



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:06 PM EDT

PDB ID : 4HJH / pdb_00004hjh
Title : Iodide SAD phased crystal structure of a phosphoglucomutase from *Brucella melitensis* complexed with glucose-6-phosphate
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2012-10-12
Resolution : 2.10 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

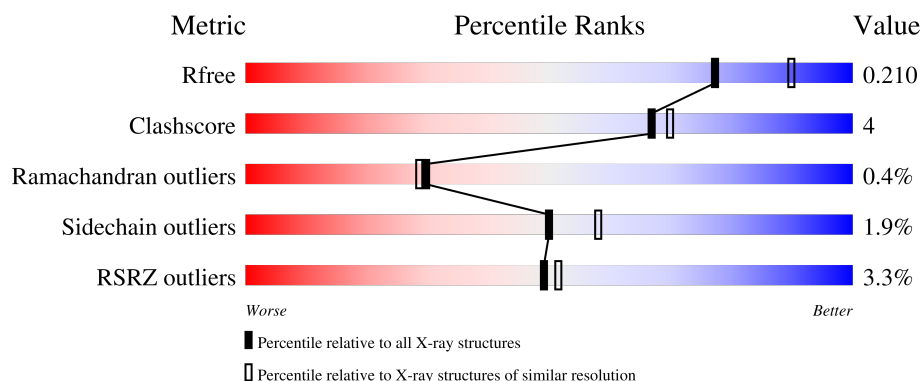
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

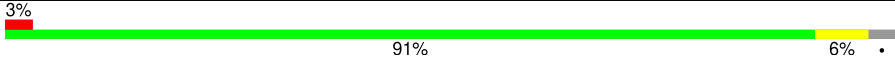
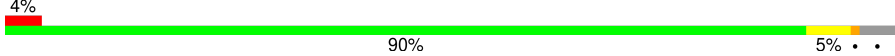
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	481	
1	B	481	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IOD	A	516	-	-	X	-
2	IOD	A	534	-	-	X	-
2	IOD	A	536	-	-	X	-
2	IOD	B	527	-	-	X	-
3	G6Q	A	544	-	X	-	-
3	G6Q	B	533	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7469 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 Phosphomannomutase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	P	S	0	7	0
			3422	2161	594	657	1	9			
1	B	464	Total	C	N	O	P	S	0	1	0
			3302	2083	570	638	1	10			

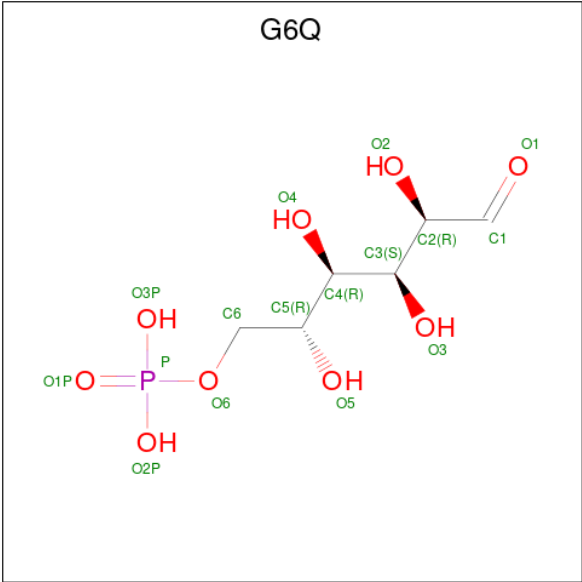
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP D0B6G5
A	-2	PRO	-	expression tag	UNP D0B6G5
B	-3	GLY	-	expression tag	UNP D0B6G5
B	-2	PRO	-	expression tag	UNP D0B6G5

- Molecule 2 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	43	Total	I	0	0
			43	43		
2	B	32	Total	I	0	0
			32	32		

- Molecule 3 is GLUCOSE-6-PHOSPHATE (CCD ID: G6Q) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			16	6	9	1		
3	B	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

Continued on next page...

Continued from previous page...

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

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

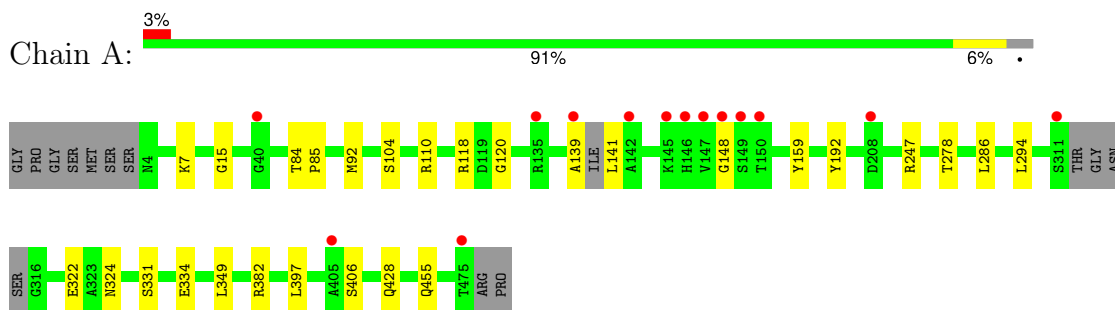
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	340	Total O 340 340	0	0
6	B	264	Total O 264 264	0	0

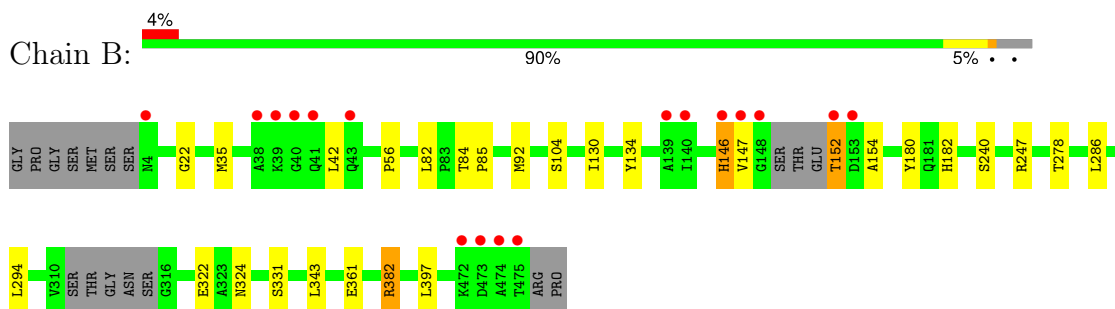
3 Residue-property plots [i](#)

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: Phosphomannomutase



- Molecule 1: Phosphomannomutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.95Å 55.98Å 131.67Å 90.00° 92.18° 90.00°	Depositor
Resolution (Å)	46.01 – 2.10 46.01 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.01-2.10) 99.8 (46.01-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.91 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.174 , 0.209 0.181 , 0.210	Depositor DCC
R_{free} test set	2695 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	16.9	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7469	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, MG, SEP, IOD, G6Q

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	0.77	0/3491	0.81	3/4756 (0.1%)
1	B	0.66	0/3351	0.80	2/4576 (0.0%)
All	All	0.72	0/6842	0.80	5/9332 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	278	THR	CA-C-N	-5.66	114.78	120.21
1	A	278	THR	C-N-CA	-5.66	114.78	120.21
1	B	278	THR	CA-C-N	-5.54	114.90	120.21
1	B	278	THR	C-N-CA	-5.54	114.90	120.21
1	A	192	TYR	CA-CB-CG	5.07	123.03	113.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	146	HIS	Peptide

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	3422	0	3359	18	0
1	B	3302	0	3173	16	0
2	A	43	0	0	17	0
2	B	32	0	0	9	0
3	A	16	0	11	5	0
3	B	16	0	11	4	0
4	A	28	0	42	2	0
4	B	4	0	6	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	340	0	0	9	0
6	B	264	0	0	3	0
All	All	7469	0	6602	50	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 4.

All (50) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ARG:HD3	2:A:516:IOD:I	1.86	1.44
1:A:110:ARG:NH1	2:A:516:IOD:I	2.32	1.32
1:B:361:GLU:OE1	2:B:527:IOD:I	2.20	1.28
1:A:110:ARG:CD	2:A:516:IOD:I	2.74	1.05
4:A:548:EDO:H12	6:A:714:HOH:O	1.66	0.94
2:A:539:IOD:I	6:A:931:HOH:O	2.59	0.90
2:A:534:IOD:I	6:A:883:HOH:O	2.67	0.81
2:A:534:IOD:I	6:A:674:HOH:O	2.70	0.79
3:B:533:G6Q:O1	3:B:533:G6Q:H62	1.84	0.77
2:A:541:IOD:I	6:A:907:HOH:O	2.74	0.75
2:A:514:IOD:I	6:A:924:HOH:O	2.77	0.72
1:A:139:ALA:O	1:A:141:LEU:N	2.24	0.71
2:A:531:IOD:I	6:A:870:HOH:O	2.82	0.67
1:A:110:ARG:CZ	2:A:516:IOD:I	3.12	0.66
2:B:504:IOD:I	6:B:693:HOH:O	2.85	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:TYR:OH	2:B:519:IOD:I	2.80	0.64
3:A:544:G6Q:O1	3:A:544:G6Q:C5	2.46	0.63
3:A:544:G6Q:O1	3:A:544:G6Q:C6	2.48	0.61
1:A:294:LEU:HD21	2:A:536:IOD:I	2.72	0.60
1:A:455[B]:GLN:NE2	6:A:926:HOH:O	2.24	0.60
2:A:508:IOD:I	6:A:828:HOH:O	2.86	0.59
1:A:247:ARG:HD3	1:A:324:ASN:HB2	1.85	0.59
1:B:56:PRO:HG3	2:B:522:IOD:I	2.73	0.58
3:A:544:G6Q:O1	3:A:544:G6Q:H62	2.05	0.57
1:B:247:ARG:HD3	1:B:324:ASN:HB2	1.86	0.57
1:B:152:THR:HA	2:B:531:IOD:I	2.76	0.55
3:B:533:G6Q:O1	3:B:533:G6Q:C6	2.54	0.54
1:A:15:GLY:HA2	2:A:516:IOD:I	2.78	0.54
1:B:35:MET:HE2	1:B:130:ILE:HG13	1.90	0.53
1:B:294:LEU:HD21	2:B:512:IOD:I	2.79	0.53
1:B:322:GLU:OE2	3:B:533:G6Q:O4	2.27	0.52
1:A:428:GLN:HG2	2:A:542:IOD:I	2.80	0.52
1:A:322:GLU:OE2	3:A:544:G6Q:O4	2.30	0.49
1:A:7:LYS:HE3	2:A:515:IOD:I	2.83	0.49
3:A:544:G6Q:O1	3:A:544:G6Q:O5	2.27	0.48
1:B:152:THR:HG23	1:B:154:ALA:HB3	1.95	0.48
1:A:334:GLU:HB3	4:A:549:EDO:H22	1.98	0.46
1:A:92:MET:SD	1:A:120:GLY:HA2	2.55	0.46
1:A:159:TYR:CE2	1:A:349[A]:LEU:HD22	2.51	0.45
1:B:361:GLU:HB2	2:B:527:IOD:I	2.86	0.45
1:A:294:LEU:CD2	2:A:536:IOD:I	3.35	0.45
1:B:84:THR:N	1:B:85:PRO:HD2	2.32	0.44
1:B:382:ARG:NH2	6:B:773:HOH:O	2.49	0.44
1:A:84:THR:N	1:A:85:PRO:HD2	2.33	0.43
2:B:513:IOD:I	6:B:819:HOH:O	2.92	0.42
1:A:118:ARG:HD3	2:A:518:IOD:I	2.89	0.42
1:B:180:TYR:HB3	1:B:240:SER:HB2	2.02	0.42
1:B:322:GLU:CD	3:B:533:G6Q:O4	2.64	0.41
1:B:22:GLY:HA2	2:B:524:IOD:I	2.90	0.41
1:B:92:MET:HE1	1:B:343:LEU:HD12	2.03	0.41

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	467/481 (97%)	461 (99%)	5 (1%)	1 (0%)	43	44
1	B	458/481 (95%)	450 (98%)	5 (1%)	3 (1%)	18	15
All	All	925/962 (96%)	911 (98%)	10 (1%)	4 (0%)	30	28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	146	HIS
1	B	147	VAL
1	A	148	GLY
1	B	182	HIS

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	338/371 (91%)	331 (98%)	7 (2%)	47	54
1	B	315/371 (85%)	308 (98%)	7 (2%)	45	53
All	All	653/742 (88%)	639 (98%)	14 (2%)	50	54

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	286	LEU
1	A	331	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	382[A]	ARG
1	A	382[B]	ARG
1	A	397	LEU
1	A	406[A]	SER
1	A	406[B]	SER
1	B	42	LEU
1	B	82	LEU
1	B	152	THR
1	B	286	LEU
1	B	331	SER
1	B	382	ARG
1	B	397	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	428	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	$\# Z > 2$
1	SEP	A	104	5,1	8,9,10	0.93	0	7,12,14	2.16	1 (14%)
1	SEP	B	104	5,1	8,9,10	0.85	0	7,12,14	2.29	1 (14%)

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
1	SEP	A	104	5,1	-	1/6/8/10	-
1	SEP	B	104	5,1	-	1/6/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	104	SEP	OG-CB-CA	5.46	113.46	108.14
1	A	104	SEP	OG-CB-CA	4.96	112.98	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	104	SEP	N-CA-CB-OG
1	B	104	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 87 ligands modelled in this entry, 77 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	$\# Z > 2$
4	EDO	A	546	-	3,3,3	0.62	0	2,2,2	0.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	550	-	3,3,3	0.33	0	2,2,2	0.57	0
4	EDO	A	549	-	3,3,3	0.43	0	2,2,2	0.34	0
4	EDO	A	547	-	3,3,3	0.36	0	2,2,2	0.73	0
4	EDO	B	534	-	3,3,3	0.47	0	2,2,2	0.40	0
3	G6Q	B	533	-	14,15,15	0.82	0	19,21,21	2.40	10 (52%)
4	EDO	A	548	-	3,3,3	0.47	0	2,2,2	0.20	0
3	G6Q	A	544	-	14,15,15	0.80	0	19,21,21	3.01	10 (52%)
4	EDO	A	545	-	3,3,3	0.57	0	2,2,2	0.09	0
4	EDO	A	551	-	3,3,3	0.46	0	2,2,2	0.11	0

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
4	EDO	A	546	-	-	1/1/1/1	-
4	EDO	A	550	-	-	0/1/1/1	-
4	EDO	A	549	-	-	1/1/1/1	-
4	EDO	A	547	-	-	1/1/1/1	-
4	EDO	B	534	-	-	1/1/1/1	-
3	G6Q	B	533	-	-	15/19/20/20	-
4	EDO	A	548	-	-	1/1/1/1	-
3	G6Q	A	544	-	-	14/19/20/20	-
4	EDO	A	545	-	-	1/1/1/1	-
4	EDO	A	551	-	-	1/1/1/1	-

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	544	G6Q	C4-C3-C2	-7.27	100.75	113.49
3	B	533	G6Q	C4-C3-C2	-5.08	104.59	113.49
3	A	544	G6Q	C5-C4-C3	4.29	119.07	112.48
3	A	544	G6Q	O2-C2-C3	4.17	119.22	109.46
3	A	544	G6Q	O4-C4-C5	-4.10	99.62	108.93
3	B	533	G6Q	O2-C2-C3	3.90	118.60	109.46
3	B	533	G6Q	C5-C4-C3	3.63	118.06	112.48
3	A	544	G6Q	O2-C2-C1	3.50	118.44	110.48
3	A	544	G6Q	O2P-P-O6	-3.19	98.35	106.67
3	B	533	G6Q	O6-C6-C5	3.11	117.68	109.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	544	G6Q	C6-C5-C4	3.10	118.07	112.22
3	A	544	G6Q	O6-C6-C5	3.09	117.61	109.36
3	B	533	G6Q	C6-C5-C4	2.76	117.42	112.22
3	B	533	G6Q	O2P-P-O6	-2.69	99.64	106.67
3	B	533	G6Q	O4-C4-C5	-2.43	103.40	108.93
3	B	533	G6Q	C3-C2-C1	-2.36	103.84	111.03
3	A	544	G6Q	C3-C2-C1	-2.26	104.15	111.03
3	A	544	G6Q	O5-C5-C4	2.14	114.26	109.25
3	B	533	G6Q	O3-C3-C2	2.05	112.95	109.13
3	B	533	G6Q	O3-C3-C4	2.00	114.14	109.46

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	544	G6Q	O1-C1-C2-C3
3	A	544	G6Q	C1-C2-C3-C4
3	A	544	G6Q	C1-C2-C3-O3
3	A	544	G6Q	O2-C2-C3-C4
3	A	544	G6Q	O2-C2-C3-O3
3	A	544	G6Q	C3-C4-C5-C6
3	A	544	G6Q	C3-C4-C5-O5
3	A	544	G6Q	O4-C4-C5-C6
3	A	544	G6Q	C4-C5-C6-O6
3	A	544	G6Q	O5-C5-C6-O6
3	B	533	G6Q	O1-C1-C2-C3
3	B	533	G6Q	C1-C2-C3-C4
3	B	533	G6Q	C1-C2-C3-O3
3	B	533	G6Q	O2-C2-C3-C4
3	B	533	G6Q	O2-C2-C3-O3
3	B	533	G6Q	O3-C3-C4-C5
3	B	533	G6Q	C3-C4-C5-C6
3	B	533	G6Q	C4-C5-C6-O6
3	A	544	G6Q	O4-C4-C5-O5
3	B	533	G6Q	C3-C4-C5-O5
3	B	533	G6Q	O4-C4-C5-C6
3	B	533	G6Q	C2-C3-C4-C5
3	B	533	G6Q	O4-C4-C5-O5
3	A	544	G6Q	O3-C3-C4-C5
4	A	551	EDO	O1-C1-C2-O2
3	A	544	G6Q	C2-C3-C4-C5
3	B	533	G6Q	C2-C3-C4-O4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	547	EDO	O1-C1-C2-O2
4	A	548	EDO	O1-C1-C2-O2
4	B	534	EDO	O1-C1-C2-O2
4	A	546	EDO	O1-C1-C2-O2
4	A	549	EDO	O1-C1-C2-O2
3	B	533	G6Q	O3-C3-C4-O4
4	A	545	EDO	O1-C1-C2-O2
3	B	533	G6Q	O5-C5-C6-O6
3	A	544	G6Q	C2-C3-C4-O4

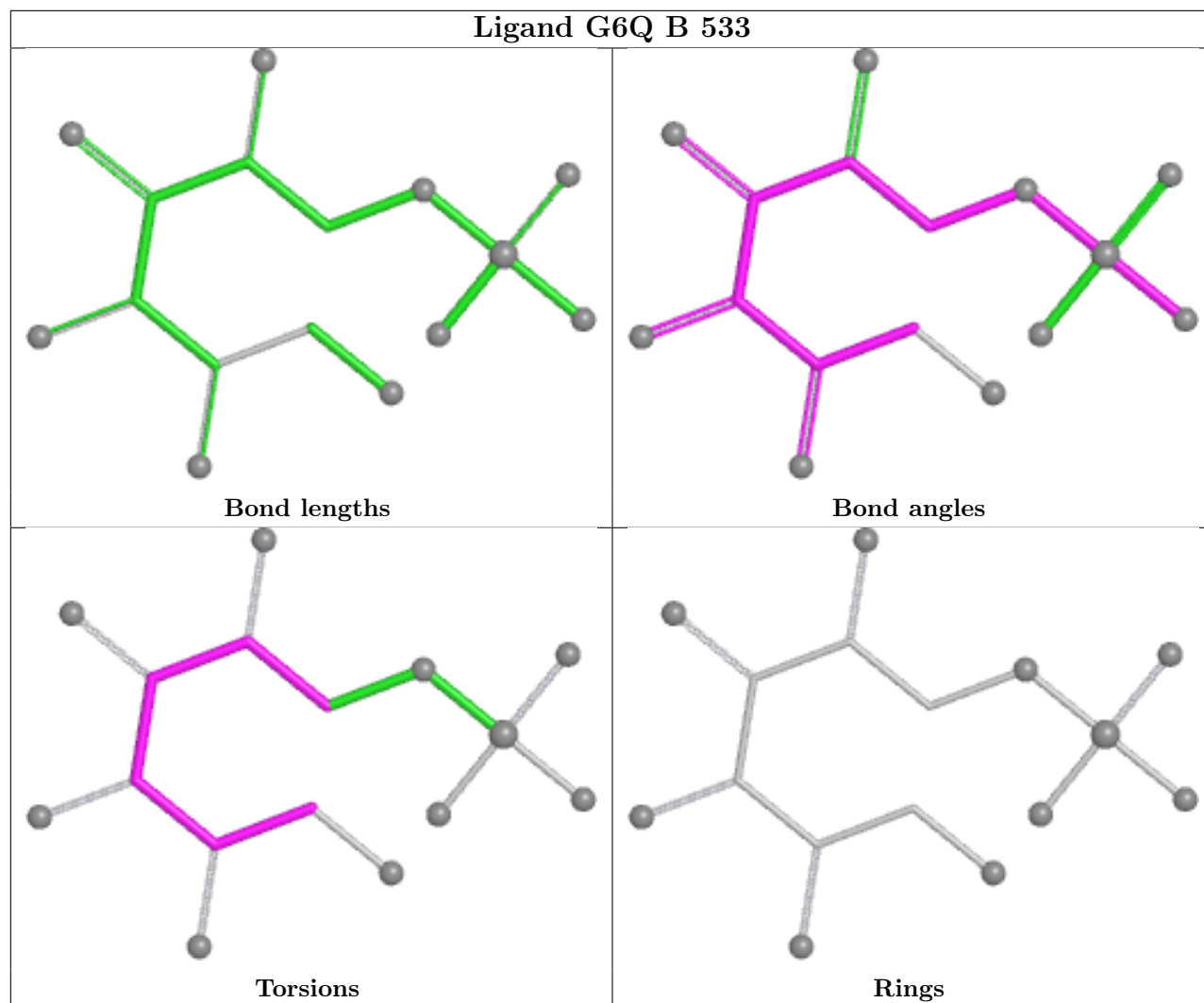
There are no ring outliers.

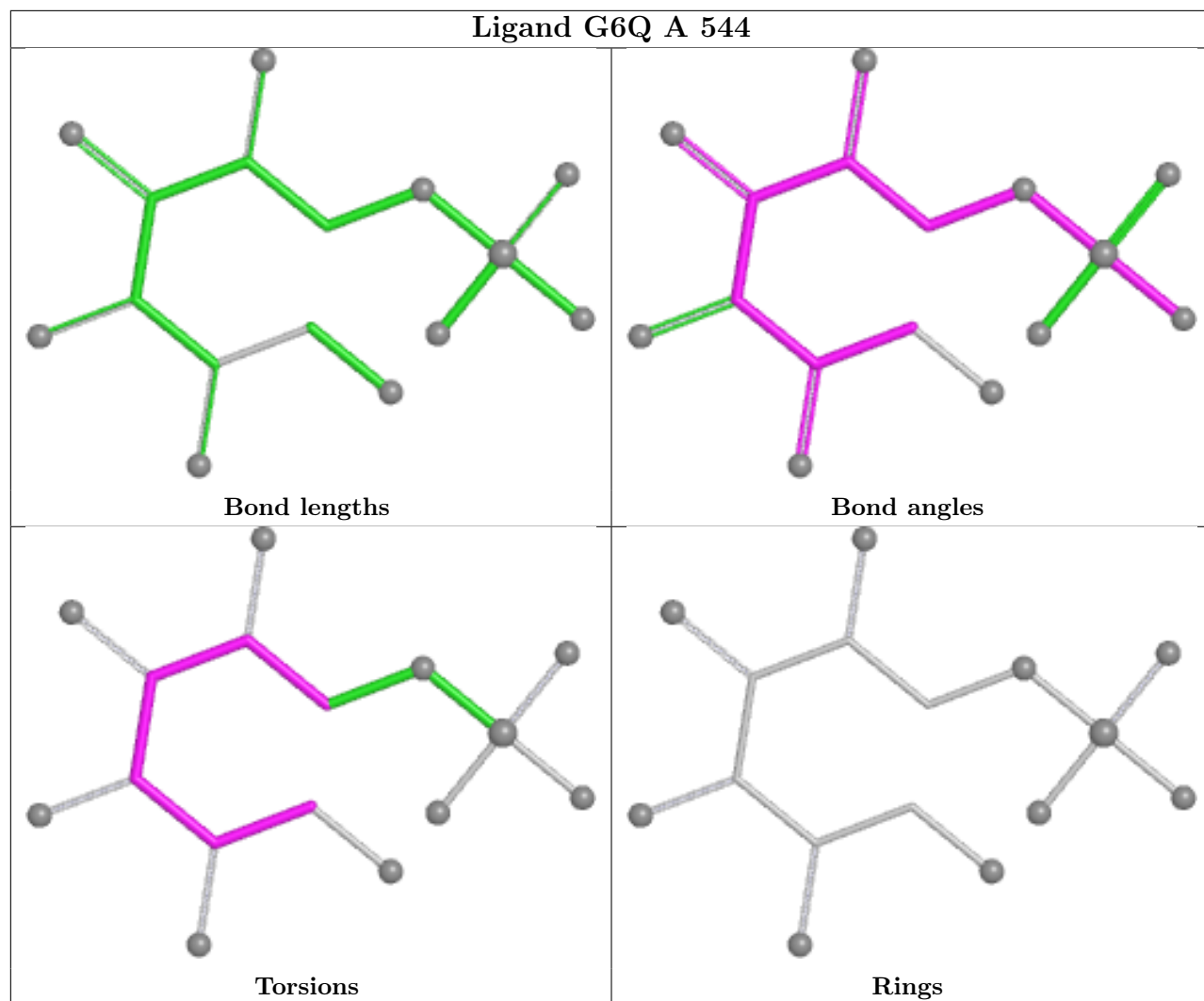
4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	549	EDO	1	0
3	B	533	G6Q	4	0
4	A	548	EDO	1	0
3	A	544	G6Q	5	0

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

Ligand G6Q B 533





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	466/481 (96%)	-0.18	14 (3%)	52 55	4, 14, 37, 51	7 (1%)
1	B	463/481 (96%)	0.07	17 (3%)	45 47	11, 22, 44, 62	1 (0%)
All	All	929/962 (96%)	-0.06	31 (3%)	49 51	4, 18, 42, 62	8 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	147	VAL	4.8
1	B	147	VAL	4.6
1	B	148	GLY	4.0
1	A	311	SER	3.9
1	A	475	THR	3.8
1	B	146	HIS	3.6
1	B	473	ASP	3.4
1	A	139	ALA	3.1
1	A	148	GLY	2.9
1	B	41	GLN	2.7
1	B	39	LYS	2.7
1	A	150	THR	2.6
1	B	38	ALA	2.5
1	A	146	HIS	2.5
1	B	43	GLN	2.4
1	A	149	SER	2.4
1	B	474	ALA	2.3
1	B	475	THR	2.3
1	B	4	ASN	2.3
1	A	142	ALA	2.3
1	B	152	THR	2.3
1	A	405	ALA	2.2
1	B	40	GLY	2.2
1	A	40	GLY	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	135	ARG	2.1
1	B	139	ALA	2.1
1	A	208	ASP	2.1
1	A	145	LYS	2.1
1	B	140	ILE	2.1
1	B	472	LYS	2.1
1	B	153	ASP	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
1	SEP	A	104	10/11	0.97	0.06	11,12,12,13	1
1	SEP	B	104	10/11	0.97	0.06	19,20,21,21	1

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	IOD	B	531	1/1	0.64	0.21	66,66,66,66	1
2	IOD	B	520	1/1	0.65	0.23	73,73,73,73	1
2	IOD	A	516	1/1	0.79	0.16	36,36,36,36	1
2	IOD	A	511	1/1	0.81	0.16	56,56,56,56	0
4	EDO	A	551	4/4	0.81	0.14	30,31,32,32	0
2	IOD	A	538	1/1	0.83	0.17	50,50,50,50	1
2	IOD	A	535	1/1	0.84	0.16	66,66,66,66	1
2	IOD	A	540	1/1	0.84	0.14	38,38,38,38	1
4	EDO	A	546	4/4	0.84	0.12	24,27,29,33	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IOD	B	515	1/1	0.84	0.14	40,40,40,40	1
2	IOD	A	537	1/1	0.86	0.19	36,36,36,36	1
2	IOD	A	503	1/1	0.86	0.12	47,47,47,47	0
2	IOD	B	506	1/1	0.87	0.13	53,53,53,53	0
2	IOD	A	517	1/1	0.87	0.12	54,54,54,54	1
4	EDO	A	549	4/4	0.87	0.16	24,27,28,32	0
2	IOD	A	525	1/1	0.87	0.14	48,48,48,48	1
2	IOD	B	527	1/1	0.88	0.13	47,47,47,47	1
2	IOD	B	530	1/1	0.88	0.11	49,49,49,49	1
2	IOD	A	530	1/1	0.88	0.12	54,54,54,54	1
4	EDO	B	534	4/4	0.88	0.13	35,36,38,39	0
2	IOD	A	539	1/1	0.89	0.15	51,51,51,51	1
2	IOD	B	532	1/1	0.89	0.09	50,50,50,50	1
2	IOD	B	522	1/1	0.89	0.15	33,33,33,33	1
2	IOD	B	525	1/1	0.89	0.13	59,59,59,59	1
2	IOD	B	512	1/1	0.89	0.13	68,68,68,68	1
2	IOD	A	529	1/1	0.89	0.11	40,40,40,40	1
2	IOD	A	521	1/1	0.90	0.17	39,39,39,39	1
4	EDO	A	547	4/4	0.90	0.11	21,21,21,21	0
2	IOD	A	536	1/1	0.90	0.11	50,50,50,50	1
2	IOD	A	518	1/1	0.90	0.10	43,43,43,43	1
2	IOD	A	532	1/1	0.90	0.18	33,33,33,33	1
3	G6Q	B	533	16/16	0.91	0.12	26,32,37,39	0
2	IOD	A	527	1/1	0.91	0.10	37,37,37,37	1
2	IOD	A	523	1/1	0.91	0.09	43,43,43,43	1
4	EDO	A	548	4/4	0.92	0.11	16,18,19,22	0
2	IOD	B	524	1/1	0.92	0.11	48,48,48,48	1
2	IOD	A	543	1/1	0.92	0.10	57,57,57,57	1
3	G6Q	A	544	16/16	0.92	0.10	16,21,23,24	0
2	IOD	B	526	1/1	0.93	0.10	47,47,47,47	1
2	IOD	A	526	1/1	0.93	0.09	45,45,45,45	1
2	IOD	B	529	1/1	0.93	0.15	31,31,31,31	1
2	IOD	B	521	1/1	0.93	0.11	50,50,50,50	1
2	IOD	A	524	1/1	0.93	0.10	57,57,57,57	1
2	IOD	A	504	1/1	0.93	0.09	35,35,35,35	1
2	IOD	B	519	1/1	0.93	0.07	38,38,38,38	1
2	IOD	A	519	1/1	0.94	0.07	39,39,39,39	1
2	IOD	B	528	1/1	0.94	0.09	47,47,47,47	1
4	EDO	A	545	4/4	0.94	0.09	17,19,20,20	0
2	IOD	A	515	1/1	0.95	0.08	47,47,47,47	1
2	IOD	B	517	1/1	0.95	0.06	39,39,39,39	1
2	IOD	B	502	1/1	0.95	0.07	44,44,44,44	1

Continued on next page...

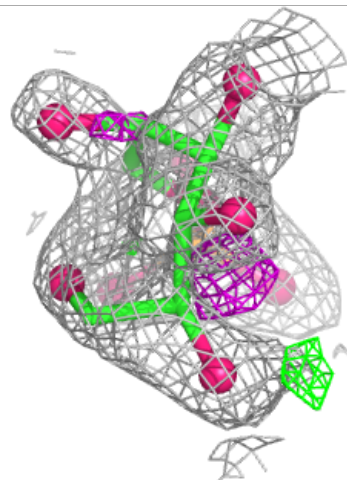
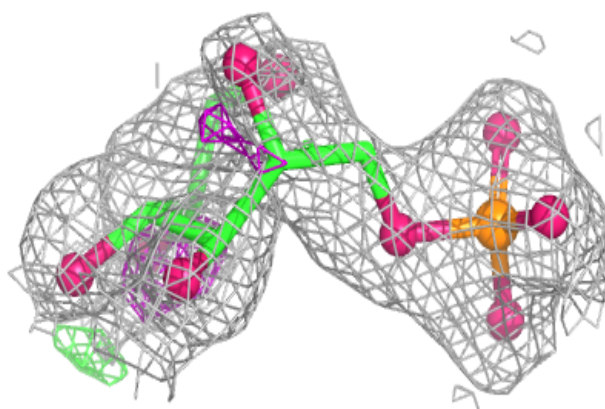
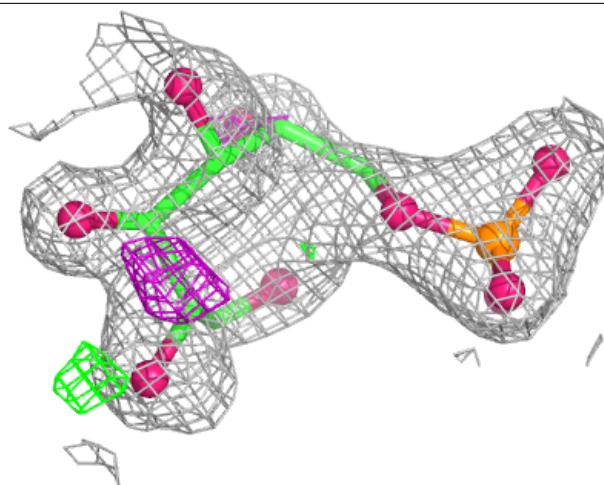
Continued from previous page...

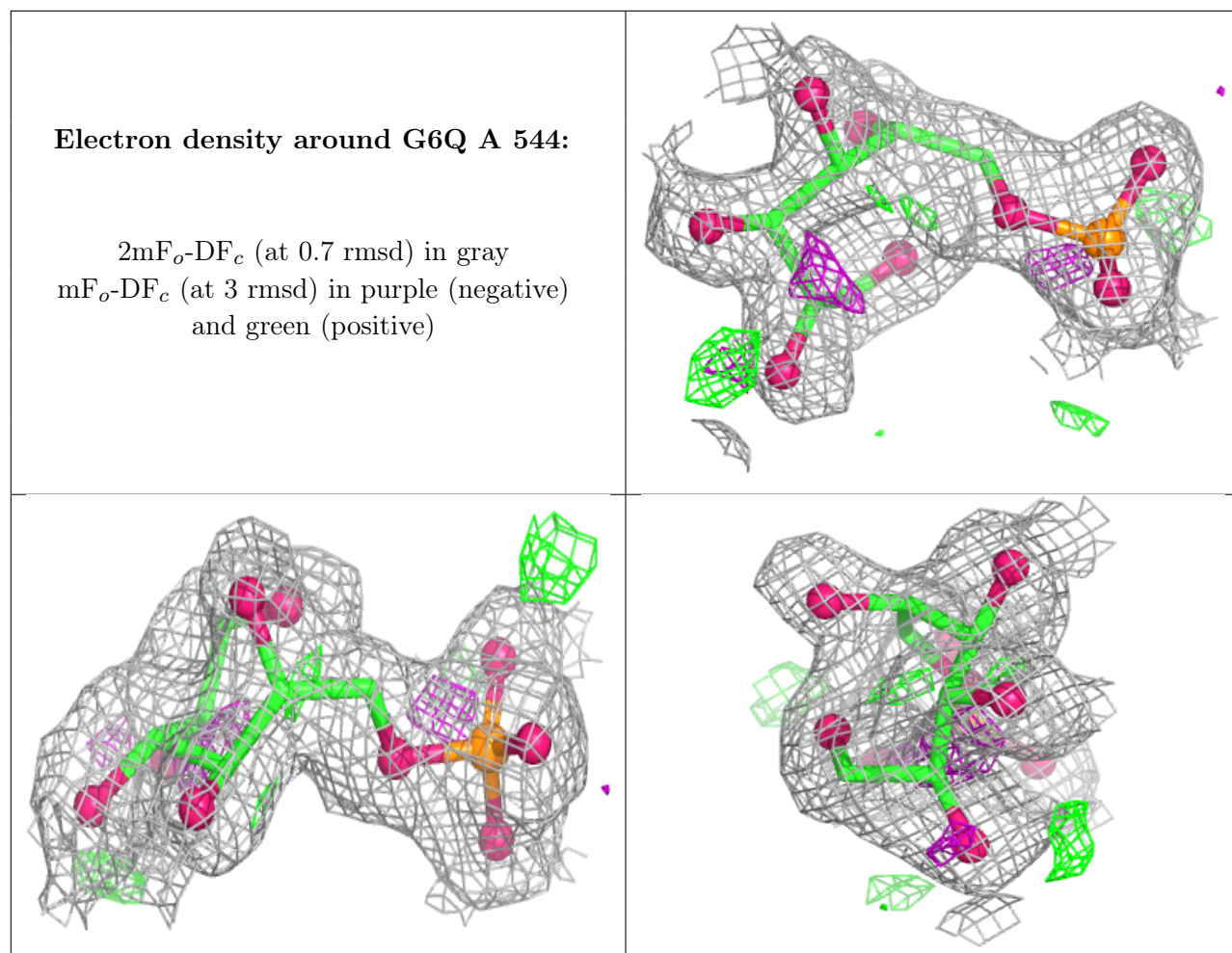
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IOD	A	522	1/1	0.95	0.09	34,34,34,34	1
2	IOD	B	509	1/1	0.95	0.08	41,41,41,41	1
2	IOD	A	534	1/1	0.95	0.12	25,25,25,25	1
2	IOD	A	520	1/1	0.96	0.09	29,29,29,29	1
2	IOD	A	528	1/1	0.96	0.09	30,30,30,30	1
2	IOD	A	541	1/1	0.96	0.06	35,35,35,35	1
2	IOD	A	531	1/1	0.96	0.10	45,45,45,45	1
2	IOD	B	513	1/1	0.97	0.05	36,36,36,36	1
2	IOD	B	505	1/1	0.97	0.05	47,47,47,47	1
2	IOD	B	516	1/1	0.97	0.04	34,34,34,34	1
2	IOD	A	512	1/1	0.97	0.06	28,28,28,28	1
2	IOD	B	518	1/1	0.97	0.04	32,32,32,32	1
2	IOD	B	508	1/1	0.97	0.08	46,46,46,46	1
2	IOD	A	513	1/1	0.97	0.05	29,29,29,29	1
2	IOD	B	510	1/1	0.97	0.07	37,37,37,37	0
2	IOD	A	506	1/1	0.97	0.05	30,30,30,30	1
2	IOD	A	510	1/1	0.98	0.05	32,32,32,32	1
2	IOD	A	514	1/1	0.98	0.05	35,35,35,35	1
2	IOD	B	507	1/1	0.98	0.07	33,33,33,33	0
2	IOD	A	501	1/1	0.98	0.05	31,31,31,31	0
2	IOD	A	509	1/1	0.98	0.04	32,32,32,32	1
2	IOD	B	501	1/1	0.98	0.05	31,31,31,31	0
2	IOD	A	533	1/1	0.98	0.10	36,36,36,36	1
4	EDO	A	550	4/4	0.98	0.05	12,13,14,16	0
2	IOD	B	504	1/1	0.98	0.04	41,41,41,41	1
2	IOD	B	523	1/1	0.98	0.04	37,37,37,37	1
2	IOD	B	503	1/1	0.99	0.05	36,36,36,36	1
2	IOD	A	542	1/1	0.99	0.05	23,23,23,23	0
2	IOD	A	505	1/1	0.99	0.03	24,24,24,24	1
2	IOD	B	511	1/1	0.99	0.03	30,30,30,30	1
2	IOD	A	507	1/1	0.99	0.03	34,34,34,34	1
2	IOD	A	508	1/1	0.99	0.03	25,25,25,25	0
2	IOD	B	514	1/1	0.99	0.05	31,31,31,31	0
5	MG	A	552	1/1	0.99	0.01	6,6,6,6	0
5	MG	B	535	1/1	0.99	0.02	14,14,14,14	0
2	IOD	A	502	1/1	1.00	0.05	19,19,19,19	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 G6Q B 533:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.