



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:18 PM GMT

PDB ID : 3TIA
Title : Crystal structure of 1957 pandemic H2N2 neuraminidase complexed with laninamivir
Authors : Vavricka, C.J.; Li, Q.; Wu, Y.; Qi, J.; Wang, M.; Liu, Y.; Gao, F.; Liu, J.; Feng, E.; He, J.; Wang, J.; Liu, H.; Jiang, H.; Gao, G.F.
Deposited on : 2011-08-20
Resolution : 1.80 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

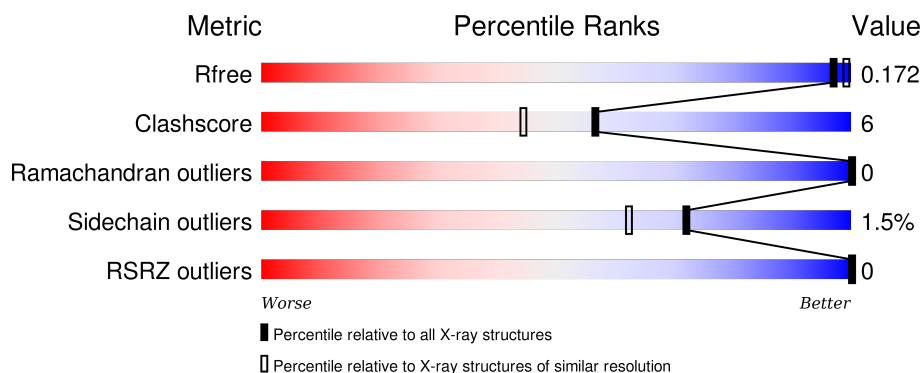
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	469	
1	B	469	
1	C	469	
1	D	469	

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
4	NAG	A	603	-	-	-	X
4	NAG	B	603	-	-	-	X
4	NAG	D	603	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 14414 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 Neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	1	0
			3023	1866	543	591	23			
1	B	388	Total	C	N	O	S	0	0	0
			3017	1863	542	589	23			
1	C	388	Total	C	N	O	S	0	1	0
			3025	1867	544	591	23			
1	D	388	Total	C	N	O	S	0	0	0
			3017	1863	542	589	23			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

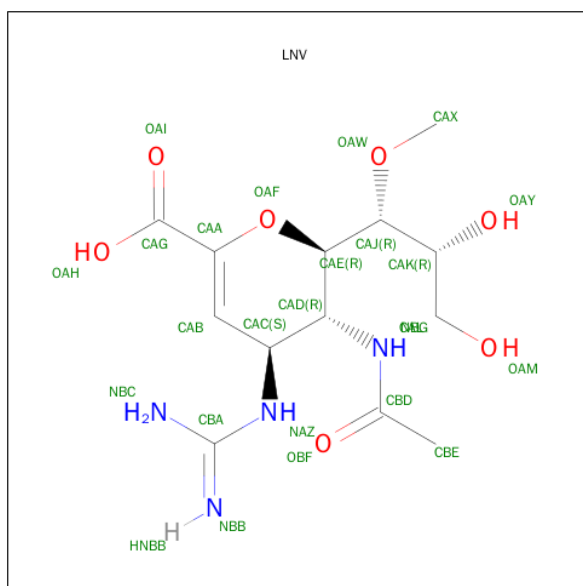
- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	C	2	Total	C	N	O	0	0
			28	16	2	10		
3	D	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is a polymer of unknown type called SUGAR (4-MER).

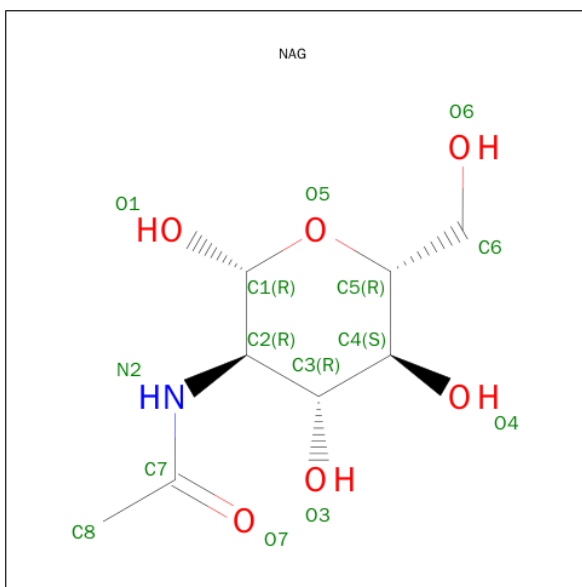
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	4	Total	C	N	O	0	0
			50	28	2	20		
4	B	4	Total	C	N	O	0	0
			50	28	2	20		
4	C	4	Total	C	N	O	0	0
			50	28	2	20		
4	D	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 5 is 5-(ACETYLAMINO)-2,6-ANHYDRO-4-CARBAMIMIDAMIDO-3,4,5-TRIDEOXY-7-O-METHYL-D-GLYCERO-D-GALACTO-NON-2-ENONIC ACID (three-letter code: LNV) (formula: $C_{13}H_{22}N_4O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			24	13	4	7		
5	B	1	Total	C	N	O	0	0
			24	13	4	7		
5	C	1	Total	C	N	O	0	0
			24	13	4	7		
5	D	1	Total	C	N	O	0	0
			24	13	4	7		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

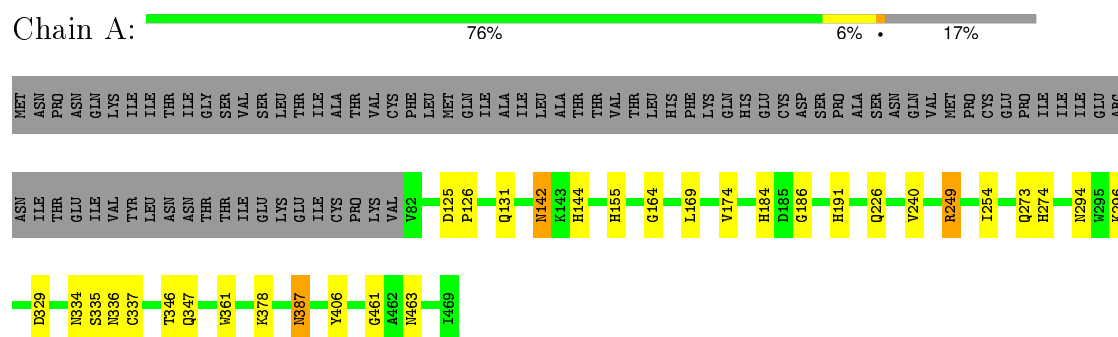
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	475	Total	O	0	0
			475	475		
7	B	494	Total	O	0	0
			494	494		
7	C	488	Total	O	0	0
			488	488		
7	D	477	Total	O	0	0
			477	477		

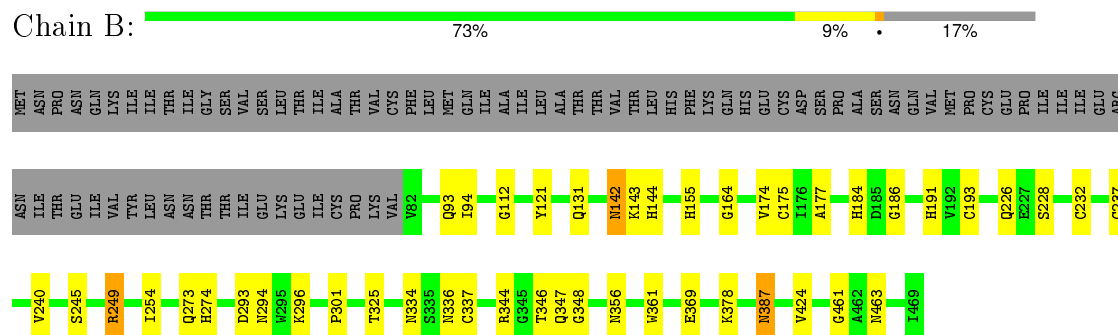
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($RSRZ > 2$). 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.

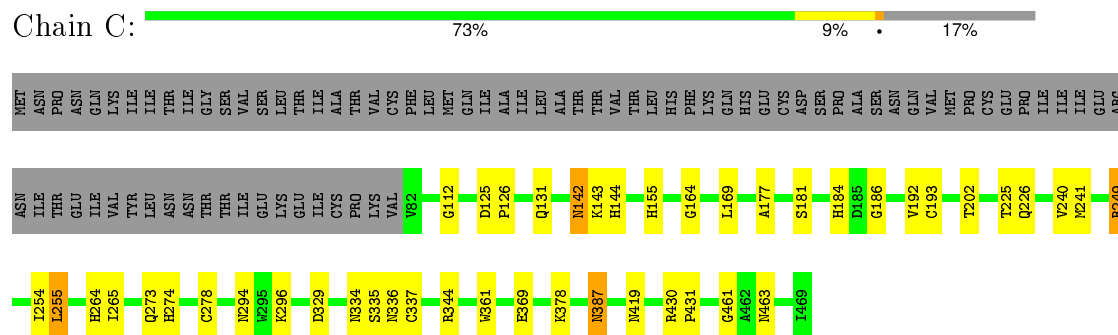
• Molecule 1: Neuraminidase



• Molecule 1: Neuraminidase



• Molecule 1: Neuraminidase



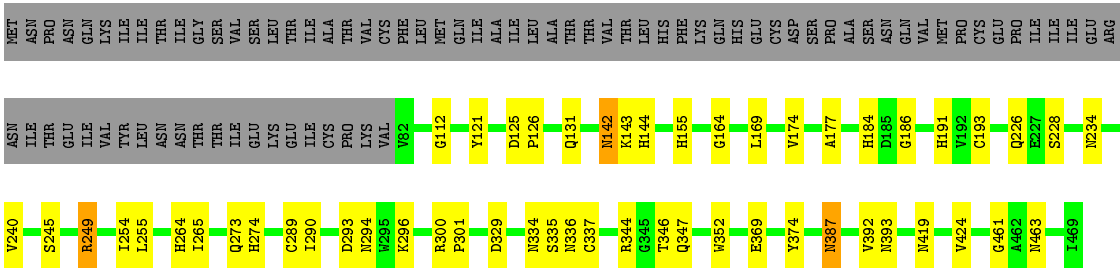
• Molecule 1: Neuraminidase

Chain D:

71%

11%

17%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.93Å 140.31Å 89.89Å 90.00° 101.54° 90.00°	Depositor
Resolution (Å)	42.99 – 1.80 42.99 – 1.80	Depositor EDS
% Data completeness (in resolution range)	94.4 (42.99-1.80) 99.6 (42.99-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.52 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.152 , 0.170 0.154 , 0.172	Depositor DCC
R_{free} test set	10137 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.0	EDS
Estimated twinning fraction	0.449 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 201286 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14414	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LNV, CA, BMA, NAG, 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	0.29	0/3096	0.51	0/4203
1	B	0.30	0/3090	0.51	0/4195
1	C	0.30	0/3098	0.51	0/4206
1	D	0.30	0/3090	0.52	0/4195
All	All	0.29	0/12374	0.51	0/16799

There are no bond length outliers.

There are no bond angle outliers.

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	3023	0	2836	29	0
1	B	3017	0	2832	39	0
1	C	3025	0	2837	45	0
1	D	3017	0	2832	45	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	28	0	25	1	0
3	D	28	0	25	0	0
4	A	50	0	43	0	0
4	B	50	0	43	0	0
4	C	50	0	43	0	0
4	D	50	0	43	0	0
5	A	24	0	18	1	0
5	B	24	0	19	0	0
5	C	24	0	18	0	0
5	D	24	0	18	0	0
6	B	14	0	13	0	0
7	A	475	0	0	2	0
7	B	494	0	0	5	0
7	C	488	0	0	2	0
7	D	477	0	0	3	0
All	All	14414	0	11670	148	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 (148) 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:B:226:GLN:HE21	1:B:240:VAL:H	1.22	0.84
1:C:226:GLN:HE21	1:C:240:VAL:H	1.25	0.83
1:C:334:ASN:HA	1:C:387:ASN:HD21	1.44	0.82
1:A:144:HIS:HE2	1:D:463:ASN:H	1.23	0.81
1:A:463:ASN:H	1:B:144:HIS:HE2	1.28	0.81
1:C:463:ASN:H	1:D:144:HIS:HE2	1.25	0.81
1:D:226:GLN:HE21	1:D:240:VAL:H	1.29	0.80
1:B:463:ASN:H	1:C:144:HIS:HE2	1.27	0.80
1:D:249:ARG:HH11	1:D:249:ARG:HB2	1.46	0.80
1:D:334:ASN:HA	1:D:387:ASN:HD21	1.47	0.78
1:A:226:GLN:HE21	1:A:240:VAL:H	1.28	0.78
1:B:334:ASN:HA	1:B:387:ASN:HD21	1.50	0.77
1:C:344:ARG:HH12	1:C:369:GLU:CD	1.86	0.76
1:C:274:HIS:HD2	1:C:294:ASN:H	1.34	0.76
1:A:334:ASN:HA	1:A:387:ASN:HD21	1.49	0.75
1:C:249:ARG:HB2	1:C:249:ARG:HH11	1.52	0.75
1:D:344:ARG:HH12	1:D:369:GLU:CD	1.90	0.74
1:B:274:HIS:HD2	1:B:294:ASN:H	1.36	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:HIS:HD2	1:A:294:ASN:H	1.40	0.70
1:B:249:ARG:HB2	1:B:249:ARG:HH11	1.55	0.70
1:D:249:ARG:NH1	1:D:249:ARG:HB2	2.06	0.69
1:D:184:HIS:HD2	1:D:186:GLY:H	1.41	0.68
1:C:249:ARG:HB2	1:C:249:ARG:NH1	2.08	0.68
1:D:184:HIS:CD2	1:D:186:GLY:H	2.13	0.67
1:C:274:HIS:CD2	1:C:294:ASN:H	2.13	0.67
1:B:344:ARG:HH12	1:B:369:GLU:CD	1.98	0.67
1:C:142:ASN:HD22	1:C:144:HIS:H	1.43	0.67
1:A:184:HIS:CD2	1:A:186:GLY:H	2.12	0.67
1:D:142:ASN:HD22	1:D:144:HIS:H	1.43	0.66
1:D:274:HIS:HD2	1:D:294:ASN:H	1.42	0.66
1:A:249:ARG:HH11	1:A:249:ARG:HB2	1.61	0.66
1:C:240:VAL:HG21	1:C:278:CYS:HB2	1.77	0.64
1:A:142:ASN:HD22	1:A:144:HIS:H	1.45	0.64
1:A:184:HIS:HD2	1:A:186:GLY:H	1.45	0.64
1:C:131:GLN:HE21	1:C:164:GLY:H	1.45	0.64
1:A:249:ARG:HB2	1:A:249:ARG:NH1	2.13	0.63
1:C:131:GLN:NE2	1:C:164:GLY:H	1.97	0.63
1:D:131:GLN:HE21	1:D:164:GLY:H	1.47	0.62
1:C:184:HIS:CD2	1:C:186:GLY:H	2.18	0.62
1:A:274:HIS:CD2	1:A:294:ASN:H	2.18	0.62
1:B:184:HIS:CD2	1:B:186:GLY:H	2.18	0.62
1:B:249:ARG:HB2	1:B:249:ARG:NH1	2.14	0.61
1:B:142:ASN:HD22	1:B:144:HIS:H	1.48	0.61
1:A:131:GLN:NE2	1:A:164:GLY:H	1.99	0.61
1:B:184:HIS:HD2	1:B:186:GLY:H	1.50	0.60
1:A:131:GLN:HE21	1:A:164:GLY:H	1.47	0.60
1:D:255:LEU:HD22	1:D:265:ILE:HG12	1.84	0.59
1:D:131:GLN:NE2	1:D:164:GLY:H	2.00	0.59
1:D:142:ASN:ND2	1:D:144:HIS:H	2.01	0.58
1:D:274:HIS:CD2	1:D:294:ASN:H	2.22	0.58
1:D:273:GLN:HE22	1:D:296:LYS:NZ	2.02	0.57
3:C:602:NAG:H2	7:C:1823:HOH:O	2.05	0.57
1:C:142:ASN:ND2	1:C:144:HIS:H	2.02	0.56
1:C:273:GLN:HE22	1:C:296:LYS:NZ	2.04	0.56
1:C:181:SER:HB3	1:C:192:VAL:CG2	2.36	0.55
1:C:184:HIS:HD2	1:C:186:GLY:H	1.52	0.55
1:B:131:GLN:HE21	1:B:164:GLY:H	1.53	0.55
1:A:142:ASN:ND2	1:A:144:HIS:H	2.05	0.54
1:B:142:ASN:ND2	1:B:144:HIS:H	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:VAL:HG21	1:C:278:CYS:SG	2.48	0.53
1:B:274:HIS:CD2	1:B:294:ASN:H	2.21	0.53
1:D:336:ASN:O	1:D:337:CYS:HB2	2.09	0.53
1:C:344:ARG:NH1	1:C:369:GLU:CD	2.59	0.52
1:C:461:GLY:HA3	1:D:155:HIS:CE1	2.43	0.52
1:B:273:GLN:HE22	1:B:296:LYS:NZ	2.06	0.52
1:A:249:ARG:HD2	7:A:1847:HOH:O	2.09	0.52
1:B:131:GLN:NE2	1:B:164:GLY:H	2.06	0.52
1:C:240:VAL:HG21	1:C:278:CYS:CB	2.40	0.51
1:A:461:GLY:HA3	1:B:155:HIS:CE1	2.45	0.51
1:B:249:ARG:HD3	7:B:1527:HOH:O	2.09	0.51
1:A:406:TYR:OH	5:A:801:LNV:CAA	2.60	0.50
1:B:93:GLN:HE22	1:B:356:ASN:HD21	1.59	0.49
1:B:94:ILE:HG22	7:B:1177:HOH:O	2.12	0.49
1:A:249:ARG:HD3	7:A:926:HOH:O	2.12	0.49
1:B:461:GLY:HA3	1:C:155:HIS:CE1	2.48	0.48
1:C:192:VAL:O	1:C:192:VAL:HG23	2.13	0.48
1:B:361:TRP:CZ2	1:B:378:LYS:HE3	2.49	0.47
1:C:334:ASN:HA	1:C:387:ASN:ND2	2.21	0.47
1:D:334:ASN:HA	1:D:387:ASN:ND2	2.25	0.47
1:A:336:ASN:O	1:A:337:CYS:HB2	2.15	0.47
1:A:155:HIS:CE1	1:D:461:GLY:HA3	2.49	0.47
1:D:234:ASN:ND2	7:D:1285:HOH:O	2.42	0.47
1:A:169:LEU:HD11	1:D:112:GLY:HA3	1.95	0.47
1:B:336:ASN:O	1:B:337:CYS:HB2	2.15	0.47
1:D:264:HIS:HE1	7:D:1389:HOH:O	1.97	0.47
1:B:226:GLN:NE2	1:B:240:VAL:H	2.02	0.47
1:B:142:ASN:HD22	1:B:143:LYS:N	2.13	0.46
7:B:583:HOH:O	1:C:202:THR:HG22	2.16	0.46
1:C:177:ALA:HB2	1:C:193:CYS:HB3	1.97	0.45
1:C:264:HIS:HE1	7:C:1057:HOH:O	2.00	0.45
1:B:174:VAL:HG11	1:B:191:HIS:CD2	2.51	0.45
1:A:273:GLN:HE22	1:A:296:LYS:NZ	2.14	0.45
1:D:273:GLN:HE22	1:D:296:LYS:HZ3	1.65	0.45
1:D:142:ASN:C	1:D:142:ASN:HD22	2.20	0.45
1:B:121:TYR:CG	1:B:228:SER:HA	2.52	0.45
1:B:334:ASN:HA	1:B:387:ASN:ND2	2.27	0.44
1:D:289:CYS:C	1:D:290:ILE:HD12	2.37	0.44
1:D:142:ASN:HD22	1:D:143:LYS:N	2.15	0.44
1:C:387:ASN:HA	1:C:387:ASN:HD22	1.62	0.44
1:D:184:HIS:HD2	1:D:186:GLY:N	2.13	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:344:ARG:HD2	7:D:1908:HOH:O	2.18	0.43
1:D:352:TRP:HE1	1:D:374:TYR:HH	1.66	0.43
1:C:335:SER:H	1:C:387:ASN:ND2	2.16	0.43
1:B:232:CYS:HA	1:B:237:CYS:HA	2.00	0.43
1:C:336:ASN:O	1:C:337:CYS:HB2	2.18	0.43
1:B:254:ILE:N	1:B:254:ILE:HD12	2.34	0.43
1:D:245:SER:O	1:D:274:HIS:HE1	2.02	0.43
1:C:181:SER:HB3	1:C:192:VAL:HG22	1.99	0.43
1:C:142:ASN:HD22	1:C:143:LYS:N	2.16	0.43
1:D:335:SER:H	1:D:387:ASN:ND2	2.15	0.43
1:D:293:ASP:HB2	1:D:301:PRO:HG3	2.01	0.43
1:C:142:ASN:C	1:C:142:ASN:HD22	2.22	0.43
1:C:240:VAL:CG2	1:C:278:CYS:HB2	2.44	0.43
1:A:254:ILE:N	1:A:254:ILE:HD12	2.34	0.42
1:C:254:ILE:N	1:C:254:ILE:HD12	2.34	0.42
1:C:255:LEU:HD12	1:C:265:ILE:HG23	2.01	0.42
1:C:112:GLY:HA3	1:D:169:LEU:HD11	2.00	0.42
1:D:177:ALA:HB2	1:D:193:CYS:HB3	2.02	0.42
1:A:387:ASN:HD22	1:A:387:ASN:HA	1.57	0.42
1:D:300:ARG:HA	1:D:301:PRO:HD3	1.96	0.42
1:C:226:GLN:CG	1:C:240:VAL:HG22	2.49	0.42
1:A:361:TRP:CZ2	1:A:378:LYS:HE3	2.55	0.42
1:D:254:ILE:N	1:D:254:ILE:HD12	2.35	0.42
1:D:387:ASN:HA	1:D:387:ASN:HD22	1.64	0.42
1:D:344:ARG:NH1	1:D:369:GLU:CD	2.66	0.42
1:A:335:SER:H	1:A:387:ASN:ND2	2.18	0.42
1:C:125:ASP:HB2	1:C:126:PRO:CD	2.50	0.41
1:B:346:THR:O	1:B:347:GLN:HB2	2.20	0.41
1:B:325:THR:O	1:B:348:GLY:HA2	2.21	0.41
1:C:225:THR:HB	1:C:241:MET:HG2	2.03	0.41
1:D:125:ASP:HB2	1:D:126:PRO:CD	2.50	0.41
1:B:142:ASN:HD22	1:B:142:ASN:C	2.24	0.41
1:D:121:TYR:CG	1:D:228:SER:HA	2.56	0.41
1:B:112:GLY:HA3	1:C:169:LEU:HD11	2.03	0.41
1:B:293:ASP:HB2	1:B:301:PRO:HG3	2.03	0.41
1:D:174:VAL:HG11	1:D:191:HIS:CD2	2.56	0.41
1:C:430:ARG:HB3	1:C:431:PRO:HA	2.03	0.41
1:C:226:GLN:HG2	1:C:240:VAL:HG22	2.02	0.41
1:B:245:SER:O	1:B:274:HIS:HE1	2.04	0.41
1:D:392:VAL:HG22	1:D:393:ASN:N	2.35	0.41
1:A:174:VAL:HG11	1:A:191:HIS:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:361:TRP:CZ2	1:C:378:LYS:HE3	2.55	0.41
1:B:249:ARG:HD2	7:B:963:HOH:O	2.20	0.40
1:D:346:THR:O	1:D:347:GLN:HB2	2.21	0.40
1:A:125:ASP:HB2	1:A:126:PRO:CD	2.51	0.40
1:B:177:ALA:HB2	1:B:193:CYS:HB3	2.04	0.40
1:A:346:THR:O	1:A:347:GLN:HB2	2.21	0.40
1:B:175:CYS:HB2	7:B:490:HOH:O	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	387/469 (82%)	370 (96%)	17 (4%)	0	100	100
1	B	386/469 (82%)	372 (96%)	14 (4%)	0	100	100
1	C	387/469 (82%)	371 (96%)	16 (4%)	0	100	100
1	D	386/469 (82%)	371 (96%)	15 (4%)	0	100	100
All	All	1546/1876 (82%)	1484 (96%)	62 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	339/414 (82%)	335 (99%)	4 (1%)	78	71
1	B	338/414 (82%)	334 (99%)	4 (1%)	78	71
1	C	339/414 (82%)	333 (98%)	6 (2%)	66	54
1	D	338/414 (82%)	332 (98%)	6 (2%)	66	54
All	All	1354/1656 (82%)	1334 (98%)	20 (2%)	72	62

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	142	ASN
1	A	249	ARG
1	A	329	ASP
1	A	387	ASN
1	B	142	ASN
1	B	249	ARG
1	B	387	ASN
1	B	424	VAL
1	C	142	ASN
1	C	249	ARG
1	C	255	LEU
1	C	329	ASP
1	C	387	ASN
1	C	419	ASN
1	D	142	ASN
1	D	249	ARG
1	D	329	ASP
1	D	387	ASN
1	D	419	ASN
1	D	424	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	104	ASN
1	A	131	GLN
1	A	142	ASN
1	A	161	ASN
1	A	184	HIS
1	A	226	GLN

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Mol	Chain	Res	Type
1	A	273	GLN
1	A	274	HIS
1	A	334	ASN
1	A	356	ASN
1	A	387	ASN
1	A	393	ASN
1	A	419	ASN
1	A	432	GLN
1	A	465	ASN
1	B	86	ASN
1	B	93	GLN
1	B	104	ASN
1	B	131	GLN
1	B	142	ASN
1	B	161	ASN
1	B	184	HIS
1	B	226	GLN
1	B	273	GLN
1	B	274	HIS
1	B	334	ASN
1	B	356	ASN
1	B	387	ASN
1	B	393	ASN
1	B	419	ASN
1	B	432	GLN
1	C	104	ASN
1	C	131	GLN
1	C	142	ASN
1	C	161	ASN
1	C	184	HIS
1	C	226	GLN
1	C	273	GLN
1	C	274	HIS
1	C	334	ASN
1	C	356	ASN
1	C	387	ASN
1	C	393	ASN
1	C	419	ASN
1	C	432	GLN
1	C	465	ASN
1	D	86	ASN
1	D	93	GLN

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Mol	Chain	Res	Type
1	D	104	ASN
1	D	131	GLN
1	D	142	ASN
1	D	161	ASN
1	D	184	HIS
1	D	226	GLN
1	D	273	GLN
1	D	274	HIS
1	D	334	ASN
1	D	356	ASN
1	D	387	ASN
1	D	393	ASN
1	D	419	ASN
1	D	432	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 ⓘ

22 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	$\# Z > 2$
3	NAG	A	601	1,3	14,14,15	0.57	0	15,19,21	0.70	0
3	NAG	A	602	3	14,14,15	0.51	0	15,19,21	0.91	1 (6%)
4	NAG	A	603	1,4	14,14,15	0.46	0	15,19,21	1.10	2 (13%)
4	NAG	A	604	4	14,14,15	0.47	0	15,19,21	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BMA	A	605	4	11,11,12	0.51	0	14,15,17	0.69	0
4	MAN	A	606	4	11,11,12	0.64	0	14,15,17	0.63	0
4	NAG	B	603	1,4	14,14,15	0.54	0	15,19,21	0.96	1 (6%)
4	NAG	B	604	4	14,14,15	0.45	0	15,19,21	0.72	0
4	BMA	B	605	4	11,11,12	0.54	0	14,15,17	0.61	0
4	MAN	B	606	4	11,11,12	0.53	0	14,15,17	0.65	0
3	NAG	C	601	1,3	14,14,15	0.55	0	15,19,21	0.71	0
3	NAG	C	602	3	14,14,15	0.53	0	15,19,21	0.62	0
4	NAG	C	603	1,4	14,14,15	0.46	0	15,19,21	1.23	2 (13%)
4	NAG	C	604	4	14,14,15	0.42	0	15,19,21	0.91	0
4	BMA	C	605	4	11,11,12	0.59	0	14,15,17	0.67	0
4	MAN	C	606	4	11,11,12	0.56	0	14,15,17	0.73	0
3	NAG	D	601	1,3	14,14,15	0.55	0	15,19,21	0.67	0
3	NAG	D	602	3	14,14,15	0.55	0	15,19,21	0.90	1 (6%)
4	NAG	D	603	1,4	14,14,15	0.48	0	15,19,21	0.88	1 (6%)
4	NAG	D	604	4	14,14,15	0.45	0	15,19,21	0.68	0
4	BMA	D	605	4	11,11,12	0.61	0	14,15,17	0.64	0
4	MAN	D	606	4	11,11,12	0.52	0	14,15,17	0.67	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
3	NAG	A	601	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	602	3	-	0/6/23/26	0/1/1/1
4	NAG	A	603	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	604	4	-	0/6/23/26	0/1/1/1
4	BMA	A	605	4	-	0/2/19/22	0/1/1/1
4	MAN	A	606	4	-	0/2/19/22	0/1/1/1
4	NAG	B	603	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	604	4	-	0/6/23/26	0/1/1/1
4	BMA	B	605	4	-	0/2/19/22	0/1/1/1
4	MAN	B	606	4	-	0/2/19/22	0/1/1/1
3	NAG	C	601	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	602	3	-	0/6/23/26	0/1/1/1
4	NAG	C	603	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	604	4	-	0/6/23/26	0/1/1/1
4	BMA	C	605	4	-	0/2/19/22	0/1/1/1
4	MAN	C	606	4	-	0/2/19/22	0/1/1/1
3	NAG	D	601	1,3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	602	3	-	0/6/23/26	0/1/1/1
4	NAG	D	603	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	604	4	-	0/6/23/26	0/1/1/1
4	BMA	D	605	4	-	0/2/19/22	0/1/1/1
4	MAN	D	606	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	603	NAG	C2-N2-C7	-2.96	119.24	123.04
4	A	603	NAG	C2-N2-C7	-2.68	119.60	123.04
4	B	603	NAG	C2-N2-C7	-2.66	119.62	123.04
3	D	602	NAG	C1-O5-C5	-2.29	109.34	112.25
3	A	602	NAG	C2-N2-C7	-2.16	120.27	123.04
4	D	603	NAG	C2-N2-C7	-2.15	120.28	123.04
4	A	603	NAG	C1-O5-C5	2.81	115.82	112.25
4	C	603	NAG	C1-O5-C5	3.19	116.30	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	602	NAG	1	0

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 4 are 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	LVN	A	801	-	18,24,24	3.99	9 (50%)	13,33,33	2.48	6 (46%)
6	NAG	B	601	1	14,14,15	0.55	0	15,19,21	0.89	1 (6%)
5	LVN	B	801	-	18,24,24	4.09	8 (44%)	13,33,33	2.84	5 (38%)
5	LVN	C	801	-	18,24,24	4.10	8 (44%)	13,33,33	2.59	5 (38%)
5	LVN	D	801	-	18,24,24	4.12	9 (50%)	13,33,33	3.02	4 (30%)

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	LVN	A	801	-	-	0/18/40/40	0/1/1/1
6	NAG	B	601	1	-	0/6/23/26	0/1/1/1
5	LVN	B	801	-	-	0/18/40/40	0/1/1/1
5	LVN	C	801	-	-	0/18/40/40	0/1/1/1
5	LVN	D	801	-	-	0/18/40/40	0/1/1/1

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	801	LVN	OAY-CAK	-6.11	1.29	1.43
5	A	801	LVN	OAY-CAK	-5.64	1.30	1.43
5	C	801	LVN	OAY-CAK	-5.45	1.31	1.43
5	C	801	LVN	OAF-CAE	-5.07	1.36	1.46
5	B	801	LVN	OAF-CAE	-4.77	1.37	1.46
5	B	801	LVN	OAY-CAK	-4.66	1.32	1.43
5	D	801	LVN	OAF-CAE	-3.89	1.38	1.46
5	B	801	LVN	CAD-NBG	-3.71	1.39	1.45
5	A	801	LVN	OAF-CAE	-3.44	1.39	1.46
5	B	801	LVN	OBF-CBD	-3.38	1.15	1.23
5	B	801	LVN	OAW-CAJ	-3.34	1.33	1.42
5	C	801	LVN	CAD-NBG	-3.31	1.40	1.45
5	D	801	LVN	OBF-CBD	-3.24	1.15	1.23
5	C	801	LVN	OBF-CBD	-3.21	1.15	1.23
5	A	801	LVN	OBF-CBD	-3.14	1.15	1.23
5	C	801	LVN	OAW-CAJ	-3.07	1.34	1.42
5	A	801	LVN	CAD-NBG	-2.84	1.41	1.45
5	D	801	LVN	CAD-NBG	-2.74	1.41	1.45
5	A	801	LVN	OAW-CAJ	-2.71	1.35	1.42
5	D	801	LVN	OAW-CAX	-2.65	1.32	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	801	LNV	OAW-CAX	-2.63	1.32	1.42
5	B	801	LNV	OAW-CAX	-2.35	1.33	1.42
5	D	801	LNV	OAW-CAJ	-2.33	1.36	1.42
5	C	801	LNV	OAW-CAX	-2.21	1.34	1.42
5	C	801	LNV	CAC-CAB	2.01	1.53	1.50
5	B	801	LNV	CAC-CAB	2.04	1.53	1.50
5	D	801	LNV	CAC-CAD	2.10	1.56	1.54
5	A	801	LNV	CAC-CAB	2.31	1.53	1.50
5	A	801	LNV	CAE-CAD	2.83	1.57	1.53
5	D	801	LNV	CAC-CAB	3.35	1.55	1.50
5	A	801	LNV	CAB-CAA	13.70	1.51	1.32
5	C	801	LNV	CAB-CAA	13.85	1.51	1.32
5	B	801	LNV	CAB-CAA	13.96	1.51	1.32
5	D	801	LNV	CAB-CAA	13.99	1.51	1.32

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	801	LNV	OAF-CAA-CAB	-4.00	118.32	124.12
5	D	801	LNV	OAF-CAA-CAB	-3.65	118.82	124.12
5	A	801	LNV	OAF-CAA-CAB	-3.48	119.07	124.12
5	C	801	LNV	OAF-CAA-CAB	-3.12	119.59	124.12
5	A	801	LNV	CBE-CBD-NBG	-3.12	110.14	116.11
6	B	601	NAG	C1-O5-C5	-2.41	109.19	112.25
5	B	801	LNV	OAY-CAK-CAL	2.06	114.02	109.22
5	A	801	LNV	CAE-CAD-NBG	2.09	114.71	111.07
5	C	801	LNV	CAX-OAW-CAJ	2.14	120.64	114.59
5	C	801	LNV	OAY-CAK-CAJ	2.25	114.33	109.10
5	B	801	LNV	CAX-OAW-CAJ	2.26	120.98	114.59
5	A	801	LNV	CAX-OAW-CAJ	2.31	121.11	114.59
5	A	801	LNV	OAY-CAK-CAJ	2.34	114.54	109.10
5	C	801	LNV	OBF-CBD-NBG	2.43	126.81	121.86
5	B	801	LNV	CAE-CAD-NBG	2.53	115.49	111.07
5	D	801	LNV	CAX-OAW-CAJ	3.02	123.11	114.59
5	D	801	LNV	CAE-CAD-NBG	3.61	117.36	111.07
5	A	801	LNV	CAE-OAF-CAA	5.80	123.77	114.79
5	C	801	LNV	CAE-OAF-CAA	6.85	125.39	114.79
5	B	801	LNV	CAE-OAF-CAA	8.30	127.63	114.79
5	D	801	LNV	CAE-OAF-CAA	8.74	128.32	114.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	801	LNV	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	388/469 (82%)	-0.74	0 100 100	4, 11, 23, 53	0
1	B	388/469 (82%)	-0.68	0 100 100	3, 11, 24, 55	0
1	C	388/469 (82%)	-0.72	0 100 100	4, 11, 24, 54	0
1	D	388/469 (82%)	-0.71	0 100 100	4, 11, 24, 50	0
All	All	1552/1876 (82%)	-0.71	0 100 100	3, 11, 24, 55	0

There are no RSRZ outliers to report.

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](#)

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
4	NAG	A	603	14/15	0.93	0.09	4.58	9,15,34,38	0
4	NAG	B	603	14/15	0.95	0.08	4.16	10,12,28,29	0
4	NAG	D	603	14/15	0.95	0.08	3.14	9,12,31,33	0
4	NAG	C	603	14/15	0.95	0.07	1.71	8,15,34,36	0
4	BMA	D	605	11/12	0.96	0.06	-	9,14,18,19	0
3	NAG	D	602	14/15	0.76	0.24	-	41,61,77,78	0
4	BMA	B	605	11/12	0.96	0.07	-	10,13,16,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	D	604	14/15	0.97	0.06	-	9,12,16,17	0
4	MAN	C	606	11/12	0.97	0.06	-	17,19,22,22	0
3	NAG	A	602	14/15	0.76	0.26	-	66,74,89,91	0
4	MAN	B	606	11/12	0.95	0.07	-	15,17,21,22	0
3	NAG	D	601	14/15	0.90	0.11	-	24,34,39,43	0
3	NAG	A	601	14/15	0.92	0.09	-	22,31,40,45	0
3	NAG	C	602	14/15	0.69	0.32	-	75,81,97,98	0
4	NAG	A	604	14/15	0.97	0.06	-	12,15,19,20	0
4	MAN	D	606	11/12	0.95	0.08	-	15,16,21,24	0
4	BMA	A	605	11/12	0.96	0.06	-	12,17,22,22	0
4	NAG	B	604	14/15	0.98	0.06	-	10,12,16,18	0
3	NAG	C	601	14/15	0.92	0.10	-	18,29,41,46	0
4	NAG	C	604	14/15	0.97	0.06	-	12,14,21,22	0
4	BMA	C	605	11/12	0.97	0.06	-	11,15,19,21	0
4	MAN	A	606	11/12	0.94	0.08	-	16,20,23,25	0

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	CA	D	501	1/1	1.00	0.09	0.54	10,10,10,10	0
2	CA	B	501	1/1	0.99	0.09	0.41	9,9,9,9	0
2	CA	A	501	1/1	1.00	0.08	0.21	9,9,9,9	0
2	CA	C	501	1/1	1.00	0.08	0.21	9,9,9,9	0
5	LNV	C	801	24/24	0.97	0.07	0.06	6,8,13,14	0
5	LNV	A	801	24/24	0.97	0.07	0.04	6,9,13,14	0
5	LNV	D	801	24/24	0.97	0.06	-0.14	5,8,11,13	0
5	LNV	B	801	24/24	0.98	0.06	-0.99	5,8,12,13	0
6	NAG	B	601	14/15	0.83	0.16	-	38,50,60,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.