



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:59 am GMT

PDB ID : 1JDN
Title : Crystal Structure of Hormone Receptor
Authors : He, X.-L.; Chow, D.-C.; Martick, M.M.; Garcia, K.C.
Deposited on : 2001-06-14
Resolution : 2.90 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

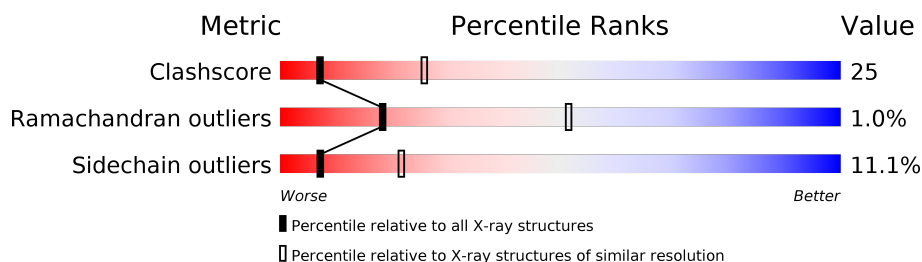
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	441	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3364 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 ATRIAL NATRIURETIC PEPTIDE CLEARANCE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3230	2048	556	610	16			

- Molecule 2 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 3 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	5	Total	C	N	O	0	0
			60	34	2	24		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

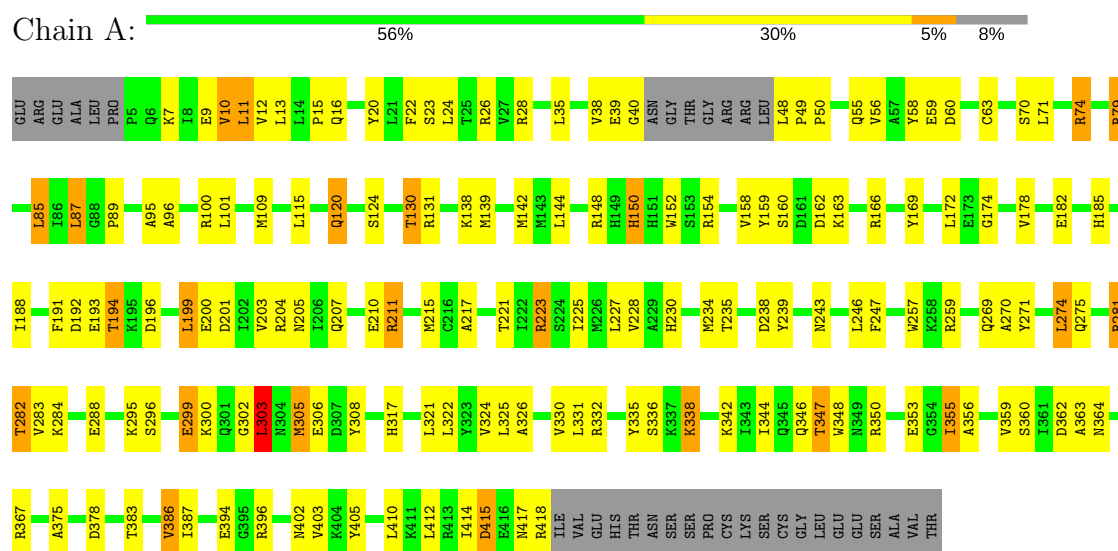
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

Note EDS was not executed.

• Molecule 1: ATRIAL NATRIURETIC PEPTIDE CLEARANCE RECEPTOR



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	217.19Å 217.19Å 130.79Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.90	Depositor
% Data completeness (in resolution range)	98.1 (50.00-2.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3364	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, CL, NDG, FUC, MAN

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	0.42	0/3303	0.65	1/4463 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	303	LEU	N-CA-C	-6.15	94.39	111.00

There are no chirality outliers.

There are no planarity outliers.

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	3230	0	3132	162	0
2	A	72	0	61	3	0
3	A	60	0	52	6	0
4	A	2	0	0	0	0
All	All	3364	0	3245	167	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 25.

All (167) 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:130:THR:HG21	1:A:347:THR:HG21	1.28	1.15
1:A:79:ARG:HH11	1:A:79:ARG:HB3	1.23	1.01
1:A:144:LEU:HD11	1:A:182:GLU:HG3	1.39	1.01
1:A:130:THR:HG21	1:A:347:THR:CG2	1.90	1.00
1:A:230:HIS:CD2	1:A:235:THR:HG21	1.97	0.98
1:A:159:TYR:HB3	1:A:172:LEU:HD12	1.45	0.96
1:A:130:THR:HG22	1:A:348:TRP:HE1	1.33	0.92
1:A:74:ARG:HG2	1:A:74:ARG:HH11	1.34	0.91
1:A:415:ASP:HB3	1:A:418:ARG:HH21	1.36	0.86
1:A:200:GLU:O	1:A:204:ARG:HG3	1.79	0.83
1:A:346:GLN:O	1:A:350:ARG:NH1	2.15	0.80
1:A:221:THR:O	1:A:225:ILE:HG12	1.83	0.78
1:A:79:ARG:HB3	1:A:79:ARG:NH1	1.98	0.78
1:A:344:ILE:O	1:A:347:THR:HG22	1.86	0.74
1:A:9:GLU:OE2	1:A:55:GLN:HG2	1.87	0.74
1:A:130:THR:HG23	1:A:344:ILE:HD12	1.71	0.73
1:A:281:ARG:HD2	1:A:386:VAL:HG11	1.71	0.73
1:A:71:LEU:HD12	1:A:101:LEU:HD13	1.72	0.71
1:A:174:GLY:O	1:A:178:VAL:HG23	1.91	0.71
1:A:305:MET:CE	1:A:305:MET:HA	2.20	0.71
1:A:10:VAL:HG22	1:A:56:VAL:HG12	1.73	0.70
1:A:79:ARG:CB	1:A:79:ARG:HH11	2.04	0.69
1:A:74:ARG:HG2	1:A:74:ARG:NH1	2.07	0.67
1:A:26:ARG:HH11	1:A:303:LEU:HD21	1.59	0.67
1:A:223:ARG:NH2	1:A:259:ARG:HG2	2.10	0.66
1:A:330:VAL:HG12	1:A:335:TYR:HB2	1.76	0.65
1:A:144:LEU:HD12	1:A:178:VAL:HG12	1.79	0.65
1:A:405:TYR:CE2	1:A:410:LEU:HB2	2.30	0.65
1:A:154:ARG:NH1	1:A:210:GLU:HG3	2.11	0.65
1:A:230:HIS:HD2	1:A:235:THR:HG21	1.56	0.64
1:A:378:ASP:HB3	1:A:383:THR:HB	1.79	0.64
1:A:275:GLN:HE21	1:A:387:ILE:HD11	1.62	0.64
1:A:162:ASP:HB2	1:A:166:ARG:HA	1.80	0.64
1:A:154:ARG:HB3	1:A:154:ARG:NH1	2.12	0.64
1:A:130:THR:CG2	1:A:348:TRP:HE1	2.10	0.63
1:A:160:SER:HA	1:A:191:PHE:O	1.98	0.63
1:A:326:ALA:O	1:A:330:VAL:HG23	1.98	0.63
1:A:23:SER:OG	1:A:26:ARG:HG2	1.99	0.62
1:A:415:ASP:CB	1:A:418:ARG:HH21	2.10	0.62
1:A:223:ARG:NH2	1:A:257:TRP:O	2.30	0.61
1:A:7:LYS:HD3	1:A:55:GLN:HB2	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:GLU:HB3	1:A:396:ARG:NH1	2.15	0.60
1:A:130:THR:CG2	1:A:344:ILE:HD12	2.30	0.60
3:A:447:NAG:H83	3:A:447:NAG:H3	1.84	0.60
1:A:415:ASP:HB3	1:A:418:ARG:NH2	2.11	0.59
1:A:335:TYR:CZ	1:A:342:LYS:HE2	2.38	0.59
1:A:230:HIS:HA	1:A:235:THR:CG2	2.33	0.58
1:A:203:VAL:HG21	1:A:228:VAL:CG1	2.33	0.58
1:A:321:LEU:O	1:A:325:LEU:HD13	2.03	0.58
3:A:448:NAG:H82	3:A:448:NAG:H3	1.85	0.58
1:A:193:GLU:OE2	1:A:217:ALA:HB1	2.03	0.58
1:A:148:ARG:HG2	1:A:148:ARG:HH21	1.68	0.58
1:A:56:VAL:HG23	1:A:58:TYR:HE1	1.69	0.58
1:A:211:ARG:HG2	1:A:414:ILE:HG23	1.86	0.58
1:A:204:ARG:HG2	1:A:204:ARG:HH11	1.70	0.57
1:A:211:ARG:HG3	1:A:238:ASP:O	2.05	0.56
1:A:284:LYS:HE2	1:A:353:GLU:OE1	2.05	0.56
1:A:162:ASP:O	1:A:163:LYS:HB2	2.05	0.56
1:A:207:GLN:HB3	1:A:234:MET:CE	2.35	0.56
1:A:74:ARG:CG	1:A:74:ARG:NH1	2.68	0.56
1:A:56:VAL:HG23	1:A:58:TYR:CE1	2.40	0.55
1:A:166:ARG:HB3	1:A:169:TYR:HB3	1.89	0.55
1:A:288:GLU:HG3	2:A:443:MAN:O2	2.06	0.54
1:A:154:ARG:HH12	1:A:210:GLU:HG3	1.71	0.54
1:A:26:ARG:NH1	1:A:303:LEU:HD21	2.22	0.54
1:A:96:ALA:O	1:A:100:ARG:HG3	2.07	0.54
1:A:305:MET:HE2	1:A:305:MET:HA	1.90	0.53
1:A:223:ARG:HH21	1:A:223:ARG:HG3	1.72	0.53
1:A:355:ILE:H	1:A:355:ILE:HD12	1.73	0.53
1:A:281:ARG:HG3	1:A:281:ARG:HH11	1.73	0.53
1:A:13:LEU:HD23	1:A:59:GLU:HB2	1.92	0.52
1:A:305:MET:O	1:A:306:GLU:HB2	2.10	0.52
1:A:355:ILE:N	1:A:355:ILE:HD12	2.25	0.52
1:A:85:LEU:CD1	1:A:87:LEU:HD13	2.40	0.52
1:A:150:HIS:HD2	1:A:152:TRP:CH2	2.28	0.51
1:A:234:MET:HB3	1:A:239:TYR:CD1	2.45	0.51
1:A:257:TRP:HB3	1:A:271:TYR:CG	2.45	0.51
1:A:20:TYR:O	1:A:26:ARG:HD2	2.09	0.51
1:A:211:ARG:NH1	1:A:239:TYR:OH	2.43	0.51
1:A:367:ARG:HG2	1:A:367:ARG:HH11	1.76	0.51
1:A:26:ARG:HH11	1:A:303:LEU:CD2	2.22	0.50
1:A:158:VAL:O	1:A:215:MET:HA	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:THR:OG1	1:A:270:ALA:HA	2.12	0.50
1:A:148:ARG:HG2	1:A:148:ARG:NH2	2.28	0.49
1:A:154:ARG:HH12	1:A:210:GLU:CG	2.25	0.48
1:A:336:SER:C	1:A:338:LYS:H	2.16	0.48
1:A:89:PRO:HD2	1:A:109:MET:HE3	1.95	0.48
1:A:363:ALA:HB2	3:A:447:NAG:H82	1.95	0.48
1:A:89:PRO:HD2	1:A:95:ALA:HA	1.95	0.48
1:A:211:ARG:HH21	1:A:418:ARG:HG3	1.77	0.48
1:A:295:LYS:O	1:A:299:GLU:HB2	2.13	0.48
1:A:70:SER:O	1:A:74:ARG:HB2	2.14	0.48
1:A:405:TYR:CZ	1:A:410:LEU:HB2	2.48	0.47
1:A:48:LEU:N	1:A:49:PRO:HD3	2.28	0.47
1:A:282:THR:O	2:A:441:NDG:H6C2	2.14	0.47
1:A:71:LEU:CD1	1:A:101:LEU:HD13	2.41	0.47
1:A:199:LEU:HD12	1:A:200:GLU:H	1.79	0.47
1:A:144:LEU:O	1:A:144:LEU:HD23	2.14	0.47
1:A:48:LEU:O	1:A:48:LEU:HD13	2.14	0.47
1:A:89:PRO:CD	1:A:109:MET:HE3	2.45	0.47
1:A:85:LEU:HD13	1:A:87:LEU:HD13	1.97	0.46
1:A:154:ARG:HA	1:A:185:HIS:O	2.16	0.46
1:A:281:ARG:NH1	2:A:441:NDG:H2	2.30	0.46
1:A:16:GLN:HB2	1:A:60:ASP:CG	2.36	0.46
1:A:246:LEU:HD13	1:A:247:PHE:CZ	2.51	0.46
1:A:355:ILE:CD1	1:A:355:ILE:H	2.29	0.46
1:A:38:VAL:HG11	1:A:324:VAL:HG21	1.97	0.45
1:A:322:LEU:HG	1:A:347:THR:OG1	2.17	0.45
1:A:188:ILE:HD12	1:A:188:ILE:N	2.31	0.45
3:A:449:MAN:H62	3:A:450:BMA:O5	2.16	0.45
1:A:288:GLU:OE2	1:A:288:GLU:N	2.49	0.45
1:A:230:HIS:CG	1:A:235:THR:HG21	2.49	0.45
1:A:336:SER:C	1:A:338:LYS:N	2.70	0.45
1:A:367:ARG:HG2	1:A:367:ARG:NH1	2.32	0.45
3:A:448:NAG:H82	3:A:448:NAG:C3	2.47	0.44
3:A:447:NAG:C8	3:A:447:NAG:H3	2.45	0.44
1:A:15:PRO:HG2	1:A:22:PHE:CE1	2.52	0.44
1:A:24:LEU:HD22	1:A:58:TYR:HB3	2.00	0.44
1:A:347:THR:HG22	1:A:348:TRP:CD1	2.52	0.44
1:A:10:VAL:CG2	1:A:56:VAL:HG12	2.44	0.44
1:A:223:ARG:NH2	1:A:223:ARG:HG3	2.32	0.44
1:A:281:ARG:HG3	1:A:281:ARG:NH1	2.33	0.44
1:A:192:ASP:OD2	1:A:194:THR:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:VAL:O	1:A:283:VAL:HG12	2.17	0.43
1:A:139:MET:O	1:A:139:MET:HE2	2.17	0.43
1:A:162:ASP:HB2	1:A:166:ARG:CA	2.48	0.43
1:A:211:ARG:HE	1:A:211:ARG:HA	1.84	0.43
1:A:11:LEU:HD12	1:A:71:LEU:HD23	2.00	0.43
1:A:199:LEU:HD12	1:A:200:GLU:N	2.34	0.43
1:A:317:HIS:CE1	1:A:355:ILE:HG13	2.53	0.43
1:A:207:GLN:HB3	1:A:234:MET:HE1	1.99	0.43
1:A:230:HIS:HA	1:A:235:THR:HG22	1.99	0.43
1:A:154:ARG:CB	1:A:154:ARG:HH11	2.32	0.43
1:A:362:ASP:OD1	1:A:364:ASN:N	2.48	0.43
1:A:120:GLN:HE21	1:A:120:GLN:HB2	1.50	0.42
1:A:130:THR:HG22	1:A:348:TRP:NE1	2.16	0.42
1:A:120:GLN:HB3	1:A:131:ARG:HH22	1.84	0.42
1:A:360:SER:O	1:A:367:ARG:HD2	2.19	0.42
1:A:295:LYS:HA	1:A:308:TYR:CD2	2.54	0.42
1:A:199:LEU:HD13	1:A:228:VAL:HG21	2.01	0.42
1:A:403:VAL:O	1:A:403:VAL:HG23	2.19	0.42
1:A:38:VAL:C	1:A:40:GLY:H	2.21	0.42
1:A:85:LEU:HD11	1:A:87:LEU:CD1	2.50	0.42
1:A:295:LYS:HG3	1:A:308:TYR:CE1	2.55	0.42
1:A:12:VAL:O	1:A:12:VAL:HG12	2.20	0.42
1:A:162:ASP:CB	1:A:166:ARG:H	2.32	0.42
1:A:299:GLU:HA	1:A:299:GLU:OE1	2.19	0.42
1:A:154:ARG:HH12	1:A:210:GLU:CD	2.23	0.41
1:A:308:TYR:CD1	1:A:308:TYR:N	2.88	0.41
1:A:227:LEU:HD23	1:A:227:LEU:HA	1.92	0.41
1:A:58:TYR:N	1:A:58:TYR:CD1	2.89	0.41
1:A:204:ARG:O	1:A:207:GLN:HG2	2.20	0.41
1:A:204:ARG:HG2	1:A:204:ARG:NH1	2.33	0.41
1:A:274:LEU:HD22	1:A:275:GLN:N	2.36	0.41
1:A:28:ARG:HG3	1:A:58:TYR:CE2	2.56	0.41
1:A:63:CYS:O	1:A:63:CYS:SG	2.79	0.41
1:A:139:MET:HE3	1:A:142:MET:HB3	2.03	0.41
1:A:144:LEU:C	1:A:144:LEU:HD23	2.41	0.41
1:A:130:THR:HG22	1:A:344:ILE:HG23	2.02	0.41
1:A:375:ALA:HB3	1:A:387:ILE:HD13	2.03	0.41
1:A:120:GLN:HB3	1:A:131:ARG:NH2	2.36	0.40
1:A:138:LYS:HA	1:A:138:LYS:HD3	1.78	0.40
1:A:163:LYS:H	1:A:166:ARG:HG3	1.86	0.40
1:A:282:THR:HG21	1:A:356:ALA:C	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:ALA:HB1	1:A:410:LEU:HD11	2.02	0.40
1:A:281:ARG:NH2	1:A:283:VAL:HG21	2.36	0.40
1:A:296:SER:O	1:A:300:LYS:HG3	2.22	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	403/441 (91%)	370 (92%)	29 (7%)	4 (1%)	18 51

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	PRO
1	A	302	GLY
1	A	124	SER
1	A	303	LEU

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	342/371 (92%)	304 (89%)	38 (11%)	7 21

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	11	LEU
1	A	35	LEU
1	A	39	GLU
1	A	74	ARG
1	A	79	ARG
1	A	85	LEU
1	A	87	LEU
1	A	115	LEU
1	A	120	GLN
1	A	130	THR
1	A	150	HIS
1	A	194	THR
1	A	196	ASP
1	A	199	LEU
1	A	201	ASP
1	A	205	ASN
1	A	211	ARG
1	A	223	ARG
1	A	243	ASN
1	A	269	GLN
1	A	274	LEU
1	A	281	ARG
1	A	282	THR
1	A	299	GLU
1	A	303	LEU
1	A	305	MET
1	A	331	LEU
1	A	332	ARG
1	A	338	LYS
1	A	347	THR
1	A	355	ILE
1	A	359	VAL
1	A	386	VAL
1	A	402	ASN
1	A	412	LEU
1	A	415	ASP
1	A	417	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	180	GLN
1	A	207	GLN
1	A	230	HIS
1	A	275	GLN
1	A	328	HIS

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 ⓘ

11 carbohydrates 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	$\# Z > 2$
2	NDG	A	440	1,2	14,14,15	1.16	1 (7%)	15,19,21	1.58	4 (26%)
2	NDG	A	441	2	14,14,15	0.59	0	15,19,21	0.91	0
2	BMA	A	442	2	11,11,12	0.97	0	13,15,17	0.82	1 (7%)
2	MAN	A	443	2	11,11,12	0.98	1 (9%)	13,15,17	1.07	1 (7%)
2	BMA	A	444	2	11,11,12	0.86	0	13,15,17	0.62	0
2	BMA	A	445	2	11,11,12	1.03	1 (9%)	13,15,17	1.07	1 (7%)
3	FUC	A	446	3	9,10,11	1.05	2 (22%)	13,14,16	2.43	3 (23%)
3	NAG	A	447	1,3	14,14,15	1.11	1 (7%)	15,19,21	1.79	4 (26%)
3	NAG	A	448	3	14,14,15	0.76	0	15,19,21	0.89	0
3	MAN	A	449	3	11,11,12	0.86	0	13,15,17	1.04	1 (7%)
3	BMA	A	450	3	11,11,12	0.62	0	13,15,17	0.44	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
2	NDG	A	440	1,2	-	0/6/23/26	0/1/1/1
2	NDG	A	441	2	-	0/6/23/26	0/1/1/1
2	BMA	A	442	2	-	0/2/19/22	1/1/1/1
2	MAN	A	443	2	-	0/2/19/22	0/1/1/1
2	BMA	A	444	2	-	0/2/19/22	0/1/1/1
2	BMA	A	445	2	-	0/2/19/22	1/1/1/1
3	FUC	A	446	3	-	0/0/17/20	0/1/1/1
3	NAG	A	447	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	448	3	-	1/6/23/26	0/1/1/1
3	MAN	A	449	3	-	0/2/19/22	0/1/1/1
3	BMA	A	450	3	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	447	NAG	C1-C2	-2.66	1.48	1.52
2	A	443	MAN	C2-C3	2.02	1.55	1.52
3	A	446	FUC	C2-C3	2.05	1.55	1.52
2	A	445	BMA	C2-C3	2.18	1.55	1.52
3	A	446	FUC	C1-C2	2.21	1.57	1.52
2	A	440	NDG	C1-C2	3.70	1.57	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	440	NDG	C3-C4-C5	-3.38	104.26	110.22
3	A	447	NAG	O5-C1-C2	-3.06	107.21	111.47
3	A	447	NAG	O4-C4-C3	-2.58	104.74	110.36
2	A	442	BMA	C2-C3-C4	-2.29	106.89	110.88
2	A	440	NDG	C2-N2-C7	-2.29	119.61	122.94
3	A	446	FUC	C2-C3-C4	2.05	114.45	110.88
3	A	447	NAG	C4-C3-C2	2.08	114.06	111.02
2	A	440	NDG	C1-O-C5	2.22	115.23	112.17
3	A	449	MAN	C1-C2-C3	2.66	113.02	109.65
2	A	443	MAN	C1-C2-C3	2.79	113.18	109.65
3	A	446	FUC	O5-C1-C2	2.97	115.44	110.79
2	A	445	BMA	C1-O5-C5	3.04	116.35	112.17
2	A	440	NDG	O-C1-C2	3.23	115.97	111.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	447	NAG	C3-C4-C5	4.24	117.69	110.22
3	A	446	FUC	C1-C2-C3	7.47	119.12	109.65

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	448	NAG	O7-C7-N2-C2

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	445	BMA	C1-C2-C3-C4-C5-O5
2	A	442	BMA	C1-C2-C3-C4-C5-O5

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	441	NDG	2	0
2	A	443	MAN	1	0
3	A	447	NAG	3	0
3	A	448	NAG	2	0
3	A	449	MAN	1	0
3	A	450	BMA	1	0

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.