



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:52 AM GMT

PDB ID : 2V5O
Title : STRUCTURE OF HUMAN IGF2R DOMAINS 11-14
Authors : Brown, J.; Delaine, C.; Zaccheo, O.J.; Siebold, C.; Gilbert, R.J.; Van Boxel, G.; Denley, A.; Wallace, J.C.; Hassan, A.B.; Forbes, B.E.; Jones, E.Y.
Deposited on : 2007-07-06
Resolution : 2.91 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

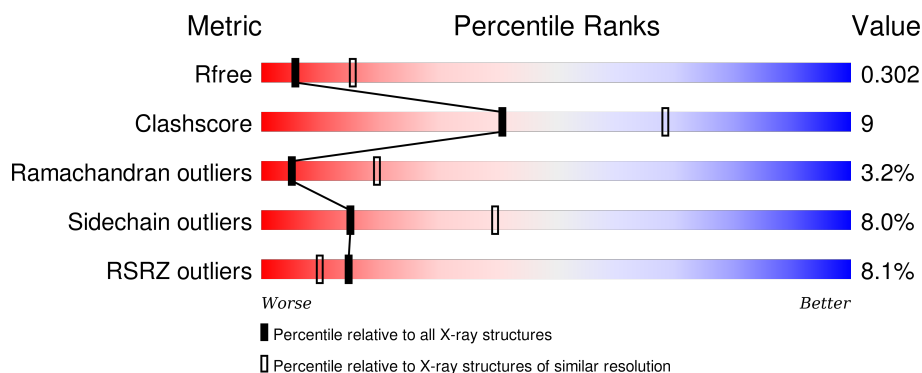
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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}	91344	1643 (2.94-2.90)
Clashscore	102246	1871 (2.94-2.90)
Ramachandran outliers	100387	1824 (2.94-2.90)
Sidechain outliers	100360	1826 (2.94-2.90)
RSRZ outliers	91569	1650 (2.94-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	627	<div> <div>8%</div> <div>72%</div> <div>21%</div> <div>.</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4686 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.

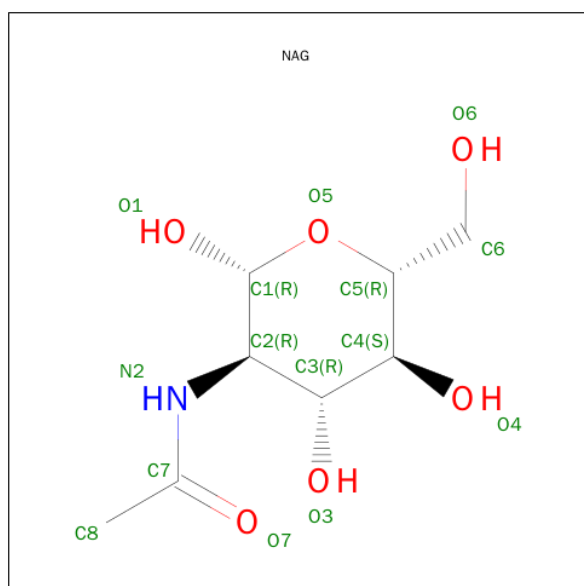
- Molecule 1 is a protein called CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	604	Total	C	N	O	S	0	0	0
			4642	2923	791	886	42			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1703	ALA	GLY	CONFLICT SEE REMARK 9	UNP P11717

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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

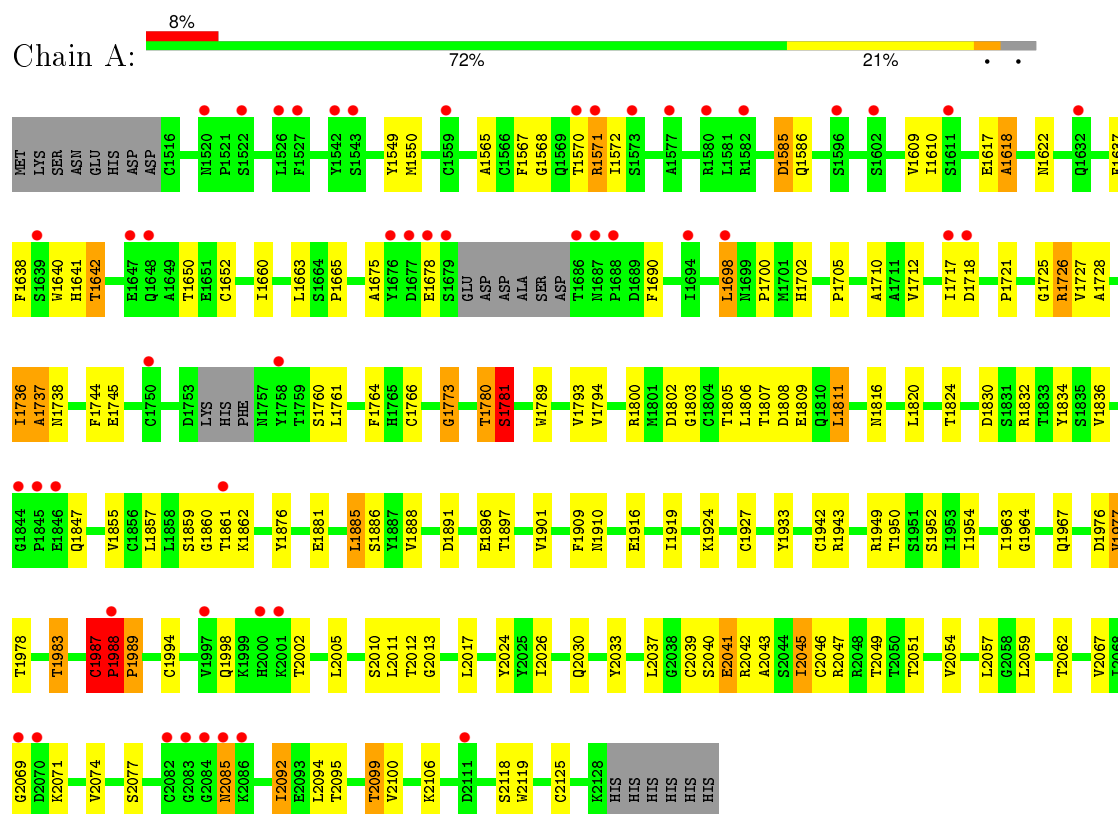
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Cl	0	0
			2	2		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.55Å 69.25Å 98.01Å 90.00° 103.25° 90.00°	Depositor
Resolution (Å)	28.46 – 2.91 28.02 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (28.46-2.91) 98.6 (28.02-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.257 , 0.304 0.265 , 0.302	Depositor DCC
R_{free} test set	1021 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	63.2	Xtriage
Anisotropy	0.472	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 68.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 19917 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4686	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NAG, CL

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	0.39	0/4751	0.56	0/6447

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	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1781	SER	Peptide
1	A	1987	CYS	Peptide
1	A	1988	PRO	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	4642	0	4494	79	0
2	A	42	0	39	0	0
3	A	2	0	0	1	0
All	All	4686	0	4533	79	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 9.

All (79) 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:1736:ILE:HG22	1:A:1737:ALA:H	0.96	1.11
1:A:1736:ILE:CG2	1:A:1737:ALA:H	1.76	0.98
1:A:1736:ILE:HG22	1:A:1737:ALA:N	1.78	0.97
1:A:1702:HIS:HB2	1:A:1924:LYS:HD3	1.54	0.89
1:A:1891:ASP:O	1:A:1949:ARG:HG3	1.71	0.88
1:A:1675:ALA:HB3	1:A:1690:PHE:HB2	1.60	0.83
1:A:1773:GLY:O	1:A:1789:TRP:NE1	2.13	0.81
1:A:1964:GLY:H	1:A:1983:THR:HG22	1.46	0.80
1:A:1885:LEU:HD12	1:A:1886:SER:N	2.02	0.74
1:A:1987:CYS:O	1:A:1989:PRO:HD3	1.88	0.72
1:A:1987:CYS:H	1:A:1988:PRO:HD3	1.54	0.71
1:A:1998:GLN:HG2	1:A:2067:VAL:HB	1.75	0.68
1:A:1808:ASP:HB3	1:A:1811:LEU:HD22	1.79	0.64
1:A:2041:GLU:O	1:A:2043:ALA:N	2.30	0.64
1:A:1964:GLY:H	1:A:1983:THR:CG2	2.11	0.64
1:A:1808:ASP:HB3	1:A:1811:LEU:CD2	2.31	0.61
1:A:2013:GLY:H	1:A:2033:TYR:HB2	1.63	0.60
1:A:1736:ILE:CG2	1:A:1737:ALA:N	2.46	0.60
1:A:1642:THR:HG22	3:A:3132:CL:CL	2.40	0.59
1:A:1806:LEU:HD11	1:A:1876:TYR:HB2	1.84	0.59
1:A:1744:PHE:HB2	1:A:1760:SER:HB3	1.86	0.57
1:A:1805:THR:HG22	1:A:1816:ASN:HA	1.88	0.56
1:A:1570:THR:O	1:A:1572:ILE:HG13	2.06	0.55
1:A:1994:CYS:HB3	1:A:2005:LEU:HB2	1.89	0.55
1:A:1954:ILE:O	1:A:1954:ILE:HG13	2.07	0.54
1:A:1927:CYS:HB3	1:A:1942:CYS:SG	2.49	0.52
1:A:1987:CYS:O	1:A:1989:PRO:CD	2.57	0.52
1:A:1820:LEU:HD23	1:A:1963:ILE:HG12	1.90	0.52
1:A:1964:GLY:N	1:A:1983:THR:HG22	2.21	0.52
1:A:1820:LEU:HD21	1:A:1983:THR:HG21	1.91	0.52
1:A:1764:PHE:HB3	1:A:1794:VAL:HG21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1705:PRO:HD2	1:A:1721:PRO:HG2	1.93	0.51
1:A:2045:ILE:HG13	1:A:2057:LEU:HB2	1.93	0.50
1:A:1780:THR:O	1:A:1781:SER:C	2.50	0.50
1:A:1641:HIS:NE2	1:A:1700:PRO:HD3	2.28	0.49
1:A:1836:VAL:HG22	1:A:1855:VAL:HG13	1.94	0.49
1:A:2059:LEU:O	1:A:2062:THR:HG22	2.12	0.49
1:A:2074:VAL:HB	1:A:2092:ILE:HG23	1.94	0.48
1:A:2094:LEU:HA	1:A:2119:TRP:O	2.13	0.48
1:A:1859:SER:O	1:A:1861:THR:N	2.46	0.48
1:A:1570:THR:O	1:A:1571:ARG:C	2.52	0.48
1:A:2011:LEU:HD23	1:A:2030:GLN:HE22	1.78	0.47
1:A:2012:THR:O	1:A:2012:THR:HG23	2.14	0.47
1:A:1663:LEU:C	1:A:1665:PRO:HD2	2.35	0.47
1:A:1717:ILE:O	1:A:1718:ASP:HB2	2.14	0.47
1:A:1952:SER:O	1:A:1978:THR:HA	2.14	0.47
1:A:1896:GLU:OE1	1:A:1943:ARG:NH2	2.42	0.47
1:A:1549:TYR:O	1:A:1565:ALA:HA	2.15	0.46
1:A:1909:PHE:HD1	1:A:1933:TYR:CD2	2.34	0.46
1:A:1876:TYR:OH	1:A:1881:GLU:HA	2.15	0.46
1:A:2041:GLU:C	1:A:2043:ALA:H	2.18	0.46
1:A:2040:SER:C	1:A:2041:GLU:O	2.54	0.45
1:A:1618:ALA:HA	1:A:1622:ASN:HD21	1.80	0.45
1:A:2047:ARG:HB2	1:A:2057:LEU:HD11	1.98	0.45
1:A:1550:MET:HB3	1:A:1565:ALA:HB2	1.99	0.44
1:A:1830:ASP:HB2	1:A:1832:ARG:NH1	2.32	0.44
1:A:2017:LEU:HG	1:A:2024:TYR:HB2	2.00	0.44
1:A:1609:VAL:HG23	1:A:1637:PHE:HA	2.00	0.44
1:A:1567:PHE:HB2	1:A:1572:ILE:HB	2.00	0.43
1:A:1712:VAL:HB	1:A:1725:GLY:HA3	2.01	0.43
1:A:1610:ILE:HA	1:A:1638:PHE:HB2	2.00	0.43
1:A:2062:THR:HG23	1:A:2077:SER:H	1.83	0.43
1:A:2094:LEU:HG	1:A:2119:TRP:HB3	2.00	0.43
1:A:1987:CYS:N	1:A:1988:PRO:HD3	2.27	0.43
1:A:2100:VAL:O	1:A:2100:VAL:HG22	2.18	0.43
1:A:1698:LEU:HB2	1:A:1710:ALA:O	2.18	0.42
1:A:1702:HIS:HB2	1:A:1924:LYS:CD	2.39	0.42
1:A:1808:ASP:OD1	1:A:1809:GLU:N	2.52	0.42
1:A:1834:TYR:CZ	1:A:1977:VAL:HG11	2.54	0.42
1:A:1950:THR:O	1:A:1976:ASP:HA	2.19	0.42
1:A:1967:GLN:HA	1:A:1967:GLN:OE1	2.20	0.42
1:A:2071:LYS:HE3	1:A:2095:THR:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1640:TRP:CD1	1:A:1642:THR:HG23	2.55	0.41
1:A:1726:ARG:N	1:A:1745:GLU:O	2.54	0.41
1:A:1710:ALA:HA	1:A:1726:ARG:HD3	2.02	0.41
1:A:2099:THR:OG1	1:A:2100:VAL:N	2.54	0.40
1:A:1800:ARG:NH1	1:A:1803:GLY:O	2.43	0.40
1:A:2106:LYS:HE3	1:A:2118:SER:HB2	2.03	0.40
1:A:1897:THR:OG1	1:A:1901:VAL:HG12	2.21	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	598/627 (95%)	521 (87%)	58 (10%)	19 (3%)	5	19

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1571	ARG
1	A	1618	ALA
1	A	1678	GLU
1	A	2041	GLU
1	A	2085	ASN
1	A	1568	GLY
1	A	1727	VAL
1	A	1736	ILE
1	A	1860	GLY
1	A	2042	ARG
1	A	2069	GLY
1	A	1728	ALA
1	A	1781	SER
1	A	1989	PRO

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Mol	Chain	Res	Type
1	A	1585	ASP
1	A	1737	ALA
1	A	1987	CYS
1	A	1773	GLY
1	A	1988	PRO

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	524/549 (95%)	482 (92%)	42 (8%)	15	39

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1585	ASP
1	A	1586	GLN
1	A	1617	GLU
1	A	1642	THR
1	A	1650	THR
1	A	1652	CYS
1	A	1660	ILE
1	A	1698	LEU
1	A	1726	ARG
1	A	1738	ASN
1	A	1761	LEU
1	A	1766	CYS
1	A	1780	THR
1	A	1793	VAL
1	A	1802	ASP
1	A	1807	THR
1	A	1811	LEU
1	A	1824	THR
1	A	1847	GLN
1	A	1857	LEU
1	A	1862	LYS

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Mol	Chain	Res	Type
1	A	1885	LEU
1	A	1888	VAL
1	A	1910	ASN
1	A	1916	GLU
1	A	1919	ILE
1	A	1977	VAL
1	A	1983	THR
1	A	2002	THR
1	A	2010	SER
1	A	2026	ILE
1	A	2037	LEU
1	A	2039	CYS
1	A	2045	ILE
1	A	2046	CYS
1	A	2049	THR
1	A	2051	THR
1	A	2054	VAL
1	A	2085	ASN
1	A	2092	ILE
1	A	2099	THR
1	A	2125	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1525	HIS
1	A	1558	ASN
1	A	1586	GLN
1	A	1589	GLN
1	A	1696	GLN
1	A	1847	GLN
1	A	1889	ASN
1	A	1910	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	NAG	A	3129	1	14,14,15	0.48	0	15,19,21	1.16	1 (6%)
2	NAG	A	3130	1	14,14,15	0.49	0	15,19,21	1.48	1 (6%)
2	NAG	A	3131	1	14,14,15	0.59	0	15,19,21	1.32	2 (13%)

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	NAG	A	3129	1	-	0/6/23/26	0/1/1/1
2	NAG	A	3130	1	-	0/6/23/26	0/1/1/1
2	NAG	A	3131	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3129	NAG	O5-C5-C6	2.62	113.03	107.35
2	A	3131	NAG	C1-O5-C5	2.69	115.66	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3131	NAG	C2-N2-C7	3.45	127.48	123.04
2	A	3130	NAG	C1-O5-C5	4.81	118.35	112.25

There are no chirality outliers.

There are no torsion outliers.

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	604/627 (96%)	0.56	49 (8%) 15 10	66, 66, 66, 66	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1845	PRO	6.5
1	A	1686	THR	5.5
1	A	2082	CYS	5.4
1	A	1679	SER	5.0
1	A	1718	ASP	4.8
1	A	2084	GLY	4.5
1	A	2083	GLY	4.4
1	A	1602	SER	4.3
1	A	2000	HIS	3.7
1	A	1580	ARG	3.6
1	A	1543	SER	3.6
1	A	1573	SER	3.5
1	A	1676	TYR	3.4
1	A	1632	GLN	3.3
1	A	1698	LEU	3.1
1	A	1861	THR	3.0
1	A	1647	GLU	3.0
1	A	1844	GLY	2.9
1	A	1750	CYS	2.9
1	A	1677	ASP	2.8
1	A	1988	PRO	2.8
1	A	1611	SER	2.8
1	A	1717	ILE	2.8
1	A	1526	LEU	2.8
1	A	1648	GLN	2.7
1	A	1596	SER	2.6
1	A	1522	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	2070	ASP	2.6
1	A	1997	VAL	2.6
1	A	1687	ASN	2.6
1	A	2001	LYS	2.5
1	A	2069	GLY	2.5
1	A	1846	GLU	2.4
1	A	2085	ASN	2.4
1	A	1520	ASN	2.3
1	A	1639	SER	2.3
1	A	1542	TYR	2.3
1	A	1559	CYS	2.2
1	A	1582	ARG	2.2
1	A	1758	TYR	2.2
1	A	1688	PRO	2.2
1	A	1694	ILE	2.2
1	A	1571	ARG	2.1
1	A	2111	ASP	2.1
1	A	2086	LYS	2.1
1	A	1577	ALA	2.1
1	A	1678	GLU	2.1
1	A	1527	PHE	2.0
1	A	1570	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	A	3131	14/15	0.85	0.25	0.76	65,65,65,65	0
2	NAG	A	3129	14/15	0.84	0.30	0.56	65,65,65,65	0
3	CL	A	3132	1/1	0.97	0.17	-2.02	65,65,65,65	0
3	CL	A	3133	1/1	0.97	0.06	-3.42	65,65,65,65	0
2	NAG	A	3130	14/15	0.86	0.44	-	65,65,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.