



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:00 AM UTC

PDB ID : 2UZA / pdb_00002uza
Title : CRYSTAL STRUCTURE OF THE FREE RADICAL INTERMEDIATE OF
PYRUVATE:FERREDOXIN OXIDOREDUCTASE FROM DESULFOVIB-
RIO AFRICANUS
Authors : Chabriere, E.; Cavazza, C.; Contreras-Martel, C.; Fontecilla-Camps, J.C.
Deposited on : 2007-04-27
Resolution : 2.42 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

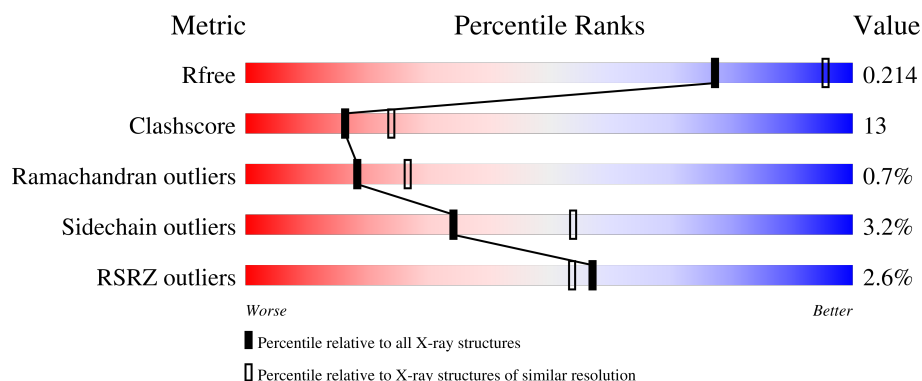
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	1231	3% 70% 27% .
1	B	1231	2% 77% 20% .

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 19846 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 PYRUVATE FERREDOXIN OXIDOREDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1231	Total	C	N	O	S	0	0	0
			9383	5941	1599	1784	59			
1	B	1231	Total	C	N	O	S	0	0	0
			9383	5941	1599	1784	59			

- Molecule 2 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



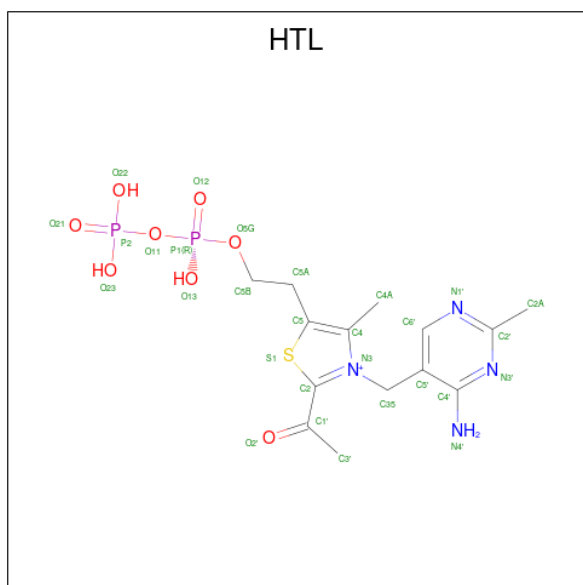
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is 2-ACETYL-THIAMINE DIPHOSPHATE (CCD ID: HTL) (formula: $C_{14}H_{21}N_4O_8P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 29	C 14	N 4	O 8	P 2	S 1	0	0
3	B	1	Total 29	C 14	N 4	O 8	P 2	S 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

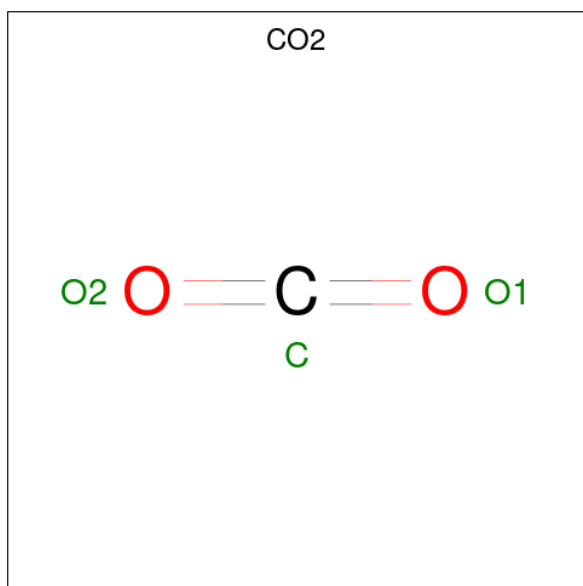
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		

- Molecule 6 is CARBON DIOXIDE (CCD ID: CO2) (formula: CO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		

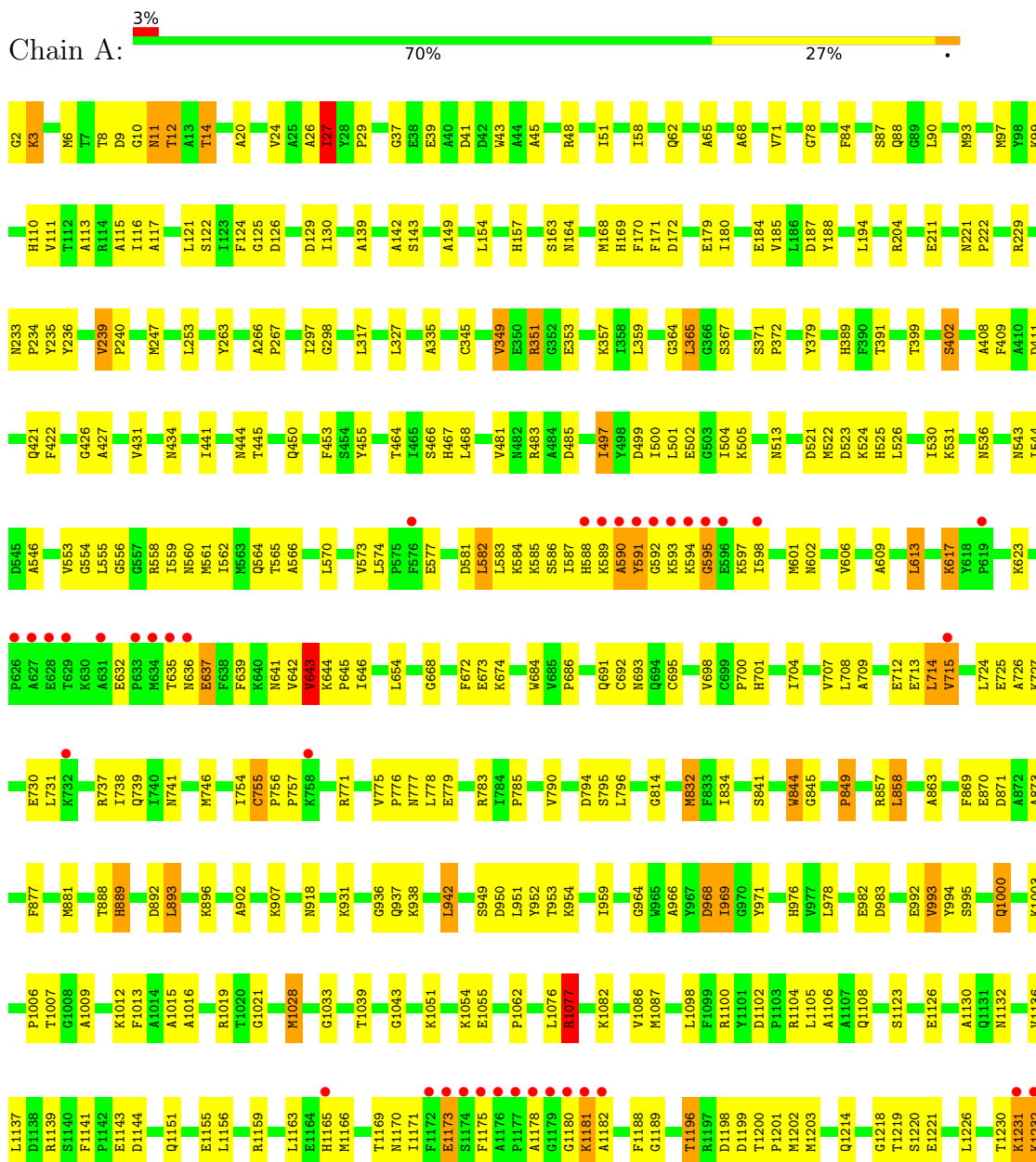
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	410	Total	O	0	0
			410	410		
7	B	554	Total	O	0	0
			554	554		

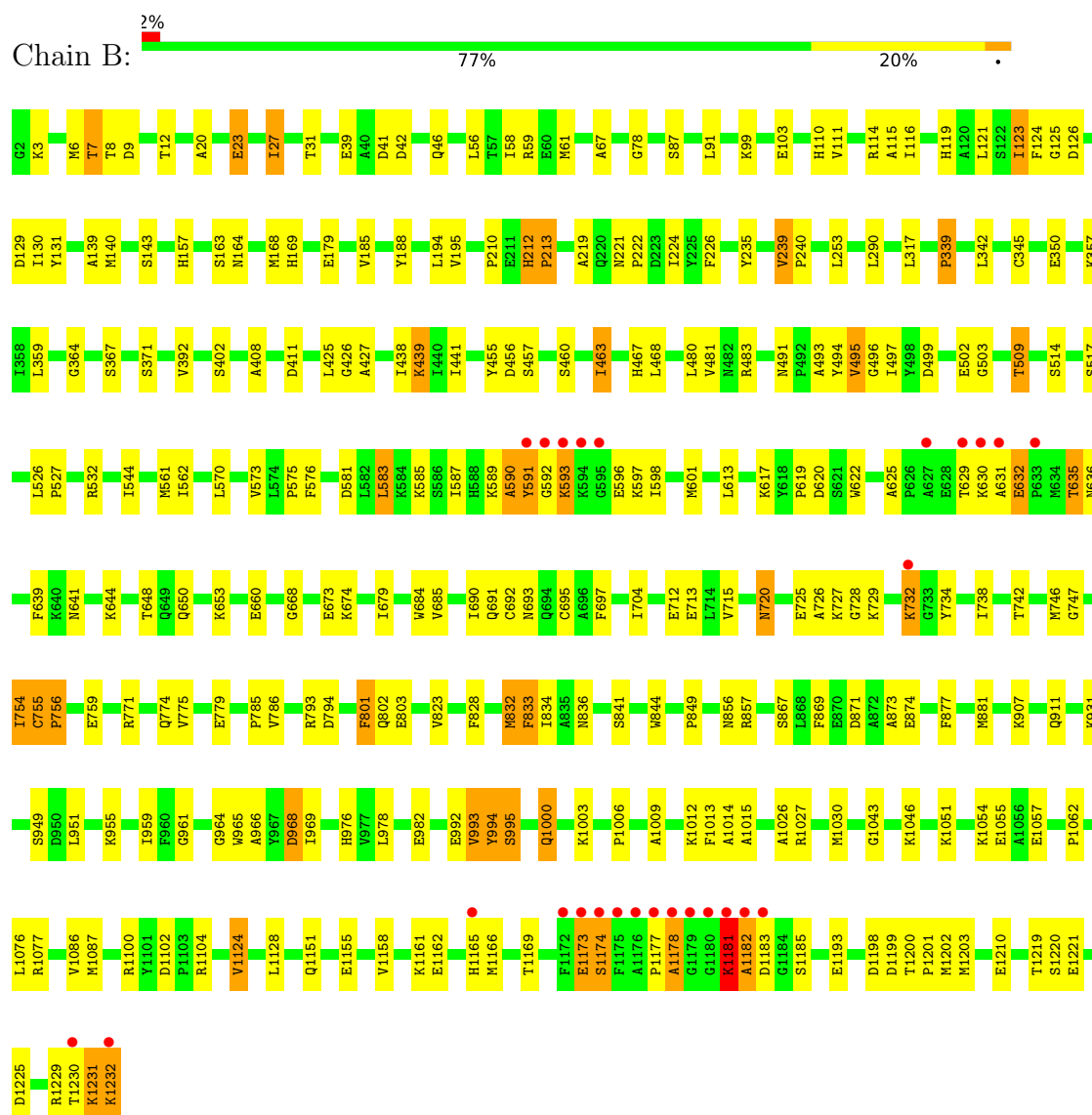
3 Residue-property plots

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: PYRUVATE FERREDOXIN OXIDOREDUCTASE



• Molecule 1: PYRUVATE FERREDOXIN OXIDOREDUCTASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.95Å 146.16Å 211.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.47 – 2.42 47.47 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.1 (47.47-2.42) 99.2 (47.47-2.42)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.93 (at 2.42Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.171 , 0.226 0.157 , 0.214	Depositor DCC
R_{free} test set	5121 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19846	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CO2, SF4, CA, HTL, MG

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	0.53	1/9585 (0.0%)	1.01	48/12954 (0.4%)
1	B	0.55	0/9585	1.02	55/12954 (0.4%)
All	All	0.54	1/19170 (0.0%)	1.01	103/25908 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1028	MET	SD-CE	-6.34	1.63	1.79

All (103) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	756	PRO	N-CA-C	10.19	123.14	110.70
1	A	125	GLY	N-CA-C	9.13	127.77	111.62
1	B	125	GLY	N-CA-C	8.79	128.46	111.31
1	B	993	VAL	CB-CA-C	-8.56	103.69	111.74
1	B	756	PRO	N-CA-C	8.52	121.10	110.70
1	A	771	ARG	N-CA-C	8.09	119.73	111.07
1	A	364	GLY	N-CA-C	7.94	126.44	114.61
1	B	755	CYS	CA-C-N	7.47	128.08	120.38
1	B	755	CYS	C-N-CA	7.47	128.08	120.38
1	B	78	GLY	N-CA-C	7.27	125.40	115.30
1	A	966	ALA	N-CA-C	7.17	119.17	111.36
1	A	969	ILE	N-CA-C	7.01	118.61	110.62
1	A	139	ALA	N-CA-C	-6.81	100.41	110.48
1	A	559	ILE	N-CA-C	6.81	122.33	113.07
1	B	966	ALA	N-CA-C	6.77	118.66	111.28
1	B	139	ALA	N-CA-C	-6.72	101.02	110.50
1	A	993	VAL	CB-CA-C	-6.59	105.55	111.74
1	A	500	ILE	N-CA-C	6.54	119.23	111.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1016	ALA	N-CA-C	-6.47	104.00	112.41
1	B	771	ARG	N-CA-C	6.46	119.15	111.33
1	A	590	ALA	N-CA-C	-6.41	102.24	110.19
1	A	844	TRP	N-CA-C	-6.33	104.26	112.23
1	B	734	TYR	N-CA-C	6.30	118.65	110.53
1	B	871	ASP	N-CA-C	6.29	120.99	112.88
1	B	801	PHE	N-CA-C	-6.20	105.02	112.59
1	B	969	ILE	N-CA-C	6.15	117.63	110.62
1	B	679	ILE	N-CA-C	-6.12	105.76	111.45
1	A	591	TYR	CB-CA-C	-6.11	109.52	116.54
1	B	1014	ALA	N-CA-C	-6.08	103.24	110.41
1	A	755	CYS	CA-C-N	6.07	126.63	120.38
1	A	755	CYS	C-N-CA	6.07	126.63	120.38
1	B	832	MET	N-CA-C	6.07	119.60	109.95
1	B	994	TYR	N-CA-C	-6.06	97.81	108.23
1	A	247	MET	N-CA-C	-6.06	104.76	111.36
1	B	339	PRO	N-CA-C	6.05	123.59	113.78
1	B	402	SER	N-CA-C	6.02	118.68	110.55
1	B	1077	ARG	N-CA-C	6.00	120.07	112.87
1	B	759	GLU	N-CA-C	-6.00	97.91	108.23
1	B	593	LYS	N-CA-C	-5.97	103.32	111.56
1	A	497	ILE	N-CA-C	5.92	118.88	112.96
1	A	27	ILE	N-CA-C	5.90	117.41	108.80
1	B	774	GLN	N-CA-C	5.88	119.72	112.54
1	A	863	ALA	N-CA-C	-5.86	98.97	108.41
1	A	588	HIS	N-CA-C	-5.82	105.02	111.36
1	A	1141	PHE	CA-C-N	5.79	125.92	119.32
1	A	1141	PHE	C-N-CA	5.79	125.92	119.32
1	A	402	SER	N-CA-C	5.76	119.47	110.32
1	A	643	VAL	N-CA-C	5.69	116.47	110.72
1	B	239	VAL	CB-CA-C	-5.67	108.31	113.70
1	A	1077	ARG	N-CA-C	5.67	119.00	111.75
1	B	833	PHE	N-CA-C	-5.67	100.47	109.59
1	A	968	ASP	N-CA-C	5.66	117.14	108.30
1	A	725	GLU	N-CA-C	-5.66	101.91	110.28
1	A	143	SER	N-CA-C	-5.64	100.21	109.40
1	B	364	GLY	N-CA-C	5.63	126.52	113.18
1	B	224	ILE	N-CA-C	5.63	121.04	109.34
1	A	637	GLU	N-CA-C	-5.60	105.26	111.36
1	B	685	VAL	CA-C-N	5.58	125.94	119.47
1	B	685	VAL	C-N-CA	5.58	125.94	119.47
1	A	757	PRO	N-CA-C	5.56	119.81	111.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	213	PRO	N-CA-C	5.51	119.21	111.33
1	B	668	GLY	N-CA-C	5.48	123.34	114.90
1	B	575	PRO	N-CA-C	-5.48	102.53	111.68
1	A	994	TYR	N-CA-C	-5.47	98.82	108.23
1	B	1173	GLU	N-CA-C	5.47	118.18	110.14
1	A	668	GLY	N-CA-C	5.47	122.76	114.61
1	B	968	ASP	N-CA-C	5.47	116.83	108.30
1	A	65	ALA	N-CA-C	-5.46	105.41	111.36
1	B	576	PHE	N-CA-C	5.44	120.29	111.37
1	B	119	HIS	N-CA-C	-5.44	105.91	112.54
1	B	23	GLU	N-CA-C	-5.43	107.20	113.88
1	A	172	ASP	N-CA-C	5.41	118.17	110.10
1	A	29	PRO	N-CA-C	5.41	118.97	110.80
1	A	832	MET	N-CA-C	5.41	118.55	109.95
1	B	195	VAL	N-CA-C	5.40	116.05	109.30
1	A	78	GLY	N-CA-C	5.38	123.90	114.76
1	A	889	HIS	N-CA-C	-5.36	105.36	111.14
1	B	219	ALA	N-CA-C	-5.36	100.45	109.07
1	B	570	LEU	N-CA-C	5.32	120.78	113.97
1	A	111	VAL	N-CA-C	5.32	115.55	108.11
1	A	485	ASP	N-CA-C	-5.29	105.97	112.90
1	B	27	ILE	N-CA-C	5.29	116.52	108.80
1	B	495	VAL	N-CA-C	5.28	115.90	110.36
1	A	871	ASP	N-CA-C	5.28	119.27	112.41
1	A	983	ASP	N-CA-C	5.25	117.66	108.52
1	B	371	SER	N-CA-C	5.25	116.16	110.13
1	B	123	ILE	N-CA-C	-5.20	107.68	112.83
1	B	1124	VAL	N-CA-C	5.20	115.93	110.62
1	A	870	GLU	N-CA-C	5.20	119.62	113.28
1	B	212	HIS	CA-C-N	5.18	125.91	120.11
1	B	212	HIS	C-N-CA	5.18	125.91	120.11
1	B	408	ALA	N-CA-C	-5.13	107.02	113.28
1	A	726	ALA	N-CA-C	5.13	117.60	109.96
1	B	742	THR	N-CA-C	5.12	118.78	112.54
1	B	641	ASN	N-CA-C	5.11	118.67	112.23
1	A	453	PHE	N-CA-C	5.10	117.38	108.76
1	B	111	VAL	N-CA-C	5.09	115.24	108.11
1	A	888	THR	N-CA-C	-5.08	105.83	112.23
1	A	698	VAL	N-CA-C	5.06	119.53	112.50
1	B	631	ALA	N-CA-C	-5.06	107.61	112.97
1	B	995	SER	N-CA-C	5.04	116.62	111.03
1	B	517	SER	N-CA-C	5.03	116.84	111.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1015	ALA	N-CA-C	5.02	118.50	112.38

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	9383	0	9262	292	0
1	B	9383	0	9262	228	0
2	A	24	0	0	0	0
2	B	24	0	0	1	0
3	A	29	0	18	2	0
3	B	29	0	18	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	3	0	0	0	0
6	B	3	0	0	1	0
7	A	410	0	0	7	0
7	B	554	0	0	13	0
All	All	19846	0	18560	485	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 13.

All (485) 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)
3:B:1236:HTL:C2	3:B:1236:HTL:C1'	1.89	1.47
3:A:1236:HTL:C1'	3:A:1236:HTL:C2	1.94	1.45
1:A:639:PHE:HA	1:A:643:VAL:HG13	1.43	1.00
1:A:635:THR:HG22	1:A:636:ASN:H	1.25	1.00
1:B:1200:THR:HG22	1:B:1202:MET:H	1.25	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:ASP:OD2	1:A:12:THR:HG23	1.66	0.94
1:A:1200:THR:HG22	1:A:1202:MET:H	1.31	0.94
1:B:12:THR:HG22	1:B:39:GLU:OE1	1.68	0.92
1:A:1230:THR:O	1:A:1232:LYS:HG2	1.71	0.91
1:A:1231:LYS:HG3	1:A:1232:LYS:H	1.36	0.90
1:B:110:HIS:HD2	1:B:169:HIS:HD2	1.23	0.87
1:B:1200:THR:HG23	1:B:1202:MET:HE3	1.57	0.87
1:B:6:MET:HE2	1:B:185:VAL:HG11	1.57	0.84
1:A:526:LEU:HD11	1:A:530:ILE:HG21	1.58	0.84
1:A:593:LYS:HG3	1:A:594:LYS:H	1.41	0.84
1:B:877:PHE:HE1	1:B:982:GLU:HG3	1.43	0.84
1:B:1200:THR:HG22	1:B:1202:MET:N	1.94	0.83
1:A:1200:THR:HG23	1:A:1202:MET:HE3	1.60	0.83
1:B:493:ALA:O	1:B:497:ILE:HD13	1.79	0.82
1:A:554:GLY:HA3	1:A:601:MET:HE2	1.59	0.82
1:B:1231:LYS:HG3	1:B:1232:LYS:H	1.46	0.81
1:B:1181:LYS:HD2	1:B:1182:ALA:H	1.46	0.80
1:A:1019:ARG:HH22	1:B:1181:LYS:HA	1.45	0.80
1:A:566:ALA:HA	1:A:613:LEU:HD21	1.63	0.80
1:A:1219:THR:HG22	1:A:1221:GLU:H	1.46	0.79
1:B:561:MET:HE1	1:B:583:LEU:HD21	1.64	0.79
1:A:1200:THR:CG2	1:A:1202:MET:HE3	2.11	0.79
1:A:24:VAL:HG13	1:B:881:MET:HE2	1.64	0.78
1:B:1200:THR:CG2	1:B:1202:MET:HE3	2.13	0.78
1:A:635:THR:HG22	1:A:636:ASN:N	1.99	0.78
1:A:110:HIS:HD2	1:A:169:HIS:HD2	1.29	0.77
1:A:635:THR:HG23	1:A:672:PHE:CD2	2.20	0.77
1:B:110:HIS:HD2	1:B:169:HIS:CD2	2.02	0.77
1:A:1200:THR:HG22	1:A:1202:MET:N	1.99	0.77
1:B:9:ASP:OD2	1:B:12:THR:HG23	1.85	0.76
1:A:522:MET:HE1	1:A:543:ASN:ND2	2.01	0.76
1:B:635:THR:CG2	1:B:639:PHE:HB3	2.16	0.76
1:A:644:LYS:HB3	1:A:645:PRO:HD3	1.68	0.76
1:B:1200:THR:CG2	1:B:1202:MET:H	1.99	0.76
1:A:1019:ARG:HH12	1:B:1181:LYS:H	1.34	0.75
1:B:877:PHE:CE1	1:B:982:GLU:HG3	2.21	0.75
1:A:1200:THR:CG2	1:A:1202:MET:H	2.00	0.73
1:A:637:GLU:HG3	1:A:641:ASN:HD21	1.54	0.73
1:A:593:LYS:HG3	1:A:594:LYS:N	2.03	0.73
1:A:1219:THR:HG22	1:A:1221:GLU:N	2.04	0.72
1:B:140:MET:HE3	1:B:168:MET:HE3	1.72	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:GLU:O	1:A:993:VAL:HG13	1.90	0.71
1:B:775:VAL:O	1:B:779:GLU:HG2	1.90	0.71
1:B:635:THR:HG23	1:B:639:PHE:HB3	1.72	0.71
1:A:97:MET:HE1	1:A:168:MET:HE3	1.71	0.71
1:B:110:HIS:CD2	1:B:169:HIS:HD2	2.07	0.70
1:A:1019:ARG:NH2	1:B:1181:LYS:HA	2.05	0.70
1:A:937:GLN:HG2	1:A:942:LEU:HB3	1.74	0.70
1:B:691:GLN:HE22	1:B:727:LYS:H	1.39	0.70
1:A:1198:ASP:OD2	1:A:1200:THR:HB	1.92	0.69
1:B:463:ILE:HD13	1:B:494:TYR:CE1	2.27	0.69
1:A:12:THR:HG22	1:A:39:GLU:OE1	1.93	0.69
1:A:357:LYS:HE3	1:A:359:LEU:HD21	1.75	0.69
1:A:110:HIS:HD2	1:A:169:HIS:CD2	2.10	0.68
1:A:602:ASN:O	1:A:606:VAL:HG23	1.94	0.68
1:A:1180:GLY:O	1:A:1181:LYS:HB2	1.93	0.68
1:A:14:THR:HG21	1:A:171:PHE:CE2	2.29	0.68
1:A:351:ARG:HD3	1:A:353:GLU:HB2	1.76	0.68
1:A:411:ASP:HB2	1:A:483:ARG:HD2	1.76	0.67
1:A:14:THR:HG22	1:A:149:ALA:HB1	1.76	0.67
1:A:1076:LEU:HD13	1:A:1086:VAL:HG21	1.75	0.67
1:A:1102:ASP:OD1	1:A:1104:ARG:HG2	1.94	0.67
1:A:591:TYR:C	1:A:593:LYS:H	2.03	0.67
1:A:902:ALA:O	1:A:907:LYS:HE3	1.95	0.67
1:B:140:MET:HE3	1:B:168:MET:CE	2.25	0.67
1:B:1198:ASP:OD2	1:B:1200:THR:HB	1.94	0.67
1:A:239:VAL:HG13	1:A:240:PRO:HD3	1.78	0.66
1:B:438:ILE:HD11	1:B:468:LEU:HD22	1.77	0.66
1:A:445:THR:HG21	1:A:574:LEU:HD21	1.76	0.66
1:B:1102:ASP:OD1	1:B:1104:ARG:HG2	1.96	0.66
1:A:99:LYS:HE3	1:B:867:SER:O	1.96	0.66
1:A:467:HIS:HD2	1:A:481:VAL:H	1.42	0.66
1:B:509:THR:HG21	7:B:2265:HOH:O	1.95	0.65
1:A:1077:ARG:HG2	1:A:1130:ALA:O	1.95	0.65
1:A:635:THR:HG21	1:A:639:PHE:CD2	2.31	0.65
1:B:1076:LEU:HD13	1:B:1086:VAL:HG21	1.78	0.65
1:A:501:LEU:O	1:A:504:ILE:HG22	1.97	0.65
1:B:467:HIS:CD2	1:B:481:VAL:H	2.15	0.65
1:A:737:ARG:HE	1:A:739:GLN:NE2	1.94	0.64
1:B:591:TYR:C	1:B:593:LYS:H	2.05	0.64
1:A:635:THR:HG23	1:A:672:PHE:CG	2.32	0.64
1:A:1201:PRO:HG3	1:B:455:TYR:HB2	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:GLN:O	1:A:1155:GLU:HG3	1.98	0.64
1:B:3:LYS:HE2	1:B:253:LEU:O	1.97	0.63
1:B:1151:GLN:O	1:B:1155:GLU:HG3	1.98	0.63
1:A:2:GLY:N	1:A:187:ASP:OD2	2.32	0.63
1:B:561:MET:HE1	1:B:583:LEU:CD2	2.28	0.63
1:B:1200:THR:CG2	1:B:1202:MET:HB2	2.29	0.63
1:B:499:ASP:OD2	1:B:502:GLU:HB2	1.98	0.62
1:B:650:GLN:HE22	1:B:653:LYS:HZ3	1.47	0.62
1:A:708:LEU:HD21	1:A:731:LEU:HD22	1.81	0.62
1:A:739:GLN:NE2	1:A:777:ASN:HB3	2.14	0.62
1:A:971:TYR:OH	1:A:1028:MET:HE2	1.99	0.62
1:B:590:ALA:O	1:B:591:TYR:C	2.41	0.62
1:A:1155:GLU:HG2	1:B:1173:GLU:OE2	2.00	0.62
1:A:873:ALA:HA	1:A:959:ILE:HD13	1.80	0.62
1:B:992:GLU:O	1:B:993:VAL:HG13	1.99	0.62
1:A:832:MET:HE2	1:A:834:ILE:HD11	1.82	0.62
1:B:691:GLN:NE2	1:B:727:LYS:H	1.97	0.62
1:A:544:ILE:HD12	1:A:613:LEU:HD13	1.80	0.61
1:B:56:LEU:HD23	1:B:58:ILE:HD11	1.80	0.61
1:A:10:GLY:O	1:A:14:THR:HG23	2.00	0.61
1:B:496:GLY:C	1:B:497:ILE:HD12	2.24	0.61
1:B:907:LYS:O	1:B:911:GLN:HG3	2.00	0.61
1:A:561:MET:HE1	1:A:583:LEU:HD11	1.82	0.61
1:A:635:THR:CG2	1:A:636:ASN:H	2.08	0.61
1:B:467:HIS:HD2	1:B:481:VAL:H	1.48	0.61
1:B:832:MET:HE2	1:B:834:ILE:HD11	1.82	0.61
1:A:467:HIS:CD2	1:A:481:VAL:H	2.19	0.61
1:A:1006:PRO:HG2	1:A:1009:ALA:HB2	1.83	0.61
1:A:110:HIS:CD2	1:A:169:HIS:HD2	2.16	0.60
1:A:558:ARG:HG2	1:A:560:ASN:ND2	2.16	0.60
1:B:1200:THR:HG21	1:B:1202:MET:HB2	1.83	0.60
1:B:8:THR:HB	1:B:12:THR:OG1	2.01	0.60
1:A:43:TRP:HB3	1:A:48:ARG:HD3	1.83	0.60
1:A:124:PHE:HB3	1:A:367:SER:HB2	1.84	0.60
1:B:598:ILE:HD13	1:B:601:MET:HE2	1.83	0.60
1:B:650:GLN:NE2	1:B:653:LYS:NZ	2.50	0.60
1:B:630:LYS:O	1:B:630:LYS:HG3	2.01	0.60
1:A:523:ASP:HA	1:A:531:LYS:NZ	2.17	0.59
1:A:553:VAL:HG23	1:A:555:LEU:HG	1.84	0.59
1:A:1051:LYS:HE3	1:A:1100:ARG:NH1	2.17	0.59
1:B:425:LEU:HD22	1:B:491:ASN:ND2	2.17	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ARG:HD2	7:B:2048:HOH:O	2.02	0.59
1:B:931:LYS:HD2	7:B:2430:HOH:O	2.01	0.59
1:A:593:LYS:CG	1:A:594:LYS:H	2.14	0.59
1:A:637:GLU:HG3	1:A:641:ASN:ND2	2.17	0.59
1:A:936:GLY:O	1:A:938:LYS:HD3	2.03	0.59
1:B:1166:MET:O	1:B:1169:THR:HG22	2.03	0.59
1:A:1231:LYS:HG3	1:A:1232:LYS:N	2.14	0.59
1:B:41:ASP:HA	1:B:58:ILE:HD12	1.85	0.58
1:A:1019:ARG:HH12	1:B:1181:LYS:N	2.01	0.58
1:B:1232:LYS:NZ	1:B:1232:LYS:HB3	2.18	0.58
1:A:24:VAL:CG1	1:B:881:MET:HE2	2.34	0.58
1:B:598:ILE:HD13	1:B:601:MET:CE	2.33	0.58
1:A:691:GLN:HE22	1:A:727:LYS:H	1.52	0.58
1:A:554:GLY:HA3	1:A:601:MET:CE	2.32	0.58
1:A:455:TYR:HB2	1:B:1201:PRO:HD3	1.85	0.58
1:B:1000:GLN:H	1:B:1000:GLN:NE2	2.02	0.58
1:A:90:LEU:HD21	1:A:168:MET:HE1	1.86	0.57
1:A:345:CYS:O	1:A:349:VAL:HG13	2.04	0.57
1:B:754:ILE:HG12	7:B:2479:HOH:O	2.03	0.57
1:A:110:HIS:HE1	1:A:157:HIS:NE2	2.02	0.57
1:B:591:TYR:C	1:B:593:LYS:N	2.57	0.57
1:B:598:ILE:HA	1:B:601:MET:HE2	1.85	0.57
1:B:124:PHE:HB3	1:B:367:SER:HB2	1.86	0.57
1:A:163:SER:O	1:A:164:ASN:HB2	2.03	0.57
1:B:650:GLN:HE22	1:B:653:LYS:NZ	2.03	0.57
1:B:1158:VAL:O	1:B:1162:GLU:HG3	2.04	0.57
1:A:3:LYS:HE2	1:A:253:LEU:O	2.05	0.57
1:A:877:PHE:HE1	1:A:982:GLU:HG3	1.70	0.56
1:A:1200:THR:CG2	1:A:1202:MET:HB2	2.35	0.56
1:B:497:ILE:HD12	1:B:497:ILE:N	2.20	0.56
1:B:644:LYS:O	1:B:648:THR:HG23	2.04	0.56
1:B:591:TYR:O	1:B:593:LYS:N	2.38	0.56
1:A:581:ASP:OD2	1:A:585:LYS:HE3	2.06	0.56
1:A:635:THR:HG21	1:A:639:PHE:CG	2.41	0.56
1:B:803:GLU:OE1	1:B:856:ASN:HB2	2.06	0.56
1:A:881:MET:HE3	1:B:59:ARG:HG2	1.86	0.56
1:B:42:ASP:O	1:B:46:GLN:HG3	2.05	0.56
1:A:950:ASP:OD2	1:B:212:HIS:HE1	1.89	0.55
1:B:61:MET:HG3	1:B:67:ALA:HA	1.86	0.55
1:A:426:GLY:O	1:A:427:ALA:HB3	2.06	0.55
1:A:731:LEU:CD2	1:A:790:VAL:HG11	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:976:HIS:HD2	1:B:1003:LYS:NZ	2.03	0.55
1:A:1188:PHE:HE1	1:A:1196:THR:HG23	1.70	0.55
1:B:20:ALA:HB2	1:B:188:TYR:CZ	2.42	0.55
1:B:1219:THR:CG2	1:B:1220:SER:N	2.70	0.55
1:A:1123:SER:O	1:A:1126:GLU:HG2	2.07	0.55
1:B:121:LEU:C	1:B:121:LEU:HD23	2.31	0.55
1:A:121:LEU:HD23	1:A:121:LEU:C	2.31	0.55
1:A:1019:ARG:NH1	1:B:1181:LYS:H	2.01	0.55
1:A:1181:LYS:O	1:A:1182:ALA:HB3	2.07	0.55
1:A:691:GLN:NE2	1:A:727:LYS:H	2.04	0.55
1:A:1003:LYS:NZ	1:B:976:HIS:HD2	2.05	0.55
1:A:27:ILE:HD11	1:A:1013:PHE:CE2	2.41	0.54
1:A:558:ARG:HG2	1:A:560:ASN:HD21	1.72	0.54
1:A:1188:PHE:CE1	1:A:1196:THR:HG23	2.42	0.54
1:B:632:GLU:O	1:B:632:GLU:CD	2.50	0.54
1:B:27:ILE:HD12	1:B:1013:PHE:CE2	2.41	0.54
1:A:881:MET:HE3	1:B:59:ARG:CG	2.37	0.54
1:A:1175:PHE:CD2	1:B:1151:GLN:HG3	2.43	0.54
1:B:163:SER:O	1:B:164:ASN:HB2	2.07	0.54
1:A:841:SER:HA	1:A:844:TRP:CE2	2.43	0.54
1:A:1200:THR:HG23	1:A:1201:PRO:HD2	1.90	0.54
1:A:775:VAL:N	1:A:776:PRO:HD2	2.23	0.54
1:A:1200:THR:HG21	1:A:1202:MET:HE3	1.90	0.54
1:A:6:MET:HE2	1:A:185:VAL:HG11	1.89	0.53
1:B:91:LEU:HD11	1:B:116:ILE:HD12	1.91	0.53
1:B:221:ASN:HB3	1:B:222:PRO:CD	2.38	0.53
1:A:692:CYS:O	1:A:693:ASN:HB2	2.08	0.53
1:B:873:ALA:HA	1:B:959:ILE:HD13	1.90	0.53
1:B:495:VAL:HG12	1:B:527:PRO:HD3	1.91	0.53
1:A:565:THR:HG21	1:A:609:ALA:HB3	1.91	0.53
1:A:9:ASP:HA	1:A:179:GLU:O	2.09	0.52
1:A:431:VAL:CG2	1:A:464:THR:HG21	2.39	0.52
1:A:1143:GLU:HG2	1:A:1144:ASP:H	1.75	0.52
1:B:841:SER:HA	1:B:844:TRP:CE2	2.44	0.52
7:A:2252:HOH:O	1:B:1219:THR:HG21	2.09	0.52
1:A:1189:GLY:CA	1:A:1196:THR:HG21	2.40	0.52
1:B:1219:THR:HG22	1:B:1221:GLU:N	2.25	0.52
1:B:581:ASP:O	1:B:585:LYS:HG2	2.10	0.51
1:B:1193:GLU:OE2	1:B:1193:GLU:N	2.43	0.51
1:A:739:GLN:HE22	1:A:777:ASN:HB3	1.74	0.51
1:A:1003:LYS:HZ3	1:B:976:HIS:HD2	1.57	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1199:ASP:HB3	7:A:2395:HOH:O	2.10	0.51
1:A:591:TYR:C	1:A:593:LYS:N	2.68	0.51
1:B:964:GLY:O	1:B:968:ASP:HB2	2.10	0.51
1:A:1165:HIS:CD2	1:B:1165:HIS:NE2	2.79	0.51
1:B:483:ARG:HA	1:B:503:GLY:O	2.11	0.51
1:B:695:CYS:HB2	1:B:704:ILE:HD13	1.92	0.51
1:B:1232:LYS:HB3	1:B:1232:LYS:HZ2	1.74	0.51
1:B:99:LYS:O	1:B:103:GLU:HG3	2.11	0.51
1:B:110:HIS:HE1	1:B:157:HIS:NE2	2.07	0.51
1:A:1200:THR:HG21	1:A:1202:MET:HB2	1.92	0.50
1:B:589:LYS:C	1:B:590:ALA:O	2.52	0.50
1:B:729:LYS:O	1:B:732:LYS:HG3	2.11	0.50
1:A:1007:THR:OG1	1:A:1021:GLY:HA2	2.11	0.50
1:A:1043:GLY:HA3	1:A:1087:MET:HB2	1.94	0.50
1:A:1166:MET:O	1:A:1169:THR:HG22	2.12	0.50
1:B:833:PHE:HE1	1:B:955:LYS:HG3	1.76	0.50
1:A:1105:LEU:O	1:A:1108:GLN:HG2	2.10	0.50
1:B:978:LEU:O	1:B:1062:PRO:HG2	2.10	0.50
1:B:1027:ARG:HA	1:B:1030:MET:HE3	1.92	0.50
1:A:441:ILE:HD13	1:A:573:VAL:HG21	1.93	0.50
1:A:1219:THR:CG2	1:A:1221:GLU:H	2.22	0.50
1:B:239:VAL:HB	1:B:240:PRO:HD3	1.93	0.50
1:B:1210:GLU:HG3	7:B:2546:HOH:O	2.11	0.50
1:A:636:ASN:ND2	1:A:672:PHE:CE1	2.80	0.50
1:A:869:PHE:CE2	1:A:969:ILE:HG21	2.47	0.50
1:B:56:LEU:HD23	1:B:58:ILE:CD1	2.42	0.50
1:A:12:THR:CG2	1:A:39:GLU:OE1	2.60	0.50
1:A:351:ARG:HD2	7:A:2154:HOH:O	2.12	0.50
1:A:609:ALA:O	1:A:613:LEU:HB2	2.13	0.49
1:A:964:GLY:O	1:A:968:ASP:HB2	2.12	0.49
1:A:434:ASN:ND2	1:A:466:SER:OG	2.45	0.49
1:A:1219:THR:CG2	1:A:1220:SER:N	2.74	0.49
1:A:421:GLN:HA	1:A:466:SER:O	2.13	0.49
1:B:690:ILE:HG12	2:B:1233:SF4:S2	2.52	0.49
1:A:1106:ALA:C	1:A:1108:GLN:H	2.20	0.49
1:B:1043:GLY:HA3	1:B:1087:MET:HB2	1.94	0.49
1:A:297:ILE:HB	1:A:379:TYR:CE2	2.47	0.49
1:B:12:THR:HG22	1:B:39:GLU:CD	2.35	0.49
1:A:6:MET:CE	1:A:185:VAL:HG11	2.43	0.49
1:A:3:LYS:HG2	1:A:184:GLU:OE2	2.12	0.49
1:A:68:ALA:HB2	1:A:93:MET:HG2	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:SER:HA	1:A:129:ASP:HB3	1.94	0.48
1:A:635:THR:CG2	1:A:639:PHE:HB3	2.43	0.48
1:A:918:ASN:HA	1:A:954:LYS:HD3	1.94	0.48
1:A:222:PRO:HD3	1:B:124:PHE:CE2	2.49	0.48
1:A:583:LEU:O	1:A:587:ILE:HG13	2.13	0.48
1:A:1015:ALA:HB3	1:B:1185:SER:HB2	1.95	0.48
1:B:467:HIS:CE1	1:B:480:LEU:HD22	2.48	0.48
1:B:1225:ASP:O	1:B:1229:ARG:HG3	2.13	0.48
1:A:467:HIS:HB3	1:A:481:VAL:HG23	1.96	0.48
1:B:1026:ALA:O	1:B:1030:MET:HG3	2.13	0.48
1:A:20:ALA:HB2	1:A:188:TYR:CZ	2.48	0.48
1:A:124:PHE:HB3	1:A:367:SER:CB	2.43	0.48
1:A:483:ARG:O	1:A:505:LYS:HE3	2.13	0.48
1:A:635:THR:HG22	1:A:639:PHE:HB3	1.95	0.48
1:A:221:ASN:HB3	1:A:222:PRO:CD	2.44	0.48
1:A:422:PHE:HE1	1:A:468:LEU:HG	1.79	0.48
1:A:1214:GLN:O	1:A:1214:GLN:HG2	2.13	0.48
1:B:495:VAL:HG11	1:B:526:LEU:HD12	1.95	0.48
1:A:1136:VAL:HG12	1:A:1139:ARG:NH1	2.28	0.48
1:B:1012:LYS:O	1:B:1013:PHE:HB2	2.14	0.48
1:A:27:ILE:CD1	1:A:1013:PHE:CE2	2.97	0.47
3:A:1236:HTL:C1'	3:A:1236:HTL:H4'2	2.27	0.47
1:A:1132:ASN:O	1:A:1136:VAL:HG22	2.14	0.47
1:A:1143:GLU:HG2	1:A:1144:ASP:N	2.29	0.47
1:B:1173:GLU:HG2	1:B:1174:SER:H	1.78	0.47
1:A:684:TRP:CE2	1:A:738:ILE:HB	2.49	0.47
1:A:1199:ASP:O	1:B:455:TYR:HB3	2.14	0.47
1:B:27:ILE:CD1	1:B:1013:PHE:CE2	2.98	0.47
1:A:10:GLY:O	1:A:14:THR:CG2	2.63	0.47
1:B:427:ALA:HA	7:B:2224:HOH:O	2.14	0.47
1:B:635:THR:CG2	1:B:636:ASN:N	2.77	0.47
1:B:1006:PRO:HG2	1:B:1009:ALA:HB2	1.97	0.47
1:A:263:TYR:OH	1:A:298:GLY:HA3	2.15	0.47
1:A:536:ASN:HA	1:A:623:LYS:HZ3	1.80	0.47
1:A:1055:GLU:O	1:A:1104:ARG:NH1	2.48	0.47
1:A:1189:GLY:HA3	1:A:1196:THR:HG21	1.97	0.47
1:B:12:THR:CG2	1:B:39:GLU:OE1	2.53	0.47
1:B:660:GLU:HB3	7:B:2309:HOH:O	2.14	0.47
1:B:1177:PRO:O	1:B:1178:ALA:HB2	2.15	0.47
1:A:992:GLU:O	1:A:993:VAL:CG1	2.62	0.47
1:B:720:ASN:H	1:B:720:ASN:ND2	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:VAL:HB	1:A:737:ARG:HB3	1.97	0.47
1:B:1231:LYS:HG3	1:B:1232:LYS:N	2.25	0.47
1:A:3:LYS:HG2	1:A:184:GLU:CD	2.40	0.47
1:A:1015:ALA:CB	1:B:1185:SER:HB2	2.45	0.46
1:A:235:TYR:O	1:A:239:VAL:HG12	2.14	0.46
1:A:949:SER:HA	1:A:952:TYR:CZ	2.50	0.46
1:A:1171:ILE:HD12	1:B:1161:LYS:HD3	1.96	0.46
1:B:713:GLU:OE1	1:B:785:PRO:HD2	2.15	0.46
1:A:586:SER:O	1:A:589:LYS:HB3	2.16	0.46
1:B:635:THR:HG22	1:B:636:ASN:O	2.15	0.46
1:A:590:ALA:O	1:A:591:TYR:C	2.59	0.46
1:A:597:LYS:O	1:A:601:MET:HG3	2.15	0.46
1:A:408:ALA:O	1:A:409:PHE:C	2.59	0.46
1:A:389:HIS:HE1	1:B:350:GLU:CD	2.23	0.46
1:A:513:ASN:ND2	1:A:546:ALA:HB3	2.31	0.46
1:A:1028:MET:HE3	7:B:2444:HOH:O	2.14	0.46
1:A:642:VAL:O	1:A:646:ILE:HG13	2.15	0.46
1:A:1136:VAL:HG23	1:A:1137:LEU:N	2.31	0.46
1:B:712:GLU:O	1:B:715:VAL:HG23	2.15	0.46
1:A:37:GLY:HA3	7:A:2011:HOH:O	2.17	0.45
1:B:949:SER:C	1:B:951:LEU:H	2.24	0.45
1:A:892:ASP:OD1	1:A:896:LYS:NZ	2.48	0.45
1:A:522:MET:HE1	1:A:543:ASN:HD22	1.75	0.45
1:A:591:TYR:O	1:A:593:LYS:N	2.50	0.45
1:A:686:PRO:HB2	1:A:724:LEU:HD21	1.97	0.45
1:A:1132:ASN:ND2	1:A:1136:VAL:CG1	2.79	0.45
1:B:27:ILE:HB	7:B:2036:HOH:O	2.16	0.45
1:B:1181:LYS:HD2	1:B:1182:ALA:N	2.23	0.45
1:A:45:ALA:HB1	1:B:1185:SER:HB3	1.99	0.45
1:A:129:ASP:OD2	1:A:130:ILE:N	2.49	0.45
1:A:335:ALA:HB2	7:A:2145:HOH:O	2.16	0.45
1:A:561:MET:HE3	1:A:564:GLN:HB3	1.99	0.45
1:B:87:SER:HA	1:B:129:ASP:HB3	1.99	0.45
1:B:720:ASN:N	1:B:720:ASN:HD22	2.14	0.45
1:B:1219:THR:HG22	1:B:1221:GLU:H	1.81	0.45
1:A:754:ILE:C	1:A:754:ILE:HD12	2.42	0.45
1:A:775:VAL:O	1:A:779:GLU:HG2	2.16	0.45
1:A:1033:GLY:HA3	1:A:1173:GLU:HG3	1.98	0.45
1:A:180:ILE:O	1:A:450:GLN:HA	2.17	0.45
1:A:731:LEU:HD23	1:A:790:VAL:HG11	1.98	0.45
1:A:1077:ARG:HG2	1:A:1130:ALA:C	2.41	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:THR:HG21	1:B:439:LYS:HA	1.99	0.45
1:B:720:ASN:H	1:B:720:ASN:HD22	1.64	0.45
1:A:426:GLY:HA3	1:B:1199:ASP:CG	2.42	0.45
1:B:1173:GLU:HG2	1:B:1174:SER:N	2.32	0.45
1:A:113:ALA:HB1	1:A:126:ASP:O	2.17	0.45
1:A:124:PHE:CE2	1:B:222:PRO:HD3	2.52	0.45
1:A:142:ALA:HB2	1:A:170:PHE:CZ	2.51	0.45
1:B:1230:THR:O	1:B:1231:LYS:C	2.60	0.45
1:A:976:HIS:HD2	1:B:1003:LYS:HZ3	1.65	0.45
1:A:1173:GLU:CD	1:A:1173:GLU:H	2.25	0.45
1:B:619:PRO:HG2	1:B:622:TRP:CD1	2.52	0.45
1:A:1230:THR:O	1:A:1231:LYS:C	2.59	0.44
1:A:524:LYS:HD2	1:A:525:HIS:CE1	2.52	0.44
1:A:978:LEU:O	1:A:1062:PRO:HG2	2.17	0.44
1:A:1226:LEU:O	1:A:1230:THR:HG23	2.17	0.44
1:B:9:ASP:HA	1:B:179:GLU:O	2.17	0.44
1:B:439:LYS:HB2	1:B:439:LYS:NZ	2.32	0.44
1:B:1200:THR:HG21	1:B:1202:MET:HE3	1.96	0.44
1:A:1159:ARG:O	1:A:1163:LEU:HG	2.17	0.44
1:B:221:ASN:HB3	1:B:222:PRO:HD2	1.98	0.44
1:A:444:ASN:CB	1:A:582:LEU:HD21	2.47	0.44
1:A:594:LYS:O	1:A:595:GLY:O	2.34	0.44
1:A:741:ASN:HA	1:A:778:LEU:HG	1.99	0.44
1:B:1231:LYS:O	1:B:1232:LYS:HB2	2.17	0.44
1:B:562:ILE:HD12	1:B:562:ILE:H	1.82	0.44
1:A:857:ARG:HG3	1:A:858:LEU:HD13	2.00	0.44
1:B:832:MET:HE2	1:B:834:ILE:CG1	2.48	0.44
1:B:212:HIS:HD2	7:B:2087:HOH:O	2.00	0.44
1:B:691:GLN:HE22	1:B:726:ALA:HA	1.81	0.44
1:B:587:ILE:O	1:B:591:TYR:HB2	2.18	0.44
1:A:26:ALA:HB3	1:A:71:VAL:HG23	2.00	0.43
1:A:700:PRO:HG2	1:A:814:GLY:HA2	1.99	0.43
1:A:1132:ASN:CG	1:A:1136:VAL:HG13	2.43	0.43
1:B:684:TRP:CE2	1:B:738:ILE:HB	2.53	0.43
1:A:643:VAL:HB	1:A:849:PRO:HB2	2.01	0.43
1:B:692:CYS:O	1:B:693:ASN:HB2	2.17	0.43
1:A:598:ILE:HG22	1:A:598:ILE:O	2.18	0.43
1:A:617:LYS:HA	1:A:617:LYS:HD3	1.86	0.43
1:A:713:GLU:OE1	1:A:785:PRO:HD2	2.18	0.43
1:A:233:ASN:HB2	1:A:234:PRO:HD3	2.00	0.43
1:A:389:HIS:CE1	1:B:350:GLU:OE1	2.71	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:PRO:O	1:B:213:PRO:HD3	2.19	0.43
1:B:441:ILE:HD13	1:B:573:VAL:HG11	2.01	0.43
1:B:630:LYS:HB2	1:B:632:GLU:HG3	2.00	0.43
1:A:41:ASP:HA	1:A:58:ILE:HD12	2.01	0.43
1:A:116:ILE:HD11	1:A:129:ASP:HB3	2.00	0.43
1:A:121:LEU:HD23	1:A:122:SER:N	2.34	0.43
1:B:495:VAL:CG1	1:B:527:PRO:HD3	2.48	0.43
1:A:84:PHE:HA	1:A:110:HIS:O	2.18	0.43
1:A:391:THR:O	1:A:402:SER:HA	2.18	0.43
1:A:1082:LYS:O	1:A:1086:VAL:HG23	2.18	0.43
1:A:841:SER:O	1:A:845:GLY:HA3	2.19	0.42
1:A:1218:GLY:N	1:B:747:GLY:O	2.52	0.42
1:B:425:LEU:O	1:B:426:GLY:C	2.62	0.42
1:B:460:SER:HB3	1:B:746:MET:HE2	2.01	0.42
1:B:697:PHE:CD2	1:B:1046:LYS:HD3	2.54	0.42
1:A:365:LEU:HD22	1:B:226:PHE:CE2	2.54	0.42
1:A:554:GLY:C	1:A:556:GLY:H	2.27	0.42
1:A:754:ILE:O	1:A:755:CYS:C	2.63	0.42
1:A:931:LYS:HE2	1:A:949:SER:HB2	2.00	0.42
1:A:1106:ALA:C	1:A:1108:GLN:N	2.77	0.42
1:B:597:LYS:O	1:B:601:MET:HG3	2.19	0.42
1:B:755:CYS:HA	1:B:756:PRO:HD3	1.81	0.42
1:A:1156:LEU:HD12	1:A:1156:LEU:C	2.44	0.42
1:B:20:ALA:HB2	1:B:188:TYR:CE2	2.54	0.42
1:B:23:GLU:C	1:B:56:LEU:HD12	2.44	0.42
1:B:1051:LYS:HE2	1:B:1100:ARG:NH1	2.34	0.42
1:A:236:TYR:HA	1:A:239:VAL:CG1	2.49	0.42
1:A:562:ILE:HD12	1:A:562:ILE:N	2.34	0.42
1:A:1039:THR:OG1	1:A:1098:LEU:HA	2.20	0.42
1:B:532:ARG:NH1	1:B:625:ALA:O	2.51	0.42
1:B:630:LYS:O	1:B:630:LYS:CG	2.67	0.42
1:B:828:PHE:CE2	1:B:1057:GLU:HG3	2.55	0.42
1:A:20:ALA:O	1:A:51:ILE:HG23	2.19	0.42
1:A:646:ILE:HB	1:A:849:PRO:HG3	2.02	0.42
1:A:779:GLU:O	1:A:783:ARG:HD3	2.20	0.42
1:B:832:MET:HE2	1:B:834:ILE:CD1	2.48	0.42
1:B:994:TYR:HB2	1:B:1000:GLN:HE21	1.84	0.42
1:A:110:HIS:CE1	1:A:157:HIS:NE2	2.85	0.42
1:A:521:ASP:O	1:A:524:LYS:HB3	2.20	0.42
1:B:31:THR:HG1	6:B:1240:CO2:C	2.32	0.42
1:A:523:ASP:HA	1:A:531:LYS:HZ3	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1028:MET:CE	7:B:2444:HOH:O	2.66	0.42
1:B:110:HIS:CE1	1:B:157:HIS:NE2	2.87	0.42
1:B:143:SER:OG	1:B:169:HIS:HE1	2.03	0.42
1:B:1219:THR:HG22	1:B:1220:SER:N	2.35	0.42
1:A:349:VAL:HG21	1:B:345:CYS:SG	2.59	0.42
1:A:695:CYS:HB2	1:A:704:ILE:CD1	2.50	0.42
1:A:1203:MET:HE2	1:B:995:SER:O	2.19	0.42
1:B:129:ASP:OD2	1:B:130:ILE:N	2.53	0.42
1:B:794:ASP:OD1	1:B:1054:LYS:HD3	2.20	0.42
1:A:573:VAL:HG23	1:A:574:LEU:HG	2.02	0.41
1:A:832:MET:HE2	1:A:834:ILE:CD1	2.49	0.41
1:A:8:THR:HB	1:A:12:THR:OG1	2.20	0.41
1:A:115:ALA:HB2	1:A:126:ASP:OD1	2.20	0.41
1:A:636:ASN:HD21	1:A:672:PHE:HE1	1.67	0.41
1:A:371:SER:HB2	1:A:372:PRO:CD	2.50	0.41
1:A:389:HIS:HE1	1:B:350:GLU:OE2	2.03	0.41
1:B:793:ARG:HG3	1:B:802:GLN:CD	2.45	0.41
1:B:544:ILE:HD12	1:B:613:LEU:HG	2.03	0.41
1:B:617:LYS:HA	1:B:617:LYS:HD3	1.79	0.41
1:B:673:GLU:O	1:B:674:LYS:C	2.63	0.41
1:A:499:ASP:OD2	1:A:502:GLU:HB2	2.20	0.41
1:A:794:ASP:OD1	1:A:1054:LYS:NZ	2.48	0.41
1:A:889:HIS:O	1:A:893:LEU:HD22	2.21	0.41
1:A:11:ASN:HD22	1:A:11:ASN:HA	1.71	0.41
1:A:544:ILE:HG23	1:A:544:ILE:O	2.21	0.41
1:A:795:SER:O	1:A:796:LEU:C	2.64	0.41
1:A:995:SER:O	1:B:1203:MET:HE2	2.21	0.41
1:A:1200:THR:HG23	1:A:1201:PRO:CD	2.49	0.41
1:A:62:GLN:HB3	1:B:976:HIS:CG	2.55	0.41
1:A:584:LYS:O	1:A:585:LYS:C	2.63	0.41
1:A:654:LEU:HD23	1:A:654:LEU:HA	1.92	0.41
1:B:961:GLY:HA3	1:B:965:TRP:CE3	2.56	0.41
1:A:88:GLN:HB3	7:A:2032:HOH:O	2.21	0.41
1:B:131:TYR:CE2	1:B:339:PRO:HB2	2.55	0.41
1:A:371:SER:HB2	1:A:372:PRO:HD2	2.03	0.41
1:A:701:HIS:CE1	1:A:746:MET:HG3	2.56	0.41
1:B:124:PHE:HB3	1:B:367:SER:CB	2.51	0.41
1:B:596:GLU:O	1:B:597:LYS:C	2.64	0.41
1:A:646:ILE:HD12	1:A:849:PRO:HB3	2.03	0.41
1:A:1000:GLN:H	1:A:1000:GLN:NE2	2.18	0.41
1:B:235:TYR:O	1:B:239:VAL:HG23	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:786:VAL:HG12	1:B:801:PHE:O	2.21	0.41
1:B:857:ARG:NH1	7:B:2393:HOH:O	2.53	0.41
1:B:1055:GLU:O	1:B:1104:ARG:NH1	2.54	0.41
1:A:712:GLU:O	1:A:715:VAL:HG23	2.21	0.40
1:A:1000:GLN:HA	1:A:1012:LYS:HB2	2.03	0.40
7:A:2205:HOH:O	1:B:1199:ASP:HB3	2.21	0.40
1:B:115:ALA:HA	1:B:126:ASP:OD2	2.21	0.40
1:B:456:ASP:OD2	1:B:457:SER:N	2.54	0.40
1:B:869:PHE:CZ	3:B:1236:HTL:H5B2	2.56	0.40
1:B:1124:VAL:O	1:B:1128:LEU:HG	2.21	0.40
1:B:1221:GLU:HB2	7:B:2552:HOH:O	2.20	0.40
1:A:695:CYS:HB2	1:A:704:ILE:HD13	2.03	0.40
1:B:114:ARG:NE	1:B:123:ILE:HA	2.36	0.40
1:B:978:LEU:HA	1:B:978:LEU:HD23	1.88	0.40
1:A:593:LYS:CG	1:A:594:LYS:N	2.73	0.40
1:A:673:GLU:O	1:A:674:LYS:C	2.64	0.40
1:A:709:ALA:HB3	1:A:714:LEU:HD21	2.03	0.40
1:A:1200:THR:HA	1:A:1201:PRO:HD3	1.93	0.40
1:B:727:LYS:HG3	1:B:728:GLY:N	2.37	0.40
1:B:1200:THR:HG22	1:B:1202:MET:HB2	2.02	0.40
1:A:949:SER:C	1:A:951:LEU:H	2.28	0.40
1:A:1230:THR:O	1:A:1232:LYS:N	2.54	0.40
1:B:695:CYS:HB2	1:B:704:ILE:CD1	2.51	0.40
1:A:117:ALA:HB1	1:B:99:LYS:HE2	2.04	0.40
1:A:266:ALA:HA	1:A:267:PRO:HD3	1.96	0.40
1:A:737:ARG:HE	1:A:739:GLN:HE21	1.66	0.40
1:A:1232:LYS:HB3	1:A:1232:LYS:NZ	2.37	0.40
1:B:411:ASP:HB2	1:B:483:ARG:HD2	2.03	0.40
1:B:794:ASP:OD2	1:B:794:ASP:N	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1229/1231 (100%)	1157 (94%)	65 (5%)	7 (1%)	21	30
1	B	1229/1231 (100%)	1175 (96%)	44 (4%)	10 (1%)	16	23
All	All	2458/2462 (100%)	2332 (95%)	109 (4%)	17 (1%)	18	27

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1231	LYS
1	B	629	THR
1	B	1181	LYS
1	B	1231	LYS
1	A	595	GLY
1	A	1178	ALA
1	A	1181	LYS
1	B	732	LYS
1	B	591	TYR
1	B	1178	ALA
1	B	1182	ALA
1	B	590	ALA
1	B	1174	SER
1	A	577	GLU
1	A	592	GLY
1	A	715	VAL
1	B	592	GLY

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	978/978 (100%)	942 (96%)	36 (4%)	30	49
1	B	978/978 (100%)	951 (97%)	27 (3%)	38	58
All	All	1956/1956 (100%)	1893 (97%)	63 (3%)	34	54

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	11	ASN
1	A	12	THR
1	A	14	THR
1	A	27	ILE
1	A	154	LEU
1	A	194	LEU
1	A	204	ARG
1	A	211	GLU
1	A	239	VAL
1	A	317	LEU
1	A	327	LEU
1	A	349	VAL
1	A	351	ARG
1	A	365	LEU
1	A	399	THR
1	A	497	ILE
1	A	570	LEU
1	A	582	LEU
1	A	613	LEU
1	A	617	LYS
1	A	632	GLU
1	A	643	VAL
1	A	714	LEU
1	A	730	GLU
1	A	849	PRO
1	A	858	LEU
1	A	893	LEU
1	A	942	LEU
1	A	953	THR
1	A	1000	GLN
1	A	1077	ARG
1	A	1170	ASN
1	A	1173	GLU
1	A	1196	THR
1	A	1232	LYS
1	B	7	THR
1	B	194	LEU
1	B	290	LEU
1	B	317	LEU
1	B	342	LEU
1	B	357	LYS
1	B	359	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	392	VAL
1	B	439	LYS
1	B	463	ILE
1	B	509	THR
1	B	514	SER
1	B	583	LEU
1	B	620	ASP
1	B	632	GLU
1	B	635	THR
1	B	720	ASN
1	B	725	GLU
1	B	754	ILE
1	B	823	VAL
1	B	836	ASN
1	B	849	PRO
1	B	874	GLU
1	B	1000	GLN
1	B	1181	LYS
1	B	1183	ASP
1	B	1232	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	A	16	HIS
1	A	46	GLN
1	A	96	ASN
1	A	110	HIS
1	A	128	GLN
1	A	164	ASN
1	A	169	HIS
1	A	197	GLN
1	A	212	HIS
1	A	220	GLN
1	A	289	HIS
1	A	389	HIS
1	A	421	GLN
1	A	434	ASN
1	A	436	GLN
1	A	467	HIS
1	A	513	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	525	HIS
1	A	536	ASN
1	A	543	ASN
1	A	560	ASN
1	A	636	ASN
1	A	641	ASN
1	A	683	GLN
1	A	688	ASN
1	A	691	GLN
1	A	701	HIS
1	A	739	GLN
1	A	765	GLN
1	A	777	ASN
1	A	880	ASN
1	A	918	ASN
1	A	976	HIS
1	A	1000	GLN
1	A	1073	ASN
1	A	1088	ASN
1	A	1165	HIS
1	A	1170	ASN
1	B	11	ASN
1	B	16	HIS
1	B	46	GLN
1	B	96	ASN
1	B	110	HIS
1	B	128	GLN
1	B	135	GLN
1	B	169	HIS
1	B	212	HIS
1	B	434	ASN
1	B	467	HIS
1	B	588	HIS
1	B	608	GLN
1	B	650	GLN
1	B	683	GLN
1	B	688	ASN
1	B	691	GLN
1	B	720	ASN
1	B	750	ASN
1	B	976	HIS
1	B	1000	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	1047	GLN
1	B	1073	ASN
1	B	1088	ASN
1	B	1108	GLN
1	B	1114	GLN
1	B	1151	GLN

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 ⓘ

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	$\# Z > 2$
2	SF4	B	1234	1	0,12,12	-	-	-		
6	CO2	B	1240	-	2,2,2	1.79	0	1,1,1	0.45	0
3	HTL	A	1236	4	29,30,30	8.11	17 (58%)	35,45,45	2.36	12 (34%)
3	HTL	B	1236	4	29,30,30	7.67	20 (68%)	35,45,45	2.76	14 (40%)
6	CO2	A	1240	-	2,2,2	2.22	1 (50%)	1,1,1	0.44	0
2	SF4	A	1234	1	0,12,12	-	-	-		
2	SF4	B	1235	1	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SF4	A	1233	1	0,12,12	-	-	-		
2	SF4	B	1233	1	0,12,12	-	-	-		
2	SF4	A	1235	1	0,12,12	-	-	-		

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	SF4	B	1234	1	-	-	0/6/5/5
3	HTL	A	1236	4	-	8/19/21/21	0/2/2/2
3	HTL	B	1236	4	-	3/19/21/21	0/2/2/2
2	SF4	A	1234	1	-	-	0/6/5/5
2	SF4	B	1235	1	-	-	0/6/5/5
2	SF4	A	1233	1	-	-	0/6/5/5
2	SF4	B	1233	1	-	-	0/6/5/5
2	SF4	A	1235	1	-	-	0/6/5/5

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1236	HTL	C1'-C2	37.71	1.94	1.48
3	B	1236	HTL	C1'-C2	33.42	1.89	1.48
3	A	1236	HTL	P1-O11	-9.73	1.49	1.59
3	A	1236	HTL	C2-N3	8.73	1.57	1.34
3	B	1236	HTL	C5-C4	8.32	1.52	1.35
3	B	1236	HTL	C2-N3	8.20	1.55	1.34
3	B	1236	HTL	C4-N3	-7.50	1.30	1.40
3	B	1236	HTL	C2'-N1'	7.09	1.45	1.34
3	B	1236	HTL	O2'-C1'	7.00	1.39	1.23
3	B	1236	HTL	C4A-C4	6.77	1.63	1.49
3	B	1236	HTL	P1-O11	-6.48	1.52	1.59
3	A	1236	HTL	C4A-C4	6.45	1.62	1.49
3	A	1236	HTL	C4'-N3'	6.36	1.43	1.35
3	B	1236	HTL	C5A-C5	5.90	1.63	1.50
3	A	1236	HTL	C5-C4	5.86	1.47	1.35
3	A	1236	HTL	C2'-N1'	5.71	1.43	1.34
3	B	1236	HTL	C3'-C1'	5.59	1.61	1.50
3	A	1236	HTL	O2'-C1'	5.34	1.35	1.23
3	B	1236	HTL	C4'-N3'	5.26	1.42	1.35
3	A	1236	HTL	C5'-C4'	5.23	1.51	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1236	HTL	P2-O23	-5.12	1.35	1.54
3	A	1236	HTL	C5-S1	4.98	1.84	1.74
3	B	1236	HTL	C5-S1	4.30	1.82	1.74
3	A	1236	HTL	P2-O21	3.66	1.61	1.50
3	A	1236	HTL	C2'-N3'	-3.58	1.27	1.34
3	B	1236	HTL	C2'-N3'	-3.53	1.28	1.34
3	B	1236	HTL	C6'-N1'	3.51	1.41	1.34
3	A	1236	HTL	C5A-C5	3.38	1.57	1.50
3	A	1236	HTL	C6'-N1'	3.37	1.41	1.34
3	A	1236	HTL	O5G-C5B	-3.16	1.32	1.44
3	B	1236	HTL	C35-C5'	-2.90	1.45	1.51
3	B	1236	HTL	C2-S1	2.78	1.81	1.71
3	A	1236	HTL	P1-O12	2.67	1.60	1.50
6	A	1240	CO2	O1-C	2.60	1.31	1.16
3	B	1236	HTL	O5G-C5B	-2.57	1.34	1.44
3	A	1236	HTL	P2-O22	-2.07	1.47	1.54
3	B	1236	HTL	C5'-C4'	2.06	1.46	1.42
3	B	1236	HTL	C5A-C5B	-2.03	1.44	1.51

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1236	HTL	C2A-C2'-N1'	8.72	126.48	117.20
3	A	1236	HTL	C2A-C2'-N1'	6.08	123.67	117.20
3	B	1236	HTL	C5A-C5-C4	-4.88	115.92	128.17
3	A	1236	HTL	C5A-C5-S1	-4.52	109.60	119.29
3	B	1236	HTL	N1'-C2'-N3'	-4.44	118.14	125.53
3	A	1236	HTL	C5A-C5-C4	-4.32	117.34	128.17
3	B	1236	HTL	C5A-C5-S1	-4.17	110.35	119.29
3	A	1236	HTL	N1'-C2'-N3'	-4.07	118.75	125.53
3	B	1236	HTL	C2'-N3'-C4'	4.00	124.25	118.10
3	B	1236	HTL	C4A-C4-N3	3.95	127.11	121.95
3	A	1236	HTL	C2'-N3'-C4'	3.84	124.00	118.10
3	B	1236	HTL	C5'-C4'-N4'	3.43	126.76	122.14
3	B	1236	HTL	N4'-C4'-N3'	-3.42	112.42	117.03
3	A	1236	HTL	C6'-N1'-C2'	3.40	121.66	116.07
3	A	1236	HTL	O23-P2-O22	3.39	120.50	107.80
3	B	1236	HTL	O2'-C1'-C2	3.34	122.21	118.80
3	B	1236	HTL	C35-N3-C4	-3.34	118.37	123.95
3	B	1236	HTL	C3'-C1'-C2	-3.32	114.82	118.17
3	A	1236	HTL	O5G-C5B-C5A	3.30	121.88	108.63
3	B	1236	HTL	C6'-N1'-C2'	2.87	120.79	116.07

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1236	HTL	C4-C5-S1	-2.74	107.73	110.56
3	B	1236	HTL	O5G-C5B-C5A	2.55	118.86	108.63
3	B	1236	HTL	P1-O5G-C5B	2.33	132.36	121.26
3	A	1236	HTL	C4A-C4-N3	2.18	124.79	121.95
3	A	1236	HTL	C6'-C5'-C4'	-2.16	112.89	115.55
3	A	1236	HTL	O11-P2-O21	-2.07	100.17	111.04

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1236	HTL	O2'-C1'-C2-S1
3	A	1236	HTL	C5B-O5G-P1-O11
3	A	1236	HTL	C5B-O5G-P1-O13
3	B	1236	HTL	O2'-C1'-C2-S1
3	A	1236	HTL	S1-C5-C5A-C5B
3	B	1236	HTL	S1-C5-C5A-C5B
3	A	1236	HTL	P2-O11-P1-O5G
3	A	1236	HTL	C5'-C35-N3-C2
3	B	1236	HTL	C5'-C35-N3-C2
3	A	1236	HTL	C5B-O5G-P1-O12
3	A	1236	HTL	C5-C5A-C5B-O5G

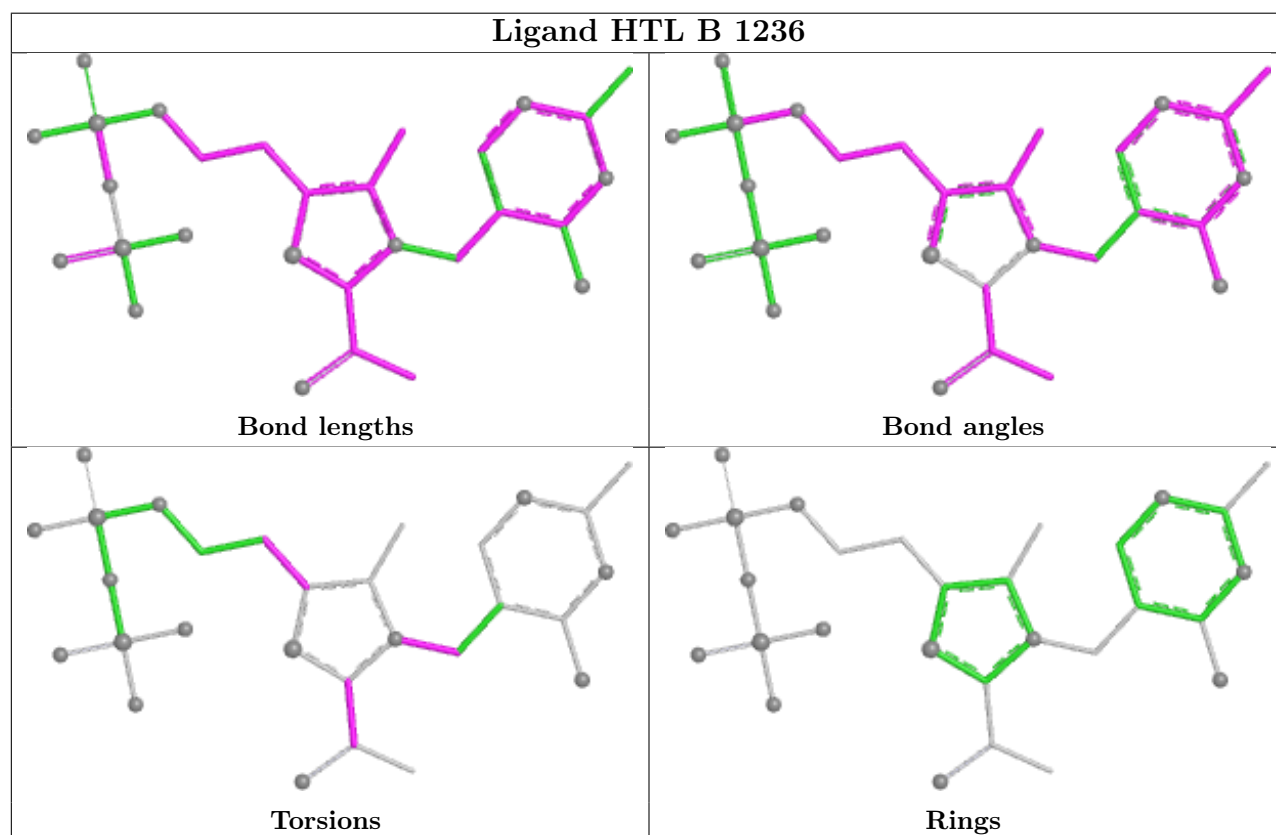
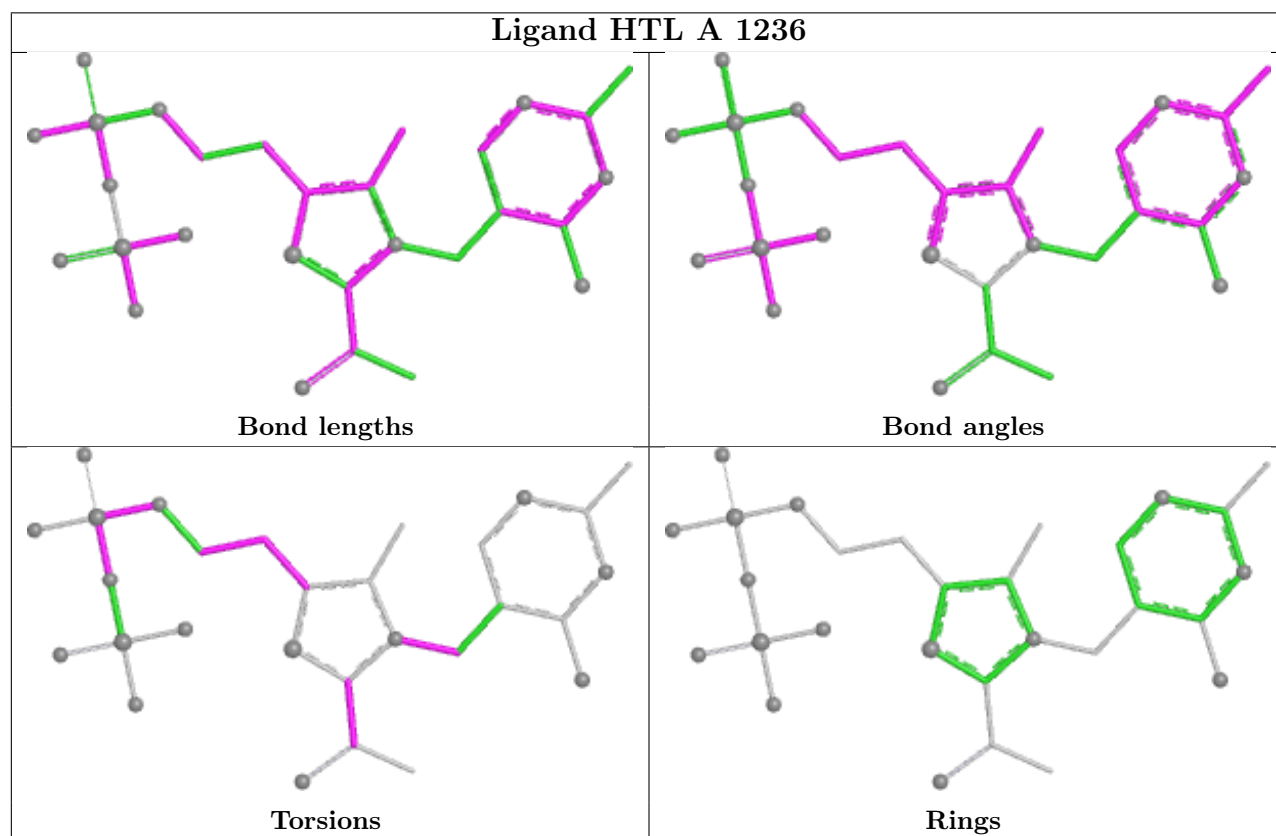
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1240	CO2	1	0
3	A	1236	HTL	2	0
3	B	1236	HTL	2	0
2	B	1233	SF4	1	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

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	1231/1231 (100%)	-0.31	38 (3%)	51	48	6, 23, 63, 111	0
1	B	1231/1231 (100%)	-0.60	26 (2%)	63	60	5, 17, 47, 99	0
All	All	2462/2462 (100%)	-0.46	64 (2%)	57	54	5, 19, 57, 111	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1175	PHE	6.3
1	A	1174	SER	5.7
1	B	1177	PRO	5.4
1	A	1178	ALA	5.2
1	A	1177	PRO	5.2
1	B	1175	PHE	5.0
1	B	1181	LYS	5.0
1	A	631	ALA	5.0
1	B	1180	GLY	4.9
1	B	1178	ALA	4.8
1	B	1165	HIS	4.5
1	B	1179	GLY	4.3
1	B	1176	ALA	4.3
1	A	1165	HIS	4.3
1	B	631	ALA	4.2
1	A	1176	ALA	4.2
1	A	1173	GLU	3.9
1	A	633	PRO	3.8
1	B	1174	SER	3.8
1	A	1179	GLY	3.8
1	B	1182	ALA	3.6
1	A	629	THR	3.6
1	A	592	GLY	3.6
1	A	591	TYR	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	1232	LYS	3.2
1	A	1181	LYS	3.2
1	A	594	LYS	3.1
1	B	1183	ASP	3.0
1	B	1173	GLU	3.0
1	A	1232	LYS	3.0
1	B	629	THR	2.9
1	A	634	MET	2.9
1	A	593	LYS	2.8
1	A	589	LYS	2.8
1	A	1231	LYS	2.8
1	A	1180	GLY	2.8
1	B	592	GLY	2.7
1	A	590	ALA	2.7
1	A	628	GLU	2.7
1	A	1182	ALA	2.7
1	A	588	HIS	2.7
1	A	1172	PHE	2.7
1	B	630	LYS	2.6
1	A	636	ASN	2.6
1	A	626	PRO	2.6
1	B	593	LYS	2.6
1	A	595	GLY	2.5
1	A	619	PRO	2.5
1	A	627	ALA	2.5
1	A	576	PHE	2.4
1	B	595	GLY	2.4
1	B	1172	PHE	2.4
1	A	598	ILE	2.4
1	B	633	PRO	2.3
1	B	732	LYS	2.3
1	A	596	GLU	2.2
1	B	591	TYR	2.1
1	A	732	LYS	2.1
1	B	594	LYS	2.1
1	A	758	LYS	2.1
1	A	715	VAL	2.1
1	B	627	ALA	2.1
1	A	635	THR	2.0
1	B	1230	THR	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](#)

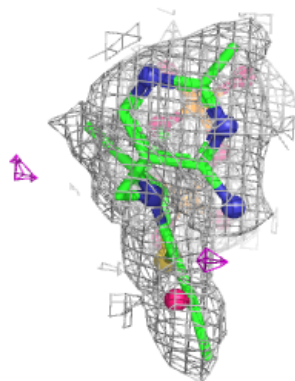
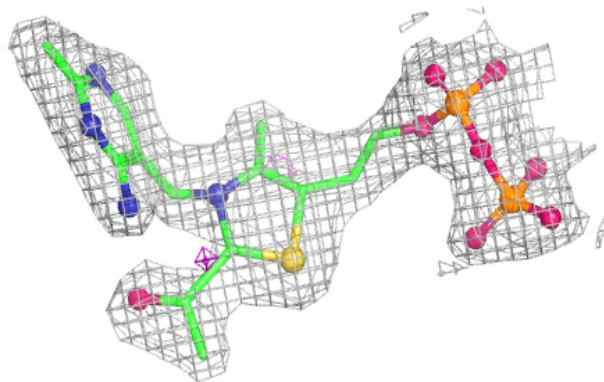
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
6	CO2	A	1240	3/3	0.90	0.16	38,38,42,46	0
5	CA	B	1239	1/1	0.96	0.14	58,58,58,58	0
3	HTL	A	1236	29/29	0.97	0.07	10,21,38,40	0
5	CA	A	1239	1/1	0.97	0.15	58,58,58,58	0
6	CO2	B	1240	3/3	0.98	0.06	29,29,31,31	0
2	SF4	B	1235	8/8	0.99	0.02	7,10,11,11	0
2	SF4	A	1233	8/8	0.99	0.05	30,31,32,33	0
3	HTL	B	1236	29/29	0.99	0.05	8,12,25,27	0
4	MG	A	1238	1/1	0.99	0.03	9,9,9,9	0
2	SF4	A	1234	8/8	0.99	0.04	22,25,27,28	0
2	SF4	A	1235	8/8	0.99	0.04	17,19,22,22	0
2	SF4	B	1233	8/8	0.99	0.03	15,18,20,20	0
2	SF4	B	1234	8/8	0.99	0.03	14,15,16,17	0
4	MG	B	1238	1/1	1.00	0.02	3,3,3,3	0

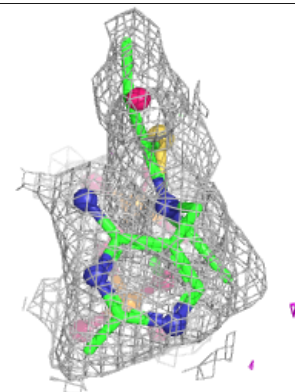
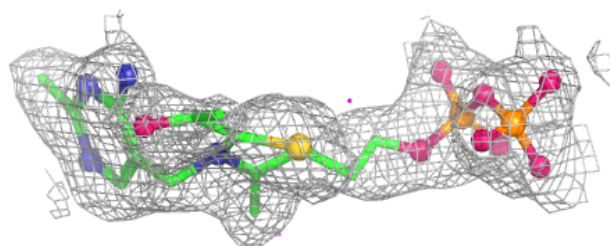
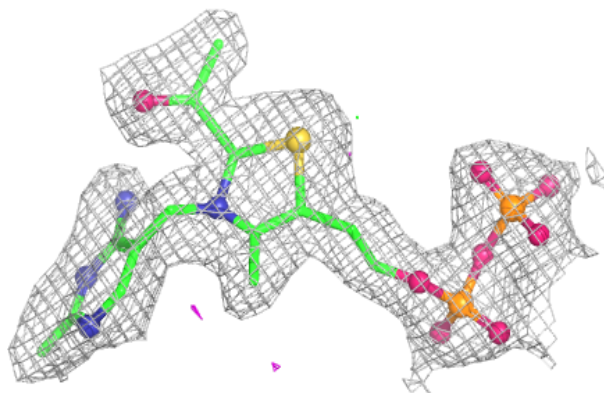
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HTL A 1236:

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

**Electron density around HTL B 1236:**

$2mF_o-DF_c$ (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.