



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 28, 2024 – 08:20 AM EDT

PDB ID : 6V55
Title : Full extracellular region of zebrafish Gpr126/Adgrg6
Authors : Leon, K.; Arac, D.
Deposited on : 2019-12-03
Resolution : 2.38 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

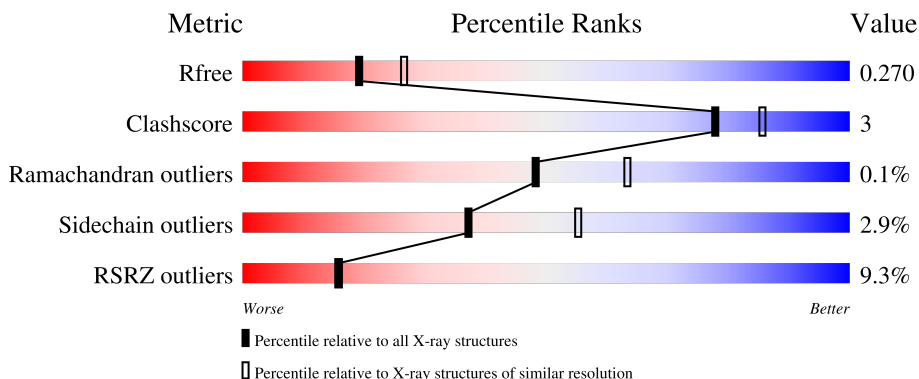
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	164625	6699 (2.40-2.36)
Clashscore	180529	7414 (2.40-2.36)
Ramachandran outliers	177936	7337 (2.40-2.36)
Sidechain outliers	177891	7338 (2.40-2.36)
RSRZ outliers	164620	6699 (2.40-2.36)

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	788	 9% 85% 9% • 5%
2	Q	12	 50% 8% 42%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6114 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 Adhesion G-protein coupled receptor G6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	746	5706	3590	941	1143	32	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	ALA	SER	conflict	UNP C6KFA3
A	234	PHE	LEU	conflict	UNP C6KFA3
A	263	GLU	GLY	conflict	UNP C6KFA3
A	?	-	ALA	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	LEU	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	VAL	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	ILE	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	SER	deletion	UNP C6KFA3
A	?	-	ILE	deletion	UNP C6KFA3
A	?	-	ALA	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	ASN	deletion	UNP C6KFA3
A	?	-	ILE	deletion	UNP C6KFA3
A	?	-	ILE	deletion	UNP C6KFA3
A	?	-	PRO	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	ASN	deletion	UNP C6KFA3
A	?	-	ALA	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	THR	deletion	UNP C6KFA3
A	?	-	HIS	deletion	UNP C6KFA3
A	461	ILE	THR	conflict	UNP C6KFA3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	804	TRP	CYS	conflict	UNP C6KFA3
A	840	HIS	-	expression tag	UNP C6KFA3
A	841	HIS	-	expression tag	UNP C6KFA3
A	842	HIS	-	expression tag	UNP C6KFA3
A	843	HIS	-	expression tag	UNP C6KFA3
A	844	HIS	-	expression tag	UNP C6KFA3
A	845	HIS	-	expression tag	UNP C6KFA3
A	846	HIS	-	expression tag	UNP C6KFA3
A	847	HIS	-	expression tag	UNP C6KFA3

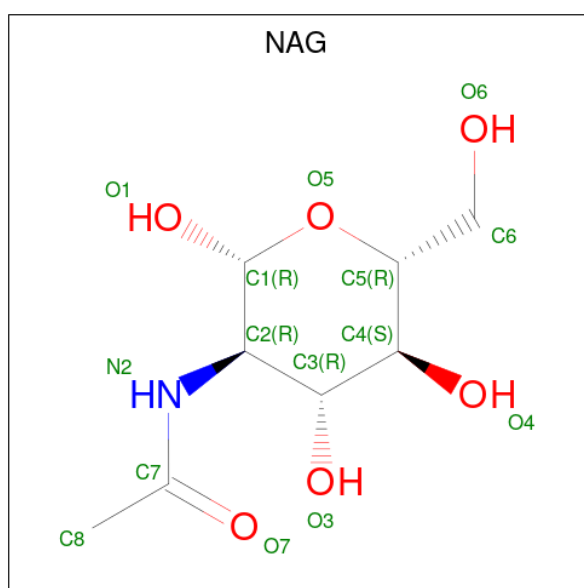
- Molecule 2 is a protein called Adhesion G-protein coupled receptor G6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Q	7	Total	C	N	O	S	0	0	0
			56	38	9	8	1			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

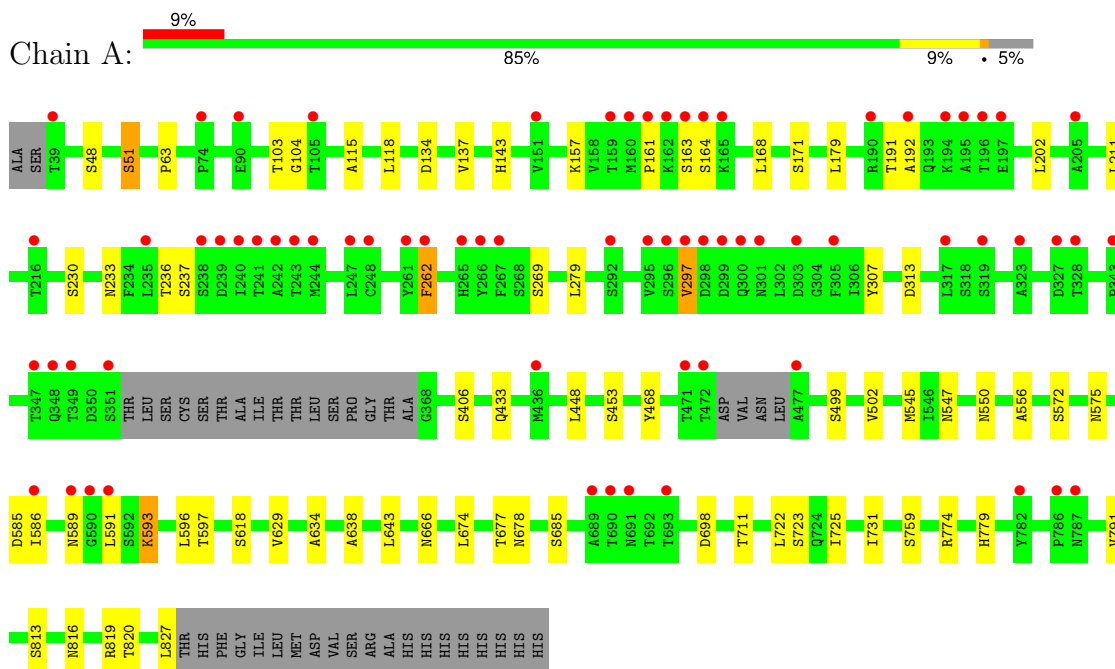
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	197	Total	O	0	0
			197	197		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Adhesion G-protein coupled receptor G6



• Molecule 2: Adhesion G-protein coupled receptor G6



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.96Å 59.45Å 168.38Å 90.00° 107.82° 90.00°	Depositor
Resolution (Å)	47.90 – 2.38 47.90 – 2.38	Depositor EDS
% Data completeness (in resolution range)	62.3 (47.90-2.38) 62.3 (47.90-2.38)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.37Å)	Xtriage
Refinement program	REFMAC 1.17.1_3660, PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.212 , 0.272 0.223 , 0.270	Depositor DCC
R_{free} test set	2739 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	1.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6114	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: NAG, CA

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	0.49	0/5816	0.71	4/7934 (0.1%)
2	Q	0.53	0/57	0.59	0/75
All	All	0.49	0/5873	0.71	4/8009 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	448	LEU	CA-CB-CG	7.69	133.00	115.30
1	A	297	VAL	CA-CB-CG2	6.46	120.59	110.90
1	A	134	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	262	PHE	CB-CG-CD2	5.12	124.39	120.80

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	5706	0	5492	31	0
2	Q	56	0	56	1	0
3	A	1	0	0	0	0
4	A	154	0	143	0	0
5	A	197	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6114	0	5691	31	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 3.

All (31) 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:164:SER:HB3	1:A:297:VAL:HG13	1.57	0.86
1:A:586:ILE:HG22	1:A:591:LEU:HD21	1.69	0.73
1:A:722:LEU:HA	1:A:725:ILE:HG22	1.76	0.68
1:A:629:VAL:HG13	1:A:666:ASN:ND2	2.17	0.60
1:A:685:SER:HB3	1:A:698:ASP:HB3	1.87	0.57
1:A:791:VAL:HG21	2:Q:833:LEU:HD13	1.86	0.56
1:A:629:VAL:CG1	1:A:666:ASN:HD21	2.18	0.55
1:A:547:ASN:ND2	1:A:550:ASN:OD1	2.41	0.54
1:A:759:SER:HB3	1:A:827:LEU:HD11	1.90	0.53
1:A:674:LEU:HD12	1:A:731:ILE:HG12	1.90	0.53
1:A:629:VAL:HG13	1:A:666:ASN:HD21	1.73	0.52
1:A:779:HIS:NE2	1:A:820:THR:OG1	2.37	0.50
1:A:179:LEU:HB2	1:A:279:LEU:HB2	1.95	0.47
1:A:593:LYS:HB2	1:A:634:ALA:HA	1.97	0.47
1:A:103:THR:OG1	1:A:104:GLY:N	2.48	0.46
1:A:711:THR:HB	1:A:774:ARG:HB3	1.96	0.46
1:A:161:PRO:HD3	1:A:168:LEU:HD13	1.98	0.46
1:A:545:MET:HG3	1:A:556:ALA:HB2	1.97	0.45
1:A:157:LYS:HG3	1:A:307:TYR:HB2	1.98	0.45
1:A:63:PRO:HG2	1:A:589:ASN:OD1	2.16	0.45
1:A:572:SER:N	1:A:575:ASN:OD1	2.44	0.45
1:A:677:THR:OG1	1:A:678:ASN:N	2.50	0.44
1:A:236:THR:OG1	1:A:237:SER:N	2.48	0.44
1:A:202:LEU:HB3	1:A:211:LEU:HB3	2.00	0.44
1:A:115:ALA:HA	1:A:118:LEU:HD22	1.99	0.43
1:A:406:SER:HB3	1:A:502:VAL:HG22	2.00	0.43
1:A:597:THR:HG22	1:A:638:ALA:HB2	2.00	0.43
1:A:51:SER:OG	1:A:143:HIS:NE2	2.51	0.43
1:A:191:THR:OG1	1:A:192:ALA:N	2.52	0.42
1:A:643:LEU:HD23	1:A:643:LEU:HA	1.95	0.41
1:A:816:ASN:HD21	1:A:819:ARG:HE	1.69	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	740/788 (94%)	703 (95%)	36 (5%)	1 (0%)	48	63
2	Q	5/12 (42%)	5 (100%)	0	0	100	100
All	All	745/800 (93%)	708 (95%)	36 (5%)	1 (0%)	48	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	VAL

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	647/695 (93%)	628 (97%)	19 (3%)	37	55
2	Q	6/10 (60%)	6 (100%)	0	100	100
All	All	653/705 (93%)	634 (97%)	19 (3%)	37	55

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	SER
1	A	51	SER
1	A	163	SER
1	A	171	SER
1	A	230	SER

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Mol	Chain	Res	Type
1	A	233	ASN
1	A	262	PHE
1	A	269	SER
1	A	313	ASP
1	A	433	GLN
1	A	453	SER
1	A	468	TYR
1	A	499	SER
1	A	585	ASP
1	A	593	LYS
1	A	596	LEU
1	A	618	SER
1	A	723	SER
1	A	813	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	348	GLN
1	A	493	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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	NAG	A	912	1	14,14,15	0.90	1 (7%)	17,19,21	0.82	1 (5%)
4	NAG	A	908	1	14,14,15	1.21	2 (14%)	17,19,21	0.72	1 (5%)
4	NAG	A	907	1	14,14,15	0.87	2 (14%)	17,19,21	0.55	0
4	NAG	A	905	1	14,14,15	0.99	2 (14%)	17,19,21	0.90	1 (5%)
4	NAG	A	902	1	14,14,15	1.08	1 (7%)	17,19,21	0.66	1 (5%)
4	NAG	A	909	1	14,14,15	0.91	1 (7%)	17,19,21	0.65	1 (5%)
4	NAG	A	911	1	14,14,15	0.79	1 (7%)	17,19,21	0.59	0
4	NAG	A	904	1	14,14,15	1.45	2 (14%)	17,19,21	1.05	1 (5%)
4	NAG	A	906	1	14,14,15	1.15	2 (14%)	17,19,21	0.94	1 (5%)
4	NAG	A	903	1	14,14,15	0.97	2 (14%)	17,19,21	1.03	1 (5%)
4	NAG	A	910	1	14,14,15	0.78	1 (7%)	17,19,21	0.65	1 (5%)

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	NAG	A	912	1	-	0/6/23/26	0/1/1/1
4	NAG	A	908	1	-	2/6/23/26	0/1/1/1
4	NAG	A	907	1	-	2/6/23/26	0/1/1/1
4	NAG	A	905	1	-	2/6/23/26	0/1/1/1
4	NAG	A	902	1	-	2/6/23/26	0/1/1/1
4	NAG	A	909	1	-	2/6/23/26	0/1/1/1
4	NAG	A	911	1	-	1/6/23/26	0/1/1/1
4	NAG	A	904	1	-	1/6/23/26	0/1/1/1
4	NAG	A	906	1	-	1/6/23/26	0/1/1/1
4	NAG	A	903	1	-	2/6/23/26	0/1/1/1
4	NAG	A	910	1	-	2/6/23/26	0/1/1/1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	904	NAG	C1-C2	3.96	1.57	1.52
4	A	902	NAG	O5-C1	3.45	1.49	1.43
4	A	908	NAG	O5-C1	3.43	1.49	1.43
4	A	904	NAG	O5-C1	3.36	1.49	1.43
4	A	906	NAG	O5-C1	3.07	1.48	1.43
4	A	906	NAG	C1-C2	2.83	1.56	1.52
4	A	903	NAG	O5-C1	2.82	1.48	1.43
4	A	908	NAG	C1-C2	2.70	1.56	1.52
4	A	912	NAG	O5-C1	2.59	1.48	1.43
4	A	905	NAG	O5-C1	2.55	1.48	1.43
4	A	909	NAG	O5-C1	2.53	1.47	1.43
4	A	905	NAG	C1-C2	2.45	1.55	1.52
4	A	910	NAG	O5-C1	2.45	1.47	1.43
4	A	907	NAG	C1-C2	2.12	1.55	1.52
4	A	907	NAG	O5-C1	2.04	1.47	1.43
4	A	903	NAG	C1-C2	2.02	1.55	1.52
4	A	911	NAG	O5-C1	2.01	1.47	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	903	NAG	C1-O5-C5	3.58	116.98	112.19
4	A	904	NAG	C1-O5-C5	3.35	116.67	112.19
4	A	906	NAG	C1-O5-C5	3.33	116.64	112.19
4	A	905	NAG	C1-O5-C5	3.22	116.50	112.19
4	A	912	NAG	C1-O5-C5	2.62	115.69	112.19
4	A	908	NAG	C1-O5-C5	2.59	115.65	112.19
4	A	910	NAG	C1-O5-C5	2.24	115.19	112.19
4	A	909	NAG	C1-O5-C5	2.04	114.92	112.19
4	A	902	NAG	C1-O5-C5	2.04	114.92	112.19

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	907	NAG	O5-C5-C6-O6
4	A	908	NAG	C4-C5-C6-O6
4	A	908	NAG	O5-C5-C6-O6
4	A	902	NAG	O5-C5-C6-O6
4	A	907	NAG	C4-C5-C6-O6
4	A	902	NAG	C4-C5-C6-O6
4	A	905	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	A	910	NAG	O5-C5-C6-O6
4	A	903	NAG	O5-C5-C6-O6
4	A	903	NAG	C4-C5-C6-O6
4	A	909	NAG	C4-C5-C6-O6
4	A	909	NAG	O5-C5-C6-O6
4	A	905	NAG	C4-C5-C6-O6
4	A	904	NAG	O5-C5-C6-O6
4	A	910	NAG	C4-C5-C6-O6
4	A	906	NAG	C4-C5-C6-O6
4	A	911	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	746/788 (94%)	0.37	70 (9%) 15 15	13, 37, 73, 102	0
2	Q	7/12 (58%)	-0.10	0 100 100	20, 24, 36, 50	0
All	All	753/800 (94%)	0.37	70 (9%) 16 16	13, 37, 73, 102	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	ALA	6.5
1	A	296	SER	5.7
1	A	690	THR	5.4
1	A	297	VAL	5.4
1	A	241	THR	5.3
1	A	243	THR	4.7
1	A	299	ASP	4.7
1	A	242	ALA	4.6
1	A	197	GLU	4.6
1	A	305	PHE	4.6
1	A	235	LEU	4.6
1	A	317	LEU	4.2
1	A	471	THR	4.2
1	A	295	VAL	4.1
1	A	39	THR	4.0
1	A	436	MET	3.9
1	A	244	MET	3.8
1	A	161	PRO	3.8
1	A	590	GLY	3.8
1	A	165	LYS	3.7
1	A	691	ASN	3.6
1	A	160	MET	3.6
1	A	261	TYR	3.6
1	A	300	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	162	LYS	3.4
1	A	328	THR	3.3
1	A	238	SER	3.2
1	A	351	SER	3.2
1	A	477	ALA	3.1
1	A	265	HIS	3.1
1	A	589	ASN	3.0
1	A	205	ALA	3.0
1	A	586	ILE	2.9
1	A	195	ALA	2.8
1	A	298	ASP	2.8
1	A	472	THR	2.8
1	A	327	ASP	2.7
1	A	164	SER	2.7
1	A	689	ALA	2.6
1	A	782	TYR	2.6
1	A	105	THR	2.6
1	A	266	TYR	2.5
1	A	262	PHE	2.5
1	A	591	LEU	2.5
1	A	240	ILE	2.4
1	A	239	ASP	2.4
1	A	292	SER	2.4
1	A	248	CYS	2.4
1	A	347	THR	2.4
1	A	151	VAL	2.4
1	A	216	THR	2.4
1	A	343	PRO	2.3
1	A	194	LYS	2.3
1	A	323	ALA	2.3
1	A	786	PRO	2.3
1	A	90	GLU	2.3
1	A	190	ARG	2.3
1	A	319	SER	2.3
1	A	301	ASN	2.3
1	A	247	LEU	2.2
1	A	693	THR	2.2
1	A	163	SER	2.2
1	A	303	ASP	2.2
1	A	267	PHE	2.2
1	A	787	ASN	2.1
1	A	159	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	349	THR	2.1
1	A	348	GLN	2.1
1	A	74	PRO	2.0
1	A	196	THR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

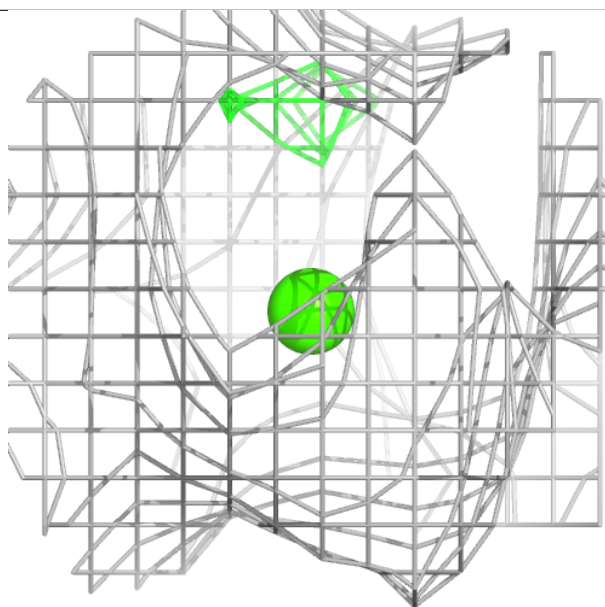
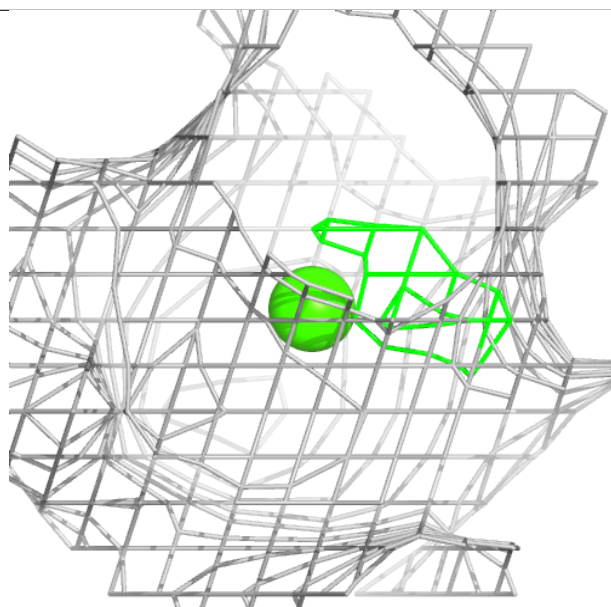
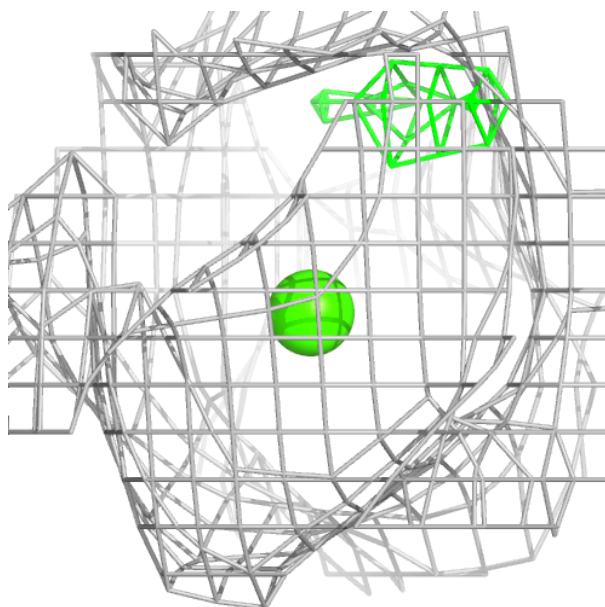
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	A	904	14/15	0.41	0.21	59,70,75,78	0
4	NAG	A	911	14/15	0.47	0.20	68,74,79,79	0
4	NAG	A	912	14/15	0.70	0.20	59,68,81,85	0
4	NAG	A	905	14/15	0.71	0.18	60,67,80,83	0
4	NAG	A	907	14/15	0.74	0.18	49,59,74,79	0
4	NAG	A	910	14/15	0.77	0.14	62,68,73,73	0
4	NAG	A	906	14/15	0.78	0.13	56,62,65,66	0
4	NAG	A	909	14/15	0.84	0.12	46,51,56,56	0
4	NAG	A	902	14/15	0.84	0.13	41,46,52,53	0
4	NAG	A	908	14/15	0.86	0.12	52,60,70,70	0
3	CA	A	901	1/1	0.94	0.03	19,19,19,19	0
4	NAG	A	903	14/15	0.95	0.07	30,38,43,44	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 CA A 901:

$2mF_o-DF_c$ (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.