



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:26 AM UTC

PDB ID : 1U25 / pdb_00001u25
Title : Crystal structure of Selenomonas ruminantium phytase complexed with per-sulfated phytate in the C2221 crystal form
Authors : Chu, H.M.; Guo, R.T.; Lin, T.W.; Chou, C.C.; Shr, H.L.; Lai, H.L.; Tang, T.Y.; Cheng, K.J.; Selinger, B.L.; Wang, A.H.-J.
Deposited on : 2004-07-16
Resolution : 2.50 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

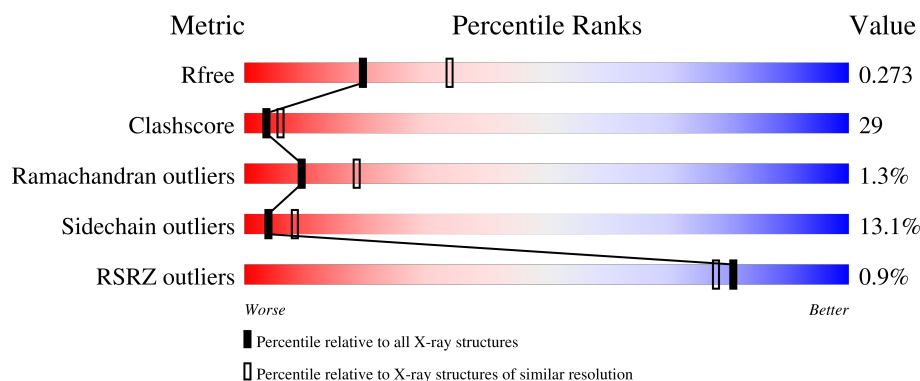
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	337	% 46% 37% 8% • 8%
1	B	337	% 48% 34% 10% • 7%
1	C	337	% 41% 39% 10% • 8%

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
2	IHS	A	2167	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8652 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 myo-inositol hexaphosphate phosphohydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	Se	0	0	0
			2534	1614	454	459	1	6			
1	B	312	Total	C	N	O	S	Se	0	0	0
			2542	1620	455	460	1	6			
1	C	310	Total	C	N	O	S	Se	0	0	0
			2527	1610	453	457	1	6			

There are 54 discrepancies between the modelled and reference sequences:

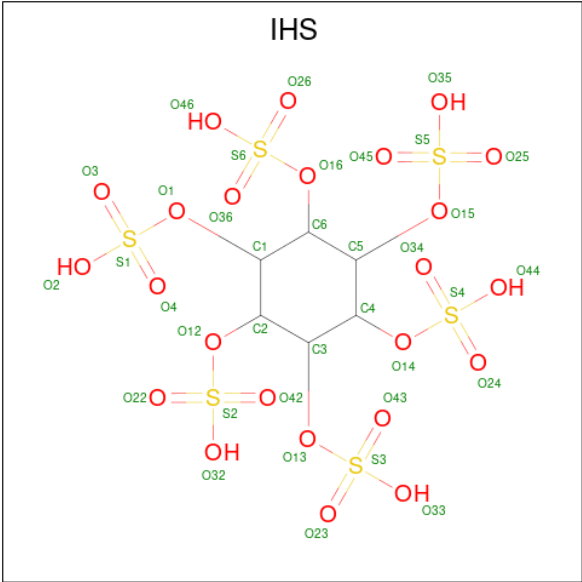
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP Q7WUJ1
A	2	ALA	-	expression tag	UNP Q7WUJ1
A	3	SER	-	expression tag	UNP Q7WUJ1
A	4	MSE	-	expression tag	UNP Q7WUJ1
A	5	THR	-	expression tag	UNP Q7WUJ1
A	6	GLY	-	expression tag	UNP Q7WUJ1
A	7	GLY	-	expression tag	UNP Q7WUJ1
A	8	GLN	-	expression tag	UNP Q7WUJ1
A	9	GLN	-	expression tag	UNP Q7WUJ1
A	10	MSE	-	expression tag	UNP Q7WUJ1
A	11	GLY	-	expression tag	UNP Q7WUJ1
A	12	ARG	-	expression tag	UNP Q7WUJ1
A	13	GLY	-	expression tag	UNP Q7WUJ1
A	14	SER	-	expression tag	UNP Q7WUJ1
A	15	GLU	-	expression tag	UNP Q7WUJ1
A	16	PHE	-	expression tag	UNP Q7WUJ1
A	336	LEU	-	expression tag	UNP Q7WUJ1
A	337	GLU	-	expression tag	UNP Q7WUJ1
B	1	MSE	-	expression tag	UNP Q7WUJ1
B	2	ALA	-	expression tag	UNP Q7WUJ1
B	3	SER	-	expression tag	UNP Q7WUJ1
B	4	MSE	-	expression tag	UNP Q7WUJ1
B	5	THR	-	expression tag	UNP Q7WUJ1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	6	GLY	-	expression tag	UNP Q7WUJ1
B	7	GLY	-	expression tag	UNP Q7WUJ1
B	8	GLN	-	expression tag	UNP Q7WUJ1
B	9	GLN	-	expression tag	UNP Q7WUJ1
B	10	MSE	-	expression tag	UNP Q7WUJ1
B	11	GLY	-	expression tag	UNP Q7WUJ1
B	12	ARG	-	expression tag	UNP Q7WUJ1
B	13	GLY	-	expression tag	UNP Q7WUJ1
B	14	SER	-	expression tag	UNP Q7WUJ1
B	15	GLU	-	expression tag	UNP Q7WUJ1
B	16	PHE	-	expression tag	UNP Q7WUJ1
B	336	LEU	-	expression tag	UNP Q7WUJ1
B	337	GLU	-	expression tag	UNP Q7WUJ1
C	1	MSE	-	expression tag	UNP Q7WUJ1
C	2	ALA	-	expression tag	UNP Q7WUJ1
C	3	SER	-	expression tag	UNP Q7WUJ1
C	4	MSE	-	expression tag	UNP Q7WUJ1
C	5	THR	-	expression tag	UNP Q7WUJ1
C	6	GLY	-	expression tag	UNP Q7WUJ1
C	7	GLY	-	expression tag	UNP Q7WUJ1
C	8	GLN	-	expression tag	UNP Q7WUJ1
C	9	GLN	-	expression tag	UNP Q7WUJ1
C	10	MSE	-	expression tag	UNP Q7WUJ1
C	11	GLY	-	expression tag	UNP Q7WUJ1
C	12	ARG	-	expression tag	UNP Q7WUJ1
C	13	GLY	-	expression tag	UNP Q7WUJ1
C	14	SER	-	expression tag	UNP Q7WUJ1
C	15	GLU	-	expression tag	UNP Q7WUJ1
C	16	PHE	-	expression tag	UNP Q7WUJ1
C	336	LEU	-	expression tag	UNP Q7WUJ1
C	337	GLU	-	expression tag	UNP Q7WUJ1

- Molecule 2 is D-MYO-INOSITOL-HEXASULPHATE (CCD ID: IHS) (formula: $C_6H_{12}O_{24}S_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			36	6	24	6		
2	A	1	Total	C	O	S	0	0
			36	6	24	6		
2	C	1	Total	C	O	S	0	0
			36	6	24	6		

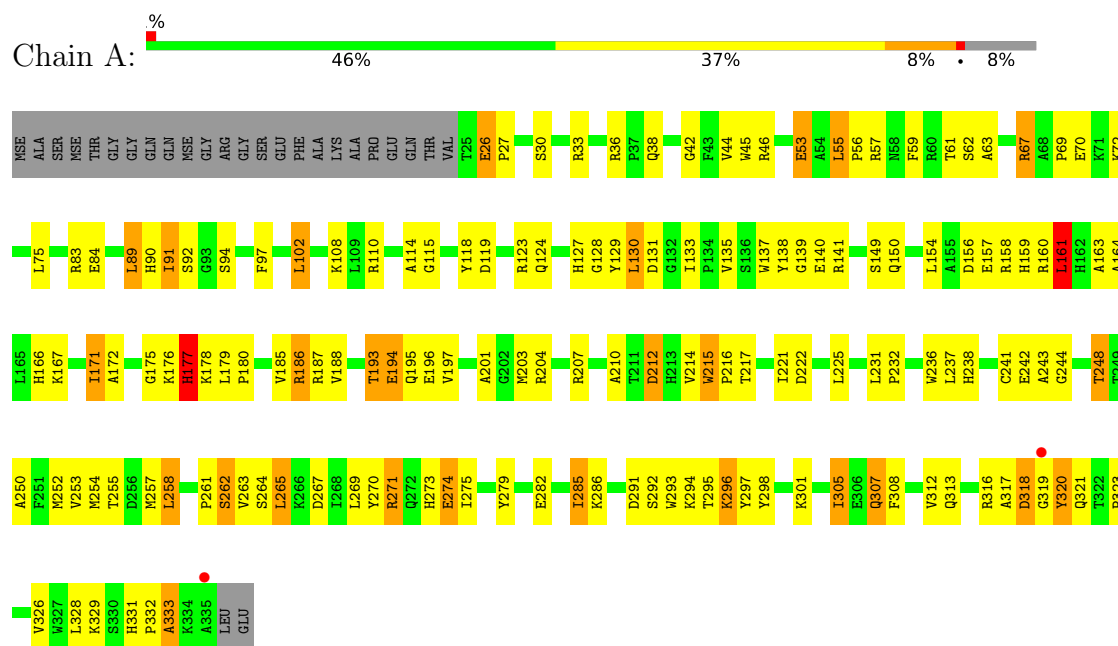
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	389	Total	O	0	0
			389	389		
3	B	317	Total	O	0	0
			317	317		
3	C	235	Total	O	0	0
			235	235		

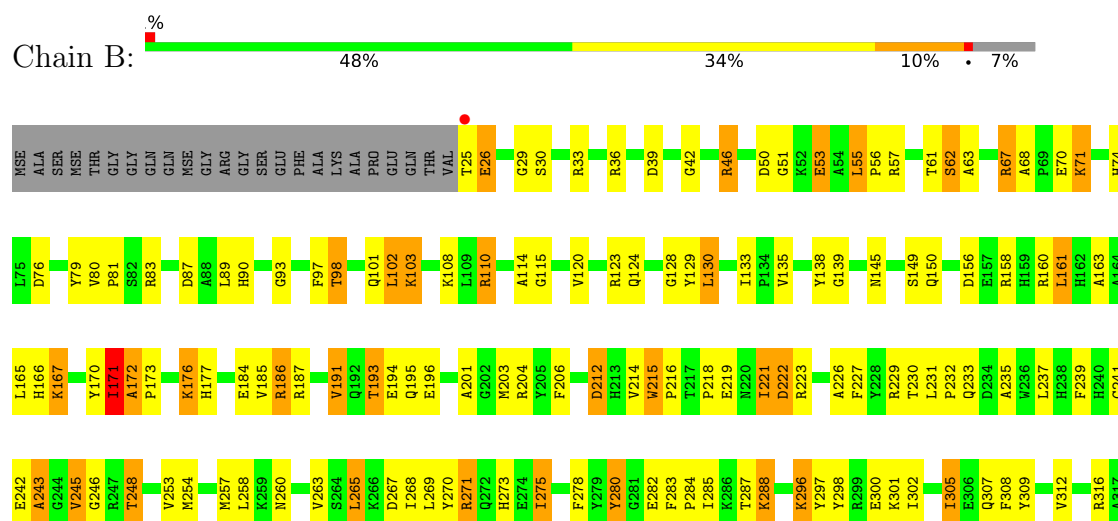
3 Residue-property plots

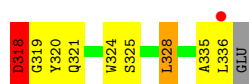
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: myo-inositol hexaphosphate phosphohydrolase

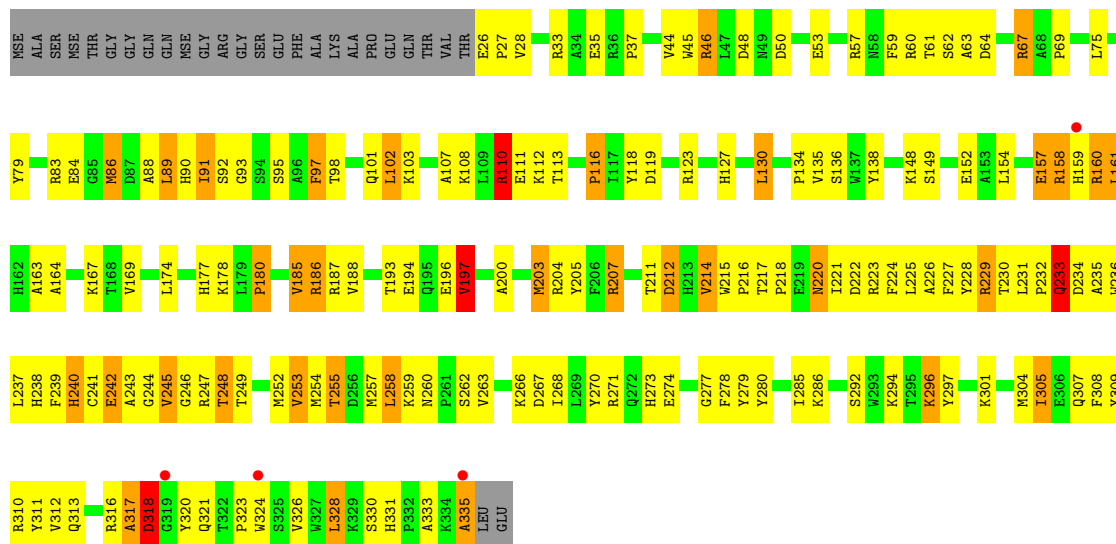
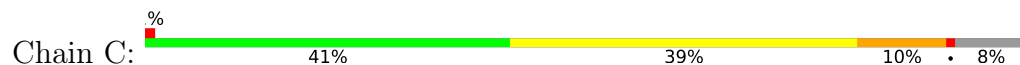


- Molecule 1: myo-inositol hexaphosphate phosphohydrolase





- Molecule 1: myo-inositol hexaphosphate phosphohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	128.38Å 228.75Å 91.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.21 – 2.50 35.21 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (35.21-2.50) 83.2 (35.21-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.179 , 0.265 0.189 , 0.273	Depositor DCC
R_{free} test set	2110 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 57.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.026 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.039 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8652	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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: IHS

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.07	1/2602 (0.0%)	1.40	34/3514 (1.0%)
1	B	1.05	4/2610 (0.2%)	1.37	36/3525 (1.0%)
1	C	0.92	1/2595 (0.0%)	1.22	14/3504 (0.4%)
All	All	1.01	6/7807 (0.1%)	1.33	84/10543 (0.8%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	136	SER	CA-C	6.38	1.60	1.52
1	B	171	ILE	CA-CB	5.84	1.61	1.54
1	B	120	VAL	CA-C	5.81	1.58	1.53
1	B	191	VAL	CA-CB	5.75	1.61	1.54
1	A	312	VAL	CA-CB	5.62	1.60	1.54
1	B	173	PRO	CA-C	5.51	1.58	1.52

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	ASP	N-CA-C	14.17	128.31	111.02
1	C	212	ASP	N-CA-C	10.33	125.97	113.16
1	B	243	ALA	N-CA-C	-9.67	94.87	109.86
1	A	212	ASP	CA-C-N	-9.21	108.76	122.86
1	A	212	ASP	C-N-CA	-9.21	108.76	122.86
1	A	138	TYR	N-CA-C	9.19	123.72	108.73
1	B	275	ILE	N-CA-C	-8.49	104.42	112.83
1	B	215	TRP	CA-C-N	-8.49	111.63	120.03
1	B	215	TRP	C-N-CA	-8.49	111.63	120.03
1	B	222	ASP	N-CA-C	-8.41	101.02	111.11
1	B	280	TYR	N-CA-C	8.19	122.10	112.93
1	B	133	ILE	CB-CA-C	-8.18	101.96	110.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	177	HIS	N-CA-C	-8.14	93.45	110.80
1	A	275	ILE	N-CA-C	-7.88	104.69	112.17
1	A	264	SER	N-CA-C	7.58	121.19	110.50
1	A	231	LEU	N-CA-C	7.41	119.05	109.64
1	B	203	MSE	N-CA-C	7.40	122.08	110.17
1	A	291	ASP	N-CA-C	7.39	121.20	112.93
1	B	212	ASP	CA-C-N	-7.30	111.13	122.37
1	B	212	ASP	C-N-CA	-7.30	111.13	122.37
1	B	138	TYR	N-CA-C	7.22	120.44	108.96
1	A	161	LEU	N-CA-C	-7.21	102.83	111.69
1	A	255	THR	N-CA-C	-7.18	103.53	111.36
1	B	309	TYR	N-CA-C	-6.92	104.10	112.54
1	C	285	ILE	N-CA-C	6.89	117.91	109.30
1	A	159	HIS	N-CA-C	6.89	119.37	111.11
1	B	212	ASP	N-CA-C	6.68	125.04	110.80
1	B	114	ALA	N-CA-C	-6.61	104.44	113.30
1	A	320	TYR	N-CA-C	-6.59	96.77	110.80
1	A	175	GLY	CA-C-N	-6.40	113.46	123.13
1	A	175	GLY	C-N-CA	-6.40	113.46	123.13
1	C	110	ARG	N-CA-C	-6.23	104.41	111.14
1	B	278	PHE	N-CA-C	-6.21	102.52	110.53
1	B	123	ARG	N-CA-C	6.21	118.85	108.73
1	B	80	VAL	CA-C-N	6.17	126.18	119.89
1	B	80	VAL	C-N-CA	6.17	126.18	119.89
1	A	232	PRO	N-CA-C	-6.16	101.53	111.14
1	C	86	MSE	N-CA-C	6.12	120.82	113.23
1	A	204	ARG	N-CA-C	-5.98	101.92	110.59
1	B	68	ALA	CA-C-N	-5.87	114.22	120.03
1	B	68	ALA	C-N-CA	-5.87	114.22	120.03
1	A	285	ILE	N-CA-C	5.83	115.94	108.12
1	C	180	PRO	N-CA-C	5.75	120.63	111.26
1	B	98	THR	N-CA-C	-5.72	102.69	110.36
1	A	149	SER	N-CA-C	-5.68	102.89	110.55
1	B	221	ILE	CB-CA-C	-5.68	104.70	111.97
1	B	158	ARG	N-CA-C	-5.66	104.80	110.97
1	A	172	ALA	N-CA-C	5.63	114.62	108.14
1	A	217	THR	N-CA-C	5.63	118.84	110.39
1	A	124	GLN	N-CA-C	-5.62	105.15	112.23
1	A	62	SER	N-CA-C	-5.62	106.27	113.01
1	C	294	LYS	N-CA-C	5.61	118.33	111.82
1	B	271	ARG	N-CA-CB	-5.58	101.77	109.91
1	C	255	THR	N-CA-C	-5.54	105.24	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	335	ALA	N-CA-C	-5.54	95.48	111.00
1	C	304	MSE	N-CA-C	5.53	118.23	111.82
1	A	333	ALA	N-CA-C	-5.52	102.59	110.59
1	B	318	ASP	CB-CA-C	-5.52	104.49	113.37
1	A	26	GLU	N-CA-C	5.50	118.27	110.24
1	B	271	ARG	CA-CB-CG	5.46	125.03	114.10
1	C	138	TYR	N-CA-C	5.38	118.38	109.46
1	A	312	VAL	N-CA-C	-5.36	105.27	110.42
1	B	176	LYS	N-CA-C	-5.33	101.84	110.32
1	A	215	TRP	CA-C-N	-5.31	114.47	119.89
1	A	215	TRP	C-N-CA	-5.31	114.47	119.89
1	A	118	TYR	N-CA-C	5.29	117.87	109.24
1	C	309	TYR	N-CA-C	-5.29	105.52	111.28
1	A	222	ASP	N-CA-C	-5.27	105.54	111.28
1	B	71	LYS	N-CA-C	5.26	117.42	111.11
1	C	97	PHE	N-CA-C	5.24	117.03	109.07
1	B	204	ARG	N-CA-C	-5.24	103.48	110.55
1	B	319	GLY	N-CA-C	-5.23	100.79	113.18
1	A	274	GLU	N-CA-C	5.21	119.50	113.20
1	C	157	GLU	N-CA-C	-5.20	105.51	111.07
1	A	123	ARG	N-CA-C	5.19	118.07	109.46
1	A	114	ALA	N-CA-C	-5.18	106.87	114.39
1	B	172	ALA	N-CA-C	5.14	117.50	108.82
1	B	218	PRO	N-CA-C	-5.09	106.45	113.53
1	B	83	ARG	N-CA-C	-5.05	106.43	112.59
1	B	62	SER	N-CA-C	-5.04	107.10	113.20
1	B	270	TYR	CA-C-N	5.04	127.31	120.65
1	B	270	TYR	C-N-CA	5.04	127.31	120.65
1	A	175	GLY	N-CA-C	-5.03	101.25	113.18
1	C	207	ARG	N-CA-C	5.02	116.59	108.26

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	2534	0	2453	146	1
1	B	2542	0	2464	132	0
1	C	2527	0	2446	163	0
2	A	72	0	22	9	1
2	C	36	0	12	5	0
3	A	389	0	0	18	0
3	B	317	0	0	13	0
3	C	235	0	0	7	0
All	All	8652	0	7397	442	1

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 29.

All (442) 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:150:GLN:HG2	2:A:2167:IHS:O46	1.31	1.26
1:A:36:ARG:NH1	1:A:38:GLN:HE21	1.45	1.13
1:A:61:THR:HG22	1:A:63:ALA:H	0.99	1.12
1:B:61:THR:HG22	1:B:63:ALA:H	1.11	1.12
1:B:186:ARG:HG2	1:B:186:ARG:HH11	1.09	1.11
1:C:61:THR:HG22	1:C:63:ALA:H	1.00	1.10
1:A:176:LYS:HB3	3:A:3315:HOH:O	1.51	1.09
1:A:193:THR:HG22	1:A:196:GLU:HG3	1.42	1.01
1:A:301:LYS:O	1:A:305:ILE:HG23	1.61	1.00
1:C:119:ASP:HB2	1:C:203:MSE:HE2	1.45	0.98
1:A:267:ASP:O	1:A:271:ARG:HB2	1.63	0.98
1:B:229:ARG:HD2	3:B:2772:HOH:O	1.64	0.97
1:A:36:ARG:NH1	1:A:38:GLN:NE2	2.14	0.95
1:C:232:PRO:HD2	1:C:235:ALA:HB2	1.48	0.95
1:A:67:ARG:HG3	1:A:67:ARG:HH11	1.33	0.94
1:A:150:GLN:CG	2:A:2167:IHS:O46	2.16	0.93
1:C:61:THR:HB	1:C:64:ASP:OD1	1.68	0.93
1:C:61:THR:HG22	1:C:63:ALA:N	1.85	0.91
1:A:61:THR:HG22	1:A:63:ALA:N	1.84	0.91
1:A:110:ARG:NH2	1:A:115:GLY:O	2.02	0.91
1:C:130:LEU:HD22	1:C:135:VAL:HG21	1.53	0.89
1:A:36:ARG:HH11	1:A:38:GLN:NE2	1.69	0.89
1:C:241:CYS:SG	1:C:248:THR:HG22	2.12	0.89
1:B:61:THR:HG22	1:B:63:ALA:N	1.88	0.89
1:B:193:THR:HG22	1:B:196:GLU:H	1.37	0.88
1:C:211:THR:O	1:C:247:ARG:HD3	1.76	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ILE:HD13	1:A:254:MSE:HE1	1.57	0.85
1:A:176:LYS:HB2	3:A:3273:HOH:O	1.77	0.84
1:A:193:THR:CG2	1:A:196:GLU:HG3	2.07	0.84
1:A:176:LYS:HD3	3:A:3273:HOH:O	1.77	0.83
1:B:318:ASP:HB3	1:B:321:GLN:HG3	1.61	0.83
1:C:253:VAL:HG13	1:C:257:MSE:HE3	1.60	0.83
1:B:285:ILE:HD13	1:B:298:TYR:HB3	1.60	0.82
1:A:254:MSE:HE2	1:A:308:PHE:CG	2.15	0.82
1:C:127:HIS:HE2	1:C:194:GLU:HG3	1.43	0.81
1:B:226:ALA:O	1:B:230:THR:HG23	1.81	0.81
1:A:36:ARG:HH11	1:A:38:GLN:HE21	1.25	0.81
1:B:70:GLU:H	1:B:273:HIS:HE1	1.25	0.81
1:A:176:LYS:CB	3:A:3315:HOH:O	2.16	0.80
1:C:97:PHE:CE1	1:C:102:LEU:HG	2.17	0.80
1:C:187:ARG:HH11	1:C:187:ARG:HB3	1.45	0.80
1:A:176:LYS:CD	3:A:3273:HOH:O	2.29	0.79
1:A:317:ALA:O	1:A:318:ASP:O	1.99	0.79
1:B:263:VAL:HG23	1:B:268:ILE:HD11	1.62	0.79
1:B:318:ASP:CB	1:B:321:GLN:HG3	2.13	0.79
1:B:265:LEU:HD13	3:B:3288:HOH:O	1.80	0.79
1:B:263:VAL:CG2	1:B:268:ILE:HD11	2.13	0.78
1:C:159:HIS:HB3	3:C:2789:HOH:O	1.83	0.78
1:A:319:GLY:C	1:A:321:GLN:N	2.37	0.78
1:A:193:THR:HG22	1:A:196:GLU:H	1.49	0.77
2:A:2167:IHS:O34	3:A:2664:HOH:O	2.02	0.76
1:C:205:TYR:OH	1:C:207:ARG:HD3	1.85	0.76
1:A:207:ARG:HB3	2:A:2167:IHS:O45	1.85	0.76
1:C:307:GLN:HG3	1:C:333:ALA:HB2	1.67	0.76
1:B:245:VAL:HG13	1:B:246:GLY:H	1.51	0.76
1:C:260:ASN:O	1:C:263:VAL:HG22	1.86	0.75
1:C:61:THR:CG2	1:C:63:ALA:H	1.92	0.75
1:A:176:LYS:C	1:A:177:HIS:ND1	2.45	0.75
1:B:71:LYS:HG3	3:B:2720:HOH:O	1.87	0.75
1:B:130:LEU:HD22	1:B:135:VAL:HG21	1.68	0.75
1:A:241:CYS:SG	1:A:248:THR:HG23	2.26	0.74
1:B:253:VAL:O	1:B:257:MSE:HG3	1.87	0.74
1:B:186:ARG:HH11	1:B:186:ARG:CG	1.94	0.74
1:C:221:ILE:HD12	1:C:254:MSE:HE1	1.70	0.73
1:A:254:MSE:HE2	1:A:308:PHE:CD1	2.24	0.73
1:A:177:HIS:CD2	1:A:179:LEU:HB2	2.23	0.73
1:A:241:CYS:SG	1:A:248:THR:CG2	2.76	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:286:LYS:NZ	2:C:2166:IHS:H3	2.03	0.73
1:C:127:HIS:NE2	1:C:194:GLU:HG3	2.04	0.72
1:A:36:ARG:HH12	1:A:38:GLN:HE21	1.38	0.72
1:A:176:LYS:HG2	3:A:3315:HOH:O	1.89	0.72
1:A:307:GLN:HG3	1:A:333:ALA:HB2	1.72	0.71
1:B:288:LYS:NZ	1:B:288:LYS:H	1.89	0.70
1:B:282:GLU:HA	1:B:302:ILE:HD13	1.71	0.70
1:A:242:GLU:CD	1:A:243:ALA:H	1.98	0.70
1:C:241:CYS:SG	1:C:248:THR:CG2	2.79	0.70
1:A:59:PHE:HE2	1:A:108:LYS:HD3	1.56	0.70
1:A:176:LYS:CG	3:A:3315:HOH:O	2.37	0.69
1:C:26:GLU:OE2	1:C:27:PRO:HD2	1.92	0.69
1:C:286:LYS:HZ1	2:C:2166:IHS:H3	1.56	0.69
1:C:186:ARG:HG2	1:C:186:ARG:HH11	1.58	0.69
1:B:186:ARG:HG2	1:B:186:ARG:NH1	1.90	0.68
1:B:216:PRO:HB2	1:B:221:ILE:HD11	1.76	0.67
1:A:59:PHE:CE2	1:A:108:LYS:HD3	2.30	0.67
1:B:193:THR:CG2	1:B:196:GLU:H	2.05	0.66
1:C:163:ALA:O	1:C:167:LYS:HE2	1.94	0.66
1:B:288:LYS:H	1:B:288:LYS:CE	2.09	0.66
1:C:59:PHE:HE2	1:C:108:LYS:HD3	1.60	0.66
1:A:70:GLU:H	1:A:273:HIS:HE1	1.43	0.66
1:B:53:GLU:HG2	1:B:57:ARG:NH2	2.11	0.65
1:B:214:VAL:HG12	1:B:297:TYR:CD2	2.30	0.65
1:C:253:VAL:CG1	1:C:257:MSE:HE3	2.26	0.65
1:B:260:ASN:O	1:B:263:VAL:HG22	1.97	0.65
1:B:307:GLN:HE21	1:B:307:GLN:HA	1.62	0.64
1:B:56:PRO:HA	3:B:2892:HOH:O	1.96	0.64
1:B:307:GLN:HA	1:B:307:GLN:NE2	2.12	0.64
1:B:280:TYR:CG	1:B:305:ILE:HD12	2.33	0.64
1:C:323:PRO:HG2	1:C:326:VAL:CG2	2.27	0.64
1:C:28:VAL:HG21	1:C:335:ALA:HB3	1.79	0.64
1:A:253:VAL:O	1:A:257:MSE:HG3	1.97	0.64
1:C:187:ARG:HB3	1:C:187:ARG:NH1	2.11	0.64
1:C:323:PRO:HG2	1:C:326:VAL:HG23	1.80	0.64
1:A:215:TRP:HH2	1:A:254:MSE:HE3	1.63	0.63
1:B:70:GLU:H	1:B:273:HIS:CE1	2.11	0.63
1:A:83:ARG:HB2	1:B:229:ARG:HH11	1.64	0.63
1:A:67:ARG:HH11	1:A:67:ARG:CG	2.07	0.63
1:C:204:ARG:HA	3:C:3057:HOH:O	1.98	0.63
1:B:336:LEU:HA	3:B:3292:HOH:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ILE:HD13	1:A:171:ILE:O	1.98	0.63
1:A:307:GLN:CG	1:A:333:ALA:HB2	2.29	0.62
1:B:156:ASP:O	1:B:160:ARG:HG3	1.99	0.62
1:A:131:ASP:OD2	1:A:186:ARG:NE	2.31	0.62
1:A:215:TRP:CH2	1:A:254:MSE:HE3	2.35	0.62
1:B:232:PRO:HD2	1:B:235:ALA:HB2	1.82	0.62
1:B:254:MSE:HG2	1:B:308:PHE:CE2	2.34	0.62
1:A:70:GLU:H	1:A:273:HIS:CE1	2.17	0.62
1:C:107:ALA:O	1:C:110:ARG:HB2	1.99	0.62
1:A:319:GLY:C	1:A:321:GLN:H	2.09	0.61
1:A:323:PRO:HG2	1:A:326:VAL:HG23	1.83	0.61
1:A:171:ILE:HD13	1:A:171:ILE:C	2.26	0.61
1:C:212:ASP:CG	1:C:212:ASP:O	2.42	0.61
1:C:308:PHE:O	1:C:312:VAL:HG23	2.00	0.61
1:B:176:LYS:O	1:B:177:HIS:HB2	2.00	0.61
1:B:93:GLY:HA2	1:B:239:PHE:O	2.00	0.61
1:C:197:VAL:O	1:C:200:ALA:HB3	2.01	0.60
1:C:232:PRO:O	1:C:234:ASP:N	2.34	0.60
1:A:176:LYS:CB	3:A:3273:HOH:O	2.42	0.60
1:A:319:GLY:CA	1:A:321:GLN:HG2	2.31	0.60
1:A:55:LEU:HD23	3:A:3250:HOH:O	2.00	0.60
1:A:102:LEU:HD12	1:A:197:VAL:HG12	1.84	0.60
1:A:319:GLY:H	1:A:321:GLN:HG2	1.66	0.60
1:B:245:VAL:HG22	1:B:246:GLY:N	2.17	0.60
1:C:217:THR:O	1:C:220:ASN:HB2	2.02	0.60
1:B:160:ARG:NH2	3:B:3297:HOH:O	2.34	0.59
1:A:141:ARG:HG2	1:A:293:TRP:CZ2	2.37	0.59
1:B:97:PHE:CE1	1:B:102:LEU:HG	2.38	0.59
1:C:286:LYS:NZ	3:C:3065:HOH:O	2.29	0.59
1:B:74:HIS:CD2	1:B:284:PRO:HG3	2.37	0.59
1:C:48:ASP:HB2	1:C:134:PRO:HB2	1.84	0.59
1:C:158:ARG:HG3	1:C:158:ARG:HH11	1.68	0.59
1:B:193:THR:HG23	1:B:195:GLN:N	2.18	0.59
1:C:312:VAL:HG13	1:C:320:TYR:OH	2.02	0.59
1:A:254:MSE:O	1:A:258:LEU:HB2	2.03	0.58
1:B:212:ASP:OD1	1:B:212:ASP:O	2.21	0.58
1:C:60:ARG:HE	1:C:252:MSE:SE	2.37	0.58
1:C:228:TYR:CE2	1:C:258:LEU:HB3	2.38	0.58
1:A:156:ASP:OD2	1:A:160:ARG:NH1	2.35	0.58
1:C:232:PRO:O	1:C:235:ALA:N	2.36	0.58
1:B:242:GLU:HB3	3:B:2827:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:ILE:HD13	1:A:298:TYR:HB3	1.85	0.58
1:C:211:THR:HG22	1:C:212:ASP:H	1.68	0.58
1:A:319:GLY:N	1:A:321:GLN:HG2	2.18	0.58
1:C:244:GLY:HA2	1:C:248:THR:HG21	1.86	0.58
1:A:285:ILE:HD13	1:A:298:TYR:CB	2.34	0.58
1:B:29:GLY:N	1:B:300:GLU:OE2	2.34	0.58
1:C:245:VAL:HG22	1:C:246:GLY:N	2.19	0.58
1:C:86:MSE:SE	1:C:271:ARG:HD2	2.53	0.58
1:C:75:LEU:HD22	1:C:270:TYR:CE2	2.38	0.57
1:C:160:ARG:NH2	3:C:2993:HOH:O	2.37	0.57
1:C:119:ASP:CB	1:C:203:MSE:HE2	2.29	0.57
1:B:267:ASP:O	1:B:271:ARG:CB	2.53	0.57
1:B:227:PHE:CZ	1:B:231:LEU:HD21	2.39	0.57
1:C:232:PRO:HD2	1:C:235:ALA:CB	2.27	0.57
1:A:67:ARG:HG3	1:A:67:ARG:NH1	2.13	0.56
1:C:57:ARG:NH1	3:C:2513:HOH:O	2.38	0.56
1:B:25:THR:O	1:B:26:GLU:C	2.47	0.56
1:B:53:GLU:OE1	1:B:53:GLU:HA	2.04	0.56
1:C:193:THR:OG1	1:C:194:GLU:N	2.36	0.56
1:B:280:TYR:HB3	1:B:305:ILE:HD12	1.86	0.56
1:C:211:THR:HG22	1:C:212:ASP:N	2.20	0.56
1:A:317:ALA:C	1:A:318:ASP:O	2.48	0.56
1:C:194:GLU:HB3	1:C:205:TYR:CE1	2.40	0.56
1:B:221:ILE:HD12	1:B:254:MSE:SE	2.56	0.56
1:B:241:CYS:SG	1:B:248:THR:HG23	2.46	0.55
1:C:61:THR:CB	1:C:64:ASP:OD1	2.48	0.55
1:C:79:TYR:CZ	1:C:266:LYS:HE2	2.41	0.55
1:C:177:HIS:O	1:C:178:LYS:HB2	2.04	0.55
1:C:318:ASP:OD1	1:C:318:ASP:N	2.38	0.55
1:C:254:MSE:HG2	1:C:308:PHE:CD2	2.41	0.55
1:A:90:HIS:HE1	3:A:2605:HOH:O	1.89	0.55
1:B:110:ARG:NH2	1:B:115:GLY:O	2.39	0.55
1:B:171:ILE:HD13	1:B:171:ILE:O	2.07	0.55
1:A:313:GLN:HE22	1:A:316:ARG:HH21	1.52	0.55
1:B:193:THR:HG22	1:B:196:GLU:N	2.16	0.55
1:A:242:GLU:CG	1:A:243:ALA:N	2.70	0.55
1:C:75:LEU:HD21	1:C:279:TYR:CZ	2.41	0.55
1:C:240:HIS:ND1	1:C:240:HIS:C	2.63	0.55
1:A:61:THR:HG21	1:A:63:ALA:HB3	1.90	0.54
1:A:154:LEU:HB3	2:A:2167:IHS:O44	2.07	0.54
1:B:156:ASP:OD1	1:B:160:ARG:HD2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:164:ALA:O	1:C:188:VAL:HB	2.08	0.54
1:A:319:GLY:O	1:A:320:TYR:C	2.50	0.54
1:A:163:ALA:O	1:A:167:LYS:HD2	2.07	0.54
1:C:310:ARG:O	1:C:313:GLN:N	2.41	0.54
1:C:267:ASP:O	1:C:271:ARG:HB2	2.08	0.54
1:C:222:ASP:O	1:C:223:ARG:C	2.49	0.54
1:A:297:TYR:O	1:A:301:LYS:HG3	2.08	0.54
1:B:280:TYR:CB	1:B:305:ILE:HD12	2.38	0.53
1:B:267:ASP:O	1:B:271:ARG:HB2	2.08	0.53
1:A:89:LEU:HD22	1:A:91:ILE:HD13	1.90	0.53
1:B:53:GLU:OE1	1:B:53:GLU:CA	2.56	0.53
1:C:263:VAL:CG2	1:C:268:ILE:HD11	2.38	0.53
1:A:193:THR:CG2	1:A:196:GLU:H	2.20	0.53
1:B:30:SER:O	1:B:33:ARG:HB2	2.09	0.53
1:B:61:THR:HG22	1:B:62:SER:N	2.22	0.53
1:C:310:ARG:O	1:C:311:TYR:C	2.52	0.53
1:A:214:VAL:HG12	1:A:297:TYR:CD2	2.44	0.52
1:B:193:THR:HG23	1:B:195:GLN:H	1.74	0.52
1:C:313:GLN:HA	1:C:313:GLN:NE2	2.25	0.52
1:B:129:TYR:CD2	1:B:129:TYR:N	2.78	0.52
1:A:83:ARG:O	1:A:84:GLU:C	2.53	0.52
1:C:95:SER:HB3	1:C:243:ALA:O	2.09	0.52
1:C:225:LEU:HD11	1:C:324:TRP:HB2	1.90	0.52
1:C:127:HIS:N	1:C:157:GLU:OE1	2.35	0.52
1:A:269:LEU:HD21	1:A:305:ILE:CD1	2.41	0.51
1:C:75:LEU:HD22	1:C:270:TYR:CZ	2.45	0.51
1:C:242:GLU:HG2	1:C:247:ARG:HH21	1.75	0.51
1:A:130:LEU:HD22	1:A:135:VAL:HG21	1.92	0.51
1:B:165:LEU:HG	1:B:166:HIS:CD2	2.45	0.51
1:C:232:PRO:O	1:C:233:GLN:C	2.53	0.51
1:C:221:ILE:O	1:C:224:PHE:HB3	2.10	0.51
1:B:243:ALA:HB3	1:B:245:VAL:HG12	1.91	0.51
1:C:110:ARG:C	1:C:112:LYS:H	2.19	0.51
1:C:59:PHE:CE2	1:C:108:LYS:HD3	2.44	0.51
1:C:193:THR:HG23	1:C:196:GLU:H	1.75	0.51
1:C:324:TRP:O	1:C:328:LEU:HB2	2.10	0.51
1:A:265:LEU:HD22	1:A:269:LEU:CD1	2.40	0.51
1:A:164:ALA:O	1:A:188:VAL:HB	2.11	0.50
1:A:244:GLY:HA2	1:A:248:THR:HG21	1.93	0.50
1:C:35:GLU:O	1:C:37:PRO:HD3	2.11	0.50
1:C:90:HIS:O	1:C:91:ILE:HD13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:263:VAL:HG23	1:C:268:ILE:HD11	1.93	0.50
1:B:282:GLU:HA	1:B:302:ILE:CD1	2.41	0.50
1:C:245:VAL:HG23	1:C:278:PHE:HB2	1.94	0.50
1:B:215:TRP:CZ2	1:B:254:MSE:HE3	2.46	0.50
1:B:328:LEU:CD2	1:B:328:LEU:O	2.60	0.50
1:C:249:THR:HG22	1:C:280:TYR:CE1	2.46	0.50
1:B:267:ASP:O	1:B:271:ARG:HB3	2.12	0.50
1:B:318:ASP:OD1	1:B:318:ASP:N	2.41	0.50
1:C:69:PRO:HA	1:C:273:HIS:HE1	1.76	0.50
1:B:296:LYS:NZ	3:B:2679:HOH:O	2.32	0.50
1:C:227:PHE:CZ	1:C:231:LEU:HD21	2.46	0.50
1:B:124:GLN:HG2	1:B:145:ASN:HB2	1.94	0.50
1:B:161:LEU:O	1:B:191:VAL:HG11	2.12	0.50
1:C:61:THR:CG2	1:C:62:SER:N	2.74	0.50
1:A:157:GLU:O	1:A:161:LEU:HB2	2.11	0.50
1:C:67:ARG:O	1:C:274:GLU:HG2	2.11	0.50
1:B:50:ASP:OD1	1:B:51:GLY:N	2.45	0.49
1:C:312:VAL:O	1:C:316:ARG:HB2	2.12	0.49
1:B:222:ASP:CG	1:B:325:SER:HB3	2.38	0.49
1:C:280:TYR:CG	1:C:305:ILE:HD12	2.48	0.49
1:C:44:VAL:HG23	3:C:2375:HOH:O	2.12	0.49
1:A:72:LYS:HD2	2:C:2166:IHS:O42	2.13	0.49
1:A:176:LYS:CE	3:A:3273:HOH:O	2.56	0.49
1:C:91:ILE:HD11	1:C:255:THR:HG21	1.95	0.49
1:C:221:ILE:HD12	1:C:254:MSE:CE	2.43	0.49
1:A:127:HIS:HE1	1:A:207:ARG:CZ	2.26	0.49
1:A:166:HIS:HE1	3:A:2757:HOH:O	1.95	0.49
1:C:222:ASP:C	1:C:224:PHE:N	2.68	0.48
1:A:75:LEU:HD21	1:A:279:TYR:CE1	2.48	0.48
1:B:170:TYR:CZ	1:B:172:ALA:HB2	2.48	0.48
1:B:283:PHE:HB2	1:B:284:PRO:HD2	1.93	0.48
1:C:212:ASP:O	1:C:212:ASP:OD1	2.31	0.48
1:B:263:VAL:HG21	1:B:268:ILE:HD11	1.91	0.48
1:C:60:ARG:NH1	1:C:277:GLY:HA2	2.29	0.48
1:A:171:ILE:HD11	3:A:2973:HOH:O	2.13	0.48
1:A:319:GLY:O	1:A:321:GLN:N	2.45	0.48
1:A:154:LEU:CD1	2:A:2167:IHS:H5	2.44	0.48
1:C:44:VAL:HG22	1:C:45:TRP:N	2.28	0.48
1:C:59:PHE:HA	1:C:93:GLY:O	2.13	0.48
1:A:154:LEU:HD13	2:A:2167:IHS:S4	2.53	0.48
1:B:254:MSE:HE2	1:B:308:PHE:CD1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:LEU:O	1:B:328:LEU:HD23	2.14	0.48
1:B:335:ALA:O	1:B:336:LEU:HG	2.14	0.48
1:C:186:ARG:HH11	1:C:186:ARG:CG	2.26	0.48
1:C:236:TRP:C	1:C:236:TRP:CD1	2.91	0.48
1:A:212:ASP:OD1	1:A:212:ASP:C	2.57	0.48
1:A:242:GLU:HG2	1:A:243:ALA:N	2.28	0.47
1:B:221:ILE:O	1:B:222:ASP:C	2.58	0.47
1:C:215:TRP:CZ3	1:C:305:ILE:HG13	2.49	0.47
1:C:228:TYR:C	1:C:230:THR:H	2.22	0.47
1:A:44:VAL:HG22	1:A:45:TRP:N	2.28	0.47
1:A:67:ARG:CG	1:A:67:ARG:NH1	2.73	0.47
1:B:280:TYR:HE2	1:B:301:LYS:HD3	1.80	0.47
1:C:148:LYS:C	1:C:149:SER:O	2.56	0.47
1:C:280:TYR:HE2	1:C:301:LYS:HD2	1.80	0.47
1:A:269:LEU:HD21	1:A:305:ILE:HD13	1.97	0.47
1:B:283:PHE:CZ	1:B:285:ILE:HG12	2.48	0.47
1:C:226:ALA:O	1:C:230:THR:HG23	2.14	0.47
1:C:260:ASN:O	1:C:263:VAL:CG2	2.60	0.47
1:B:287:THR:HA	1:B:288:LYS:HZ2	1.80	0.47
1:B:336:LEU:HD23	3:B:3292:HOH:O	2.14	0.47
1:A:176:LYS:O	1:A:177:HIS:ND1	2.47	0.47
1:C:110:ARG:O	1:C:112:LYS:N	2.48	0.47
1:C:116:PRO:O	1:C:116:PRO:HG2	2.15	0.46
1:A:156:ASP:OD1	1:A:160:ARG:HD2	2.15	0.46
1:A:171:ILE:CD1	3:A:2973:HOH:O	2.63	0.46
1:A:210:ALA:HB1	3:A:3277:HOH:O	2.14	0.46
1:C:83:ARG:O	1:C:84:GLU:C	2.58	0.46
1:C:296:LYS:HD3	1:C:297:TYR:CE1	2.50	0.46
1:A:119:ASP:HB2	1:A:203:MSE:HE2	1.96	0.46
1:B:79:TYR:O	1:B:81:PRO:HD3	2.15	0.46
1:B:149:SER:O	1:B:150:GLN:C	2.58	0.46
1:C:127:HIS:HE1	1:C:207:ARG:NH2	2.13	0.46
1:C:244:GLY:HA2	1:C:248:THR:CG2	2.45	0.46
1:B:25:THR:O	1:B:26:GLU:O	2.34	0.46
1:B:98:THR:OG1	1:B:101:GLN:HG3	2.15	0.46
1:C:88:ALA:HA	1:C:90:HIS:NE2	2.31	0.46
1:C:254:MSE:HE2	1:C:308:PHE:CE1	2.51	0.46
1:A:244:GLY:HA2	1:A:248:THR:CG2	2.45	0.46
1:C:79:TYR:CE1	1:C:266:LYS:HE2	2.51	0.46
1:C:228:TYR:O	1:C:230:THR:N	2.49	0.46
1:C:254:MSE:HE2	1:C:308:PHE:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:ARG:HD2	3:B:3110:HOH:O	2.15	0.46
1:B:296:LYS:HB2	3:B:2450:HOH:O	2.15	0.46
1:C:169:VAL:O	1:C:185:VAL:HA	2.16	0.46
1:A:69:PRO:HA	1:A:273:HIS:HE1	1.81	0.46
1:B:280:TYR:HB3	1:B:305:ILE:CD1	2.46	0.46
1:C:212:ASP:OD2	1:C:242:GLU:HG2	2.16	0.46
1:B:61:THR:CG2	1:B:62:SER:N	2.78	0.45
1:C:46:ARG:CG	1:C:174:LEU:HG	2.46	0.45
1:B:74:HIS:HD2	3:B:2953:HOH:O	1.98	0.45
1:C:88:ALA:C	1:C:90:HIS:CD2	2.94	0.45
1:A:241:CYS:SG	1:A:248:THR:HG22	2.55	0.45
1:B:288:LYS:H	1:B:288:LYS:CD	2.28	0.45
1:B:307:GLN:HE21	1:B:307:GLN:CA	2.25	0.45
1:C:93:GLY:HA2	1:C:239:PHE:O	2.16	0.45
1:C:194:GLU:HB3	1:C:205:TYR:HE1	1.80	0.45
1:B:288:LYS:H	1:B:288:LYS:HZ3	1.64	0.45
1:B:55:LEU:HD22	3:B:3285:HOH:O	2.17	0.45
1:A:53:GLU:HG2	1:A:57:ARG:NH2	2.31	0.45
1:C:28:VAL:CG2	1:C:335:ALA:HB3	2.45	0.45
1:A:141:ARG:CZ	1:A:293:TRP:CG	3.00	0.45
1:A:215:TRP:O	1:A:216:PRO:C	2.59	0.45
1:B:36:ARG:NH2	1:B:39:ASP:OD1	2.50	0.45
1:B:318:ASP:C	1:B:320:TYR:H	2.24	0.45
1:C:317:ALA:O	1:C:318:ASP:O	2.34	0.45
1:A:157:GLU:O	1:A:158:ARG:C	2.58	0.45
1:C:186:ARG:HG2	1:C:186:ARG:NH1	2.31	0.45
1:C:88:ALA:HA	1:C:90:HIS:HE2	1.82	0.44
1:C:118:TYR:O	1:C:238:HIS:HB3	2.17	0.44
1:C:205:TYR:HH	1:C:207:ARG:HD3	1.81	0.44
1:A:139:GLY:O	1:A:140:GLU:C	2.59	0.44
1:B:167:LYS:O	1:B:187:ARG:HA	2.17	0.44
1:C:98:THR:OG1	1:C:101:GLN:HG3	2.17	0.44
1:A:97:PHE:CE1	1:A:102:LEU:HG	2.52	0.44
1:B:308:PHE:HA	1:B:324:TRP:CZ3	2.52	0.44
1:B:171:ILE:HD12	1:B:184:GLU:HG2	1.99	0.44
1:C:215:TRP:CZ2	1:C:254:MSE:HE3	2.53	0.44
1:A:61:THR:CG2	1:A:63:ALA:HB3	2.48	0.44
1:A:69:PRO:HA	1:A:273:HIS:CE1	2.53	0.44
1:A:92:SER:CA	1:A:252:MSE:HE3	2.48	0.44
1:A:92:SER:OG	1:A:238:HIS:HD2	2.01	0.44
1:A:270:TYR:O	1:A:274:GLU:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:ILE:HG22	1:C:252:MSE:HE3	1.99	0.44
1:C:216:PRO:HB2	1:C:221:ILE:HD11	1.99	0.44
1:A:90:HIS:C	1:A:91:ILE:HD12	2.43	0.44
1:A:296:LYS:HD2	3:A:2733:HOH:O	2.18	0.44
1:B:171:ILE:HD13	1:B:171:ILE:C	2.43	0.44
1:B:184:GLU:OE1	1:B:186:ARG:NH1	2.51	0.44
1:B:42:GLY:HA2	1:B:139:GLY:CA	2.48	0.43
1:C:154:LEU:HD23	1:C:207:ARG:HH12	1.83	0.43
1:C:223:ARG:NH2	3:C:3308:HOH:O	2.50	0.43
1:A:90:HIS:HA	1:A:236:TRP:CZ3	2.53	0.43
1:C:90:HIS:HA	1:C:236:TRP:CZ3	2.53	0.43
1:A:26:GLU:OE2	1:A:27:PRO:HD2	2.18	0.43
1:A:242:GLU:CD	1:A:243:ALA:N	2.72	0.43
1:A:261:PRO:HB2	1:A:316:ARG:HD2	1.99	0.43
1:A:262:SER:HB2	3:A:2371:HOH:O	2.17	0.43
1:B:193:THR:CG2	1:B:195:GLN:HB3	2.47	0.43
1:B:206:PHE:CZ	1:B:227:PHE:HB2	2.53	0.43
1:C:161:LEU:HD12	1:C:161:LEU:HA	1.82	0.43
1:C:245:VAL:O	1:C:249:THR:HB	2.18	0.43
1:A:67:ARG:HG2	1:A:274:GLU:O	2.17	0.43
1:A:241:CYS:SG	1:A:244:GLY:HA2	2.59	0.43
1:C:127:HIS:CE1	1:C:207:ARG:NH2	2.87	0.43
1:A:92:SER:C	1:A:252:MSE:HE3	2.43	0.43
1:B:288:LYS:HB2	1:B:288:LYS:HE2	1.91	0.43
1:C:286:LYS:HZ3	2:C:2166:IHS:H3	1.81	0.43
1:C:324:TRP:CZ2	1:C:328:LEU:HG	2.54	0.43
1:A:177:HIS:HD2	1:A:179:LEU:HB2	1.79	0.43
1:B:70:GLU:N	1:B:273:HIS:HE1	2.05	0.43
1:B:222:ASP:OD1	1:B:325:SER:HB3	2.19	0.43
1:C:91:ILE:CG2	1:C:92:SER:N	2.81	0.43
1:B:215:TRP:CH2	1:B:254:MSE:HE3	2.54	0.43
1:C:214:VAL:HG12	1:C:297:TYR:CD2	2.54	0.43
1:A:154:LEU:HD13	2:A:2167:IHS:O34	2.19	0.43
1:A:254:MSE:HE2	1:A:308:PHE:CD2	2.54	0.43
1:B:245:VAL:HG13	1:B:246:GLY:N	2.27	0.43
1:C:310:ARG:HH21	1:C:331:HIS:HB3	1.83	0.43
1:A:236:TRP:CD1	1:A:236:TRP:C	2.97	0.42
1:C:97:PHE:CD1	1:C:102:LEU:HG	2.54	0.42
1:C:123:ARG:HA	1:C:247:ARG:NH1	2.33	0.42
1:C:268:ILE:O	1:C:271:ARG:HB3	2.19	0.42
1:A:70:GLU:N	1:A:273:HIS:HE1	2.15	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:50:ASP:N	1:C:50:ASP:OD1	2.51	0.42
1:B:57:ARG:HA	1:B:57:ARG:NE	2.34	0.42
1:B:171:ILE:CD1	1:B:184:GLU:HG2	2.50	0.42
1:A:36:ARG:HB3	1:A:38:GLN:NE2	2.34	0.42
1:A:129:TYR:HE2	1:A:194:GLU:HG2	1.85	0.42
1:C:89:LEU:HD22	1:C:91:ILE:HG12	2.02	0.42
1:A:128:GLY:HA3	1:A:161:LEU:HD21	2.02	0.42
1:B:219:GLU:CD	1:B:219:GLU:H	2.27	0.42
1:A:30:SER:O	1:A:33:ARG:HG3	2.20	0.42
1:A:294:LYS:O	1:A:295:THR:C	2.63	0.42
1:B:87:ASP:O	1:B:90:HIS:CE1	2.72	0.42
1:C:221:ILE:HG21	1:C:324:TRP:CG	2.55	0.42
1:A:177:HIS:ND1	1:A:177:HIS:N	2.68	0.42
1:A:285:ILE:HD13	1:A:298:TYR:HB2	2.01	0.42
1:A:193:THR:HG23	1:A:195:GLN:N	2.35	0.41
1:B:103:LYS:NZ	1:B:201:ALA:O	2.53	0.41
1:B:318:ASP:HB2	1:B:321:GLN:HG3	1.98	0.41
1:A:301:LYS:O	1:A:305:ILE:CG2	2.50	0.41
1:C:211:THR:CG2	1:C:212:ASP:H	2.32	0.41
1:C:311:TYR:CE1	1:C:324:TRP:HA	2.55	0.41
2:C:2166:IHS:O43	2:C:2166:IHS:H4	2.19	0.41
1:C:88:ALA:O	1:C:259:LYS:NZ	2.53	0.41
1:A:250:ALA:O	1:A:254:MSE:HG3	2.21	0.41
1:B:46:ARG:HH11	1:B:46:ARG:HD3	1.73	0.41
1:B:241:CYS:SG	1:B:248:THR:CG2	3.09	0.41
1:C:163:ALA:O	1:C:167:LYS:CE	2.64	0.41
1:A:42:GLY:HA3	1:A:137:TRP:NE1	2.35	0.41
1:A:92:SER:OG	1:A:238:HIS:CD2	2.74	0.41
1:A:193:THR:HG23	1:A:195:GLN:H	1.86	0.41
1:A:286:LYS:HE3	2:A:2165:IHS:O32	2.20	0.41
1:A:331:HIS:N	1:A:332:PRO:CD	2.84	0.41
1:A:56:PRO:HB3	1:A:97:PHE:HB3	2.03	0.41
1:B:128:GLY:C	1:B:129:TYR:CD2	2.99	0.41
1:C:212:ASP:OD2	1:C:247:ARG:NH2	2.54	0.41
1:A:102:LEU:HD13	1:A:201:ALA:CB	2.50	0.41
1:B:67:ARG:NH2	1:B:275:ILE:O	2.52	0.41
1:B:265:LEU:HD22	1:B:269:LEU:HG	2.02	0.41
1:C:154:LEU:CD2	1:C:207:ARG:NH1	2.84	0.41
1:B:280:TYR:CE2	1:B:301:LYS:HD3	2.56	0.40
1:B:76:ASP:OD1	1:B:76:ASP:C	2.64	0.40
1:B:163:ALA:O	1:B:167:LYS:HG3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:245:VAL:CG2	1:C:246:GLY:N	2.80	0.40
1:B:267:ASP:O	1:B:271:ARG:HD3	2.21	0.40
1:C:228:TYR:C	1:C:230:THR:N	2.80	0.40
1:C:280:TYR:CD2	1:C:305:ILE:HD12	2.56	0.40
1:B:308:PHE:O	1:B:312:VAL:HG23	2.22	0.40
1:C:61:THR:HG22	1:C:62:SER:N	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ARG:CB	2:A:2167:IHS:O42[3_555]	2.11	0.09

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	309/337 (92%)	283 (92%)	23 (7%)	3 (1%)	12	24
1	B	310/337 (92%)	292 (94%)	16 (5%)	2 (1%)	21	38
1	C	308/337 (91%)	266 (86%)	35 (11%)	7 (2%)	5	8
All	All	927/1011 (92%)	841 (91%)	74 (8%)	12 (1%)	9	18

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	177	HIS
1	A	318	ASP
1	C	111	GLU
1	C	233	GLN
1	C	318	ASP
1	C	229	ARG

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Mol	Chain	Res	Type
1	C	321	GLN
1	B	26	GLU
1	C	197	VAL
1	C	317	ALA
1	A	180	PRO
1	B	245	VAL

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	259/269 (96%)	225 (87%)	34 (13%)	4	8
1	B	260/269 (97%)	232 (89%)	28 (11%)	6	13
1	C	258/269 (96%)	218 (84%)	40 (16%)	2	5
All	All	777/807 (96%)	675 (87%)	102 (13%)	4	8

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ARG
1	A	53	GLU
1	A	55	LEU
1	A	67	ARG
1	A	89	LEU
1	A	91	ILE
1	A	94	SER
1	A	102	LEU
1	A	130	LEU
1	A	133	ILE
1	A	161	LEU
1	A	171	ILE
1	A	177	HIS
1	A	178	LYS
1	A	185	VAL
1	A	186	ARG

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Mol	Chain	Res	Type
1	A	187	ARG
1	A	193	THR
1	A	194	GLU
1	A	225	LEU
1	A	237	LEU
1	A	248	THR
1	A	258	LEU
1	A	262	SER
1	A	263	VAL
1	A	265	LEU
1	A	271	ARG
1	A	282	GLU
1	A	292	SER
1	A	296	LYS
1	A	305	ILE
1	A	307	GLN
1	A	328	LEU
1	A	329	LYS
1	B	46	ARG
1	B	53	GLU
1	B	55	LEU
1	B	67	ARG
1	B	89	LEU
1	B	102	LEU
1	B	103	LYS
1	B	108	LYS
1	B	110	ARG
1	B	130	LEU
1	B	161	LEU
1	B	167	LYS
1	B	171	ILE
1	B	185	VAL
1	B	186	ARG
1	B	193	THR
1	B	194	GLU
1	B	233	GLN
1	B	237	LEU
1	B	248	THR
1	B	258	LEU
1	B	265	LEU
1	B	288	LYS
1	B	296	LYS

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Mol	Chain	Res	Type
1	B	305	ILE
1	B	316	ARG
1	B	318	ASP
1	B	328	LEU
1	C	33	ARG
1	C	46	ARG
1	C	53	GLU
1	C	67	ARG
1	C	89	LEU
1	C	91	ILE
1	C	102	LEU
1	C	103	LYS
1	C	110	ARG
1	C	113	THR
1	C	116	PRO
1	C	130	LEU
1	C	152	GLU
1	C	158	ARG
1	C	160	ARG
1	C	161	LEU
1	C	180	PRO
1	C	185	VAL
1	C	186	ARG
1	C	197	VAL
1	C	203	MSE
1	C	214	VAL
1	C	218	PRO
1	C	220	ASN
1	C	229	ARG
1	C	233	GLN
1	C	237	LEU
1	C	240	HIS
1	C	242	GLU
1	C	245	VAL
1	C	248	THR
1	C	253	VAL
1	C	258	LEU
1	C	262	SER
1	C	292	SER
1	C	296	LYS
1	C	305	ILE
1	C	318	ASP

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Mol	Chain	Res	Type
1	C	328	LEU
1	C	330	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	90	HIS
1	A	166	HIS
1	A	238	HIS
1	A	260	ASN
1	A	273	HIS
1	A	313	GLN
1	A	315	ASN
1	B	74	HIS
1	B	90	HIS
1	B	124	GLN
1	B	166	HIS
1	B	233	GLN
1	B	238	HIS
1	B	260	ASN
1	B	273	HIS
1	B	307	GLN
1	B	315	ASN
1	C	166	HIS
1	C	189	GLN
1	C	195	GLN
1	C	233	GLN
1	C	260	ASN
1	C	307	GLN
1	C	313	GLN
1	C	315	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	IHS	A	2167	-	36,36,36	2.22	9 (25%)	48,60,60	1.87	8 (16%)
2	IHS	A	2165	-	36,36,36	1.83	11 (30%)	48,60,60	1.54	9 (18%)
2	IHS	C	2166	-	36,36,36	2.10	10 (27%)	48,60,60	1.72	11 (22%)

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
2	IHS	A	2167	-	-	12/30/54/54	0/1/1/1
2	IHS	A	2165	-	-	4/30/54/54	0/1/1/1
2	IHS	C	2166	-	-	9/30/54/54	0/1/1/1

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2167	IHS	O13-S3	7.11	1.78	1.57
2	A	2167	IHS	O23-S3	-5.47	1.21	1.45
2	C	2166	IHS	C6-C1	5.06	1.62	1.52
2	A	2167	IHS	O44-S4	-4.64	1.22	1.50
2	C	2166	IHS	C6-C5	4.04	1.60	1.52
2	C	2166	IHS	O1-S1	3.90	1.69	1.57
2	C	2166	IHS	C3-C2	3.72	1.59	1.52
2	C	2166	IHS	O12-C2	-3.38	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2165	IHS	C6-C1	3.36	1.59	1.52
2	C	2166	IHS	O15-S5	3.27	1.67	1.57
2	A	2165	IHS	O15-S5	3.21	1.67	1.57
2	A	2165	IHS	O13-S3	3.18	1.66	1.57
2	A	2167	IHS	O43-S3	-2.98	1.32	1.45
2	A	2165	IHS	O12-C2	-2.98	1.39	1.46
2	C	2166	IHS	O3-S1	2.76	1.57	1.45
2	A	2167	IHS	C6-C1	2.74	1.57	1.52
2	A	2165	IHS	C5-C4	2.70	1.57	1.52
2	A	2167	IHS	O12-C2	-2.62	1.40	1.46
2	A	2167	IHS	O15-C5	-2.48	1.40	1.46
2	A	2165	IHS	C6-C5	2.45	1.57	1.52
2	A	2165	IHS	O23-S3	2.41	1.55	1.45
2	C	2166	IHS	O12-S2	2.32	1.64	1.57
2	A	2165	IHS	O3-S1	2.29	1.55	1.45
2	C	2166	IHS	O25-S5	2.27	1.55	1.45
2	A	2165	IHS	O34-S4	2.26	1.55	1.45
2	A	2165	IHS	C3-C2	2.24	1.56	1.52
2	A	2165	IHS	O26-S6	2.21	1.55	1.45
2	C	2166	IHS	C2-C1	2.16	1.56	1.52
2	A	2167	IHS	O12-S2	2.10	1.63	1.57
2	A	2167	IHS	C6-C5	2.09	1.56	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2167	IHS	O33-S3-O43	7.54	134.95	108.56
2	A	2167	IHS	C3-O13-S3	5.13	131.35	119.04
2	C	2166	IHS	O35-S5-O15	-3.75	97.76	106.37
2	A	2165	IHS	O15-C5-C4	3.66	116.54	108.56
2	C	2166	IHS	C5-C4-C3	3.37	117.82	110.43
2	C	2166	IHS	O14-C4-C5	-3.23	101.51	108.56
2	C	2166	IHS	C1-O1-S1	3.21	126.75	119.04
2	A	2167	IHS	O35-S5-O15	-3.17	99.10	106.37
2	C	2166	IHS	O35-S5-O25	3.11	119.44	108.56
2	A	2165	IHS	C4-O14-S4	3.07	126.40	119.04
2	C	2166	IHS	C6-C1-C2	-3.05	103.73	110.43
2	A	2165	IHS	O14-C4-C5	-3.00	102.01	108.56
2	A	2167	IHS	O33-S3-O13	-2.98	99.54	106.37
2	C	2166	IHS	O16-C6-C5	-2.90	102.22	108.56
2	A	2167	IHS	C5-C4-C3	2.88	116.75	110.43
2	A	2165	IHS	C5-C4-C3	2.82	116.62	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2166	IHS	C4-O14-S4	2.75	125.64	119.04
2	A	2165	IHS	C2-O12-S2	-2.63	112.74	119.04
2	A	2165	IHS	O35-S5-O25	2.52	117.36	108.56
2	C	2166	IHS	C5-C6-C1	2.41	115.71	110.43
2	C	2166	IHS	O13-C3-C4	-2.31	103.51	108.56
2	A	2165	IHS	C3-C2-C1	2.30	115.48	110.43
2	A	2165	IHS	C6-C1-C2	-2.26	105.47	110.43
2	C	2166	IHS	O13-C3-C2	2.18	113.32	108.56
2	A	2165	IHS	C5-C6-C1	2.11	115.06	110.43
2	A	2167	IHS	C3-C2-C1	2.10	115.03	110.43
2	A	2167	IHS	O14-C4-C5	-2.04	104.10	108.56
2	A	2167	IHS	O44-S4-O34	-2.01	101.52	108.56

There are no chirality outliers.

All (25) torsion outliers are listed below:

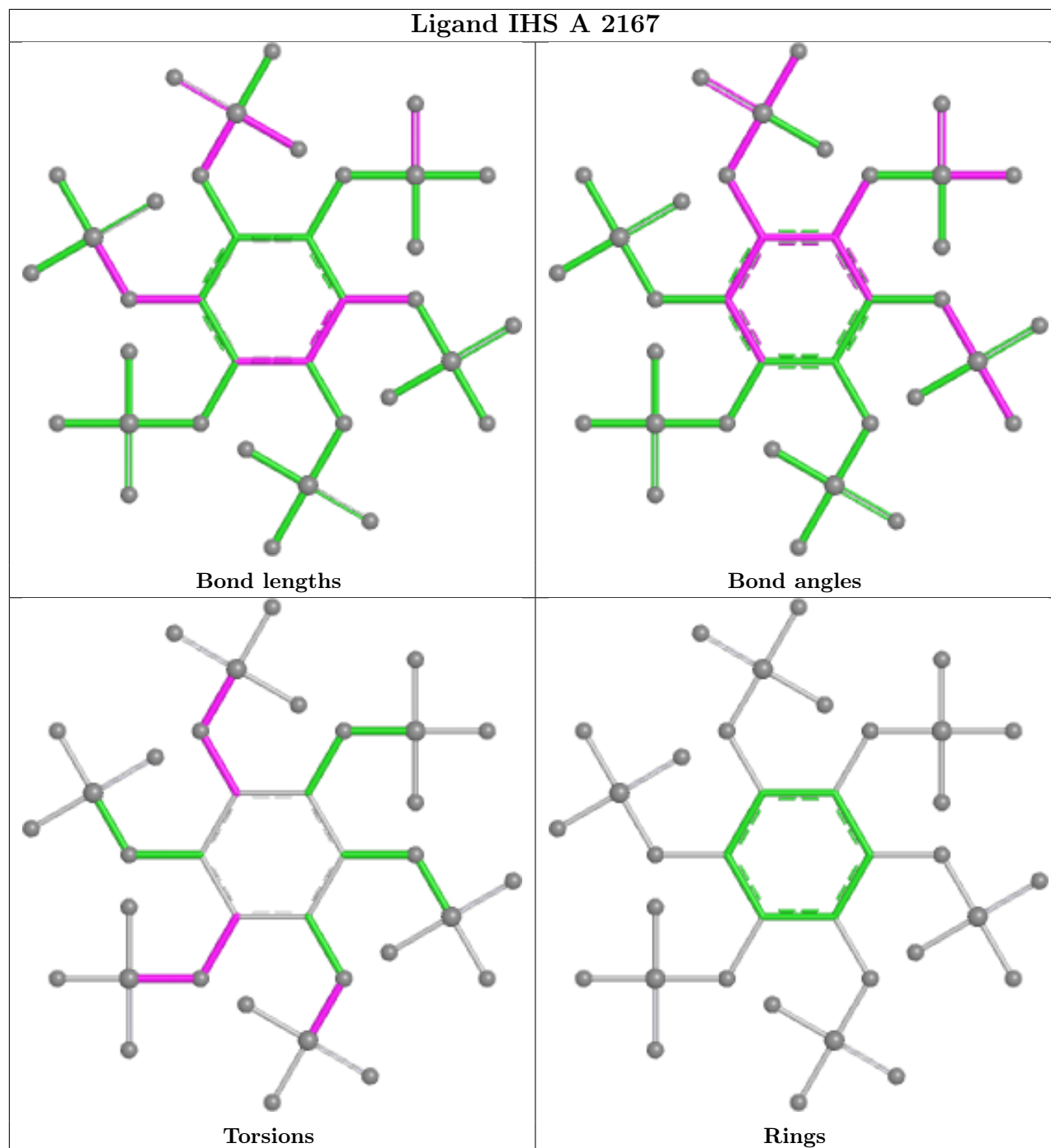
Mol	Chain	Res	Type	Atoms
2	A	2165	IHS	C3-C4-O14-S4
2	A	2167	IHS	C6-C1-O1-S1
2	A	2167	IHS	C1-O1-S1-O2
2	A	2167	IHS	C1-O1-S1-O3
2	C	2166	IHS	C1-O1-S1-O2
2	C	2166	IHS	C4-C3-O13-S3
2	C	2166	IHS	C3-C4-O14-S4
2	A	2167	IHS	C1-O1-S1-O4
2	A	2167	IHS	C3-O13-S3-O23
2	A	2167	IHS	C3-O13-S3-O43
2	C	2166	IHS	C1-O1-S1-O3
2	C	2166	IHS	C1-O1-S1-O4
2	A	2167	IHS	C6-O16-S6-O36
2	A	2165	IHS	C5-C4-O14-S4
2	A	2167	IHS	C2-C1-O1-S1
2	A	2167	IHS	C4-C3-O13-S3
2	C	2166	IHS	C2-C3-O13-S3
2	A	2167	IHS	C3-O13-S3-O33
2	A	2167	IHS	C6-O16-S6-O26
2	A	2167	IHS	C6-O16-S6-O46
2	C	2166	IHS	C5-O15-S5-O35
2	A	2165	IHS	C1-O1-S1-O2
2	C	2166	IHS	C5-O15-S5-O25
2	A	2165	IHS	C6-C1-O1-S1
2	C	2166	IHS	C1-C6-O16-S6

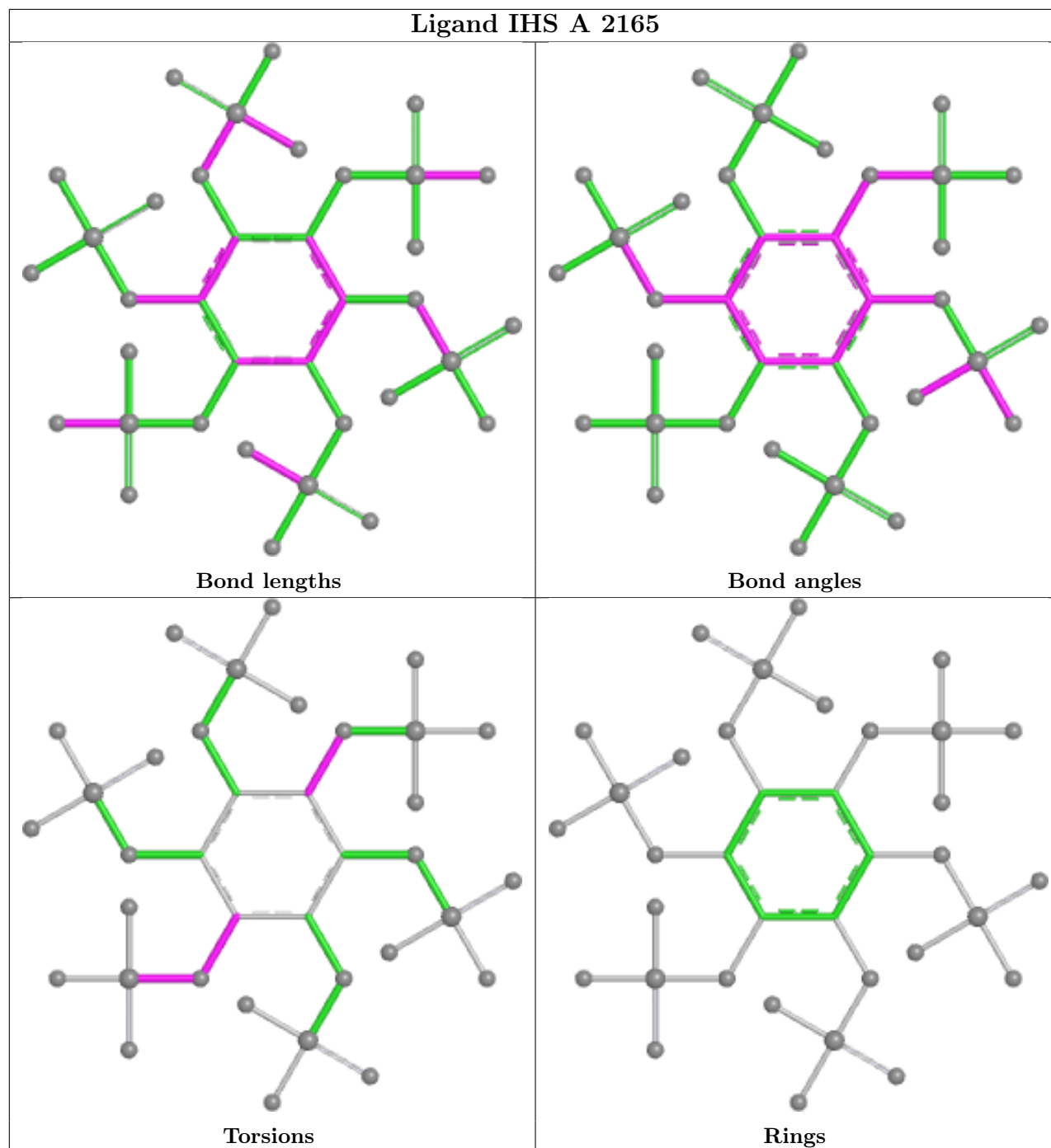
There are no ring outliers.

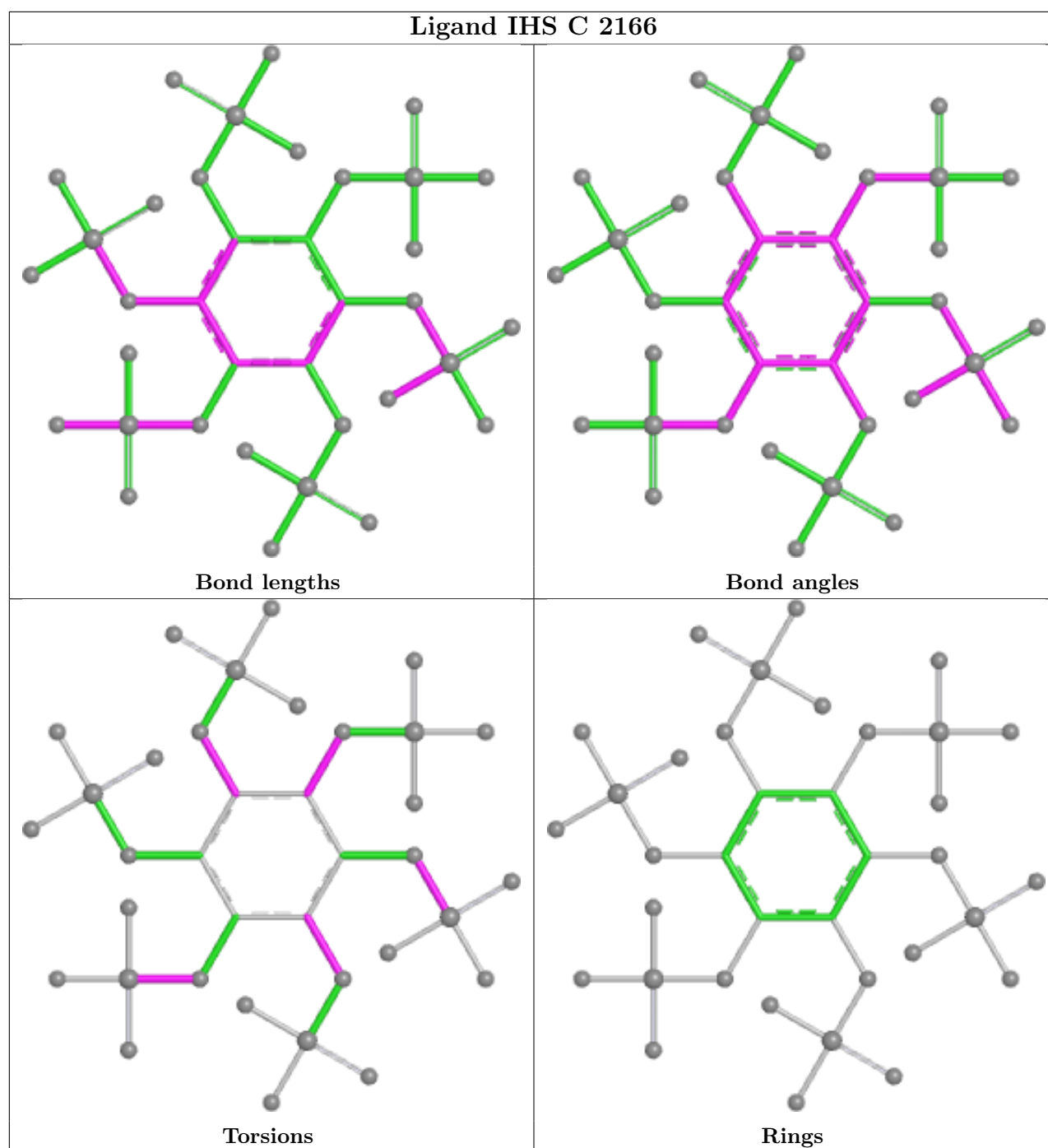
3 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2167	IHS	8	1
2	A	2165	IHS	1	0
2	C	2166	IHS	5	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	305/337 (90%)	-0.57	2 (0%) 84 81	4, 20, 39, 60	0
1	B	306/337 (90%)	-0.45	2 (0%) 84 81	11, 23, 45, 66	0
1	C	304/337 (90%)	0.09	4 (1%) 75 71	11, 35, 63, 71	0
All	All	915/1011 (90%)	-0.31	8 (0%) 81 78	4, 25, 54, 71	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	335	ALA	3.1
1	B	336	LEU	3.0
1	A	319	GLY	2.8
1	C	335	ALA	2.3
1	B	25	THR	2.2
1	C	319	GLY	2.2
1	C	159	HIS	2.1
1	C	324	TRP	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.

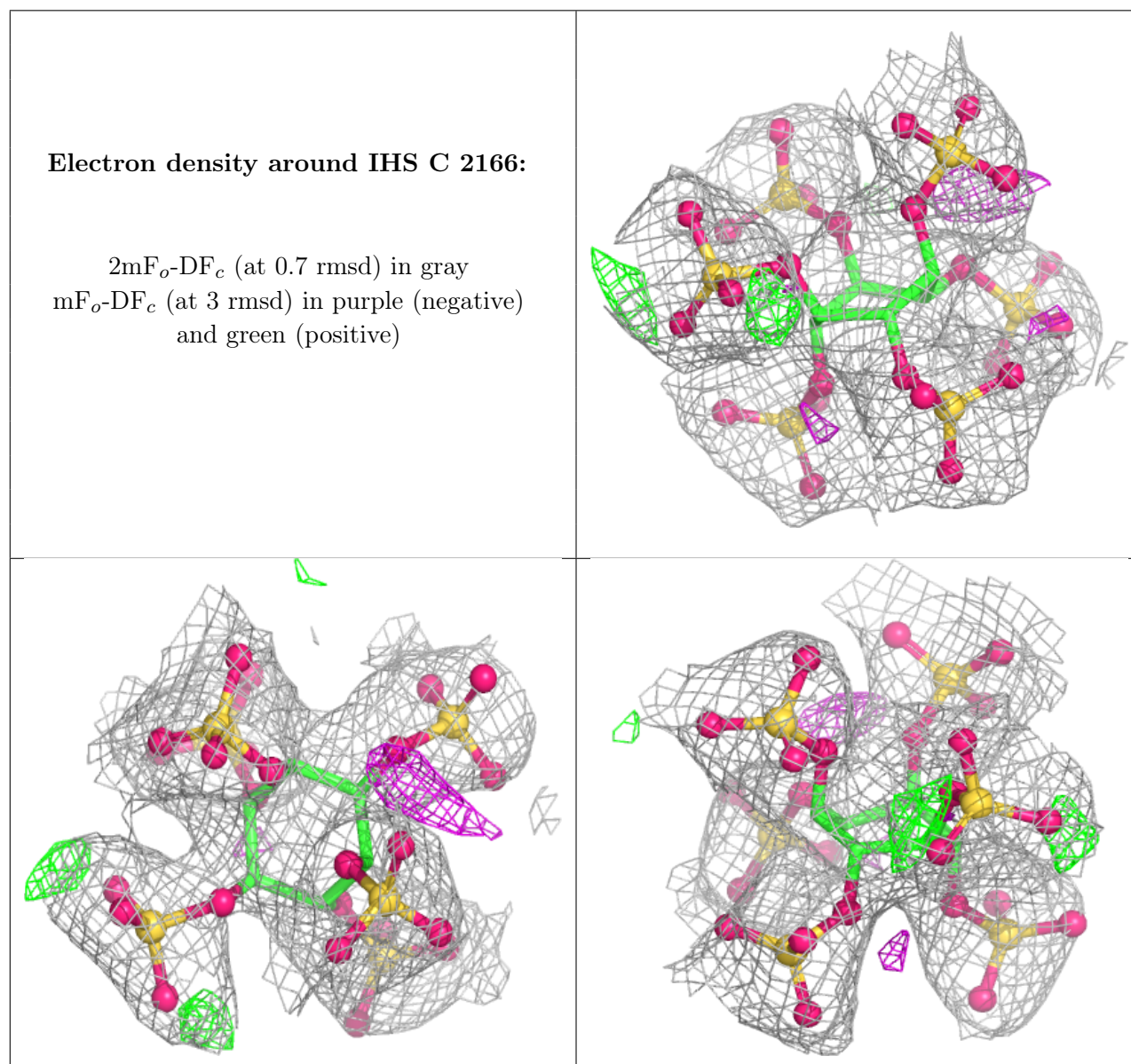
6.4 Ligands [i](#)

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.

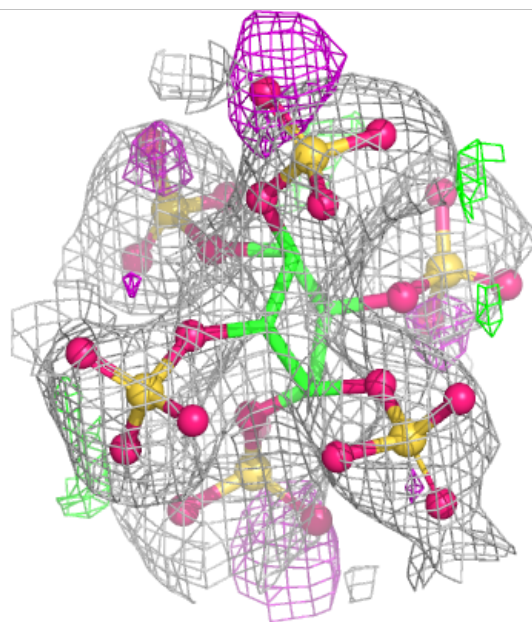
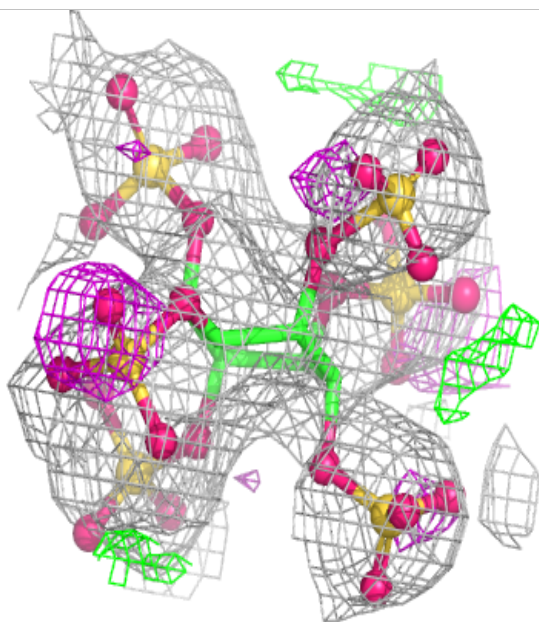
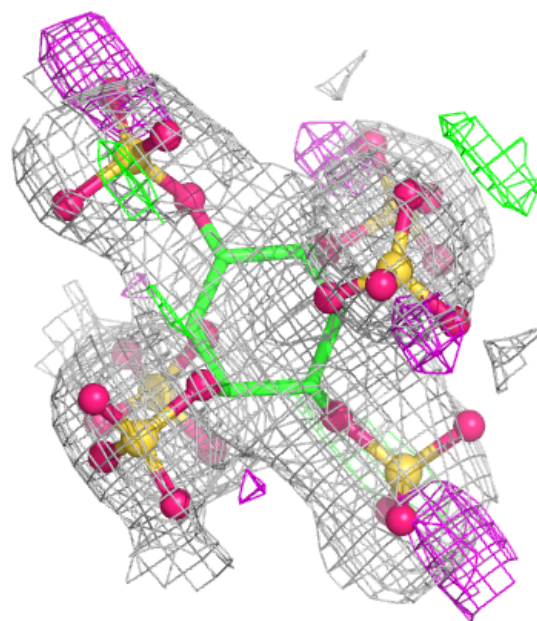
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IHS	C	2166	36/36	0.90	0.11	54,62,67,68	0
2	IHS	A	2167	36/36	0.91	0.12	54,57,60,61	36
2	IHS	A	2165	36/36	0.93	0.10	51,62,69,70	0

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.



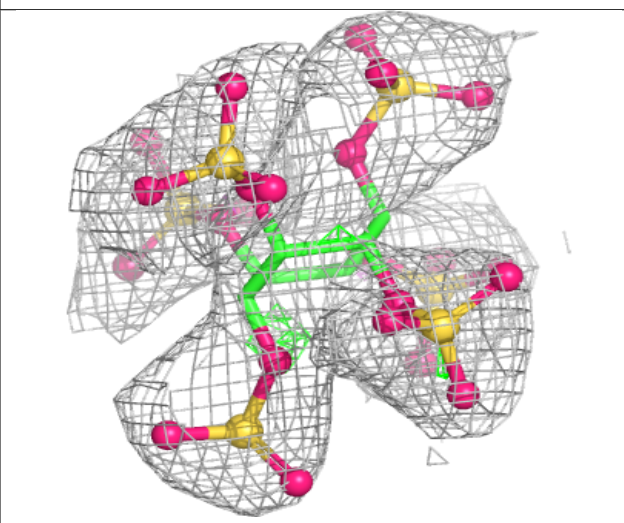
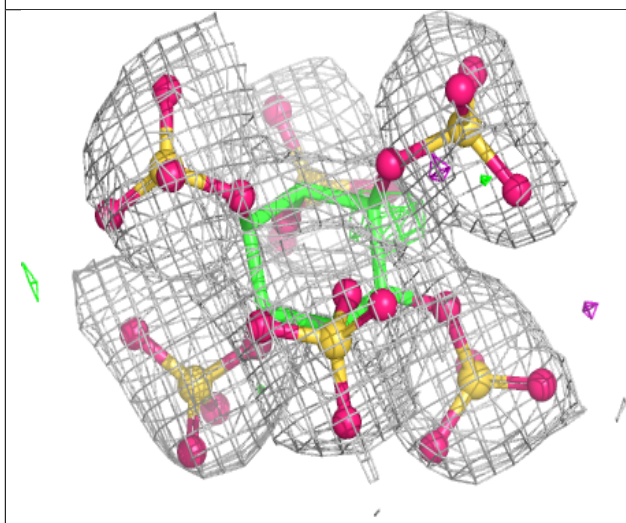
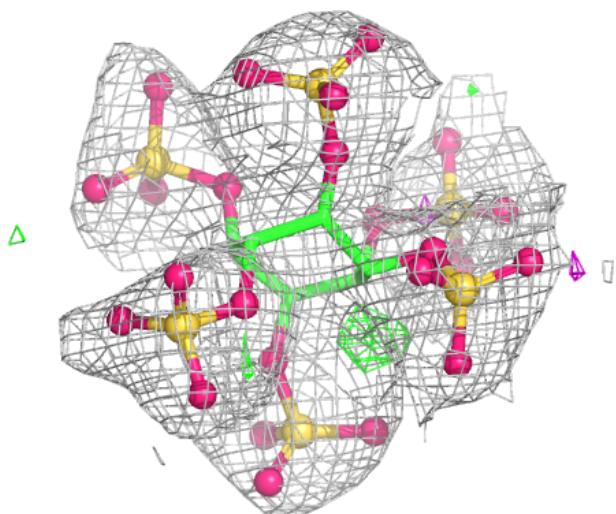
Electron density around IHS A 2167:

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



Electron density around IHS A 2165:

$2mF_o-DF_c$ (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.