Full wwPDB X-ray Structure Validation Report ⓘ

Feb 18, 2024 – 08:59 PM EST

PDB ID	:	4GUK
Title	:	New crystal form structure of human NCS1
Authors	:	Fan, C.; Lolis, E.
Deposited on	:	2012-08-29
Resolution	:	1.75 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:

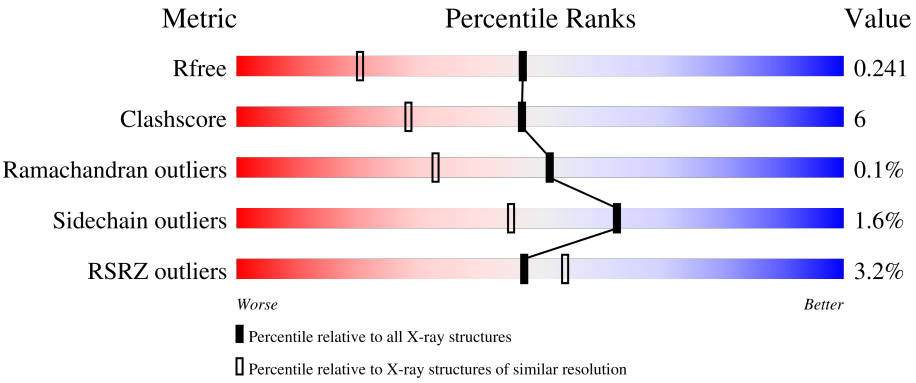
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 <=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	190	2% 84% 12%
1	B	190	3% 79% 15% 6%
1	C	190	4% 81% 14%
1	D	190	3% 82% 13% 5%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 6402 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 Neuronal calcium sensor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	183	Total	C	N	O	S	0	0	0
			1475	944	238	288	5			
1	C	182	Total	C	N	O	S	0	0	0
			1469	941	237	286	5			
1	B	179	Total	C	N	O	S	0	0	0
			1454	932	234	283	5			
1	D	180	Total	C	N	O	S	0	0	0
			1460	936	235	284	5			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P62166
A	2	GLY	-	expression tag	UNP P62166
A	3	LYS	-	expression tag	UNP P62166
A	4	SER	-	expression tag	UNP P62166
A	5	ASN	-	expression tag	UNP P62166
A	189	LEU	-	expression tag	UNP P62166
A	190	VAL	-	expression tag	UNP P62166
C	-4	MET	-	initiating methionine	UNP P62166
C	-3	GLY	-	expression tag	UNP P62166
C	-2	LYS	-	expression tag	UNP P62166
C	-1	SER	-	expression tag	UNP P62166
C	0	ASN	-	expression tag	UNP P62166
C	182	LEU	-	expression tag	UNP P62166
C	183	VAL	-	expression tag	UNP P62166
B	1	MET	-	initiating methionine	UNP P62166
B	2	GLY	-	expression tag	UNP P62166
B	3	LYS	-	expression tag	UNP P62166
B	4	SER	-	expression tag	UNP P62166
B	5	ASN	-	expression tag	UNP P62166
B	189	LEU	-	expression tag	UNP P62166
B	190	VAL	-	expression tag	UNP P62166

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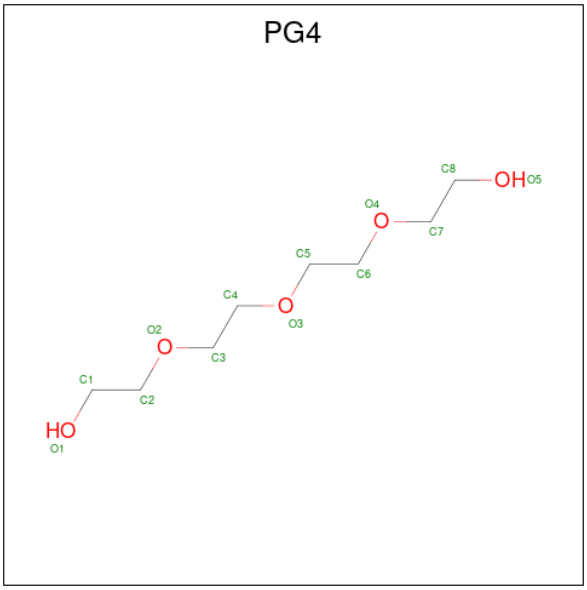
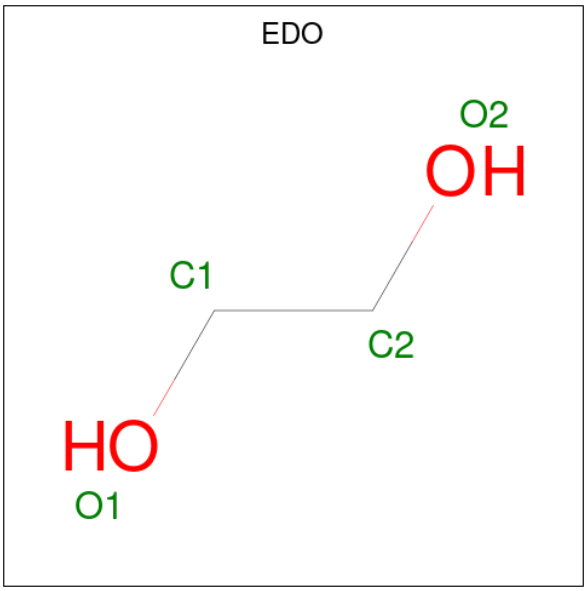
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP P62166
D	2	GLY	-	expression tag	UNP P62166
D	3	LYS	-	expression tag	UNP P62166
D	4	SER	-	expression tag	UNP P62166
D	5	ASN	-	expression tag	UNP P62166
D	189	LEU	-	expression tag	UNP P62166
D	190	VAL	-	expression tag	UNP P62166

- Molecule 2 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 8 5	0	0
2	A	1	Total C O 13 8 5	0	0
2	C	1	Total C O 13 8 5	0	0
2	B	1	Total C O 13 8 5	0	0
2	B	1	Total C O 13 8 5	0	0
2	D	1	Total C O 13 8 5	0	0
2	D	1	Total C O 13 8 5	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

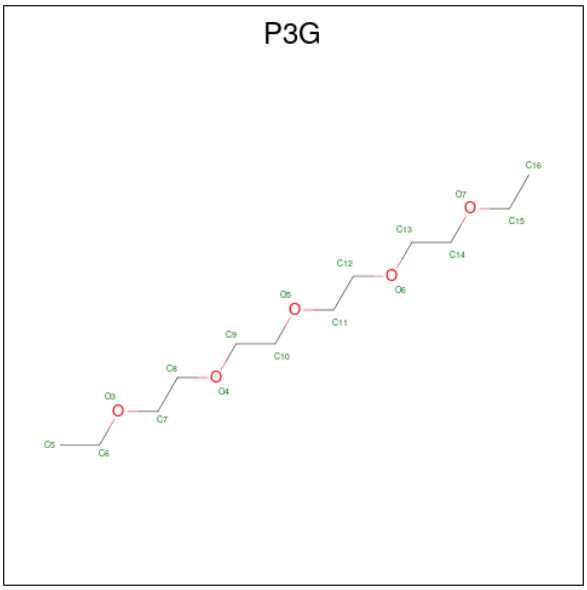
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total Ca 3 3	0	0
4	C	3	Total Ca 3 3	0	0
4	B	3	Total Ca 3 3	0	0
4	D	3	Total Ca 3 3	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

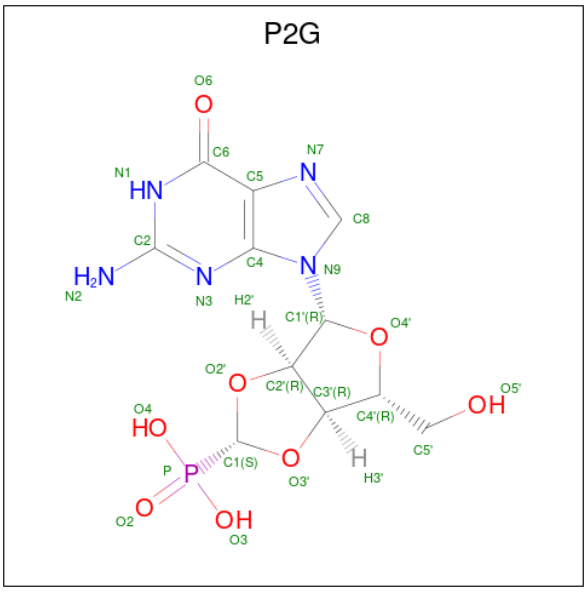
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Na 1 1	0	0
5	C	1	Total Na 1 1	0	0
5	B	1	Total Na 1 1	0	0
5	D	1	Total Na 1 1	0	0

- Molecule 6 is 3,6,9,12,15-PENTAOXAHEPTADECANE (three-letter code: P3G) (formula: $C_{12}H_{26}O_5$).



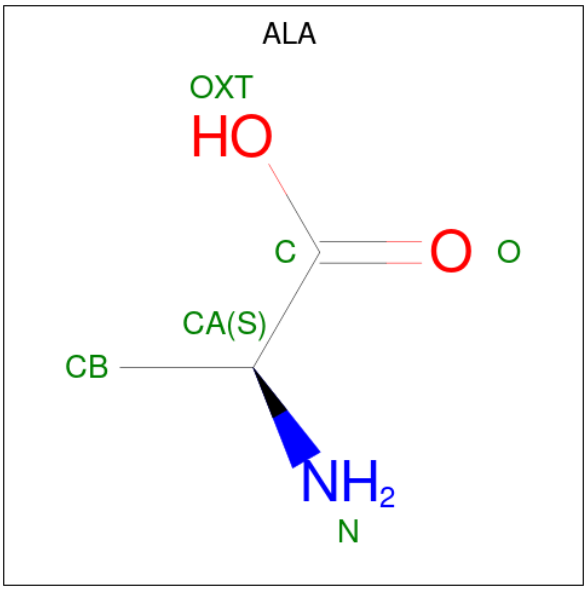
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C O 10 6 4	0	0

- Molecule 7 is (2S,4R,6R,6AS)-4-(2-AMINO-6-OXO-1,6-DIHYDROPURIN-9-YL)-6-(HYDROXYMETHYL)-TETRAHYDROFURO[3,4-D][1,3]DIOXOL-2-YLPHOSPHONI C ACID (three-letter code: P2G) (formula: $C_{11}H_{14}N_5O_8P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total C O 7 4 3	0	0
7	B	1	Total C O 7 4 3	0	0
7	B	1	Total C O 7 4 3	0	0
7	D	1	Total C O 7 4 3	0	0

- Molecule 8 is ALANINE (three-letter code: ALA) (formula: $C_3H_7NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 9 is water.

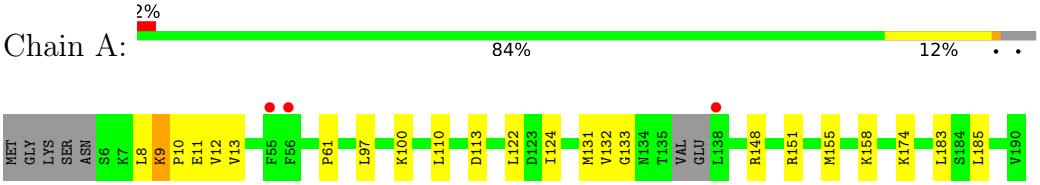
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	85	Total	O	0	0
			85	85		
9	C	96	Total	O	0	0
			96	96		
9	B	102	Total	O	0	0
			102	102		
9	D	91	Total	O	0	0
			91	91		

3 Residue-property plots (i)

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.

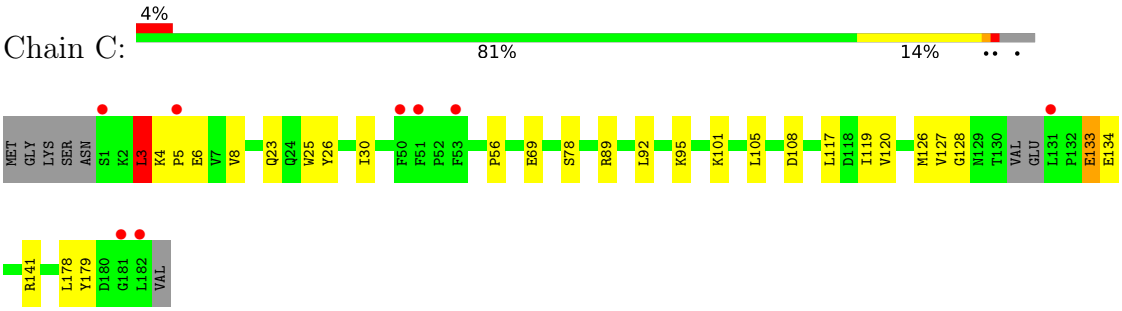
• Molecule 1: Neuronal calcium sensor 1

Chain A:



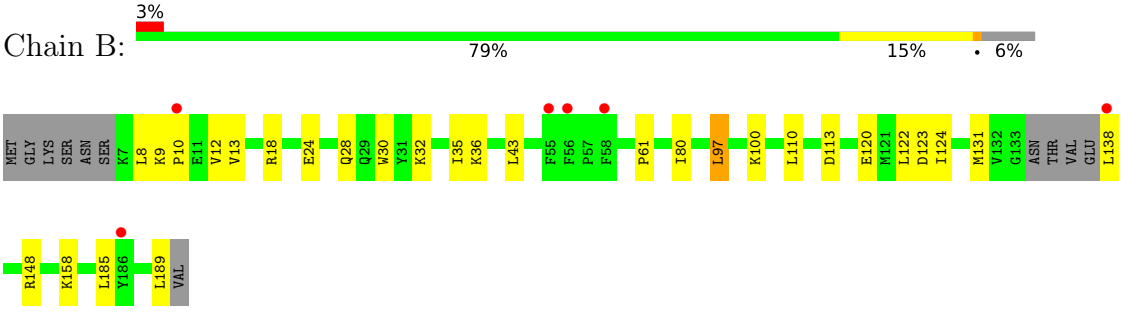
• Molecule 1: Neuronal calcium sensor 1

Chain C:



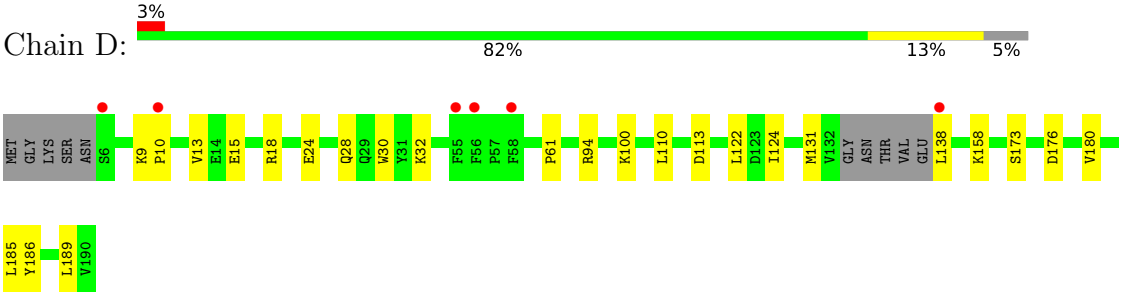
• Molecule 1: Neuronal calcium sensor 1

Chain B:



• Molecule 1: Neuronal calcium sensor 1

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	54.99Å 54.99Å 213.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.75 47.62 – 1.75	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.75) 97.5 (47.62-1.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.03 (at 1.75Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.201 , 0.243 0.200 , 0.241	Depositor DCC
R_{free} test set	2010 reflections (2.75%)	wwPDB-VP
Wilson B-factor (Å^2)	24.3	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.467 for -h,-k,l 0.477 for h,-h-k,-l 0.467 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6402	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: P3G, P2G, NA, PG4, CA, EDO

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	0.92	0/1505	0.88	2/2027 (0.1%)
1	B	0.95	2/1484 (0.1%)	0.91	3/1998 (0.2%)
1	C	0.94	0/1499	0.91	3/2019 (0.1%)
1	D	0.94	0/1490	0.89	1/2007 (0.0%)
All	All	0.94	2/5978 (0.0%)	0.90	9/8051 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	120	GLU	CG-CD	-5.57	1.43	1.51
1	B	24	GLU	CB-CG	-5.03	1.42	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	97	LEU	CB-CG-CD1	-7.70	97.91	111.00
1	A	113	ASP	CB-CG-OD1	7.49	125.04	118.30
1	C	108	ASP	CB-CG-OD1	7.37	124.93	118.30
1	C	3	LEU	CA-CB-CG	7.36	132.22	115.30
1	D	113	ASP	CB-CG-OD1	6.94	124.55	118.30
1	A	97	LEU	CB-CG-CD1	-6.92	99.24	111.00
1	C	92	LEU	CB-CG-CD1	-6.42	100.08	111.00
1	B	113	ASP	CB-CG-OD1	6.13	123.81	118.30
1	B	18	ARG	NE-CZ-NH2	-5.06	117.77	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	1475	0	1418	13	0
1	B	1454	0	1407	18	0
1	C	1469	0	1416	21	0
1	D	1460	0	1408	19	1
2	A	26	0	36	2	0
2	B	26	0	36	4	0
2	C	13	0	18	4	0
2	D	26	0	36	2	0
3	A	12	0	18	0	0
3	B	4	0	6	0	0
3	D	4	0	6	0	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	C	3	0	0	0	0
4	D	3	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	C	10	0	12	2	0
7	B	14	0	6	0	0
7	C	7	0	3	0	0
7	D	7	0	3	0	0
8	B	5	0	4	1	0
9	A	85	0	0	0	6
9	B	102	0	0	2	6
9	C	96	0	0	3	4
9	D	91	0	0	4	3
All	All	6402	0	5833	74	10

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:TRP:HE1	2:B:209:PG4:H62	1.32	0.93
1:D:15:GLU:OE1	1:D:18:ARG:NH2	2.11	0.83
1:D:28:GLN:O	1:D:32:LYS:HD3	1.82	0.80
1:D:9:LYS:HG3	1:D:10:PRO:HD2	1.65	0.76
1:D:30:TRP:HE1	2:D:206:PG4:H62	1.51	0.75
1:B:9:LYS:HG3	1:B:10:PRO:HD2	1.68	0.74
1:A:148:ARG:HE	2:A:202:PG4:H71	1.50	0.74
1:B:32:LYS:O	1:B:36:LYS:HD3	1.88	0.74
1:B:148:ARG:HE	2:B:204:PG4:H12	1.52	0.73
1:D:173:SER:O	9:D:303:HOH:O	2.07	0.72
1:D:180:VAL:HG23	9:D:303:HOH:O	1.89	0.72
1:B:123:ASP:OD2	9:B:365:HOH:O	2.10	0.68
1:C:8:VAL:HG11	1:C:23:GLN:NE2	2.09	0.68
1:D:13:VAL:HG21	1:D:28:GLN:NE2	2.09	0.68
1:B:13:VAL:HG21	1:B:28:GLN:NE2	2.10	0.67
1:C:78:SER:OG	9:C:359:HOH:O	2.14	0.66
1:C:4:LYS:HG3	1:C:5:PRO:HD2	1.76	0.65
1:D:176:ASP:N	9:D:303:HOH:O	2.31	0.63
1:B:61:PRO:HB3	1:B:131:MET:HG3	1.81	0.63
1:A:9:LYS:HD3	1:A:12:VAL:HG21	1.82	0.62
1:D:28:GLN:OE1	1:D:32:LYS:NZ	2.33	0.61
1:D:13:VAL:HG11	1:D:24:GLU:HG3	1.83	0.60
1:C:141:ARG:HE	2:C:201:PG4:H12	1.66	0.59
1:B:185:LEU:HD23	8:B:205:ALA:HB2	1.88	0.55
1:C:105:LEU:HD21	1:C:119:ILE:HD11	1.89	0.55
1:D:61:PRO:HB3	1:D:131:MET:HG3	1.91	0.53
1:A:61:PRO:HB3	1:A:131:MET:HG3	1.91	0.52
1:A:110:LEU:HD21	1:A:124:ILE:HD11	1.91	0.52
2:B:204:PG4:H71	9:B:401:HOH:O	2.10	0.52
1:C:127:VAL:HG23	1:C:128:GLY:H	1.77	0.50
1:D:176:ASP:O	9:D:303:HOH:O	2.20	0.50
1:B:30:TRP:NE1	2:B:209:PG4:H62	2.14	0.50
1:C:120:VAL:HG22	2:C:201:PG4:H21	1.94	0.50
1:D:13:VAL:CG1	1:D:24:GLU:HG3	2.42	0.49
1:C:56:PRO:HB3	1:C:126:MET:HG3	1.94	0.49
1:D:100:LYS:NZ	1:D:185:LEU:O	2.46	0.49
1:B:158:LYS:HA	1:B:158:LYS:HD2	1.73	0.47
1:A:100:LYS:NZ	1:A:185:LEU:O	2.48	0.47
1:C:133:GLU:HG2	1:C:134:GLU:H	1.79	0.47
1:C:101:LYS:NZ	9:C:322:HOH:O	2.48	0.46
2:C:201:PG4:H32	9:C:393:HOH:O	2.15	0.46
1:A:8:LEU:HB3	1:A:13:VAL:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:LYS:HE3	1:A:174:LYS:HB2	1.58	0.46
1:B:100:LYS:NZ	1:B:185:LEU:O	2.49	0.46
1:A:151:ARG:O	1:A:155:MET:HG3	2.16	0.45
1:A:183:LEU:HD21	2:A:202:PG4:H11	1.98	0.45
1:D:110:LEU:HD21	1:D:124:ILE:HD11	1.99	0.45
1:A:132:VAL:CG2	1:A:133:GLY:H	2.30	0.45
1:D:158:LYS:HA	1:D:158:LYS:HD2	1.71	0.45
1:C:127:VAL:HG23	1:C:128:GLY:N	2.32	0.45
1:D:32:LYS:N	1:D:32:LYS:HD2	2.32	0.44
1:C:4:LYS:NZ	1:C:6:GLU:HG3	2.32	0.44
1:A:158:LYS:HA	1:A:158:LYS:HD2	1.77	0.44
1:B:185:LEU:HD13	1:B:189:LEU:H	1.83	0.43
1:B:8:LEU:HD22	1:B:12:VAL:HG11	1.99	0.43
1:C:3:LEU:HD13	1:C:26:TYR:CE2	2.53	0.42
1:C:127:VAL:CG2	1:C:128:GLY:H	2.32	0.42
1:B:110:LEU:HD21	1:B:124:ILE:HD11	2.00	0.42
2:C:201:PG4:H31	2:C:201:PG4:H52	1.81	0.42
1:D:94:ARG:HD3	1:D:186:TYR:OH	2.20	0.42
1:A:61:PRO:HB3	1:A:131:MET:SD	2.59	0.42
1:B:185:LEU:HD22	1:B:189:LEU:HA	2.01	0.42
1:C:25:TRP:CE2	6:C:202:P3G:H131	2.54	0.42
1:D:30:TRP:NE1	2:D:206:PG4:H62	2.27	0.42
1:C:25:TRP:NE1	6:C:202:P3G:H131	2.34	0.41
1:C:95:LYS:NZ	1:C:178:LEU:O	2.53	0.41
1:C:4:LYS:HZ2	1:C:6:GLU:HB2	1.86	0.41
1:C:30:ILE:HD13	1:C:30:ILE:HA	1.89	0.41
1:C:3:LEU:HD23	1:C:8:VAL:HG12	2.02	0.41
1:B:35:ILE:HD13	1:B:35:ILE:HA	1.82	0.41
1:C:89:ARG:HD3	1:C:179:TYR:OH	2.21	0.40
1:B:97:LEU:HA	1:B:97:LEU:HD12	1.84	0.40
1:A:10:PRO:HG2	1:A:11:GLU:OE2	2.21	0.40
1:B:43:LEU:HB3	1:B:80:ILE:HB	2.03	0.40

All (10) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:385:HOH:O	9:B:382:HOH:O[1_655]	1.56	0.64
9:A:305:HOH:O	9:B:318:HOH:O[1_655]	1.66	0.54
9:C:316:HOH:O	9:D:380:HOH:O[2_565]	1.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:374:HOH:O	9:B:318:HOH:O[1_655]	1.78	0.42
9:C:385:HOH:O	9:D:380:HOH:O[2_565]	1.84	0.36
9:A:320:HOH:O	9:B:397:HOH:O[1_665]	2.01	0.19
9:A:385:HOH:O	9:B:317:HOH:O[1_655]	2.01	0.19
9:A:368:HOH:O	9:B:373:HOH:O[1_655]	2.04	0.16
9:C:374:HOH:O	9:D:371:HOH:O[2_665]	2.18	0.02
1:D:189:LEU:O	9:C:384:HOH:O[3_454]	2.19	0.01

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	179/190 (94%)	173 (97%)	6 (3%)	0	100 100
1	B	175/190 (92%)	170 (97%)	5 (3%)	0	100 100
1	C	178/190 (94%)	171 (96%)	6 (3%)	1 (1%)	25 10
1	D	176/190 (93%)	172 (98%)	4 (2%)	0	100 100
All	All	708/760 (93%)	686 (97%)	21 (3%)	1 (0%)	51 33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	3	LEU

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	157/168 (94%)	155 (99%)	2 (1%)	69	54
1	B	156/168 (93%)	154 (99%)	2 (1%)	69	54
1	C	156/168 (93%)	152 (97%)	4 (3%)	46	23
1	D	156/168 (93%)	154 (99%)	2 (1%)	69	54
All	All	625/672 (93%)	615 (98%)	10 (2%)	62	45

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LYS
1	A	122	LEU
1	C	3	LEU
1	C	69	GLU
1	C	117	LEU
1	C	133	GLU
1	B	122	LEU
1	B	138	LEU
1	D	122	LEU
1	D	138	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 34 ligands modelled in this entry, 16 are monoatomic - leaving 18 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	PG4	C	201	-	12,12,12	0.57	0	11,11,11	1.77	3 (27%)
7	P2G	D	205	-	6,6,28	0.53	0	5,5,44	1.59	1 (20%)
2	PG4	A	201	-	12,12,12	0.72	0	11,11,11	1.53	1 (9%)
2	PG4	B	209	-	12,12,12	0.52	0	11,11,11	1.81	4 (36%)
2	PG4	B	204	-	12,12,12	0.57	0	11,11,11	1.80	2 (18%)
2	PG4	D	206	-	12,12,12	0.51	0	11,11,11	1.95	4 (36%)
2	PG4	A	202	-	12,12,12	0.57	0	11,11,11	1.59	4 (36%)
3	EDO	D	204	-	3,3,3	0.54	0	2,2,2	0.81	0
7	P2G	B	207	-	6,6,28	0.47	0	5,5,44	1.70	0
8	ALA	B	205	-	3,4,5	0.67	0	2,4,6	0.77	0
3	EDO	B	206	-	3,3,3	0.50	0	2,2,2	0.91	0
6	P3G	C	202	-	9,9,16	0.51	0	8,8,15	1.80	4 (50%)
3	EDO	A	205	-	3,3,3	0.53	0	2,2,2	0.89	0
3	EDO	A	203	-	3,3,3	0.50	0	2,2,2	0.55	0
2	PG4	D	207	-	12,12,12	0.34	0	11,11,11	2.12	5 (45%)
7	P2G	C	206	-	6,6,28	0.41	0	5,5,44	1.46	1 (20%)
3	EDO	A	204	-	3,3,3	0.55	0	2,2,2	0.72	0
7	P2G	B	208	-	6,6,28	0.63	0	5,5,44	1.36	1 (20%)

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	PG4	C	201	-	-	5/10/10/10	-
7	P2G	D	205	-	-	3/4/4/36	-
2	PG4	A	201	-	-	6/10/10/10	-
2	PG4	B	209	-	-	7/10/10/10	-
2	PG4	B	204	-	-	5/10/10/10	-
2	PG4	D	206	-	-	7/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PG4	A	202	-	-	4/10/10/10	-
3	EDO	D	204	-	-	1/1/1/1	-
7	P2G	B	207	-	-	2/4/4/36	-
8	ALA	B	205	-	-	0/0/2/4	-
3	EDO	B	206	-	-	1/1/1/1	-
6	P3G	C	202	-	-	3/7/7/14	-
3	EDO	A	205	-	-	1/1/1/1	-
3	EDO	A	203	-	-	1/1/1/1	-
2	PG4	D	207	-	-	7/10/10/10	-
7	P2G	C	206	-	-	3/4/4/36	-
3	EDO	A	204	-	-	1/1/1/1	-
7	P2G	B	208	-	-	3/4/4/36	-

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	204	PG4	O4-C7-C8	3.87	127.09	110.07
2	D	207	PG4	O2-C3-C4	3.82	127.62	110.39
2	C	201	PG4	O3-C5-C6	3.58	126.54	110.39
2	B	204	PG4	O3-C5-C6	3.26	125.11	110.39
2	C	201	PG4	C7-O4-C6	3.06	126.56	113.29
2	D	207	PG4	O3-C5-C6	3.04	124.12	110.39
2	D	207	PG4	O2-C2-C1	2.77	122.26	110.07
2	D	207	PG4	O4-C7-C8	2.76	122.20	110.07
2	A	202	PG4	O2-C2-C1	2.67	121.82	110.07
2	A	202	PG4	O2-C3-C4	2.53	121.79	110.39
2	D	206	PG4	O4-C6-C5	2.45	121.46	110.39
6	C	202	P3G	O6-C12-C11	2.30	120.75	110.39
2	D	206	PG4	C5-O3-C4	2.29	123.20	113.29
2	B	209	PG4	O4-C6-C5	2.28	120.66	110.39
2	D	207	PG4	C3-O2-C2	2.28	123.15	113.29
2	D	206	PG4	O2-C3-C4	2.22	120.42	110.39
2	A	202	PG4	O3-C5-C6	2.22	120.40	110.39
6	C	202	P3G	C11-O5-C10	2.21	122.85	113.29
7	B	208	P2G	C4'-O4'-C1'	2.20	122.84	113.29
2	D	206	PG4	C7-O4-C6	2.19	122.78	113.29
6	C	202	P3G	C13-O6-C12	2.18	122.75	113.29
7	C	206	P2G	O4'-C4'-C5'	2.16	119.55	110.07
2	B	209	PG4	C5-O3-C4	2.15	122.61	113.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	201	PG4	O4-C7-C8	2.13	119.42	110.07
7	D	205	P2G	O5'-C5'-C4'	2.10	124.02	111.81
2	A	202	PG4	O1-C1-C2	2.09	123.95	111.81
2	B	209	PG4	O2-C3-C4	2.07	119.72	110.39
6	C	202	P3G	O6-C13-C14	2.07	119.15	110.07
2	B	209	PG4	O3-C4-C3	2.04	119.59	110.39
2	C	201	PG4	O2-C3-C4	2.00	119.42	110.39

There are no chirality outliers.

All (60) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	209	PG4	C1-C2-O2-C3
2	D	206	PG4	C1-C2-O2-C3
7	C	206	P2G	C5'-C4'-O4'-C1'
7	B	207	P2G	C2'-C1'-O4'-C4'
2	A	201	PG4	C1-C2-O2-C3
2	D	206	PG4	C8-C7-O4-C6
6	C	202	P3G	C11-C12-O6-C13
2	D	207	PG4	C1-C2-O2-C3
2	B	209	PG4	O2-C3-C4-O3
2	B	209	PG4	O3-C5-C6-O4
2	D	206	PG4	O2-C3-C4-O3
2	B	209	PG4	C8-C7-O4-C6
6	C	202	P3G	O5-C11-C12-O6
2	C	201	PG4	O3-C5-C6-O4
2	B	204	PG4	C3-C4-O3-C5
6	C	202	P3G	O5-C10-C9-O4
7	D	205	P2G	O4'-C1'-C2'-O2'
2	B	204	PG4	C5-C6-O4-C7
2	A	202	PG4	O2-C3-C4-O3
2	D	206	PG4	O3-C5-C6-O4
7	C	206	P2G	O4'-C1'-C2'-O2'
7	B	208	P2G	O4'-C4'-C5'-O5'
2	B	209	PG4	O4-C7-C8-O5
2	D	206	PG4	O4-C7-C8-O5
7	B	207	P2G	O4'-C1'-C2'-O2'
7	D	205	P2G	O4'-C4'-C5'-O5'
3	A	204	EDO	O1-C1-C2-O2
3	D	204	EDO	O1-C1-C2-O2
2	D	206	PG4	C3-C4-O3-C5
2	D	207	PG4	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	B	204	PG4	O4-C7-C8-O5
7	B	208	P2G	O4'-C1'-C2'-O2'
2	D	207	PG4	C3-C4-O3-C5
2	D	207	PG4	C5-C6-O4-C7
2	B	209	PG4	C3-C4-O3-C5
2	C	201	PG4	C5-C6-O4-C7
2	A	201	PG4	C3-C4-O3-C5
7	B	208	P2G	C2'-C1'-O4'-C4'
2	C	201	PG4	C3-C4-O3-C5
7	D	205	P2G	C5'-C4'-O4'-C1'
2	D	207	PG4	C4-C3-O2-C2
2	A	202	PG4	O3-C5-C6-O4
3	A	205	EDO	O1-C1-C2-O2
3	B	206	EDO	O1-C1-C2-O2
2	A	202	PG4	C3-C4-O3-C5
2	C	201	PG4	O2-C3-C4-O3
2	C	201	PG4	O1-C1-C2-O2
7	C	206	P2G	C2'-C1'-O4'-C4'
2	A	201	PG4	O2-C3-C4-O3
2	A	201	PG4	C5-C6-O4-C7
3	A	203	EDO	O1-C1-C2-O2
2	D	207	PG4	O2-C3-C4-O3
2	D	207	PG4	O3-C5-C6-O4
2	B	209	PG4	C6-C5-O3-C4
2	D	206	PG4	C6-C5-O3-C4
2	A	202	PG4	C1-C2-O2-C3
2	B	204	PG4	O3-C5-C6-O4
2	A	201	PG4	O4-C7-C8-O5
2	B	204	PG4	O2-C3-C4-O3
2	A	201	PG4	C6-C5-O3-C4

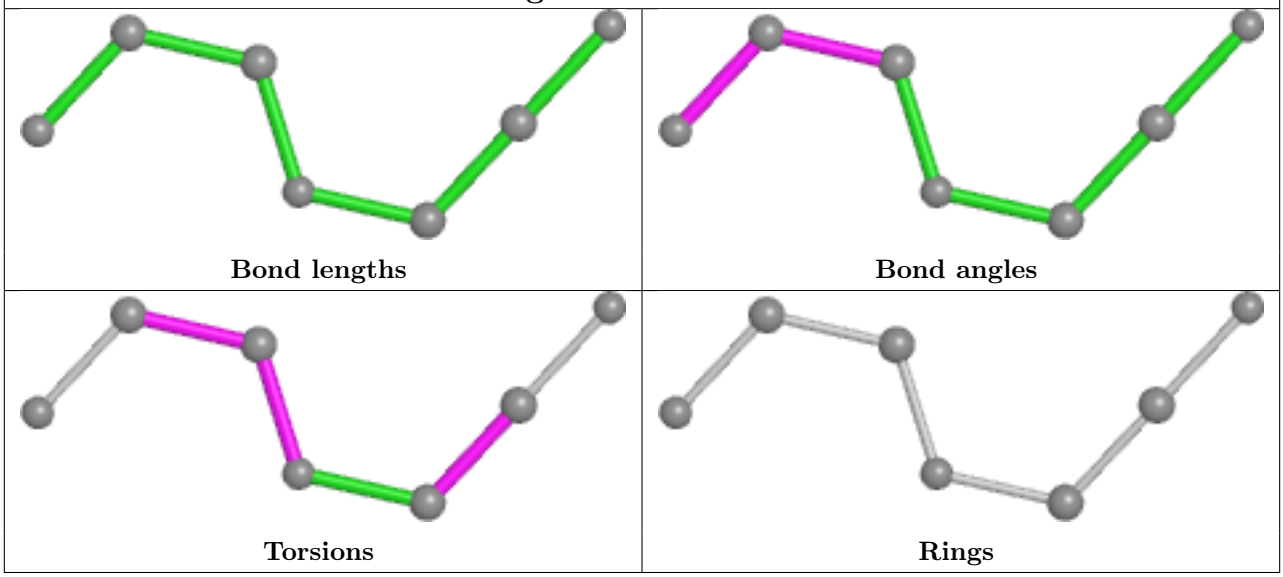
There are no ring outliers.

7 monomers are involved in 15 short contacts:

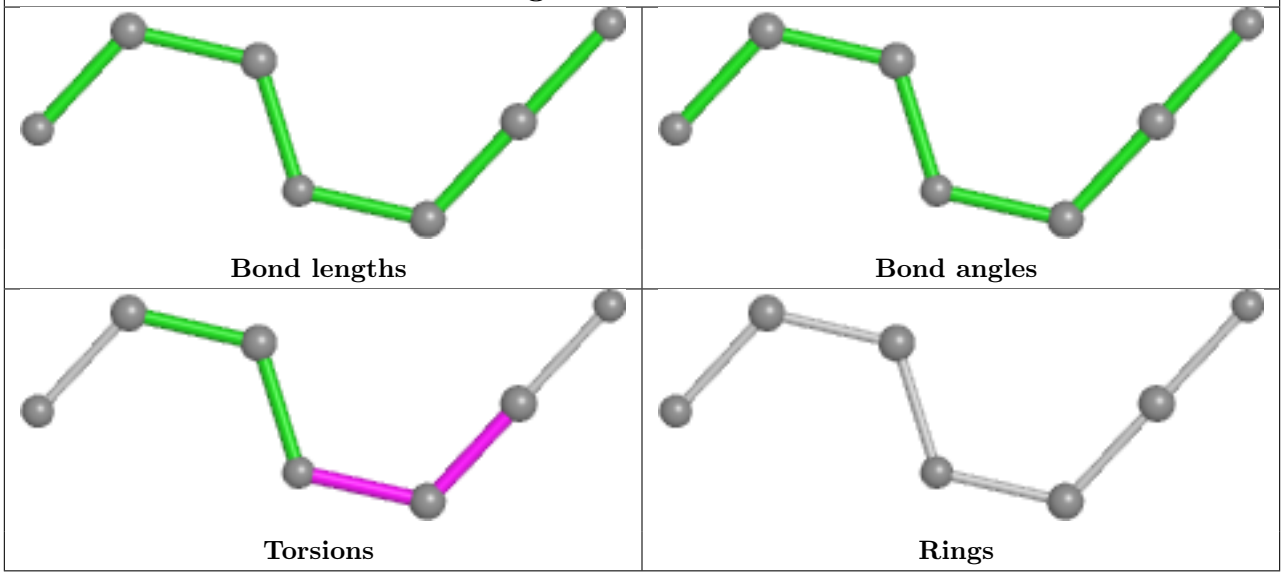
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	201	PG4	4	0
2	B	209	PG4	2	0
2	B	204	PG4	2	0
2	D	206	PG4	2	0
2	A	202	PG4	2	0
8	B	205	ALA	1	0
6	C	202	P3G	2	0

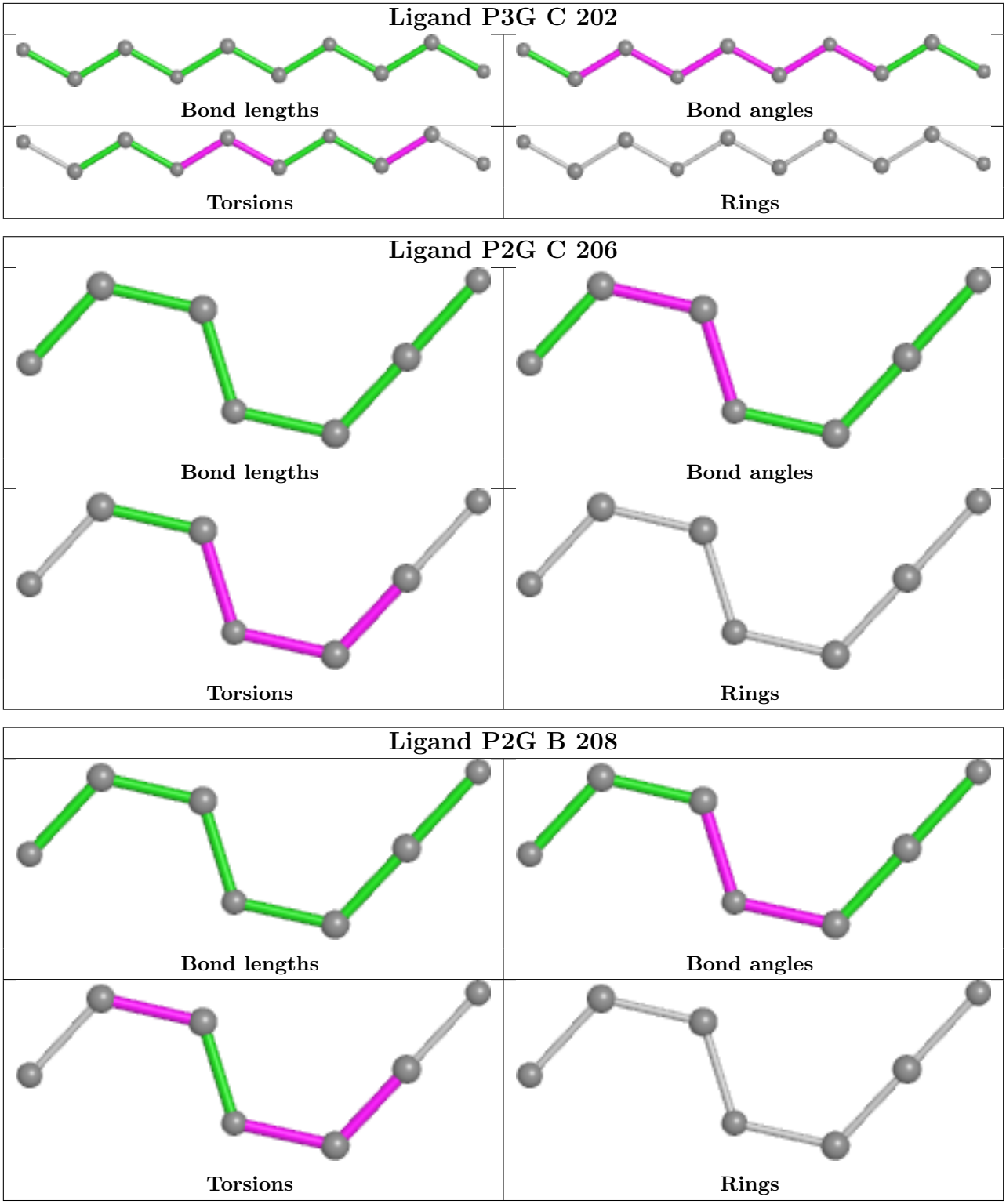
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand P2G D 205



Ligand P2G B 207





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, 95^{th} 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	183/190 (96%)	-0.01	3 (1%)	72	79	21, 37, 86, 100	0
1	B	179/190 (94%)	0.00	6 (3%)	45	51	20, 37, 82, 100	1 (0%)
1	C	182/190 (95%)	0.06	8 (4%)	34	40	20, 37, 85, 100	0
1	D	180/190 (94%)	-0.03	6 (3%)	46	53	20, 37, 85, 100	1 (0%)
All	All	724/760 (95%)	0.00	23 (3%)	47	54	20, 37, 86, 100	2 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	51	PHE	6.7
1	B	56	PHE	5.6
1	D	56	PHE	5.5
1	A	56	PHE	5.1
1	C	5	PRO	5.1
1	B	55	PHE	4.6
1	C	50	PHE	3.8
1	D	6	SER	3.6
1	D	58	PHE	3.6
1	A	55	PHE	3.5
1	D	10	PRO	3.4
1	B	138	LEU	3.0
1	D	55	PHE	3.0
1	B	58	PHE	2.8
1	D	138	LEU	2.8
1	C	182	LEU	2.5
1	C	53	PHE	2.5
1	A	138	LEU	2.4
1	C	131	LEU	2.3
1	C	1	SER	2.2
1	B	10	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	181	GLY	2.1
1	B	186	TYR	2.0

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

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

6.3 Carbohydrates (i)

There are no 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, 95^{th} 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
8	ALA	B	205	5/6	0.69	0.17	86,87,91,92	0
3	EDO	A	205	4/4	0.81	0.13	62,64,65,69	0
6	P3G	C	202	10/17	0.83	0.12	44,48,56,59	0
7	P2G	C	206	7/25	0.86	0.10	48,61,68,72	0
7	P2G	B	207	7/25	0.87	0.13	60,63,67,70	0
2	PG4	B	209	13/13	0.87	0.10	45,58,68,70	0
3	EDO	A	203	4/4	0.88	0.17	53,54,60,62	0
3	EDO	A	204	4/4	0.89	0.10	62,62,63,66	0
3	EDO	D	204	4/4	0.90	0.14	62,62,64,65	0
2	PG4	D	206	13/13	0.91	0.08	46,57,69,69	0
2	PG4	C	201	13/13	0.91	0.10	19,38,48,49	0
2	PG4	A	201	13/13	0.91	0.08	42,48,60,61	0
3	EDO	B	206	4/4	0.92	0.12	53,55,62,62	0
7	P2G	B	208	7/25	0.92	0.10	44,50,66,66	0
2	PG4	B	204	13/13	0.92	0.10	21,33,48,51	0
5	NA	B	210	1/1	0.93	0.07	27,27,27,27	0
7	P2G	D	205	7/25	0.93	0.10	47,50,67,69	0
2	PG4	A	202	13/13	0.93	0.09	23,40,49,54	0
5	NA	C	207	1/1	0.94	0.08	28,28,28,28	0
5	NA	A	209	1/1	0.94	0.06	27,27,27,27	0
4	CA	D	201	1/1	0.95	0.06	29,29,29,29	0

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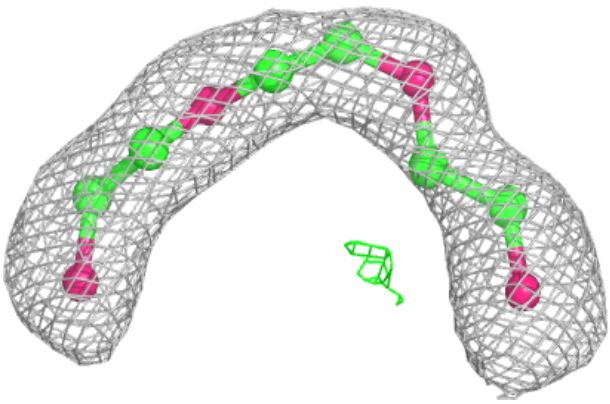
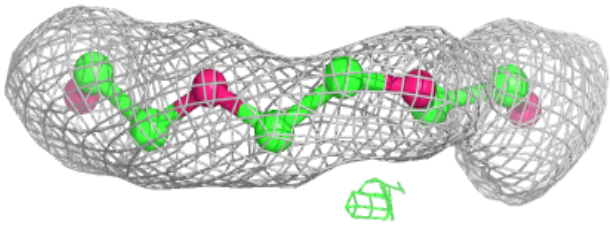
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PG4	D	207	13/13	0.95	0.08	22,40,62,65	0
4	CA	A	206	1/1	0.96	0.06	30,30,30,30	0
4	CA	A	208	1/1	0.96	0.08	25,25,25,25	0
4	CA	C	203	1/1	0.96	0.06	30,30,30,30	0
4	CA	B	201	1/1	0.96	0.05	31,31,31,31	0
4	CA	B	203	1/1	0.96	0.07	25,25,25,25	0
4	CA	D	203	1/1	0.97	0.07	24,24,24,24	0
4	CA	C	205	1/1	0.97	0.07	24,24,24,24	0
4	CA	C	204	1/1	0.98	0.06	21,21,21,21	0
4	CA	D	202	1/1	0.98	0.06	22,22,22,22	0
4	CA	B	202	1/1	0.98	0.06	22,22,22,22	0
4	CA	A	207	1/1	0.98	0.06	22,22,22,22	0
5	NA	D	208	1/1	0.99	0.31	18,18,18,18	0

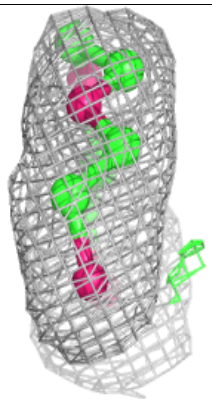
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around P3G C 202:

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

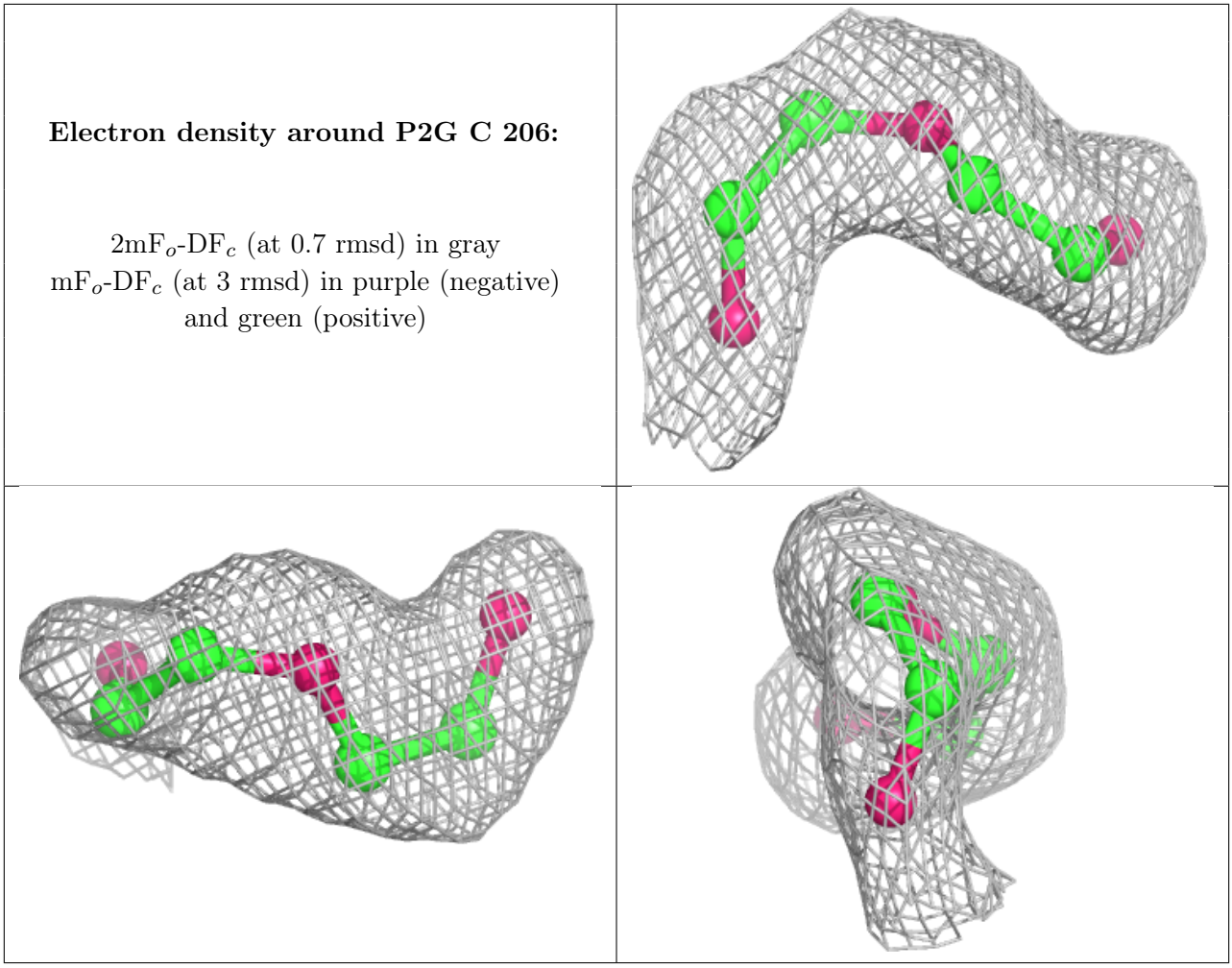






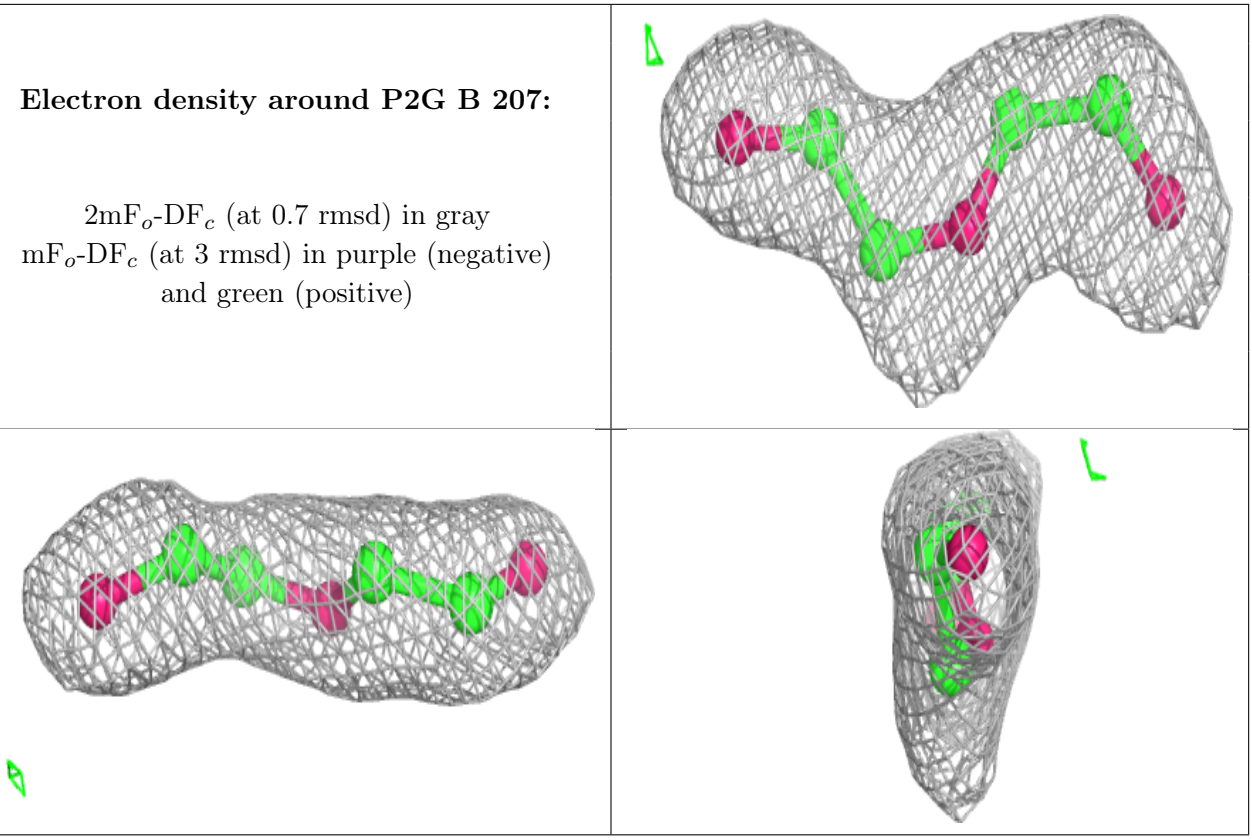
Electron density around P2G C 206:

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



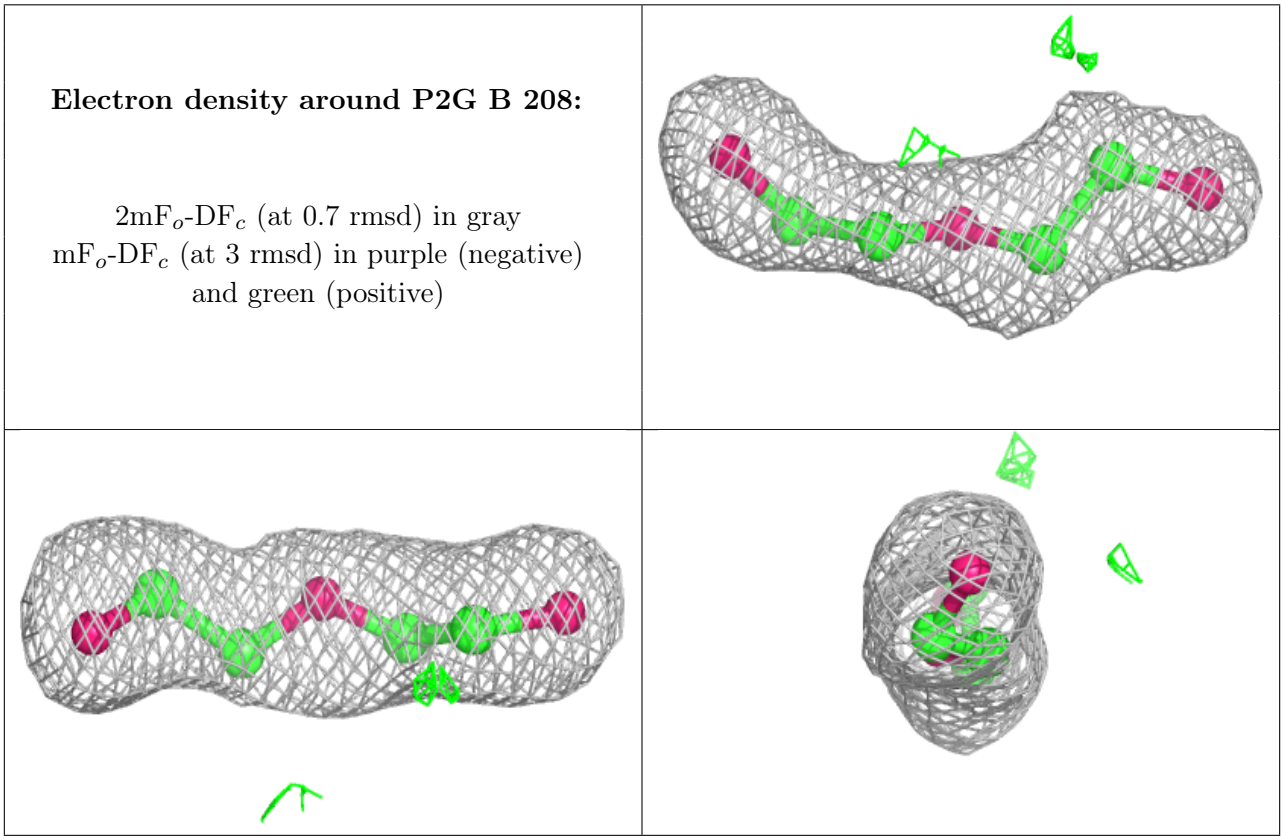
Electron density around P2G B 207:

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



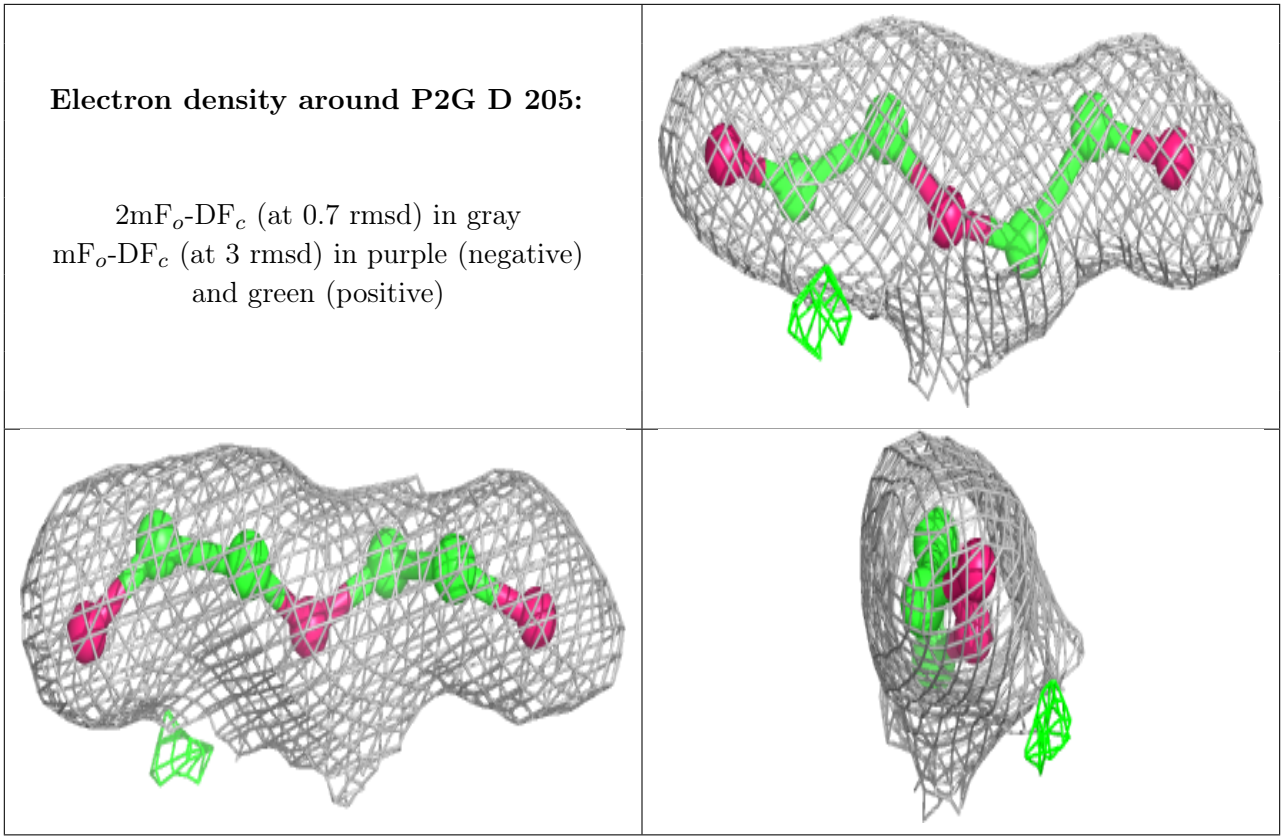
Electron density around P2G B 208:

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



Electron density around P2G D 205:

$2mF_o$-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.