



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 01:10 PM EDT

PDB ID : 8EG3 / pdb_00008eg3
Title : Structure of human placental steroid (estrone/DHEA) sulfatase at 2.0 angstrom resolution
Authors : Ghosh, D.
Deposited on : 2022-09-10
Resolution : 2.04 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

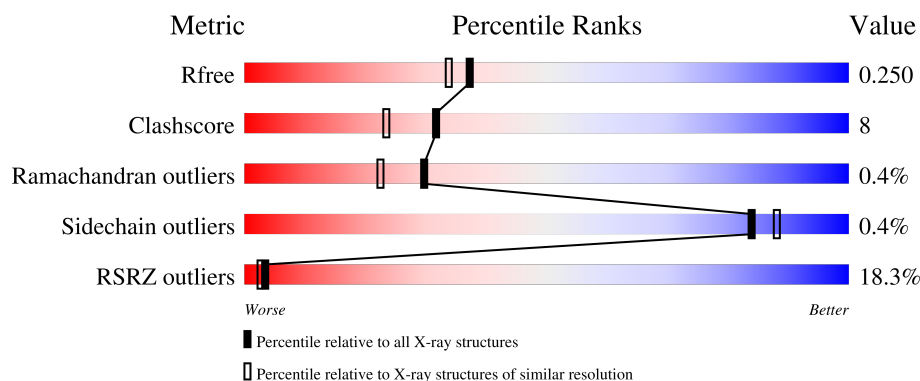
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	583	

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
3	NAG	A	601	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4575 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 Steryl-sulfatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	554	4368	2803	750	789	26	0	0	0

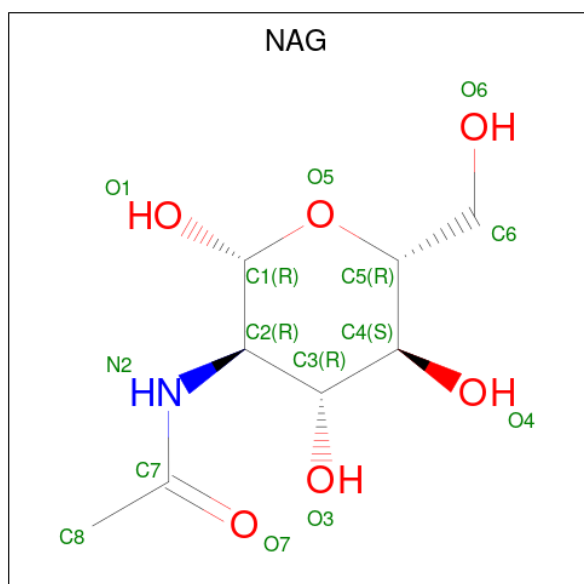
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	ALS	CYS	conflict	UNP P08842

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

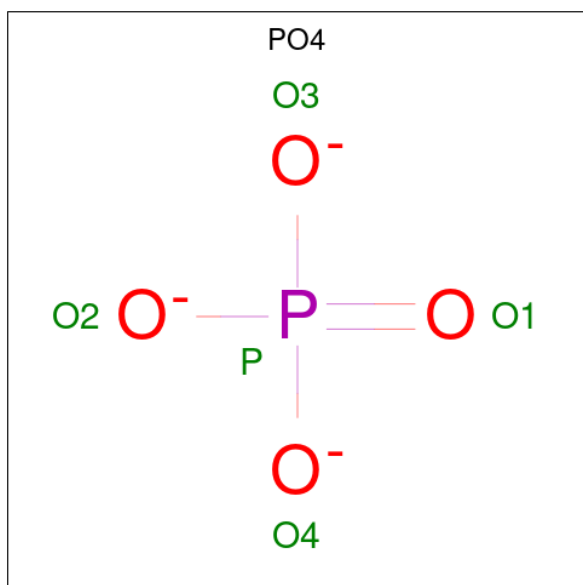
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



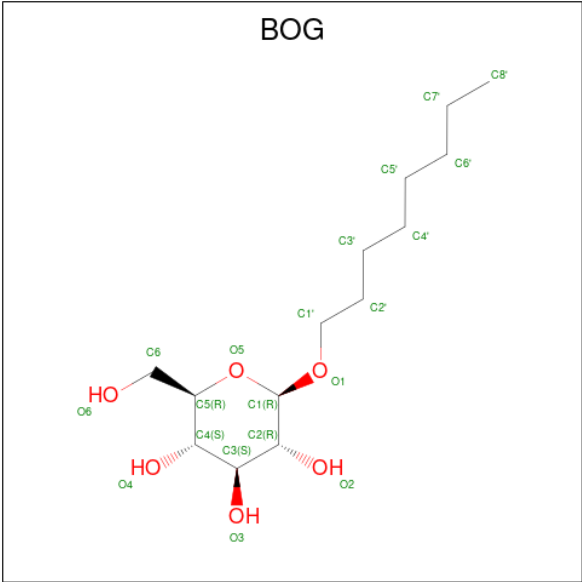
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: $C_{14}H_{28}O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			20	14	6		
5	A	1	Total	C	O	0	0
			20	14	6		

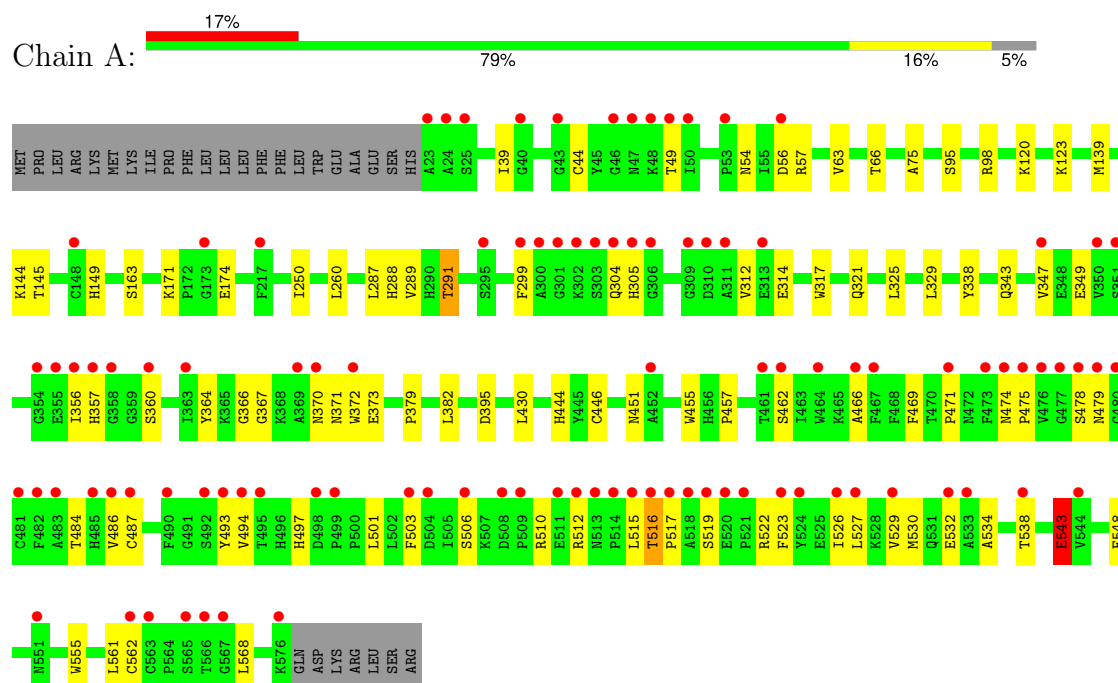
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	133	Total	O	0	0
			133	133		

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: Steryl-sulfatase



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.19Å 117.19Å 102.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.13 – 2.04 32.13 – 2.04	Depositor EDS
% Data completeness (in resolution range)	98.8 (32.13-2.04) 98.8 (32.13-2.04)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.220 , 0.251 0.220 , 0.250	Depositor DCC
R_{free} test set	2539 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.631	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 69.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4575	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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: PO4, CA, BOG, ALS, NAG

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	0.38	0/4482	0.66	3/6092 (0.0%)

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	A	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	543	GLU	CA-CB-CG	13.55	141.19	114.10
1	A	543	GLU	CB-CA-C	7.54	123.89	111.23
1	A	543	GLU	N-CA-CB	-5.08	102.30	110.69

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	291	THR	Peptide
1	A	543	GLU	Sidechain

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	4368	0	4260	70	0
2	A	1	0	0	0	0
3	A	28	0	26	1	0
4	A	5	0	0	0	0
5	A	40	0	56	7	0
6	A	133	0	0	3	0
All	All	4575	0	4342	71	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 8.

All (71) 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:510:ARG:HD3	1:A:512:ARG:HD2	1.61	0.83
1:A:370:ASN:HD22	1:A:372:TRP:HD1	1.25	0.82
1:A:370:ASN:HD22	1:A:372:TRP:CD1	1.97	0.82
1:A:370:ASN:ND2	1:A:372:TRP:HD1	1.85	0.74
1:A:366:GLY:HA3	1:A:370:ASN:HD21	1.58	0.69
1:A:139:MET:HE2	1:A:163:SER:CB	2.23	0.69
1:A:555:TRP:CD1	5:A:605:BOG:H61	2.34	0.62
1:A:66:THR:HB	1:A:395:ASP:HA	1.83	0.61
1:A:370:ASN:ND2	1:A:372:TRP:CD1	2.63	0.61
1:A:364:TYR:HB3	1:A:373:GLU:HB3	1.83	0.61
1:A:291:THR:HG21	1:A:349:GLU:HG2	1.83	0.61
1:A:349:GLU:HG3	1:A:357:HIS:HB2	1.82	0.60
1:A:98:ARG:NH2	1:A:493:TYR:OH	2.35	0.59
1:A:291:THR:HG21	1:A:349:GLU:CD	2.28	0.58
1:A:555:TRP:CG	5:A:605:BOG:H61	2.39	0.57
1:A:304:GLN:CD	1:A:305:HIS:HB2	2.30	0.57
1:A:260:LEU:HD21	1:A:287:LEU:HD22	1.88	0.56
1:A:382:LEU:HG	1:A:430:LEU:HD21	1.89	0.54
1:A:299:PHE:CD1	1:A:314:GLU:HG3	2.42	0.54
1:A:503:PHE:HA	1:A:515:LEU:HD23	1.88	0.54
1:A:95:SER:HB3	1:A:548:PHE:CB	2.38	0.54
1:A:519:SER:HB3	1:A:522:ARG:HE	1.72	0.54
1:A:291:THR:HG21	1:A:349:GLU:CG	2.37	0.53
1:A:304:GLN:NE2	1:A:305:HIS:HB2	2.24	0.53
1:A:54:ASN:OD1	1:A:57:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:SER:HB3	1:A:548:PHE:HB3	1.91	0.51
1:A:139:MET:HE2	1:A:163:SER:HB3	1.92	0.50
1:A:149:HIS:HD2	6:A:751:HOH:O	1.93	0.50
1:A:123:LYS:NZ	6:A:706:HOH:O	2.43	0.50
1:A:516:THR:H	1:A:517:PRO:CD	2.25	0.50
1:A:49:THR:HB	1:A:304:GLN:HG3	1.94	0.49
1:A:562:CYS:O	5:A:604:BOG:H8'3	2.12	0.48
1:A:144:LYS:HE2	5:A:604:BOG:H5'1	1.96	0.48
1:A:360:SER:HB2	3:A:601:NAG:H4	1.96	0.48
1:A:474:ASN:HB2	1:A:475:PRO:HD3	1.95	0.48
1:A:250:ILE:HD11	1:A:561:LEU:HB3	1.96	0.47
1:A:367:GLY:O	1:A:370:ASN:OD1	2.32	0.47
1:A:44:CYS:HB3	1:A:56:ASP:CB	2.43	0.47
1:A:497:HIS:CD2	1:A:501:LEU:HD13	2.49	0.47
1:A:510:ARG:HG3	1:A:512:ARG:HB2	1.97	0.47
1:A:568:LEU:O	5:A:604:BOG:O6	2.32	0.47
1:A:120:LYS:HD2	6:A:816:HOH:O	2.15	0.46
1:A:462:SER:HA	1:A:506:SER:HB3	1.97	0.46
1:A:475:PRO:HB2	1:A:478:SER:HB2	1.95	0.46
1:A:347:VAL:HG11	1:A:479:ASN:HB3	1.99	0.45
1:A:325:LEU:HG	1:A:329:LEU:HD23	1.98	0.45
1:A:455:TRP:HZ3	1:A:526:ILE:HB	1.82	0.45
1:A:289:VAL:HG11	1:A:312:VAL:HG22	1.98	0.44
1:A:529:VAL:O	1:A:532:GLU:HG3	2.18	0.44
1:A:501:LEU:HD23	1:A:503:PHE:HE2	1.83	0.44
5:A:604:BOG:H8'2	5:A:604:BOG:H5'2	1.78	0.43
1:A:455:TRP:O	1:A:457:PRO:HD3	2.18	0.43
1:A:305:HIS:NE2	1:A:356:ILE:HG21	2.32	0.43
1:A:527:LEU:HD23	1:A:530:MET:HE2	2.01	0.43
1:A:371:ASN:OD1	1:A:444:HIS:HB3	2.18	0.42
1:A:534:ALA:O	1:A:538:THR:HG23	2.19	0.42
1:A:39:ILE:HA	1:A:379:PRO:HD3	2.01	0.42
1:A:446:CYS:HB2	1:A:451:ASN:HD22	1.85	0.42
1:A:317:TRP:O	1:A:321:GLN:HG2	2.19	0.42
1:A:466:ALA:HB2	1:A:530:MET:HE1	2.01	0.42
1:A:562:CYS:H	5:A:604:BOG:H7'1	1.84	0.42
1:A:139:MET:HE2	1:A:163:SER:OG	2.21	0.41
1:A:171:LYS:HD3	1:A:174:GLU:HG3	2.01	0.41
1:A:288:HIS:HA	1:A:289:VAL:HA	1.76	0.41
1:A:144:LYS:HG3	1:A:145:THR:HG23	2.02	0.41
1:A:338:TYR:HB2	1:A:382:LEU:HD13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:PRO:HB2	1:A:487:CYS:SG	2.60	0.41
1:A:63:VAL:CG1	1:A:382:LEU:HB2	2.51	0.40
1:A:484:THR:C	1:A:486:VAL:H	2.29	0.40
1:A:49:THR:CB	1:A:304:GLN:HG3	2.51	0.40
1:A:469:PHE:HB2	1:A:494:VAL:HG22	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	551/583 (94%)	512 (93%)	37 (7%)	2 (0%)	30 22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	516	THR
1	A	523	PHE

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	473/501 (94%)	471 (100%)	2 (0%)	84 88

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	343	GLN
1	A	543	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	HIS
1	A	273	GLN
1	A	321	GLN
1	A	389	GLN
1	A	451	ASN
1	A	456	HIS
1	A	485	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	ALS	A	75	2,1	8,10,11	1.19	1 (12%)	7,14,16	1.04	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
1	ALS	A	75	2,1	-	1/3/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	75	ALS	OS1-CB	-2.16	1.38	1.46

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	75	ALS	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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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
5	BOG	A	605	-	20,20,20	1.44	2 (10%)	25,25,25	2.59	10 (40%)
3	NAG	A	602	1	14,14,15	0.28	0	17,19,21	0.46	0
5	BOG	A	604	-	20,20,20	1.39	2 (10%)	25,25,25	0.99	2 (8%)
4	PO4	A	603	-	4,4,4	3.66	3 (75%)	6,6,6	0.83	0
3	NAG	A	601	1	14,14,15	0.23	0	17,19,21	0.48	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
5	BOG	A	604	-	-	8/11/31/31	0/1/1/1
5	BOG	A	605	-	-	9/11/31/31	0/1/1/1
3	NAG	A	601	1	-	2/6/23/26	0/1/1/1
3	NAG	A	602	1	-	2/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	PO4	P-O1	5.92	1.64	1.50
5	A	604	BOG	O5-C1	4.59	1.53	1.41
5	A	605	BOG	O5-C1	4.44	1.53	1.41
4	A	603	PO4	P-O3	3.06	1.63	1.54
4	A	603	PO4	P-O4	-2.72	1.46	1.54
5	A	605	BOG	O1-C1	-2.46	1.36	1.40
5	A	604	BOG	O1-C1	-2.23	1.36	1.40

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	605	BOG	C3-C4-C5	5.46	120.14	110.23
5	A	605	BOG	C4-C3-C2	4.88	119.40	110.83
5	A	605	BOG	C6-C5-C4	-4.65	101.61	113.02
5	A	605	BOG	O5-C5-C4	4.03	116.96	109.70
5	A	605	BOG	O1-C1-C2	-3.83	102.46	108.27
5	A	605	BOG	O3-C3-C4	-3.60	101.90	110.38
5	A	605	BOG	O3-C3-C2	-3.49	102.16	110.38
5	A	605	BOG	O5-C1-C2	3.04	116.61	110.37
5	A	605	BOG	C1-O5-C5	2.69	118.97	113.72
5	A	605	BOG	C1-C2-C3	2.62	115.53	110.01
5	A	604	BOG	O3-C3-C2	-2.26	105.06	110.38
5	A	604	BOG	C6-C5-C4	-2.03	108.05	113.02

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	604	BOG	O5-C5-C6-O6

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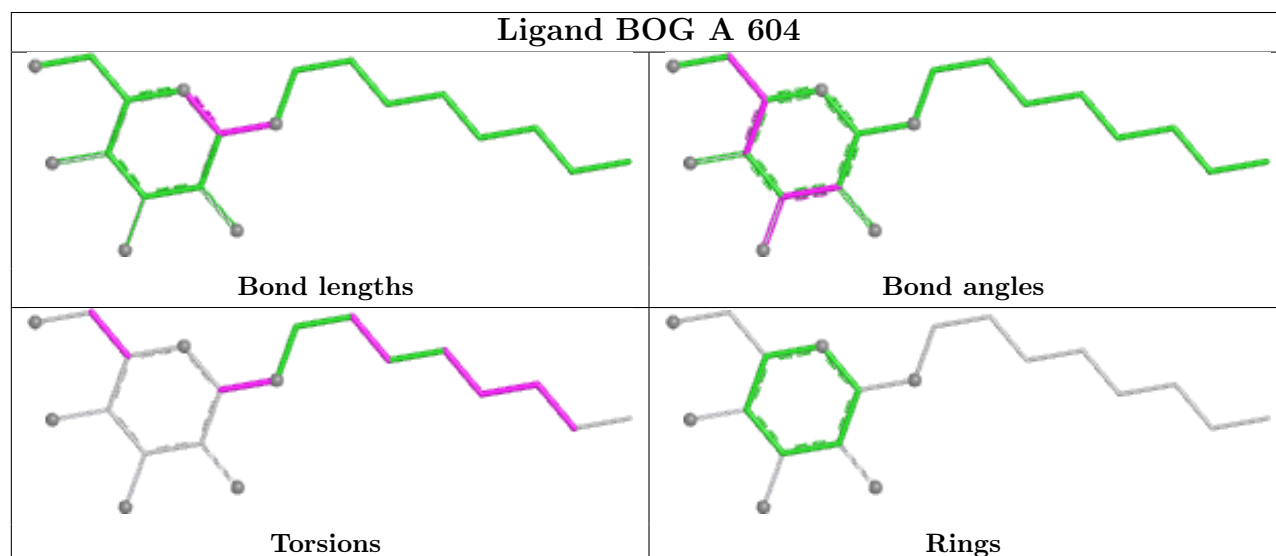
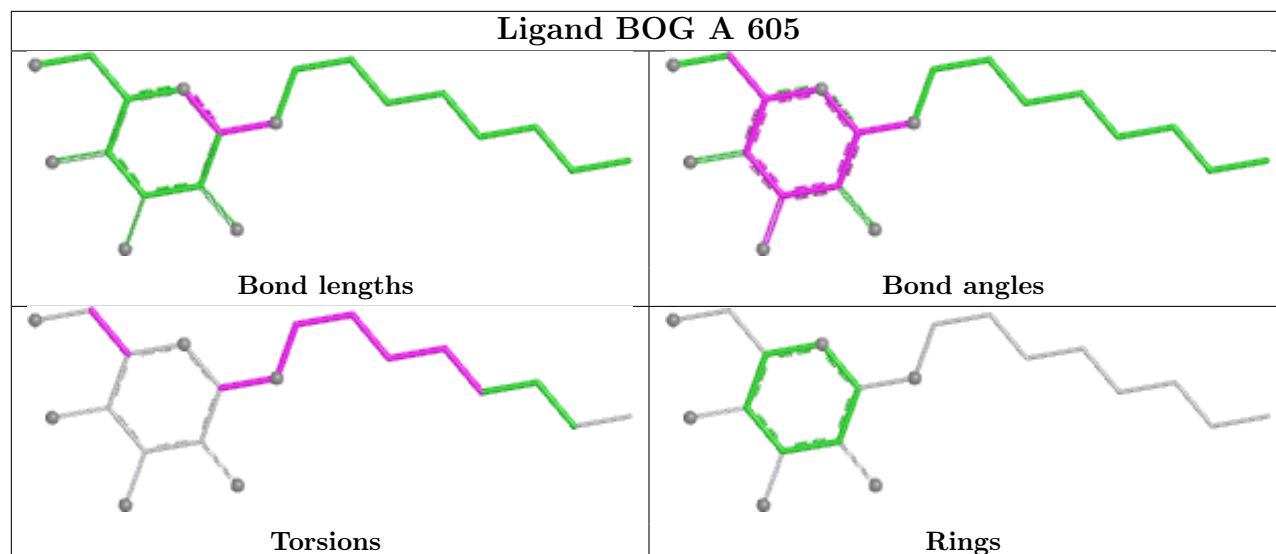
Mol	Chain	Res	Type	Atoms
3	A	601	NAG	O5-C5-C6-O6
3	A	601	NAG	C4-C5-C6-O6
5	A	604	BOG	C4-C5-C6-O6
5	A	605	BOG	O5-C5-C6-O6
5	A	604	BOG	O5-C1-O1-C1'
5	A	605	BOG	O5-C1-O1-C1'
5	A	605	BOG	C4-C5-C6-O6
5	A	604	BOG	C2-C1-O1-C1'
5	A	605	BOG	C2-C1-O1-C1'
5	A	605	BOG	C1'-C2'-C3'-C4'
5	A	604	BOG	C3'-C4'-C5'-C6'
3	A	602	NAG	C4-C5-C6-O6
3	A	602	NAG	O5-C5-C6-O6
5	A	605	BOG	C2'-C1'-O1-C1
5	A	604	BOG	C4'-C5'-C6'-C7'
5	A	605	BOG	C3'-C4'-C5'-C6'
5	A	604	BOG	C5'-C6'-C7'-C8'
5	A	605	BOG	O1-C1'-C2'-C3'
5	A	604	BOG	C1'-C2'-C3'-C4'
5	A	605	BOG	C2'-C3'-C4'-C5'

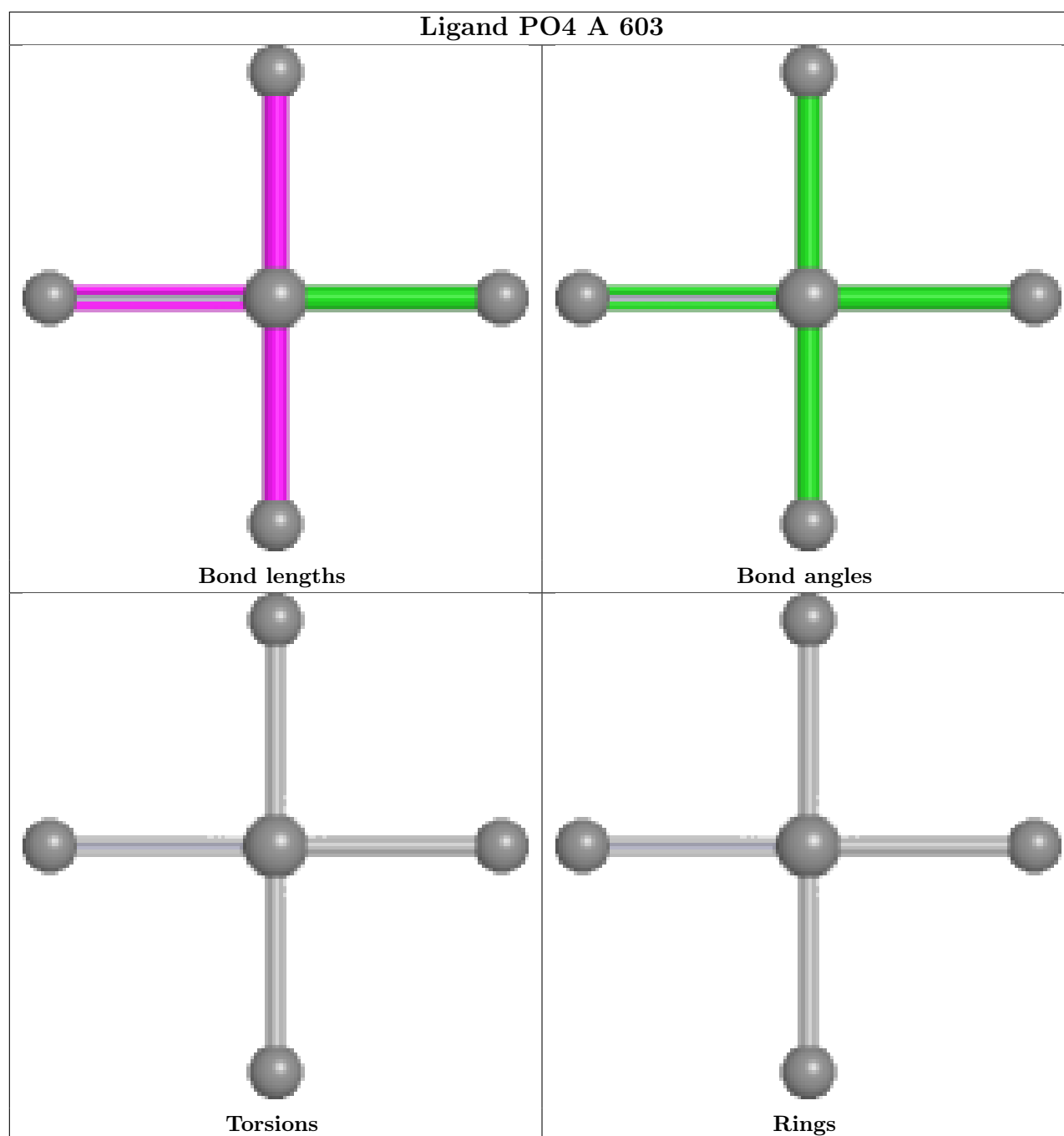
There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	605	BOG	2	0
5	A	604	BOG	5	0
3	A	601	NAG	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	553/583 (94%)	0.86	101 (18%) 3 3	31, 60, 127, 195	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	487	CYS	6.4
1	A	474	ASN	6.1
1	A	304	GLN	5.9
1	A	518	ALA	4.9
1	A	517	PRO	4.9
1	A	24	ALA	4.8
1	A	303	SER	4.7
1	A	300	ALA	4.6
1	A	495	THR	4.3
1	A	306	GLY	4.2
1	A	360	SER	4.1
1	A	356	ILE	4.0
1	A	358	GLY	4.0
1	A	49	THR	3.9
1	A	504	ASP	3.9
1	A	524	TYR	3.8
1	A	521	PRO	3.8
1	A	475	PRO	3.7
1	A	485	HIS	3.7
1	A	302	LYS	3.6
1	A	494	VAL	3.6
1	A	523	PHE	3.5
1	A	305	HIS	3.5
1	A	516	THR	3.5
1	A	514	PRO	3.4
1	A	473	PHE	3.4
1	A	526	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	56	ASP	3.4
1	A	499	PRO	3.4
1	A	23	ALA	3.4
1	A	350	VAL	3.4
1	A	527	LEU	3.4
1	A	483	ALA	3.3
1	A	476	VAL	3.3
1	A	533	ALA	3.2
1	A	565	SER	3.2
1	A	309	GLY	3.2
1	A	532	GLU	3.1
1	A	480	GLY	3.1
1	A	50	ILE	3.1
1	A	481	CYS	3.1
1	A	508	ASP	3.1
1	A	498	ASP	3.0
1	A	25	SER	3.0
1	A	529	VAL	2.9
1	A	515	LEU	2.9
1	A	173	GLY	2.9
1	A	47	ASN	2.8
1	A	370	ASN	2.8
1	A	299	PHE	2.8
1	A	217	PHE	2.8
1	A	40	GLY	2.8
1	A	486	VAL	2.8
1	A	310	ASP	2.7
1	A	355	GLU	2.7
1	A	363	ILE	2.7
1	A	372	TRP	2.7
1	A	301	GLY	2.7
1	A	354	GLY	2.7
1	A	369	ALA	2.7
1	A	538	THR	2.6
1	A	479	ASN	2.6
1	A	471	PRO	2.6
1	A	357	HIS	2.6
1	A	43	GLY	2.6
1	A	347	VAL	2.5
1	A	493	TYR	2.5
1	A	509	PRO	2.5
1	A	53	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	466	ALA	2.5
1	A	511	GLU	2.4
1	A	566	THR	2.4
1	A	478	SER	2.4
1	A	506	SER	2.4
1	A	576	LYS	2.4
1	A	563	CYS	2.4
1	A	520	GLU	2.4
1	A	461	THR	2.4
1	A	311	ALA	2.3
1	A	490	PHE	2.3
1	A	551	ASN	2.3
1	A	46	GLY	2.3
1	A	482	PHE	2.3
1	A	513	ASN	2.3
1	A	464	TRP	2.3
1	A	313	GLU	2.2
1	A	295	SER	2.2
1	A	492	SER	2.2
1	A	544	VAL	2.2
1	A	148	CYS	2.2
1	A	519	SER	2.2
1	A	503	PHE	2.2
1	A	562	CYS	2.2
1	A	351	SER	2.2
1	A	467	PHE	2.1
1	A	462	SER	2.1
1	A	48	LYS	2.1
1	A	512	ARG	2.1
1	A	452	ALA	2.0
1	A	477	GLY	2.0
1	A	567	GLY	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	ALS	A	75	11/12	0.97	0.08	35,39,47,50	0

6.3 Carbohydrates [i](#)

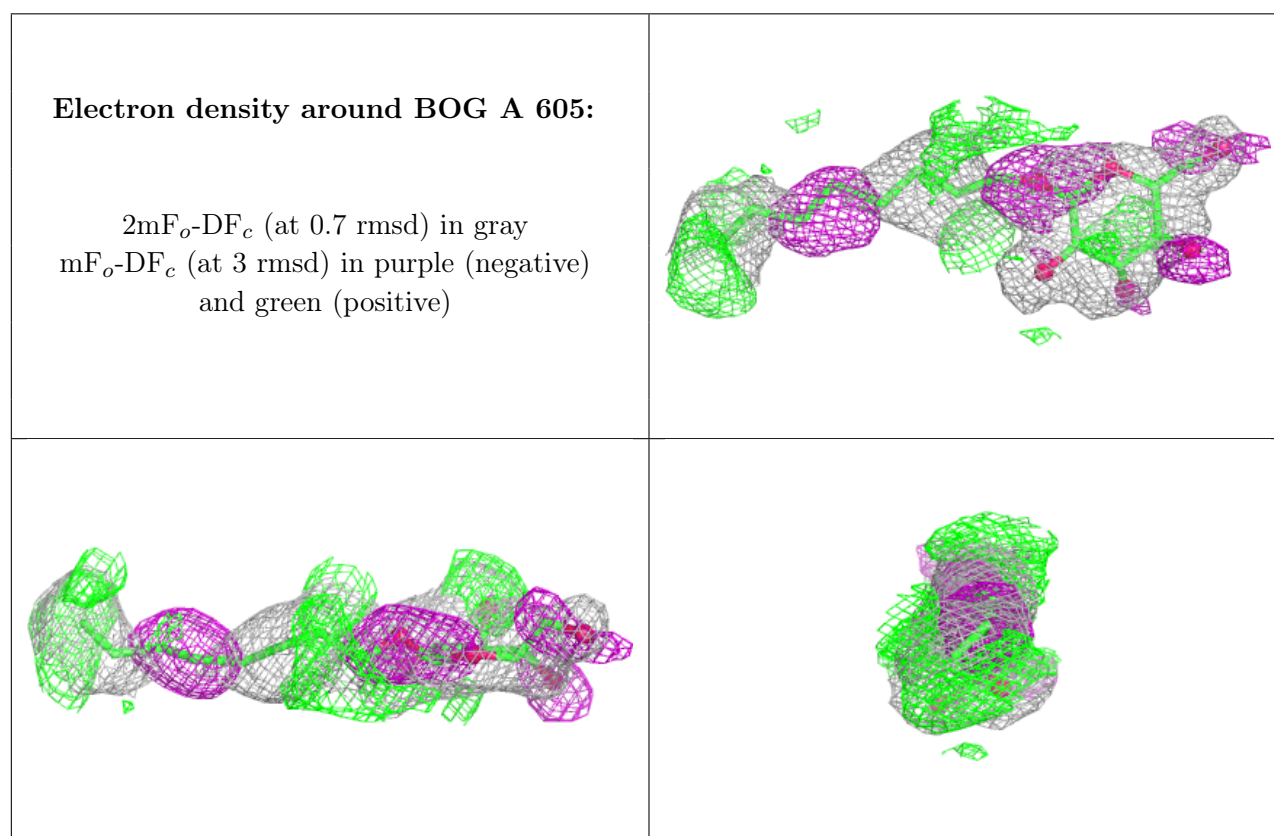
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

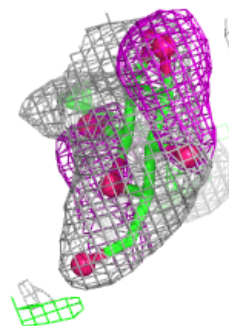
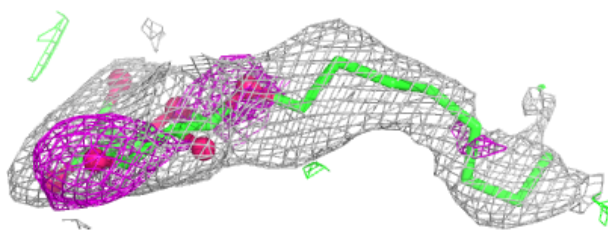
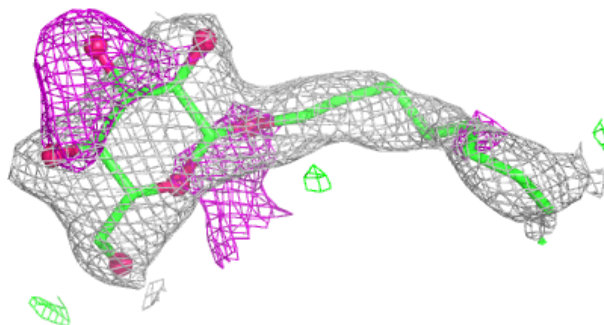
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	BOG	A	605	20/20	0.62	0.20	38,50,54,61	0
5	BOG	A	604	20/20	0.73	0.15	52,60,68,69	0
3	NAG	A	601	14/15	0.77	0.42	81,89,99,100	14
3	NAG	A	602	14/15	0.77	0.19	65,67,70,71	14
4	PO4	A	603	5/5	0.92	0.15	41,44,45,50	5
2	CA	A	600	1/1	0.94	0.08	46,46,46,46	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.



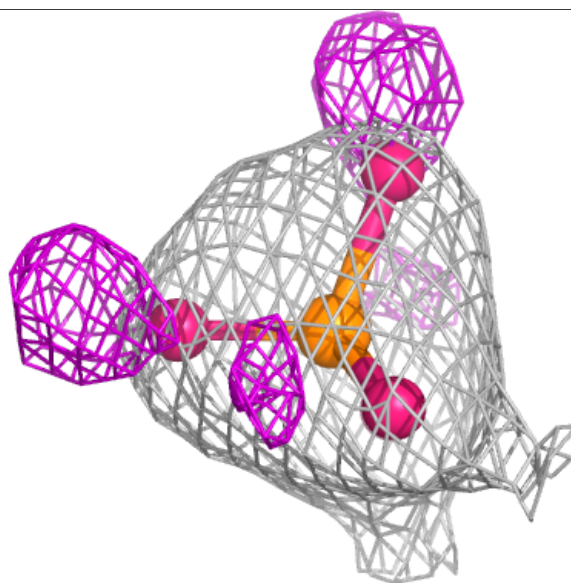
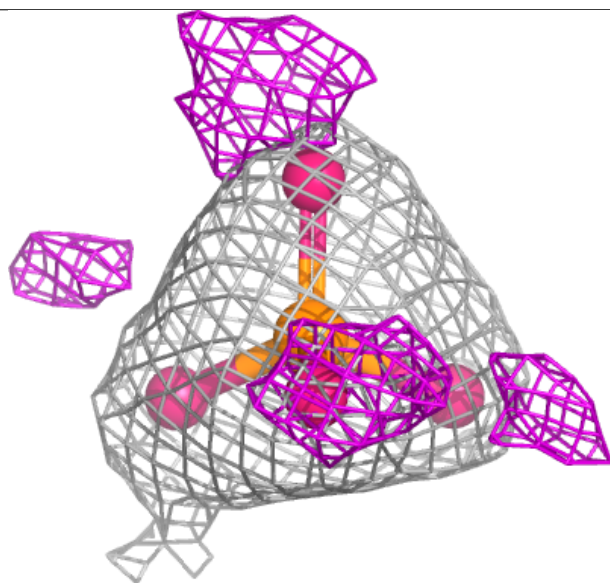
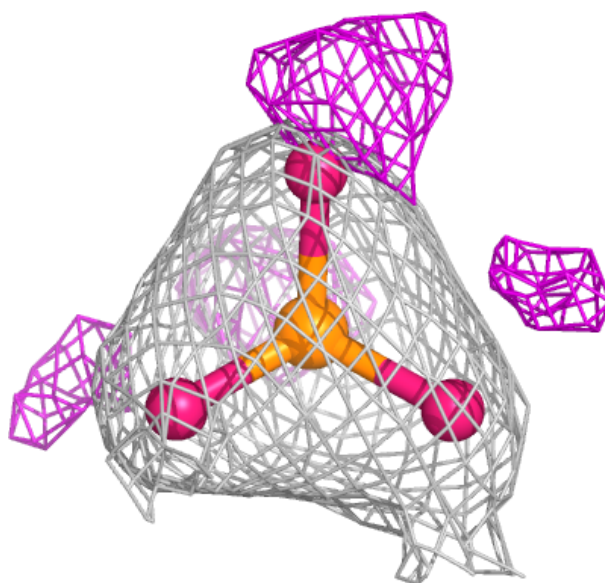
Electron density around BOG A 604:

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



Electron density around PO4 A 603:

$2mF_o-DF_c$ (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.