



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2017 – 03:35 AM EDT

PDB ID : 3BEQ
Title : Neuraminidase of A/Brevig Mission/1/1918 H1N1 strain
Authors : Xu, X.; Zhu, X.; Wilson, I.A.
Deposited on : unknown
Resolution : 1.64 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) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

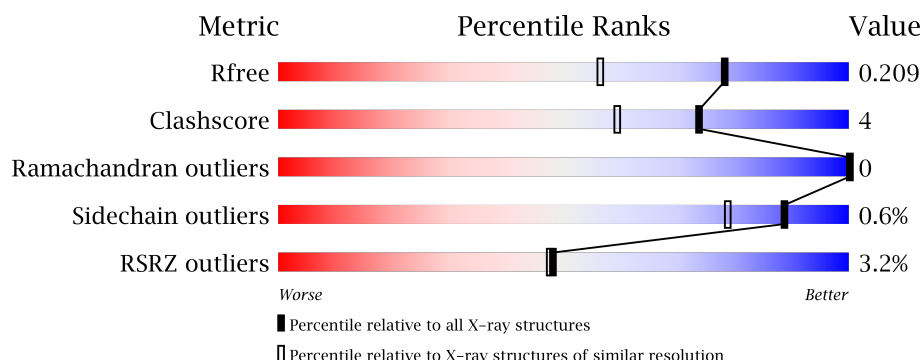
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.64 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}	100719	2211 (1.66-1.62)
Clashscore	112137	2356 (1.66-1.62)
Ramachandran outliers	110173	2315 (1.66-1.62)
Sidechain outliers	110143	2315 (1.66-1.62)
RSRZ outliers	101464	2219 (1.66-1.62)

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	385	<div> <div>2%</div> <div>92%</div> <div>8%</div> </div>
1	B	385	<div> <div>4%</div> <div>92%</div> <div>8%</div> </div>

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	ACT	A	3000	-	-	-	X
4	ACT	A	3002	-	-	X	X
4	ACT	B	3004	-	-	X	X
5	PO4	A	1000	-	-	-	X
6	GOL	A	1003	-	-	-	X
6	GOL	A	1005	-	-	-	X
6	GOL	A	1009	-	-	-	X
6	GOL	A	3004	-	-	-	X
6	GOL	A	3005	-	-	-	X
6	GOL	B	1002	-	-	-	X
6	GOL	B	1004	-	-	-	X
6	GOL	B	1006	-	-	-	X
6	GOL	B	1007	-	-	-	X
6	GOL	B	1008	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 6873 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	385	Total	C	N	O	S	0	4	0
			2983	1867	512	581	23			
1	B	385	Total	C	N	O	S	0	3	0
			2980	1865	512	580	23			

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

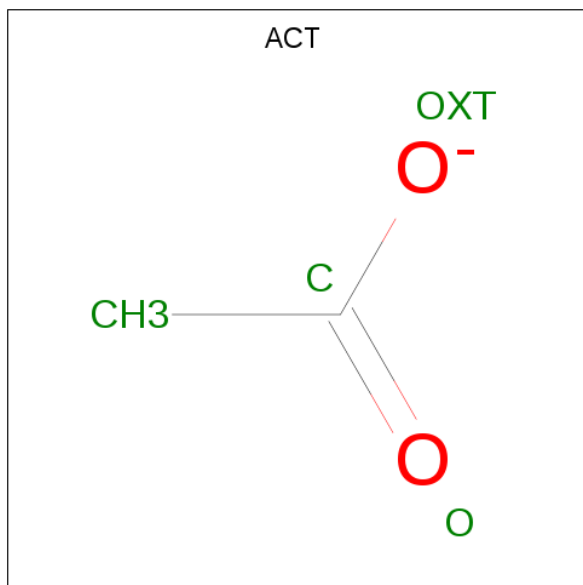


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Ca 2 2	0	0
3	A	3	Total Ca 3 3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



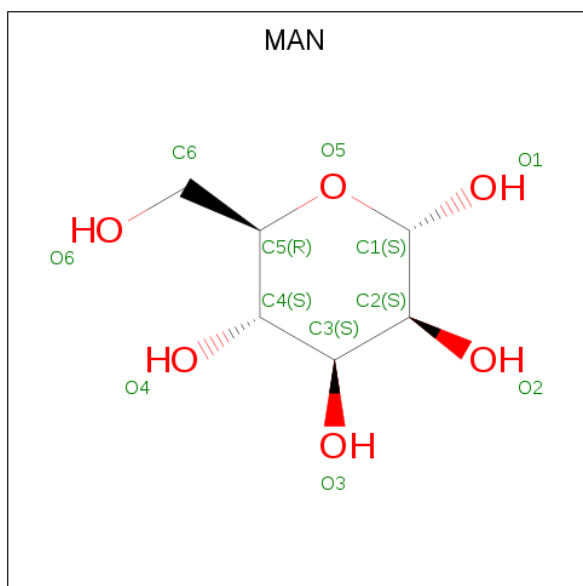
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 7 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			11	6	5		
7	B	1	Total	C	O	0	0
			11	6	5		

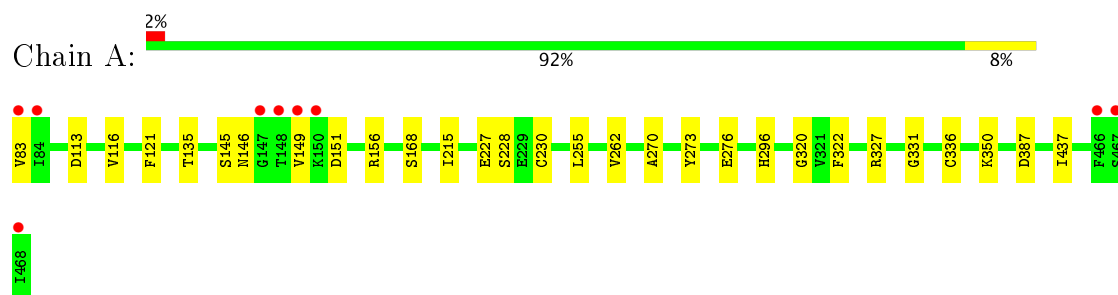
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	395	Total 397	O 397	0	2
8	B	359	Total 359	O 359	0	0

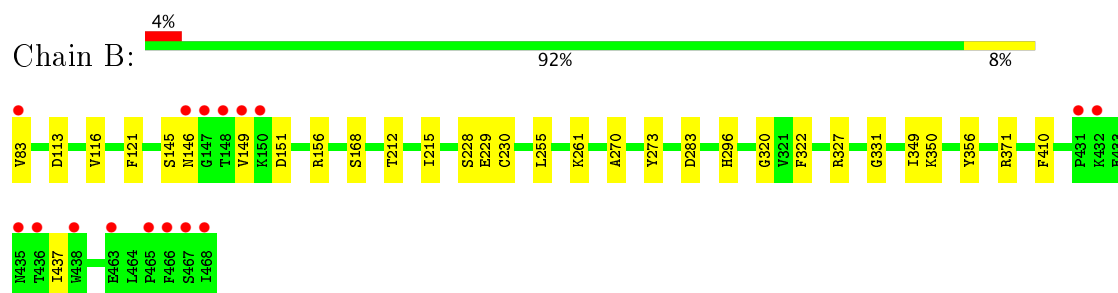
3 Residue-property plots [i](#)

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

• Molecule 1: Neuramininidase



• Molecule 1: Neuramininidase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	117.73Å 138.47Å 117.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.86 – 1.64 44.88 – 1.64	Depositor EDS
% Data completeness (in resolution range)	97.1 (44.86-1.64) 97.1 (44.88-1.64)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.64Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.180 , 0.210 0.179 , 0.209	Depositor DCC
R_{free} test set	5652 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	14.3	Xtriage
Anisotropy	0.834	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6873	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, PO4, ACT, CA, 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	0.62	0/3073	0.70	0/4177
1	B	0.63	0/3067	0.69	0/4169
All	All	0.62	0/6140	0.69	0/8346

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

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	2983	0	2806	23	0
1	B	2980	0	2801	18	0
2	A	14	0	13	1	0
2	B	28	0	24	1	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
4	A	12	0	9	2	0
4	B	8	0	6	3	0
5	A	5	0	0	1	0
6	A	30	0	40	2	0
6	B	30	0	40	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	22	0	19	0	0
8	A	397	0	0	2	0
8	B	359	0	0	0	0
All	All	6873	0	5758	45	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 4.

All (45) 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:227:GLU:OE2	4:A:3002:ACT:H1	1.80	0.80
4:B:3004:ACT:H1	6:B:1008:GOL:H2	1.70	0.72
1:A:336:CYS:HB2	8:A:3171:HOH:O	1.98	0.63
1:A:83:VAL:HG23	1:A:83:VAL:O	1.98	0.62
1:B:356:TYR:CD2	6:B:1002:GOL:H32	2.36	0.60
1:A:83:VAL:HA	8:A:3372:HOH:O	2.02	0.58
1:A:83:VAL:CG2	1:A:83:VAL:O	2.53	0.57
1:B:151:ASP:O	1:B:156:ARG:HD2	2.04	0.57
1:B:270:ALA:HB1	1:B:273:TYR:HB2	1.88	0.55
1:A:146:ASN:O	1:A:149:VAL:HG23	2.06	0.55
1:A:113:ASP:O	1:A:168[B]:SER:HB2	2.06	0.55
1:B:437:ILE:HG21	2:B:2001:NAG:H82	1.90	0.53
1:B:212:THR:O	1:B:261:LYS:HD3	2.09	0.52
1:A:387:ASP:HA	6:A:1009:GOL:H31	1.93	0.50
1:A:151:ASP:O	1:A:156:ARG:HD2	2.11	0.49
1:A:116:VAL:HG21	1:A:145:SER:HB2	1.94	0.49
1:B:146:ASN:O	1:B:149:VAL:HG23	2.13	0.49
1:B:83:VAL:CG2	1:B:83:VAL:O	2.62	0.48
1:B:228:SER:HB3	1:B:350:LYS:HE2	1.94	0.48
1:B:83:VAL:HG23	1:B:83:VAL:O	2.14	0.47
1:A:387:ASP:HA	6:A:1009:GOL:C3	2.44	0.47
1:B:320:GLY:HA3	1:B:331:GLY:O	2.15	0.47
1:A:215:ILE:HD13	1:A:255:LEU:CD1	2.45	0.47
1:B:322:PHE:HB2	1:B:327:ARG:HD2	1.97	0.47
1:A:270:ALA:HB1	1:A:273:TYR:HB2	1.98	0.46
1:A:228:SER:HB3	1:A:350:LYS:HE2	1.98	0.46
1:A:320:GLY:HA3	1:A:331:GLY:O	2.16	0.46
1:A:215:ILE:CD1	1:A:255:LEU:HD13	2.47	0.45
1:B:121:PHE:CG	1:B:228:SER:HA	2.52	0.45
1:B:116:VAL:HG21	1:B:145:SER:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:ILE:HG21	2:A:1001:NAG:H82	1.98	0.45
4:B:3004:ACT:OXT	6:B:1004:GOL:O1	2.27	0.44
1:B:113:ASP:O	1:B:168[B]:SER:HB2	2.18	0.44
1:A:215:ILE:HD13	1:A:255:LEU:HD11	1.99	0.43
1:B:215:ILE:HD13	1:B:255:LEU:CD1	2.48	0.42
1:A:135:THR:O	1:A:156:ARG:HA	2.19	0.42
1:A:276:GLU:OE1	5:A:1000:PO4:O3	2.37	0.42
1:A:322:PHE:HB2	1:A:327:ARG:HD2	2.01	0.42
1:A:121:PHE:CG	1:A:228:SER:HA	2.55	0.42
1:A:215:ILE:HD11	1:A:262:VAL:HG21	2.02	0.41
4:B:3004:ACT:CH3	6:B:1008:GOL:H12	2.51	0.41
4:A:3002:ACT:C	4:A:3003:ACT:H3	2.50	0.41
1:B:229:GLU:OE2	1:B:410:PHE:HA	2.21	0.41
1:B:283:ASP:HB3	6:B:1006:GOL:H31	2.02	0.41
1:B:349:ILE:HD12	1:B:371:ARG:HG2	2.03	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	387/385 (100%)	370 (96%)	17 (4%)	0	100	100
1	B	386/385 (100%)	367 (95%)	19 (5%)	0	100	100
All	All	773/770 (100%)	737 (95%)	36 (5%)	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	334/330 (101%)	332 (99%)	2 (1%)	89	79
1	B	333/330 (101%)	331 (99%)	2 (1%)	89	79
All	All	667/660 (101%)	663 (99%)	4 (1%)	89	79

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230	CYS
1	A	296	HIS
1	B	230	CYS
1	B	296	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 26 ligands modelled in this entry, 5 are monoatomic - leaving 21 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	PO4	A	1000	-	4,4,4	0.67	0	6,6,6	0.65	0
2	NAG	A	1001	1	14,14,15	0.44	0	15,19,21	0.96	1 (6%)
6	GOL	A	1003	-	5,5,5	0.33	0	5,5,5	0.28	0
6	GOL	A	1005	-	5,5,5	0.30	0	5,5,5	0.27	0
6	GOL	A	1009	-	5,5,5	0.30	0	5,5,5	0.29	0
4	ACT	A	3000	-	1,3,3	1.62	0	0,3,3	0.00	-
4	ACT	A	3002	-	1,3,3	1.03	0	0,3,3	0.00	-
4	ACT	A	3003	-	1,3,3	0.97	0	0,3,3	0.00	-
6	GOL	A	3004	-	5,5,5	0.36	0	5,5,5	0.15	0
6	GOL	A	3005	-	5,5,5	0.31	0	5,5,5	0.50	0
6	GOL	B	1002	-	5,5,5	0.35	0	5,5,5	0.42	0
6	GOL	B	1004	-	5,5,5	0.41	0	5,5,5	0.46	0
6	GOL	B	1006	-	5,5,5	0.29	0	5,5,5	0.62	0
6	GOL	B	1007	-	5,5,5	0.34	0	5,5,5	0.48	0
6	GOL	B	1008	-	5,5,5	0.44	0	5,5,5	0.13	0
2	NAG	B	2001	1,2	14,14,15	0.48	0	15,19,21	0.74	1 (6%)
2	NAG	B	2002	2,7	14,14,15	0.61	0	15,19,21	1.24	2 (13%)
7	MAN	B	2003	2,7	11,11,12	0.53	0	13,15,17	1.19	2 (15%)
7	MAN	B	2004	7	11,11,12	0.51	0	13,15,17	1.11	1 (7%)
4	ACT	B	3001	-	1,3,3	0.73	0	0,3,3	0.00	-
4	ACT	B	3004	-	1,3,3	0.36	0	0,3,3	0.00	-

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	PO4	A	1000	-	-	0/0/0/0	0/0/0/0
2	NAG	A	1001	1	-	0/6/23/26	0/1/1/1
6	GOL	A	1003	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1005	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1009	-	-	0/4/4/4	0/0/0/0
4	ACT	A	3000	-	-	0/0/0/0	0/0/0/0
4	ACT	A	3002	-	-	0/0/0/0	0/0/0/0
4	ACT	A	3003	-	-	0/0/0/0	0/0/0/0
6	GOL	A	3004	-	-	0/4/4/4	0/0/0/0
6	GOL	A	3005	-	-	0/4/4/4	0/0/0/0
6	GOL	B	1002	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	B	1004	-	-	0/4/4/4	0/0/0/0
6	GOL	B	1006	-	-	0/4/4/4	0/0/0/0
6	GOL	B	1007	-	-	0/4/4/4	0/0/0/0
6	GOL	B	1008	-	-	0/4/4/4	0/0/0/0
2	NAG	B	2001	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2002	2,7	-	0/6/23/26	0/1/1/1
7	MAN	B	2003	2,7	-	0/2/19/22	0/1/1/1
7	MAN	B	2004	7	-	0/2/19/22	0/1/1/1
4	ACT	B	3001	-	-	0/0/0/0	0/0/0/0
4	ACT	B	3004	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	NAG	C1-O5-C5	2.03	114.96	112.17
2	B	2002	NAG	C2-N2-C7	2.06	125.95	122.94
2	B	2002	NAG	O7-C7-N2	2.69	127.10	121.92
7	B	2003	MAN	C1-O5-C5	2.74	115.95	112.17
7	B	2004	MAN	C1-O5-C5	2.75	115.96	112.17
7	B	2003	MAN	C1-C2-C3	2.80	113.20	109.65
2	A	1001	NAG	C1-O5-C5	3.12	116.47	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1000	PO4	1	0
2	A	1001	NAG	1	0
6	A	1009	GOL	2	0
4	A	3002	ACT	2	0
4	A	3003	ACT	1	0
6	B	1002	GOL	1	0
6	B	1004	GOL	1	0
6	B	1006	GOL	1	0
6	B	1008	GOL	2	0
2	B	2001	NAG	1	0
4	B	3004	ACT	3	0

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	385/385 (100%)	-0.20	9 (2%) 61 61	9, 15, 28, 52	0
1	B	385/385 (100%)	-0.10	16 (4%) 37 34	10, 15, 29, 52	0
All	All	770/770 (100%)	-0.15	25 (3%) 48 47	9, 15, 29, 52	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	468	ILE	9.8
1	A	149	VAL	8.1
1	B	149	VAL	7.5
1	B	468	ILE	7.2
1	B	467	SER	7.2
1	A	148	THR	6.1
1	A	467	SER	5.8
1	B	147	GLY	5.7
1	B	435	ASN	5.1
1	B	148	THR	4.0
1	B	466	PHE	3.8
1	A	83	VAL	3.4
1	B	150	LYS	3.3
1	A	150	LYS	3.2
1	B	83	VAL	3.2
1	B	465	PRO	2.9
1	B	431	PRO	2.8
1	A	147	GLY	2.8
1	A	84	ILE	2.6
1	B	146	ASN	2.4
1	A	466	PHE	2.3
1	B	463	GLU	2.2
1	B	432	LYS	2.1
1	B	436	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	438	TRP	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
6	GOL	B	1007	6/6	0.83	0.27	18.49	34,38,39,42	0
6	GOL	A	1003	6/6	0.77	0.23	18.14	32,48,52,59	0
6	GOL	A	1009	6/6	0.85	0.35	17.42	26,39,40,46	0
4	ACT	A	3000	4/4	0.69	0.39	12.45	54,54,54,55	0
5	PO4	A	1000	5/5	0.68	0.19	9.80	46,53,57,63	0
4	ACT	B	3004	4/4	0.90	0.24	8.36	20,27,29,30	0
4	ACT	A	3002	4/4	0.86	0.21	7.46	26,30,30,33	0
6	GOL	A	1005	6/6	0.91	0.17	5.66	32,44,46,50	0
6	GOL	A	3004	6/6	0.73	0.20	5.28	40,52,53,54	0
6	GOL	B	1006	6/6	0.77	0.21	4.84	27,29,38,43	0
6	GOL	B	1004	6/6	0.89	0.13	4.12	38,42,45,46	0
6	GOL	A	3005	6/6	0.92	0.10	3.97	22,25,34,47	0
6	GOL	B	1002	6/6	0.93	0.11	3.82	20,32,35,40	0
6	GOL	B	1008	6/6	0.77	0.18	2.29	40,55,58,59	0
4	ACT	A	3003	4/4	0.83	0.15	1.44	53,54,54,54	0
4	ACT	B	3001	4/4	0.92	0.12	0.86	48,48,49,49	0
3	CA	B	4	1/1	1.00	0.04	-1.30	14,14,14,14	0
3	CA	A	1	1/1	0.99	0.04	-1.79	14,14,14,14	0
3	CA	A	2	1/1	0.99	0.04	-2.74	14,14,14,14	0
3	CA	B	3	1/1	0.99	0.04	-3.32	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	CA	A	5	1/1	0.73	0.11	-	65,65,65,65	1
7	MAN	B	2004	11/12	0.69	0.26	-	46,56,62,63	0
2	NAG	B	2001	14/15	0.61	0.30	-	57,63,68,76	0
7	MAN	B	2003	11/12	0.50	0.37	-	72,80,84,85	0
2	NAG	B	2002	14/15	0.60	0.40	-	80,83,88,88	0
2	NAG	A	1001	14/15	0.48	0.25	-	53,59,63,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.