



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:52 AM GMT

PDB ID : 2J4G
Title : BACTEROIDES THETA IOTAOMICRON GH84 O-GLCNACASE IN COM-
PLEX WITH N-BUTYL-THIAZOLINE INHIBITOR
Authors : Dennis, R.J.; Davies, G.J.
Deposited on : 2006-08-31
Resolution : 2.25 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

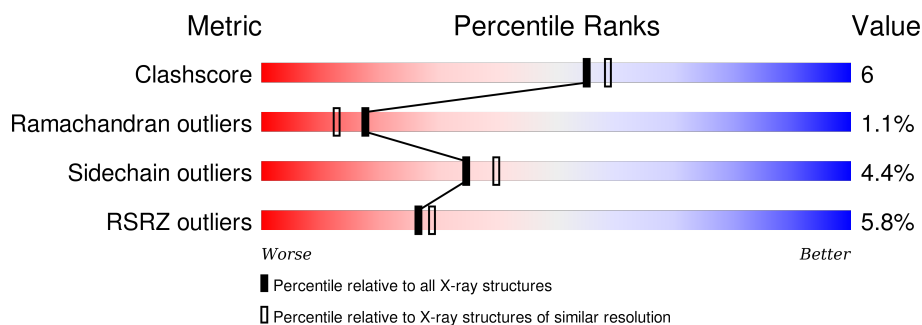
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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	715	
1	B	715	

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	ACT	B	1591	-	-	-	X

2 Entry composition [i](#)

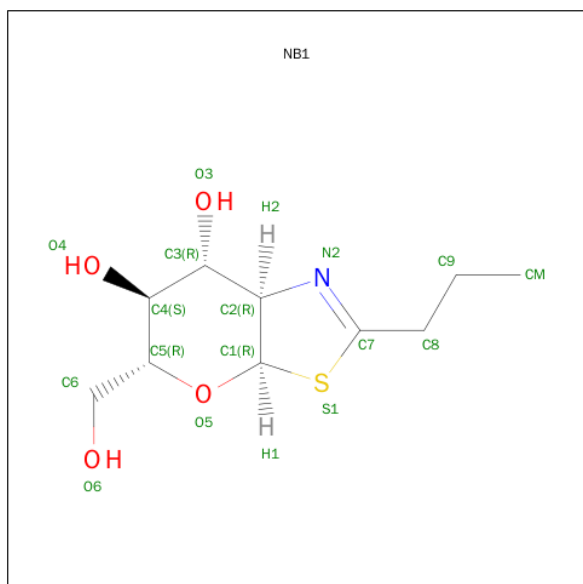
There are 5 unique types of molecules in this entry. The entry contains 10075 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HYALURONOGLUCOSAMINIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	586	Total	C	N	O	S	0	1	0
			4759	3040	806	897	16			
1	B	580	Total	C	N	O	S	0	0	0
			4706	3009	794	887	16			

- Molecule 2 is (3AR,5R,6S,7R,7AR)-5-(HYDROXYMETHYL)-2-PROPYL-5,6,7,7A-TE TRAHYDRO-3AH-PYRANO[3,2-D][1,3]THIAZOLE-6,7-DIOL (three-letter code: NB1) (formula: C₁₀H₁₇NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			16	10	1	4	1		
2	B	1	Total	C	N	O	S	0	0
			16	10	1	4	1		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	280	Total 280	O 280	0	0
5	B	278	Total 278	O 278	0	0

ARG	LEU
VAL	LYS
LEU	GLN
ILE	LYS
SER	GLU
PRO	SER
ALA	ARG
ASN	LEU
GLU	SER
VAL	ALA
VAL	GLY
LYS	LEU
TRP	GLN
ALA	LYS
ALA	ALA
GLY	PRO
ASN	VAL
SER	LYS
SER	PHE
VAL	VAL
GLU	ARG
ILE	PHE
GLU	THR
LEU	ASN
ASP	VAL
ALA	SER
ILE	ASP
TYR	GLU
PRO	GLU
GLY	GLN
GLU	GLN
ASN	VAL
ILE	TYR
GLN	LEU
ILE	ARG
ASN	GLN
PHE	PHE
GLY	VAL
LYS	LEU
ASP	THR
ALA	ILE
PRO	GLU
CYS	LYS
THR	LYS
TRP	LYS
GLY	ARG
ARG	LEU
LEU	GLU
GLU	ILE
ILE	SER
SER	THR
THR	ASP
GLY	LYS
LYS	GLU
TRP	THR
LYS	LYS
THR	VAL
VAL	ASP
ASP	

LEU
LYS
GLN
LYS
GLU
SER
ARG
LEU
SER
ALA
GLY
LEU
GLN
LYS
ALA
PRO
VAL
LYS
PHE
VAL
ARG
PHE
THR
ASN
VAL
SER
ASP
GLU
GLU
GLN
GLN
VAL
TYR
LEU
ARG
GLN
PHE
VAL
LEU
THR
ILE
GLU
LYS
LYS

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	185.11Å 51.71Å 172.78Å 90.00° 100.11° 90.00°	Depositor
Resolution (Å)	169.03 – 2.25 39.38 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (169.03-2.25) 99.6 (39.38-2.25)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.06 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.220 , 0.284 0.221 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	4 of 76925 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10075	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 63.56 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 9.4882e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: GOL, NB1, ACT

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	0.70	0/4886	0.75	2/6626 (0.0%)
1	B	0.71	0/4827	0.76	6/6544 (0.1%)
All	All	0.70	0/9713	0.76	8/13170 (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	A	0	3
1	B	0	4
All	All	0	7

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	6	GLN	N-CA-C	9.37	136.29	111.00
1	B	364	LYS	N-CA-C	-8.90	86.96	111.00
1	A	5	LEU	C-N-CA	7.28	139.89	121.70
1	B	6	GLN	N-CA-CB	-5.63	100.47	110.60
1	B	342	VAL	N-CA-C	-5.57	95.97	111.00
1	B	341	PRO	N-CA-C	5.35	126.00	112.10
1	A	104	LEU	CA-CB-CG	-5.32	103.08	115.30
1	B	291	GLY	N-CA-C	-5.18	100.15	113.10

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	PRO	Peptide
1	A	341	PRO	Peptide
1	A	5	LEU	Peptide
1	B	174	PRO	Peptide
1	B	341	PRO	Peptide
1	B	363	ALA	Peptide
1	B	5	LEU	Peptide

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	4759	0	4642	58	0
1	B	4706	0	4583	61	0
2	A	16	0	17	0	0
2	B	16	0	17	0	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
5	A	280	0	0	9	0
5	B	278	0	0	10	0
All	All	10075	0	9281	119	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 6.

All (119) 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:245:SER:HB3	5:A:2121:HOH:O	1.66	0.94
1:B:532:LYS:O	1:B:536:GLN:HG3	1.85	0.77
1:B:570:ALA:O	1:B:574:LYS:HE3	1.89	0.72
1:A:277:MET:CE	1:A:307:ILE:HG23	2.20	0.71
1:B:441:MET:HB2	5:B:2222:HOH:O	1.95	0.67
1:A:6:GLN:H	1:A:7:PRO:C	1.99	0.65
1:A:62:LYS:HD3	5:A:2036:HOH:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:ASN:HD22	1:B:292:ASN:H	1.45	0.64
1:A:245:SER:CB	5:A:2121:HOH:O	2.34	0.64
1:B:6:GLN:HA	1:B:7:PRO:C	2.18	0.62
1:A:277:MET:HE2	1:A:307:ILE:HG23	1.80	0.61
1:B:557:ALA:HB1	1:B:561:ILE:HB	1.81	0.61
1:A:83:LEU:HD22	1:A:121:ILE:HD12	1.81	0.60
1:A:46:SER:O	1:A:47:GLY:O	2.21	0.59
1:A:245:SER:CA	5:A:2121:HOH:O	2.50	0.58
1:B:81:TYR:CE2	1:B:123:ASP:HB3	2.40	0.57
1:B:515:MET:HG3	1:B:527:LYS:HB3	1.87	0.57
1:B:539:PHE:O	1:B:543:GLN:HG2	2.04	0.56
1:A:7:PRO:HB3	1:A:389:SER:HA	1.87	0.56
1:B:416:GLU:HB3	1:B:474:ARG:NH2	2.21	0.56
1:B:292:ASN:N	1:B:292:ASN:HD22	2.04	0.56
1:A:562:LYS:HB3	1:A:563:PRO:HD3	1.88	0.55
1:B:86:ASN:HA	1:B:118:GLU:HG3	1.89	0.55
1:B:306:GLN:HE21	1:B:306:GLN:HA	1.71	0.55
1:A:21:LEU:HD12	1:A:22:PRO:HD2	1.89	0.55
1:B:74:ILE:HD11	1:B:93:ALA:HB1	1.89	0.54
1:B:308:MET:HA	1:B:335:TYR:O	2.08	0.54
1:A:81:TYR:CE2	1:A:123:ASP:HB3	2.43	0.54
1:A:308:MET:HA	1:A:335:TYR:O	2.08	0.54
1:A:296:THR:O	1:A:300:LYS:HB2	2.09	0.53
1:B:21:LEU:HD13	1:B:111:LEU:HD13	1.91	0.52
1:B:46:SER:O	1:B:47:GLY:O	2.28	0.52
1:A:70:TYR:OH	1:A:89:GLU:OE2	2.27	0.52
1:B:458:LYS:HE2	5:B:2226:HOH:O	2.09	0.51
1:B:306:GLN:NE2	1:B:306:GLN:HA	2.26	0.51
1:A:47:GLY:HA3	1:A:48:LYS:HD2	1.93	0.51
1:B:81:TYR:CZ	1:B:123:ASP:HB3	2.45	0.51
1:A:17:LYS:NZ	1:A:87:GLU:HG2	2.25	0.51
1:B:515:MET:CG	1:B:527:LYS:HB3	2.40	0.51
1:B:277:MET:HG2	1:B:301:LEU:HD11	1.93	0.51
1:A:144:GLN:HG2	5:A:2068:HOH:O	2.10	0.51
1:A:41:LEU:HB2	1:A:104:LEU:HD21	1.93	0.49
1:A:445:PRO:HD2	5:A:2225:HOH:O	2.12	0.49
1:B:240:PHE:HA	1:B:278:CYS:HB3	1.95	0.49
1:A:454:PHE:C	1:A:456:GLU:H	2.15	0.49
1:A:98:ARG:HG3	1:A:199:GLU:HB3	1.94	0.49
1:B:364:LYS:CB	5:B:2179:HOH:O	2.60	0.49
1:A:131:GLY:HA2	1:A:158:MET:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:MET:HG3	1:A:527:LYS:HB3	1.95	0.49
1:A:141:TRP:CZ3	1:A:149:GLN:HG3	2.48	0.48
1:A:557:ALA:HB1	1:A:561:ILE:HB	1.94	0.48
1:B:458:LYS:O	1:B:459:ASN:HB2	2.14	0.48
1:A:132:VAL:HG22	1:A:371:THR:HG23	1.97	0.47
1:A:462:LYS:O	1:A:466:GLU:HG2	2.15	0.47
1:B:364:LYS:HB3	5:B:2179:HOH:O	2.14	0.47
1:A:527:LYS:HD3	1:A:527:LYS:HA	1.66	0.47
1:B:301:LEU:HD12	1:B:307:ILE:HD11	1.97	0.46
1:B:57:ILE:HG12	1:B:90:ILE:HB	1.98	0.46
1:B:22:PRO:HG2	1:B:57:ILE:HD11	1.96	0.46
1:A:81:TYR:CZ	1:A:123:ASP:HB3	2.50	0.46
1:B:536:GLN:OE1	5:B:2255:HOH:O	2.20	0.46
1:A:214:TRP:CD2	1:A:253:LYS:HB3	2.51	0.45
1:A:408[B]:ARG:NE	5:A:2209:HOH:O	2.43	0.45
1:A:514:LYS:NZ	5:A:2252:HOH:O	2.50	0.45
1:B:527:LYS:N	1:B:527:LYS:HD2	2.31	0.44
1:A:240:PHE:HA	1:A:278:CYS:HB3	1.99	0.44
1:A:306:GLN:HA	1:A:306:GLN:HE21	1.82	0.44
1:B:543:GLN:NE2	5:B:2257:HOH:O	2.50	0.44
1:A:37:ALA:HB1	1:A:104:LEU:HD13	1.98	0.44
1:B:338:TRP:CH2	1:B:355:VAL:HG13	2.52	0.44
1:B:262:ASP:HA	1:B:266:ALA:HB3	1.99	0.44
1:B:533:ALA:O	1:B:537:GLN:HG3	2.18	0.44
1:A:176:TRP:HE3	1:A:206:ILE:HD11	1.83	0.44
1:A:262:ASP:HA	1:A:266:ALA:HB3	2.00	0.44
1:A:178:LEU:O	1:A:225:LYS:NZ	2.44	0.44
1:A:174:PRO:HD2	5:A:2082:HOH:O	2.19	0.43
1:B:364:LYS:HZ3	1:B:364:LYS:HB2	1.84	0.43
1:A:238:ALA:HA	1:A:276:VAL:O	2.19	0.43
1:B:261:ILE:O	1:B:265:PHE:HB3	2.18	0.43
1:A:6:GLN:OE1	1:A:6:GLN:HA	2.19	0.43
1:B:302:ASN:HB3	5:B:2146:HOH:O	2.18	0.43
1:A:168:ASP:HA	1:A:169:PRO:HD2	1.82	0.43
1:B:364:LYS:HZ2	1:B:364:LYS:HA	1.84	0.43
1:A:41:LEU:HB2	1:A:104:LEU:CD2	2.49	0.43
1:A:340:PHE:HA	1:A:341:PRO:HA	1.63	0.42
1:B:501:GLN:HA	1:B:501:GLN:OE1	2.19	0.42
1:B:102:TYR:CE1	1:B:157:LYS:HA	2.53	0.42
1:B:193:ALA:O	1:B:197:GLU:HG3	2.18	0.42
1:B:7:PRO:HB3	1:B:389:SER:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:ARG:HG3	1:B:199:GLU:HB3	2.01	0.42
1:B:77:HIS:HB3	5:B:2030:HOH:O	2.20	0.42
1:A:17:LYS:HZ2	1:A:87:GLU:HG2	1.85	0.42
1:B:214:TRP:CD2	1:B:253:LYS:HB3	2.54	0.42
1:A:475:MET:HG2	1:A:502:PHE:CZ	2.55	0.42
1:A:6:GLN:HG3	1:A:385:TYR:OH	2.20	0.42
1:B:292:ASN:N	1:B:292:ASN:ND2	2.68	0.42
1:A:21:LEU:HD22	1:A:111:LEU:HD11	2.00	0.42
1:B:271:ASP:N	1:B:271:ASP:OD1	2.52	0.42
1:B:22:PRO:HB2	1:B:25:TYR:HB3	2.01	0.42
1:A:86:ASN:HA	1:A:118:GLU:HG3	2.02	0.41
1:A:147:LEU:HD22	1:A:194:VAL:HG21	2.02	0.41
1:A:271:ASP:OD1	1:A:271:ASP:N	2.53	0.41
1:B:364:LYS:HB2	5:B:2179:HOH:O	2.20	0.41
1:B:412:PRO:HD2	1:B:487:GLU:OE2	2.20	0.41
1:B:449:ARG:HD2	1:B:464:ASP:OD2	2.19	0.41
1:A:176:TRP:CE3	1:A:206:ILE:HD11	2.56	0.41
1:A:306:GLN:HA	1:A:306:GLN:NE2	2.36	0.41
1:A:341:PRO:HD2	1:A:373:PRO:HA	2.03	0.41
1:B:70:TYR:OH	1:B:89:GLU:OE1	2.38	0.41
1:B:458:LYS:HB2	1:B:458:LYS:HE3	1.90	0.41
1:B:130:ARG:HG2	1:B:391:ALA:HB1	2.03	0.41
1:B:289:PRO:HD2	1:B:290:ASN:H	1.86	0.41
1:B:204:TRP:CE3	1:B:229:MET:HG3	2.55	0.41
1:B:284:LYS:HB3	1:B:312:ASP:HA	2.02	0.40
1:B:451:LEU:HD21	1:B:567:ARG:HD2	2.03	0.40
1:A:6:GLN:HA	1:A:7:PRO:HA	1.93	0.40
1:B:4:SER:HA	5:B:2001:HOH:O	2.21	0.40
1:A:576:PHE:C	1:A:578:GLN:H	2.25	0.40
1:B:216:LYS:HB2	1:B:216:LYS:HE3	1.81	0.40

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	585/715 (82%)	553 (94%)	24 (4%)	8 (1%)	14	9
1	B	572/715 (80%)	544 (95%)	23 (4%)	5 (1%)	21	18
All	All	1157/1430 (81%)	1097 (95%)	47 (4%)	13 (1%)	17	13

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	47	GLY
1	A	342	VAL
1	B	47	GLY
1	A	455	LYS
1	A	518	GLY
1	B	363	ALA
1	B	518	GLY
1	B	453	ALA
1	A	459	ASN
1	A	53	LYS
1	A	456	GLU
1	B	459	ASN

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	513/629 (82%)	491 (96%)	22 (4%)	35	41
1	B	507/629 (81%)	483 (95%)	24 (5%)	32	36
All	All	1020/1258 (81%)	974 (96%)	46 (4%)	35	38

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	PRO
1	A	20	ASP
1	A	45	LEU
1	A	70	TYR
1	A	87	GLU
1	A	104	LEU
1	A	113	ASP
1	A	120	GLU
1	A	178	LEU
1	A	221	LEU
1	A	277	MET
1	A	323	ILE
1	A	341	PRO
1	A	342	VAL
1	A	371	THR
1	A	408[A]	ARG
1	A	408[B]	ARG
1	A	454	PHE
1	A	458	LYS
1	A	469	GLN
1	A	474	ARG
1	A	574	LYS
1	B	11	GLN
1	B	18	THR
1	B	26	GLN
1	B	27	LEU
1	B	32	GLU
1	B	49	GLN
1	B	65	LYS
1	B	72	ARG
1	B	113	ASP
1	B	178	LEU
1	B	213	LYS
1	B	216	LYS
1	B	285	SER
1	B	292	ASN
1	B	323	ILE
1	B	342	VAL
1	B	364	LYS
1	B	371	THR
1	B	416	GLU
1	B	467	THR
1	B	469	GLN

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Mol	Chain	Res	Type
1	B	527	LYS
1	B	574	LYS
1	B	581	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	198	ASN
1	A	231	GLN
1	A	254	GLN
1	A	274	GLN
1	A	306	GLN
1	A	349	HIS
1	A	547	GLN
1	B	273	ASN
1	B	292	ASN
1	B	306	GLN

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 ⓘ

6 ligands 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	NB1	A	1590	-	14,17,17	2.45	2 (14%)	11,24,24	1.42	2 (18%)
3	ACT	A	1591	-	1,3,3	1.55	0	0,3,3	0.00	-
4	GOL	A	1719	-	5,5,5	0.34	0	5,5,5	1.08	0
2	NB1	B	1590	-	14,17,17	2.88	2 (14%)	11,24,24	1.31	2 (18%)
3	ACT	B	1591	-	1,3,3	1.59	0	0,3,3	0.00	-
4	GOL	B	1719	-	5,5,5	0.55	0	5,5,5	0.27	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	NB1	A	1590	-	-	0/5/33/33	0/2/2/2
3	ACT	A	1591	-	-	0/0/0/0	0/0/0/0
4	GOL	A	1719	-	-	0/4/4/4	0/0/0/0
2	NB1	B	1590	-	-	0/5/33/33	0/2/2/2
3	ACT	B	1591	-	-	0/0/0/0	0/0/0/0
4	GOL	B	1719	-	-	0/4/4/4	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1590	NB1	C7-S1	-3.40	1.70	1.77
2	B	1590	NB1	C7-S1	-2.74	1.71	1.77
2	A	1590	NB1	C7-N2	7.98	1.34	1.27
2	B	1590	NB1	C7-N2	10.12	1.35	1.27

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1590	NB1	O4-C4-C3	-2.81	104.01	110.34
2	A	1590	NB1	O4-C4-C3	-2.54	104.61	110.34
2	B	1590	NB1	C1-O5-C5	2.82	118.11	112.74
2	A	1590	NB1	C1-O5-C5	3.31	119.05	112.74

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	586/715 (81%)	0.15	35 (5%)	25 27	13, 27, 63, 77	0
1	B	580/715 (81%)	0.18	33 (5%)	27 30	13, 26, 63, 78	0
All	All	1166/1430 (81%)	0.17	68 (5%)	26 29	13, 27, 63, 78	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	52	LYS	8.2
1	A	457	GLY	6.2
1	A	54	GLY	5.4
1	B	24	VAL	5.1
1	B	19	ILE	3.9
1	B	113	ASP	3.7
1	A	16	ASN	3.6
1	B	47	GLY	3.6
1	B	22	PRO	3.6
1	B	582	ALA	3.6
1	B	454	PHE	3.6
1	B	518	GLY	3.5
1	B	49	GLN	3.5
1	B	17	LYS	3.4
1	B	21	LEU	3.4
1	B	581	ASN	3.3
1	A	51	SER	3.2
1	A	455	LYS	3.2
1	A	113	ASP	3.2
1	A	19	ILE	3.2
1	A	459	ASN	3.2
1	A	575	PHE	3.1
1	A	539	PHE	3.1
1	A	18	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	54	GLY	3.0
1	B	583	HIS	3.0
1	B	291	GLY	3.0
1	A	589	ASP	2.9
1	A	582	ALA	2.9
1	A	17	LYS	2.9
1	A	23	ALA	2.9
1	B	26	GLN	2.8
1	A	24	VAL	2.8
1	A	115	LYS	2.7
1	A	456	GLU	2.7
1	B	580	PHE	2.7
1	B	578	GLN	2.7
1	B	16	ASN	2.6
1	A	454	PHE	2.6
1	A	578	GLN	2.6
1	A	518	GLY	2.6
1	B	587	THR	2.6
1	B	33	ALA	2.6
1	B	457	GLY	2.6
1	B	46	SER	2.6
1	B	290	ASN	2.6
1	A	580	PHE	2.5
1	B	63	GLY	2.5
1	A	583	HIS	2.5
1	A	581	ASN	2.5
1	B	15	GLN	2.5
1	B	539	PHE	2.5
1	A	31	GLU	2.3
1	A	15	GLN	2.3
1	A	14	VAL	2.3
1	A	584	LEU	2.2
1	B	133	VAL	2.2
1	A	47	GLY	2.2
1	A	50	SER	2.2
1	B	25	TYR	2.1
1	A	53	LYS	2.1
1	A	55	MET	2.1
1	A	519	ARG	2.1
1	A	21	LEU	2.1
1	B	18	THR	2.0
1	B	459	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	88	LYS	2.0
1	B	451	LEU	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(Å ²)	Q<0.9
3	ACT	B	1591	4/4	0.86	0.19	2.51	52,52,52,52	0
4	GOL	B	1719	6/6	0.93	0.13	0.62	35,37,42,44	0
2	NB1	B	1590	16/16	0.96	0.14	0.09	15,19,20,20	0
4	GOL	A	1719	6/6	0.91	0.13	-0.11	25,31,32,36	0
2	NB1	A	1590	16/16	0.98	0.14	-0.25	14,18,19,21	0
3	ACT	A	1591	4/4	0.94	0.10	-0.79	56,56,56,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.