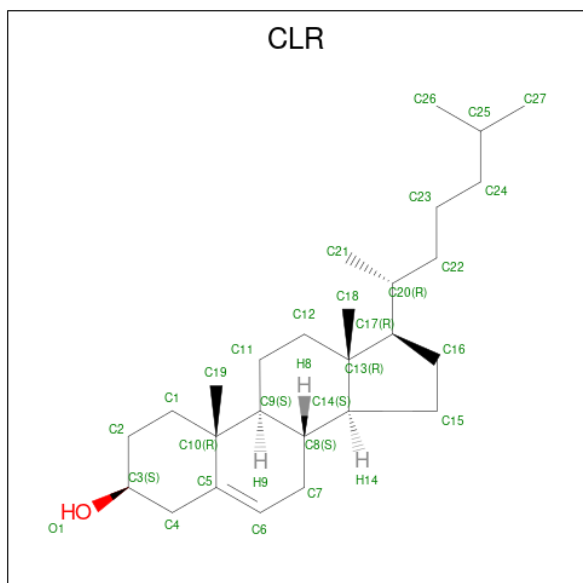


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

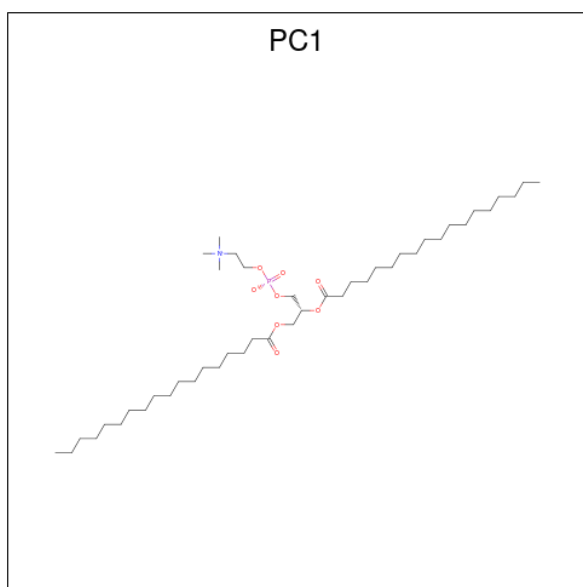
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	4	Total	Na	0	0
			4	4		
7	C	4	Total	Na	0	0
			4	4		

- Molecule 8 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



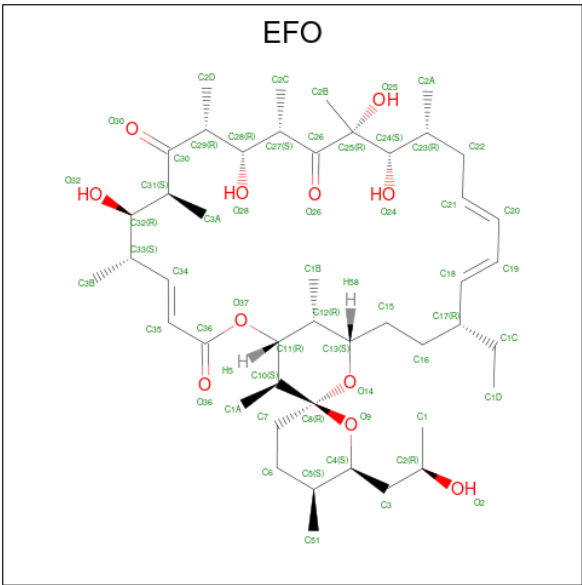
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			28	27	1		
8	A	1	Total	C	O	0	0
			28	27	1		
8	G	1	Total	C	O	0	0
			28	27	1		
8	D	1	Total	C	O	0	0
			28	27	1		
8	D	1	Total	C	O	0	0
			28	27	1		
8	E	1	Total	C	O	0	0
			28	27	1		

- Molecule 9 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



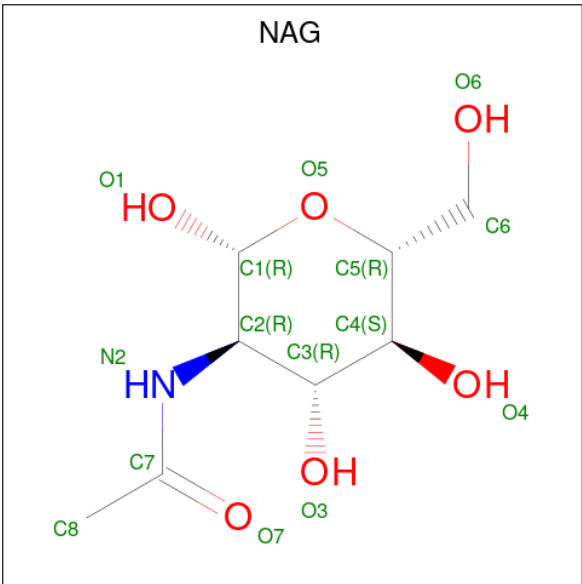
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	B	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	D	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 10 is Oligomycin A (CCD ID: EFO) (formula: C₄₅H₇₄O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			56	45	11		
10	C	1	Total	C	O	0	0
			56	45	11		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	D	1	Total	C	N	O	0	0
			14	8	1	5		

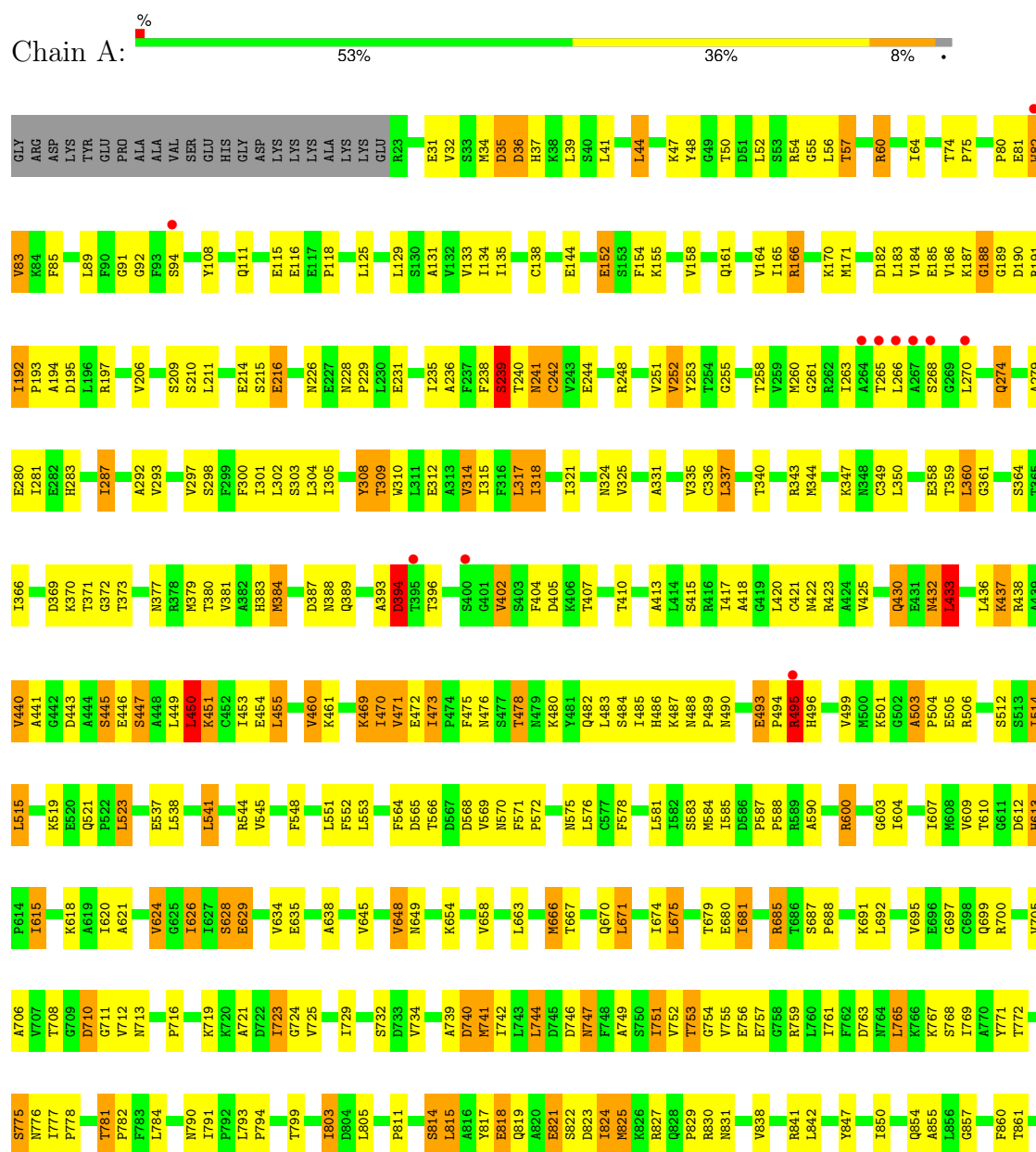
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	24	Total	O	0	0
			24	24		
12	B	2	Total	O	0	0
			2	2		
12	C	20	Total	O	0	0
			20	20		
12	D	2	Total	O	0	0
			2	2		

3 Residue-property plots

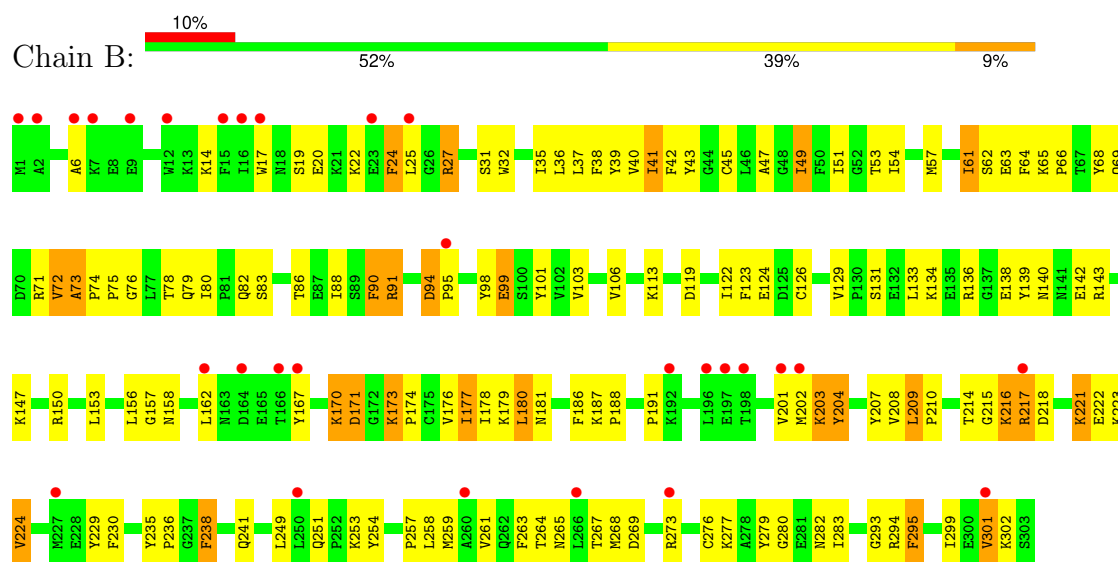
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

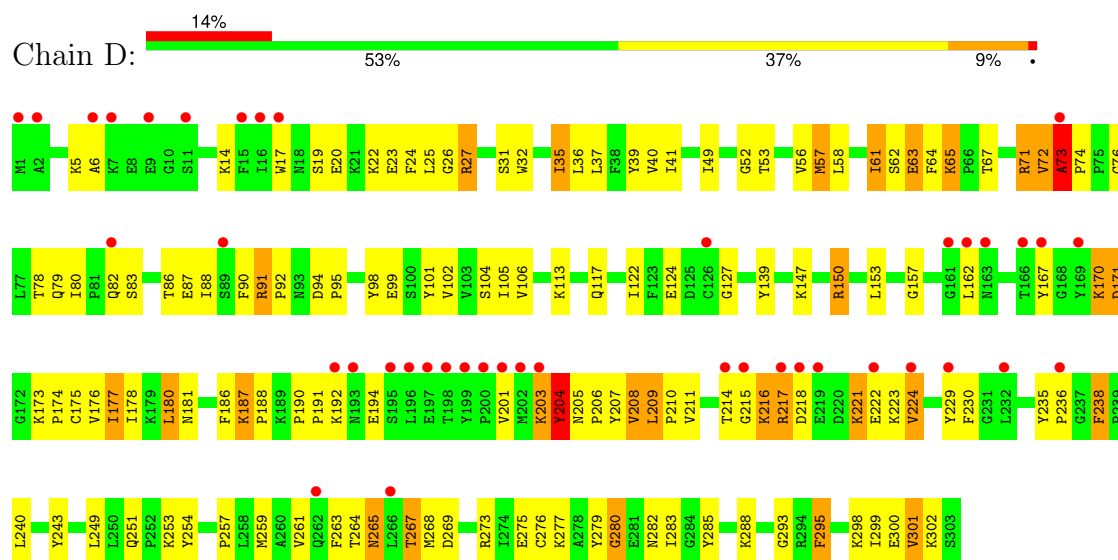




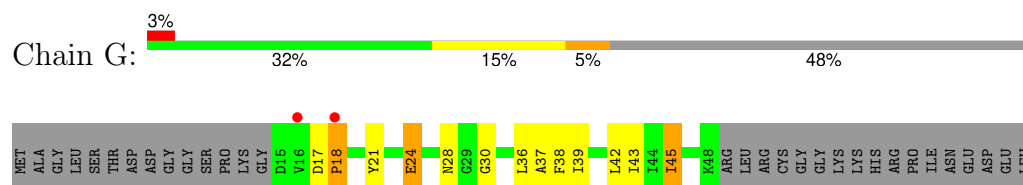
• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1



• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1



• Molecule 3: Na⁺/K⁺ ATPase gamma subunit transcript variant a



• Molecule 3: Na⁺/K⁺ ATPase gamma subunit transcript variant a





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.28Å 210.18Å 256.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.99 – 2.80 15.99 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.4 (15.99-2.80) 93.8 (15.99-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.270 , 0.298 0.272 , 0.299	Depositor DCC
R_{free} test set	3965 reflections (2.82%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.15 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	21909	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ALF, NA, PC1, MG, EFO, NAG, CLR, ADP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.60	0/7864	1.01	26/10671 (0.2%)
1	C	0.51	0/7864	0.92	15/10671 (0.1%)
2	B	0.42	0/2544	0.92	11/3426 (0.3%)
2	D	0.44	0/2544	0.92	11/3426 (0.3%)
3	E	0.49	0/287	0.94	0/389
3	G	0.46	0/276	0.85	0/375
All	All	0.53	0/21379	0.95	63/28958 (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
3	E	0	1

There are no bond length outliers.

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	495	ARG	CB-CA-C	-18.33	91.69	109.83
2	B	73	ALA	CA-C-N	-12.49	107.52	120.38
2	B	73	ALA	C-N-CA	-12.49	107.52	120.38
2	D	73	ALA	CA-C-N	-11.36	108.68	120.38
2	D	73	ALA	C-N-CA	-11.36	108.68	120.38
1	C	192	ILE	CA-C-N	7.54	127.06	118.85
1	C	192	ILE	C-N-CA	7.54	127.06	118.85
1	C	495	ARG	CB-CA-C	-6.64	97.67	110.35
1	C	705	VAL	N-CA-C	6.62	118.13	108.53
1	A	54	ARG	N-CA-C	-6.44	106.01	114.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	239	SER	CB-CA-C	-6.32	97.85	110.42
1	A	649	ASN	CA-C-N	6.22	127.62	119.84
1	A	649	ASN	C-N-CA	6.22	127.62	119.84
2	D	209	LEU	CA-C-N	6.15	126.10	119.76
2	D	209	LEU	C-N-CA	6.15	126.10	119.76
1	A	977	LYS	CA-C-N	6.15	127.53	119.84
1	A	977	LYS	C-N-CA	6.15	127.53	119.84
2	B	173	LYS	N-CA-C	6.10	123.28	109.81
1	C	800	ILE	N-CA-C	-6.10	104.80	110.53
1	A	239	SER	CB-CA-C	-6.05	97.57	110.76
1	A	34	MET	N-CA-CB	-5.96	100.81	110.71
1	A	931	LYS	N-CA-C	-5.93	106.18	113.41
2	B	91	ARG	CA-C-N	5.82	127.12	119.84
2	B	91	ARG	C-N-CA	5.82	127.12	119.84
2	B	209	LEU	CA-C-N	5.81	125.74	119.76
2	B	209	LEU	C-N-CA	5.81	125.74	119.76
2	B	238	PHE	CA-C-N	5.76	127.04	119.84
2	B	238	PHE	C-N-CA	5.76	127.04	119.84
1	A	75	PRO	CA-C-N	5.76	126.31	120.38
1	A	75	PRO	C-N-CA	5.76	126.31	120.38
2	D	238	PHE	CA-C-N	5.75	127.03	119.84
2	D	238	PHE	C-N-CA	5.75	127.03	119.84
1	C	649	ASN	CA-C-N	5.70	125.37	119.56
1	C	649	ASN	C-N-CA	5.70	125.37	119.56
1	A	712	VAL	N-CA-C	-5.68	104.61	112.50
1	A	626	ILE	N-CA-C	-5.67	105.00	110.72
1	A	613	HIS	CA-C-N	5.64	125.75	119.32
1	A	613	HIS	C-N-CA	5.64	125.75	119.32
1	A	503	ALA	CA-C-N	5.64	125.75	119.32
1	A	503	ALA	C-N-CA	5.64	125.75	119.32
1	A	74	THR	CA-C-N	5.59	126.14	120.38
1	A	74	THR	C-N-CA	5.59	126.14	120.38
1	C	553	LEU	CA-C-N	5.58	126.46	119.98
1	C	553	LEU	C-N-CA	5.58	126.46	119.98
1	A	35	ASP	N-CA-C	5.51	115.67	108.07
1	A	433	LEU	CA-C-N	5.41	125.41	119.89
1	A	433	LEU	C-N-CA	5.41	125.41	119.89
1	C	580	GLY	N-CA-C	5.38	118.84	110.88
1	A	240	THR	N-CA-C	-5.30	102.17	110.17
2	D	91	ARG	CA-C-N	5.25	126.40	119.84
2	D	91	ARG	C-N-CA	5.25	126.40	119.84
1	C	240	THR	N-CA-C	-5.20	101.80	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	94	ASP	CA-C-N	5.18	124.68	119.19
2	B	94	ASP	C-N-CA	5.18	124.68	119.19
1	A	739	ALA	N-CA-C	5.15	116.58	110.19
1	C	592	VAL	CB-CA-C	-5.11	108.84	113.70
1	A	228	ASN	CA-C-N	5.10	125.38	119.47
1	A	228	ASN	C-N-CA	5.10	125.38	119.47
1	C	558	PHE	CA-C-N	5.07	125.08	120.21
1	C	558	PHE	C-N-CA	5.07	125.08	120.21
2	D	65	LYS	CA-C-N	5.03	124.79	119.76
2	D	65	LYS	C-N-CA	5.03	124.79	119.76
2	D	280	GLY	N-CA-C	5.02	117.36	110.69

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	17	ASP	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7714	0	7770	314	0
1	C	7714	0	7769	283	0
2	B	2479	0	2458	103	0
2	D	2479	0	2458	101	0
3	E	281	0	285	14	0
3	G	270	0	272	12	0
4	A	2	0	0	0	0
4	C	2	0	0	0	0
5	A	5	0	0	1	0
5	C	5	0	0	3	0
6	A	27	0	12	3	0
6	C	27	0	12	6	0
7	A	4	0	0	0	0
7	C	4	0	0	0	0
8	A	56	0	92	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	56	0	92	29	0
8	E	28	0	45	13	0
8	G	28	0	45	9	0
9	A	216	0	352	14	0
9	B	54	0	88	2	0
9	C	216	0	352	15	0
9	D	54	0	88	2	0
10	A	56	0	74	0	0
10	C	56	0	74	0	0
11	B	14	0	13	0	0
11	D	14	0	13	0	0
12	A	24	0	0	0	0
12	B	2	0	0	0	0
12	C	20	0	0	2	0
12	D	2	0	0	0	0
All	All	21909	0	22364	883	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 20.

All (883) 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)
8:A:2009:CLR:C11	8:A:2009:CLR:C9	1.77	1.62
8:D:3002:CLR:C12	8:D:3002:CLR:C11	1.74	1.60
8:A:2010:CLR:C11	8:A:2010:CLR:C9	1.76	1.59
8:D:3001:CLR:C11	8:D:3001:CLR:C9	1.78	1.57
8:E:101:CLR:C11	8:E:101:CLR:C9	1.78	1.56
8:D:3002:CLR:C11	8:D:3002:CLR:C9	1.78	1.55
8:G:101:CLR:C11	8:G:101:CLR:C9	1.79	1.54
1:C:495:ARG:HG3	1:C:495:ARG:O	1.42	1.11
1:C:493:GLU:HG2	1:C:495:ARG:H	1.24	1.03
1:A:600:ARG:HG2	1:A:600:ARG:HH11	1.33	0.94
2:D:221:LYS:HE3	2:D:223:LYS:HB2	1.49	0.93
1:A:417:ILE:HD11	1:A:548:PHE:HB3	1.48	0.93
1:A:493:GLU:HG2	1:A:495:ARG:H	1.35	0.91
8:A:2010:CLR:C11	8:A:2010:CLR:C10	2.50	0.90
2:B:76:GLY:HA2	2:B:293:GLY:H	1.37	0.90
1:C:44:LEU:HD11	1:C:197:ARG:HG2	1.54	0.90
2:B:221:LYS:HE3	2:B:223:LYS:HB2	1.52	0.90
1:A:790:ASN:HD22	1:A:880:ARG:HD2	1.38	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:ARG:NH1	1:C:182:ASP:OD1	2.06	0.88
1:A:57:THR:HG23	1:A:60:ARG:HB2	1.56	0.87
2:D:124:GLU:HB2	2:D:147:LYS:HD3	1.56	0.87
2:B:188:PRO:HB3	2:B:209:LEU:HD22	1.56	0.86
8:A:2009:CLR:C11	8:A:2009:CLR:C10	2.52	0.86
8:D:3002:CLR:C11	8:D:3002:CLR:C10	2.54	0.86
2:D:216:LYS:HG2	2:D:221:LYS:HB2	1.59	0.85
2:D:269:ASP:HA	2:D:302:LYS:HA	1.56	0.85
1:A:480:LYS:HE3	6:A:2004:ADP:H5'2	1.57	0.85
1:A:443:ASP:HB2	1:A:446:GLU:HB2	1.60	0.84
8:D:3001:CLR:C11	8:D:3001:CLR:C10	2.55	0.84
1:A:494:PRO:HG2	1:A:552:PHE:HB3	1.59	0.83
8:E:101:CLR:C11	8:E:101:CLR:C10	2.56	0.82
1:A:679:THR:HG23	1:A:680:GLU:HG3	1.61	0.82
1:C:454:GLU:HG2	1:C:460:VAL:HG23	1.59	0.82
2:B:216:LYS:HG2	2:B:221:LYS:HB2	1.62	0.81
1:A:799:THR:HG21	1:A:912:HIS:HB3	1.62	0.81
1:C:195:ASP:HB2	1:C:253:TYR:HB2	1.61	0.81
1:C:763:ASP:OD2	12:C:2114:HOH:O	1.97	0.81
1:A:495:ARG:HG3	1:A:495:ARG:O	1.77	0.81
1:C:384:MET:HE1	1:C:393:ALA:HB2	1.61	0.81
1:C:495:ARG:O	1:C:495:ARG:CG	2.27	0.80
1:C:165:ILE:HB	1:C:183:LEU:HD21	1.62	0.80
1:C:872:LEU:HD12	1:C:873:PRO:HD2	1.64	0.79
8:D:3001:CLR:H212	8:D:3001:CLR:H121	1.64	0.78
2:B:79:GLN:HB3	2:B:295:PHE:HZ	1.49	0.78
2:D:79:GLN:HB3	2:D:295:PHE:CZ	2.19	0.78
2:D:79:GLN:HB3	2:D:295:PHE:HZ	1.46	0.78
1:C:514:ILE:HG13	1:C:523:LEU:HG	1.66	0.77
1:C:565:ASP:H	1:C:570:ASN:HB2	1.51	0.76
2:B:79:GLN:HB3	2:B:295:PHE:CZ	2.21	0.75
1:C:57:THR:HG23	1:C:60:ARG:HB2	1.68	0.75
1:C:600:ARG:HH11	1:C:600:ARG:HB3	1.52	0.75
1:A:472:GLU:HB2	1:A:484:SER:HB3	1.68	0.75
2:B:124:GLU:HB2	2:B:147:LYS:HD3	1.69	0.75
1:A:165:ILE:HB	1:A:183:LEU:HD21	1.67	0.74
1:A:195:ASP:HB2	1:A:253:TYR:HB2	1.70	0.74
1:C:986:PRO:HG3	8:D:3002:CLR:H152	1.70	0.74
2:D:122:ILE:HG21	2:D:253:LYS:HE2	1.70	0.74
2:D:173:LYS:HG2	2:D:264:THR:HA	1.69	0.74
8:E:101:CLR:H121	8:E:101:CLR:H212	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:ARG:O	1:A:495:ARG:CG	2.35	0.73
1:C:309:THR:HG23	1:C:312:GLU:HB2	1.70	0.73
8:G:101:CLR:C11	8:G:101:CLR:C8	2.66	0.73
1:C:946:ILE:HG13	3:E:45:ILE:HD11	1.70	0.73
2:D:188:PRO:HB3	2:D:209:LEU:HD22	1.71	0.72
2:B:269:ASP:HA	2:B:302:LYS:HA	1.71	0.72
1:C:663:LEU:HA	1:C:666:MET:HE2	1.69	0.72
1:C:759:ARG:HH12	1:C:829:PRO:HA	1.54	0.72
2:B:122:ILE:HG21	2:B:253:LYS:HE2	1.70	0.72
1:A:963:TYR:CE2	8:G:101:CLR:H21	2.24	0.71
1:C:56:LEU:HD11	1:C:182:ASP:HB3	1.72	0.71
2:D:187:LYS:O	2:D:282:ASN:ND2	2.22	0.71
1:A:977:LYS:H	1:A:980:TRP:CD1	2.07	0.71
8:G:101:CLR:C11	8:G:101:CLR:C10	2.63	0.71
1:A:44:LEU:HD11	1:A:197:ARG:HG2	1.72	0.71
1:A:811:PRO:HB3	1:A:927:LEU:HD22	1.72	0.71
2:B:57:MET:HE3	2:B:61:ILE:HD11	1.72	0.70
1:C:685:ARG:NH2	6:C:2004:ADP:O3'	2.22	0.70
1:A:473:ILE:HD11	1:A:483:LEU:HD23	1.72	0.70
1:C:1003:ARG:HD2	9:C:2011:PC1:H122	1.72	0.70
8:D:3002:CLR:C11	8:D:3002:CLR:C8	2.68	0.70
8:A:2010:CLR:C11	8:A:2010:CLR:C8	2.64	0.70
1:C:643:ILE:HD11	1:C:648:VAL:HG22	1.73	0.70
1:A:255:GLY:O	1:A:258:THR:HG22	1.92	0.70
1:C:277:ILE:HD12	1:C:358:GLU:HG3	1.74	0.69
1:A:420:LEU:HB3	1:A:486:HIS:CE1	2.28	0.69
1:A:166:ARG:NH1	1:A:182:ASP:OD1	2.25	0.69
8:A:2009:CLR:H121	8:A:2009:CLR:H212	1.73	0.69
9:C:2012:PC1:H351	9:C:2012:PC1:H251	1.75	0.69
8:D:3001:CLR:C11	8:D:3001:CLR:C8	2.67	0.69
1:A:50:THR:HG22	1:A:56:LEU:HB3	1.75	0.69
1:A:551:LEU:HD22	1:A:553:LEU:HD23	1.75	0.69
1:C:50:THR:HG22	1:C:56:LEU:HD23	1.75	0.68
1:C:600:ARG:NH1	12:C:2120:HOH:O	2.25	0.68
2:B:14:LYS:HA	2:B:17:TRP:HB3	1.75	0.68
1:C:696:GLU:HG3	1:C:720:LYS:HE2	1.75	0.68
8:A:2010:CLR:H121	8:A:2010:CLR:H212	1.73	0.68
1:C:241:ASN:N	1:C:241:ASN:OD1	2.24	0.68
1:A:1002:ILE:HG23	1:A:1011:GLU:HB2	1.76	0.68
9:A:2013:PC1:H292	9:A:2013:PC1:H3B2	1.74	0.68
1:A:239:SER:O	1:A:239:SER:OG	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:17:ASP:HB3	3:G:18:PRO:HD2	1.76	0.68
1:A:493:GLU:HG2	1:A:495:ARG:N	2.09	0.67
3:G:24:GLU:O	3:G:28:ASN:ND2	2.26	0.67
1:C:421:CYS:O	1:C:501:LYS:NZ	2.23	0.67
1:C:867:ALA:HB2	1:C:873:PRO:HD3	1.76	0.67
2:D:209:LEU:HD21	2:D:283:ILE:HD11	1.77	0.67
2:D:191:PRO:HG3	2:D:280:GLY:HA2	1.77	0.67
2:B:88:ILE:HB	2:B:299:ILE:HG22	1.76	0.67
1:C:417:ILE:HD11	1:C:548:PHE:HB3	1.75	0.66
1:C:488:ASN:HB3	1:C:493:GLU:HG3	1.75	0.66
2:D:216:LYS:HB3	2:D:273:ARG:HB2	1.76	0.66
2:B:90:PHE:CD2	2:B:98:TYR:HB3	2.31	0.66
2:D:14:LYS:HA	2:D:17:TRP:HB3	1.77	0.66
1:A:108:TYR:HA	1:A:111:GLN:HE21	1.60	0.66
1:A:394:ASP:OD1	1:A:394:ASP:N	2.28	0.66
1:C:445:SER:OG	1:C:544:ARG:NH1	2.29	0.66
1:A:154:PHE:HB3	1:A:350:LEU:HD13	1.78	0.66
1:C:719:LYS:NZ	1:C:738:ALA:O	2.28	0.66
1:A:505:GLU:HG3	1:A:506:ARG:H	1.61	0.65
9:C:2009:PC1:H2D2	9:C:2012:PC1:H3F2	1.78	0.65
1:A:759:ARG:HH12	1:A:829:PRO:HA	1.60	0.65
8:D:3002:CLR:C11	8:D:3002:CLR:C13	2.68	0.65
2:D:229:TYR:HD1	2:D:261:VAL:HG12	1.60	0.65
9:C:2009:PC1:H2I3	9:C:2009:PC1:H3I1	1.78	0.65
1:A:514:ILE:HG12	1:A:578:PHE:HB3	1.77	0.65
1:A:842:LEU:HD12	1:A:1016:TYR:HD2	1.61	0.65
1:A:258:THR:HG23	1:A:261:GLY:H	1.60	0.65
1:C:777:ILE:HD11	1:C:847:TYR:HA	1.79	0.64
1:C:372:GLY:HA2	1:C:377:ASN:HB2	1.79	0.64
1:C:679:THR:HG23	1:C:680:GLU:HG3	1.79	0.64
8:A:2010:CLR:H193	8:A:2010:CLR:H111	1.79	0.64
1:A:790:ASN:ND2	1:A:880:ARG:HD2	2.11	0.64
1:A:274:GLN:HE22	1:A:279:ALA:HB2	1.62	0.64
2:D:217:ARG:HD2	2:D:218:ASP:H	1.62	0.64
2:B:27:ARG:HD3	2:B:32:TRP:HE3	1.62	0.64
1:A:1009:TRP:HZ2	2:B:35:ILE:HG22	1.63	0.64
1:C:211:LEU:HD23	1:C:212:THR:HG23	1.80	0.64
1:A:613:HIS:CD2	1:A:615:ILE:HG12	2.33	0.63
1:A:613:HIS:NE2	1:A:615:ILE:HG12	2.14	0.63
8:A:2009:CLR:C11	8:A:2009:CLR:C8	2.65	0.63
1:C:299:PHE:HB3	1:C:316:PHE:HE2	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:173:LYS:HG2	2:B:264:THR:HA	1.81	0.63
1:C:426:PHE:HE2	1:C:454:GLU:HG3	1.63	0.63
3:E:33:PHE:CE1	8:E:101:CLR:H183	2.34	0.63
2:B:224:VAL:HB	2:B:267:THR:HG21	1.81	0.62
1:A:36:ASP:OD1	1:A:47:LYS:NZ	2.32	0.62
1:C:963:TYR:CE2	8:E:101:CLR:H21	2.33	0.62
9:C:2011:PC1:H2H2	8:D:3002:CLR:H272	1.80	0.62
2:B:216:LYS:H	2:B:216:LYS:HD2	1.63	0.62
1:A:152:GLU:HA	1:A:155:LYS:HG2	1.82	0.62
1:A:209:SER:HB3	1:A:215:SER:HA	1.82	0.62
1:C:998:ARG:HE	1:C:1014:THR:HB	1.65	0.62
2:B:229:TYR:HD1	2:B:261:VAL:HG12	1.64	0.62
1:C:854:GLN:HG2	1:C:922:VAL:HB	1.81	0.62
1:C:266:LEU:HD22	1:C:270:LEU:HA	1.82	0.62
1:A:324:ASN:HA	1:A:776:ASN:OD1	2.00	0.61
1:A:708:THR:HG22	1:A:725:VAL:HB	1.81	0.61
2:D:83:SER:HB3	2:D:86:THR:HA	1.80	0.61
1:C:258:THR:HG23	1:C:261:GLY:H	1.64	0.61
1:A:483:LEU:HD21	1:A:571:PHE:HE2	1.65	0.61
1:A:946:ILE:HG13	3:G:45:ILE:HD11	1.81	0.61
1:C:777:ILE:HD12	1:C:777:ILE:H	1.65	0.61
1:C:186:VAL:HG11	1:C:192:ILE:HD13	1.81	0.61
1:C:480:LYS:HG2	6:C:2004:ADP:H5'1	1.83	0.61
1:A:1016:TYR:HD1	1:A:1016:TYR:H	1.48	0.61
1:C:956:ALA:HB2	3:E:37:ALA:HB3	1.83	0.61
2:B:209:LEU:HD21	2:B:283:ILE:HD11	1.82	0.60
1:C:471:VAL:HG21	1:C:564:PHE:HB2	1.83	0.60
1:C:982:PHE:HA	1:C:985:PHE:CD1	2.36	0.60
8:A:2009:CLR:H111	8:A:2009:CLR:H193	1.82	0.60
2:D:91:ARG:HG3	2:D:302:LYS:O	2.01	0.60
2:D:106:VAL:HG22	2:D:167:TYR:HB2	1.83	0.60
3:E:17:ASP:HB3	3:E:18:PRO:HD2	1.81	0.60
2:D:87:GLU:HA	2:D:298:LYS:O	2.02	0.60
2:D:73:ALA:HB3	2:D:74:PRO:HD3	1.83	0.60
1:A:343:ARG:HD2	1:A:757:GLU:OE2	2.02	0.60
1:A:360:LEU:HA	1:A:723:ILE:HD13	1.83	0.60
1:C:125:LEU:O	1:C:129:LEU:HB2	2.01	0.60
1:A:35:ASP:HB2	1:A:37:HIS:ND1	2.16	0.60
1:A:818:GLU:HG2	1:A:944:ASN:HD22	1.66	0.60
1:C:385:TRP:HB3	1:C:581:LEU:HB2	1.83	0.60
1:C:469:LYS:HA	1:C:486:HIS:HA	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:494:PRO:HG2	1:C:552:PHE:HB3	1.82	0.60
2:D:88:ILE:HB	2:D:299:ILE:HG22	1.82	0.60
1:A:514:ILE:HG13	1:A:523:LEU:HG	1.84	0.59
1:A:80:PRO:HG2	1:A:83:VAL:HB	1.83	0.59
2:B:73:ALA:HB3	2:B:74:PRO:HD3	1.84	0.59
1:C:398:ASN:HB2	1:C:455:LEU:HD13	1.84	0.59
1:C:31:GLU:HG3	1:C:32:VAL:H	1.68	0.59
8:D:3002:CLR:H193	8:D:3002:CLR:H111	1.84	0.59
1:C:152:GLU:C	1:C:154:PHE:H	2.09	0.59
1:C:827:ARG:HH12	1:C:933:ARG:HH21	1.50	0.59
1:A:433:LEU:HD12	1:A:437:LYS:HB3	1.85	0.59
2:D:76:GLY:HA2	2:D:293:GLY:H	1.66	0.59
1:A:372:GLY:HA2	1:A:377:ASN:HB2	1.85	0.59
1:C:365:THR:HB	1:C:705:VAL:HG12	1.84	0.59
1:C:191:ARG:HA	1:C:241:ASN:HB3	1.85	0.58
1:C:549:CYS:HA	1:C:579:VAL:HG23	1.84	0.58
1:A:874:ILE:H	1:A:874:ILE:HD12	1.68	0.58
1:A:986:PRO:CG	8:A:2010:CLR:H181	2.33	0.58
5:A:2002:ALF:F1	6:A:2004:ADP:O3B	2.11	0.58
1:A:496:HIS:HB2	1:A:553:LEU:HB2	1.84	0.58
2:B:216:LYS:HB3	2:B:273:ARG:HB2	1.85	0.58
1:C:281:ILE:HD11	1:C:765:LEU:HD13	1.85	0.58
1:C:906:ILE:O	1:C:910:THR:OG1	2.22	0.58
8:D:3002:CLR:H121	8:D:3002:CLR:H212	1.85	0.58
1:A:383:HIS:C	1:A:384:MET:HE3	2.29	0.58
1:A:831:ASN:HD21	2:B:6:ALA:HB2	1.69	0.58
1:C:496:HIS:HB2	1:C:553:LEU:HB2	1.84	0.58
1:A:824:ILE:HD12	1:A:825:MET:H	1.68	0.58
1:A:889:ASN:HD22	1:A:900:THR:HB	1.69	0.58
1:C:902:GLU:O	1:C:906:ILE:HG12	2.03	0.58
1:A:873:PRO:HA	1:A:876:LEU:HD12	1.86	0.58
8:A:2010:CLR:C11	8:A:2010:CLR:C19	2.82	0.57
1:A:927:LEU:HG	1:A:947:LEU:HD21	1.87	0.57
1:C:553:LEU:HD22	1:C:558:PHE:CE2	2.39	0.57
8:A:2010:CLR:C9	8:A:2010:CLR:C12	2.79	0.57
1:C:551:LEU:HD12	1:C:576:LEU:HA	1.87	0.57
1:C:303:SER:O	1:C:308:TYR:HB2	2.04	0.57
2:D:186:PHE:CZ	2:D:282:ASN:HB3	2.40	0.57
1:A:340:THR:HG22	1:A:757:GLU:OE1	2.04	0.57
1:A:857:GLY:O	1:A:861:THR:HG23	2.04	0.57
1:A:300:PHE:HB2	1:A:317:LEU:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:628:SER:OG	1:A:680:GLU:OE2	2.21	0.57
1:A:263:ILE:HG13	1:A:263:ILE:O	2.05	0.56
1:C:420:LEU:HB3	1:C:486:HIS:CE1	2.39	0.56
1:A:370:LYS:NZ	1:A:612:ASP:OD2	2.37	0.56
1:A:671:LEU:O	1:A:675:LEU:HD22	2.06	0.56
1:C:60:ARG:O	1:C:64:ILE:HG13	2.05	0.56
1:C:126:GLY:O	1:C:130:SER:OG	2.17	0.56
1:A:420:LEU:HD13	1:A:486:HIS:ND1	2.20	0.56
1:A:638:ALA:HB2	1:A:648:VAL:HG21	1.87	0.56
1:A:902:GLU:O	1:A:906:ILE:HG12	2.05	0.56
1:C:206:VAL:HA	1:C:242:CYS:HA	1.87	0.56
1:C:538:LEU:HA	1:C:541:LEU:HD22	1.88	0.56
1:C:987:TYR:OH	2:D:53:THR:HG21	2.06	0.56
2:B:214:THR:OG1	2:B:215:GLY:N	2.35	0.56
1:C:99:ILE:O	1:C:103:LEU:HG	2.06	0.56
9:C:2012:PC1:H3B2	9:C:2012:PC1:H361	1.88	0.56
2:D:268:MET:HA	2:D:301:VAL:HG23	1.87	0.56
1:A:963:TYR:HE1	1:A:976:LEU:H	1.54	0.56
1:A:777:ILE:HD11	1:A:847:TYR:CG	2.41	0.55
1:A:892:GLU:HA	1:A:897:GLN:O	2.06	0.55
1:C:369:ASP:OD1	5:C:2002:ALF:F1	2.14	0.55
1:C:985:PHE:HZ	8:E:101:CLR:H221	1.72	0.55
2:B:217:ARG:HD2	2:B:218:ASP:H	1.71	0.55
1:C:565:ASP:H	1:C:570:ASN:CB	2.19	0.55
1:A:469:LYS:HB2	1:A:486:HIS:CD2	2.42	0.55
2:B:27:ARG:HD3	2:B:32:TRP:CE3	2.41	0.55
1:C:67:ARG:NH1	1:C:68:ASP:OD2	2.39	0.55
2:D:61:ILE:HG23	2:D:67:THR:HG23	1.87	0.55
1:A:350:LEU:HD23	1:A:742:ILE:HD12	1.88	0.55
1:A:768:SER:HA	1:A:815:LEU:HD23	1.89	0.55
1:A:963:TYR:CD2	3:G:30:GLY:HA3	2.41	0.55
2:B:178:ILE:HD11	2:B:276:CYS:SG	2.47	0.55
1:C:469:LYS:HB3	1:C:486:HIS:CE1	2.40	0.55
2:D:27:ARG:HD3	2:D:32:TRP:HE3	1.71	0.55
8:E:101:CLR:H111	8:E:101:CLR:H193	1.88	0.55
1:A:607:ILE:HG12	1:A:681:ILE:HG13	1.88	0.55
2:B:238:PHE:HD1	2:B:257:PRO:HB2	1.72	0.55
1:A:55:GLY:HA3	1:A:165:ILE:O	2.07	0.55
1:C:460:VAL:HG11	1:C:464:ARG:HH21	1.71	0.55
1:A:706:ALA:HA	1:A:723:ILE:HG13	1.88	0.55
2:B:113:LYS:HA	2:B:153:LEU:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:2012:PC1:H3B1	9:C:2012:PC1:H282	1.87	0.55
2:B:80:ILE:HB	2:B:177:ILE:HG23	1.89	0.55
1:A:183:LEU:HD23	1:A:183:LEU:H	1.73	0.54
1:A:475:PHE:H	1:A:482:GLN:HG3	1.72	0.54
1:A:777:ILE:HD11	1:A:847:TYR:HA	1.90	0.54
2:B:138:GLU:O	2:B:140:ASN:N	2.39	0.54
1:C:255:GLY:O	1:C:258:THR:HG22	2.07	0.54
1:A:60:ARG:O	1:A:64:ILE:HG13	2.07	0.54
1:C:799:THR:HG22	1:C:973:MET:HE3	1.88	0.54
1:C:861:THR:HG21	1:C:918:SER:OG	2.07	0.54
1:A:666:MET:HG3	1:A:670:GLN:HB3	1.90	0.54
1:C:747:ASN:HD21	1:C:749:ALA:HB3	1.72	0.54
9:A:2014:PC1:H122	2:B:25:LEU:HD11	1.89	0.54
1:C:306:LEU:HD12	1:C:880:ARG:HE	1.73	0.54
8:D:3001:CLR:C9	8:D:3001:CLR:C12	2.84	0.54
1:A:977:LYS:HD3	2:B:68:TYR:CE1	2.43	0.54
3:G:17:ASP:CB	3:G:18:PRO:HD2	2.38	0.54
2:B:90:PHE:HD2	2:B:98:TYR:HB3	1.72	0.54
1:C:801:LEU:O	1:C:805:LEU:HG	2.07	0.54
1:A:336:CYS:O	1:A:340:THR:HG23	2.08	0.54
1:A:854:GLN:HE22	1:A:923:GLN:HE21	1.55	0.54
1:A:888:ILE:O	1:A:904:ARG:NH2	2.41	0.54
1:C:143:GLN:HE21	1:C:335:VAL:HG22	1.73	0.54
1:C:613:HIS:HD2	1:C:615:ILE:HB	1.72	0.54
1:A:472:GLU:CB	1:A:484:SER:HB3	2.36	0.53
1:C:814:SER:HB3	1:C:946:ILE:HG22	1.89	0.53
1:A:131:ALA:O	1:A:135:ILE:HG12	2.09	0.53
1:A:440:VAL:HG12	1:A:441:ALA:H	1.74	0.53
1:A:603:GLY:HA3	1:A:829:PRO:HD3	1.90	0.53
1:A:899:TRP:CE3	2:B:72:VAL:HG13	2.43	0.53
1:C:854:GLN:HE22	1:C:923:GLN:HE21	1.57	0.53
1:A:476:ASN:OD1	1:A:478:THR:HG23	2.08	0.53
1:C:50:THR:HG21	1:C:181:GLY:C	2.33	0.53
8:A:2009:CLR:C11	8:A:2009:CLR:C19	2.87	0.53
9:A:2013:PC1:H292	9:A:2013:PC1:C3B	2.39	0.53
2:B:83:SER:HB3	2:B:86:THR:HA	1.89	0.53
1:C:317:LEU:O	1:C:321:ILE:HG12	2.09	0.53
1:A:861:THR:HG21	1:A:918:SER:OG	2.08	0.53
2:B:106:VAL:HG22	2:B:167:TYR:HB2	1.91	0.53
1:A:505:GLU:OE2	1:A:613:HIS:ND1	2.34	0.53
1:A:951:LEU:O	1:A:955:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:176:VAL:HB	2:B:261:VAL:HG23	1.90	0.53
1:C:440:VAL:HG21	1:C:451:LYS:HE3	1.90	0.53
1:A:335:VAL:HG11	1:A:817:TYR:CE2	2.43	0.53
1:A:609:VAL:HG12	1:A:691:LYS:HE2	1.89	0.53
1:A:1001:ILE:CG2	1:A:1010:VAL:HG21	2.39	0.53
8:E:101:CLR:C11	8:E:101:CLR:C8	2.69	0.53
1:A:421:CYS:O	1:A:482:GLN:NE2	2.42	0.52
1:C:58:PRO:HD3	1:C:167:ASN:HB2	1.91	0.52
1:C:184:VAL:HG11	1:C:193:PRO:HG3	1.91	0.52
1:C:916:PHE:O	1:C:920:VAL:HG23	2.10	0.52
2:D:176:VAL:HB	2:D:261:VAL:HG23	1.90	0.52
8:E:101:CLR:C9	8:E:101:CLR:C12	2.83	0.52
8:A:2010:CLR:H121	8:A:2010:CLR:C21	2.39	0.52
2:D:224:VAL:HB	2:D:267:THR:HG21	1.91	0.52
1:A:997:VAL:O	1:A:1001:ILE:HG13	2.09	0.52
1:A:184:VAL:HG11	1:A:193:PRO:HG2	1.91	0.52
1:A:393:ALA:HA	1:A:402:VAL:HA	1.91	0.52
1:A:771:TYR:CE1	1:A:927:LEU:HB2	2.44	0.52
1:A:1009:TRP:CZ2	2:B:35:ILE:HG22	2.43	0.52
9:C:2009:PC1:H3A1	9:C:2009:PC1:H291	1.92	0.52
1:A:89:LEU:HD21	1:A:134:ILE:HA	1.91	0.52
1:A:422:ASN:OD1	1:A:423:ARG:N	2.42	0.52
1:A:921:VAL:HG22	1:A:924:TRP:CH2	2.45	0.52
2:D:90:PHE:CD2	2:D:98:TYR:HB3	2.44	0.52
1:C:986:PRO:CG	8:D:3002:CLR:H152	2.39	0.52
8:A:2010:CLR:C11	8:A:2010:CLR:H193	2.40	0.52
1:C:801:LEU:HD12	1:C:805:LEU:HD11	1.92	0.52
1:A:56:LEU:HG	1:A:182:ASP:HB3	1.91	0.52
1:A:777:ILE:HD12	1:A:777:ILE:H	1.74	0.52
1:A:790:ASN:C	1:A:880:ARG:HB2	2.35	0.52
1:C:493:GLU:HG2	1:C:495:ARG:N	2.08	0.52
1:C:514:ILE:HD12	1:C:527:LEU:HD13	1.90	0.52
1:A:501:LYS:HE3	6:A:2004:ADP:N1	2.24	0.52
2:B:76:GLY:H	2:B:181:ASN:HD22	1.56	0.52
1:A:258:THR:HG23	1:A:261:GLY:N	2.24	0.51
1:C:893:ASP:OD2	1:C:897:GLN:HG3	2.10	0.51
9:D:3003:PC1:H242	8:E:101:CLR:H6	1.92	0.51
2:B:251:GLN:HB3	2:B:254:TYR:HB2	1.92	0.51
1:C:115:GLU:HG2	1:C:116:GLU:H	1.74	0.51
1:C:283:HIS:NE2	1:C:287:ILE:HD11	2.25	0.51
1:C:531:PHE:HE2	1:C:581:LEU:HD21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:LYS:HG3	1:A:753:THR:HG21	1.92	0.51
1:A:818:GLU:OE2	1:A:931:LYS:NZ	2.39	0.51
1:A:986:PRO:HG3	8:A:2010:CLR:H181	1.92	0.51
2:B:202:MET:SD	2:B:236:PRO:HG2	2.50	0.51
1:C:43:GLU:O	1:C:46:ARG:HG2	2.10	0.51
1:C:551:LEU:HD13	1:C:576:LEU:HD23	1.92	0.51
1:C:600:ARG:HH21	1:C:680:GLU:HG2	1.76	0.51
1:C:196:LEU:HB2	1:C:236:ALA:HB3	1.93	0.51
1:C:340:THR:HG21	1:C:357:VAL:HG11	1.91	0.51
1:C:997:VAL:O	1:C:1001:ILE:HG13	2.11	0.51
1:A:263:ILE:HD12	1:A:265:THR:OG1	2.10	0.51
1:A:889:ASN:ND2	1:A:901:TYR:H	2.08	0.51
1:A:44:LEU:HD11	1:A:197:ARG:CG	2.38	0.51
1:A:986:PRO:HG3	8:A:2010:CLR:H152	1.91	0.51
1:C:827:ARG:NH1	1:C:933:ARG:HH21	2.08	0.51
3:E:24:GLU:O	3:E:28:ASN:ND2	2.43	0.51
1:C:375:THR:HA	1:C:588:PRO:HA	1.92	0.51
1:C:698:CYS:HB2	1:C:705:VAL:HG11	1.93	0.51
1:A:31:GLU:HG3	1:A:32:VAL:H	1.76	0.51
2:D:192:LYS:HZ1	2:D:205:ASN:HB3	1.75	0.51
2:B:136:ARG:HD2	2:B:143:ARG:HH12	1.76	0.50
1:C:689:GLN:O	1:C:693:ILE:HG12	2.10	0.50
1:A:37:HIS:HB3	1:A:235:ILE:HD11	1.93	0.50
2:D:14:LYS:HZ3	2:D:17:TRP:HE3	1.58	0.50
1:C:782:PRO:HG3	1:C:795:LEU:HD23	1.94	0.50
1:C:376:GLN:HG3	1:C:589:ARG:HA	1.93	0.50
1:A:420:LEU:HB3	1:A:486:HIS:HE1	1.73	0.50
2:D:57:MET:HE2	2:D:58:LEU:HA	1.94	0.50
1:A:185:GLU:HG3	1:A:248:ARG:HG2	1.93	0.50
1:A:211:LEU:HD12	1:A:260:MET:SD	2.52	0.50
1:A:298:SER:HB2	9:A:2014:PC1:H3F1	1.93	0.50
2:B:90:PHE:CZ	2:B:174:PRO:HG3	2.46	0.50
1:C:824:ILE:HD12	1:C:825:MET:H	1.77	0.50
2:D:117:GLN:HB3	2:D:150:ARG:HD3	1.93	0.50
1:A:769:ILE:HA	1:A:772:THR:HG22	1.94	0.50
2:B:280:GLY:HA3	2:B:283:ILE:HD13	1.94	0.50
1:C:757:GLU:O	1:C:761:ILE:HG22	2.11	0.50
1:A:620:ILE:O	1:A:624:VAL:HG13	2.12	0.49
2:D:24:PHE:C	2:D:26:GLY:H	2.20	0.49
8:D:3002:CLR:C11	8:D:3002:CLR:C14	2.89	0.49
1:A:725:VAL:HG11	1:A:751:ILE:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:759:ARG:HH22	1:A:829:PRO:HG3	1.76	0.49
1:A:781:THR:HG22	8:A:2009:CLR:C27	2.41	0.49
1:C:131:ALA:O	1:C:135:ILE:HG12	2.12	0.49
2:D:56:VAL:HG11	8:D:3002:CLR:H122	1.92	0.49
1:A:928:VAL:O	1:A:931:LYS:HB3	2.12	0.49
1:A:998:ARG:HA	1:A:1001:ILE:HD12	1.94	0.49
8:A:2009:CLR:H191	2:B:39:TYR:CZ	2.46	0.49
2:B:35:ILE:HG13	2:B:36:LEU:N	2.26	0.49
2:B:191:PRO:HG3	2:B:280:GLY:HA2	1.93	0.49
1:C:503:ALA:HB1	1:C:685:ARG:NH1	2.26	0.49
9:C:2009:PC1:H291	9:C:2009:PC1:H391	1.94	0.49
2:D:178:ILE:HD11	2:D:276:CYS:SG	2.52	0.49
2:D:251:GLN:HB3	2:D:254:TYR:HB2	1.93	0.49
1:A:545:VAL:HG22	1:A:583:SER:HB3	1.94	0.49
2:B:42:PHE:HD2	2:B:43:TYR:CD1	2.30	0.49
2:B:138:GLU:HG3	2:B:140:ASN:ND2	2.27	0.49
1:C:861:THR:O	1:C:865:ILE:HD12	2.12	0.49
1:C:93:PHE:CZ	1:C:285:ILE:HG23	2.48	0.49
1:C:430:GLN:HA	1:C:430:GLN:HE21	1.76	0.49
1:A:192:ILE:HD12	1:A:236:ALA:HB1	1.95	0.49
1:A:413:ALA:O	1:A:417:ILE:HG23	2.12	0.49
1:A:454:GLU:HG2	1:A:460:VAL:HG23	1.94	0.49
2:B:37:LEU:O	2:B:41:ILE:HG23	2.13	0.49
8:G:101:CLR:H183	8:G:101:CLR:H212	1.94	0.49
1:C:777:ILE:CD1	1:C:847:TYR:HA	2.43	0.49
2:D:57:MET:HA	8:D:3002:CLR:H11	1.93	0.49
2:D:57:MET:HE3	2:D:61:ILE:HD11	1.93	0.49
8:E:101:CLR:C11	8:E:101:CLR:C19	2.90	0.49
1:A:688:PRO:HG3	1:A:713:ASN:HB2	1.94	0.49
1:C:977:LYS:H	1:C:980:TRP:CD1	2.30	0.49
2:D:36:LEU:O	2:D:40:VAL:HG23	2.13	0.49
8:D:3002:CLR:C11	8:D:3002:CLR:C19	2.91	0.49
1:A:191:ARG:HA	1:A:241:ASN:HB3	1.95	0.49
1:A:283:HIS:O	1:A:287:ILE:HG12	2.12	0.49
1:A:317:LEU:O	1:A:321:ILE:HG12	2.13	0.49
1:A:710:ASP:OD1	1:A:711:GLY:N	2.44	0.49
1:A:861:THR:HG22	1:A:983:CYS:HB3	1.95	0.49
1:A:777:ILE:CD1	1:A:847:TYR:HA	2.42	0.49
1:A:882:ASN:HB3	1:A:888:ILE:HD12	1.95	0.49
2:B:157:GLY:H	2:B:230:PHE:HB3	1.78	0.49
1:C:607:ILE:HG23	1:C:681:ILE:HG13	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:90:PHE:CZ	2:D:174:PRO:HG3	2.48	0.49
1:C:426:PHE:CE2	1:C:454:GLU:HG3	2.47	0.48
1:C:763:ASP:O	1:C:767:LYS:HG3	2.13	0.48
1:C:1009:TRP:HZ2	2:D:35:ILE:HG22	1.78	0.48
2:D:214:THR:OG1	2:D:215:GLY:N	2.45	0.48
2:B:91:ARG:NH2	2:D:94:ASP:OD1	2.45	0.48
1:C:611:GLY:O	6:C:2004:ADP:H5'2	2.12	0.48
8:D:3001:CLR:H121	8:D:3001:CLR:C21	2.40	0.48
1:A:944:ASN:ND2	1:A:947:LEU:HB2	2.29	0.48
1:A:182:ASP:O	1:A:251:VAL:HG23	2.13	0.48
2:B:268:MET:HA	2:B:301:VAL:HG23	1.95	0.48
1:A:752:VAL:O	1:A:755:VAL:HG12	2.13	0.48
1:C:1001:ILE:CG2	1:C:1010:VAL:HG21	2.43	0.48
2:D:62:SER:C	2:D:64:PHE:H	2.22	0.48
1:A:340:THR:HG21	1:A:761:ILE:CD1	2.43	0.48
1:A:937:VAL:HG21	1:A:992:PHE:CE1	2.49	0.48
8:A:2010:CLR:H111	8:A:2010:CLR:C19	2.44	0.48
2:B:209:LEU:HD12	2:B:210:PRO:HD2	1.96	0.48
1:A:185:GLU:HG3	1:A:248:ARG:CG	2.43	0.48
1:A:838:VAL:HG13	1:A:842:LEU:HD22	1.95	0.48
2:B:36:LEU:O	2:B:40:VAL:HG23	2.14	0.48
3:G:38:PHE:O	3:G:42:LEU:HG	2.12	0.48
1:C:565:ASP:CB	1:C:570:ASN:HD22	2.26	0.48
1:A:565:ASP:HB3	1:A:570:ASN:HB2	1.95	0.48
2:B:238:PHE:CD1	2:B:257:PRO:HB2	2.49	0.48
1:C:305:ILE:C	1:C:307:GLU:H	2.21	0.48
1:C:899:TRP:CE3	2:D:72:VAL:HG13	2.49	0.48
2:D:192:LYS:NZ	2:D:205:ASN:HB3	2.29	0.48
2:D:216:LYS:H	2:D:216:LYS:HD2	1.77	0.48
8:E:101:CLR:H121	8:E:101:CLR:C21	2.43	0.48
1:A:387:ASP:O	1:A:389:GLN:N	2.46	0.48
1:A:777:ILE:HD12	1:A:777:ILE:N	2.29	0.48
1:A:793:LEU:O	1:A:912:HIS:NE2	2.43	0.48
1:C:147:SER:HB2	1:C:338:THR:HG23	1.96	0.48
1:C:556:GLU:OE1	1:C:556:GLU:N	2.43	0.48
1:C:613:HIS:CD2	1:C:615:ILE:HB	2.48	0.48
1:C:692:LEU:O	1:C:696:GLU:HB2	2.14	0.48
1:A:37:HIS:CE1	1:A:229:PRO:HG3	2.49	0.47
1:A:303:SER:O	1:A:308:TYR:HB2	2.14	0.47
8:A:2009:CLR:H111	8:A:2009:CLR:C19	2.44	0.47
9:A:2013:PC1:H261	9:A:2013:PC1:H291	1.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:52:GLY:O	2:D:56:VAL:HG23	2.13	0.47
2:D:204:TYR:CE2	2:D:207:TYR:HB2	2.48	0.47
1:A:956:ALA:HB2	3:G:37:ALA:HB3	1.95	0.47
1:A:1009:TRP:CE2	1:A:1013:GLU:HG3	2.48	0.47
2:B:38:PHE:HD2	2:B:39:TYR:CD1	2.32	0.47
2:B:277:LYS:HD2	2:B:279:TYR:CE2	2.49	0.47
1:A:815:LEU:HD12	1:A:815:LEU:HA	1.71	0.47
8:D:3001:CLR:H111	8:D:3001:CLR:H193	1.96	0.47
2:D:17:TRP:CZ2	2:D:19:SER:HB3	2.49	0.47
1:A:402:VAL:HG21	1:A:404:PHE:CZ	2.49	0.47
2:B:99:GLU:O	2:B:103:VAL:HG23	2.14	0.47
1:C:103:LEU:HD12	1:C:318:ILE:HD11	1.95	0.47
9:D:3003:PC1:H2B2	9:D:3003:PC1:H282	1.60	0.47
1:A:349:CYS:SG	1:A:741:MET:HG2	2.55	0.47
1:A:445:SER:HB3	1:A:584:MET:HE1	1.97	0.47
1:A:512:SER:OG	1:A:575:ASN:HA	2.13	0.47
1:A:803:ILE:HG23	1:A:919:ILE:HG21	1.96	0.47
2:B:131:SER:HB2	2:B:241:GLN:HB3	1.97	0.47
2:B:186:PHE:CZ	2:B:282:ASN:HB3	2.50	0.47
2:B:204:TYR:HB3	2:B:208:VAL:HB	1.97	0.47
1:C:25:MET:O	1:C:29:LYS:HG3	2.15	0.47
1:C:804:ASP:O	1:C:808:ASP:HB2	2.15	0.47
2:D:98:TYR:CZ	2:D:171:ASP:HB3	2.50	0.47
1:A:192:ILE:HA	1:A:193:PRO:HD3	1.71	0.47
2:B:170:LYS:N	2:B:170:LYS:HD2	2.30	0.47
2:B:173:LYS:HA	2:B:174:PRO:HD3	1.79	0.47
1:C:972:ARG:HH12	2:D:288:LYS:NZ	2.12	0.47
2:D:49:ILE:O	2:D:53:THR:HG22	2.14	0.47
2:D:102:VAL:HA	2:D:105:ILE:HG22	1.95	0.47
2:D:238:PHE:HD1	2:D:257:PRO:HB2	1.78	0.47
1:A:814:SER:HB2	1:A:946:ILE:HG22	1.97	0.47
1:A:861:THR:HG22	1:A:983:CYS:CB	2.45	0.47
1:A:864:VAL:HG22	2:B:57:MET:SD	2.54	0.47
1:C:613:HIS:CD2	1:C:615:ILE:H	2.32	0.47
1:A:188:GLY:HA2	1:A:244:GLU:HA	1.97	0.46
1:A:920:VAL:HG13	1:A:954:GLU:HG2	1.97	0.46
1:C:27:GLU:C	1:C:29:LYS:H	2.23	0.46
1:A:504:PRO:HB3	1:A:581:LEU:CD2	2.45	0.46
1:C:544:ARG:NH2	6:C:2004:ADP:O1B	2.48	0.46
2:D:277:LYS:HD2	2:D:279:TYR:CE2	2.51	0.46
3:E:39:ILE:O	3:E:43:ILE:HG12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:942:MET:HE3	1:A:948:ILE:HG12	1.97	0.46
1:C:778:PRO:HB3	1:C:855:ALA:HA	1.97	0.46
1:C:901:TYR:OH	1:C:905:LYS:HE3	2.15	0.46
3:E:47:SER:O	3:E:47:SER:OG	2.29	0.46
1:A:670:GLN:O	1:A:674:ILE:HG13	2.15	0.46
1:C:83:VAL:O	1:C:87:ARG:HG2	2.15	0.46
1:C:825:MET:HE2	1:C:825:MET:HA	1.97	0.46
1:A:280:GLU:OE1	1:A:830:ARG:NH2	2.48	0.46
1:C:370:LYS:HB2	1:C:610:THR:HB	1.97	0.46
1:A:387:ASP:C	1:A:389:GLN:H	2.23	0.46
1:A:985:PHE:HZ	8:G:101:CLR:H221	1.80	0.46
1:C:430:GLN:O	1:C:432:ASN:N	2.41	0.46
1:C:914:ALA:O	1:C:918:SER:N	2.44	0.46
2:D:101:TYR:O	2:D:104:SER:OG	2.33	0.46
1:A:301:ILE:HD11	9:A:2014:PC1:H3I1	1.98	0.46
1:C:324:ASN:N	1:C:324:ASN:HD22	2.13	0.46
1:A:85:PHE:CZ	1:A:138:CYS:HB3	2.51	0.46
1:A:488:ASN:OD1	1:A:490:ASN:ND2	2.49	0.46
1:A:827:ARG:NH2	1:A:934:ARG:HD3	2.30	0.46
1:A:977:LYS:HD3	2:B:68:TYR:CZ	2.50	0.46
2:B:49:ILE:O	2:B:53:THR:HG22	2.16	0.46
2:B:62:SER:C	2:B:64:PHE:H	2.23	0.46
2:D:23:GLU:HG2	2:D:24:PHE:H	1.81	0.46
1:A:36:ASP:HB3	1:A:39:LEU:HD12	1.97	0.46
1:A:384:MET:HE1	1:A:393:ALA:CB	2.46	0.46
1:A:410:THR:HG23	1:A:515:LEU:HD22	1.98	0.46
1:A:551:LEU:HD12	1:A:576:LEU:HD23	1.97	0.46
1:A:847:TYR:CD2	9:A:2011:PC1:H381	2.51	0.46
1:C:483:LEU:HB2	1:C:500:MET:HE2	1.98	0.46
1:C:781:THR:N	1:C:782:PRO:HD2	2.31	0.46
1:C:1002:ILE:HG23	1:C:1011:GLU:HB2	1.98	0.46
1:A:430:GLN:C	1:A:432:ASN:H	2.24	0.46
1:A:473:ILE:H	1:A:473:ILE:HG12	1.64	0.46
1:A:898:GLN:OE1	2:B:181:ASN:HA	2.16	0.46
1:A:968:GLY:HA2	1:A:973:MET:N	2.30	0.46
1:C:383:HIS:CD2	1:C:392:GLU:HG2	2.51	0.46
1:C:883:TRP:HZ2	1:C:908:GLU:HB2	1.81	0.46
1:C:901:TYR:HA	1:C:904:ARG:CZ	2.46	0.46
1:C:935:ASN:HA	1:C:1003:ARG:HD3	1.98	0.46
1:A:781:THR:HG22	8:A:2009:CLR:H273	1.98	0.45
1:A:977:LYS:HG2	3:G:21:TYR:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:PRO:O	1:C:77:PRO:HD3	2.16	0.45
1:C:811:PRO:HB3	1:C:927:LEU:HD22	1.97	0.45
2:D:76:GLY:H	2:D:181:ASN:HD22	1.62	0.45
1:A:226:ASN:HB3	1:A:231:GLU:HB2	1.99	0.45
1:A:505:GLU:CD	1:A:685:ARG:HH11	2.24	0.45
1:A:1016:TYR:N	1:A:1016:TYR:CD1	2.84	0.45
1:C:360:LEU:HA	1:C:723:ILE:HD13	1.98	0.45
1:C:589:ARG:NH1	1:C:746:ASP:HB3	2.32	0.45
1:C:755:VAL:HG13	1:C:825:MET:HE1	1.99	0.45
2:D:180:LEU:HD13	2:D:181:ASN:N	2.30	0.45
2:D:275:GLU:HA	2:D:295:PHE:O	2.15	0.45
1:A:747:ASN:HD21	1:A:749:ALA:HB3	1.80	0.45
1:A:860:PHE:CE1	2:B:53:THR:HG23	2.51	0.45
2:B:215:GLY:HA3	2:B:221:LYS:HZ1	1.81	0.45
1:A:318:ILE:HD13	1:A:318:ILE:HA	1.81	0.45
1:A:436:LEU:HG	1:A:455:LEU:HD11	1.97	0.45
9:A:2014:PC1:H361	9:A:2014:PC1:H2B2	1.98	0.45
1:C:71:ASN:OD1	1:C:254:THR:HG22	2.17	0.45
1:C:183:LEU:HB2	1:C:249:GLY:O	2.16	0.45
1:C:483:LEU:HD21	1:C:571:PHE:HE2	1.81	0.45
1:C:753:THR:O	1:C:757:GLU:HG2	2.17	0.45
2:D:27:ARG:HD3	2:D:32:TRP:CE3	2.51	0.45
8:D:3001:CLR:C11	8:D:3001:CLR:C19	2.94	0.45
8:D:3002:CLR:H111	8:D:3002:CLR:C19	2.47	0.45
2:B:203:LYS:HB2	2:B:235:TYR:HE2	1.82	0.45
1:C:993:VAL:O	1:C:997:VAL:HG13	2.15	0.45
1:A:194:ALA:HA	1:A:238:PHE:HB2	1.99	0.45
1:A:475:PHE:N	1:A:482:GLN:HG3	2.32	0.45
1:A:968:GLY:HA3	1:A:974:TYR:CE2	2.52	0.45
1:C:811:PRO:O	1:C:814:SER:OG	2.33	0.45
2:D:80:ILE:HB	2:D:177:ILE:HG23	1.97	0.45
1:A:50:THR:CG2	1:A:56:LEU:HD23	2.47	0.45
1:A:445:SER:OG	1:A:544:ARG:NH1	2.50	0.45
2:B:157:GLY:N	2:B:230:PHE:HB3	2.32	0.45
1:C:405:ASP:C	1:C:407:THR:H	2.23	0.45
1:C:886:ARG:HA	1:C:901:TYR:CD1	2.51	0.45
1:A:977:LYS:N	1:A:980:TRP:CD1	2.80	0.45
1:A:1001:ILE:HG21	1:A:1010:VAL:HG21	1.99	0.45
2:B:91:ARG:HH21	2:B:94:ASP:HB2	1.82	0.45
2:B:95:PRO:HA	2:B:98:TYR:CE1	2.51	0.45
2:B:134:LYS:HB2	2:B:136:ARG:HH12	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:425:VAL:HG12	1:C:426:PHE:O	2.16	0.45
1:C:790:ASN:C	1:C:880:ARG:HB2	2.42	0.45
2:D:95:PRO:HA	2:D:98:TYR:CE1	2.52	0.45
2:D:229:TYR:CD1	2:D:261:VAL:HG12	2.47	0.45
1:A:214:GLU:HB2	1:A:216:GLU:HG3	1.99	0.45
2:B:98:TYR:HA	2:B:101:TYR:HD1	1.81	0.45
1:C:55:GLY:HA2	1:C:183:LEU:HD22	1.98	0.45
1:C:565:ASP:OD2	1:C:568:ASP:HB2	2.16	0.45
1:C:977:LYS:HG2	3:E:21:TYR:HE2	1.82	0.45
1:C:565:ASP:HB2	1:C:570:ASN:HD22	1.82	0.45
1:C:611:GLY:HA2	1:C:686:THR:H	1.82	0.45
1:A:654:LYS:HA	1:A:654:LYS:HD3	1.75	0.44
1:A:927:LEU:HD11	1:A:947:LEU:HG	1.99	0.44
1:C:695:VAL:O	1:C:699:GLN:HG3	2.18	0.44
1:A:238:PHE:CD2	1:A:258:THR:HG21	2.52	0.44
8:A:2009:CLR:C11	8:A:2009:CLR:H193	2.47	0.44
2:B:42:PHE:HD2	2:B:43:TYR:HD1	1.63	0.44
2:B:203:LYS:HE2	2:B:203:LYS:HB3	1.82	0.44
1:C:972:ARG:HH12	2:D:288:LYS:HZ1	1.65	0.44
9:C:2009:PC1:H3H2	9:C:2012:PC1:H2H1	1.99	0.44
2:D:37:LEU:O	2:D:41:ILE:HG23	2.16	0.44
1:A:81:GLU:HG3	1:A:82:TRP:H	1.83	0.44
1:A:450:LEU:HD23	1:A:460:VAL:HG21	1.99	0.44
1:A:900:THR:HG23	1:A:903:GLN:NE2	2.33	0.44
9:A:2012:PC1:H2E2	9:A:2012:PC1:H2A2	1.99	0.44
3:G:45:ILE:HD12	3:G:45:ILE:HA	1.71	0.44
1:C:209:SER:C	1:C:211:LEU:H	2.25	0.44
2:D:204:TYR:HD2	2:D:207:TYR:H	1.65	0.44
1:A:756:GLU:HB2	1:A:825:MET:SD	2.57	0.44
1:C:199:ILE:HA	1:C:199:ILE:HD13	1.57	0.44
1:C:550:HIS:CD2	1:C:550:HIS:C	2.95	0.44
1:C:870:GLY:O	1:C:893:ASP:HB2	2.18	0.44
1:C:929:ILE:HB	1:C:995:ASP:OD2	2.16	0.44
2:D:88:ILE:HG23	2:D:101:TYR:CE2	2.52	0.44
8:D:3001:CLR:H212	8:D:3001:CLR:C12	2.42	0.44
1:A:350:LEU:HB2	1:A:744:LEU:HD21	1.98	0.44
1:A:695:VAL:O	1:A:699:GLN:HG3	2.17	0.44
1:C:420:LEU:C	1:C:422:ASN:H	2.26	0.44
1:C:460:VAL:HG12	1:C:464:ARG:HE	1.82	0.44
1:C:487:LYS:HB3	1:C:487:LYS:HE2	1.85	0.44
1:C:592:VAL:O	1:C:596:VAL:HG13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:28:ASN:O	3:E:32:ILE:HG12	2.17	0.44
1:A:315:ILE:HD13	1:A:315:ILE:HA	1.88	0.44
1:A:763:ASP:O	1:A:767:LYS:HG3	2.18	0.44
1:A:821:GLU:HA	1:A:940:GLN:OE1	2.17	0.44
2:B:204:TYR:CE2	2:B:207:TYR:HB2	2.52	0.44
2:D:31:SER:O	2:D:35:ILE:HG23	2.17	0.44
1:A:443:ASP:O	1:A:447:SER:OG	2.29	0.44
1:A:1001:ILE:O	1:A:1005:ARG:HB2	2.17	0.44
1:C:37:HIS:HB3	1:C:235:ILE:HD11	1.98	0.44
1:C:488:ASN:CG	1:C:493:GLU:HB2	2.42	0.44
1:C:613:HIS:NE2	1:C:615:ILE:HD13	2.32	0.44
2:D:98:TYR:OH	2:D:171:ASP:HB3	2.18	0.44
1:A:618:LYS:O	1:A:621:ALA:HB3	2.17	0.44
9:A:2013:PC1:H2C2	9:B:401:PC1:H3I1	1.99	0.44
2:B:17:TRP:CZ2	2:B:19:SER:HB3	2.52	0.44
1:C:28:LEU:C	1:C:31:GLU:HG2	2.43	0.44
1:C:228:ASN:HA	1:C:229:PRO:HD3	1.86	0.44
1:C:759:ARG:HE	1:C:825:MET:CE	2.30	0.44
1:A:303:SER:HB2	1:A:308:TYR:CD2	2.52	0.44
1:A:488:ASN:O	1:A:493:GLU:HG3	2.17	0.44
1:A:724:GLY:N	1:A:740:ASP:OD2	2.41	0.44
1:A:755:VAL:HG13	1:A:825:MET:HE1	1.99	0.44
9:A:2013:PC1:H3F1	9:B:401:PC1:H3H2	2.00	0.44
1:C:841:ARG:HB2	1:C:1016:TYR:HA	2.00	0.44
1:C:925:ALA:O	1:C:929:ILE:HG12	2.18	0.44
1:C:1001:ILE:HG21	1:C:1010:VAL:HG21	1.99	0.44
1:A:300:PHE:HE1	1:A:314:VAL:HG12	1.83	0.43
1:A:609:VAL:O	1:A:691:LYS:HE2	2.18	0.43
8:A:2010:CLR:C11	8:A:2010:CLR:C1	2.95	0.43
9:A:2013:PC1:H122	9:A:2013:PC1:H11	1.99	0.43
1:C:50:THR:CG2	1:C:56:LEU:HD23	2.44	0.43
1:C:794:PRO:HG2	1:C:859:PHE:HE2	1.83	0.43
2:D:157:GLY:H	2:D:230:PHE:HB3	1.83	0.43
1:A:781:THR:HA	1:A:784:LEU:HD12	2.00	0.43
2:B:88:ILE:HG23	2:B:101:TYR:CE2	2.54	0.43
1:C:366:ILE:HG13	1:C:604:ILE:HG21	2.00	0.43
1:C:505:GLU:OE2	1:C:613:HIS:ND1	2.49	0.43
1:C:645:VAL:C	1:C:647:GLN:H	2.26	0.43
1:A:304:LEU:HD23	1:A:304:LEU:HA	1.84	0.43
8:A:2009:CLR:H121	8:A:2009:CLR:C21	2.46	0.43
1:C:258:THR:HG23	1:C:261:GLY:N	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:430:GLN:HE21	1:C:433:LEU:HD21	1.83	0.43
1:C:503:ALA:HA	1:C:504:PRO:HD3	1.88	0.43
2:D:209:LEU:HD12	2:D:210:PRO:HD2	2.00	0.43
1:A:35:ASP:HB2	1:A:37:HIS:CE1	2.53	0.43
1:A:115:GLU:HG2	1:A:116:GLU:N	2.34	0.43
1:A:206:VAL:HA	1:A:242:CYS:HA	2.00	0.43
1:A:418:ALA:O	1:A:422:ASN:HB2	2.18	0.43
1:A:471:VAL:HG21	1:A:564:PHE:HB2	2.00	0.43
1:A:624:VAL:CG2	1:A:626:ILE:HG12	2.49	0.43
1:C:610:THR:OG1	5:C:2002:ALF:F1	2.25	0.43
1:A:697:GLY:HA2	1:A:700:ARG:NH2	2.34	0.43
3:G:39:ILE:O	3:G:43:ILE:HG12	2.19	0.43
1:C:483:LEU:HD12	1:C:484:SER:N	2.33	0.43
1:C:514:ILE:HG22	1:C:516:ILE:HG12	2.01	0.43
1:C:873:PRO:HA	1:C:876:LEU:HD12	1.99	0.43
2:D:178:ILE:HD13	2:D:211:VAL:HG11	2.01	0.43
2:D:203:LYS:HE2	2:D:203:LYS:HB3	1.79	0.43
1:A:292:ALA:O	1:A:321:ILE:HD13	2.18	0.43
1:A:621:ALA:O	1:A:626:ILE:N	2.49	0.43
1:A:815:LEU:O	1:A:818:GLU:HB2	2.18	0.43
1:A:864:VAL:HA	2:B:57:MET:SD	2.58	0.43
1:A:977:LYS:HG2	3:G:21:TYR:HE2	1.83	0.43
2:B:98:TYR:CZ	2:B:171:ASP:HB3	2.54	0.43
2:B:186:PHE:HZ	2:B:282:ASN:HB3	1.84	0.43
1:C:372:GLY:O	1:C:589:ARG:NH2	2.52	0.43
1:C:612:ASP:O	1:C:684:ALA:HB1	2.19	0.43
1:C:654:LYS:HB3	1:C:679:THR:HG22	2.00	0.43
1:C:963:TYR:CZ	8:E:101:CLR:H21	2.53	0.43
2:D:113:LYS:HA	2:D:153:LEU:HD11	2.01	0.43
1:A:752:VAL:HA	1:A:755:VAL:HG12	2.01	0.43
1:A:781:THR:N	1:A:782:PRO:HD2	2.34	0.43
1:A:1009:TRP:CZ2	1:A:1013:GLU:HG3	2.54	0.43
2:B:62:SER:OG	2:B:65:LYS:HG2	2.19	0.43
2:B:123:PHE:HB3	2:B:150:ARG:HG3	2.00	0.43
1:C:263:ILE:HG13	1:C:267:ALA:HA	1.99	0.43
1:C:549:CYS:HB2	1:C:577:CYS:O	2.19	0.43
1:C:900:THR:H	1:C:903:GLN:HE21	1.67	0.43
2:D:277:LYS:HG2	2:D:285:TYR:CE2	2.54	0.43
2:B:88:ILE:HG23	2:B:101:TYR:CD2	2.54	0.43
1:C:462:GLU:O	1:C:466:ARG:HG3	2.18	0.43
1:A:358:GLU:O	1:A:361:GLY:N	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:654:LYS:O	1:A:679:THR:HG22	2.19	0.43
1:A:692:LEU:HD12	1:A:716:PRO:HB2	2.01	0.43
1:A:901:TYR:HA	1:A:904:ARG:CZ	2.49	0.43
1:A:957:LEU:HD22	1:A:957:LEU:HA	1.87	0.43
1:C:89:LEU:HD22	1:C:134:ILE:HD13	2.01	0.43
2:D:39:TYR:CE2	8:D:3001:CLR:H182	2.54	0.43
2:D:90:PHE:O	2:D:92:PRO:HD3	2.19	0.43
2:D:204:TYR:HB3	2:D:208:VAL:HB	2.00	0.43
1:A:571:PHE:HB2	1:A:572:PRO:HD2	2.00	0.42
1:C:410:THR:HG23	1:C:515:LEU:HD22	2.00	0.42
1:C:483:LEU:HD12	1:C:484:SER:H	1.84	0.42
1:C:963:TYR:CD2	3:E:30:GLY:HA3	2.53	0.42
2:D:62:SER:OG	2:D:65:LYS:HG2	2.19	0.42
1:A:366:ILE:HG13	1:A:604:ILE:HG21	2.01	0.42
1:A:841:ARG:HG3	1:A:841:ARG:HH11	1.82	0.42
1:C:55:GLY:HA3	1:C:165:ILE:O	2.19	0.42
1:C:340:THR:CG2	1:C:357:VAL:HG11	2.48	0.42
1:C:360:LEU:HG	1:C:723:ILE:HD13	2.00	0.42
1:C:514:ILE:HG12	1:C:578:PHE:HB3	2.00	0.42
1:C:982:PHE:O	1:C:985:PHE:HB2	2.19	0.42
1:A:483:LEU:HD12	1:A:499:VAL:O	2.18	0.42
1:A:565:ASP:OD2	1:A:568:ASP:HB2	2.17	0.42
1:A:765:LEU:O	1:A:769:ILE:HG13	2.19	0.42
2:B:47:ALA:O	2:B:51:ILE:HG13	2.19	0.42
2:D:238:PHE:CD1	2:D:257:PRO:HB2	2.54	0.42
1:A:430:GLN:HB3	1:A:438:ARG:HB3	2.01	0.42
1:A:503:ALA:HB3	1:A:506:ARG:HB2	2.02	0.42
1:C:152:GLU:C	1:C:154:PHE:N	2.77	0.42
1:A:405:ASP:C	1:A:407:THR:H	2.27	0.42
1:A:450:LEU:HB3	1:A:451:LYS:H	1.73	0.42
1:A:600:ARG:HG2	1:A:600:ARG:NH1	2.11	0.42
1:C:31:GLU:HG3	1:C:32:VAL:N	2.31	0.42
1:A:293:VAL:HA	1:A:321:ILE:CD1	2.50	0.42
1:A:470:ILE:H	1:A:470:ILE:HG13	1.70	0.42
1:A:759:ARG:HD2	1:A:825:MET:HE3	2.01	0.42
1:A:503:ALA:HA	1:A:504:PRO:HD3	1.78	0.42
1:A:538:LEU:HA	1:A:538:LEU:HD23	1.76	0.42
2:B:27:ARG:HG3	2:B:31:SER:HB3	2.02	0.42
2:B:177:ILE:HD11	2:B:258:LEU:HD13	2.00	0.42
2:B:180:LEU:HD13	2:B:181:ASN:N	2.34	0.42
1:C:209:SER:HB3	1:C:215:SER:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:374:LEU:HD12	1:C:608:MET:HE2	2.02	0.42
1:C:479:ASN:O	1:C:480:LYS:HB2	2.20	0.42
1:C:899:TRP:CH2	2:D:72:VAL:HG22	2.55	0.42
1:C:1013:GLU:CD	2:D:27:ARG:HH21	2.26	0.42
9:C:2011:PC1:H272	9:C:2011:PC1:H2A1	1.70	0.42
3:E:18:PRO:HB2	3:E:19:PHE:H	1.52	0.42
1:A:778:PRO:HB3	1:A:855:ALA:HA	2.00	0.42
1:A:867:ALA:HB2	1:A:873:PRO:HD3	2.02	0.42
1:A:952:PHE:HD2	3:G:37:ALA:HA	1.84	0.42
1:C:311:LEU:O	1:C:315:ILE:HG12	2.20	0.42
9:C:2012:PC1:H221	9:C:2012:PC1:H2	1.78	0.42
1:A:187:LYS:HG2	1:A:190:ASP:OD2	2.20	0.42
1:A:331:ALA:O	1:A:335:VAL:HG23	2.20	0.42
1:A:360:LEU:HD23	1:A:723:ILE:CD1	2.50	0.42
1:A:968:GLY:HA2	1:A:973:MET:H	1.85	0.42
1:C:165:ILE:HB	1:C:183:LEU:CD2	2.44	0.42
1:C:565:ASP:HB3	1:C:570:ASN:HB2	2.00	0.42
1:C:649:ASN:HA	1:C:650:PRO:HD3	1.91	0.42
5:C:2002:ALF:F1	6:C:2004:ADP:O3B	2.28	0.42
3:E:38:PHE:CZ	3:E:42:LEU:HD11	2.55	0.42
1:A:192:ILE:CD1	1:A:236:ALA:HB1	2.50	0.42
1:A:587:PRO:HA	1:A:588:PRO:HD3	1.92	0.42
8:G:101:CLR:C9	8:G:101:CLR:C12	2.89	0.42
1:C:24:ASP:OD2	1:C:26:ASP:HB2	2.20	0.42
1:C:422:ASN:OD1	1:C:446:GLU:HB3	2.20	0.42
1:C:535:TYR:CE2	1:C:545:VAL:HB	2.55	0.42
9:C:2009:PC1:H112	9:C:2009:PC1:H132	1.80	0.42
2:D:190:PRO:HA	2:D:191:PRO:HD3	1.85	0.42
2:D:277:LYS:HB3	2:D:279:TYR:CE1	2.55	0.42
1:A:609:VAL:CG1	1:A:691:LYS:HG2	2.49	0.41
1:A:638:ALA:HB2	1:A:648:VAL:CG2	2.49	0.41
1:A:854:GLN:NE2	1:A:923:GLN:HE21	2.16	0.41
1:C:606:VAL:HG11	1:C:626:ILE:HD12	2.00	0.41
1:A:48:TYR:OH	1:A:252:VAL:HB	2.20	0.41
1:A:864:VAL:HG13	2:B:57:MET:HG3	2.01	0.41
1:A:913:THR:HG23	1:A:973:MET:HE2	2.00	0.41
1:C:791:ILE:HG12	1:C:792:PRO:O	2.20	0.41
8:D:3002:CLR:C12	8:D:3002:CLR:H212	2.49	0.41
1:A:471:VAL:HG11	1:A:566:THR:HB	2.02	0.41
1:A:827:ARG:HH21	1:A:934:ARG:HD3	1.85	0.41
1:C:908:GLU:O	1:C:911:CYS:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:368:SER:HB2	1:C:708:THR:OG1	2.20	0.41
1:C:519:LYS:H	1:C:519:LYS:HG2	1.69	0.41
1:C:883:TRP:O	1:C:904:ARG:HD2	2.21	0.41
2:D:71:ARG:HE	2:D:71:ARG:HA	1.85	0.41
2:D:300:GLU:HG2	2:D:302:LYS:HB2	2.01	0.41
1:C:293:VAL:HA	1:C:321:ILE:HD12	2.02	0.41
1:C:460:VAL:CG1	1:C:464:ARG:HH21	2.32	0.41
1:C:803:ILE:HD12	1:C:919:ILE:HG21	2.03	0.41
1:C:1009:TRP:CZ2	2:D:35:ILE:HG22	2.55	0.41
2:D:216:LYS:HE2	2:D:273:ARG:O	2.21	0.41
2:D:277:LYS:HB3	2:D:279:TYR:CZ	2.54	0.41
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.89	0.41
1:A:966:GLY:O	1:A:969:VAL:HG22	2.21	0.41
2:B:24:PHE:HD2	2:B:24:PHE:HA	1.73	0.41
2:B:179:LYS:HE2	2:B:179:LYS:HB3	1.80	0.41
1:C:32:VAL:O	1:C:262:ARG:NH1	2.54	0.41
6:C:2004:ADP:O2B	6:C:2004:ADP:H3'	2.19	0.41
2:D:35:ILE:HG13	2:D:36:LEU:N	2.36	0.41
1:A:370:LYS:HB2	1:A:610:THR:HB	2.02	0.41
1:A:866:LEU:HD13	1:A:876:LEU:HD21	2.02	0.41
2:B:216:LYS:HE2	2:B:273:ARG:HB2	2.02	0.41
1:C:238:PHE:HB3	1:C:258:THR:HG1	1.85	0.41
1:C:763:ASP:HB3	1:C:767:LYS:HE3	2.03	0.41
1:C:861:THR:HG22	1:C:983:CYS:HB3	2.02	0.41
8:D:3001:CLR:C11	8:D:3001:CLR:C1	2.99	0.41
1:A:274:GLN:HE21	1:A:274:GLN:HB3	1.59	0.41
1:A:337:LEU:HD12	1:A:337:LEU:HA	1.90	0.41
1:A:369:ASP:HB3	1:A:373:THR:OG1	2.21	0.41
1:A:729:ILE:HB	1:A:746:ASP:CG	2.45	0.41
8:G:101:CLR:H121	8:G:101:CLR:C21	2.50	0.41
1:C:589:ARG:HD3	1:C:746:ASP:O	2.20	0.41
1:C:777:ILE:HD12	1:C:777:ILE:N	2.32	0.41
9:C:2009:PC1:H272	8:D:3001:CLR:H14	2.03	0.41
8:D:3002:CLR:C11	8:D:3002:CLR:C1	2.98	0.41
1:A:301:ILE:HG13	1:A:302:LEU:N	2.36	0.41
1:A:344:MET:HE1	1:A:754:GLY:HA2	2.03	0.41
1:A:402:VAL:HG21	1:A:404:PHE:CE1	2.55	0.41
2:B:66:PRO:HG2	2:B:69:GLN:HG3	2.02	0.41
2:B:204:TYR:HD2	2:B:207:TYR:H	1.68	0.41
1:C:471:VAL:HG11	1:C:566:THR:HB	2.03	0.41
1:C:613:HIS:HD2	1:C:615:ILE:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:857:GLY:O	1:C:861:THR:HG23	2.20	0.41
1:C:866:LEU:HD23	1:C:866:LEU:HA	1.86	0.41
1:A:537:GLU:O	1:A:541:LEU:HD22	2.20	0.41
1:C:953:GLU:OE2	3:E:41:GLY:HA3	2.20	0.41
9:C:2009:PC1:H3C2	9:C:2009:PC1:H2A1	2.03	0.41
1:A:384:MET:HE1	1:A:393:ALA:HB2	2.02	0.40
1:A:629:GLU:N	1:A:629:GLU:OE1	2.55	0.40
1:A:648:VAL:H	1:A:648:VAL:HG23	1.68	0.40
1:A:870:GLY:O	1:A:893:ASP:HB2	2.21	0.40
2:B:74:PRO:HA	2:B:75:PRO:HD3	1.86	0.40
2:B:91:ARG:HG3	2:B:302:LYS:O	2.21	0.40
8:G:101:CLR:H212	8:G:101:CLR:H121	2.03	0.40
1:C:445:SER:HG	1:C:544:ARG:NH1	2.19	0.40
1:C:565:ASP:N	1:C:570:ASN:HB2	2.28	0.40
1:C:900:THR:H	1:C:903:GLN:NE2	2.19	0.40
2:D:188:PRO:HG2	2:D:243:TYR:CD1	2.57	0.40
1:A:189:GLY:HA2	1:A:734:VAL:HG21	2.04	0.40
1:A:998:ARG:NH1	1:A:999:LYS:HG3	2.37	0.40
1:C:318:ILE:O	1:C:322:VAL:HG23	2.20	0.40
1:C:476:ASN:O	1:C:478:THR:N	2.53	0.40
1:C:783:PHE:O	1:C:787:ILE:HG13	2.21	0.40
1:C:784:LEU:O	1:C:788:ILE:HG12	2.20	0.40
1:C:799:THR:O	1:C:803:ILE:HG12	2.21	0.40
2:D:5:LYS:HB3	2:D:6:ALA:H	1.73	0.40
2:D:170:LYS:HD2	2:D:170:LYS:N	2.36	0.40
3:E:15:ASP:HB3	3:E:16:VAL:H	1.64	0.40
1:A:309:THR:HG23	1:A:312:GLU:HB2	2.02	0.40
1:A:793:LEU:HD12	1:A:794:PRO:HD2	2.02	0.40
9:A:2012:PC1:H152	9:A:2012:PC1:H112	1.88	0.40
2:B:126:CYS:HB3	2:B:241:GLN:OE1	2.21	0.40
1:C:84:LYS:HE2	1:C:84:LYS:HB3	1.93	0.40
1:C:111:GLN:HB3	1:C:118:PRO:CB	2.51	0.40
1:C:850:ILE:O	1:C:854:GLN:HG3	2.21	0.40
2:D:235:TYR:HA	2:D:236:PRO:HD3	1.70	0.40
8:A:2010:CLR:H191	8:A:2010:CLR:H8	1.92	0.40
9:A:2013:PC1:H2C1	9:A:2013:PC1:H381	2.02	0.40
2:B:94:ASP:HA	2:B:95:PRO:HD3	1.84	0.40
1:C:214:GLU:HB2	1:C:216:GLU:HG3	2.03	0.40
1:C:301:ILE:O	1:C:305:ILE:HG12	2.22	0.40
1:C:748:PHE:O	1:C:751:ILE:HD12	2.21	0.40
1:C:854:GLN:NE2	1:C:923:GLN:HE21	2.17	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:879:LEU:O	1:C:880:ARG:C	2.64	0.40
2:D:207:TYR:C	2:D:240:LEU:HD13	2.47	0.40
2:D:265:ASN:HD22	2:D:267:THR:HG23	1.87	0.40
1:A:921:VAL:HG12	1:A:988:SER:HB2	2.03	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	992/1016 (98%)	859 (87%)	114 (12%)	19 (2%)	6	22
1	C	992/1016 (98%)	884 (89%)	91 (9%)	17 (2%)	7	25
2	B	301/303 (99%)	238 (79%)	55 (18%)	8 (3%)	4	15
2	D	301/303 (99%)	231 (77%)	59 (20%)	11 (4%)	2	9
3	E	33/65 (51%)	31 (94%)	1 (3%)	1 (3%)	3	12
3	G	32/65 (49%)	27 (84%)	4 (12%)	1 (3%)	3	12
All	All	2651/2768 (96%)	2270 (86%)	324 (12%)	57 (2%)	5	19

All (57) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	388	ASN
1	A	402	VAL
2	B	82	GLN
2	B	139	TYR
3	G	18	PRO
1	C	267	ALA
1	C	398	ASN
1	C	880	ARG

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Mol	Chain	Res	Type
3	E	18	PRO
1	A	381	VAL
1	A	710	ASP
2	B	201	VAL
2	B	204	TYR
2	B	265	ASN
1	C	34	MET
1	C	92	GLY
1	C	629	GLU
1	C	961	LEU
2	D	82	GLN
2	D	201	VAL
2	D	204	TYR
2	D	265	ASN
1	A	450	LEU
1	A	721	ALA
1	A	775	SER
1	A	821	GLU
2	B	133	LEU
2	B	156	LEU
1	C	167	ASN
1	C	210	SER
1	C	404	PHE
1	C	569	VAL
1	C	859	PHE
2	D	63	GLU
1	A	359	THR
1	A	451	LYS
1	A	590	ALA
2	B	142	GLU
1	C	944	ASN
2	D	194	GLU
2	D	206	PRO
1	A	92	GLY
1	A	118	PRO
1	A	394	ASP
1	C	306	LEU
1	C	835	ASP
2	D	139	TYR
1	A	52	LEU
1	A	569	VAL
2	D	25	LEU

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Mol	Chain	Res	Type
1	C	255	GLY
2	D	73	ALA
1	A	188	GLY
1	C	402	VAL
2	D	127	GLY
1	A	91	GLY
1	A	489	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	844/861 (98%)	707 (84%)	137 (16%)	2	8
1	C	844/861 (98%)	749 (89%)	95 (11%)	5	19
2	B	269/269 (100%)	233 (87%)	36 (13%)	4	13
2	D	269/269 (100%)	236 (88%)	33 (12%)	4	16
3	E	29/52 (56%)	23 (79%)	6 (21%)	1	4
3	G	28/52 (54%)	25 (89%)	3 (11%)	6	21
All	All	2283/2364 (97%)	1973 (86%)	310 (14%)	3	13

All (310) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ASP
1	A	41	LEU
1	A	44	LEU
1	A	57	THR
1	A	60	ARG
1	A	82	TRP
1	A	83	VAL
1	A	94	SER
1	A	125	LEU
1	A	129	LEU
1	A	133	VAL

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Mol	Chain	Res	Type
1	A	144	GLU
1	A	152	GLU
1	A	158	VAL
1	A	161	GLN
1	A	164	VAL
1	A	166	ARG
1	A	170	LYS
1	A	171	MET
1	A	186	VAL
1	A	192	ILE
1	A	210	SER
1	A	216	GLU
1	A	239	SER
1	A	241	ASN
1	A	242	CYS
1	A	252	VAL
1	A	266	LEU
1	A	268	SER
1	A	270	LEU
1	A	274	GLN
1	A	281	ILE
1	A	287	ILE
1	A	297	VAL
1	A	305	ILE
1	A	308	TYR
1	A	309	THR
1	A	310	TRP
1	A	314	VAL
1	A	317	LEU
1	A	318	ILE
1	A	325	VAL
1	A	337	LEU
1	A	360	LEU
1	A	364	SER
1	A	371	THR
1	A	379	MET
1	A	380	THR
1	A	384	MET
1	A	394	ASP
1	A	396	THR
1	A	415	SER
1	A	425	VAL

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Mol	Chain	Res	Type
1	A	430	GLN
1	A	432	ASN
1	A	433	LEU
1	A	437	LYS
1	A	440	VAL
1	A	445	SER
1	A	447	SER
1	A	449	LEU
1	A	450	LEU
1	A	453	ILE
1	A	455	LEU
1	A	460	VAL
1	A	461	LYS
1	A	469	LYS
1	A	470	ILE
1	A	471	VAL
1	A	473	ILE
1	A	478	THR
1	A	485	ILE
1	A	487	LYS
1	A	493	GLU
1	A	495	ARG
1	A	514	ILE
1	A	515	LEU
1	A	519	LYS
1	A	521	GLN
1	A	523	LEU
1	A	541	LEU
1	A	585	ILE
1	A	600	ARG
1	A	615	ILE
1	A	624	VAL
1	A	628	SER
1	A	629	GLU
1	A	634	VAL
1	A	635	GLU
1	A	645	VAL
1	A	648	VAL
1	A	658	VAL
1	A	663	LEU
1	A	666	MET
1	A	667	THR

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Mol	Chain	Res	Type
1	A	671	LEU
1	A	675	LEU
1	A	681	ILE
1	A	685	ARG
1	A	687	SER
1	A	705	VAL
1	A	719	LYS
1	A	723	ILE
1	A	732	SER
1	A	740	ASP
1	A	741	MET
1	A	744	LEU
1	A	747	ASN
1	A	751	ILE
1	A	753	THR
1	A	765	LEU
1	A	775	SER
1	A	781	THR
1	A	791	ILE
1	A	803	ILE
1	A	805	LEU
1	A	814	SER
1	A	815	LEU
1	A	818	GLU
1	A	819	GLN
1	A	822	SER
1	A	823	ASP
1	A	824	ILE
1	A	825	MET
1	A	850	ILE
1	A	865	ILE
1	A	881	VAL
1	A	882	ASN
1	A	900	THR
1	A	911	CYS
1	A	922	VAL
1	A	946	ILE
1	A	957	LEU
1	A	969	VAL
1	A	1004	ARG
1	A	1010	VAL
1	A	1016	TYR

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Mol	Chain	Res	Type
2	B	20	GLU
2	B	22	LYS
2	B	24	PHE
2	B	27	ARG
2	B	41	ILE
2	B	45	CYS
2	B	49	ILE
2	B	54	ILE
2	B	61	ILE
2	B	63	GLU
2	B	71	ARG
2	B	72	VAL
2	B	78	THR
2	B	90	PHE
2	B	99	GLU
2	B	119	ASP
2	B	129	VAL
2	B	158	ASN
2	B	162	LEU
2	B	170	LYS
2	B	171	ASP
2	B	177	ILE
2	B	180	LEU
2	B	187	LYS
2	B	203	LYS
2	B	216	LYS
2	B	217	ARG
2	B	221	LYS
2	B	222	GLU
2	B	224	VAL
2	B	249	LEU
2	B	259	MET
2	B	263	PHE
2	B	294	ARG
2	B	295	PHE
2	B	301	VAL
3	G	24	GLU
3	G	36	LEU
3	G	45	ILE
1	C	36	ASP
1	C	41	LEU
1	C	44	LEU

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Mol	Chain	Res	Type
1	C	56	LEU
1	C	57	THR
1	C	60	ARG
1	C	82	TRP
1	C	86	CYS
1	C	114	THR
1	C	125	LEU
1	C	129	LEU
1	C	136	THR
1	C	154	PHE
1	C	161	GLN
1	C	166	ARG
1	C	171	MET
1	C	172	SER
1	C	191	ARG
1	C	199	ILE
1	C	241	ASN
1	C	242	CYS
1	C	250	ILE
1	C	254	THR
1	C	274	GLN
1	C	277	ILE
1	C	287	ILE
1	C	293	VAL
1	C	308	TYR
1	C	309	THR
1	C	310	TRP
1	C	317	LEU
1	C	336	CYS
1	C	347	LYS
1	C	360	LEU
1	C	371	THR
1	C	380	THR
1	C	394	ASP
1	C	403	SER
1	C	412	LEU
1	C	417	ILE
1	C	423	ARG
1	C	430	GLN
1	C	450	LEU
1	C	455	LEU
1	C	461	LYS

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Mol	Chain	Res	Type
1	C	473	ILE
1	C	478	THR
1	C	483	LEU
1	C	485	ILE
1	C	493	GLU
1	C	495	ARG
1	C	514	ILE
1	C	519	LYS
1	C	520	GLU
1	C	521	GLN
1	C	523	LEU
1	C	541	LEU
1	C	576	LEU
1	C	600	ARG
1	C	629	GLU
1	C	645	VAL
1	C	662	ASP
1	C	667	THR
1	C	671	LEU
1	C	681	ILE
1	C	687	SER
1	C	708	THR
1	C	719	LYS
1	C	723	ILE
1	C	741	MET
1	C	744	LEU
1	C	747	ASN
1	C	761	ILE
1	C	772	THR
1	C	791	ILE
1	C	801	LEU
1	C	805	LEU
1	C	815	LEU
1	C	818	GLU
1	C	824	ILE
1	C	825	MET
1	C	859	PHE
1	C	861	THR
1	C	869	ASN
1	C	886	ARG
1	C	888	ILE
1	C	894	SER

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Mol	Chain	Res	Type
1	C	897	GLN
1	C	900	THR
1	C	903	GLN
1	C	904	ARG
1	C	969	VAL
1	C	1000	LEU
1	C	1004	ARG
1	C	1010	VAL
2	D	20	GLU
2	D	22	LYS
2	D	27	ARG
2	D	35	ILE
2	D	57	MET
2	D	61	ILE
2	D	63	GLU
2	D	71	ARG
2	D	72	VAL
2	D	78	THR
2	D	99	GLU
2	D	150	ARG
2	D	162	LEU
2	D	170	LYS
2	D	171	ASP
2	D	175	CYS
2	D	177	ILE
2	D	180	LEU
2	D	187	LYS
2	D	203	LYS
2	D	204	TYR
2	D	208	VAL
2	D	216	LYS
2	D	217	ARG
2	D	221	LYS
2	D	222	GLU
2	D	224	VAL
2	D	249	LEU
2	D	259	MET
2	D	263	PHE
2	D	267	THR
2	D	295	PHE
2	D	301	VAL
3	E	17	ASP

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Mol	Chain	Res	Type
3	E	20	TYR
3	E	24	GLU
3	E	36	LEU
3	E	45	ILE
3	E	48	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	A	156	ASN
1	A	161	GLN
1	A	274	GLN
1	A	324	ASN
1	A	388	ASN
1	A	430	GLN
1	A	479	ASN
1	A	678	HIS
1	A	699	GLN
1	A	701	GLN
1	A	747	ASN
1	A	790	ASN
1	A	882	ASN
1	A	889	ASN
1	A	903	GLN
1	A	923	GLN
1	A	944	ASN
2	B	140	ASN
2	B	262	GLN
2	B	292	GLN
3	G	28	ASN
1	C	119	GLN
1	C	120	ASN
1	C	143	GLN
1	C	156	ASN
1	C	161	GLN
1	C	274	GLN
1	C	324	ASN
1	C	399	GLN
1	C	430	GLN
1	C	550	HIS
1	C	570	ASN

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Mol	Chain	Res	Type
1	C	790	ASN
1	C	819	GLN
1	C	854	GLN
1	C	875	HIS
1	C	889	ASN
1	C	903	GLN
1	C	923	GLN
2	D	84	GLN
2	D	93	ASN
2	D	128	ASN
2	D	140	ASN
2	D	158	ASN
2	D	181	ASN
2	D	205	ASN
2	D	262	GLN
3	E	28	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 12 are monoatomic - leaving 24 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
8	CLR	E	101	-	31,31,31	4.80	14 (45%)	48,48,48	2.49	15 (31%)
9	PC1	A	2012	-	53,53,53	0.95	3 (5%)	59,61,61	1.42	7 (11%)
11	NAG	B	402	-	14,14,15	0.21	0	17,19,21	0.45	0
8	CLR	G	101	-	31,31,31	4.80	13 (41%)	48,48,48	2.73	15 (31%)
9	PC1	C	2012	-	53,53,53	0.93	4 (7%)	59,61,61	1.28	4 (6%)
9	PC1	D	3003	-	53,53,53	0.95	5 (9%)	59,61,61	1.21	5 (8%)
9	PC1	A	2011	-	53,53,53	0.94	4 (7%)	59,61,61	1.32	6 (10%)
9	PC1	A	2013	-	53,53,53	0.93	4 (7%)	59,61,61	1.19	5 (8%)
6	ADP	C	2004	5	28,29,29	1.36	5 (17%)	43,45,45	1.84	10 (23%)
5	ALF	A	2002	6,1	4,4,4	1.40	0	-		
8	CLR	A	2010	-	31,31,31	4.59	11 (35%)	48,48,48	2.29	16 (33%)
9	PC1	A	2014	-	53,53,53	0.94	3 (5%)	59,61,61	1.35	4 (6%)
10	EFO	A	2015	-	57,58,58	2.21	20 (35%)	72,85,85	3.79	25 (34%)
9	PC1	C	2009	-	53,53,53	0.95	4 (7%)	59,61,61	1.29	6 (10%)
9	PC1	B	401	-	53,53,53	0.93	4 (7%)	59,61,61	1.31	5 (8%)
11	NAG	D	3004	-	14,14,15	0.23	0	17,19,21	0.52	0
8	CLR	A	2009	-	31,31,31	4.62	12 (38%)	48,48,48	2.24	16 (33%)
9	PC1	C	2011	-	53,53,53	0.98	5 (9%)	59,61,61	1.32	5 (8%)
10	EFO	C	2013	-	57,58,58	2.29	21 (36%)	72,85,85	3.77	26 (36%)
8	CLR	D	3002	-	31,31,31	4.69	12 (38%)	48,48,48	2.00	15 (31%)
6	ADP	A	2004	4,5	28,29,29	1.43	3 (10%)	43,45,45	2.02	9 (20%)
9	PC1	C	2010	-	53,53,53	0.92	3 (5%)	59,61,61	1.39	5 (8%)
5	ALF	C	2002	6,1	4,4,4	1.33	0	-		
8	CLR	D	3001	-	31,31,31	4.63	12 (38%)	48,48,48	2.22	15 (31%)

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
8	CLR	E	101	-	-	0/10/68/68	0/4/4/4
9	PC1	A	2012	-	-	29/57/57/57	-
11	NAG	B	402	-	-	0/6/23/26	0/1/1/1
8	CLR	G	101	-	-	1/10/68/68	0/4/4/4
9	PC1	C	2012	-	-	24/57/57/57	-
9	PC1	D	3003	-	-	29/57/57/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	PC1	A	2011	-	-	23/57/57/57	-
9	PC1	A	2013	-	-	29/57/57/57	-
6	ADP	C	2004	5	-	1/16/32/32	0/3/3/3
8	CLR	A	2010	-	-	1/10/68/68	0/4/4/4
9	PC1	A	2014	-	-	30/57/57/57	-
10	EFO	A	2015	-	-	9/72/110/110	0/2/3/3
9	PC1	C	2009	-	-	27/57/57/57	-
9	PC1	B	401	-	-	32/57/57/57	-
11	NAG	D	3004	-	-	1/6/23/26	0/1/1/1
8	CLR	A	2009	-	-	0/10/68/68	0/4/4/4
9	PC1	C	2011	-	-	32/57/57/57	-
10	EFO	C	2013	-	-	11/72/110/110	0/2/3/3
8	CLR	D	3002	-	-	1/10/68/68	0/4/4/4
6	ADP	A	2004	4,5	-	6/16/32/32	0/3/3/3
9	PC1	C	2010	-	-	33/57/57/57	-
8	CLR	D	3001	-	-	0/10/68/68	0/4/4/4

All (162) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	G	101	CLR	C11-C9	15.69	1.79	1.53
8	D	3002	CLR	C11-C9	15.09	1.78	1.53
8	E	101	CLR	C11-C9	14.94	1.78	1.53
8	D	3001	CLR	C11-C9	14.82	1.78	1.53
8	A	2009	CLR	C11-C9	14.36	1.77	1.53
8	A	2010	CLR	C11-C9	13.96	1.76	1.53
8	A	2010	CLR	C10-C9	-12.82	1.35	1.56
8	E	101	CLR	C10-C9	-12.78	1.35	1.56
8	A	2009	CLR	C10-C9	-12.69	1.35	1.56
8	G	101	CLR	C10-C9	-12.68	1.35	1.56
8	D	3002	CLR	C10-C9	-12.58	1.36	1.56
8	D	3001	CLR	C10-C9	-12.32	1.36	1.56
8	D	3002	CLR	C12-C11	10.75	1.74	1.53
8	G	101	CLR	C12-C11	10.33	1.74	1.53
8	D	3001	CLR	C12-C11	10.00	1.73	1.53
8	A	2009	CLR	C12-C11	9.76	1.72	1.53
8	E	101	CLR	C12-C11	9.69	1.72	1.53
8	A	2010	CLR	C12-C11	9.22	1.71	1.53
8	E	101	CLR	C6-C5	7.41	1.48	1.33
8	A	2009	CLR	C6-C5	7.31	1.48	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	C	2013	EFO	C15-C13	-7.23	1.36	1.52
8	D	3002	CLR	C6-C5	7.19	1.47	1.33
8	D	3001	CLR	C6-C5	7.16	1.47	1.33
8	A	2010	CLR	C6-C5	7.13	1.47	1.33
8	G	101	CLR	C6-C5	6.95	1.47	1.33
10	A	2015	EFO	C15-C13	-6.94	1.37	1.52
8	E	101	CLR	C8-C14	-6.49	1.41	1.53
8	A	2010	CLR	C13-C14	-6.42	1.43	1.55
8	E	101	CLR	C13-C14	-6.32	1.43	1.55
8	D	3001	CLR	C13-C14	-6.13	1.43	1.55
8	D	3002	CLR	C13-C14	-5.98	1.44	1.55
8	A	2009	CLR	C13-C14	-5.84	1.44	1.55
8	A	2010	CLR	C8-C14	-5.60	1.43	1.53
8	G	101	CLR	C13-C14	-5.51	1.44	1.55
8	D	3001	CLR	C8-C14	-5.19	1.43	1.53
8	G	101	CLR	C8-C14	-5.18	1.43	1.53
8	A	2009	CLR	C8-C14	-5.10	1.44	1.53
8	G	101	CLR	C12-C13	-5.07	1.45	1.54
8	A	2010	CLR	C12-C13	-4.87	1.45	1.54
8	E	101	CLR	C12-C13	-4.69	1.46	1.54
8	D	3002	CLR	C8-C14	-4.56	1.45	1.53
8	A	2009	CLR	C12-C13	-4.54	1.46	1.54
10	C	2013	EFO	O37-C11	4.53	1.51	1.44
10	A	2015	EFO	O37-C11	4.49	1.51	1.44
8	A	2009	CLR	C16-C15	4.43	1.66	1.54
6	A	2004	ADP	C5-C4	4.31	1.46	1.39
8	D	3001	CLR	C12-C13	-4.30	1.46	1.54
8	D	3002	CLR	C12-C13	-4.29	1.46	1.54
8	D	3002	CLR	C16-C15	4.22	1.65	1.54
10	A	2015	EFO	C10-C11	-4.21	1.43	1.53
10	C	2013	EFO	C10-C11	-4.19	1.43	1.53
8	E	101	CLR	C16-C15	4.04	1.65	1.54
10	C	2013	EFO	C6-C5	-4.03	1.43	1.53
8	G	101	CLR	C16-C15	4.01	1.65	1.54
8	D	3001	CLR	C16-C15	3.99	1.64	1.54
10	A	2015	EFO	C6-C5	-3.95	1.43	1.53
8	A	2010	CLR	C16-C15	3.92	1.64	1.54
10	C	2013	EFO	C35-C34	3.92	1.41	1.32
10	C	2013	EFO	O14-C13	3.89	1.52	1.44
10	A	2015	EFO	O14-C13	3.87	1.51	1.44
6	C	2004	ADP	C5-C4	3.75	1.45	1.39
10	C	2013	EFO	C1A-C10	3.71	1.60	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	2015	EFO	C35-C34	3.68	1.40	1.32
10	C	2013	EFO	C7-C6	-3.65	1.46	1.53
10	A	2015	EFO	C1A-C10	3.64	1.60	1.53
10	A	2015	EFO	C7-C6	-3.62	1.46	1.53
9	A	2012	PC1	O31-C31	3.46	1.43	1.33
9	C	2010	PC1	O31-C31	3.45	1.43	1.33
9	A	2014	PC1	O31-C31	3.43	1.43	1.33
10	C	2013	EFO	C19-C18	3.38	1.45	1.33
8	G	101	CLR	C20-C17	-3.36	1.48	1.54
8	E	101	CLR	C20-C17	-3.31	1.48	1.54
6	A	2004	ADP	C5-C6	3.31	1.50	1.41
10	C	2013	EFO	C23-C24	3.30	1.59	1.53
10	A	2015	EFO	C19-C18	3.29	1.45	1.33
8	G	101	CLR	C10-C5	3.29	1.59	1.52
10	C	2013	EFO	C17-C18	3.27	1.57	1.50
10	A	2015	EFO	C17-C18	3.21	1.56	1.50
9	D	3003	PC1	O31-C31	3.19	1.42	1.33
9	C	2009	PC1	O31-C31	3.18	1.42	1.33
9	C	2011	PC1	O31-C31	3.18	1.42	1.33
8	D	3001	CLR	C20-C17	-3.18	1.48	1.54
9	C	2012	PC1	O31-C31	3.14	1.42	1.33
10	A	2015	EFO	C2D-C29	-3.09	1.46	1.53
9	B	401	PC1	O31-C31	3.08	1.42	1.33
10	A	2015	EFO	C23-C24	3.08	1.59	1.53
8	A	2009	CLR	C10-C5	3.06	1.58	1.52
8	A	2010	CLR	C10-C5	3.03	1.58	1.52
8	G	101	CLR	C15-C14	3.03	1.60	1.54
10	C	2013	EFO	C2D-C29	-3.02	1.46	1.53
10	A	2015	EFO	C12-C11	-2.93	1.47	1.53
8	A	2010	CLR	C15-C14	2.93	1.60	1.54
6	C	2004	ADP	C5-N7	-2.92	1.33	1.39
9	A	2011	PC1	O31-C31	2.88	1.41	1.33
8	A	2009	CLR	C15-C14	2.85	1.60	1.54
8	A	2010	CLR	C20-C17	-2.85	1.49	1.54
9	A	2013	PC1	O31-C31	2.85	1.41	1.33
10	C	2013	EFO	C8-C10	-2.80	1.50	1.53
10	C	2013	EFO	C12-C11	-2.77	1.47	1.53
10	A	2015	EFO	C20-C21	2.75	1.42	1.33
10	C	2013	EFO	C27-C28	2.75	1.59	1.53
8	E	101	CLR	O1-C3	-2.73	1.35	1.43
10	C	2013	EFO	C20-C21	2.69	1.42	1.33
8	D	3002	CLR	C10-C5	2.68	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	3001	CLR	C10-C5	2.67	1.58	1.52
9	C	2011	PC1	C2A-C29	-2.67	1.38	1.51
8	E	101	CLR	C10-C5	2.66	1.57	1.52
9	A	2013	PC1	O21-C2	-2.64	1.40	1.46
10	C	2013	EFO	O26-C26	2.62	1.25	1.21
10	C	2013	EFO	O37-C36	2.60	1.40	1.34
9	A	2011	PC1	C3A-C39	-2.60	1.38	1.51
9	C	2011	PC1	C3A-C39	-2.58	1.38	1.51
6	C	2004	ADP	PA-O3A	2.58	1.62	1.59
9	A	2013	PC1	C3A-C39	-2.57	1.39	1.51
10	A	2015	EFO	O37-C36	2.57	1.40	1.34
10	C	2013	EFO	O30-C30	2.57	1.25	1.21
9	B	401	PC1	C3A-C39	-2.55	1.39	1.51
9	C	2012	PC1	C3A-C39	-2.52	1.39	1.51
9	C	2009	PC1	O21-C2	-2.52	1.40	1.46
9	C	2009	PC1	C3A-C39	-2.50	1.39	1.51
9	D	3003	PC1	C3A-C39	-2.50	1.39	1.51
10	A	2015	EFO	O30-C30	2.46	1.25	1.21
9	C	2010	PC1	C3A-C39	-2.45	1.39	1.51
9	A	2011	PC1	O21-C21	2.45	1.41	1.34
10	A	2015	EFO	O26-C26	2.43	1.25	1.21
9	A	2014	PC1	C3A-C39	-2.43	1.39	1.51
8	D	3001	CLR	C15-C14	2.42	1.59	1.54
9	D	3003	PC1	O21-C2	-2.41	1.40	1.46
6	A	2004	ADP	C5-N7	-2.40	1.34	1.39
9	B	401	PC1	O21-C2	-2.39	1.41	1.46
10	A	2015	EFO	C8-C10	-2.39	1.50	1.53
8	D	3002	CLR	C15-C14	2.36	1.59	1.54
6	C	2004	ADP	C4-N9	-2.35	1.32	1.37
9	A	2014	PC1	O21-C21	2.34	1.40	1.34
8	G	101	CLR	O1-C3	-2.34	1.36	1.43
9	A	2012	PC1	C3A-C39	-2.34	1.40	1.51
9	A	2011	PC1	O21-C2	-2.34	1.41	1.46
8	E	101	CLR	C4-C3	-2.34	1.48	1.52
10	A	2015	EFO	C19-C20	2.33	1.51	1.44
10	C	2013	EFO	C19-C20	2.32	1.51	1.44
9	C	2012	PC1	O21-C21	2.30	1.40	1.34
8	E	101	CLR	C15-C14	2.30	1.59	1.54
9	C	2010	PC1	O21-C21	2.26	1.40	1.34
9	C	2011	PC1	O21-C21	2.24	1.40	1.34
8	A	2009	CLR	C20-C17	-2.23	1.50	1.54
9	A	2013	PC1	C2A-C29	-2.21	1.40	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	401	PC1	O21-C21	2.19	1.40	1.34
8	G	101	CLR	C16-C17	-2.18	1.49	1.54
8	D	3001	CLR	O1-C3	-2.17	1.37	1.43
10	A	2015	EFO	C27-C28	2.16	1.58	1.53
9	C	2011	PC1	O21-C2	-2.15	1.41	1.46
8	D	3002	CLR	O1-C3	-2.13	1.37	1.43
8	D	3002	CLR	C7-C6	2.12	1.54	1.50
9	C	2012	PC1	O21-C2	-2.11	1.41	1.46
9	A	2012	PC1	O21-C2	-2.10	1.41	1.46
9	D	3003	PC1	C2A-C29	-2.09	1.41	1.51
9	C	2009	PC1	O21-C21	2.09	1.40	1.34
9	D	3003	PC1	O21-C21	2.08	1.40	1.34
8	E	101	CLR	C7-C6	2.05	1.54	1.50
6	C	2004	ADP	C8-N7	2.04	1.35	1.31
10	C	2013	EFO	C35-C36	2.03	1.52	1.48
8	A	2009	CLR	C7-C6	2.00	1.54	1.50

All (214) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	2015	EFO	O9-C8-O14	21.09	161.70	109.73
10	C	2013	EFO	O9-C8-O14	20.49	160.24	109.73
10	A	2015	EFO	O14-C8-C7	-12.65	63.03	107.36
10	C	2013	EFO	O14-C8-C7	-12.17	64.72	107.36
10	C	2013	EFO	O9-C4-C3	9.91	118.41	105.95
8	G	101	CLR	C7-C8-C14	-9.60	97.33	110.93
8	E	101	CLR	C15-C14-C8	-8.36	105.77	119.10
10	C	2013	EFO	C31-C32-C33	8.22	124.67	114.70
10	A	2015	EFO	O9-C4-C3	8.11	116.14	105.95
8	G	101	CLR	C15-C14-C8	-8.10	106.18	119.10
8	E	101	CLR	C7-C8-C14	-7.56	100.23	110.93
10	A	2015	EFO	C31-C32-C33	7.23	123.48	114.70
6	A	2004	ADP	C5-C4-N3	-6.65	117.56	126.72
10	A	2015	EFO	O14-C13-C12	-6.30	102.23	109.97
8	G	101	CLR	C12-C13-C17	-5.94	107.85	116.60
8	A	2009	CLR	C12-C13-C17	-5.79	108.08	116.60
8	A	2010	CLR	C11-C9-C10	-5.78	105.96	113.08
8	A	2010	CLR	C7-C8-C14	-5.76	102.78	110.93
6	C	2004	ADP	C5-C4-N3	-5.71	118.86	126.72
8	D	3001	CLR	C7-C8-C14	-5.45	103.22	110.93
8	A	2010	CLR	C12-C13-C17	-5.37	108.70	116.60
8	A	2009	CLR	C7-C8-C14	-5.32	103.40	110.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2009	CLR	C11-C9-C10	-5.25	106.61	113.08
10	A	2015	EFO	O14-C13-C15	4.96	113.78	106.24
8	D	3002	CLR	C11-C9-C10	-4.87	107.08	113.08
8	D	3001	CLR	C15-C14-C8	-4.76	111.51	119.10
10	A	2015	EFO	C1A-C10-C8	4.72	119.40	111.92
6	A	2004	ADP	N3-C4-N9	4.69	135.15	127.17
6	C	2004	ADP	N3-C4-N9	4.65	135.08	127.17
8	D	3001	CLR	C12-C13-C17	-4.65	109.75	116.60
10	C	2013	EFO	O37-C36-C35	4.65	121.50	111.39
9	A	2011	PC1	O21-C21-C22	4.60	121.44	111.48
10	C	2013	EFO	O14-C13-C12	-4.56	104.37	109.97
10	C	2013	EFO	C8-O14-C13	-4.54	105.35	114.77
8	G	101	CLR	C16-C15-C14	-4.54	96.26	105.14
8	D	3002	CLR	C15-C14-C8	-4.52	111.88	119.10
8	A	2009	CLR	C15-C14-C8	-4.52	111.89	119.10
10	C	2013	EFO	C28-C27-C26	4.49	119.42	110.56
10	C	2013	EFO	O14-C13-C15	4.47	113.04	106.24
9	B	401	PC1	O21-C21-C22	4.46	121.12	111.48
10	A	2015	EFO	C8-O14-C13	-4.41	105.63	114.77
10	C	2013	EFO	C22-C21-C20	-4.38	119.86	125.44
9	C	2011	PC1	O21-C21-C22	4.38	120.95	111.48
8	A	2010	CLR	C15-C14-C8	-4.37	112.13	119.10
8	E	101	CLR	C12-C13-C17	-4.36	110.18	116.60
10	C	2013	EFO	C8-O9-C4	-4.34	105.77	114.77
9	C	2012	PC1	O21-C21-C22	4.29	120.75	111.48
10	A	2015	EFO	C8-O9-C4	-4.27	105.92	114.77
9	A	2014	PC1	O31-C3-C2	4.21	120.52	108.40
8	G	101	CLR	C11-C12-C13	-4.16	105.71	112.74
9	A	2014	PC1	O21-C21-C22	4.09	120.32	111.48
9	B	401	PC1	C15-N-C13	4.08	119.70	108.98
6	A	2004	ADP	C4-C5-N7	-4.06	105.94	110.58
8	E	101	CLR	C8-C7-C6	-4.05	107.15	112.76
10	A	2015	EFO	O37-C36-C35	4.03	120.17	111.39
9	C	2010	PC1	O31-C3-C2	4.02	119.99	108.40
9	C	2010	PC1	C15-N-C13	4.02	119.53	108.98
8	E	101	CLR	C11-C12-C13	-4.01	105.97	112.74
9	A	2013	PC1	O21-C21-C22	4.01	120.15	111.48
8	G	101	CLR	C21-C20-C17	4.00	118.89	112.88
6	A	2004	ADP	C2-N3-C4	3.98	121.56	111.83
9	C	2009	PC1	O21-C21-C22	3.97	120.07	111.48
9	D	3003	PC1	O31-C3-C2	3.96	119.80	108.40
10	C	2013	EFO	C15-C16-C17	3.94	120.22	114.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2010	CLR	C11-C9-C8	-3.94	106.29	111.78
8	G	101	CLR	C11-C9-C8	-3.92	106.31	111.78
9	C	2009	PC1	C15-N-C13	3.91	119.25	108.98
8	D	3001	CLR	C11-C9-C10	-3.91	108.27	113.08
9	A	2012	PC1	C15-N-C13	3.84	119.06	108.98
8	D	3001	CLR	C17-C13-C14	3.81	104.47	100.10
8	A	2009	CLR	C17-C13-C14	3.81	104.47	100.10
9	A	2011	PC1	C15-N-C13	3.80	118.96	108.98
6	C	2004	ADP	C2-N3-C4	3.79	121.09	111.83
8	D	3002	CLR	C7-C8-C14	-3.78	105.58	110.93
8	A	2010	CLR	C12-C11-C9	-3.73	106.79	113.14
8	A	2009	CLR	C11-C9-C8	-3.73	106.57	111.78
8	D	3002	CLR	C13-C14-C8	3.73	119.71	114.41
9	A	2012	PC1	O31-C3-C2	3.70	119.07	108.40
9	C	2012	PC1	O31-C3-C2	3.70	119.06	108.40
8	A	2010	CLR	C22-C20-C17	-3.66	102.75	110.33
8	A	2010	CLR	C11-C12-C13	-3.64	106.59	112.74
9	C	2011	PC1	C15-N-C13	3.64	118.53	108.98
9	A	2014	PC1	C15-N-C13	3.63	118.52	108.98
8	E	101	CLR	C11-C9-C10	-3.62	108.62	113.08
10	A	2015	EFO	C15-C16-C17	3.62	119.72	114.13
9	A	2013	PC1	C15-N-C13	3.61	118.47	108.98
8	A	2010	CLR	C4-C5-C10	3.60	121.03	116.42
10	C	2013	EFO	C1A-C10-C8	3.58	117.59	111.92
8	D	3002	CLR	C12-C13-C17	-3.56	111.35	116.60
10	A	2015	EFO	C17-C18-C19	-3.56	117.68	126.30
8	G	101	CLR	C8-C7-C6	-3.52	107.88	112.76
8	E	101	CLR	C22-C20-C17	-3.50	103.07	110.33
10	A	2015	EFO	C22-C21-C20	-3.50	120.98	125.44
9	D	3003	PC1	C15-N-C13	3.49	118.15	108.98
6	C	2004	ADP	N3-C2-N1	-3.46	123.35	128.58
8	D	3001	CLR	C16-C17-C20	-3.44	106.98	112.18
8	D	3002	CLR	C19-C10-C9	3.43	115.51	111.66
9	C	2012	PC1	C15-N-C13	3.40	117.92	108.98
8	A	2009	CLR	C10-C5-C6	-3.40	117.97	122.93
9	A	2012	PC1	O21-C21-C22	3.36	118.75	111.48
6	A	2004	ADP	O4'-C1'-N9	3.34	114.50	108.09
8	G	101	CLR	C19-C10-C9	3.30	115.36	111.66
8	D	3002	CLR	C11-C9-C8	-3.29	107.18	111.78
8	E	101	CLR	C12-C13-C14	3.26	112.12	107.25
9	C	2010	PC1	O21-C21-C22	3.25	118.51	111.48
9	C	2009	PC1	O31-C3-C2	3.23	117.72	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	3001	CLR	C10-C5-C6	-3.22	118.22	122.93
8	D	3001	CLR	C11-C9-C8	-3.14	107.40	111.78
10	C	2013	EFO	O37-C36-O36	-3.12	118.35	123.34
10	A	2015	EFO	O25-C25-C26	-3.11	105.34	108.81
8	E	101	CLR	C12-C11-C9	-3.09	107.89	113.14
6	A	2004	ADP	N3-C2-N1	-3.06	123.95	128.58
9	C	2010	PC1	C2-O21-C21	3.05	125.09	117.80
8	E	101	CLR	C16-C15-C14	-3.02	99.22	105.14
9	C	2011	PC1	O31-C31-C32	3.00	120.98	111.83
10	A	2015	EFO	C6-C7-C8	2.98	116.60	111.93
8	D	3001	CLR	C12-C11-C9	-2.97	108.08	113.14
9	A	2011	PC1	O31-C31-O32	-2.97	116.19	123.63
8	D	3002	CLR	C12-C13-C14	2.96	111.67	107.25
9	C	2010	PC1	O31-C31-C32	2.95	120.84	111.83
6	C	2004	ADP	C4-C5-N7	-2.95	107.21	110.58
9	A	2014	PC1	O31-C31-C32	2.93	120.78	111.83
10	C	2013	EFO	C23-C22-C21	2.91	118.67	114.11
8	A	2009	CLR	C22-C20-C17	-2.91	104.30	110.33
8	D	3001	CLR	C4-C5-C10	2.91	120.14	116.42
6	C	2004	ADP	C4-N9-C8	2.90	108.79	105.74
8	A	2009	CLR	C4-C5-C10	2.90	120.13	116.42
8	A	2010	CLR	C10-C5-C6	-2.89	118.71	122.93
10	C	2013	EFO	C33-C34-C35	-2.88	118.69	126.30
8	A	2009	CLR	C11-C12-C13	-2.87	107.90	112.74
8	D	3002	CLR	C10-C5-C6	-2.86	118.75	122.93
8	G	101	CLR	C4-C5-C10	2.84	120.06	116.42
9	B	401	PC1	O31-C3-C2	2.82	116.53	108.40
10	A	2015	EFO	C33-C34-C35	-2.82	118.84	126.30
8	E	101	CLR	C10-C5-C6	-2.81	118.82	122.93
6	A	2004	ADP	C5-N7-C8	2.80	107.85	103.45
8	D	3001	CLR	C19-C10-C9	2.78	114.78	111.66
8	E	101	CLR	C16-C17-C20	-2.77	107.98	112.18
8	D	3002	CLR	C2-C3-C4	-2.77	106.39	110.29
10	A	2015	EFO	C28-C27-C26	2.75	115.99	110.56
6	A	2004	ADP	O3A-PA-O1A	2.75	118.96	110.70
10	C	2013	EFO	C17-C18-C19	-2.73	119.69	126.30
10	A	2015	EFO	C32-C31-C30	2.72	114.94	110.11
8	D	3001	CLR	C11-C12-C13	-2.72	108.16	112.74
9	D	3003	PC1	O31-C31-C32	2.71	120.11	111.83
8	A	2010	CLR	C2-C3-C4	-2.71	106.48	110.29
8	D	3001	CLR	C22-C20-C17	-2.71	104.72	110.33
6	A	2004	ADP	O2A-PA-O3A	-2.71	99.96	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2011	PC1	O31-C3-C2	2.71	116.20	108.40
8	D	3002	CLR	C8-C7-C6	-2.68	109.06	112.76
10	A	2015	EFO	C27-C28-C29	-2.65	111.49	114.70
9	A	2011	PC1	O31-C31-C32	2.64	119.90	111.83
10	A	2015	EFO	C12-C11-C10	2.64	117.39	112.40
8	D	3001	CLR	C12-C13-C14	2.61	111.16	107.25
9	A	2012	PC1	O31-C31-C32	2.61	119.79	111.83
10	C	2013	EFO	C1D-C1C-C17	2.58	119.20	113.69
9	A	2012	PC1	C2-O21-C21	2.58	123.97	117.80
9	A	2013	PC1	O31-C3-C2	2.55	115.76	108.40
8	G	101	CLR	C2-C3-C4	-2.54	106.71	110.29
10	C	2013	EFO	O9-C4-C5	-2.54	106.91	110.39
8	A	2009	CLR	C7-C8-C9	-2.48	106.85	109.72
8	A	2009	CLR	C7-C6-C5	-2.48	120.83	125.02
8	A	2009	CLR	C8-C7-C6	-2.47	109.33	112.76
10	A	2015	EFO	C11-O37-C36	2.46	121.33	117.42
9	D	3003	PC1	O21-C21-C22	2.44	116.77	111.48
8	D	3001	CLR	C18-C13-C17	-2.43	107.26	111.68
9	C	2011	PC1	O31-C31-O32	-2.42	117.56	123.63
8	E	101	CLR	C17-C13-C14	2.41	102.86	100.10
8	D	3002	CLR	C2-C1-C10	-2.40	107.67	112.78
9	C	2012	PC1	O31-C31-C32	2.40	119.15	111.83
6	C	2004	ADP	C5-N7-C8	2.38	107.19	103.45
9	C	2009	PC1	O31-C31-C32	2.37	119.06	111.83
8	G	101	CLR	C7-C6-C5	-2.37	121.02	125.02
9	B	401	PC1	O31-C31-C32	2.35	119.00	111.83
9	A	2012	PC1	O21-C21-O22	-2.32	118.29	123.70
8	A	2010	CLR	C17-C13-C14	2.31	102.75	100.10
8	D	3002	CLR	C1-C2-C3	-2.29	107.44	110.48
8	E	101	CLR	C15-C14-C13	2.26	106.50	103.84
10	A	2015	EFO	O28-C28-C29	2.26	114.02	108.59
6	C	2004	ADP	N9-C8-N7	-2.25	110.75	113.94
10	C	2013	EFO	O28-C28-C29	2.24	113.99	108.59
10	C	2013	EFO	O25-C25-C26	-2.23	106.32	108.81
10	C	2013	EFO	C11-C12-C13	2.23	112.87	108.21
8	G	101	CLR	C10-C5-C6	-2.22	119.69	122.93
9	C	2011	PC1	O31-C3-C2	2.21	114.77	108.40
9	B	401	PC1	O13-C11-C12	2.21	120.28	109.65
8	D	3002	CLR	C23-C22-C20	-2.21	108.91	115.08
10	A	2015	EFO	C11-C12-C13	2.20	112.81	108.21
6	C	2004	ADP	C2'-C1'-N9	-2.20	107.83	113.30
8	D	3002	CLR	C4-C5-C10	2.17	119.21	116.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2010	CLR	C16-C17-C20	-2.17	108.90	112.18
8	A	2009	CLR	C12-C11-C9	-2.16	109.46	113.14
9	A	2013	PC1	O31-C31-C32	2.14	118.36	111.83
8	A	2010	CLR	C8-C7-C6	-2.14	109.80	112.76
8	G	101	CLR	C19-C10-C5	-2.13	105.13	108.38
10	A	2015	EFO	O37-C36-O36	-2.13	119.93	123.34
10	C	2013	EFO	C2C-C27-C28	-2.12	108.68	112.42
8	A	2009	CLR	C19-C10-C9	2.12	114.03	111.66
10	A	2015	EFO	C23-C22-C21	2.11	117.40	114.11
10	C	2013	EFO	C12-C11-C10	2.11	116.38	112.40
9	A	2012	PC1	C34-C33-C32	2.11	120.86	113.13
9	C	2009	PC1	O31-C31-O32	-2.10	118.38	123.63
6	C	2004	ADP	O4'-C1'-N9	2.09	112.11	108.09
9	A	2013	PC1	O13-C11-C12	2.08	119.67	109.65
8	A	2009	CLR	C2-C3-C4	-2.08	107.36	110.29
10	C	2013	EFO	C2B-C25-C26	2.07	111.06	106.99
9	C	2009	PC1	O21-C21-O22	-2.07	118.87	123.70
9	A	2011	PC1	O22-C21-C22	-2.04	115.79	123.78
8	A	2010	CLR	C7-C6-C5	-2.04	121.57	125.02
8	A	2010	CLR	C12-C13-C14	2.02	110.27	107.25
8	G	101	CLR	C12-C13-C14	2.02	110.27	107.25
10	C	2013	EFO	C51-C5-C4	-2.02	109.24	112.62
9	D	3003	PC1	O31-C31-O32	-2.00	118.61	123.63
8	E	101	CLR	C7-C6-C5	-2.00	121.64	125.02

There are no chirality outliers.

All (319) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2004	ADP	C5'-O5'-PA-O1A
6	A	2004	ADP	C5'-O5'-PA-O2A
6	A	2004	ADP	C5'-O5'-PA-O3A
6	A	2004	ADP	O4'-C4'-C5'-O5'
9	A	2011	PC1	O13-C11-C12-N
9	A	2012	PC1	C11-O13-P-O12
9	A	2012	PC1	C11-O13-P-O14
9	A	2012	PC1	C11-O13-P-O11
9	A	2012	PC1	O13-C11-C12-N
9	A	2014	PC1	C22-C21-O21-C2
9	B	401	PC1	C1-O11-P-O14
9	B	401	PC1	O13-C11-C12-N
9	B	401	PC1	C22-C21-O21-C2

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Mol	Chain	Res	Type	Atoms
9	C	2009	PC1	C11-O13-P-O12
9	C	2009	PC1	C11-O13-P-O11
9	C	2009	PC1	C1-O11-P-O12
9	C	2009	PC1	C1-O11-P-O13
9	C	2009	PC1	O13-C11-C12-N
9	C	2010	PC1	O13-C11-C12-N
9	C	2011	PC1	C11-O13-P-O14
9	C	2011	PC1	C11-O13-P-O11
9	C	2011	PC1	O13-C11-C12-N
9	C	2012	PC1	O22-C21-O21-C2
9	C	2012	PC1	C22-C21-O21-C2
9	D	3003	PC1	O22-C21-O21-C2
9	D	3003	PC1	C22-C21-O21-C2
10	A	2015	EFO	C12-C13-C15-C16
10	A	2015	EFO	C2-C3-C4-O9
10	A	2015	EFO	C2-C3-C4-C5
10	C	2013	EFO	C12-C13-C15-C16
10	C	2013	EFO	C1-C2-C3-C4
10	C	2013	EFO	O2-C2-C3-C4
9	A	2014	PC1	O22-C21-O21-C2
9	C	2010	PC1	O22-C21-O21-C2
9	C	2011	PC1	C32-C31-O31-C3
9	A	2011	PC1	O22-C21-O21-C2
9	C	2009	PC1	C38-C39-C3A-C3B
9	D	3003	PC1	C28-C29-C2A-C2B
9	C	2012	PC1	C38-C39-C3A-C3B
9	C	2010	PC1	C32-C31-O31-C3
9	A	2013	PC1	C22-C21-O21-C2
9	C	2012	PC1	C28-C29-C2A-C2B
6	A	2004	ADP	C3'-C4'-C5'-O5'
9	A	2012	PC1	C2-C1-O11-P
9	D	3003	PC1	C38-C39-C3A-C3B
9	A	2013	PC1	C26-C27-C28-C29
9	B	401	PC1	C24-C25-C26-C27
9	C	2010	PC1	C28-C29-C2A-C2B
9	C	2010	PC1	O32-C31-O31-C3
9	C	2009	PC1	O22-C21-O21-C2
9	A	2012	PC1	C28-C29-C2A-C2B
9	A	2013	PC1	C38-C39-C3A-C3B
9	A	2014	PC1	C24-C25-C26-C27
9	B	401	PC1	C38-C39-C3A-C3B
9	C	2011	PC1	O32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
9	B	401	PC1	O22-C21-O21-C2
9	C	2010	PC1	O11-C1-C2-O21
9	A	2012	PC1	C21-C22-C23-C24
9	C	2011	PC1	C27-C28-C29-C2A
9	C	2011	PC1	C11-C12-N-C14
9	C	2010	PC1	C22-C21-O21-C2
9	A	2011	PC1	C21-C22-C23-C24
9	C	2009	PC1	C31-C32-C33-C34
9	D	3003	PC1	C21-C22-C23-C24
9	C	2009	PC1	C28-C29-C2A-C2B
9	A	2014	PC1	C32-C31-O31-C3
9	C	2012	PC1	O32-C31-O31-C3
9	A	2012	PC1	O22-C21-O21-C2
9	A	2011	PC1	C32-C31-O31-C3
9	C	2012	PC1	C32-C31-O31-C3
9	C	2009	PC1	C21-C22-C23-C24
9	A	2013	PC1	O22-C21-O21-C2
9	C	2010	PC1	C11-C12-N-C15
9	C	2009	PC1	C32-C31-O31-C3
9	C	2011	PC1	C11-C12-N-C13
9	C	2012	PC1	C21-C22-C23-C24
9	A	2013	PC1	C27-C28-C29-C2A
9	A	2013	PC1	C36-C37-C38-C39
9	C	2011	PC1	C35-C36-C37-C38
9	A	2011	PC1	C24-C25-C26-C27
9	A	2013	PC1	C24-C25-C26-C27
9	A	2014	PC1	C2D-C2E-C2F-C2G
9	C	2009	PC1	C36-C37-C38-C39
9	C	2009	PC1	C39-C3A-C3B-C3C
9	C	2011	PC1	C22-C23-C24-C25
9	C	2011	PC1	C3C-C3D-C3E-C3F
9	A	2013	PC1	C3C-C3D-C3E-C3F
9	D	3003	PC1	C26-C27-C28-C29
9	C	2009	PC1	C35-C36-C37-C38
9	C	2012	PC1	C24-C25-C26-C27
9	C	2011	PC1	C21-C22-C23-C24
9	A	2011	PC1	C3A-C3B-C3C-C3D
9	C	2012	PC1	C23-C24-C25-C26
9	C	2009	PC1	C22-C21-O21-C2
9	D	3003	PC1	C2B-C2C-C2D-C2E
9	C	2009	PC1	C3A-C3B-C3C-C3D
9	B	401	PC1	C2C-C2D-C2E-C2F

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Mol	Chain	Res	Type	Atoms
9	B	401	PC1	C33-C34-C35-C36
9	C	2009	PC1	C26-C27-C28-C29
9	A	2012	PC1	C2D-C2E-C2F-C2G
9	A	2014	PC1	C23-C24-C25-C26
9	B	401	PC1	C39-C3A-C3B-C3C
9	A	2013	PC1	C29-C2A-C2B-C2C
9	A	2013	PC1	C2B-C2C-C2D-C2E
9	A	2013	PC1	C2C-C2D-C2E-C2F
9	C	2012	PC1	C27-C28-C29-C2A
9	C	2009	PC1	C34-C35-C36-C37
9	C	2012	PC1	C36-C37-C38-C39
9	D	3003	PC1	C25-C26-C27-C28
9	C	2010	PC1	C24-C25-C26-C27
9	C	2012	PC1	C34-C35-C36-C37
9	C	2011	PC1	C29-C2A-C2B-C2C
9	A	2011	PC1	C27-C28-C29-C2A
9	B	401	PC1	C2B-C2C-C2D-C2E
9	C	2010	PC1	C2A-C2B-C2C-C2D
9	D	3003	PC1	C2C-C2D-C2E-C2F
9	C	2011	PC1	C24-C25-C26-C27
9	A	2014	PC1	C3D-C3E-C3F-C3G
9	A	2014	PC1	C2B-C2C-C2D-C2E
9	A	2013	PC1	C37-C38-C39-C3A
9	C	2011	PC1	C34-C35-C36-C37
9	A	2013	PC1	C32-C31-O31-C3
9	A	2014	PC1	C36-C37-C38-C39
9	C	2009	PC1	C2A-C2B-C2C-C2D
9	C	2011	PC1	C28-C29-C2A-C2B
10	A	2015	EFO	O14-C13-C15-C16
10	C	2013	EFO	O14-C13-C15-C16
9	A	2012	PC1	C26-C27-C28-C29
9	A	2014	PC1	C29-C2A-C2B-C2C
9	C	2010	PC1	C29-C2A-C2B-C2C
9	B	401	PC1	C3E-C3F-C3G-C3H
9	D	3003	PC1	C23-C24-C25-C26
9	A	2011	PC1	C22-C21-O21-C2
9	D	3003	PC1	C3C-C3D-C3E-C3F
9	A	2011	PC1	C2D-C2E-C2F-C2G
9	B	401	PC1	C21-C22-C23-C24
9	D	3003	PC1	C36-C37-C38-C39
9	C	2011	PC1	C26-C27-C28-C29
9	D	3003	PC1	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
9	A	2012	PC1	C22-C21-O21-C2
9	A	2013	PC1	C2D-C2E-C2F-C2G
9	B	401	PC1	C28-C29-C2A-C2B
9	A	2014	PC1	C35-C36-C37-C38
9	C	2009	PC1	C2B-C2C-C2D-C2E
9	A	2011	PC1	C34-C35-C36-C37
9	C	2012	PC1	C2B-C2C-C2D-C2E
9	A	2014	PC1	C27-C28-C29-C2A
9	B	401	PC1	C2D-C2E-C2F-C2G
9	A	2014	PC1	O32-C31-O31-C3
9	A	2014	PC1	C3B-C3C-C3D-C3E
9	C	2011	PC1	C2B-C2C-C2D-C2E
9	D	3003	PC1	C3B-C3C-C3D-C3E
9	A	2014	PC1	C33-C34-C35-C36
9	B	401	PC1	C2A-C2B-C2C-C2D
9	B	401	PC1	C3C-C3D-C3E-C3F
9	C	2010	PC1	C2B-C2C-C2D-C2E
9	D	3003	PC1	C27-C28-C29-C2A
9	B	401	PC1	O11-C1-C2-C3
9	C	2012	PC1	O11-C1-C2-C3
9	A	2013	PC1	C3B-C3C-C3D-C3E
9	C	2009	PC1	C29-C2A-C2B-C2C
9	D	3003	PC1	C29-C2A-C2B-C2C
9	D	3003	PC1	C31-C32-C33-C34
9	A	2014	PC1	C26-C27-C28-C29
10	A	2015	EFO	C34-C35-C36-O37
10	C	2013	EFO	C34-C35-C36-O37
9	C	2009	PC1	C23-C24-C25-C26
9	C	2010	PC1	C25-C26-C27-C28
9	D	3003	PC1	C1-C2-C3-O31
9	B	401	PC1	C32-C33-C34-C35
9	C	2011	PC1	C38-C39-C3A-C3B
9	A	2012	PC1	C33-C34-C35-C36
9	A	2013	PC1	C22-C23-C24-C25
9	B	401	PC1	C27-C28-C29-C2A
9	A	2013	PC1	C32-C33-C34-C35
9	C	2011	PC1	C23-C24-C25-C26
9	C	2011	PC1	C3B-C3C-C3D-C3E
9	A	2014	PC1	C31-C32-C33-C34
9	A	2011	PC1	C29-C2A-C2B-C2C
9	A	2012	PC1	C22-C23-C24-C25
9	C	2010	PC1	C34-C35-C36-C37

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Mol	Chain	Res	Type	Atoms
9	A	2012	PC1	C2C-C2D-C2E-C2F
9	C	2009	PC1	C3D-C3E-C3F-C3G
9	A	2012	PC1	C34-C35-C36-C37
9	C	2010	PC1	C3C-C3D-C3E-C3F
9	B	401	PC1	C35-C36-C37-C38
9	B	401	PC1	C34-C35-C36-C37
9	A	2013	PC1	C2F-C2G-C2H-C2I
9	A	2012	PC1	C35-C36-C37-C38
9	C	2009	PC1	C3E-C3F-C3G-C3H
9	A	2012	PC1	C27-C28-C29-C2A
9	C	2010	PC1	C3B-C3C-C3D-C3E
9	D	3003	PC1	C34-C35-C36-C37
9	C	2011	PC1	C2F-C2G-C2H-C2I
9	A	2013	PC1	C34-C35-C36-C37
9	C	2009	PC1	C2D-C2E-C2F-C2G
9	C	2011	PC1	C2D-C2E-C2F-C2G
9	C	2010	PC1	C11-C12-N-C14
9	B	401	PC1	C26-C27-C28-C29
9	C	2009	PC1	C3C-C3D-C3E-C3F
9	A	2011	PC1	C26-C27-C28-C29
9	A	2013	PC1	C23-C24-C25-C26
9	D	3003	PC1	C3A-C3B-C3C-C3D
10	C	2013	EFO	C2-C3-C4-O9
9	C	2012	PC1	C32-C33-C34-C35
9	C	2012	PC1	C3A-C3B-C3C-C3D
9	D	3003	PC1	C22-C23-C24-C25
9	A	2012	PC1	O11-C1-C2-C3
9	C	2010	PC1	O11-C1-C2-C3
9	C	2011	PC1	O11-C1-C2-C3
9	A	2014	PC1	C3A-C3B-C3C-C3D
9	A	2013	PC1	C21-C22-C23-C24
9	A	2011	PC1	C2F-C2G-C2H-C2I
9	A	2014	PC1	C28-C29-C2A-C2B
9	C	2012	PC1	C37-C38-C39-C3A
9	D	3003	PC1	C24-C25-C26-C27
9	C	2012	PC1	C3C-C3D-C3E-C3F
9	B	401	PC1	O11-C1-C2-O21
10	A	2015	EFO	C28-C29-C30-O30
9	C	2010	PC1	C2C-C2D-C2E-C2F
9	C	2012	PC1	C3F-C3G-C3H-C3I
9	A	2013	PC1	C3D-C3E-C3F-C3G
9	D	3003	PC1	C2A-C2B-C2C-C2D

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Mol	Chain	Res	Type	Atoms
6	A	2004	ADP	PB-O3A-PA-O5'
6	C	2004	ADP	PB-O3A-PA-O5'
9	A	2012	PC1	O32-C31-O31-C3
9	A	2011	PC1	C37-C38-C39-C3A
9	D	3003	PC1	C3F-C3G-C3H-C3I
9	B	401	PC1	C29-C2A-C2B-C2C
10	A	2015	EFO	C28-C29-C30-C31
9	C	2011	PC1	C25-C26-C27-C28
9	A	2014	PC1	C3C-C3D-C3E-C3F
9	A	2013	PC1	O32-C31-O31-C3
8	A	2010	CLR	C22-C23-C24-C25
9	A	2014	PC1	C3F-C3G-C3H-C3I
9	A	2014	PC1	C21-C22-C23-C24
9	C	2011	PC1	C11-C12-N-C15
9	C	2010	PC1	C3-C2-O21-C21
9	A	2012	PC1	C38-C39-C3A-C3B
9	C	2011	PC1	C2C-C2D-C2E-C2F
9	C	2011	PC1	C32-C33-C34-C35
9	A	2011	PC1	O11-C1-C2-O21
9	A	2012	PC1	O11-C1-C2-O21
9	A	2013	PC1	O11-C1-C2-O21
9	C	2011	PC1	O11-C1-C2-O21
9	A	2013	PC1	C1-C2-C3-O31
9	C	2010	PC1	C1-C2-C3-O31
9	B	401	PC1	C31-C32-C33-C34
9	C	2010	PC1	C3F-C3G-C3H-C3I
9	A	2011	PC1	C12-C11-O13-P
9	B	401	PC1	C12-C11-O13-P
9	C	2011	PC1	C3F-C3G-C3H-C3I
9	C	2010	PC1	C36-C37-C38-C39
9	D	3003	PC1	C39-C3A-C3B-C3C
9	A	2011	PC1	C2A-C2B-C2C-C2D
9	C	2010	PC1	C39-C3A-C3B-C3C
9	A	2013	PC1	O13-C11-C12-N
9	A	2011	PC1	O11-C1-C2-C3
9	A	2014	PC1	O11-C1-C2-C3
10	C	2013	EFO	C2-C3-C4-C5
9	D	3003	PC1	C3E-C3F-C3G-C3H
9	B	401	PC1	O32-C31-O31-C3
9	A	2012	PC1	C3E-C3F-C3G-C3H
9	A	2014	PC1	C34-C35-C36-C37
9	A	2014	PC1	O11-C1-C2-O21

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Mol	Chain	Res	Type	Atoms
9	C	2010	PC1	O21-C2-C3-O31
9	D	3003	PC1	O21-C2-C3-O31
9	A	2011	PC1	C36-C37-C38-C39
9	D	3003	PC1	C32-C33-C34-C35
9	C	2010	PC1	C11-C12-N-C13
9	C	2012	PC1	C1-O11-P-O14
8	G	101	CLR	C21-C20-C22-C23
9	A	2012	PC1	C3-C2-O21-C21
9	A	2011	PC1	C39-C3A-C3B-C3C
9	C	2012	PC1	O11-C1-C2-O21
9	C	2012	PC1	C25-C26-C27-C28
9	C	2011	PC1	C31-C32-C33-C34
9	C	2011	PC1	C39-C3A-C3B-C3C
9	A	2011	PC1	C23-C24-C25-C26
9	A	2014	PC1	C32-C33-C34-C35
9	B	401	PC1	C32-C31-O31-C3
9	A	2013	PC1	C2A-C2B-C2C-C2D
9	B	401	PC1	C23-C24-C25-C26
9	A	2012	PC1	C3A-C3B-C3C-C3D
11	D	3004	NAG	O5-C5-C6-O6
9	D	3003	PC1	O21-C21-C22-C23
10	A	2015	EFO	C15-C16-C17-C18
10	C	2013	EFO	C15-C16-C17-C18
9	C	2012	PC1	C3D-C3E-C3F-C3G
9	A	2012	PC1	C29-C2A-C2B-C2C
9	A	2014	PC1	C3E-C3F-C3G-C3H
9	C	2010	PC1	C2-C1-O11-P
9	C	2010	PC1	C2D-C2E-C2F-C2G
9	C	2012	PC1	C31-C32-C33-C34
9	A	2013	PC1	C35-C36-C37-C38
9	C	2010	PC1	C38-C39-C3A-C3B
9	B	401	PC1	C3F-C3G-C3H-C3I
9	A	2012	PC1	C2F-C2G-C2H-C2I
9	B	401	PC1	C2F-C2G-C2H-C2I
9	A	2012	PC1	C3C-C3D-C3E-C3F
9	C	2010	PC1	C22-C23-C24-C25
9	A	2014	PC1	C38-C39-C3A-C3B
9	A	2011	PC1	O32-C31-O31-C3
10	C	2013	EFO	C18-C19-C20-C21
9	A	2013	PC1	O11-C1-C2-C3
9	C	2010	PC1	C37-C38-C39-C3A
9	C	2010	PC1	O21-C21-C22-C23

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Mol	Chain	Res	Type	Atoms
9	A	2014	PC1	O21-C21-C22-C23
10	C	2013	EFO	C28-C29-C30-C31
8	D	3002	CLR	C23-C24-C25-C27
10	A	2015	EFO	C2D-C29-C30-C31
10	C	2013	EFO	C2D-C29-C30-C31
9	B	401	PC1	C22-C23-C24-C25
9	C	2009	PC1	O32-C31-O31-C3
9	A	2011	PC1	C3D-C3E-C3F-C3G
9	C	2010	PC1	C33-C34-C35-C36
9	A	2012	PC1	O31-C31-C32-C33
9	A	2014	PC1	O22-C21-C22-C23
9	A	2012	PC1	C2B-C2C-C2D-C2E

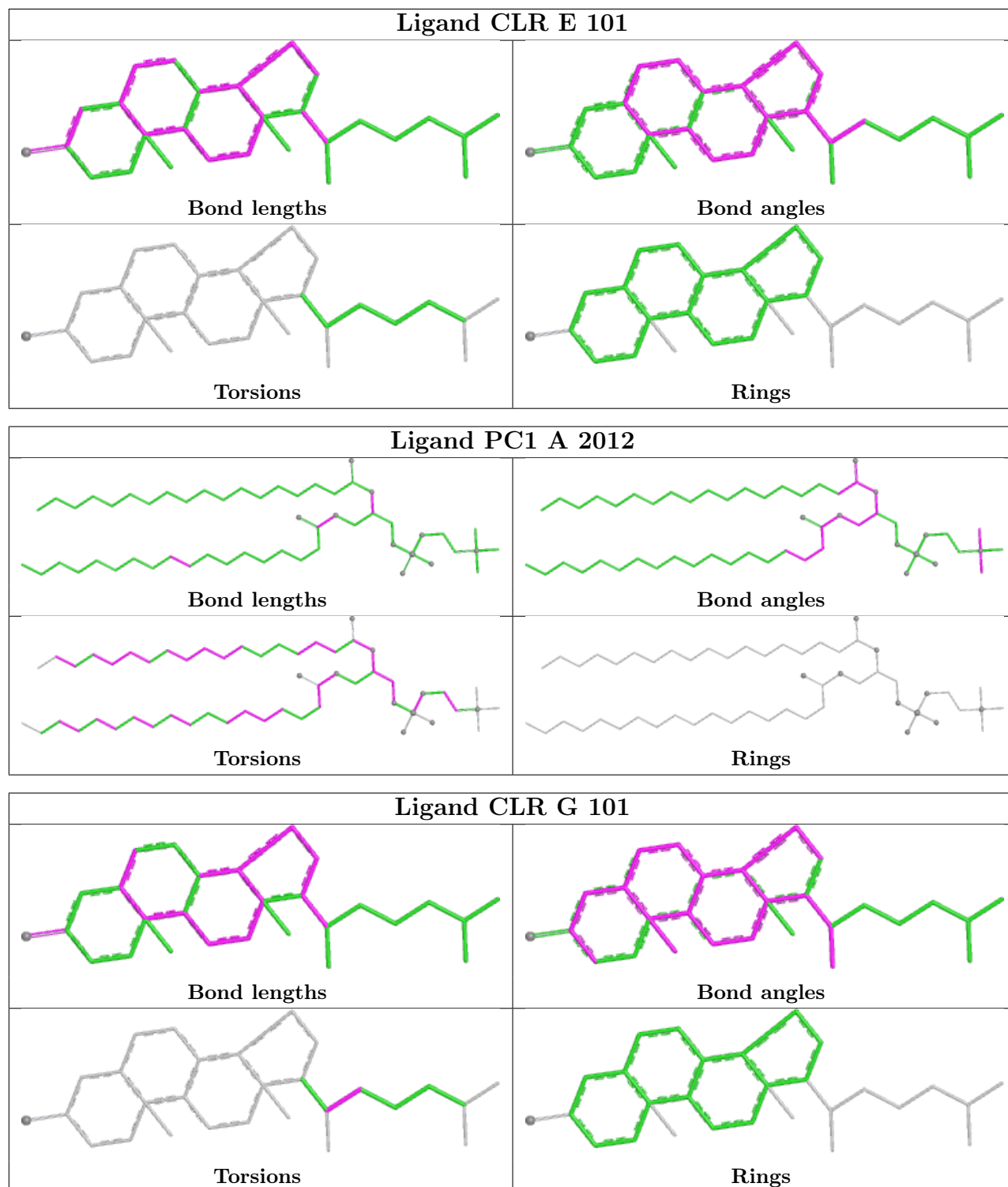
There are no ring outliers.

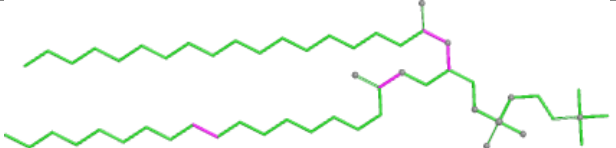
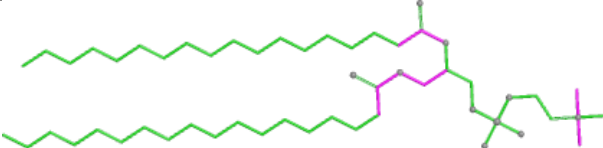
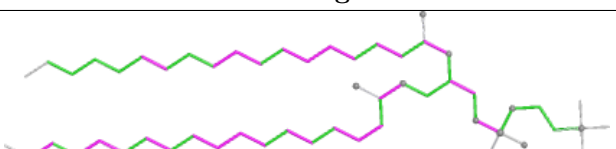
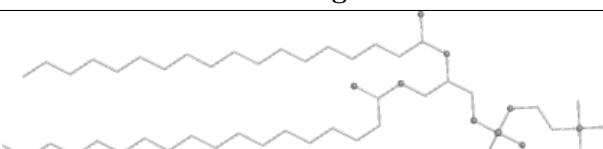
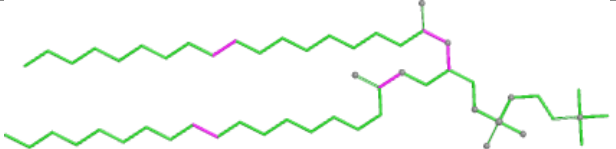
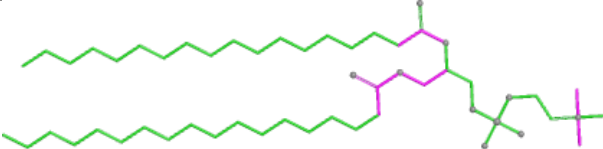
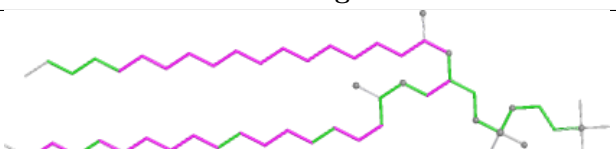
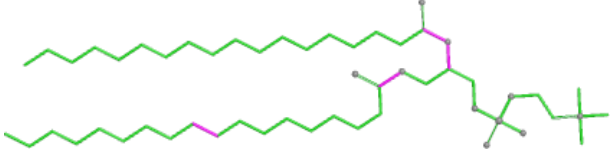
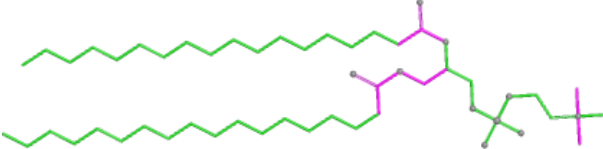
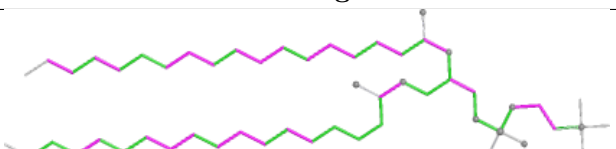
19 monomers are involved in 117 short contacts:

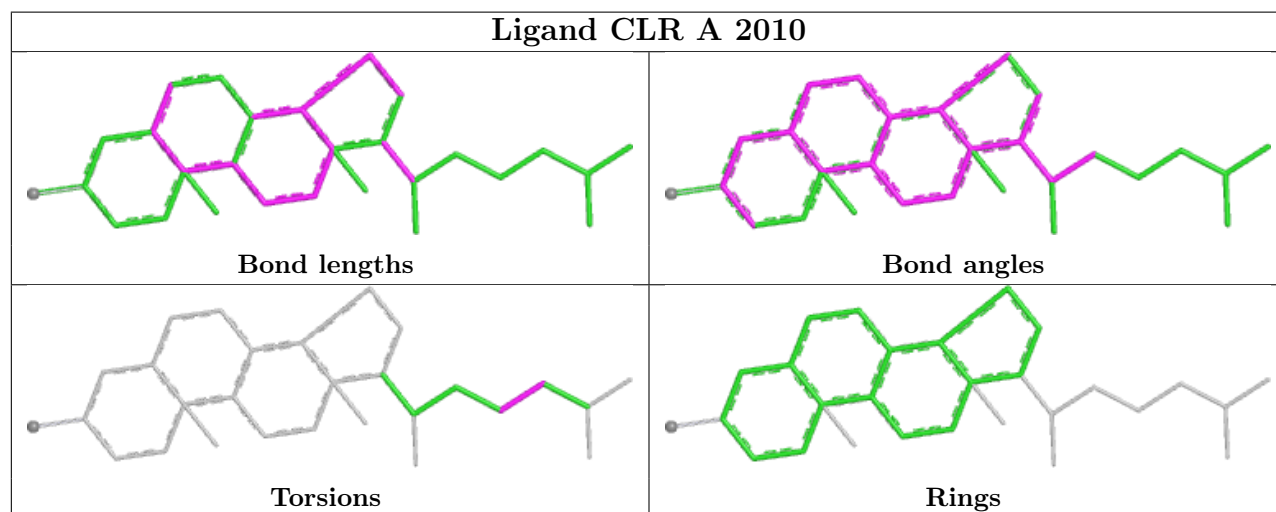
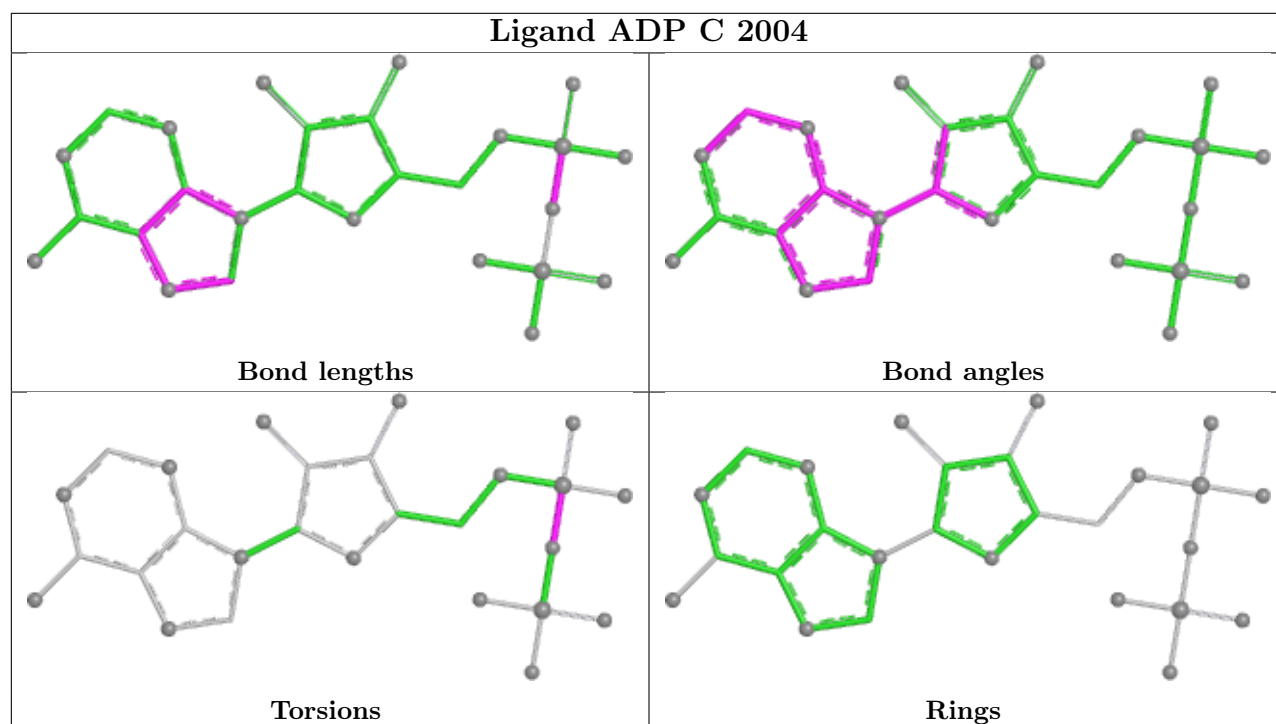
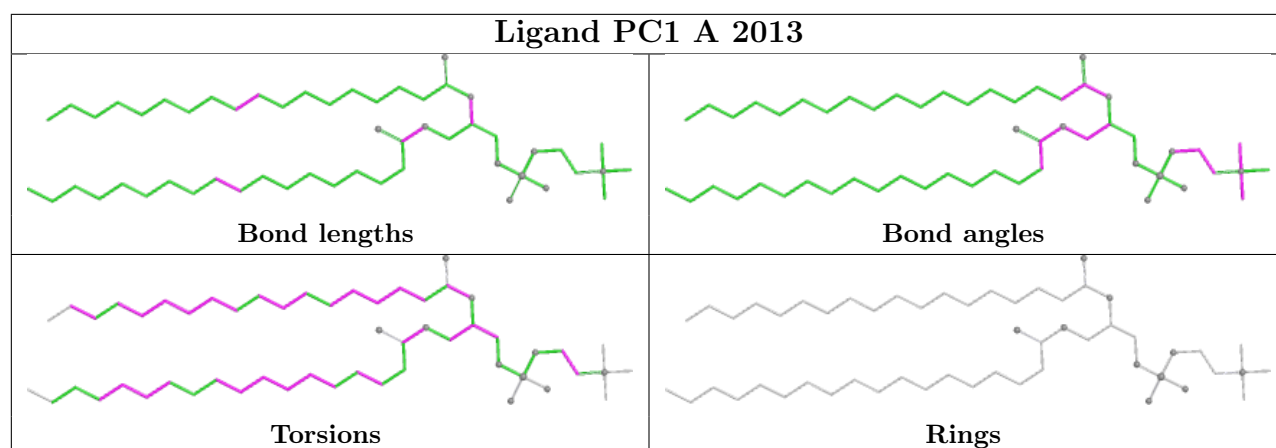
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	E	101	CLR	13	0
9	A	2012	PC1	2	0
8	G	101	CLR	9	0
9	C	2012	PC1	6	0
9	D	3003	PC1	2	0
9	A	2011	PC1	1	0
9	A	2013	PC1	7	0
6	C	2004	ADP	6	0
5	A	2002	ALF	1	0
8	A	2010	CLR	15	0
9	A	2014	PC1	4	0
9	C	2009	PC1	8	0
9	B	401	PC1	2	0
8	A	2009	CLR	12	0
9	C	2011	PC1	3	0
8	D	3002	CLR	17	0
6	A	2004	ADP	3	0
5	C	2002	ALF	3	0
8	D	3001	CLR	12	0

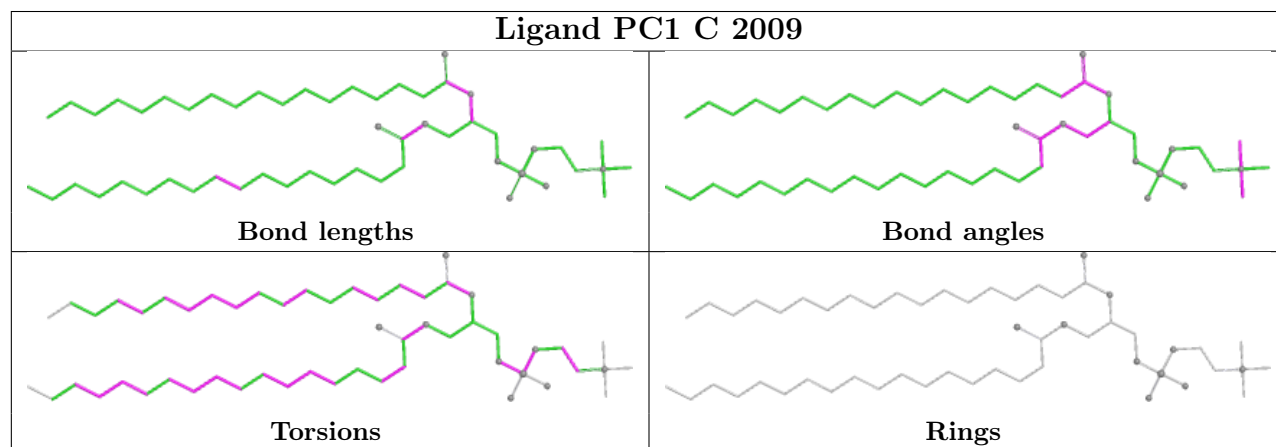
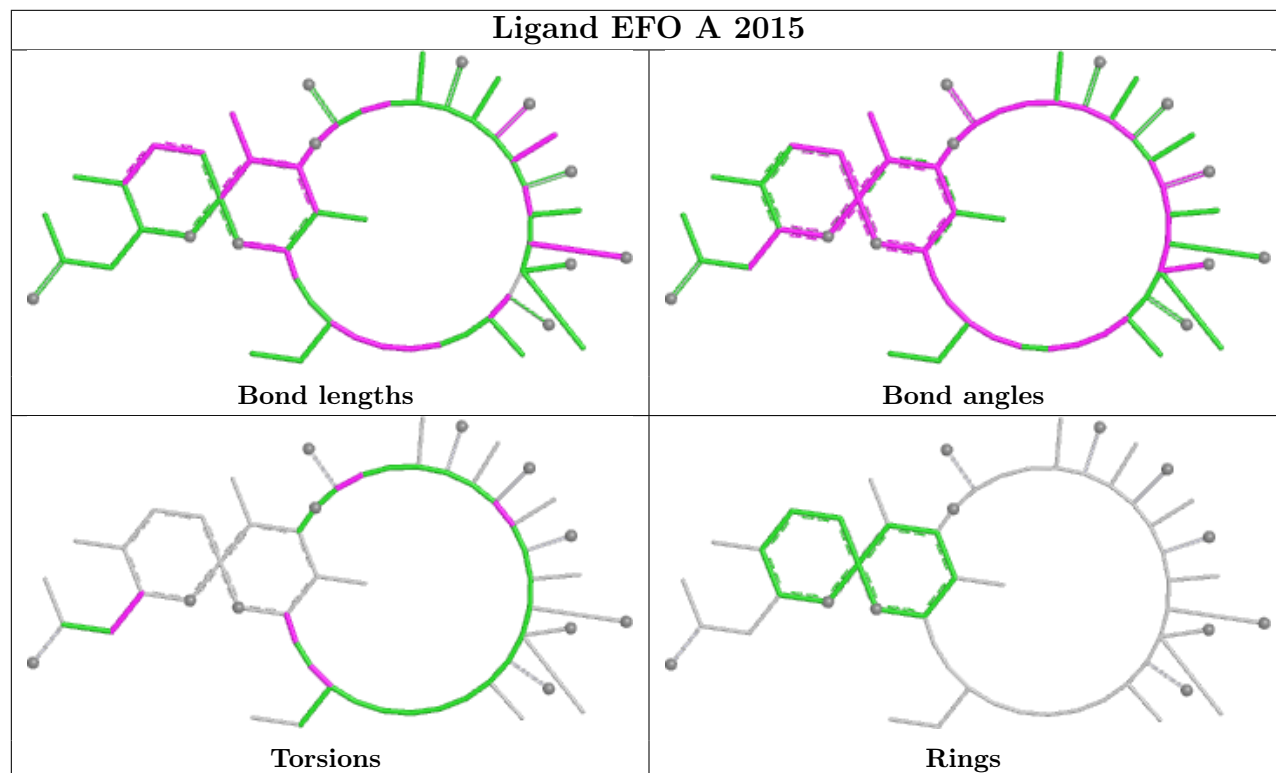
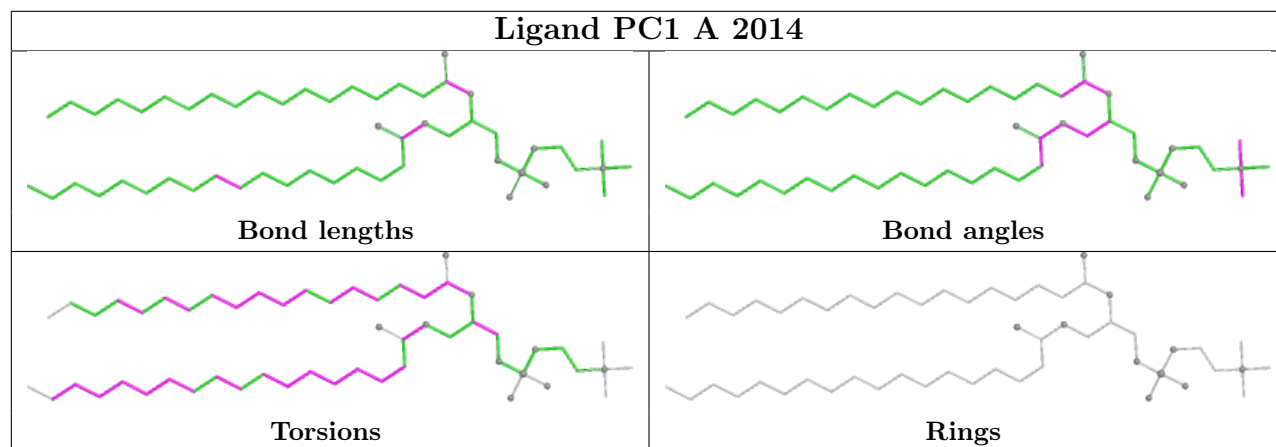
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

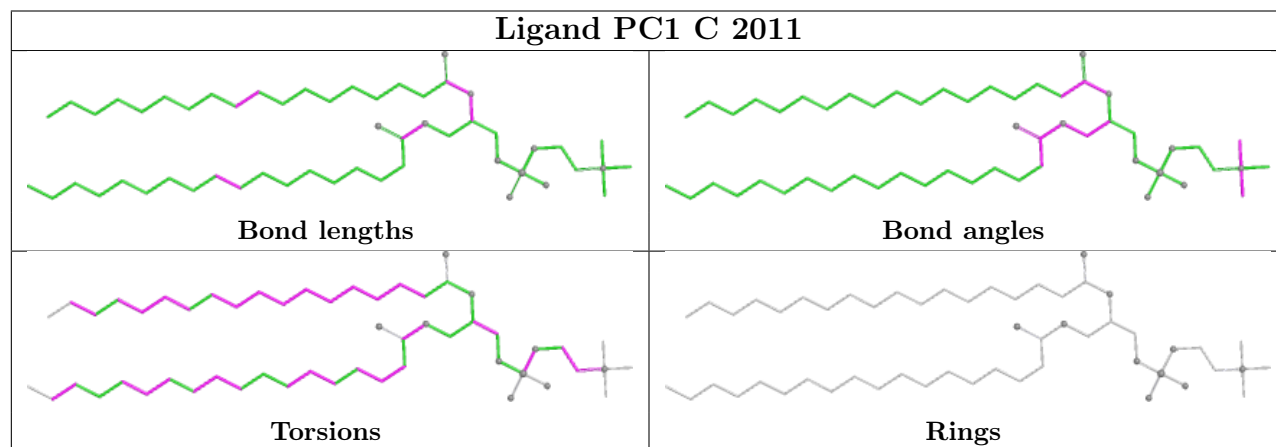
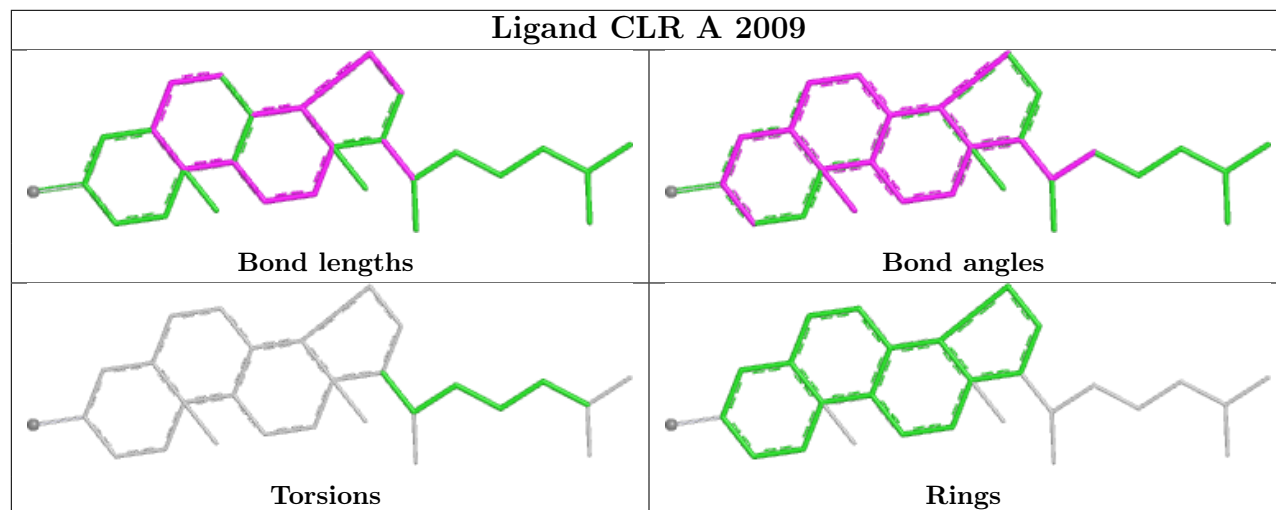
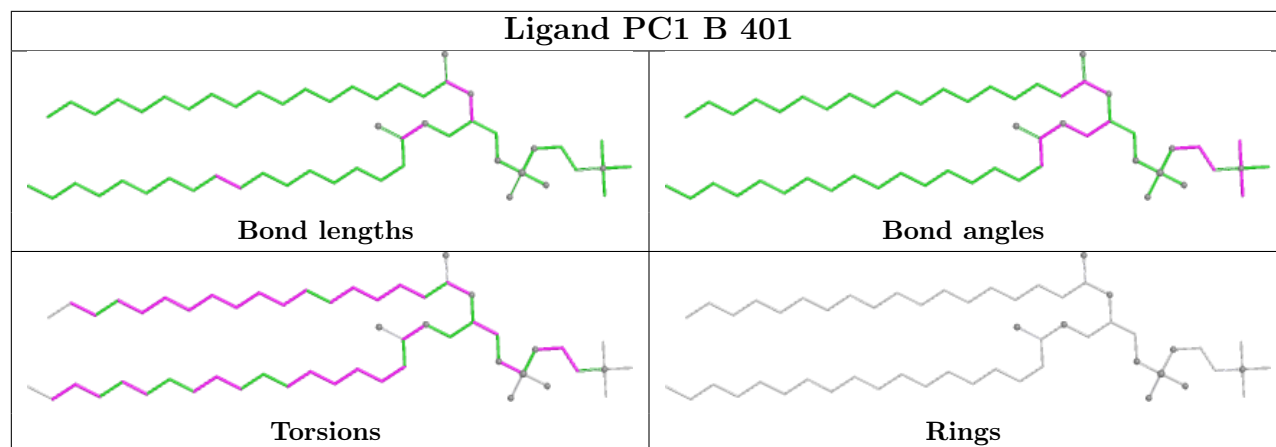
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

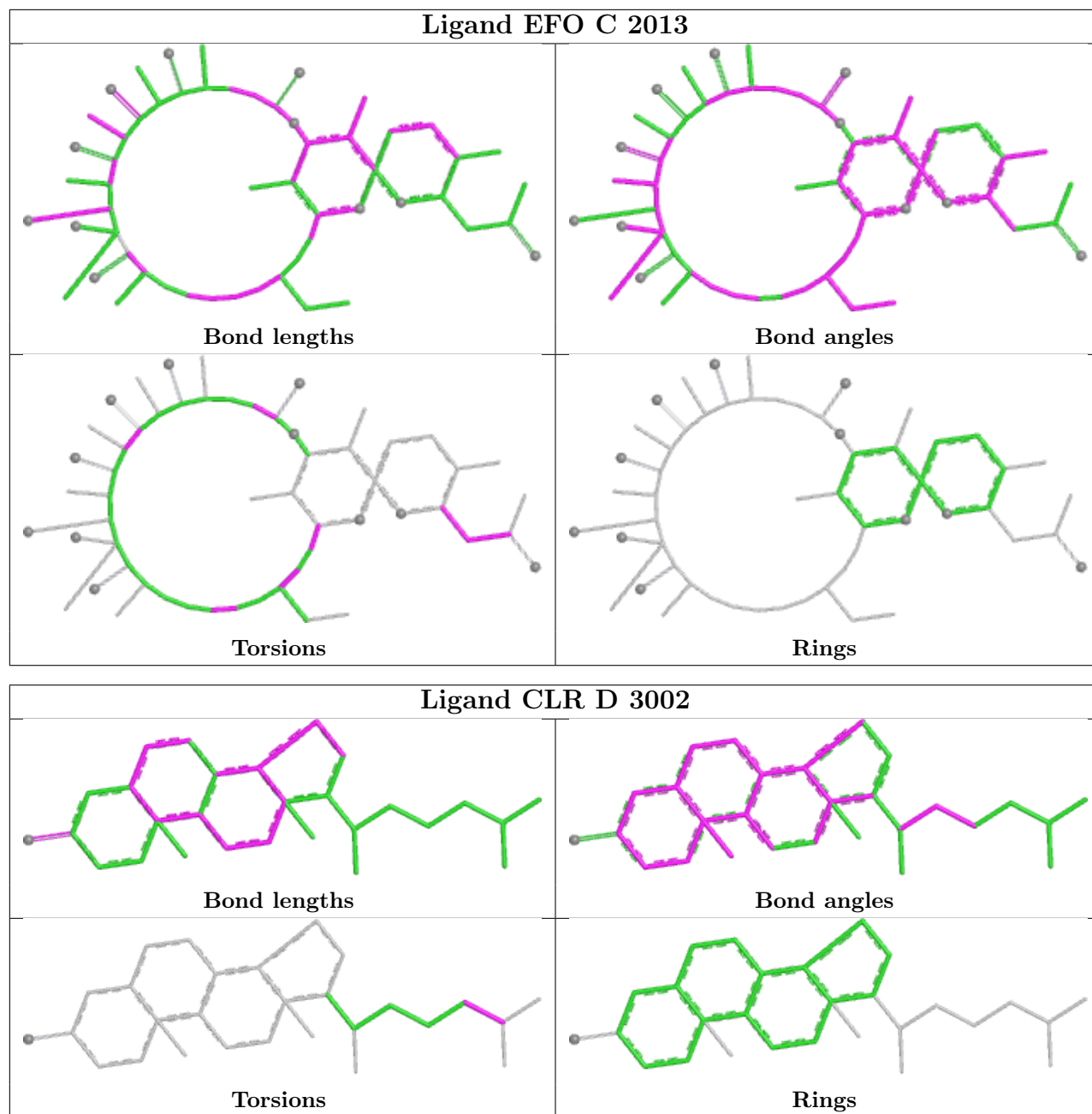


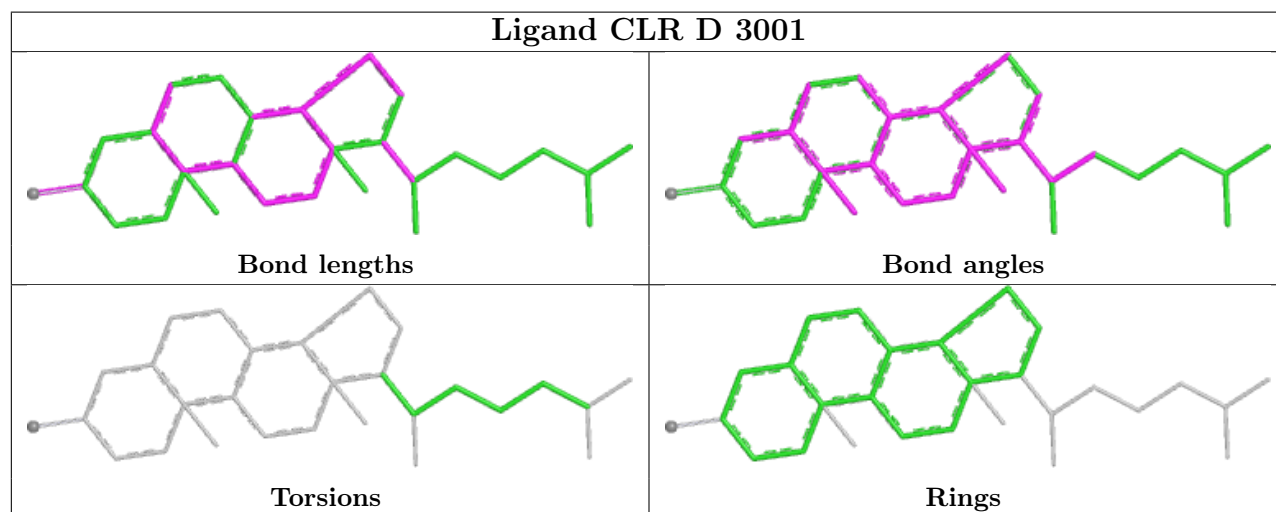
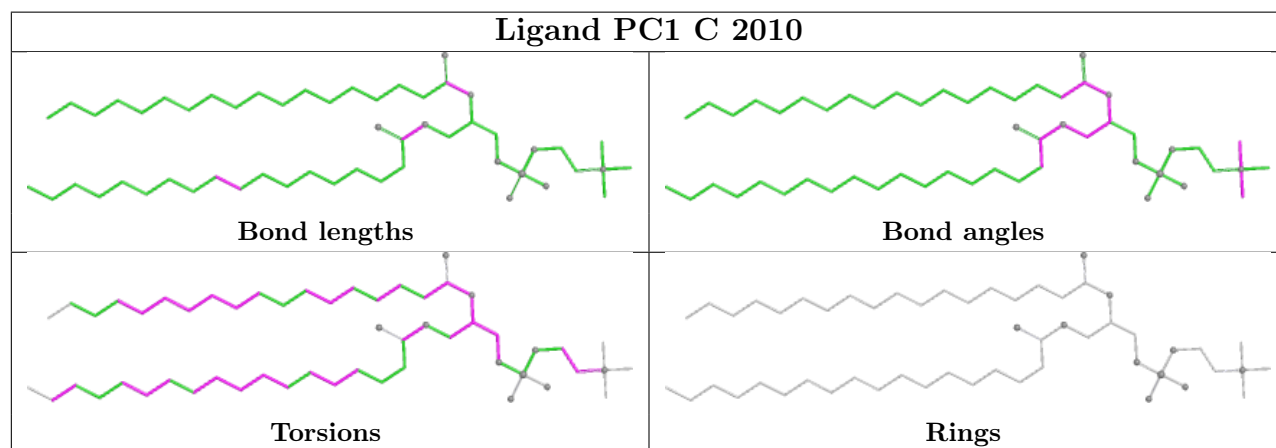
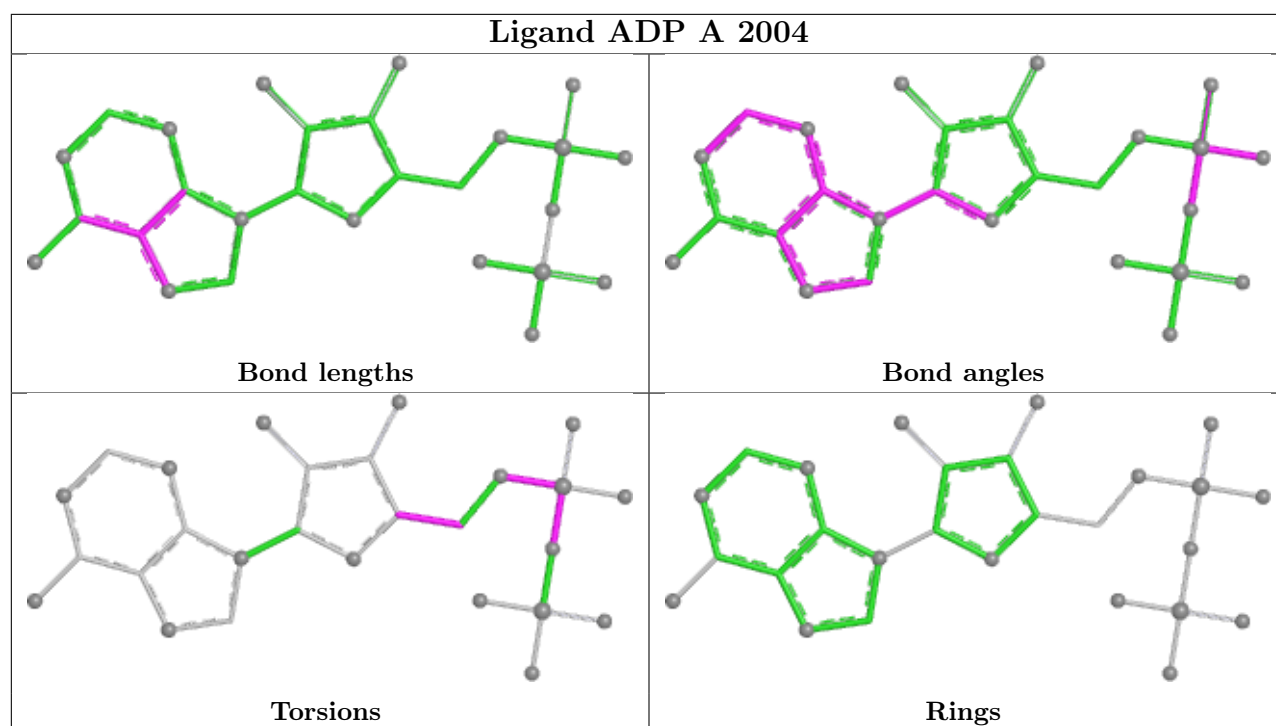
Ligand PC1 C 2012	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PC1 D 3003	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PC1 A 2011	
 Bond lengths	 Bond angles
 Torsions	 Rings











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	994/1016 (97%)	-0.55	11 (1%)	78	70	17, 57, 117, 181	0
1	C	994/1016 (97%)	-0.24	30 (3%)	52	42	34, 74, 143, 199	0
2	B	303/303 (100%)	0.68	29 (9%)	13	10	59, 130, 199, 229	0
2	D	303/303 (100%)	0.76	42 (13%)	6	5	68, 127, 205, 239	0
3	E	35/65 (53%)	0.14	1 (2%)	53	43	70, 88, 165, 168	0
3	G	34/65 (52%)	0.06	2 (5%)	28	21	75, 91, 164, 175	0
All	All	2663/2768 (96%)	-0.13	115 (4%)	40	31	17, 77, 161, 239	0

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	201	VAL	7.1
2	D	218	ASP	7.0
1	C	395	THR	6.6
2	D	166	THR	6.1
2	D	196	LEU	5.6
3	G	16	VAL	5.4
2	D	167	TYR	5.4
3	E	16	VAL	5.3
2	B	266	LEU	5.0
2	D	201	VAL	4.8
1	A	270	LEU	4.7
1	A	265	THR	4.5
1	C	396	THR	4.4
2	D	2	ALA	4.3
2	B	217	ARG	4.3
2	B	166	THR	4.2
2	D	266	LEU	4.0
2	B	15	PHE	3.8
2	B	1	MET	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	267	ALA	3.8
1	C	398	ASN	3.6
2	B	23	GLU	3.5
1	C	121	ASP	3.5
2	D	162	LEU	3.3
2	B	2	ALA	3.3
1	A	268	SER	3.3
2	B	25	LEU	3.3
2	D	17	TRP	3.3
1	C	495	ARG	3.3
1	A	267	ALA	3.3
2	D	9	GLU	3.3
1	C	645	VAL	3.3
2	D	217	ARG	3.2
2	B	7	LYS	3.2
2	D	219	GLU	3.2
1	C	268	SER	3.2
2	D	197	GLU	3.1
2	B	167	TYR	3.0
2	B	197	GLU	3.0
2	B	6	ALA	3.0
2	D	1	MET	3.0
1	C	265	THR	3.0
1	C	28	LEU	2.9
1	A	395	THR	2.9
2	D	15	PHE	2.9
2	D	89	SER	2.9
1	A	82	TRP	2.9
1	A	400	SER	2.9
2	D	202	MET	2.8
2	D	16	ILE	2.8
2	D	192	LYS	2.8
2	B	202	MET	2.8
2	D	7	LYS	2.8
2	D	195	SER	2.8
1	C	270	LEU	2.7
2	B	16	ILE	2.7
2	D	82	GLN	2.7
2	B	227	MET	2.7
2	D	198	THR	2.7
1	C	264	ALA	2.6
2	D	200	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	266	LEU	2.6
1	A	264	ALA	2.6
2	B	198	THR	2.6
2	D	11	SER	2.6
2	B	192	LYS	2.5
1	C	78	THR	2.5
1	C	632	GLU	2.5
2	D	262	GLN	2.5
1	C	143	GLN	2.4
1	C	406	LYS	2.4
2	D	199	TYR	2.4
1	C	427	GLN	2.4
2	D	229	TYR	2.4
1	C	24	ASP	2.4
2	B	164	ASP	2.4
2	B	9	GLU	2.4
2	D	222	GLU	2.4
2	D	6	ALA	2.4
2	B	162	LEU	2.4
2	B	95	PRO	2.4
1	C	642	ASN	2.3
1	C	537	GLU	2.3
2	D	232	LEU	2.3
2	B	17	TRP	2.3
2	D	161	GLY	2.3
1	C	82	TRP	2.3
2	B	12	TRP	2.3
1	C	402	VAL	2.3
1	C	109	GLY	2.3
1	A	266	LEU	2.2
2	B	196	LEU	2.2
2	D	193	ASN	2.2
2	B	273	ARG	2.2
2	B	260	ALA	2.2
3	G	18	PRO	2.2
2	D	214	THR	2.2
1	A	495	ARG	2.1
2	D	163	ASN	2.1
2	B	301	VAL	2.1
1	C	393	ALA	2.1
2	D	73	ALA	2.1
1	C	648	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	650	PRO	2.1
2	D	236	PRO	2.1
2	D	203	LYS	2.1
1	C	108	TYR	2.1
1	C	84	LYS	2.1
2	D	126	CYS	2.1
1	C	311	LEU	2.1
2	D	215	GLY	2.0
1	A	94	SER	2.0
2	D	224	VAL	2.0
2	B	250	LEU	2.0
2	D	169	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	NAG	B	402	14/15	0.66	0.15	126,137,144,146	0
9	PC1	C	2012	54/54	0.68	0.16	79,133,162,185	0
9	PC1	A	2014	54/54	0.69	0.18	86,123,160,189	0
9	PC1	A	2012	54/54	0.76	0.17	61,117,163,176	0
11	NAG	D	3004	14/15	0.78	0.12	96,123,132,133	0
9	PC1	C	2010	54/54	0.79	0.14	68,101,143,205	0
7	NA	C	2006	1/1	0.80	0.08	83,83,83,83	0
10	EFO	C	2013	56/56	0.81	0.18	49,150,194,195	0
9	PC1	C	2011	54/54	0.81	0.20	77,117,163,173	0
9	PC1	B	401	54/54	0.81	0.15	61,90,146,170	0
9	PC1	A	2013	54/54	0.85	0.16	71,103,124,174	0

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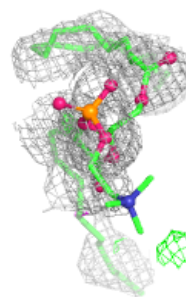
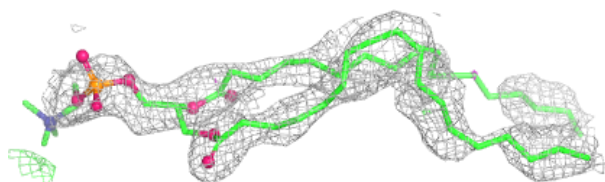
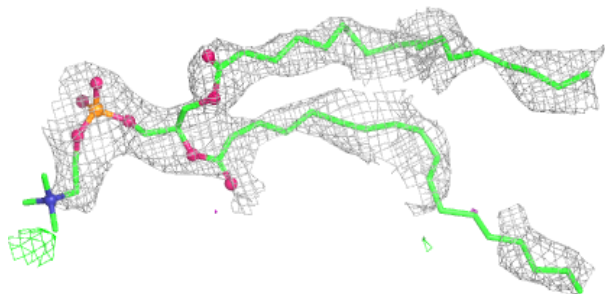
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	PC1	C	2009	54/54	0.86	0.14	59,107,140,145	0
7	NA	A	2006	1/1	0.86	0.08	65,65,65,65	0
9	PC1	D	3003	54/54	0.86	0.11	44,80,121,142	0
7	NA	A	2007	1/1	0.87	0.14	98,98,98,98	0
8	CLR	A	2010	28/28	0.87	0.14	60,98,131,138	0
10	EFO	A	2015	56/56	0.88	0.14	91,134,150,160	0
9	PC1	A	2011	54/54	0.89	0.14	57,97,128,130	0
8	CLR	G	101	28/28	0.89	0.11	54,91,100,131	0
8	CLR	A	2009	28/28	0.90	0.11	62,93,107,147	0
8	CLR	E	101	28/28	0.90	0.11	37,77,109,172	0
8	CLR	D	3002	28/28	0.91	0.13	13,97,131,141	0
7	NA	C	2008	1/1	0.92	0.08	46,46,46,46	0
7	NA	A	2008	1/1	0.92	0.11	59,59,59,59	0
8	CLR	D	3001	28/28	0.94	0.10	35,83,89,92	0
7	NA	A	2005	1/1	0.95	0.04	95,95,95,95	0
4	MG	A	2001	1/1	0.95	0.13	61,61,61,61	0
7	NA	C	2007	1/1	0.96	0.05	77,77,77,77	0
7	NA	C	2005	1/1	0.96	0.06	103,103,103,103	0
6	ADP	C	2004	27/27	0.98	0.05	31,47,57,60	0
6	ADP	A	2004	27/27	0.99	0.04	10,23,38,47	0
4	MG	A	2003	1/1	0.99	0.05	15,15,15,15	0
4	MG	C	2001	1/1	0.99	0.11	54,54,54,54	0
4	MG	C	2003	1/1	0.99	0.03	51,51,51,51	0
5	ALF	A	2002	5/5	0.99	0.04	14,14,28,29	0
5	ALF	C	2002	5/5	1.00	0.04	20,24,71,106	0

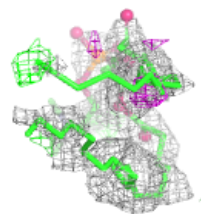
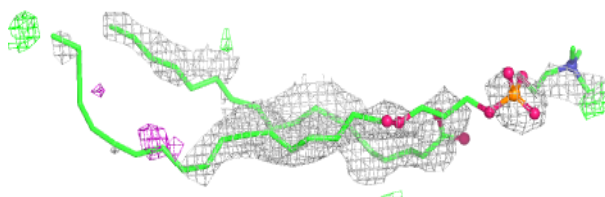
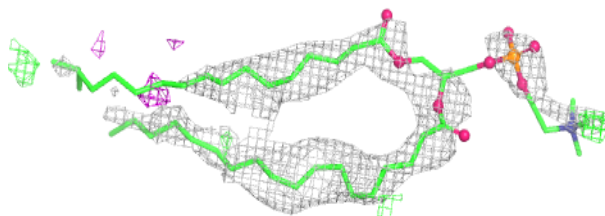
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PC1 C 2012:

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

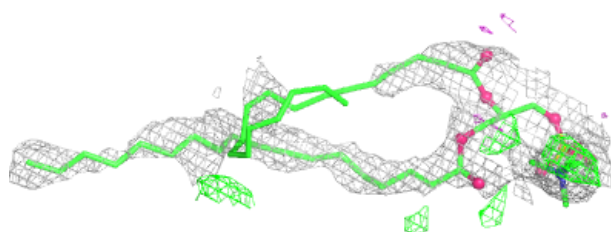
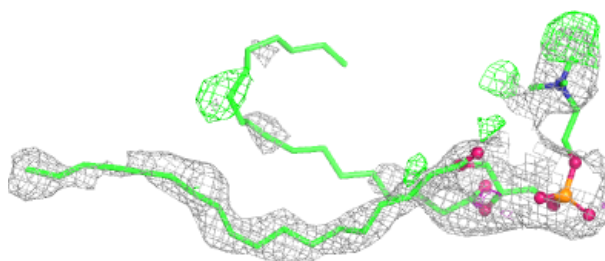
**Electron density around PC1 A 2014:**

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

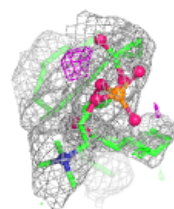
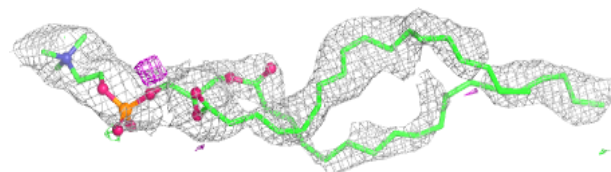


Electron density around PC1 A 2012:

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

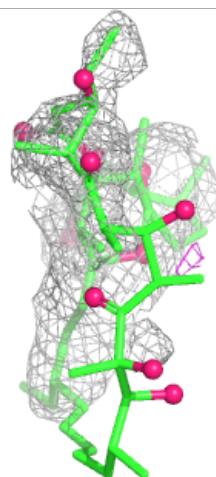
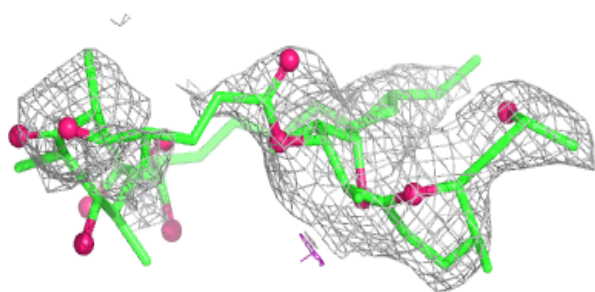
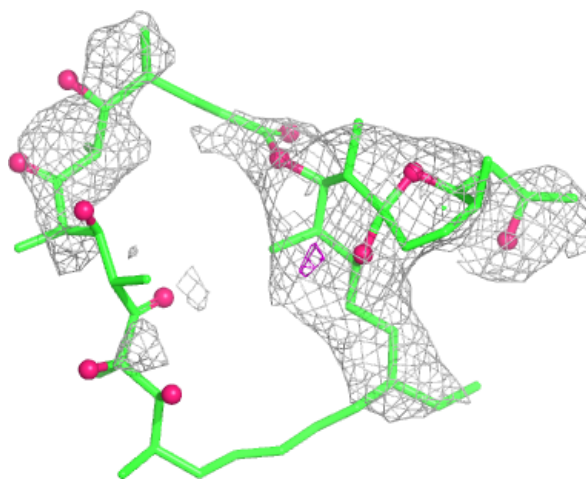
**Electron density around PC1 C 2010:**

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



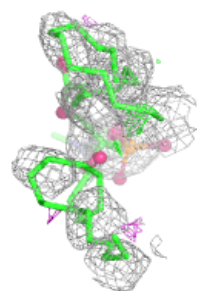
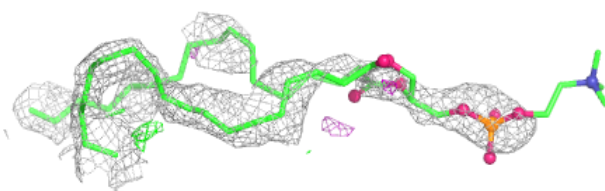
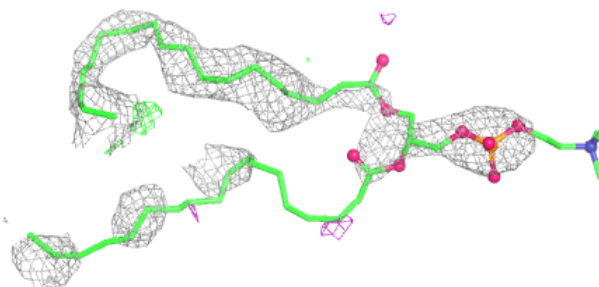
Electron density around EFO C 2013:

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

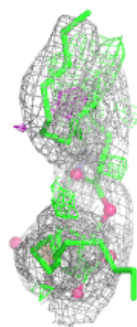
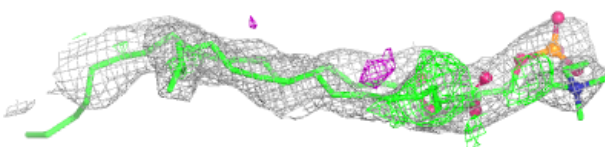
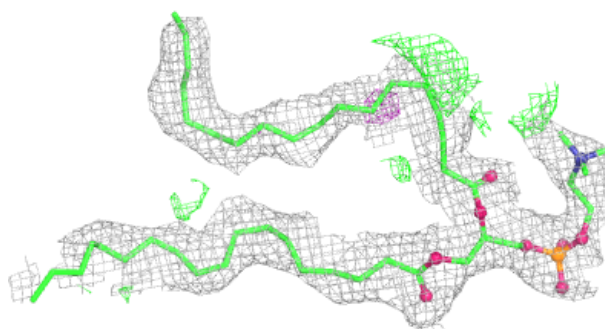


Electron density around PC1 C 2011:

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

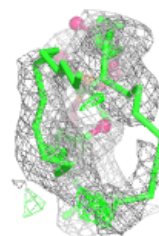
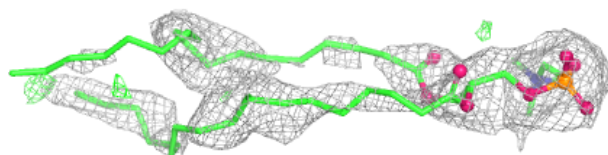
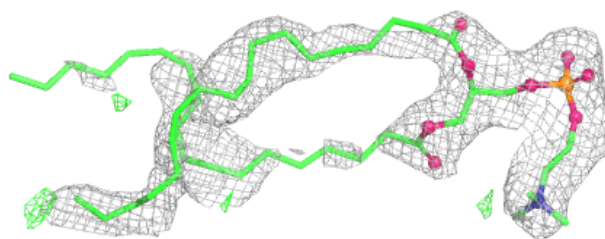
**Electron density around PC1 B 401:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

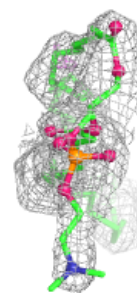
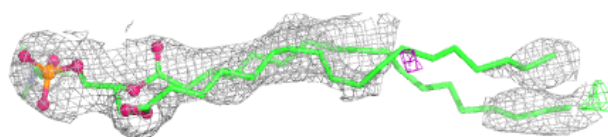
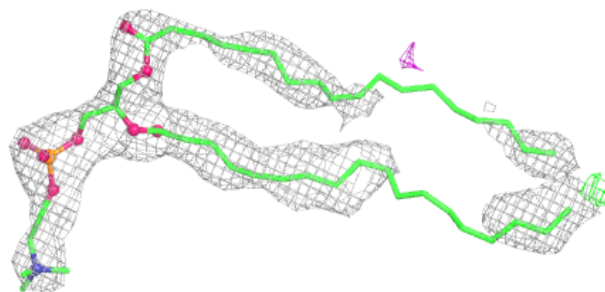


Electron density around PC1 A 2013:

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

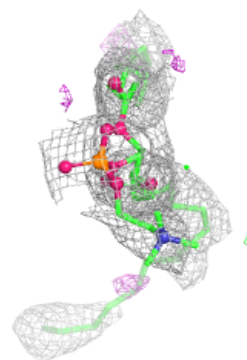
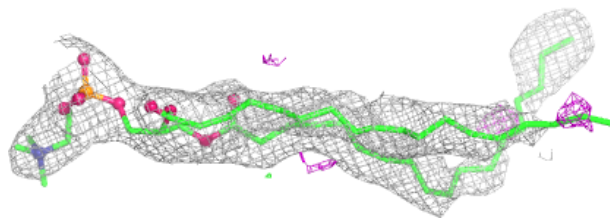
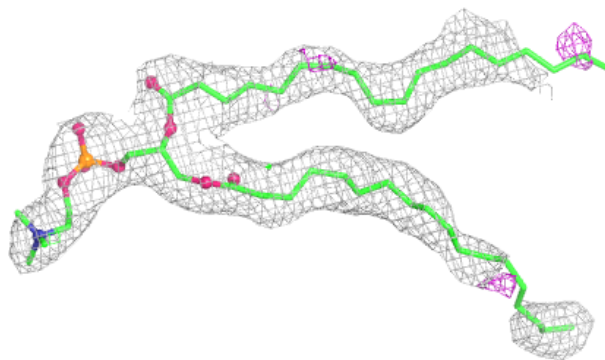
**Electron density around PC1 C 2009:**

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

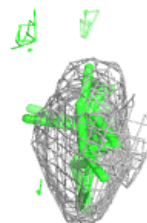
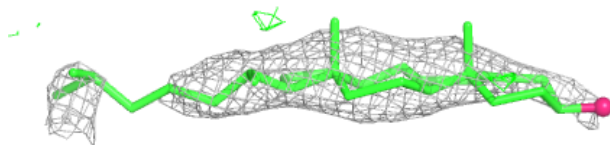


Electron density around PC1 D 3003:

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

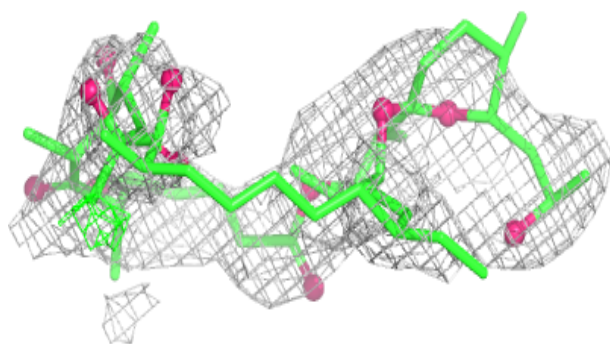
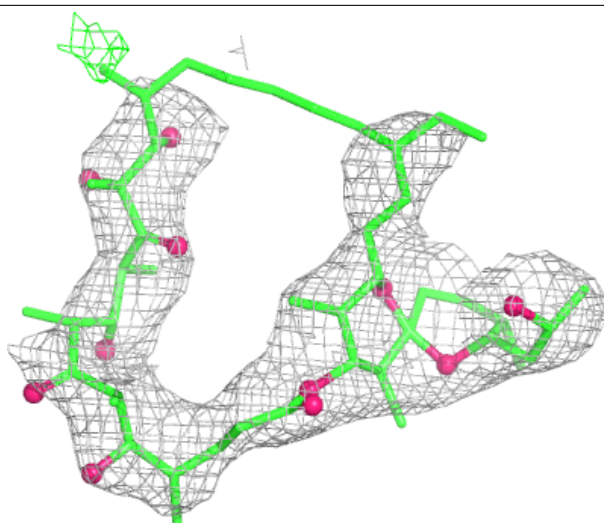
**Electron density around CLR A 2010:**

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



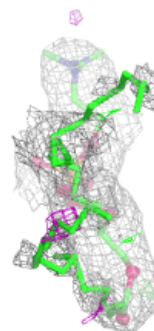
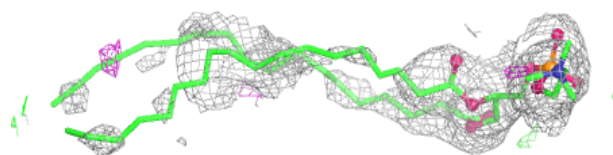
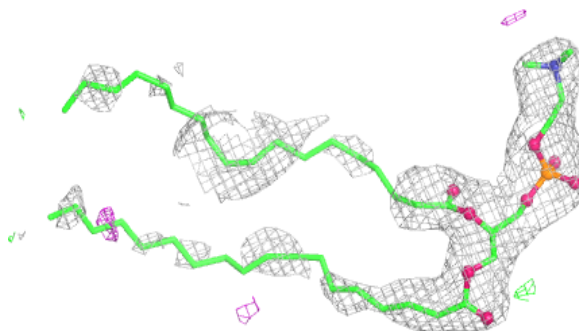
Electron density around EFO A 2015:

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

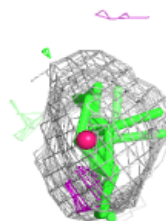
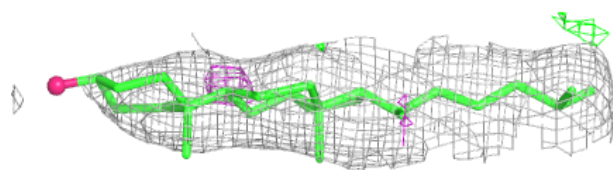
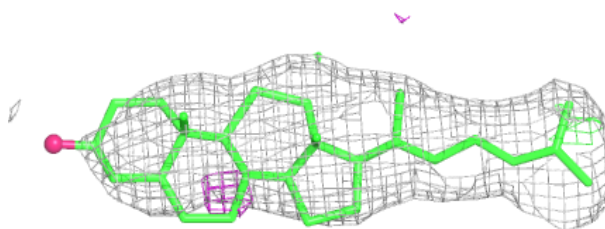


Electron density around PC1 A 2011:

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

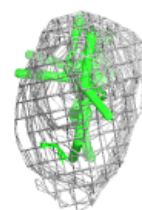
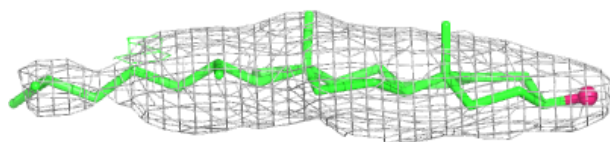
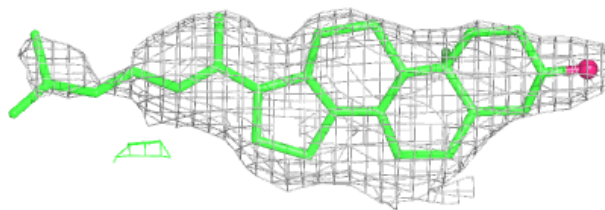
**Electron density around CLR G 101:**

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

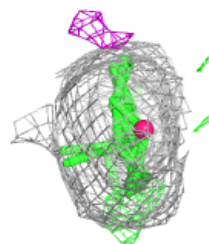
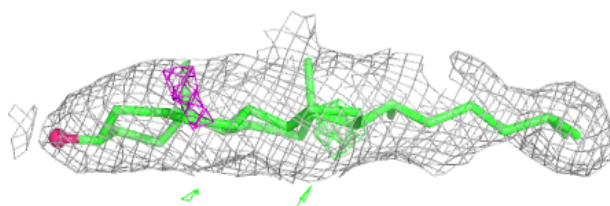
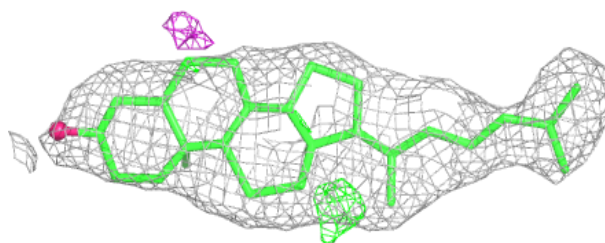


Electron density around CLR A 2009:

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

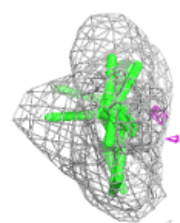
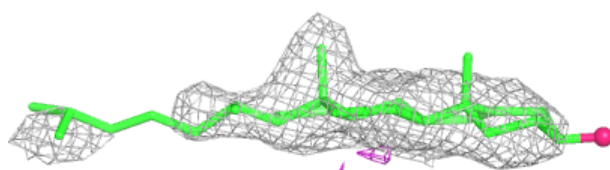
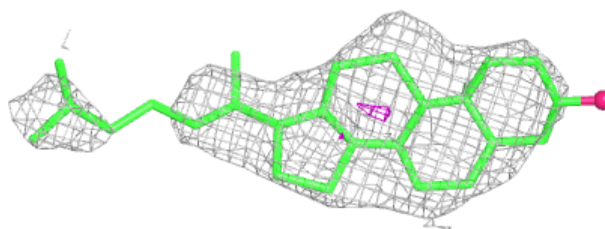
**Electron density around CLR E 101:**

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

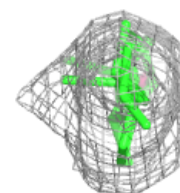
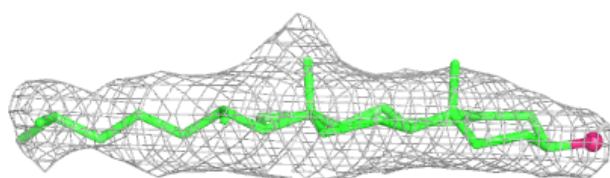
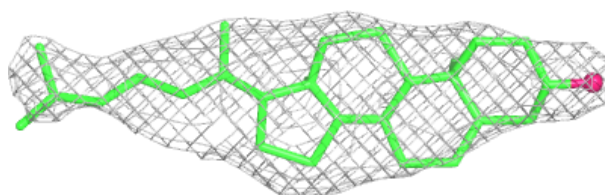


Electron density around CLR D 3002:

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

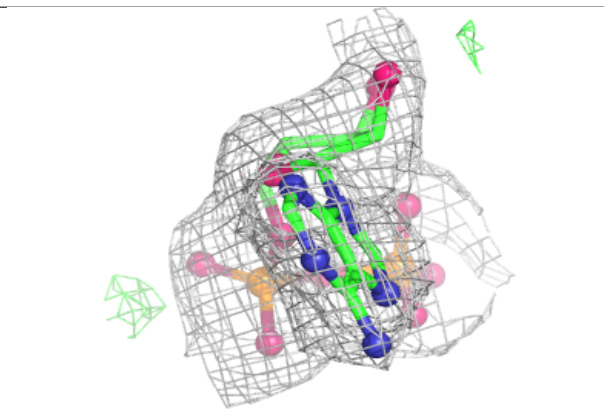
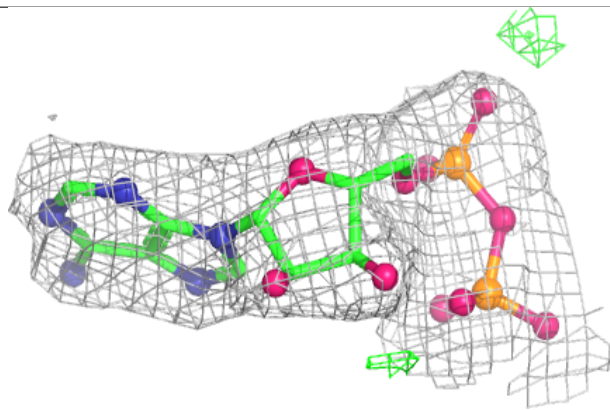
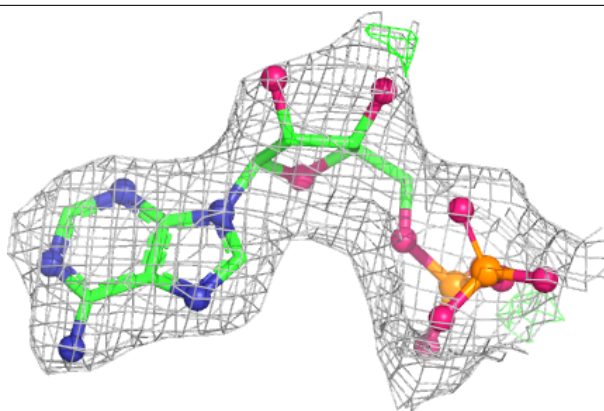
**Electron density around CLR D 3001:**

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

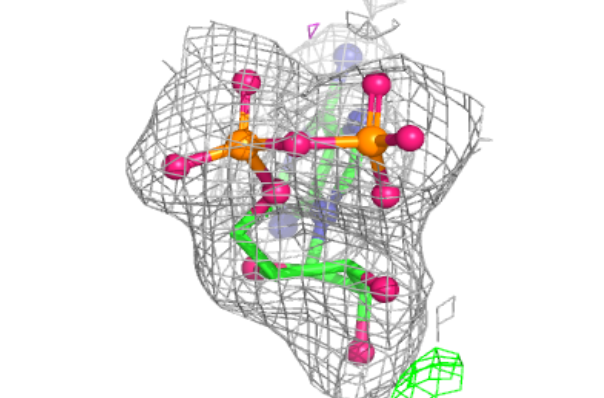
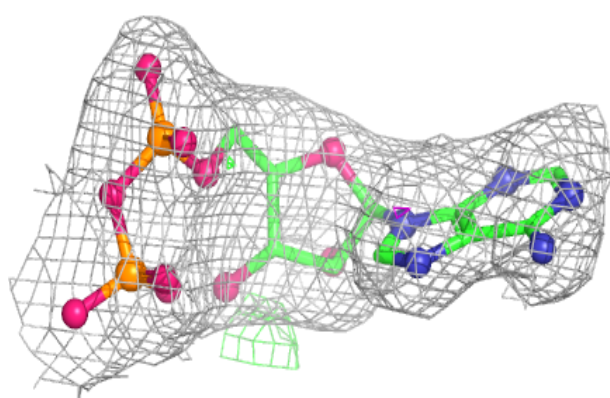
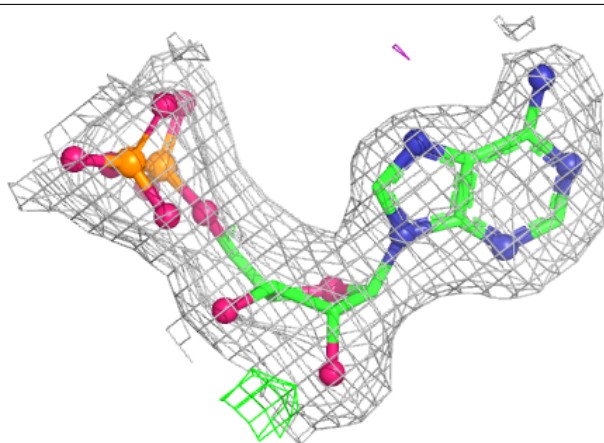


Electron density around ADP C 2004:

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

**Electron density around ADP A 2004:**

$2mF_o - DF_c$ (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.