



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 09:22 PM EDT

PDB ID : 3EXH
Title : Crystal structure of the pyruvate dehydrogenase (E1p) component of human pyruvate dehydrogenase complex
Authors : Kato, M.; Wynn, R.M.; Chuang, J.L.; Tso, S.-C.; Machius, M.; Li, J.; Chuang, D.T.
Deposited on : 2008-10-16
Resolution : 2.44 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

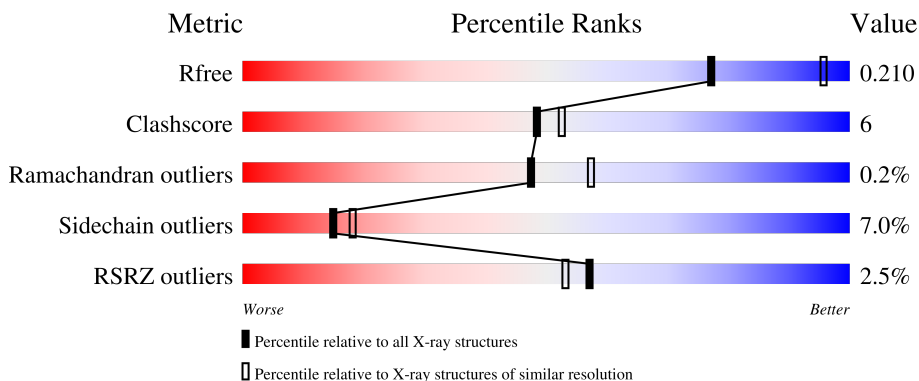
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 Å.

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



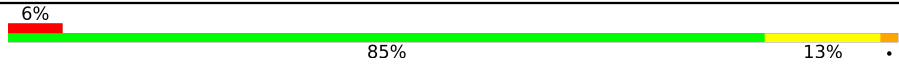

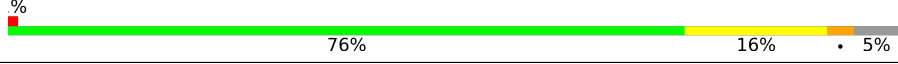
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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	382	
1	E	382	
2	B	329	
2	D	329	
2	F	329	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	329	 <p>6% 85% 13% • 5%</p>
3	C	382	 <p>% 77% 15% • 5%</p>
3	G	382	 <p>% 76% 16% • 5%</p>

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 22035 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 dehydrogenase E1 component subunit alpha, somatic form, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	359	2802	1760	493	525	24	0	0	0
1	E	331	2573	1621	448	482	22	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP P08559
A	-19	GLY	-	expression tag	UNP P08559
A	-18	SER	-	expression tag	UNP P08559
A	-17	SER	-	expression tag	UNP P08559
A	-16	HIS	-	expression tag	UNP P08559
A	-15	HIS	-	expression tag	UNP P08559
A	-14	HIS	-	expression tag	UNP P08559
A	-13	HIS	-	expression tag	UNP P08559
A	-12	HIS	-	expression tag	UNP P08559
A	-11	HIS	-	expression tag	UNP P08559
A	-10	SER	-	expression tag	UNP P08559
A	-9	SER	-	expression tag	UNP P08559
A	-8	GLY	-	expression tag	UNP P08559
A	-7	LEU	-	expression tag	UNP P08559
A	-6	VAL	-	expression tag	UNP P08559
A	-5	PRO	-	expression tag	UNP P08559
A	-4	ARG	-	expression tag	UNP P08559
A	-3	GLY	-	expression tag	UNP P08559
A	-2	SER	-	expression tag	UNP P08559
A	-1	HIS	-	expression tag	UNP P08559
A	0	MET	-	expression tag	UNP P08559
A	203	ALA	SER	engineered mutation	UNP P08559
A	271	ALA	SER	engineered mutation	UNP P08559
E	-20	MET	-	expression tag	UNP P08559

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	GLY	-	expression tag	UNP P08559
E	-18	SER	-	expression tag	UNP P08559
E	-17	SER	-	expression tag	UNP P08559
E	-16	HIS	-	expression tag	UNP P08559
E	-15	HIS	-	expression tag	UNP P08559
E	-14	HIS	-	expression tag	UNP P08559
E	-13	HIS	-	expression tag	UNP P08559
E	-12	HIS	-	expression tag	UNP P08559
E	-11	HIS	-	expression tag	UNP P08559
E	-10	SER	-	expression tag	UNP P08559
E	-9	SER	-	expression tag	UNP P08559
E	-8	GLY	-	expression tag	UNP P08559
E	-7	LEU	-	expression tag	UNP P08559
E	-6	VAL	-	expression tag	UNP P08559
E	-5	PRO	-	expression tag	UNP P08559
E	-4	ARG	-	expression tag	UNP P08559
E	-3	GLY	-	expression tag	UNP P08559
E	-2	SER	-	expression tag	UNP P08559
E	-1	HIS	-	expression tag	UNP P08559
E	0	MET	-	expression tag	UNP P08559
E	203	ALA	SER	engineered mutation	UNP P08559
E	271	ALA	SER	engineered mutation	UNP P08559

- Molecule 2 is a protein called Pyruvate dehydrogenase E1 component subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	D	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	F	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	H	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			

- Molecule 3 is a protein called Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
3	C	362	Total	C	N	O	P	S	0	0	0
			2825	1772	496	532	1	24			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
3	G	362	2825	1772	496	532	1	24	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	MET	-	expression tag	UNP P08559
C	-19	GLY	-	expression tag	UNP P08559
C	-18	SER	-	expression tag	UNP P08559
C	-17	SER	-	expression tag	UNP P08559
C	-16	HIS	-	expression tag	UNP P08559
C	-15	HIS	-	expression tag	UNP P08559
C	-14	HIS	-	expression tag	UNP P08559
C	-13	HIS	-	expression tag	UNP P08559
C	-12	HIS	-	expression tag	UNP P08559
C	-11	HIS	-	expression tag	UNP P08559
C	-10	SER	-	expression tag	UNP P08559
C	-9	SER	-	expression tag	UNP P08559
C	-8	GLY	-	expression tag	UNP P08559
C	-7	LEU	-	expression tag	UNP P08559
C	-6	VAL	-	expression tag	UNP P08559
C	-5	PRO	-	expression tag	UNP P08559
C	-4	ARG	-	expression tag	UNP P08559
C	-3	GLY	-	expression tag	UNP P08559
C	-2	SER	-	expression tag	UNP P08559
C	-1	HIS	-	expression tag	UNP P08559
C	0	MET	-	expression tag	UNP P08559
C	203	ALA	SER	engineered mutation	UNP P08559
C	271	ALA	SER	engineered mutation	UNP P08559
G	-20	MET	-	expression tag	UNP P08559
G	-19	GLY	-	expression tag	UNP P08559
G	-18	SER	-	expression tag	UNP P08559
G	-17	SER	-	expression tag	UNP P08559
G	-16	HIS	-	expression tag	UNP P08559
G	-15	HIS	-	expression tag	UNP P08559
G	-14	HIS	-	expression tag	UNP P08559
G	-13	HIS	-	expression tag	UNP P08559
G	-12	HIS	-	expression tag	UNP P08559
G	-11	HIS	-	expression tag	UNP P08559
G	-10	SER	-	expression tag	UNP P08559
G	-9	SER	-	expression tag	UNP P08559
G	-8	GLY	-	expression tag	UNP P08559

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	-7	LEU	-	expression tag	UNP P08559
G	-6	VAL	-	expression tag	UNP P08559
G	-5	PRO	-	expression tag	UNP P08559
G	-4	ARG	-	expression tag	UNP P08559
G	-3	GLY	-	expression tag	UNP P08559
G	-2	SER	-	expression tag	UNP P08559
G	-1	HIS	-	expression tag	UNP P08559
G	0	MET	-	expression tag	UNP P08559
G	203	ALA	SER	engineered mutation	UNP P08559
G	271	ALA	SER	engineered mutation	UNP P08559

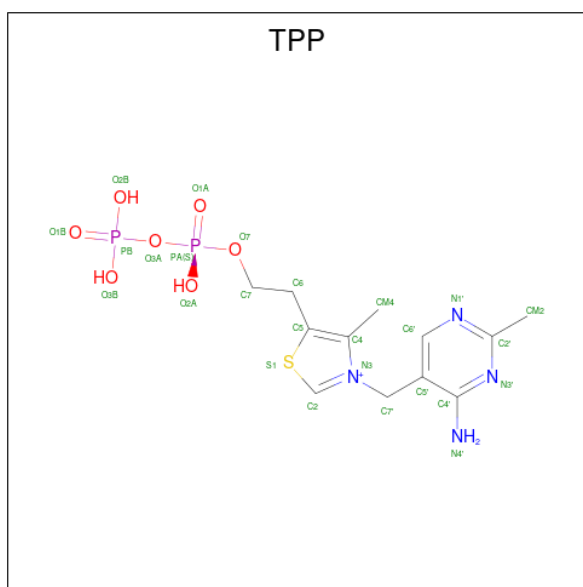
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mn 1 1	0	0
4	C	1	Total Mn 1 1	0	0
4	E	1	Total Mn 1 1	0	0
4	G	1	Total Mn 1 1	0	0

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

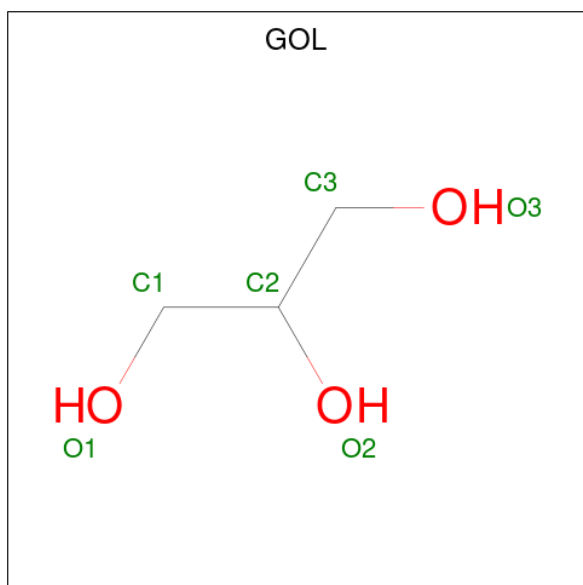
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total K 1 1	0	0
5	C	1	Total K 1 1	0	0
5	E	1	Total K 1 1	0	0
5	G	1	Total K 1 1	0	0

- Molecule 6 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
6	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
6	C	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
6	E	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
6	G	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



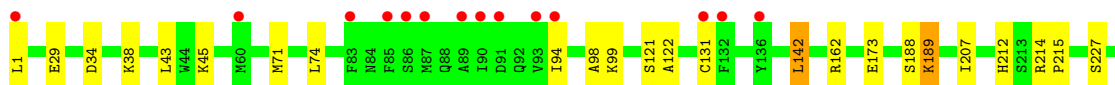
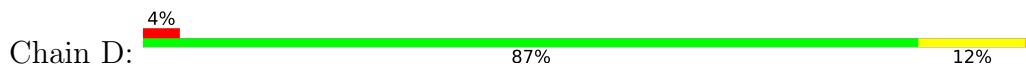
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	E	1	Total	C	O	0	0
			6	3	3		
7	G	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is water.

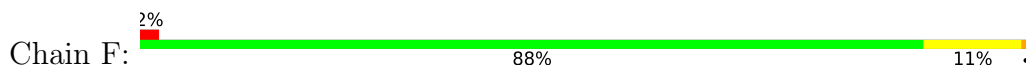
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	93	Total	O	0	0
			93	93		
8	B	114	Total	O	0	0
			114	114		
8	C	80	Total	O	0	0
			80	80		
8	D	97	Total	O	0	0
			97	97		
8	E	89	Total	O	0	0
			89	89		
8	F	121	Total	O	0	0
			121	121		
8	G	97	Total	O	0	0
			97	97		
8	H	101	Total	O	0	0
			101	101		



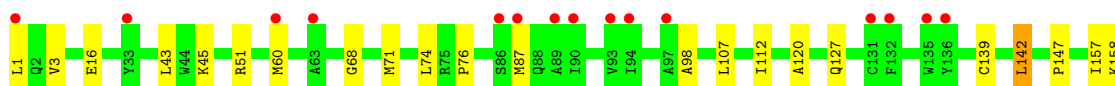
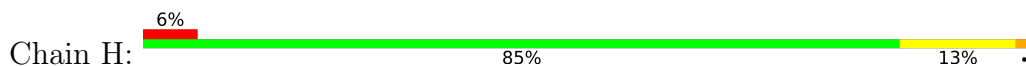
- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial



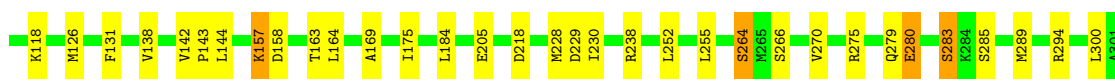
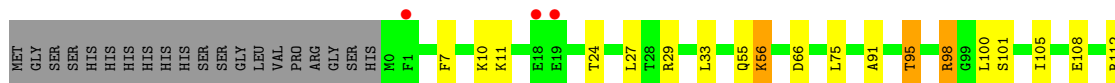
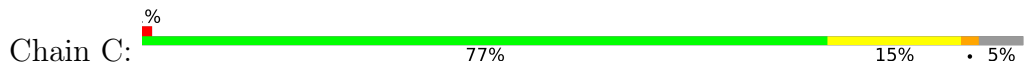
- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial




- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

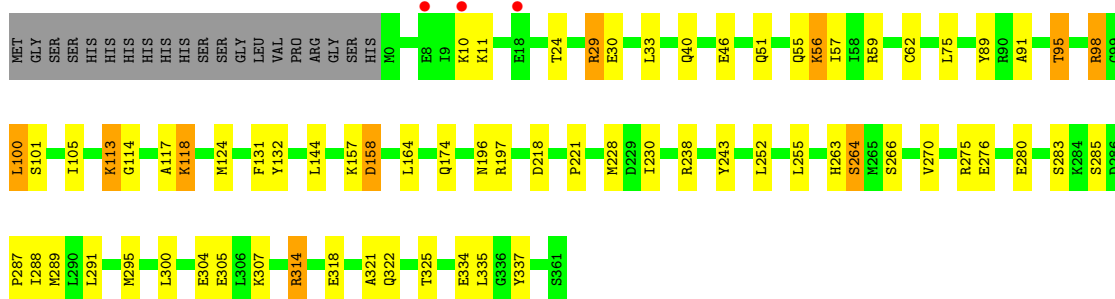


- Molecule 3: Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial



- Molecule 3: Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial

Chain G:  %



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	257.06Å 115.61Å 127.59Å 90.00° 113.64° 90.00°	Depositor
Resolution (Å)	50.00 – 2.44 47.46 – 2.44	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-2.44) 97.8 (47.46-2.44)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.28 (at 2.45Å)	Xtrriage
Refinement program	REFMAC 5.4.0069	Depositor
R, R_{free}	0.165 , 0.211 0.166 , 0.210	Depositor DCC
R_{free} test set	6182 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.4	Xtrriage
Anisotropy	0.144	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22035	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: TPP, MN, SEP, K, GOL

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	0.95	2/2857 (0.1%)	0.89	2/3845 (0.1%)
1	E	0.93	1/2621 (0.0%)	0.88	5/3527 (0.1%)
2	B	0.99	0/2574	0.95	7/3488 (0.2%)
2	D	0.96	3/2574 (0.1%)	0.91	2/3488 (0.1%)
2	F	0.99	2/2574 (0.1%)	0.92	2/3488 (0.1%)
2	H	0.98	1/2574 (0.0%)	0.90	3/3488 (0.1%)
3	C	0.94	2/2870 (0.1%)	0.87	1/3864 (0.0%)
3	G	0.93	1/2870 (0.0%)	0.86	1/3864 (0.0%)
All	All	0.96	12/21514 (0.1%)	0.90	23/29052 (0.1%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	29	GLU	CG-CD	6.55	1.61	1.51
3	G	62	CYS	CB-SG	-6.08	1.72	1.82
1	A	176	PHE	CE2-CZ	5.89	1.48	1.37
3	C	205	GLU	CG-CD	5.55	1.60	1.51
2	F	136	TYR	CD1-CE1	-5.49	1.31	1.39
3	C	280	GLU	CG-CD	5.33	1.59	1.51
2	D	250	GLU	CD-OE2	5.29	1.31	1.25
1	A	333	GLU	CG-CD	5.24	1.59	1.51
2	D	131	CYS	CB-SG	5.16	1.91	1.82
1	E	176	PHE	CE2-CZ	5.07	1.47	1.37
2	F	91	ASP	CB-CG	5.04	1.62	1.51
2	H	139	CYS	CB-SG	5.01	1.90	1.82

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	162	ARG	NE-CZ-NH2	-9.03	115.78	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	14	ASP	CB-CG-OD1	8.83	126.25	118.30
2	B	162	ARG	NE-CZ-NH1	8.21	124.40	120.30
1	E	197	ARG	NE-CZ-NH1	8.13	124.37	120.30
2	F	162	ARG	NE-CZ-NH1	7.13	123.87	120.30
2	H	162	ARG	NE-CZ-NH2	-6.78	116.91	120.30
2	B	14	ASP	CB-CG-OD2	-6.46	112.48	118.30
2	D	299	ASP	CB-CG-OD1	6.17	123.86	118.30
1	A	289	MET	CG-SD-CE	6.03	109.85	100.20
2	H	162	ARG	NE-CZ-NH1	5.62	123.11	120.30
2	B	152	ASP	CB-CG-OD2	-5.58	113.28	118.30
1	E	286	ASP	CB-CG-OD2	5.55	123.30	118.30
1	E	349	ARG	NE-CZ-NH2	-5.52	117.54	120.30
2	D	162	ARG	NE-CZ-NH2	-5.50	117.55	120.30
2	B	139	CYS	CA-CB-SG	-5.47	104.16	114.00
3	G	314	ARG	NE-CZ-NH1	5.42	123.01	120.30
2	B	152	ASP	CB-CG-OD1	5.30	123.07	118.30
2	F	162	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	98	ARG	NE-CZ-NH1	-5.17	117.72	120.30
2	H	214	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	E	71	CYS	CA-CB-SG	-5.08	104.85	114.00
1	E	99	GLY	N-CA-C	5.07	125.77	113.10
3	C	317	ILE	CG1-CB-CG2	-5.00	100.39	111.40

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	2802	0	2755	39	0
1	E	2573	0	2543	41	0
2	B	2519	0	2517	27	0
2	D	2519	0	2517	20	0
2	F	2519	0	2517	24	0
2	H	2519	0	2517	27	0
3	C	2825	0	2775	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	2825	0	2775	44	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
6	A	26	0	16	2	0
6	C	26	0	16	4	0
6	E	26	0	16	3	0
6	G	26	0	16	7	0
7	A	12	0	16	0	0
7	C	6	0	8	0	0
7	E	6	0	8	0	0
7	G	6	0	8	0	0
8	A	93	0	0	2	0
8	B	114	0	0	1	0
8	C	80	0	0	1	0
8	D	97	0	0	0	0
8	E	89	0	0	3	0
8	F	121	0	0	2	0
8	G	97	0	0	5	0
8	H	101	0	0	3	0
All	All	22035	0	21020	253	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 6.

All (253) 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:G:264:SEP:O3P	3:G:266:SER:HB2	1.34	1.26
3:C:270:VAL:HG21	3:C:275:ARG:NH1	1.62	1.14
3:C:264:SEP:O3P	3:C:266:SER:HB2	1.48	1.11
1:E:206:ARG:HG3	1:E:206:ARG:HH11	1.03	1.06
1:A:68:GLN:HE22	1:A:196:ASN:HD22	1.07	1.03
3:C:98:ARG:HG2	3:C:131:PHE:HB2	1.41	0.99
3:G:98:ARG:HG2	3:G:131:PHE:HB2	1.46	0.98
1:E:206:ARG:HG3	1:E:206:ARG:NH1	1.77	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:98:ALA:HB2	2:H:142:LEU:HD13	1.53	0.91
2:F:118:ASN:HD21	2:F:132:PHE:H	1.17	0.89
1:A:68:GLN:NE2	1:A:196:ASN:HD22	1.72	0.87
2:H:317:LYS:HE3	8:H:2624:HOH:O	1.76	0.85
3:G:264:SEP:O3P	3:G:266:SER:CB	2.22	0.83
2:F:139:CYS:HB3	8:F:2605:HOH:O	1.79	0.81
3:G:276:GLU:O	3:G:280:GLU:HG2	1.81	0.80
2:F:16:GLU:OE1	2:F:162:ARG:HD2	1.85	0.77
2:B:118:ASN:HD21	2:B:132:PHE:H	1.28	0.76
3:C:270:VAL:CG2	3:C:275:ARG:NH1	2.47	0.75
2:F:104:SER:O	2:F:107:LEU:HD22	1.88	0.73
1:A:334:GLU:HG2	1:A:337:TYR:CE2	2.24	0.72
2:D:98:ALA:HB2	2:D:142:LEU:HD13	1.71	0.71
1:E:39:MET:CE	1:E:291:LEU:CD2	2.70	0.70
1:E:206:ARG:NH1	1:E:206:ARG:CG	2.52	0.69
1:E:39:MET:CE	1:E:291:LEU:HD23	2.22	0.69
2:B:199:LYS:HE2	2:B:239:ARG:NH2	2.07	0.69
1:E:39:MET:HE1	1:E:291:LEU:CD2	2.22	0.69
3:G:55:GLN:O	3:G:56:LYS:HB2	1.93	0.69
1:E:39:MET:HE1	1:E:291:LEU:HD22	1.75	0.68
3:C:270:VAL:HG21	3:C:275:ARG:CZ	2.22	0.68
1:A:68:GLN:HE22	1:A:196:ASN:ND2	1.87	0.67
1:A:223:LEU:HD21	1:A:253:MET:HG3	1.75	0.67
3:C:108:GLU:HB3	3:C:126:MET:HE1	1.76	0.66
3:G:59:ARG:HD2	8:G:2582:HOH:O	1.94	0.66
2:F:172:ASN:HD22	2:F:175:MET:H	1.42	0.66
2:F:118:ASN:HD21	2:F:132:PHE:N	1.92	0.65
2:B:207:ILE:HD11	2:B:260:VAL:HG23	1.79	0.65
3:C:91:ALA:O	3:C:95:THR:HG23	1.98	0.64
1:A:291:LEU:O	1:A:295:MET:HG3	1.97	0.63
2:B:172:ASN:HD22	2:B:175:MET:H	1.43	0.63
6:G:1502:TPP:HN42	6:G:1502:TPP:H2	1.63	0.63
1:E:29:ARG:NH2	1:E:305:GLU:OE1	2.31	0.63
3:G:118:LYS:HB2	8:G:2742:HOH:O	1.99	0.62
2:D:189:LYS:HB2	2:D:189:LYS:NZ	2.13	0.62
2:F:75:ARG:HH12	2:F:164:ASN:ND2	1.98	0.61
3:C:55:GLN:O	3:C:56:LYS:HB2	2.00	0.60
2:F:33:TYR:O	2:F:34:ASP:HB2	2.00	0.60
3:G:304:GLU:HG3	8:G:2727:HOH:O	2.01	0.60
2:D:259:LEU:HD22	2:D:279:ILE:HG13	1.82	0.60
6:C:1502:TPP:H2	8:C:2592:HOH:O	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:270:VAL:HG11	3:G:275:ARG:NH2	2.16	0.59
2:H:16:GLU:OE1	2:H:162:ARG:HD2	2.03	0.59
1:A:68:GLN:NE2	1:A:259:ARG:HB3	2.18	0.59
6:C:1502:TPP:H2	6:C:1502:TPP:HN42	1.66	0.59
3:G:334:GLU:HG2	3:G:337:TYR:CD2	2.38	0.59
1:E:223:LEU:N	1:E:223:LEU:HD23	2.18	0.58
3:G:101:SER:O	3:G:105:ILE:HG13	2.03	0.58
1:E:39:MET:CE	1:E:291:LEU:HD22	2.34	0.57
6:E:1502:TPP:H2	6:E:1502:TPP:HN42	1.69	0.57
1:A:223:LEU:HD23	1:A:252:LEU:O	2.06	0.56
2:B:203:GLN:NE2	8:B:2667:HOH:O	2.39	0.56
2:H:212:HIS:HB3	2:H:238:MET:CE	2.36	0.56
2:B:24:PHE:CZ	2:B:76:PRO:HB3	2.40	0.56
1:E:157:LYS:O	1:E:158:ASP:HB2	2.05	0.56
3:G:113:LYS:HG2	3:G:114:GLY:N	2.20	0.56
2:F:153:ALA:O	2:F:157:ILE:HG22	2.06	0.55
1:E:334:GLU:HG2	1:E:337:TYR:CE2	2.41	0.55
3:G:91:ALA:O	3:G:95:THR:CG2	2.55	0.55
2:B:16:GLU:OE1	2:B:162:ARG:HD2	2.08	0.54
1:A:223:LEU:HD23	1:A:223:LEU:N	2.21	0.54
2:B:118:ASN:HD21	2:B:132:PHE:N	2.01	0.54
1:A:196:ASN:O	1:A:197:ARG:HB2	2.08	0.54
3:G:29:ARG:NH2	3:G:305:GLU:OE1	2.41	0.54
1:E:308:GLU:HB3	8:E:2731:HOH:O	2.08	0.54
2:F:251:ALA:HA	2:F:254:MET:HE2	1.90	0.53
2:H:120:ALA:HB1	2:H:313:ILE:HD11	1.89	0.53
3:C:279:GLN:O	3:C:283:SER:HB3	2.08	0.53
3:G:321:ALA:O	3:G:325:THR:HG23	2.08	0.53
1:A:172:GLN:HB2	1:A:175:ILE:HD13	1.91	0.53
1:A:101:SER:OG	1:A:104:GLU:HG3	2.09	0.53
1:E:127:TYR:CD1	1:E:127:TYR:N	2.77	0.53
1:A:40:GLN:O	1:A:44:ARG:HG2	2.09	0.52
1:E:103:ARG:HG2	1:E:323:PHE:CD2	2.44	0.52
3:G:157:LYS:O	3:G:158:ASP:CB	2.56	0.52
2:B:104:SER:O	2:B:107:LEU:HD22	2.08	0.52
3:C:270:VAL:HG21	3:C:275:ARG:HH12	1.66	0.51
3:G:228:MET:HE3	3:G:285:SER:O	2.09	0.51
3:G:228:MET:HE3	3:G:287:PRO:HD3	1.92	0.51
2:B:246:MET:CE	2:B:279:ILE:HG12	2.40	0.51
1:A:341:SER:HB2	2:B:101:TYR:CE1	2.45	0.51
6:A:1502:TPP:H2	8:A:2278:HOH:O	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:246:MET:CE	2:H:279:ILE:HG12	2.41	0.51
3:C:157:LYS:O	3:C:158:ASP:HB2	2.09	0.51
1:E:223:LEU:HD23	1:E:223:LEU:H	1.76	0.50
6:E:1502:TPP:H2	8:E:2668:HOH:O	2.10	0.50
1:E:302:SER:OG	1:E:305:GLU:HG3	2.11	0.50
3:G:334:GLU:HG2	3:G:337:TYR:CE2	2.46	0.50
3:G:89:TYR:OH	6:G:1502:TPP:H71	2.11	0.50
3:C:29:ARG:NH2	3:C:305:GLU:OE1	2.45	0.50
2:H:212:HIS:HB3	2:H:238:MET:HE2	1.94	0.50
2:H:120:ALA:CB	2:H:313:ILE:HD11	2.41	0.50
2:B:237:ASN:C	2:B:237:ASN:HD22	2.16	0.49
1:A:95:THR:HG23	1:A:100:LEU:HD22	1.94	0.49
2:B:33:TYR:O	2:B:34:ASP:HB2	2.12	0.49
2:D:259:LEU:CD2	2:D:279:ILE:HG13	2.42	0.49
1:A:223:LEU:HD23	1:A:223:LEU:H	1.77	0.49
3:C:108:GLU:HB3	3:C:126:MET:CE	2.42	0.49
1:A:304:GLU:HG3	1:A:305:GLU:N	2.26	0.49
2:H:263:GLU:HB2	8:H:2720:HOH:O	2.12	0.49
1:A:103:ARG:HG2	1:A:323:PHE:CD2	2.48	0.49
3:G:335:LEU:C	3:G:335:LEU:HD23	2.31	0.49
2:H:237:ASN:C	2:H:237:ASN:HD22	2.16	0.49
1:E:229:ASP:C	1:E:229:ASP:OD1	2.48	0.49
2:D:189:LYS:HB2	2:D:189:LYS:HZ3	1.77	0.49
1:E:66:ASP:HA	1:E:69:GLU:OE2	2.12	0.49
1:A:302:SER:OG	1:A:305:GLU:HB2	2.13	0.49
1:E:212:ASP:HB3	1:E:215:LYS:HG3	1.95	0.48
1:E:95:THR:HG23	1:E:100:LEU:HD22	1.95	0.48
2:F:184:PRO:HA	2:F:187:GLN:NE2	2.29	0.48
3:C:142:VAL:HB	3:C:143:PRO:HD3	1.95	0.48
2:F:256:THR:O	2:F:257:ASN:HB2	2.13	0.48
3:C:144:LEU:HD13	2:D:71:MET:HE1	1.95	0.48
2:D:280:MET:HE2	2:D:285:PHE:CE1	2.48	0.48
3:G:263:HIS:CE1	6:G:1502:TPP:S1	3.07	0.48
3:G:91:ALA:O	3:G:95:THR:HG22	2.14	0.48
3:C:229:ASP:CG	3:C:294:ARG:HH12	2.16	0.48
2:B:285:PHE:O	2:B:288:LEU:HB2	2.14	0.47
2:B:154:LYS:O	2:B:157:ILE:HG22	2.13	0.47
3:C:335:LEU:HD23	3:C:335:LEU:O	2.14	0.47
3:C:101:SER:O	3:C:105:ILE:HG13	2.14	0.47
3:G:144:LEU:HD22	2:H:71:MET:HE1	1.95	0.47
1:A:229:ASP:OD1	1:A:229:ASP:C	2.52	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:GLU:HB3	2:B:58:SER:HB3	1.96	0.47
1:E:162:LEU:N	1:E:162:LEU:HD12	2.30	0.47
1:A:138:VAL:HG13	1:A:169:ALA:HB2	1.96	0.47
3:C:335:LEU:HD23	3:C:335:LEU:C	2.36	0.47
2:D:246:MET:CE	2:D:279:ILE:HG12	2.45	0.47
1:A:68:GLN:HE21	1:A:259:ARG:HB3	1.79	0.46
2:D:302:MET:CE	2:D:313:ILE:HD11	2.45	0.46
1:E:89:TYR:OH	6:E:1502:TPP:H71	2.16	0.46
1:E:290:LEU:HD22	1:E:294:ARG:HD2	1.98	0.46
1:A:132:TYR:N	1:A:132:TYR:CD1	2.84	0.45
3:G:89:TYR:HB2	3:G:124:MET:HG2	1.98	0.45
1:A:32:GLY:HA3	1:A:295:MET:HE1	1.98	0.45
3:C:228:MET:HE3	3:C:285:SER:O	2.16	0.45
1:E:196:ASN:HA	1:E:257:THR:HG22	1.97	0.45
1:A:55:GLN:O	1:A:56:LYS:HB2	2.16	0.45
1:E:292:LYS:HG3	1:E:306:LEU:CD1	2.46	0.45
3:C:302:SER:OG	3:C:305:GLU:HB2	2.16	0.45
2:B:3:VAL:HG13	2:B:182:PHE:HB2	1.98	0.45
2:B:256:THR:O	2:B:257:ASN:HB2	2.16	0.45
3:C:66:ASP:OD1	3:C:66:ASP:N	2.43	0.45
3:G:132:TYR:N	3:G:132:TYR:CD1	2.84	0.45
3:G:291:LEU:O	3:G:295:MET:HG3	2.17	0.45
1:E:258:TYR:N	1:E:258:TYR:CD2	2.85	0.45
2:D:324:LYS:HG2	2:D:329:ILE:HG13	1.99	0.45
1:A:228:MET:HE3	1:A:287:PRO:HD3	1.99	0.45
2:D:94:ILE:HG22	2:D:99:LYS:HE3	1.99	0.45
1:A:95:THR:CG2	1:A:100:LEU:HD22	2.46	0.45
1:A:216:ARG:HH11	1:A:216:ARG:HG3	1.81	0.44
1:E:283:SER:O	1:E:289:MET:HG2	2.17	0.44
3:G:91:ALA:O	3:G:95:THR:HG23	2.16	0.44
6:G:1502:TPP:HN42	6:G:1502:TPP:C2	2.30	0.44
2:D:212:HIS:HB3	2:D:238:MET:HE3	1.99	0.44
2:H:147:PRO:HD2	2:H:170:LEU:O	2.17	0.44
6:A:1502:TPP:H2	6:A:1502:TPP:HN42	1.82	0.44
3:C:112:ARG:HD2	3:C:327:ASP:O	2.18	0.44
2:F:21:GLU:HG2	8:F:2205:HOH:O	2.17	0.44
1:E:174:GLN:HB3	2:F:60:MET:HG2	1.98	0.44
2:B:1:LEU:HD12	2:B:3:VAL:HG12	2.00	0.44
3:G:117:ALA:O	3:G:118:LYS:HB2	2.17	0.44
3:C:327:ASP:HA	3:C:328:PRO:HD3	1.90	0.44
2:D:214:ARG:HB3	2:D:215:PRO:HD3	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:46:GLU:HA	3:G:46:GLU:OE1	2.18	0.44
3:G:221:PRO:HG2	3:G:243:TYR:OH	2.18	0.44
3:C:7:PHE:O	3:C:24:THR:HA	2.18	0.43
3:G:55:GLN:O	3:G:56:LYS:CB	2.61	0.43
3:G:164:LEU:HD12	3:G:164:LEU:N	2.33	0.43
1:A:172:GLN:HB2	1:A:175:ILE:CD1	2.48	0.43
2:B:237:ASN:C	2:B:237:ASN:ND2	2.71	0.43
3:C:229:ASP:OD1	3:C:229:ASP:C	2.56	0.43
1:A:32:GLY:HA3	1:A:295:MET:CE	2.48	0.43
6:C:1502:TPP:HN42	6:C:1502:TPP:C2	2.31	0.43
2:F:237:ASN:HD22	2:F:237:ASN:C	2.21	0.43
2:H:212:HIS:HB3	2:H:238:MET:HE3	2.00	0.43
2:B:202:ARG:O	2:B:234:GLU:HA	2.18	0.43
3:G:51:GLN:NE2	8:G:2252:HOH:O	2.51	0.43
1:A:341:SER:HB2	2:B:101:TYR:CZ	2.54	0.43
3:G:29:ARG:HH22	3:G:305:GLU:CD	2.22	0.43
1:A:343:ASP:HB3	1:A:344:PRO:HD2	1.99	0.43
3:G:157:LYS:HB2	8:G:2711:HOH:O	2.18	0.43
2:H:157:ILE:HG13	2:H:158:LYS:N	2.33	0.43
2:D:279:ILE:HD13	2:D:279:ILE:HA	1.90	0.43
1:E:315:LYS:HB2	1:E:315:LYS:HE2	1.69	0.43
2:F:95:ASN:ND2	2:H:87:MET:CE	2.82	0.43
2:D:207:ILE:HG13	2:D:258:HIS:HB2	2.01	0.43
2:H:259:LEU:HD22	2:H:279:ILE:HG13	2.01	0.43
1:E:164:LEU:HG	1:E:192:ILE:HB	2.00	0.42
2:H:302:MET:SD	2:H:303:PRO:HD2	2.59	0.42
1:E:164:LEU:N	1:E:164:LEU:HD12	2.33	0.42
1:A:257:THR:OG1	1:A:258:TYR:N	2.52	0.42
3:C:108:GLU:CG	3:C:126:MET:HE2	2.49	0.42
2:D:302:MET:HA	2:D:303:PRO:HD2	1.92	0.42
1:E:223:LEU:HD23	1:E:252:LEU:O	2.19	0.42
2:H:280:MET:HE3	2:H:285:PHE:CE1	2.55	0.42
2:F:154:LYS:O	2:F:157:ILE:HG22	2.19	0.42
3:C:138:VAL:HG13	3:C:169:ALA:HB2	2.01	0.42
3:C:334:GLU:HG2	3:C:337:TYR:CE2	2.55	0.42
2:D:280:MET:HG3	2:D:285:PHE:CE1	2.54	0.42
2:F:118:ASN:ND2	2:F:132:PHE:H	2.00	0.42
1:A:150:LEU:HA	1:A:187:LEU:HD22	2.01	0.42
2:H:237:ASN:ND2	8:H:2754:HOH:O	2.52	0.42
2:F:172:ASN:HD22	2:F:175:MET:N	2.13	0.42
2:H:107:LEU:HD12	2:H:107:LEU:O	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:222:GLY:HA2	1:E:252:LEU:O	2.20	0.42
3:G:40:GLN:NE2	3:G:288:ILE:HD13	2.35	0.42
2:H:76:PRO:HG2	2:H:112:ILE:HG13	2.02	0.42
1:A:58:ILE:HD13	1:A:109:LEU:HG	2.02	0.42
1:E:125:HIS:HE1	2:H:127:GLN:OE1	2.03	0.42
3:G:100:LEU:HD12	3:G:100:LEU:HA	1.88	0.42
3:G:196:ASN:O	3:G:197:ARG:HB2	2.20	0.42
1:E:58:ILE:HD13	1:E:109:LEU:HG	2.02	0.42
2:F:57:ILE:CD1	6:G:1502:TPP:HM41	2.50	0.42
1:A:58:ILE:HD13	1:A:109:LEU:HB3	2.01	0.41
1:A:174:GLN:HB3	2:B:60:MET:HG2	2.01	0.41
3:C:164:LEU:HD12	3:C:164:LEU:N	2.35	0.41
3:C:321:ALA:O	3:C:325:THR:HG23	2.20	0.41
3:C:142:VAL:HA	3:C:163:THR:CG2	2.50	0.41
2:D:121:SER:OG	2:D:122:ALA:N	2.53	0.41
1:A:56:LYS:HD3	8:A:2676:HOH:O	2.20	0.41
2:B:70:ALA:HB1	2:B:111:PRO:HD2	2.03	0.41
3:G:263:HIS:HE1	6:G:1502:TPP:S1	2.44	0.41
3:G:55:GLN:HE21	3:G:57:ILE:HD12	1.86	0.41
3:G:157:LYS:O	3:G:158:ASP:HB2	2.18	0.41
1:E:206:ARG:H	1:E:206:ARG:HG2	1.41	0.41
2:F:57:ILE:HD13	6:G:1502:TPP:CM4	2.50	0.41
3:C:55:GLN:O	3:C:56:LYS:CB	2.64	0.41
3:C:169:ALA:O	3:C:175:ILE:HD12	2.21	0.41
2:D:34:ASP:O	2:D:38:LYS:HA	2.20	0.41
3:G:174:GLN:HB3	2:H:60:MET:HG2	2.03	0.41
2:F:237:ASN:C	2:F:237:ASN:ND2	2.74	0.41
3:G:270:VAL:O	3:G:270:VAL:HG12	2.21	0.41
2:H:237:ASN:C	2:H:237:ASN:ND2	2.74	0.41
2:F:99:LYS:HG2	2:H:301:PRO:HB3	2.03	0.40
2:B:59:GLU:OE2	6:C:1502:TPP:N1'	2.55	0.40
2:B:288:LEU:HD23	2:D:280:MET:CE	2.51	0.40
1:E:357:PHE:HB3	8:E:2023:HOH:O	2.21	0.40
2:H:68:GLY:HA2	2:H:71:MET:HE2	2.02	0.40
1:E:74:GLY:N	1:E:230:ILE:HD12	2.37	0.40
1:E:47:LEU:HD23	1:E:47:LEU:HA	1.77	0.40
2:F:75:ARG:HH12	2:F:164:ASN:HD22	1.67	0.40
2:H:184:PRO:HA	2:H:187:GLN:NE2	2.37	0.40
2:B:259:LEU:CD2	2:B:279:ILE:HG13	2.52	0.40
1:E:343:ASP:HB3	1:E:344:PRO:HD2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	355/382 (93%)	343 (97%)	9 (2%)	3 (1%)	19	22
1	E	325/382 (85%)	317 (98%)	7 (2%)	1 (0%)	41	49
2	B	327/329 (99%)	315 (96%)	12 (4%)	0	100	100
2	D	327/329 (99%)	319 (98%)	8 (2%)	0	100	100
2	F	327/329 (99%)	314 (96%)	13 (4%)	0	100	100
2	H	327/329 (99%)	315 (96%)	12 (4%)	0	100	100
3	C	359/382 (94%)	348 (97%)	10 (3%)	1 (0%)	41	49
3	G	359/382 (94%)	346 (96%)	12 (3%)	1 (0%)	41	49
All	All	2706/2844 (95%)	2617 (97%)	83 (3%)	6 (0%)	47	57

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	MET
3	C	218	ASP
1	E	218	ASP
3	G	218	ASP
1	A	88	ALA
1	A	218	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	290/310 (94%)	269 (93%)	21 (7%)	14	17
1	E	267/310 (86%)	243 (91%)	24 (9%)	9	10
2	B	268/268 (100%)	253 (94%)	15 (6%)	21	27
2	D	268/268 (100%)	254 (95%)	14 (5%)	23	31
2	F	268/268 (100%)	255 (95%)	13 (5%)	25	33
2	H	268/268 (100%)	251 (94%)	17 (6%)	18	23
3	C	291/309 (94%)	266 (91%)	25 (9%)	10	11
3	G	291/309 (94%)	266 (91%)	25 (9%)	10	11
All	All	2211/2310 (96%)	2057 (93%)	154 (7%)	15	18

All (154) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	10	LYS
1	A	24	THR
1	A	27	LEU
1	A	29	ARG
1	A	33	LEU
1	A	75	LEU
1	A	100	LEU
1	A	109	LEU
1	A	129	LYS
1	A	157	LYS
1	A	230	ILE
1	A	253	MET
1	A	255	LEU
1	A	279	GLN
1	A	285	SER
1	A	289	MET
1	A	304	GLU
1	A	307	LYS
1	A	322	GLN
1	A	342	SER
2	B	1	LEU
2	B	18	GLU
2	B	43	LEU
2	B	45	LYS
2	B	74	LEU
2	B	107	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	121	SER
2	B	162	ARG
2	B	172	ASN
2	B	173	GLU
2	B	185	GLU
2	B	197	LYS
2	B	237	ASN
2	B	279	ILE
2	B	288	LEU
3	C	10	LYS
3	C	11	LYS
3	C	27	LEU
3	C	33	LEU
3	C	56	LYS
3	C	75	LEU
3	C	95	THR
3	C	98	ARG
3	C	100	LEU
3	C	118	LYS
3	C	157	LYS
3	C	184	LEU
3	C	230	ILE
3	C	238	ARG
3	C	252	LEU
3	C	255	LEU
3	C	280	GLU
3	C	283	SER
3	C	289	MET
3	C	300	LEU
3	C	307	LYS
3	C	314	ARG
3	C	317	ILE
3	C	342	SER
3	C	360	VAL
2	D	1	LEU
2	D	43	LEU
2	D	45	LYS
2	D	74	LEU
2	D	142	LEU
2	D	173	GLU
2	D	188	SER
2	D	189	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	227	SER
2	D	237	ASN
2	D	255	LYS
2	D	279	ILE
2	D	288	LEU
2	D	306	LYS
1	E	3	ASN
1	E	10	LYS
1	E	22	PRO
1	E	24	THR
1	E	27	LEU
1	E	29	ARG
1	E	33	LEU
1	E	34	LYS
1	E	75	LEU
1	E	100	LEU
1	E	103	ARG
1	E	109	LEU
1	E	205	GLU
1	E	206	ARG
1	E	210	SER
1	E	230	ILE
1	E	255	LEU
1	E	257	THR
1	E	283	SER
1	E	290	LEU
1	E	314	ARG
1	E	315	LYS
1	E	322	GLN
1	E	342	SER
2	F	1	LEU
2	F	3	VAL
2	F	43	LEU
2	F	45	LYS
2	F	74	LEU
2	F	107	LEU
2	F	157	ILE
2	F	192	LEU
2	F	237	ASN
2	F	246	MET
2	F	279	ILE
2	F	288	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	F	317	LYS
3	G	10	LYS
3	G	11	LYS
3	G	24	THR
3	G	29	ARG
3	G	30	GLU
3	G	33	LEU
3	G	56	LYS
3	G	75	LEU
3	G	95	THR
3	G	98	ARG
3	G	100	LEU
3	G	113	LYS
3	G	118	LYS
3	G	158	ASP
3	G	230	ILE
3	G	238	ARG
3	G	252	LEU
3	G	255	LEU
3	G	283	SER
3	G	289	MET
3	G	300	LEU
3	G	307	LYS
3	G	314	ARG
3	G	318	GLU
3	G	322	GLN
2	H	1	LEU
2	H	3	VAL
2	H	43	LEU
2	H	45	LYS
2	H	51	ARG
2	H	74	LEU
2	H	142	LEU
2	H	173	GLU
2	H	185	GLU
2	H	188	SER
2	H	189	LYS
2	H	197	LYS
2	H	237	ASN
2	H	279	ILE
2	H	288	LEU
2	H	306	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	H	317	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	130	ASN
1	A	279	GLN
1	A	297	ASN
2	B	32	GLN
2	B	118	ASN
2	B	172	ASN
2	B	187	GLN
2	B	203	GLN
2	B	237	ASN
2	B	257	ASN
2	B	328	ASN
3	C	40	GLN
3	C	51	GLN
3	C	55	GLN
3	C	263	HIS
3	C	299	ASN
3	C	353	GLN
2	D	237	ASN
1	E	55	GLN
1	E	130	ASN
1	E	297	ASN
2	F	32	GLN
2	F	118	ASN
2	F	164	ASN
2	F	172	ASN
2	F	187	GLN
2	F	237	ASN
2	F	257	ASN
2	F	328	ASN
3	G	3	ASN
3	G	40	GLN
3	G	51	GLN
3	G	55	GLN
3	G	80	ASN
3	G	263	HIS
3	G	299	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	G	353	GLN
2	H	237	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SEP	G	264	3	8,9,10	1.51	1 (12%)	8,12,14	1.85	4 (50%)
3	SEP	C	264	3	8,9,10	1.73	2 (25%)	8,12,14	1.64	3 (37%)

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. ^{1,2} means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SEP	G	264	3	-	2/5/8/10	-
3	SEP	C	264	3	-	2/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	264	SEP	P-O1P	3.60	1.62	1.50
3	G	264	SEP	P-O1P	2.99	1.60	1.50
3	C	264	SEP	P-O2P	2.42	1.64	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	264	SEP	O2P-P-OG	-2.43	100.27	106.73
3	C	264	SEP	OG-CB-CA	-2.33	105.88	108.14
3	G	264	SEP	O3P-P-O2P	2.32	116.52	107.64
3	G	264	SEP	O3P-P-OG	2.28	112.80	106.73
3	G	264	SEP	O3P-P-O1P	-2.12	102.37	110.68
3	C	264	SEP	O2P-P-OG	-2.09	101.18	106.73
3	C	264	SEP	OG-P-O1P	2.07	112.28	106.47

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	264	SEP	CB-OG-P-O2P
3	C	264	SEP	CB-OG-P-O3P
3	G	264	SEP	CB-OG-P-O2P
3	G	264	SEP	CB-OG-P-O3P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	264	SEP	2	0
3	C	264	SEP	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 8 are monoatomic - leaving 9 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
7	GOL	G	1905	-	5,5,5	0.57	0	5,5,5	0.79	0
6	TPP	E	1502	4	22,27,27	1.92	5 (22%)	29,40,40	3.10	14 (48%)
7	GOL	A	1901	-	5,5,5	0.20	0	5,5,5	1.30	1 (20%)
7	GOL	C	1903	-	5,5,5	0.42	0	5,5,5	0.77	0
6	TPP	G	1502	4	22,27,27	1.62	4 (18%)	29,40,40	2.41	12 (41%)
7	GOL	E	1904	-	5,5,5	0.33	0	5,5,5	0.53	0
6	TPP	A	1502	4	22,27,27	1.37	4 (18%)	29,40,40	2.33	12 (41%)
7	GOL	A	1902	-	5,5,5	0.34	0	5,5,5	0.55	0
6	TPP	C	1502	4	22,27,27	1.96	3 (13%)	29,40,40	2.43	16 (55%)

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
7	GOL	G	1905	-	-	4/4/4/4	-
6	TPP	E	1502	4	-	1/16/17/17	0/2/2/2
7	GOL	A	1901	-	-	4/4/4/4	-
7	GOL	C	1903	-	-	3/4/4/4	-
6	TPP	G	1502	4	-	2/16/17/17	0/2/2/2
7	GOL	E	1904	-	-	4/4/4/4	-
6	TPP	A	1502	4	-	4/16/17/17	0/2/2/2
7	GOL	A	1902	-	-	2/4/4/4	-
6	TPP	C	1502	4	-	0/16/17/17	0/2/2/2

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1502	TPP	C6-C5	7.31	1.54	1.50
6	E	1502	TPP	C6-C5	6.47	1.53	1.50
6	G	1502	TPP	C7'-N3	-3.67	1.41	1.48
6	A	1502	TPP	C2'-N3'	3.54	1.40	1.34
6	G	1502	TPP	C6-C5	3.30	1.52	1.50
6	G	1502	TPP	C5'-C4'	-2.76	1.38	1.42
6	G	1502	TPP	C4-N3	-2.56	1.37	1.39
6	C	1502	TPP	C7'-N3	-2.54	1.44	1.48
6	A	1502	TPP	C7'-N3	-2.39	1.44	1.48
6	E	1502	TPP	C4'-N3'	2.38	1.38	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	1502	TPP	C7'-N3	-2.32	1.44	1.48
6	E	1502	TPP	C2'-N3'	2.23	1.38	1.34
6	A	1502	TPP	C5'-C4'	-2.19	1.39	1.42
6	A	1502	TPP	C4'-N3'	2.06	1.38	1.35
6	E	1502	TPP	PB-O2B	-2.01	1.47	1.54
6	C	1502	TPP	C5'-C4'	-2.00	1.39	1.42

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1502	TPP	C6-C5-C4	7.37	133.35	127.43
6	E	1502	TPP	C7'-N3-C2	-6.95	112.80	125.35
6	E	1502	TPP	CM4-C4-N3	6.00	130.18	122.53
6	G	1502	TPP	C7'-N3-C2	-5.03	116.27	125.35
6	A	1502	TPP	C6-C5-C4	4.78	131.27	127.43
6	C	1502	TPP	CM4-C4-N3	4.75	128.59	122.53
6	C	1502	TPP	C5'-C7'-N3	-4.70	105.46	113.28
6	G	1502	TPP	CM4-C4-N3	4.64	128.45	122.53
6	E	1502	TPP	N1'-C2'-N3'	-4.48	117.83	125.54
6	C	1502	TPP	C7'-N3-C2	-4.41	117.39	125.35
6	A	1502	TPP	N1'-C2'-N3'	-4.37	118.02	125.54
6	G	1502	TPP	C5'-C7'-N3	-4.13	106.40	113.28
6	A	1502	TPP	CM4-C4-N3	4.12	127.78	122.53
6	G	1502	TPP	N1'-C2'-N3'	-4.11	118.47	125.54
6	G	1502	TPP	CM2-C2'-N3'	4.00	123.39	117.15
6	A	1502	TPP	C7'-N3-C2	-3.96	118.19	125.35
6	A	1502	TPP	CM2-C2'-N3'	3.84	123.15	117.15
6	E	1502	TPP	C2'-N3'-C4'	3.84	124.07	118.08
6	C	1502	TPP	N1'-C2'-N3'	-3.69	119.19	125.54
6	C	1502	TPP	C6'-C5'-C4'	3.62	120.65	115.72
6	E	1502	TPP	CM2-C2'-N3'	3.62	122.80	117.15
6	E	1502	TPP	CM4-C4-C5	-3.53	119.88	127.60
6	E	1502	TPP	C7'-C5'-C6'	-3.46	114.07	120.69
6	E	1502	TPP	O3B-PB-O3A	3.38	115.98	104.64
6	G	1502	TPP	C6'-C5'-C4'	3.33	120.25	115.72
6	C	1502	TPP	O3B-PB-O3A	3.31	115.73	104.64
6	G	1502	TPP	C2'-N3'-C4'	3.27	123.18	118.08
6	E	1502	TPP	C5'-C4'-N3'	-3.20	116.21	121.24
6	G	1502	TPP	C5'-C4'-N3'	-3.01	116.51	121.24
6	E	1502	TPP	C5'-C7'-N3	-3.01	108.27	113.28
6	A	1502	TPP	C2'-N3'-C4'	2.97	122.71	118.08
6	A	1502	TPP	C5'-C7'-N3	-2.94	108.38	113.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1502	TPP	CM2-C2'-N1'	2.89	120.31	117.14
6	C	1502	TPP	C6-C5-C4	2.79	129.68	127.43
6	G	1502	TPP	C7'-C5'-C6'	-2.73	115.47	120.69
6	E	1502	TPP	C6'-C5'-C4'	2.72	119.42	115.72
6	C	1502	TPP	C6'-N1'-C2'	2.71	120.57	115.96
6	C	1502	TPP	CM4-C4-C5	-2.66	121.77	127.60
6	G	1502	TPP	C6'-N1'-C2'	2.59	120.37	115.96
6	A	1502	TPP	O3B-PB-O3A	2.58	113.28	104.64
6	C	1502	TPP	C2'-N3'-C4'	2.56	122.08	118.08
6	A	1502	TPP	C6'-C5'-C4'	2.55	119.20	115.72
6	A	1502	TPP	C7'-C5'-C6'	-2.45	116.01	120.69
6	C	1502	TPP	C5'-C4'-N3'	-2.40	117.48	121.24
6	E	1502	TPP	C6'-N1'-C2'	2.39	120.03	115.96
7	A	1901	GOL	O3-C3-C2	-2.36	98.90	110.20
6	A	1502	TPP	C5'-C4'-N3'	-2.35	117.55	121.24
6	C	1502	TPP	C5'-C6'-N1'	-2.30	120.00	123.82
6	G	1502	TPP	N4'-C4'-N3'	2.20	120.15	117.03
6	C	1502	TPP	PA-O3A-PB	-2.19	125.31	132.83
6	A	1502	TPP	C6'-N1'-C2'	2.16	119.65	115.96
6	C	1502	TPP	CM2-C2'-N3'	2.13	120.48	117.15
6	C	1502	TPP	C7'-C5'-C6'	-2.12	116.63	120.69
6	G	1502	TPP	C6-C5-C4	2.08	129.10	127.43
6	E	1502	TPP	CM2-C2'-N1'	2.03	119.36	117.14

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1502	TPP	C5-C6-C7-O7
6	A	1502	TPP	C7-O7-PA-O1A
6	E	1502	TPP	PB-O3A-PA-O7
6	G	1502	TPP	PA-O3A-PB-O2B
7	A	1901	GOL	O1-C1-C2-O2
7	A	1901	GOL	O1-C1-C2-C3
7	C	1903	GOL	O1-C1-C2-C3
7	E	1904	GOL	O1-C1-C2-C3
7	E	1904	GOL	C1-C2-C3-O3
7	E	1904	GOL	O2-C2-C3-O3
7	A	1902	GOL	C1-C2-C3-O3
7	G	1905	GOL	O1-C1-C2-C3
7	G	1905	GOL	C1-C2-C3-O3
7	A	1901	GOL	O2-C2-C3-O3

Continued on next page...

Continued from previous page...

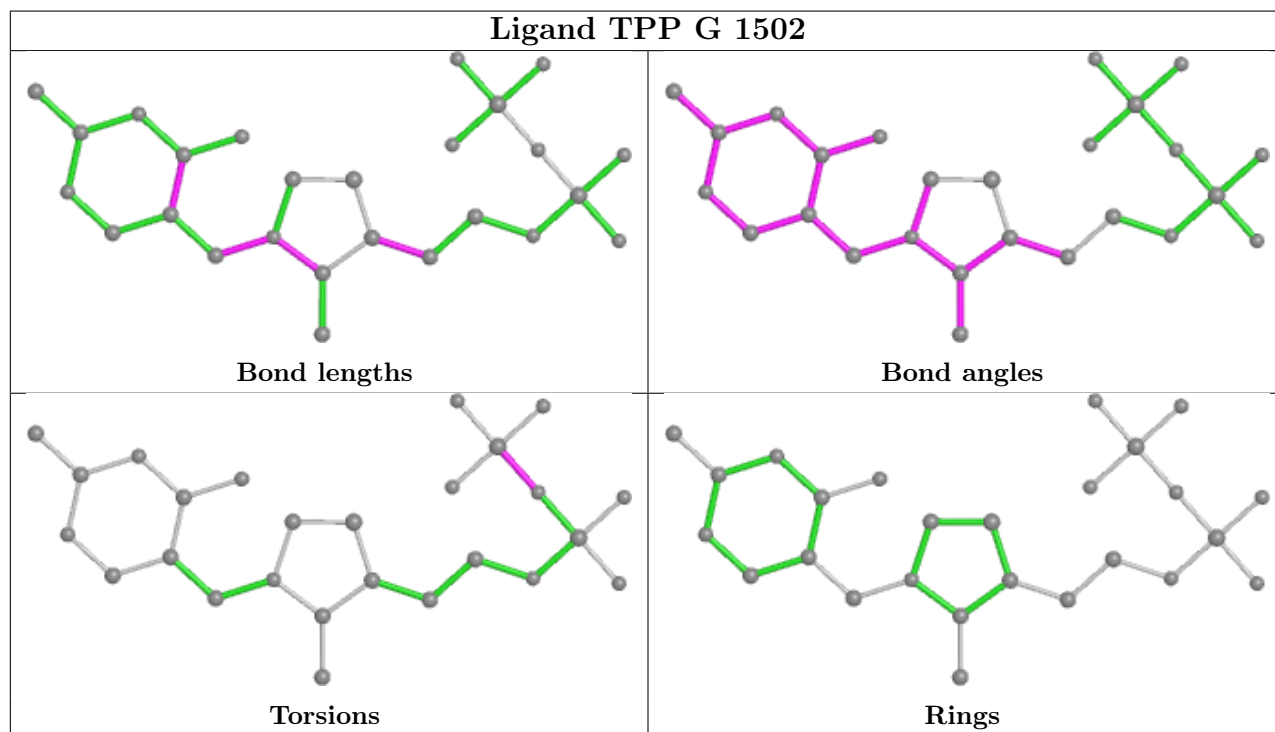
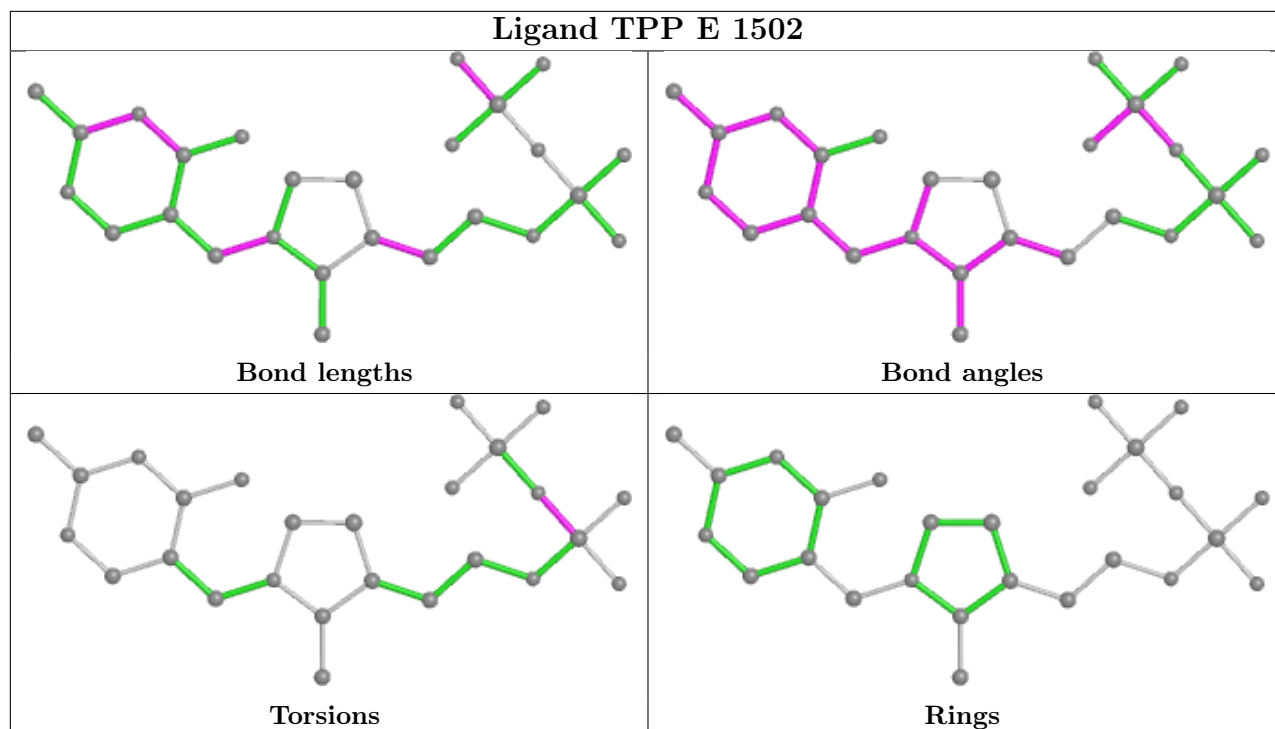
Mol	Chain	Res	Type	Atoms
7	C	1903	GOL	O1-C1-C2-O2
7	E	1904	GOL	O1-C1-C2-O2
7	G	1905	GOL	O1-C1-C2-O2
7	G	1905	GOL	O2-C2-C3-O3
7	A	1902	GOL	O2-C2-C3-O3
6	A	1502	TPP	C7-O7-PA-O3A
6	A	1502	TPP	C7-O7-PA-O2A
6	G	1502	TPP	PA-O3A-PB-O3B
7	A	1901	GOL	C1-C2-C3-O3
7	C	1903	GOL	O2-C2-C3-O3

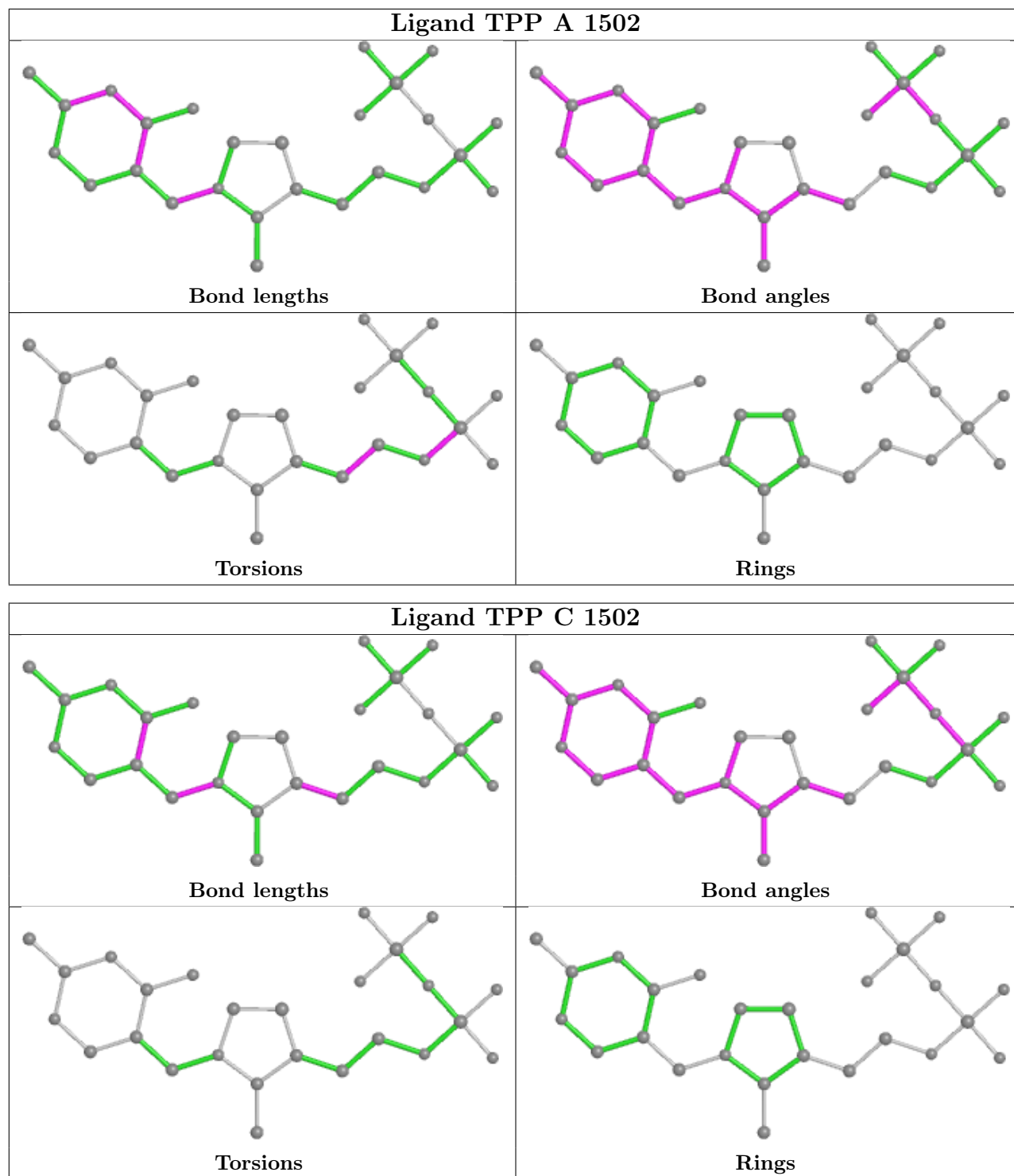
There are no ring outliers.

4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	1502	TPP	3	0
6	G	1502	TPP	7	0
6	A	1502	TPP	2	0
6	C	1502	TPP	4	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

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	359/382 (93%)	-0.22	3 (0%) 86 85	10, 18, 32, 55	0
1	E	331/382 (86%)	-0.18	12 (3%) 42 39	10, 18, 29, 48	0
2	B	329/329 (100%)	-0.29	6 (1%) 68 64	10, 16, 27, 37	0
2	D	329/329 (100%)	-0.05	14 (4%) 35 32	10, 17, 28, 39	0
2	F	329/329 (100%)	-0.18	8 (2%) 59 54	11, 16, 27, 40	0
2	H	329/329 (100%)	0.03	20 (6%) 21 17	10, 17, 28, 41	0
3	C	361/382 (94%)	-0.28	3 (0%) 86 85	10, 18, 32, 44	0
3	G	361/382 (94%)	-0.24	3 (0%) 86 85	10, 18, 30, 42	0
All	All	2728/2844 (95%)	-0.18	69 (2%) 57 53	10, 17, 29, 55	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	90	ILE	4.7
2	D	90	ILE	4.1
2	D	1	LEU	3.6
3	C	18	GLU	3.4
2	F	1	LEU	3.4
2	H	93	VAL	3.3
2	H	60	MET	3.2
1	E	285	SER	3.1
2	B	1	LEU	3.1
1	E	205	GLU	2.9
1	E	308	GLU	2.9
2	D	136	TYR	2.9
2	D	60	MET	2.9
2	D	89	ALA	2.9
1	E	1	PHE	2.9
2	H	94	ILE	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	131	CYS	2.8
2	D	87	MET	2.8
1	E	3	ASN	2.8
2	H	136	TYR	2.8
2	H	33	TYR	2.7
1	E	18	GLU	2.7
2	F	135	TRP	2.7
2	H	89	ALA	2.7
2	H	87	MET	2.7
2	H	132	PHE	2.7
2	B	184	PRO	2.6
2	D	94	ILE	2.6
1	A	301	ALA	2.6
2	D	132	PHE	2.5
2	B	90	ILE	2.5
2	H	86	SER	2.5
2	H	181	GLU	2.5
2	B	87	MET	2.5
2	F	90	ILE	2.5
2	F	87	MET	2.4
2	H	329	ILE	2.4
1	E	310	ASP	2.4
2	H	1	LEU	2.4
2	F	183	PRO	2.4
2	F	185	GLU	2.4
2	B	89	ALA	2.3
2	D	86	SER	2.3
1	A	296	VAL	2.3
1	E	33	LEU	2.3
3	C	1	PHE	2.3
2	D	85	PHE	2.3
3	G	18	GLU	2.3
3	G	10	LYS	2.3
2	F	184	PRO	2.3
1	E	309	ILE	2.2
2	H	184	PRO	2.2
2	H	131	CYS	2.2
2	H	183	PRO	2.2
2	H	135	TRP	2.2
2	D	93	VAL	2.1
2	B	135	TRP	2.1
1	E	301	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	F	89	ALA	2.1
3	G	8	GLU	2.1
1	E	0	MET	2.1
1	E	284	LYS	2.1
1	A	205	GLU	2.1
2	D	83	PHE	2.1
3	C	19	GLU	2.1
2	H	97	ALA	2.1
2	D	91	ASP	2.1
2	H	63	ALA	2.0
2	H	168	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SEP	G	264	10/11	0.94	0.15	27,31,37,39	0
3	SEP	C	264	10/11	0.96	0.15	30,35,44,45	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

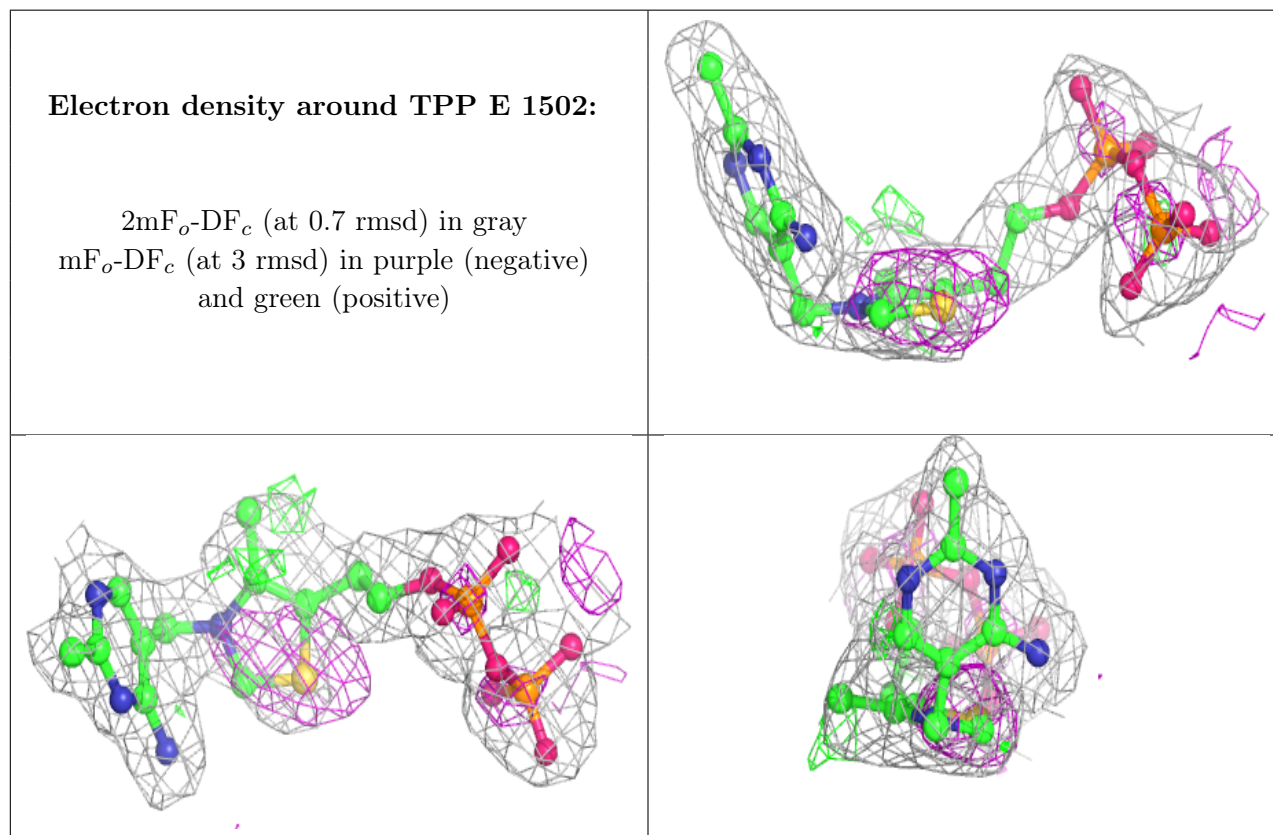
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	K	E	1501	1/1	0.79	0.10	48,48,48,48	0
7	GOL	C	1903	6/6	0.80	0.17	45,51,52,53	0
7	GOL	A	1902	6/6	0.88	0.15	46,51,52,52	0
7	GOL	A	1901	6/6	0.88	0.13	43,43,46,48	0
7	GOL	E	1904	6/6	0.88	0.15	45,48,50,52	0

Continued on next page...

Continued from previous page...

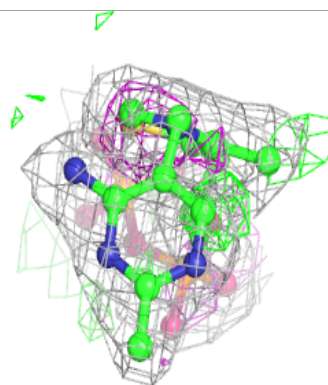
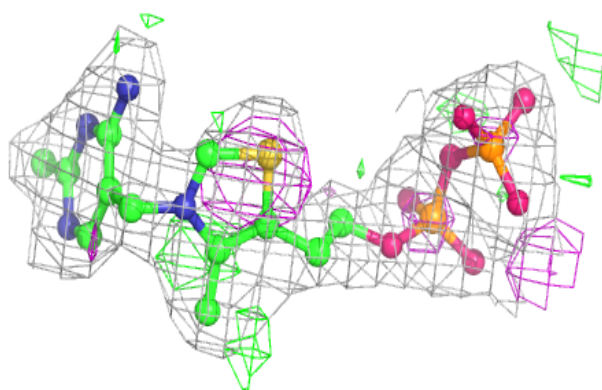
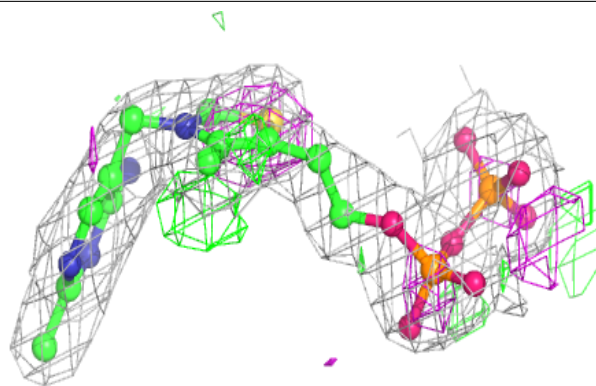
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	GOL	G	1905	6/6	0.89	0.15	44,47,49,49	0
6	TPP	E	1502	26/26	0.96	0.12	7,16,31,40	0
6	TPP	G	1502	26/26	0.97	0.11	9,14,25,31	0
6	TPP	C	1502	26/26	0.97	0.11	10,14,26,34	0
6	TPP	A	1502	26/26	0.97	0.12	9,16,27,28	0
5	K	C	1501	1/1	0.98	0.13	32,32,32,32	0
5	K	A	1501	1/1	0.98	0.14	36,36,36,36	0
5	K	G	1501	1/1	0.98	0.14	41,41,41,41	0
4	MN	G	1500	1/1	0.99	0.02	13,13,13,13	0
4	MN	E	1500	1/1	1.00	0.01	14,14,14,14	0
4	MN	A	1500	1/1	1.00	0.02	14,14,14,14	0
4	MN	C	1500	1/1	1.00	0.01	12,12,12,12	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.

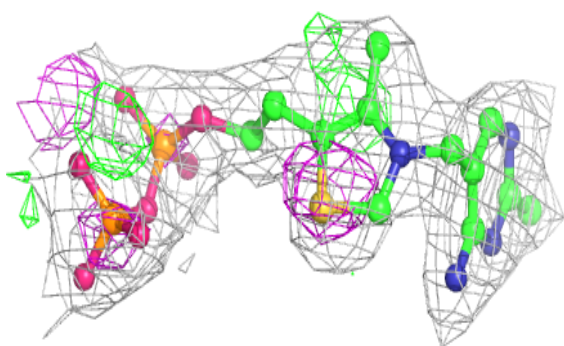
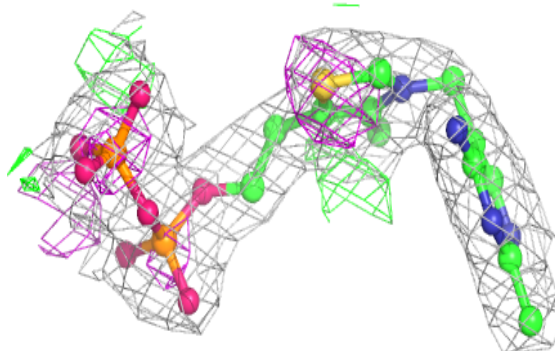


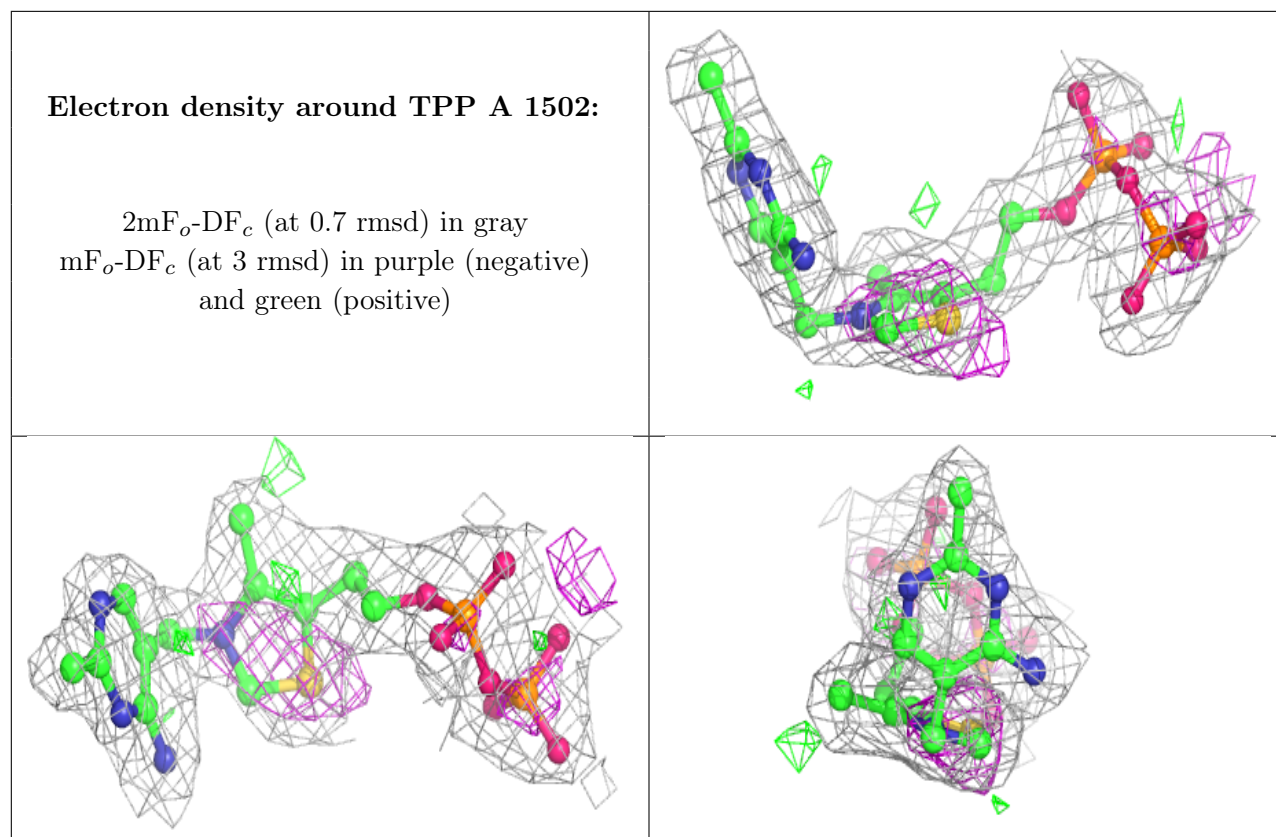
Electron density around TPP G 1502:

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

**Electron density around TPP C 1502:**

$2mF_o-DF_c$ (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.