



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:10 PM UTC

PDB ID : 1IK3 / pdb_00001ik3
Title : LIPOXYGENASE-3 (SOYBEAN) COMPLEX WITH 13(S)-HYDROPEROXY-9(Z),11(E)-OCTADECADIENOIC ACID
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Deposited on : 2001-05-01
Resolution : 2.00 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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

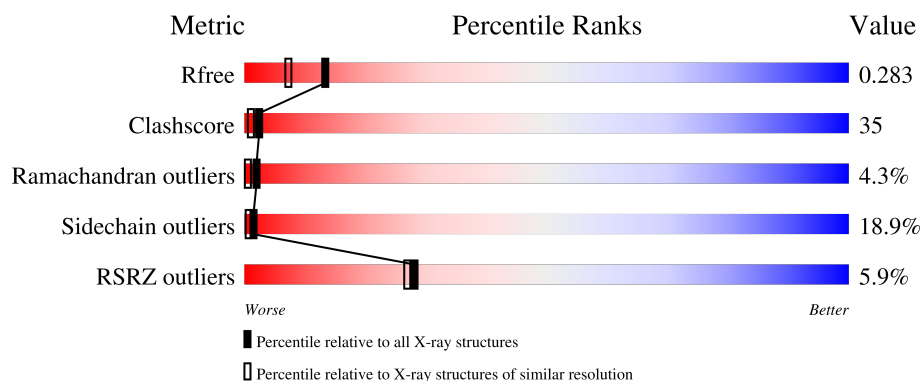
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	857	

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
3	13S	A	1859[A]	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7314 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.

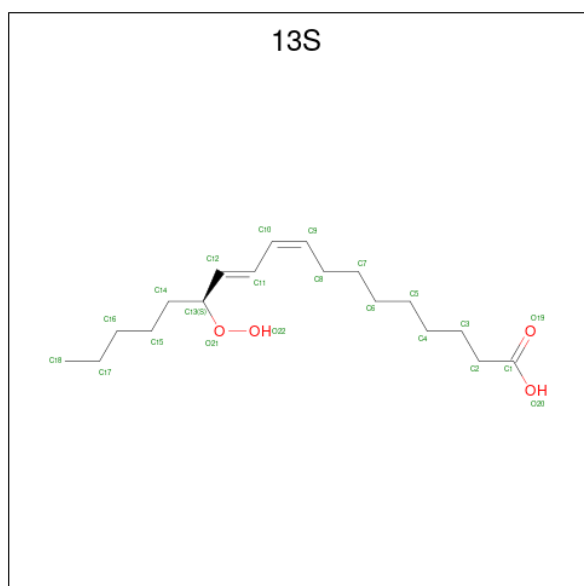
- Molecule 1 is a protein called LIPOXYGENASE-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	836	Total	C	N	O	S	0	0	0
			6696	4278	1149	1251	18			

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

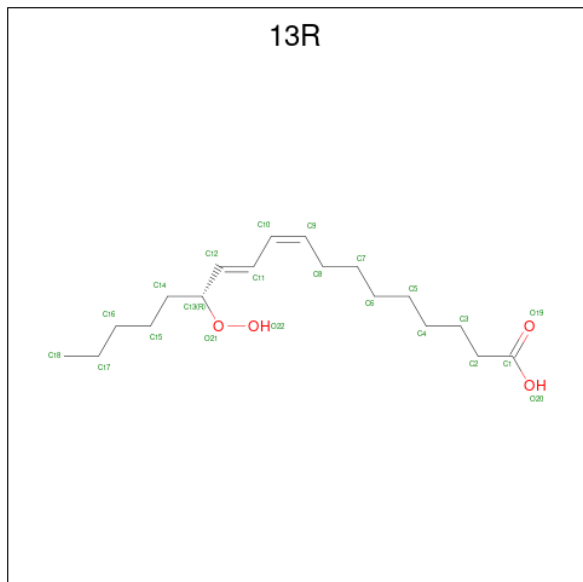
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		

- Molecule 3 is 13(S)-HYDROPEROXY-9(Z),11(E)-OCTADECADIENOIC ACID (CCD ID: 13S) (formula: C₁₈H₃₂O₄).



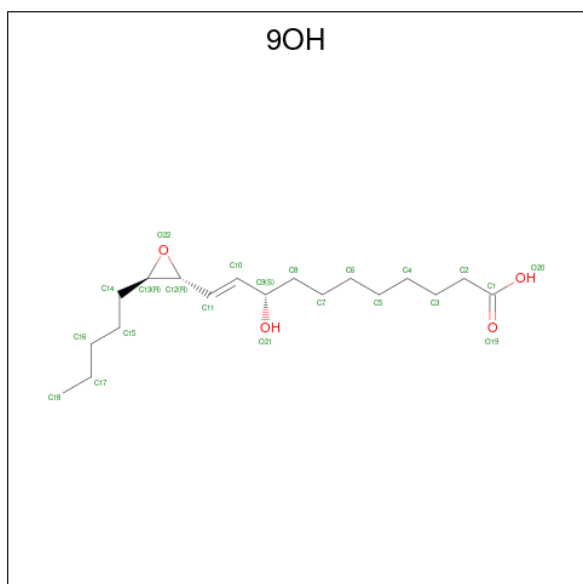
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			22	18	4		

- Molecule 4 is 13(R)-HYDROPEROXY-9(Z),11(E)-OCTADECADIENOIC ACID (CCD ID: 13R) (formula: C₁₈H₃₂O₄).



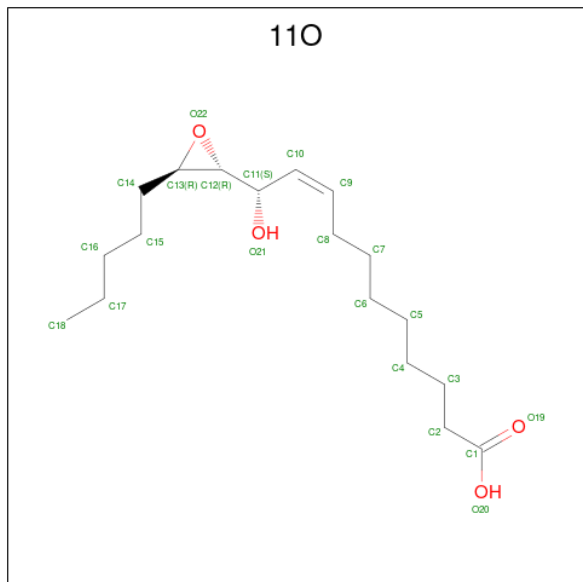
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	22	1
			22	18	4		

- Molecule 5 is (TRANS-12,13-EPOXY)-9-HYDROXY-10(E)-OCTADECENOIC ACID (CCD ID: 9OH) (formula: C₁₈H₃₂O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	22	1
			22	18	4		

- Molecule 6 is (TRANS-12,13-EPOXY)-11-HYDROXY-9(Z)-OCTADECENOIC ACID (CCD ID: 11O) (formula: C₁₈H₃₂O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	22	1
			22	18	4		

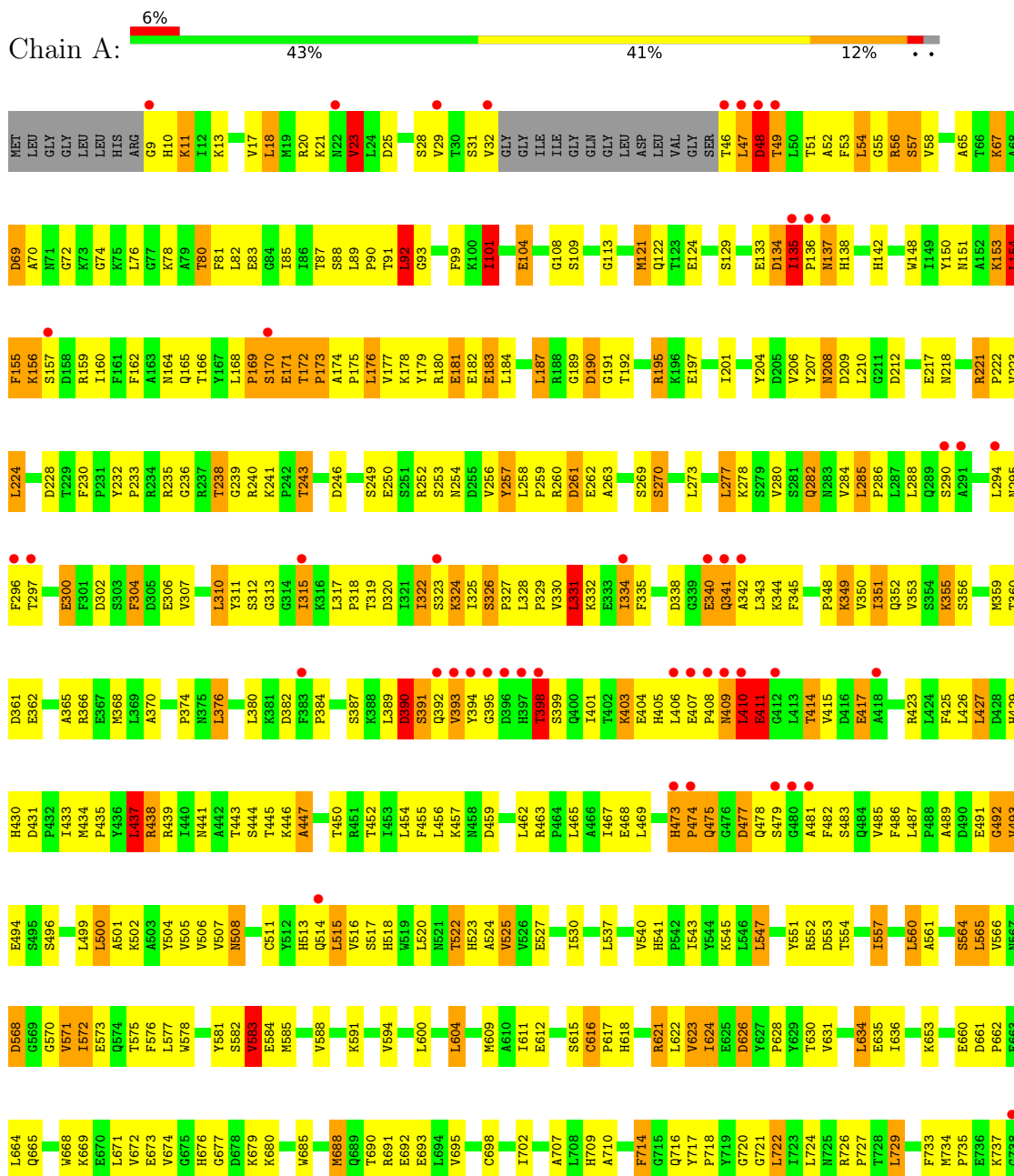
- Molecule 7 is water.

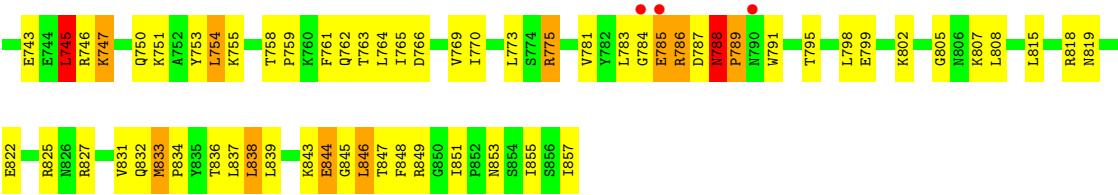
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	529	Total	O	0	0
			529	529		

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: LIPOXYGENASE-3





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.65Å 137.28Å 61.89Å 90.00° 95.56° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 40.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	84.0 (40.00-2.00) 65.4 (40.00-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.92 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.196 , 0.296 0.196 , 0.283	Depositor DCC
R_{free} test set	4949 reflections (10.16%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 106.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7314	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.85% 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: 13R, FE, 9OH, 13S, 11O

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	0.46	0/6867	1.03	38/9326 (0.4%)

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	THR	N-CA-C	-10.20	100.58	113.23
1	A	171	GLU	N-CA-C	-8.70	103.20	113.38
1	A	238	THR	N-CA-C	-7.91	95.62	109.06
1	A	170	SER	N-CA-C	-7.84	102.14	112.34
1	A	121	MET	N-CA-C	7.24	121.69	113.01
1	A	23	VAL	N-CA-C	-7.21	106.46	113.53
1	A	361	ASP	N-CA-C	-7.09	103.56	111.71
1	A	450	THR	N-CA-C	7.00	120.88	110.52
1	A	623	VAL	N-CA-C	-6.87	98.42	108.87
1	A	197	GLU	N-CA-C	6.70	119.44	111.33
1	A	583	VAL	N-CA-C	6.59	117.38	110.72
1	A	491	GLU	N-CA-C	6.58	120.24	109.85
1	A	714	PHE	N-CA-C	6.57	121.13	113.18
1	A	474	PRO	N-CA-C	-6.57	104.60	113.40
1	A	129	SER	N-CA-C	6.30	117.80	108.60
1	A	745	LEU	N-CA-C	-6.29	104.42	111.28
1	A	154	LEU	N-CA-C	6.29	120.56	113.02
1	A	155	PHE	N-CA-C	6.24	121.29	113.43
1	A	437	LEU	N-CA-C	6.19	117.70	111.07
1	A	431	ASP	N-CA-C	6.02	120.94	112.75
1	A	376	LEU	N-CA-C	6.01	120.81	112.45
1	A	524	ALA	N-CA-C	5.97	117.46	111.07
1	A	398	THR	N-CA-C	5.75	123.04	110.80
1	A	552	ARG	N-CA-C	5.54	118.61	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	VAL	N-CA-C	5.45	120.49	113.07
1	A	500	LEU	N-CA-C	-5.43	105.78	112.90
1	A	391	SER	N-CA-C	5.38	119.59	113.19
1	A	228	ASP	N-CA-C	5.33	117.09	111.28
1	A	165	GLN	N-CA-C	5.20	117.76	109.96
1	A	392	GLN	N-CA-C	-5.19	103.69	110.53
1	A	447	ALA	N-CA-C	5.18	117.28	109.41
1	A	616	CYS	N-CA-C	5.14	116.98	109.84
1	A	707	ALA	N-CA-C	5.09	116.82	111.28
1	A	304	PHE	N-CA-C	-5.03	105.98	111.82
1	A	212	ASP	CA-C-N	5.02	124.81	119.28
1	A	212	ASP	C-N-CA	5.02	124.81	119.28
1	A	616	CYS	CA-C-N	5.02	126.12	119.84
1	A	616	CYS	C-N-CA	5.02	126.12	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6696	0	6615	470	0
2	A	1	0	0	0	0
3	A	22	0	30	20	0
4	A	22	0	30	0	0
5	A	22	0	29	0	0
6	A	22	0	31	0	0
7	A	529	0	0	63	0
All	All	7314	0	6735	470	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 35.

All (470) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:TYR:HB3	1:A:481:ALA:HB2	1.23	1.15
1:A:788:ASN:HB2	1:A:789:PRO:HD3	1.26	1.09
1:A:389:LEU:HD13	1:A:394:TYR:HE2	1.16	1.03
1:A:243:THR:HG22	1:A:246:ASP:O	1.60	1.02
1:A:734:MET:HE3	1:A:735:PRO:HD2	1.42	1.00
1:A:785:GLU:O	1:A:785:GLU:HG3	1.60	1.00
1:A:847:THR:HG22	1:A:849:ARG:HG2	1.49	0.95
1:A:315:ILE:HG23	1:A:343:LEU:HB3	1.48	0.93
1:A:514:GLN:HE22	1:A:515:LEU:HD23	1.34	0.93
1:A:604:LEU:HD21	1:A:630:THR:HG23	1.50	0.93
1:A:387:SER:HB3	1:A:395:GLY:HA2	1.47	0.93
1:A:518:HIS:HD1	3:A:1859[A]:13S:H81	1.31	0.92
1:A:169:PRO:HG3	1:A:661:ASP:OD1	1.70	0.92
1:A:389:LEU:HD13	1:A:394:TYR:CE2	2.06	0.90
1:A:349:LYS:HB3	1:A:833:MET:HE3	1.53	0.89
1:A:584:GLU:HG3	7:A:971:HOH:O	1.71	0.89
1:A:514:GLN:NE2	1:A:515:LEU:HD23	1.90	0.87
1:A:611:ILE:HD11	1:A:621:ARG:HD2	1.57	0.86
1:A:135:ILE:HG23	1:A:136:PRO:HD3	1.57	0.85
1:A:581:TYR:HB2	1:A:585:MET:HE2	1.60	0.84
1:A:514:GLN:HB2	3:A:1859[A]:13S:H61	1.59	0.84
1:A:690:THR:HG22	1:A:692:GLU:H	1.42	0.84
1:A:394:TYR:HB3	1:A:481:ALA:CB	2.06	0.83
1:A:578:TRP:HB3	1:A:585:MET:HE3	1.59	0.83
1:A:438:ARG:HG2	1:A:473:HIS:CE1	2.14	0.82
1:A:788:ASN:HB2	1:A:789:PRO:CD	2.07	0.82
1:A:775:ARG:HG3	1:A:775:ARG:HH11	1.43	0.82
1:A:169:PRO:HD3	1:A:541:HIS:CE1	2.14	0.81
1:A:238:THR:HG23	1:A:250:GLU:OE2	1.82	0.80
1:A:775:ARG:NH1	1:A:846:LEU:HD13	1.98	0.79
1:A:447:ALA:HB2	1:A:577:LEU:HD11	1.64	0.79
1:A:502:LYS:HB2	7:A:1283:HOH:O	1.81	0.78
1:A:169:PRO:HG3	1:A:661:ASP:CG	2.08	0.78
1:A:169:PRO:HG2	7:A:934:HOH:O	1.83	0.77
1:A:235:ARG:HH12	1:A:238:THR:HG22	1.50	0.77
1:A:408:PRO:O	1:A:409:ASN:HB3	1.84	0.77
1:A:511:CYS:O	1:A:514:GLN:HG3	1.84	0.76
1:A:522:THR:HG21	1:A:709:HIS:CD2	2.20	0.76
1:A:304:PHE:H	1:A:750:GLN:NE2	1.84	0.76
1:A:611:ILE:HD11	1:A:621:ARG:HH21	1.51	0.75
1:A:831:VAL:HG13	1:A:833:MET:HB2	1.69	0.74
1:A:135:ILE:HG12	1:A:136:PRO:N	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:819:ASN:HD22	1:A:827:ARG:HE	1.35	0.74
1:A:10:HIS:CD2	1:A:11:LYS:H	2.06	0.74
1:A:57:SER:HB2	7:A:1348:HOH:O	1.86	0.74
1:A:384:PRO:HD2	1:A:398:THR:HG21	1.68	0.74
1:A:729:LEU:HD11	1:A:758:THR:HG23	1.70	0.73
1:A:438:ARG:HH22	1:A:439:ARG:NH2	1.86	0.72
1:A:224:LEU:HD12	1:A:230:PHE:HB3	1.70	0.72
1:A:819:ASN:ND2	1:A:827:ARG:HE	1.86	0.72
1:A:46:THR:C	1:A:48:ASP:H	1.97	0.72
1:A:172:THR:HB	1:A:173:PRO:HD3	1.72	0.72
1:A:578:TRP:HB3	1:A:585:MET:CE	2.20	0.72
1:A:124:GLU:HB2	7:A:1385:HOH:O	1.89	0.72
1:A:169:PRO:O	1:A:171:GLU:HG2	1.89	0.72
1:A:522:THR:HG22	1:A:523:HIS:N	2.04	0.72
1:A:401:ILE:HD11	1:A:468:GLU:HB2	1.72	0.71
1:A:260:ARG:O	1:A:261:ASP:HB2	1.89	0.71
1:A:326:SER:H	1:A:327:PRO:HD2	1.56	0.71
1:A:438:ARG:HG3	7:A:939:HOH:O	1.89	0.71
1:A:525:VAL:HG23	7:A:1375:HOH:O	1.88	0.71
1:A:254:ASN:HB2	7:A:1181:HOH:O	1.90	0.71
1:A:836:THR:HG23	1:A:848:PHE:O	1.90	0.71
1:A:622:LEU:HD21	1:A:630:THR:HG21	1.70	0.70
1:A:284:VAL:O	1:A:288:LEU:HB2	1.91	0.70
1:A:25:ASP:O	1:A:29:VAL:HG23	1.90	0.70
1:A:492:GLY:HA3	7:A:1254:HOH:O	1.91	0.70
1:A:121:MET:O	1:A:122:GLN:HB2	1.89	0.69
1:A:151:ASN:OD1	1:A:153:LYS:HB2	1.92	0.69
1:A:518:HIS:ND1	3:A:1859[A]:13S:H81	2.06	0.69
1:A:160:ILE:CG2	1:A:183:GLU:HG3	2.22	0.69
1:A:277:LEU:HD23	3:A:1859[A]:13S:H182	1.75	0.69
1:A:403:LYS:HE2	1:A:404:GLU:HB3	1.74	0.69
1:A:847:THR:CG2	1:A:849:ARG:HG2	2.22	0.69
1:A:566:VAL:HG22	1:A:583:VAL:CG2	2.23	0.68
1:A:565:LEU:HD12	1:A:571:VAL:HG21	1.75	0.68
1:A:360:THR:HG22	1:A:362:GLU:H	1.58	0.68
1:A:690:THR:HG22	1:A:692:GLU:N	2.08	0.68
1:A:455:PHE:HB2	1:A:465:LEU:HD22	1.74	0.68
1:A:408:PRO:HD2	1:A:463:ARG:HH22	1.59	0.68
1:A:142:HIS:HB2	7:A:997:HOH:O	1.94	0.67
1:A:661:ASP:O	1:A:665:GLN:HG2	1.94	0.67
1:A:581:TYR:CB	1:A:585:MET:HE2	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:836:THR:OG1	1:A:839:LEU:HD22	1.95	0.67
1:A:317:LEU:O	1:A:341:GLN:HA	1.95	0.66
1:A:360:THR:CG2	1:A:362:GLU:HB2	2.25	0.66
1:A:315:ILE:HB	7:A:1114:HOH:O	1.95	0.66
1:A:438:ARG:HH22	1:A:439:ARG:HH21	1.43	0.66
1:A:783:LEU:O	1:A:785:GLU:N	2.29	0.66
1:A:522:THR:HG21	1:A:709:HIS:HD2	1.60	0.66
1:A:387:SER:OG	1:A:389:LEU:HD12	1.97	0.65
1:A:764:LEU:HD22	7:A:1360:HOH:O	1.96	0.65
1:A:65:ALA:HB2	1:A:113:GLY:HA3	1.77	0.65
1:A:172:THR:HB	1:A:173:PRO:CD	2.27	0.65
1:A:734:MET:SD	7:A:1225:HOH:O	2.55	0.65
1:A:170:SER:C	1:A:172:THR:H	2.04	0.65
1:A:668:TRP:O	1:A:672:VAL:HG23	1.96	0.64
1:A:504:TYR:O	1:A:507:VAL:HG12	1.98	0.64
1:A:454:LEU:HB2	7:A:1248:HOH:O	1.97	0.64
1:A:166:THR:HB	1:A:545:LYS:HE3	1.80	0.64
1:A:446:LYS:HD2	1:A:733:PHE:CE2	2.33	0.63
1:A:441:ASN:HD21	1:A:447:ALA:H	1.47	0.63
1:A:51:THR:HA	1:A:54:LEU:HD22	1.81	0.62
1:A:547:LEU:HD21	7:A:1311:HOH:O	1.99	0.62
1:A:243:THR:HG23	1:A:246:ASP:H	1.65	0.61
1:A:511:CYS:HG	1:A:578:TRP:CG	2.19	0.61
1:A:604:LEU:HD21	1:A:630:THR:CG2	2.28	0.61
1:A:425:PHE:HB2	7:A:1248:HOH:O	1.99	0.61
1:A:18:LEU:HD21	1:A:99:PHE:HE2	1.65	0.61
1:A:394:TYR:CB	1:A:481:ALA:HB2	2.15	0.61
1:A:716:GLN:OE1	3:A:1859[A]:13S:H51	2.01	0.61
1:A:514:GLN:HE22	1:A:515:LEU:CD2	2.10	0.60
1:A:530:ILE:HB	7:A:1245:HOH:O	2.01	0.60
1:A:566:VAL:CG2	1:A:583:VAL:HG22	2.32	0.60
1:A:788:ASN:CB	1:A:789:PRO:HD3	2.17	0.60
1:A:583:VAL:HG23	7:A:1193:HOH:O	2.02	0.60
1:A:571:VAL:HB	7:A:935:HOH:O	2.01	0.60
1:A:300:GLU:HG2	7:A:1222:HOH:O	2.01	0.60
1:A:408:PRO:HD2	1:A:463:ARG:NH2	2.16	0.59
1:A:170:SER:C	1:A:172:THR:N	2.59	0.59
1:A:775:ARG:HG3	1:A:775:ARG:NH1	2.14	0.59
1:A:350:VAL:HG13	1:A:351:ILE:HG23	1.84	0.59
1:A:243:THR:CG2	1:A:246:ASP:H	2.16	0.59
1:A:319:THR:HG23	1:A:340:GLU:CD	2.27	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:VAL:C	1:A:332:LYS:H	2.10	0.59
1:A:565:LEU:HD21	3:A:1859[A]:13S:H152	1.84	0.58
1:A:273:LEU:HD13	1:A:857:ILE:HD13	1.83	0.58
1:A:360:THR:CG2	1:A:362:GLU:OE1	2.51	0.58
1:A:374:PRO:HD2	7:A:1210:HOH:O	2.02	0.58
1:A:857:ILE:O	3:A:1859[A]:13S:H162	2.02	0.58
1:A:360:THR:HG21	1:A:362:GLU:HB2	1.86	0.58
1:A:221:ARG:HG2	7:A:1191:HOH:O	2.03	0.58
1:A:576:PHE:HZ	3:A:1859[A]:13S:H41	1.68	0.58
1:A:588:VAL:O	1:A:591:LYS:HB2	2.04	0.58
1:A:410:LEU:HD21	1:A:457:LYS:HD2	1.86	0.57
1:A:766:ASP:O	1:A:770:ILE:HG12	2.05	0.57
1:A:104:GLU:HB2	7:A:1083:HOH:O	2.02	0.57
1:A:403:LYS:HB2	1:A:415:VAL:HG21	1.86	0.57
1:A:566:VAL:HG22	1:A:583:VAL:HG22	1.86	0.57
1:A:91:THR:O	1:A:92:LEU:O	2.23	0.57
1:A:530:ILE:HD12	7:A:1242:HOH:O	2.04	0.57
1:A:349:LYS:HA	1:A:352:GLN:HG3	1.86	0.57
1:A:691:ARG:O	1:A:695:VAL:HG23	2.05	0.57
1:A:136:PRO:O	1:A:138:HIS:N	2.37	0.57
1:A:515:LEU:HD21	1:A:582:SER:HB3	1.87	0.57
1:A:561:ALA:HA	1:A:565:LEU:CD2	2.35	0.57
1:A:312:SER:O	1:A:344:LYS:HD3	2.05	0.57
1:A:514:GLN:HG2	1:A:576:PHE:CD1	2.39	0.56
1:A:843:LYS:O	1:A:844:GLU:CB	2.52	0.56
1:A:56:ARG:HG2	1:A:81:PHE:CE2	2.40	0.56
1:A:171:GLU:HA	1:A:180:ARG:HH11	1.71	0.56
1:A:9:GLY:O	1:A:10:HIS:HB2	2.03	0.56
1:A:441:ASN:HD22	1:A:446:LYS:HA	1.70	0.56
1:A:169:PRO:C	1:A:171:GLU:N	2.62	0.56
1:A:172:THR:O	1:A:173:PRO:C	2.48	0.56
1:A:609:MET:O	1:A:623:VAL:HG22	2.05	0.56
1:A:134:ASP:CG	1:A:135:ILE:H	2.14	0.56
1:A:221:ARG:HG3	1:A:222:PRO:HD2	1.87	0.56
1:A:791:TRP:H	1:A:791:TRP:CD1	2.22	0.56
1:A:326:SER:H	1:A:327:PRO:CD	2.18	0.56
1:A:729:LEU:O	1:A:729:LEU:HD22	2.05	0.56
1:A:611:ILE:HG13	1:A:621:ARG:HB3	1.87	0.56
1:A:190:ASP:OD1	1:A:191:GLY:N	2.39	0.56
1:A:338:ASP:HB3	1:A:342:ALA:HB3	1.86	0.55
1:A:168:LEU:C	1:A:170:SER:H	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:THR:HG22	7:A:1022:HOH:O	2.06	0.55
1:A:290:SER:O	1:A:294:LEU:HB2	2.06	0.55
1:A:527:GLU:HG3	7:A:1245:HOH:O	2.05	0.55
1:A:302:ASP:HB2	1:A:306:GLU:OE1	2.07	0.55
1:A:239:GLY:N	7:A:1021:HOH:O	2.32	0.55
1:A:438:ARG:NH2	1:A:439:ARG:HE	2.05	0.55
1:A:514:GLN:NE2	1:A:515:LEU:CD2	2.67	0.55
1:A:566:VAL:HG22	1:A:583:VAL:HG21	1.87	0.55
1:A:572:ILE:HD11	3:A:1859[A]:13S:H71	1.87	0.55
1:A:729:LEU:HD21	1:A:758:THR:HA	1.89	0.55
1:A:496:SER:HB3	1:A:745:LEU:HD22	1.88	0.54
1:A:561:ALA:HA	1:A:565:LEU:HB2	1.88	0.54
1:A:173:PRO:HB2	1:A:176:LEU:HB2	1.89	0.54
1:A:348:PRO:HG2	1:A:351:ILE:HD12	1.88	0.54
1:A:137:ASN:HB3	7:A:1232:HOH:O	2.07	0.54
1:A:168:LEU:O	1:A:170:SER:N	2.40	0.54
1:A:172:THR:CB	1:A:173:PRO:HD3	2.38	0.54
1:A:171:GLU:HB2	1:A:177:VAL:HG22	1.88	0.54
1:A:844:GLU:HG2	1:A:845:GLY:N	2.23	0.54
1:A:151:ASN:OD1	1:A:153:LYS:HD2	2.08	0.54
1:A:313:GLY:O	1:A:344:LYS:HG2	2.08	0.54
1:A:160:ILE:HG21	1:A:183:GLU:HG3	1.91	0.53
1:A:387:SER:HG	1:A:389:LEU:HD12	1.72	0.53
1:A:328:LEU:N	1:A:328:LEU:HD23	2.24	0.53
1:A:410:LEU:HD23	1:A:463:ARG:NH1	2.23	0.53
1:A:499:LEU:C	7:A:1283:HOH:O	2.51	0.53
1:A:57:SER:HB3	1:A:121:MET:HG2	1.90	0.53
1:A:514:GLN:HB2	3:A:1859[A]:13S:C6	2.37	0.53
1:A:169:PRO:HB2	1:A:662:PRO:HD2	1.91	0.53
1:A:423:ARG:NH1	1:A:456:LEU:O	2.42	0.53
1:A:474:PRO:C	1:A:475:GLN:HG3	2.33	0.53
1:A:827:ARG:O	1:A:834:PRO:HA	2.09	0.53
1:A:135:ILE:CG2	1:A:136:PRO:HD3	2.34	0.53
1:A:201:ILE:O	1:A:259:PRO:HG3	2.08	0.53
1:A:240:ARG:NH2	7:A:966:HOH:O	2.41	0.53
1:A:324:LYS:O	1:A:327:PRO:HD2	2.08	0.53
1:A:447:ALA:CB	1:A:577:LEU:HD11	2.36	0.53
1:A:10:HIS:CD2	1:A:11:LYS:N	2.77	0.53
1:A:565:LEU:HD12	1:A:571:VAL:CG2	2.38	0.53
1:A:785:GLU:HB2	1:A:805:GLY:HA3	1.90	0.53
1:A:441:ASN:ND2	1:A:446:LYS:HA	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:773:LEU:CD1	3:A:1859[A]:13S:H161	2.39	0.53
1:A:322:ILE:HG21	1:A:340:GLU:HG3	1.90	0.52
1:A:410:LEU:HD12	1:A:411:GLU:H	1.73	0.52
1:A:664:LEU:HD11	1:A:688:MET:HG3	1.91	0.52
1:A:743:GLU:O	1:A:747:LYS:HD3	2.09	0.52
1:A:775:ARG:HH11	1:A:846:LEU:HD13	1.71	0.52
1:A:133:GLU:HG2	7:A:1153:HOH:O	2.09	0.52
1:A:479:SER:HB2	7:A:1332:HOH:O	2.08	0.52
1:A:169:PRO:CG	1:A:662:PRO:HD2	2.40	0.52
1:A:58:VAL:HG23	7:A:1348:HOH:O	2.09	0.52
1:A:433:ILE:HD12	1:A:578:TRP:NE1	2.25	0.52
1:A:541:HIS:HD2	1:A:543:ILE:H	1.55	0.52
1:A:17:VAL:HG12	7:A:1011:HOH:O	2.09	0.52
1:A:750:GLN:O	1:A:754:LEU:HD22	2.09	0.52
1:A:243:THR:HG22	1:A:246:ASP:C	2.32	0.52
1:A:235:ARG:NH1	1:A:238:THR:HG22	2.24	0.52
1:A:285:LEU:CB	1:A:286:PRO:HD3	2.39	0.52
1:A:29:VAL:O	1:A:269:SER:HB2	2.10	0.51
1:A:353:VAL:HG11	1:A:832:GLN:OE1	2.10	0.51
1:A:307:VAL:O	1:A:310:LEU:HB2	2.11	0.51
1:A:46:THR:O	1:A:48:ASP:N	2.42	0.51
1:A:159:ARG:NH1	7:A:1139:HOH:O	2.44	0.51
1:A:360:THR:HG22	1:A:362:GLU:HB2	1.91	0.51
1:A:502:LYS:CB	7:A:1283:HOH:O	2.49	0.51
1:A:90:PRO:HB2	7:A:1246:HOH:O	2.11	0.51
1:A:455:PHE:HB2	1:A:465:LEU:CD2	2.41	0.51
1:A:576:PHE:CZ	3:A:1859[A]:13S:H41	2.44	0.51
1:A:171:GLU:HA	1:A:180:ARG:NH1	2.26	0.51
1:A:769:VAL:O	1:A:773:LEU:HD13	2.11	0.51
1:A:729:LEU:HD22	1:A:729:LEU:C	2.36	0.51
1:A:393:VAL:HG12	1:A:393:VAL:O	2.11	0.51
1:A:514:GLN:OE1	1:A:515:LEU:HD22	2.10	0.51
1:A:238:THR:HG21	7:A:966:HOH:O	2.10	0.51
1:A:433:ILE:HD12	1:A:578:TRP:CD1	2.46	0.51
1:A:53:PHE:HA	7:A:1348:HOH:O	2.09	0.51
1:A:660:GLU:O	1:A:662:PRO:HD3	2.11	0.51
1:A:677:GLY:O	1:A:680:LYS:HG2	2.11	0.51
1:A:499:LEU:HA	7:A:1283:HOH:O	2.10	0.50
1:A:523:HIS:HE1	1:A:557:ILE:HD12	1.77	0.50
1:A:581:TYR:HB2	1:A:585:MET:CE	2.38	0.50
1:A:393:VAL:H	1:A:479:SER:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:SER:HB2	1:A:468:GLU:OE1	2.11	0.50
1:A:187:LEU:HD13	7:A:1054:HOH:O	2.12	0.50
1:A:516:VAL:HG13	1:A:520:LEU:HD23	1.94	0.50
1:A:393:VAL:HB	1:A:479:SER:HA	1.92	0.50
1:A:522:THR:HG23	1:A:855:ILE:CD1	2.42	0.50
1:A:568:ASP:O	1:A:573:GLU:OE1	2.30	0.50
1:A:729:LEU:CD2	1:A:758:THR:HA	2.42	0.50
1:A:278:LYS:O	1:A:282:GLN:HG3	2.11	0.50
1:A:300:GLU:HG3	7:A:1115:HOH:O	2.09	0.50
1:A:493:VAL:HG21	1:A:746:ARG:HH11	1.77	0.50
1:A:609:MET:C	1:A:623:VAL:HG22	2.36	0.50
1:A:236:GLY:N	1:A:527:GLU:OE2	2.42	0.50
1:A:315:ILE:O	1:A:315:ILE:HG12	2.11	0.50
1:A:317:LEU:HG	1:A:318:PRO:HD2	1.93	0.50
1:A:438:ARG:NH2	1:A:439:ARG:NE	2.60	0.50
1:A:134:ASP:OD2	1:A:138:HIS:HB3	2.12	0.49
1:A:609:MET:HA	1:A:623:VAL:CG2	2.42	0.49
1:A:433:ILE:HG12	1:A:437:LEU:HD13	1.93	0.49
1:A:847:THR:C	1:A:849:ARG:H	2.21	0.49
1:A:207:TYR:CD1	1:A:232:TYR:HD2	2.30	0.49
1:A:356:SER:O	1:A:359:MET:HG3	2.12	0.49
1:A:434:MET:HB3	1:A:435:PRO:CD	2.41	0.49
1:A:489:ALA:CB	1:A:494:GLU:HB3	2.42	0.49
1:A:505:VAL:O	1:A:508:ASN:HB2	2.13	0.49
1:A:710:ALA:HA	1:A:714:PHE:HD2	1.76	0.49
1:A:618:HIS:HE1	1:A:635:GLU:OE2	1.95	0.49
1:A:362:GLU:H	1:A:362:GLU:CD	2.21	0.49
1:A:626:ASP:CB	7:A:1190:HOH:O	2.60	0.49
1:A:172:THR:CB	1:A:173:PRO:CD	2.90	0.49
1:A:273:LEU:HD13	1:A:857:ILE:CD1	2.42	0.49
1:A:315:ILE:HD11	1:A:317:LEU:HD13	1.94	0.49
1:A:360:THR:HG22	1:A:362:GLU:OE1	2.13	0.49
1:A:168:LEU:C	1:A:170:SER:N	2.70	0.49
1:A:360:THR:HG22	1:A:362:GLU:CD	2.38	0.49
1:A:729:LEU:CD1	1:A:758:THR:HG23	2.40	0.48
1:A:775:ARG:NH1	1:A:775:ARG:CG	2.77	0.48
1:A:631:VAL:HG12	1:A:818:ARG:CZ	2.42	0.48
1:A:169:PRO:HD3	1:A:541:HIS:HE1	1.76	0.48
1:A:430:HIS:CE1	1:A:434:MET:HE2	2.49	0.48
1:A:522:THR:HG23	1:A:855:ILE:HG12	1.94	0.48
1:A:761:PHE:CE2	1:A:765:ILE:HD11	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:857:ILE:HG13	3:A:1859[A]:13S:H183	1.94	0.48
1:A:304:PHE:H	1:A:750:GLN:HE21	1.61	0.48
1:A:365:ALA:O	1:A:368:MET:HB2	2.14	0.48
1:A:791:TRP:CD1	1:A:791:TRP:N	2.81	0.48
1:A:148:TRP:HB3	7:A:1385:HOH:O	2.13	0.48
1:A:18:LEU:C	1:A:18:LEU:HD23	2.39	0.48
1:A:159:ARG:HG2	7:A:915:HOH:O	2.13	0.48
1:A:169:PRO:CB	1:A:662:PRO:HD2	2.44	0.47
1:A:206:VAL:CG1	1:A:207:TYR:N	2.76	0.47
1:A:623:VAL:O	1:A:624:ILE:HB	2.13	0.47
1:A:192:THR:O	1:A:195:ARG:NH2	2.47	0.47
1:A:208:ASN:HD22	1:A:208:ASN:H	1.61	0.47
1:A:174:ALA:HB3	1:A:175:PRO:HD3	1.96	0.47
1:A:257:TYR:CD1	1:A:257:TYR:C	2.92	0.47
1:A:208:ASN:ND2	1:A:235:ARG:HH21	2.12	0.47
1:A:260:ARG:O	1:A:261:ASP:CB	2.58	0.47
1:A:557:ILE:HB	7:A:1166:HOH:O	2.14	0.47
1:A:190:ASP:CG	1:A:191:GLY:N	2.73	0.47
1:A:233:PRO:HB3	1:A:676:HIS:CE1	2.50	0.47
1:A:362:GLU:HB3	7:A:1202:HOH:O	2.15	0.47
1:A:403:LYS:HZ3	1:A:404:GLU:HG2	1.80	0.47
1:A:516:VAL:HA	1:A:520:LEU:HB3	1.97	0.47
1:A:836:THR:OG1	1:A:849:ARG:HB3	2.15	0.47
1:A:560:LEU:HD23	1:A:565:LEU:CD2	2.44	0.47
1:A:729:LEU:C	1:A:729:LEU:CD2	2.88	0.47
1:A:273:LEU:HD12	7:A:1207:HOH:O	2.13	0.47
1:A:403:LYS:HD3	1:A:403:LYS:H	1.80	0.47
1:A:441:ASN:ND2	1:A:447:ALA:H	2.11	0.47
1:A:575:THR:HG21	1:A:766:ASP:HB2	1.97	0.47
1:A:168:LEU:HD23	1:A:168:LEU:HA	1.78	0.47
1:A:473:HIS:HB3	1:A:477:ASP:HA	1.97	0.47
1:A:206:VAL:HG11	1:A:223:VAL:CG2	2.45	0.46
1:A:751:LYS:HD2	1:A:755:LYS:HG3	1.97	0.46
1:A:410:LEU:CD1	1:A:411:GLU:H	2.27	0.46
1:A:831:VAL:CG1	1:A:833:MET:HB2	2.44	0.46
1:A:69:ASP:CG	1:A:70:ALA:N	2.73	0.46
1:A:775:ARG:HG3	1:A:846:LEU:HD13	1.97	0.46
1:A:171:GLU:CD	1:A:180:ARG:HD3	2.40	0.46
1:A:486:PHE:C	1:A:487:LEU:HD12	2.40	0.46
1:A:717:TYR:O	1:A:721:GLY:N	2.49	0.46
1:A:151:ASN:O	1:A:154:LEU:HD12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:THR:HG22	1:A:523:HIS:H	1.77	0.46
1:A:631:VAL:HG12	1:A:818:ARG:NH1	2.31	0.46
1:A:348:PRO:O	1:A:351:ILE:HD13	2.16	0.46
1:A:351:ILE:HG21	1:A:722:LEU:HG	1.98	0.46
1:A:622:LEU:HD21	1:A:630:THR:CG2	2.42	0.46
1:A:857:ILE:O	3:A:1859[A]:13S:O22	2.33	0.46
1:A:496:SER:HB3	1:A:745:LEU:CD2	2.45	0.45
1:A:833:MET:C	7:A:1374:HOH:O	2.60	0.45
1:A:46:THR:C	1:A:48:ASP:N	2.67	0.45
1:A:438:ARG:HG3	1:A:438:ARG:H	1.48	0.45
1:A:522:THR:CG2	1:A:523:HIS:N	2.76	0.45
1:A:672:VAL:HG11	7:A:1026:HOH:O	2.16	0.45
1:A:330:VAL:O	1:A:332:LYS:N	2.49	0.45
1:A:427:LEU:HD13	1:A:429:HIS:CD2	2.51	0.45
1:A:612:GLU:HB2	7:A:1285:HOH:O	2.15	0.45
1:A:781:VAL:HG13	1:A:786:ARG:HG2	1.98	0.45
1:A:561:ALA:HA	1:A:565:LEU:HD23	1.98	0.45
1:A:76:LEU:N	1:A:76:LEU:HD12	2.32	0.45
1:A:150:TYR:HB2	1:A:155:PHE:HZ	1.82	0.45
1:A:133:GLU:O	1:A:134:ASP:O	2.35	0.45
1:A:296:PHE:HB3	1:A:318:PRO:HD3	1.98	0.45
1:A:390:ASP:HB3	1:A:391:SER:H	1.58	0.45
1:A:513:HIS:HA	1:A:517:SER:HB2	1.98	0.45
1:A:564:SER:O	1:A:571:VAL:HG22	2.17	0.45
1:A:46:THR:HG22	1:A:47:LEU:N	2.32	0.44
1:A:434:MET:HB3	1:A:435:PRO:HD3	1.98	0.44
1:A:500:LEU:HD12	1:A:753:TYR:HD1	1.81	0.44
1:A:20:ARG:O	1:A:23:VAL:HB	2.17	0.44
1:A:690:THR:HB	1:A:693:GLU:HG3	2.00	0.44
1:A:457:LYS:HB2	1:A:459:ASP:OD1	2.18	0.44
1:A:506:VAL:CG1	1:A:727:PRO:HD2	2.47	0.44
1:A:781:VAL:HG12	1:A:853:ASN:ND2	2.32	0.44
1:A:781:VAL:HG12	1:A:786:ARG:HB3	1.99	0.44
1:A:258:LEU:HD12	1:A:262:GLU:HB2	1.99	0.44
1:A:438:ARG:NH2	1:A:439:ARG:HH21	2.12	0.44
1:A:277:LEU:CD2	3:A:1859[A]:13S:H182	2.43	0.44
1:A:530:ILE:HG12	1:A:551:TYR:CD1	2.53	0.44
1:A:600:LEU:HD23	1:A:634:LEU:HD13	1.99	0.44
1:A:168:LEU:HB3	1:A:169:PRO:HD2	1.99	0.44
1:A:208:ASN:HD21	1:A:235:ARG:NH2	2.16	0.44
1:A:788:ASN:CB	1:A:789:PRO:CD	2.87	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:LYS:HG2	1:A:108:GLY:O	2.18	0.44
1:A:330:VAL:C	1:A:332:LYS:N	2.76	0.44
1:A:29:VAL:HG13	1:A:32:VAL:HB	2.00	0.44
1:A:92:LEU:HB3	1:A:93:GLY:H	1.55	0.44
1:A:351:ILE:HB	1:A:355:LYS:HA	2.00	0.44
1:A:403:LYS:NZ	1:A:404:GLU:HG2	2.33	0.44
1:A:332:LYS:O	1:A:334:ILE:N	2.44	0.43
1:A:626:ASP:O	1:A:628:PRO:HD3	2.18	0.43
1:A:836:THR:HG1	1:A:839:LEU:HD22	1.83	0.43
1:A:370:ALA:HB2	1:A:628:PRO:HG2	2.00	0.43
1:A:785:GLU:HB2	1:A:805:GLY:CA	2.47	0.43
1:A:169:PRO:C	1:A:171:GLU:H	2.26	0.43
1:A:561:ALA:HA	1:A:565:LEU:HD22	2.00	0.43
1:A:626:ASP:HB2	7:A:1190:HOH:O	2.17	0.43
1:A:664:LEU:HD22	7:A:1259:HOH:O	2.19	0.43
1:A:819:ASN:HD21	1:A:827:ARG:HH21	1.67	0.43
1:A:482:PHE:CD1	1:A:482:PHE:C	2.96	0.43
1:A:785:GLU:CB	1:A:805:GLY:HA3	2.47	0.43
1:A:581:TYR:O	1:A:585:MET:HG3	2.19	0.43
1:A:362:GLU:CD	1:A:362:GLU:N	2.77	0.43
1:A:609:MET:HA	1:A:623:VAL:HG22	2.00	0.43
1:A:155:PHE:O	1:A:156:LYS:HB2	2.19	0.43
1:A:349:LYS:CB	1:A:833:MET:HE3	2.38	0.43
1:A:331:LEU:HD12	1:A:335:PHE:CZ	2.53	0.43
1:A:781:VAL:CG1	1:A:786:ARG:HB3	2.48	0.43
1:A:29:VAL:O	1:A:29:VAL:HG12	2.19	0.43
1:A:206:VAL:HG12	1:A:207:TYR:N	2.32	0.43
1:A:69:ASP:O	1:A:70:ALA:C	2.62	0.42
1:A:169:PRO:O	1:A:171:GLU:CG	2.63	0.42
1:A:178:LYS:O	1:A:182:GLU:HB2	2.19	0.42
1:A:232:TYR:CG	1:A:233:PRO:HD2	2.54	0.42
1:A:384:PRO:HD2	1:A:398:THR:CG2	2.43	0.42
1:A:717:TYR:HB3	1:A:718:PRO:HD3	2.01	0.42
1:A:189:GLY:O	1:A:190:ASP:HB3	2.18	0.42
1:A:653:LYS:HG3	7:A:932:HOH:O	2.18	0.42
1:A:91:THR:O	1:A:91:THR:OG1	2.35	0.42
1:A:170:SER:HB2	7:A:992:HOH:O	2.18	0.42
1:A:178:LYS:HB2	7:A:1027:HOH:O	2.18	0.42
1:A:669:LYS:HE2	1:A:673:GLU:OE2	2.19	0.42
1:A:773:LEU:HD11	3:A:1859[A]:13S:H161	2.02	0.42
1:A:785:GLU:OE1	1:A:802:LYS:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:LEU:O	1:A:259:PRO:C	2.60	0.42
1:A:360:THR:HG22	1:A:362:GLU:CB	2.49	0.42
1:A:501:ALA:N	7:A:1225:HOH:O	2.51	0.42
1:A:80:THR:HB	1:A:101:ILE:HD11	2.02	0.42
1:A:160:ILE:HD13	1:A:162:PHE:CZ	2.55	0.42
1:A:171:GLU:CB	1:A:180:ARG:HD3	2.49	0.42
1:A:243:THR:CG2	1:A:246:ASP:N	2.81	0.42
1:A:282:GLN:HG2	7:A:1182:HOH:O	2.19	0.42
1:A:761:PHE:HD2	1:A:762:GLN:OE1	2.02	0.42
1:A:438:ARG:HE	1:A:438:ARG:HB2	1.68	0.42
1:A:469:LEU:HD12	1:A:486:PHE:CE1	2.55	0.42
1:A:554:THR:HG22	7:A:1242:HOH:O	2.19	0.42
1:A:310:LEU:HD12	1:A:310:LEU:HA	1.87	0.42
1:A:618:HIS:HB2	7:A:1125:HOH:O	2.18	0.42
1:A:710:ALA:HA	1:A:714:PHE:CD2	2.54	0.42
1:A:857:ILE:CD1	3:A:1859[A]:13S:H183	2.50	0.42
1:A:88:SER:C	1:A:89:LEU:HD22	2.45	0.42
1:A:92:LEU:HD23	1:A:92:LEU:HA	1.86	0.42
1:A:160:ILE:HG22	1:A:183:GLU:HG3	1.98	0.42
1:A:21:LYS:C	1:A:23:VAL:H	2.27	0.42
1:A:174:ALA:N	1:A:175:PRO:CD	2.83	0.42
1:A:324:LYS:O	1:A:328:LEU:HD22	2.20	0.42
1:A:462:LEU:HD11	7:A:1248:HOH:O	2.20	0.42
1:A:204:TYR:CD1	1:A:674:VAL:HG11	2.55	0.41
1:A:240:ARG:HD3	1:A:253:SER:HB2	2.00	0.41
1:A:720:GLY:C	1:A:722:LEU:H	2.28	0.41
1:A:195:ARG:HD3	1:A:195:ARG:HA	1.79	0.41
1:A:467:ILE:HD11	1:A:502:LYS:HG2	2.02	0.41
1:A:171:GLU:OE1	1:A:181:GLU:HG2	2.20	0.41
1:A:360:THR:HG22	1:A:362:GLU:N	2.31	0.41
1:A:636:ILE:HD12	1:A:838:LEU:HG	2.02	0.41
1:A:258:LEU:HD11	1:A:263:ALA:HB2	2.02	0.41
1:A:414:THR:OG1	1:A:417:GLU:HB2	2.20	0.41
1:A:775:ARG:HG3	1:A:846:LEU:CD1	2.50	0.41
1:A:499:LEU:CA	7:A:1283:HOH:O	2.66	0.41
1:A:685:TRP:HB2	7:A:1265:HOH:O	2.20	0.41
1:A:208:ASN:HD22	1:A:208:ASN:N	2.16	0.41
1:A:206:VAL:CG1	1:A:223:VAL:CG2	2.99	0.41
1:A:636:ILE:HD13	1:A:851:ILE:CD1	2.51	0.41
1:A:74:GLY:H	1:A:179:TYR:HE2	1.69	0.41
1:A:171:GLU:HB3	1:A:180:ARG:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:565:LEU:HD21	3:A:1859[A]:13S:C15	2.50	0.41
1:A:636:ILE:HD11	1:A:838:LEU:O	2.21	0.41
1:A:277:LEU:CG	3:A:1859[A]:13S:H182	2.51	0.41
1:A:433:ILE:HD12	1:A:578:TRP:HE1	1.86	0.41
1:A:698:CYS:O	1:A:702:ILE:HG13	2.21	0.41
1:A:759:PRO:HG2	1:A:762:GLN:NE2	2.36	0.40
1:A:340:GLU:HG3	1:A:341:GLN:H	1.86	0.40
1:A:425:PHE:HE1	1:A:456:LEU:HB2	1.85	0.40
1:A:717:TYR:N	1:A:718:PRO:CD	2.85	0.40
1:A:857:ILE:HD11	3:A:1859[A]:13S:H183	2.03	0.40
1:A:52:ALA:HB1	1:A:121:MET:HE1	2.04	0.40
1:A:311:TYR:HA	1:A:345:PHE:O	2.21	0.40
1:A:522:THR:CG2	1:A:855:ILE:HG12	2.52	0.40
1:A:600:LEU:HG	1:A:604:LEU:HD22	2.03	0.40
1:A:616:CYS:HB3	1:A:617:PRO:HD2	2.03	0.40
1:A:788:ASN:OD1	1:A:788:ASN:N	2.54	0.40
1:A:329:PRO:O	1:A:330:VAL:HB	2.21	0.40
1:A:443:THR:C	1:A:445:THR:H	2.28	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	832/857 (97%)	730 (88%)	66 (8%)	36 (4%)	2 0

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	92	LEU
1	A	134	ASP
1	A	172	THR

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Mol	Chain	Res	Type
1	A	270	SER
1	A	390	ASP
1	A	398	THR
1	A	409	ASN
1	A	410	LEU
1	A	473	HIS
1	A	737	LYS
1	A	784	GLY
1	A	789	PRO
1	A	844	GLU
1	A	48	ASP
1	A	55	GLY
1	A	72	GLY
1	A	137	ASN
1	A	411	GLU
1	A	477	ASP
1	A	568	ASP
1	A	135	ILE
1	A	261	ASP
1	A	295	ASN
1	A	326	SER
1	A	331	LEU
1	A	341	GLN
1	A	788	ASN
1	A	69	ASP
1	A	169	PRO
1	A	101	ILE
1	A	624	ILE
1	A	492	GLY
1	A	325	ILE
1	A	570	GLY
1	A	407	GLU
1	A	173	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	735/749 (98%)	596 (81%)	139 (19%)	1 1

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	13	LYS
1	A	18	LEU
1	A	23	VAL
1	A	28	SER
1	A	31	SER
1	A	47	LEU
1	A	48	ASP
1	A	49	THR
1	A	54	LEU
1	A	56	ARG
1	A	57	SER
1	A	67	LYS
1	A	78	LYS
1	A	80	THR
1	A	82	LEU
1	A	83	GLU
1	A	85	ILE
1	A	92	LEU
1	A	101	ILE
1	A	104	GLU
1	A	109	SER
1	A	135	ILE
1	A	153	LYS
1	A	154	LEU
1	A	156	LYS
1	A	157	SER
1	A	164	ASN
1	A	176	LEU
1	A	181	GLU
1	A	183	GLU
1	A	184	LEU
1	A	187	LEU
1	A	190	ASP
1	A	195	ARG
1	A	208	ASN
1	A	209	ASP
1	A	210	LEU

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Mol	Chain	Res	Type
1	A	217	GLU
1	A	218	ASN
1	A	221	ARG
1	A	224	LEU
1	A	241	LYS
1	A	243	THR
1	A	249	SER
1	A	252	ARG
1	A	256	VAL
1	A	257	TYR
1	A	270	SER
1	A	277	LEU
1	A	280	VAL
1	A	282	GLN
1	A	285	LEU
1	A	297	THR
1	A	300	GLU
1	A	310	LEU
1	A	315	ILE
1	A	320	ASP
1	A	322	ILE
1	A	323	SER
1	A	324	LYS
1	A	331	LEU
1	A	334	ILE
1	A	340	GLU
1	A	349	LYS
1	A	351	ILE
1	A	355	LYS
1	A	366	ARG
1	A	376	LEU
1	A	380	LEU
1	A	382	ASP
1	A	390	ASP
1	A	403	LYS
1	A	405	HIS
1	A	406	LEU
1	A	410	LEU
1	A	411	GLU
1	A	414	THR
1	A	417	GLU
1	A	426	LEU

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Mol	Chain	Res	Type
1	A	427	LEU
1	A	437	LEU
1	A	438	ARG
1	A	444	SER
1	A	452	THR
1	A	475	GLN
1	A	478	GLN
1	A	483	SER
1	A	485	VAL
1	A	493	VAL
1	A	508	ASN
1	A	515	LEU
1	A	522	THR
1	A	525	VAL
1	A	537	LEU
1	A	540	VAL
1	A	547	LEU
1	A	553	ASP
1	A	557	ILE
1	A	560	LEU
1	A	564	SER
1	A	565	LEU
1	A	571	VAL
1	A	572	ILE
1	A	583	VAL
1	A	594	VAL
1	A	604	LEU
1	A	615	SER
1	A	621	ARG
1	A	626	ASP
1	A	634	LEU
1	A	671	LEU
1	A	679	LYS
1	A	688	MET
1	A	722	LEU
1	A	724	LEU
1	A	726	ARG
1	A	729	LEU
1	A	745	LEU
1	A	747	LYS
1	A	754	LEU
1	A	763	THR

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Mol	Chain	Res	Type
1	A	775	ARG
1	A	785	GLU
1	A	786	ARG
1	A	787	ASP
1	A	788	ASN
1	A	795	THR
1	A	798	LEU
1	A	799	GLU
1	A	807	LYS
1	A	808	LEU
1	A	815	LEU
1	A	822	GLU
1	A	825	ARG
1	A	833	MET
1	A	837	LEU
1	A	838	LEU
1	A	846	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	22	ASN
1	A	138	HIS
1	A	164	ASN
1	A	165	GLN
1	A	208	ASN
1	A	218	ASN
1	A	219	HIS
1	A	248	ASN
1	A	341	GLN
1	A	441	ASN
1	A	458	ASN
1	A	473	HIS
1	A	484	GLN
1	A	521	ASN
1	A	541	HIS
1	A	556	ASN
1	A	618	HIS
1	A	665	GLN
1	A	681	ASN
1	A	725	ASN

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Mol	Chain	Res	Type
1	A	750	GLN
1	A	806	ASN
1	A	813	ASN
1	A	819	ASN
1	A	826	ASN
1	A	853	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 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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$
5	9OH	A	1861[C]	2	21,22,22	0.93	1 (4%)	22,26,26	1.89	3 (13%)
3	13S	A	1859[A]	2	21,21,21	3.32	4 (19%)	19,22,22	1.05	1 (5%)
6	11O	A	1862[D]	-	22,22,22	0.97	1 (4%)	23,26,26	0.94	2 (8%)
4	13R	A	1860[B]	2	21,21,21	3.21	3 (14%)	19,22,22	1.16	2 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	9OH	A	1861[C]	2	-	13/20/25/25	0/1/1/1
3	13S	A	1859[A]	2	-	12/19/21/21	-
6	11O	A	1862[D]	-	-	9/21/26/26	0/1/1/1
4	13R	A	1860[B]	2	-	12/19/21/21	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1859[A]	13S	O22-O21	-13.88	1.22	1.46
4	A	1860[B]	13R	O22-O21	-13.87	1.22	1.46
3	A	1859[A]	13S	C14-C13	3.98	1.57	1.52
6	A	1862[D]	11O	C12-C13	2.78	1.50	1.46
4	A	1860[B]	13R	C11-C10	-2.66	1.35	1.44
3	A	1859[A]	13S	C10-C9	2.36	1.41	1.33
4	A	1860[B]	13R	O20-C1	-2.31	1.23	1.30
3	A	1859[A]	13S	O20-C1	-2.14	1.23	1.30
5	A	1861[C]	9OH	O22-C12	2.12	1.50	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1861[C]	9OH	O22-C12-C11	5.66	129.06	115.43
5	A	1861[C]	9OH	O22-C13-C14	5.31	126.90	116.78
5	A	1861[C]	9OH	O21-C9-C8	-3.39	100.08	109.23
3	A	1859[A]	13S	C15-C14-C13	-3.38	109.64	114.24
4	A	1860[B]	13R	C15-C14-C13	-2.85	110.36	114.24
6	A	1862[D]	11O	C12-O22-C13	2.63	62.28	60.62
6	A	1862[D]	11O	O22-C13-C14	-2.42	112.17	116.78
4	A	1860[B]	13R	O20-C1-C2	2.10	120.63	114.00

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1859[A]	13S	C12-C13-C14-C15
3	A	1859[A]	13S	O21-C13-C14-C15
4	A	1860[B]	13R	C11-C12-C13-O21
4	A	1860[B]	13R	C12-C13-C14-C15
4	A	1860[B]	13R	O21-C13-C14-C15

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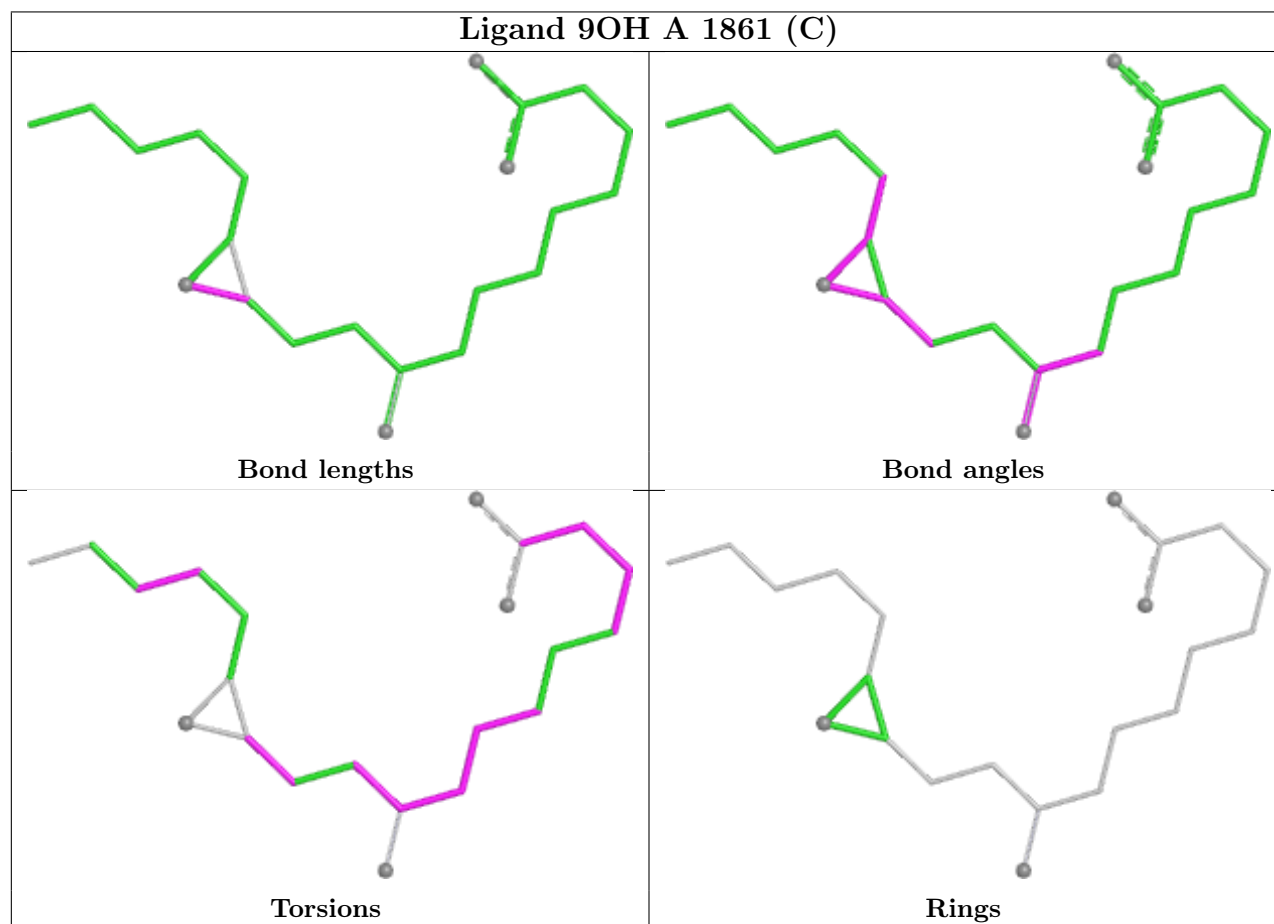
Mol	Chain	Res	Type	Atoms
5	A	1861[C]	9OH	C7-C8-C9-C10
5	A	1861[C]	9OH	C7-C8-C9-O21
5	A	1861[C]	9OH	C11-C10-C9-C8
5	A	1861[C]	9OH	C11-C10-C9-O21
5	A	1861[C]	9OH	C10-C11-C12-O22
5	A	1861[C]	9OH	C1-C2-C3-C4
6	A	1862[D]	11O	C1-C2-C3-C4
3	A	1859[A]	13S	C1-C2-C3-C4
5	A	1861[C]	9OH	C5-C6-C7-C8
4	A	1860[B]	13R	C2-C3-C4-C5
3	A	1859[A]	13S	C6-C7-C8-C9
5	A	1861[C]	9OH	C14-C15-C16-C17
3	A	1859[A]	13S	C2-C3-C4-C5
3	A	1859[A]	13S	C3-C4-C5-C6
5	A	1861[C]	9OH	C2-C3-C4-C5
3	A	1859[A]	13S	C11-C12-C13-O21
4	A	1860[B]	13R	C6-C7-C8-C9
4	A	1860[B]	13R	C5-C6-C7-C8
6	A	1862[D]	11O	C2-C3-C4-C5
3	A	1859[A]	13S	C11-C12-C13-C14
4	A	1860[B]	13R	C11-C12-C13-C14
6	A	1862[D]	11O	C5-C6-C7-C8
6	A	1862[D]	11O	O22-C13-C14-C15
4	A	1860[B]	13R	C15-C16-C17-C18
4	A	1860[B]	13R	C13-C14-C15-C16
3	A	1859[A]	13S	C13-C14-C15-C16
6	A	1862[D]	11O	C4-C5-C6-C7
5	A	1861[C]	9OH	C6-C7-C8-C9
3	A	1859[A]	13S	C15-C16-C17-C18
6	A	1862[D]	11O	O19-C1-C2-C3
6	A	1862[D]	11O	C3-C4-C5-C6
4	A	1860[B]	13R	C4-C5-C6-C7
3	A	1859[A]	13S	O19-C1-C2-C3
5	A	1861[C]	9OH	O20-C1-C2-C3
6	A	1862[D]	11O	O20-C1-C2-C3
5	A	1861[C]	9OH	O19-C1-C2-C3
6	A	1862[D]	11O	C7-C8-C9-C10
3	A	1859[A]	13S	O20-C1-C2-C3
4	A	1860[B]	13R	O20-C1-C2-C3
4	A	1860[B]	13R	O19-C1-C2-C3
5	A	1861[C]	9OH	C10-C11-C12-C13

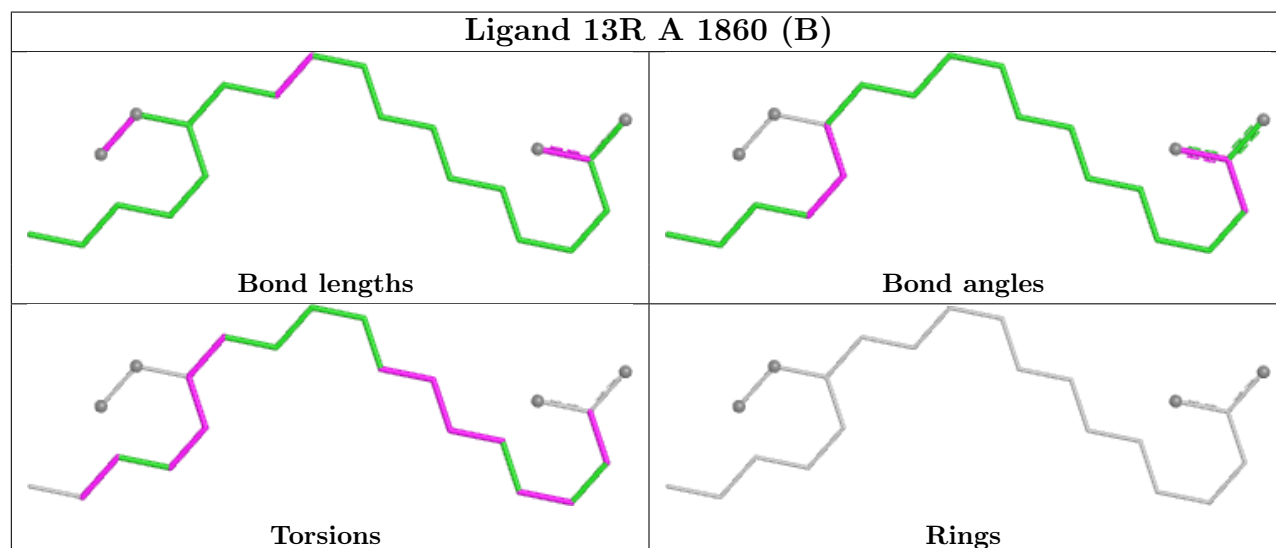
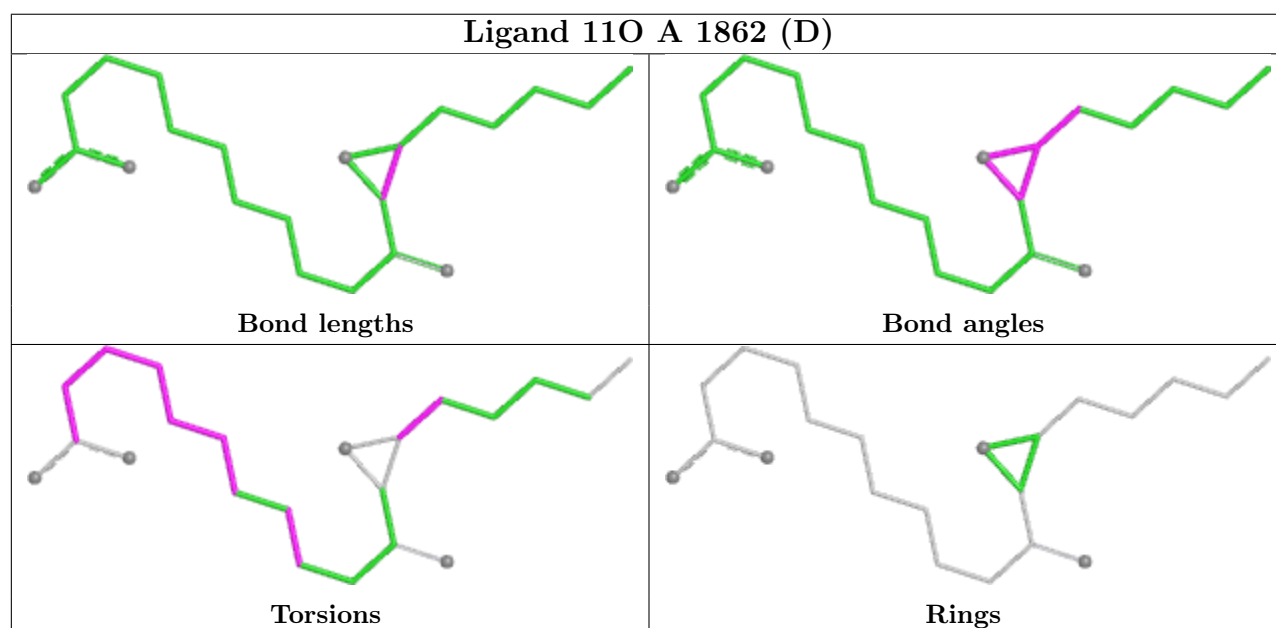
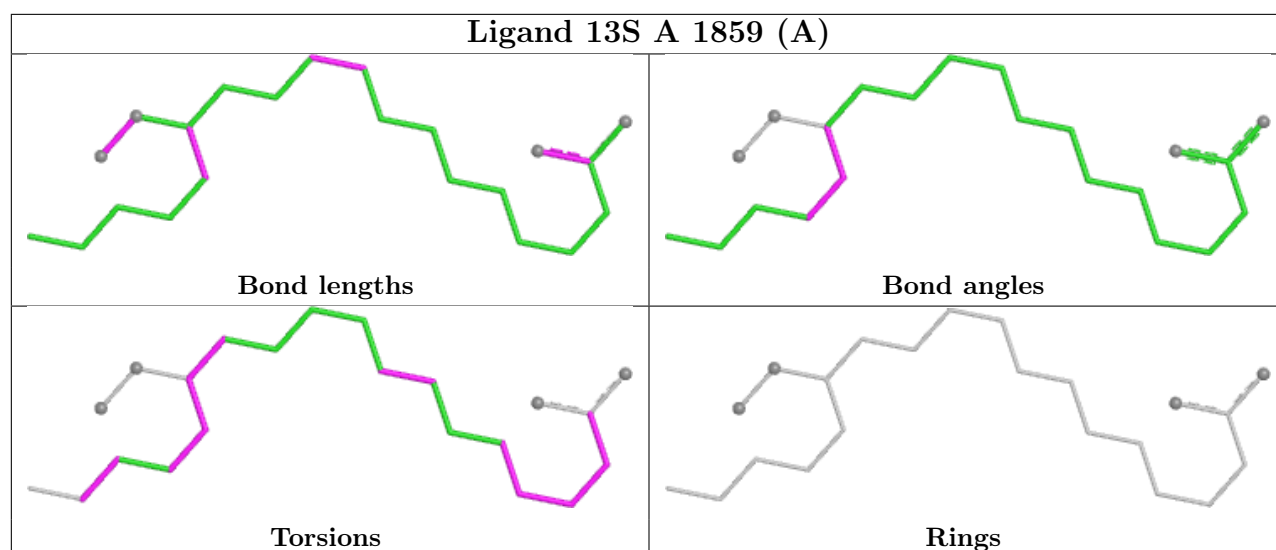
There are no ring outliers.

1 monomer is involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1859[A]	13S	20	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 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	836/857 (97%)	0.23	49 (5%) 28 27	11, 29, 74, 100	1 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	VAL	4.4
1	A	395	GLY	4.3
1	A	135	ILE	4.3
1	A	474	PRO	3.9
1	A	790	ASN	3.9
1	A	48	ASP	3.8
1	A	481	ALA	3.6
1	A	394	TYR	3.6
1	A	398	THR	3.5
1	A	412	GLY	3.4
1	A	32	VAL	3.4
1	A	334	ILE	3.3
1	A	392	GLN	3.2
1	A	170	SER	3.1
1	A	480	GLY	3.1
1	A	514	GLN	3.1
1	A	294	LEU	3.0
1	A	393	VAL	3.0
1	A	9	GLY	3.0
1	A	47	LEU	2.9
1	A	784	GLY	2.9
1	A	291	ALA	2.9
1	A	396	ASP	2.8
1	A	738	GLY	2.8
1	A	473	HIS	2.6
1	A	49	THR	2.5
1	A	136	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	157	SER	2.4
1	A	46	THR	2.4
1	A	297	THR	2.4
1	A	342	ALA	2.4
1	A	409	ASN	2.4
1	A	296	PHE	2.4
1	A	383	PHE	2.4
1	A	323	SER	2.4
1	A	408	PRO	2.3
1	A	22	ASN	2.3
1	A	406	LEU	2.3
1	A	341	GLN	2.2
1	A	137	ASN	2.2
1	A	785	GLU	2.2
1	A	315	ILE	2.2
1	A	290	SER	2.2
1	A	418	ALA	2.1
1	A	407	GLU	2.1
1	A	410	LEU	2.1
1	A	397	HIS	2.0
1	A	340	GLU	2.0
1	A	479	SER	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(Å ²)	Q<0.9
3	13S	A	1859[A]	22/22	0.83	0.13	30,46,66,72	0

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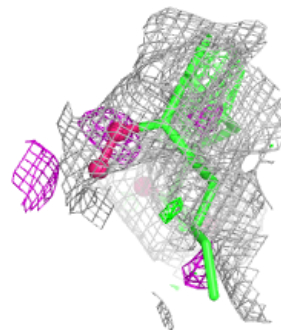
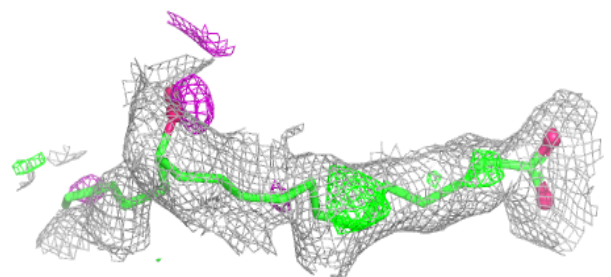
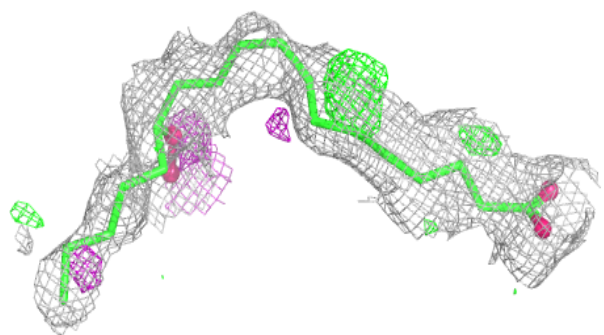
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FE	A	858	1/1	0.91	0.15	39,39,39,39	0
4	13R	A	1860[B]	22/22	-	-	33,46,66,71	22
5	9OH	A	1861[C]	22/22	-	-	0,0,0,0	22
6	11O	A	1862[D]	22/22	-	-	0,0,0,0	22

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.

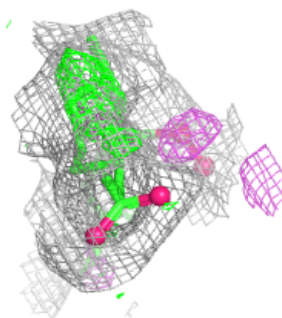
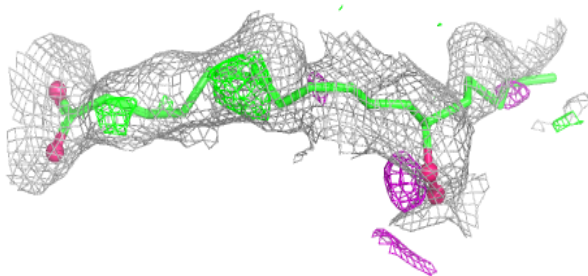
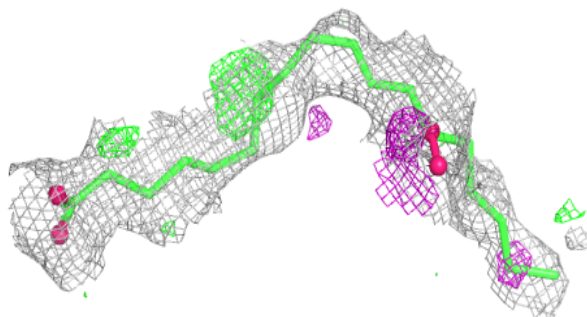
Electron density around 13S A 1859 (A):

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

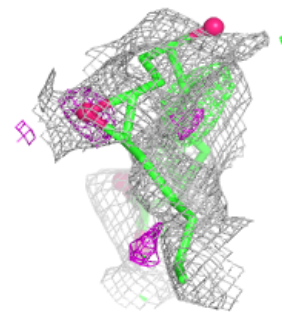
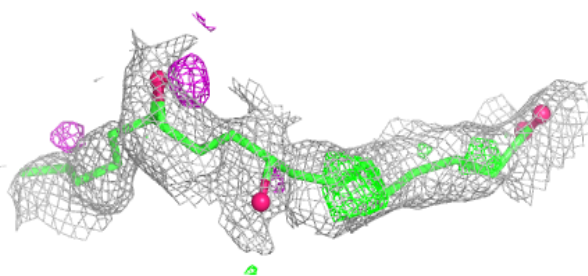
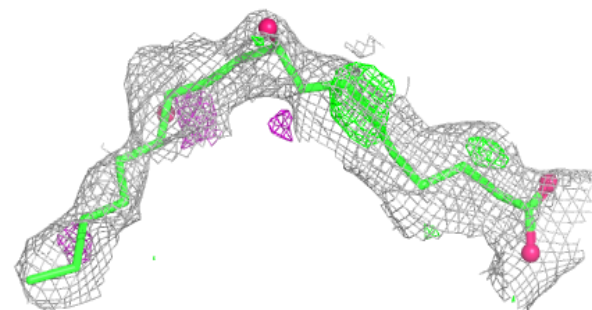


Electron density around 13R A 1860 (B):

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

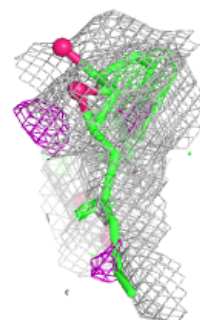
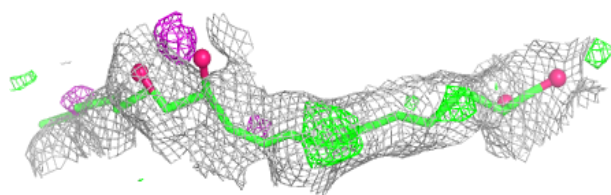
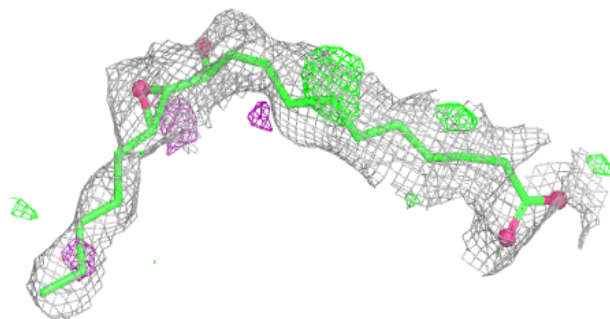
**Electron density around 9OH A 1861 (C):**

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



Electron density around 11O A 1862 (D):

$2mF_o-DF_c$ (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.