



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 09:06 PM BST

PDB ID : 4GSX
Title : High resolution structure of dengue virus serotype 1 sE containing stem
Authors : Klein, D.E.; Choi, J.L.; Harrison, S.C.
Deposited on : 2012-08-28
Resolution : 1.90 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

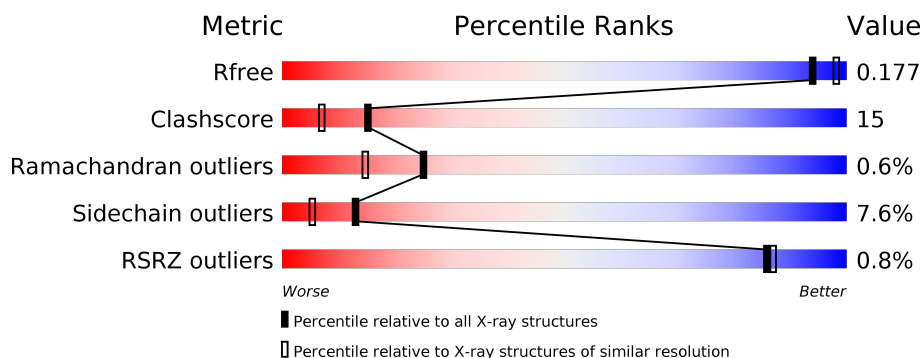
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 respectively. 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	427	<div> <div></div> <div> <div></div> <div>70%</div> <div>20%</div> <div>9%</div> </div> </div>
1	B	427	<div> <div></div> <div> <div></div> <div>62%</div> <div>26%</div> <div>9%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6673 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 Envelope protein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	4	0
			3007	1902	507	578	20			
1	B	390	Total	C	N	O	S	0	2	0
			2967	1876	498	573	20			

There are 36 discrepancies between the modelled and reference sequences:

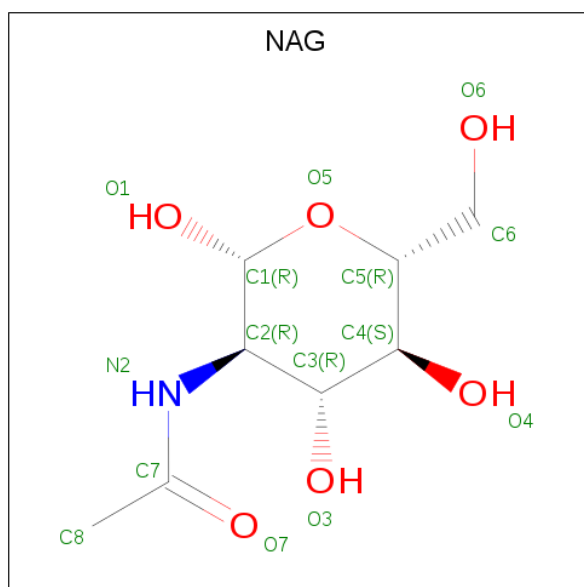
Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	GLY	-	expression tag	UNP P17763
A	-14	HIS	-	expression tag	UNP P17763
A	-13	HIS	-	expression tag	UNP P17763
A	-12	HIS	-	expression tag	UNP P17763
A	-11	HIS	-	expression tag	UNP P17763
A	-10	HIS	-	expression tag	UNP P17763
A	-9	HIS	-	expression tag	UNP P17763
A	-8	HIS	-	expression tag	UNP P17763
A	-7	HIS	-	expression tag	UNP P17763
A	-6	GLY	-	expression tag	UNP P17763
A	-5	SER	-	expression tag	UNP P17763
A	-4	SER	-	expression tag	UNP P17763
A	-3	THR	-	expression tag	UNP P17763
A	-2	SER	-	expression tag	UNP P17763
A	-1	ASN	-	expression tag	UNP P17763
A	0	GLY	-	expression tag	UNP P17763
A	101	HIS	TRP	engineered mutation	UNP P17763
A	161	ILE	THR	conflict	UNP P17763
B	-15	GLY	-	expression tag	UNP P17763
B	-14	HIS	-	expression tag	UNP P17763
B	-13	HIS	-	expression tag	UNP P17763
B	-12	HIS	-	expression tag	UNP P17763
B	-11	HIS	-	expression tag	UNP P17763
B	-10	HIS	-	expression tag	UNP P17763
B	-9	HIS	-	expression tag	UNP P17763

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	expression tag	UNP P17763
B	-7	HIS	-	expression tag	UNP P17763
B	-6	GLY	-	expression tag	UNP P17763
B	-5	SER	-	expression tag	UNP P17763
B	-4	SER	-	expression tag	UNP P17763
B	-3	THR	-	expression tag	UNP P17763
B	-2	SER	-	expression tag	UNP P17763
B	-1	ASN	-	expression tag	UNP P17763
B	0	GLY	-	expression tag	UNP P17763
B	101	HIS	TRP	engineered mutation	UNP P17763
B	161	ILE	THR	conflict	UNP P17763

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (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		

- Molecule 3 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Cd	0	0
			2	2		

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

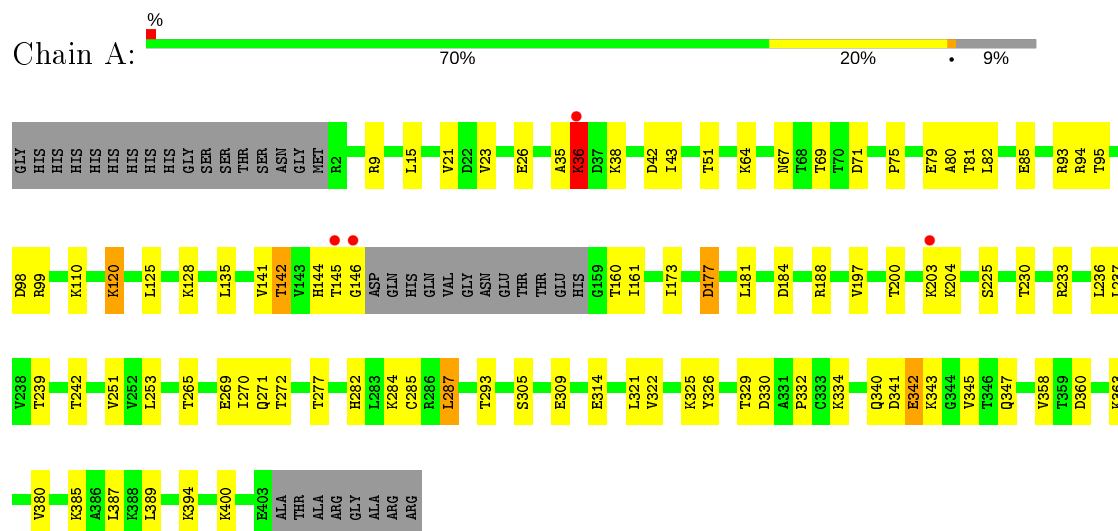
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	360	Total	O	0	0
			360	360		
5	B	306	Total	O	0	0
			306	306		

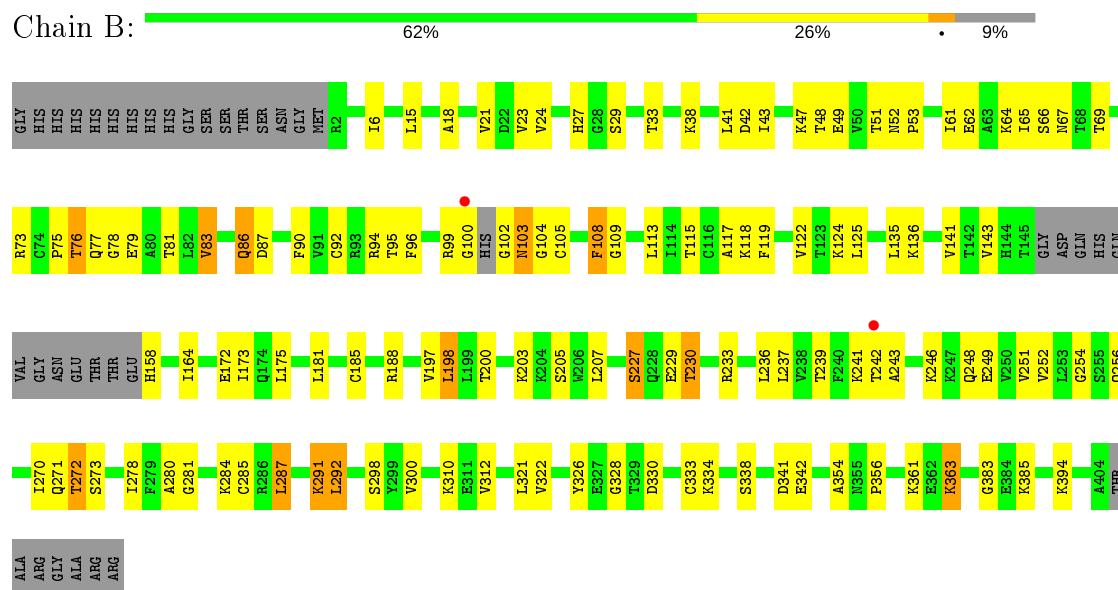
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Envelope protein E



• Molecule 1: Envelope protein E



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	77.57Å 77.57Å 292.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.13 – 1.90 29.13 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.13-1.90) 97.6 (29.13-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 1.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.161 , 0.186 0.156 , 0.177	Depositor DCC
R_{free} test set	3857 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.389 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.400 for h,-h-k,-l	Depositor
Outliers	0 of 76852 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6673	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 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, NAG, CD

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	0.55	0/3071	0.66	0/4156
1	B	0.56	0/3023	0.66	0/4097
All	All	0.55	0/6094	0.66	0/8253

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	18	ALA	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	3007	0	3050	76	0
1	B	2967	0	2974	103	0
2	A	14	0	13	5	0
2	B	14	0	13	3	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	1	0	0	0	0
5	A	360	0	0	24	3
5	B	306	0	0	25	4
All	All	6673	0	6050	179	5

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 15.

All (179) 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:67:ASN:HD21	2:A:501:NAG:C1	1.20	1.52
1:B:67:ASN:HD21	2:B:501:NAG:C1	1.23	1.46
1:A:284:LYS:NZ	5:A:831:HOH:O	1.85	1.07
1:B:333:CYS:SG	5:B:830:HOH:O	2.22	0.97
1:B:76:THR:OG1	1:B:77:GLN:OE1	1.84	0.96
1:B:328:GLY:O	1:B:361:LYS:NZ	1.98	0.95
1:B:49:GLU:OE2	5:B:798:HOH:O	1.86	0.93
1:A:309:GLU:OE2	5:A:948:HOH:O	1.87	0.91
1:B:104:GLY:O	5:B:901:HOH:O	1.87	0.90
1:B:254:GLY:O	1:B:256:GLN:NE2	2.04	0.90
1:A:71:ASP:OD1	5:A:793:HOH:O	1.90	0.88
1:B:41:LEU:HD13	1:B:143:VAL:HG22	1.59	0.83
1:B:29:SER:OG	5:B:823:HOH:O	1.97	0.81
1:B:67:ASN:HD22	2:B:501:NAG:C1	1.94	0.80
1:B:158:HIS:O	5:B:786:HOH:O	1.98	0.80
1:B:198:LEU:HD13	1:B:270:ILE:HD11	1.65	0.77
1:A:36:LYS:NZ	1:A:293:THR:OG1	2.16	0.76
1:B:227:SER:O	5:B:834:HOH:O	2.03	0.75
1:B:236:LEU:O	5:B:797:HOH:O	2.03	0.75
1:A:69:THR:OG1	5:A:935:HOH:O	2.05	0.74
1:A:242[A]:THR:HG23	5:A:728:HOH:O	1.87	0.74
1:A:79:GLU:OE2	5:A:908:HOH:O	2.05	0.74
1:A:36:LYS:NZ	5:A:859:HOH:O	2.21	0.73
1:A:329:THR:O	5:A:912:HOH:O	2.06	0.72
1:A:314:GLU:OE1	5:A:945:HOH:O	2.09	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:ILE:CD1	1:A:141:VAL:HG13	2.21	0.70
1:B:105:CYS:HA	5:B:901:HOH:O	1.92	0.69
1:B:229:GLU:OE2	5:B:803:HOH:O	2.11	0.69
1:B:246:LYS:O	5:B:814:HOH:O	2.10	0.69
1:B:200:THR:HG22	1:B:205:SER:OG	1.92	0.69
1:B:83:VAL:O	1:B:86:GLN:HG2	1.94	0.67
1:A:188:ARG:HE	1:A:282:HIS:HB3	1.61	0.66
1:A:67:ASN:HD21	2:A:501:NAG:C2	2.06	0.65
1:B:65:ILE:HG23	1:B:117:ALA:HB1	1.79	0.64
1:B:230:THR:O	1:B:230:THR:OG1	2.12	0.63
1:B:62:GLU:HA	5:B:663:HOH:O	1.99	0.62
1:A:69:THR:CB	5:A:935:HOH:O	2.47	0.62
1:A:67:ASN:HD22	2:A:501:NAG:C1	2.07	0.62
1:A:305:SER:HB3	1:A:385:LYS:HG3	1.81	0.62
1:B:67:ASN:ND2	2:B:501:NAG:O5	2.32	0.61
1:B:75:PRO:O	1:B:76:THR:OG1	2.19	0.61
1:B:87:ASP:OD1	5:B:880:HOH:O	2.16	0.60
1:B:65:ILE:HG12	1:B:252:VAL:HG13	1.85	0.58
1:A:80:ALA:O	1:A:94:ARG:NH2	2.33	0.58
1:A:161:ILE:N	1:A:161:ILE:HD12	2.20	0.57
1:A:269:GLU:OE1	5:A:844:HOH:O	2.17	0.57
1:B:38:LYS:HE3	1:B:292:LEU:HD21	1.86	0.57
1:A:345:VAL:O	1:A:347:GLN:NE2	2.38	0.56
1:A:347:GLN:OE1	5:A:938:HOH:O	2.17	0.56
1:A:334:LYS:NZ	5:A:894:HOH:O	2.38	0.56
1:B:65:ILE:HD13	1:B:119:PHE:HA	1.86	0.56
1:A:394:LYS:HG2	5:A:842:HOH:O	2.05	0.56
1:B:65:ILE:HA	1:B:118:LYS:O	2.06	0.56
1:B:41:LEU:CD1	1:B:143:VAL:HG22	2.35	0.55
1:B:61:ILE:O	1:B:256:GLN:HG2	2.06	0.55
1:B:42:ASP:O	1:B:43:ILE:HD13	2.06	0.55
1:B:100:GLY:O	1:B:108:PHE:HB2	2.07	0.55
1:B:27:HIS:CD2	1:B:280:ALA:HB1	2.41	0.55
1:B:330:ASP:N	1:B:330:ASP:OD1	2.30	0.55
1:B:67:ASN:O	1:B:69:THR:HG23	2.07	0.54
1:B:113:LEU:N	5:B:852:HOH:O	2.40	0.54
1:A:305:SER:HB3	1:A:385:LYS:CG	2.38	0.53
1:B:6:ILE:HD12	1:B:33:THR:HB	1.88	0.53
1:A:36:LYS:HE3	1:A:293:THR:CB	2.39	0.53
1:B:312:VAL:HG22	1:B:322:VAL:HG22	1.90	0.53
1:B:65:ILE:HG12	1:B:252:VAL:CG1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:GLY:O	1:B:105:CYS:N	2.31	0.53
1:B:100:GLY:C	1:B:108:PHE:HA	2.28	0.53
1:B:65:ILE:CG2	1:B:117:ALA:HB1	2.39	0.53
1:A:314:GLU:OE1	5:A:951:HOH:O	2.19	0.53
1:B:125:LEU:C	1:B:125:LEU:HD12	2.30	0.52
1:A:36:LYS:HE3	1:A:293:THR:HB	1.92	0.52
1:B:273:SER:OG	1:B:273:SER:O	2.27	0.52
1:A:36:LYS:CE	1:A:293:THR:OG1	2.57	0.52
1:B:100:GLY:O	1:B:108:PHE:CD1	2.62	0.52
1:B:95:THR:OG1	1:B:96:PHE:N	2.43	0.52
1:B:42:ASP:C	1:B:43:ILE:HD13	2.29	0.52
1:A:43:ILE:HD13	1:A:141:VAL:HG13	1.92	0.52
1:B:394:LYS:HE3	5:B:906:HOH:O	2.09	0.51
1:B:394:LYS:CE	5:B:906:HOH:O	2.57	0.51
1:B:73:ARG:HG3	1:B:78:GLY:O	2.10	0.51
1:A:265:THR:HG22	1:A:400:LYS:NZ	2.26	0.51
1:A:341:ASP:O	1:A:342:GLU:C	2.48	0.51
1:B:300:VAL:O	1:B:333:CYS:HB2	2.10	0.50
1:A:233:ARG:NH2	1:A:236:LEU:HD21	2.25	0.50
1:A:26:GLU:HG2	1:A:188:ARG:NH2	2.27	0.50
1:A:321[A]:LEU:HD23	1:A:322:VAL:N	2.27	0.50
1:A:330:ASP:OD1	1:A:330:ASP:N	2.43	0.50
1:A:36:LYS:HE3	1:A:293:THR:OG1	2.12	0.50
1:A:79:GLU:OE1	5:A:934:HOH:O	2.19	0.50
1:A:93:ARG:NH1	5:A:697:HOH:O	2.42	0.50
1:B:23:VAL:CG2	1:B:285:CYS:HB2	2.42	0.50
1:B:205:SER:OG	1:B:272:THR:CG2	2.60	0.50
1:B:94:ARG:HD3	5:B:688:HOH:O	2.10	0.49
1:A:43:ILE:HD12	1:A:141:VAL:HG22	1.94	0.49
1:B:354:ALA:O	1:B:356:PRO:HD3	2.13	0.48
1:A:69:THR:HB	5:A:935:HOH:O	2.12	0.48
1:A:21:VAL:HB	1:A:287:LEU:HB2	1.95	0.48
1:A:360:ASP:HB3	1:A:363:LYS:HG2	1.96	0.48
1:A:82:LEU:O	1:A:85:GLU:HB2	2.13	0.48
1:A:145:THR:O	1:A:146:GLY:O	2.32	0.47
1:B:241:LYS:HE3	1:B:242:THR:HG22	1.97	0.47
1:B:64:LYS:HG3	1:B:122:VAL:CG2	2.44	0.47
1:B:75:PRO:O	1:B:76:THR:CB	2.61	0.47
1:A:332:PRO:HA	1:A:358:VAL:O	2.13	0.47
1:A:360:ASP:CG	1:A:363:LYS:HG2	2.35	0.47
1:B:66:SER:O	1:B:118:LYS:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:GLY:HA2	1:B:109:GLY:N	2.29	0.47
1:B:92:CYS:HA	1:B:115:THR:O	2.15	0.47
1:B:205:SER:OG	1:B:272:THR:HG21	2.15	0.46
1:B:229:GLU:HB2	5:B:875:HOH:O	2.15	0.46
1:B:363:LYS:HE2	5:B:765:HOH:O	2.14	0.46
1:A:128:LYS:NZ	1:A:200:THR:OG1	2.40	0.46
1:A:36:LYS:NZ	5:A:826:HOH:O	2.46	0.46
1:B:243:ALA:CB	1:B:248:GLN:HG2	2.46	0.46
1:A:203:LYS:HG2	1:A:203:LYS:O	2.15	0.46
1:B:233:ARG:NE	5:B:903:HOH:O	2.49	0.46
1:B:241:LYS:NZ	1:B:242:THR:HG22	2.31	0.46
1:B:361:LYS:HD2	5:B:879:HOH:O	2.15	0.46
1:B:237:LEU:O	1:B:252:VAL:HA	2.16	0.46
1:B:354:ALA:O	1:B:356:PRO:CD	2.64	0.45
1:A:67:ASN:ND2	2:A:501:NAG:N2	2.64	0.45
1:B:47:LYS:HE2	1:B:278:ILE:CD1	2.47	0.45
1:A:237:LEU:C	1:A:253:LEU:HD23	2.37	0.45
1:B:24:VAL:HG13	1:B:188:ARG:HD2	1.99	0.45
1:B:310:LYS:HE2	5:B:667:HOH:O	2.17	0.45
1:B:75:PRO:O	1:B:76:THR:HG23	2.15	0.45
1:A:42:ASP:O	1:A:43:ILE:HD13	2.17	0.45
1:B:361:LYS:C	1:B:363:LYS:H	2.19	0.45
1:A:340:GLN:HA	1:A:345:VAL:O	2.17	0.44
1:B:43:ILE:CD1	1:B:141:VAL:HG13	2.48	0.44
1:A:125:LEU:HD12	1:A:125:LEU:C	2.37	0.44
1:A:237:LEU:O	1:A:253:LEU:HD23	2.16	0.44
1:A:35:ALA:HB3	1:A:38:LYS:HD2	1.98	0.44
1:A:67:ASN:ND2	2:A:501:NAG:C2	2.71	0.44
1:B:102:GLY:N	1:B:105:CYS:O	2.49	0.44
1:B:99:ARG:HD3	5:B:776:HOH:O	2.18	0.44
1:B:271:GLN:CG	1:B:271:GLN:O	2.65	0.44
1:A:326:TYR:OH	1:A:330:ASP:OD1	2.25	0.44
1:B:326:TYR:CZ	1:B:328:GLY:HA3	2.53	0.44
1:B:86:GLN:CD	1:B:86:GLN:N	2.71	0.44
1:B:65:ILE:CG1	1:B:252:VAL:HG13	2.46	0.43
1:B:48:THR:OG1	1:B:281:GLY:HA3	2.18	0.43
1:B:94:ARG:HG2	5:B:688:HOH:O	2.18	0.43
1:A:305:SER:HB3	1:A:385:LYS:HD2	2.00	0.43
1:A:385:LYS:HG3	1:A:385:LYS:O	2.18	0.43
1:A:142:THR:OG1	5:A:864:HOH:O	2.11	0.43
1:A:341:ASP:O	1:A:343:LYS:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:ASP:HB3	1:B:90:PHE:CD2	2.53	0.43
1:B:383:GLY:O	1:B:385:LYS:N	2.51	0.43
1:B:75:PRO:C	1:B:76:THR:HG23	2.39	0.43
1:B:52:ASN:N	1:B:53:PRO:CD	2.81	0.43
1:B:334:LYS:NZ	5:B:883:HOH:O	2.51	0.43
1:B:102:GLY:O	1:B:103:ASN:C	2.58	0.42
1:A:184:ASP:OD1	5:A:852:HOH:O	2.21	0.42
1:A:64:LYS:HG2	1:A:120:LYS:HB3	2.00	0.42
1:B:21:VAL:HB	1:B:287:LEU:HB2	2.00	0.42
1:B:64:LYS:HG3	1:B:122:VAL:HG21	2.01	0.42
1:B:23:VAL:HG23	1:B:285:CYS:HB2	2.01	0.42
1:A:282:HIS:NE2	5:A:827:HOH:O	2.25	0.42
1:B:47:LYS:CE	1:B:278:ILE:CD1	2.98	0.41
1:B:103:ASN:O	1:B:103:ASN:OD1	2.39	0.41
1:B:239:THR:HB	1:B:251:VAL:HG23	2.03	0.41
1:A:265:THR:HG22	1:A:400:LYS:HZ2	1.85	0.41
1:A:98:ASP:OD1	1:A:110:LYS:NZ	2.45	0.41
1:A:239:THR:HB	1:A:251:VAL:HG23	2.02	0.41
1:A:271:GLN:HG2	5:A:682:HOH:O	2.20	0.41
1:B:66:SER:HB2	1:B:118:LYS:HE3	2.02	0.41
1:A:75:PRO:HD3	1:A:99:ARG:HB2	2.03	0.41
1:B:341:ASP:C	1:B:341:ASP:OD1	2.58	0.41
1:B:94:ARG:HG3	5:B:852:HOH:O	2.20	0.41
1:A:23:VAL:HG22	1:A:285:CYS:HB2	2.03	0.40
1:A:177:ASP:OD2	5:A:836:HOH:O	2.20	0.40
1:A:80:ALA:O	1:A:94:ARG:NH1	2.53	0.40
1:B:175:LEU:HD11	1:B:181:LEU:HD22	2.04	0.40
1:B:164:ILE:HG21	1:B:185:CYS:HB2	2.04	0.40
1:A:160:THR:CG2	1:A:173:ILE:HD13	2.52	0.40
1:A:270:ILE:HG12	1:A:277:THR:CG2	2.52	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:919:HOH:O	5:A:928:HOH:O[3_655]	1.83	0.37
5:A:942:HOH:O	5:B:901:HOH:O[3_545]	1.83	0.37
5:B:662:HOH:O	5:B:662:HOH:O[2_445]	1.84	0.36
5:B:678:HOH:O	5:B:678:HOH:O[2_445]	2.01	0.19
5:A:811:HOH:O	5:B:754:HOH:O[3_545]	2.03	0.17

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	390/427 (91%)	378 (97%)	11 (3%)	1 (0%)	41	31
1	B	386/427 (90%)	370 (96%)	12 (3%)	4 (1%)	15	6
All	All	776/854 (91%)	748 (96%)	23 (3%)	5 (1%)	25	15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	LYS
1	B	76	THR
1	B	103	ASN
1	B	227	SER
1	B	291	LYS

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	338/363 (93%)	315 (93%)	23 (7%)	16	7
1	B	329/363 (91%)	302 (92%)	27 (8%)	11	4
All	All	667/726 (92%)	617 (92%)	50 (8%)	13	5

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG

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Mol	Chain	Res	Type
1	A	15	LEU
1	A	36	LYS
1	A	51	THR
1	A	81	THR
1	A	95	THR
1	A	120	LYS
1	A	135	LEU
1	A	142	THR
1	A	144	HIS
1	A	177	ASP
1	A	181	LEU
1	A	197	VAL
1	A	204	LYS
1	A	225	SER
1	A	230	THR
1	A	272	THR
1	A	287	LEU
1	A	325	LYS
1	A	342	GLU
1	A	380	VAL
1	A	387	LEU
1	A	389	LEU
1	B	51	THR
1	B	79	GLU
1	B	81	THR
1	B	83	VAL
1	B	86	GLN
1	B	108	PHE
1	B	124	LYS
1	B	135	LEU
1	B	136	LYS
1	B	172	GLU
1	B	173	ILE
1	B	197	VAL
1	B	198	LEU
1	B	203	LYS
1	B	207	LEU
1	B	230	THR
1	B	249	GLU
1	B	272	THR
1	B	284	LYS
1	B	287	LEU

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Mol	Chain	Res	Type
1	B	291	LYS
1	B	292	LEU
1	B	298	SER
1	B	321	LEU
1	B	338	SER
1	B	342	GLU
1	B	363	LYS

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	67	ASN
1	A	347	GLN
1	A	355	ASN
1	B	67	ASN
1	B	89	ASN
1	B	256	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	B	501	1	14,14,15	0.56	0	17,19,21	1.05	2 (11%)
2	NAG	A	501	1	14,14,15	0.57	0	17,19,21	1.42	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	501	1	-	3/6/23/26	0/1/1/1
2	NAG	A	501	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	501	NAG	C4-C3-C2	-3.75	105.52	111.02
2	A	501	NAG	C2-N2-C7	-3.39	118.07	122.90
2	B	501	NAG	C4-C3-C2	2.25	114.31	111.02
2	B	501	NAG	O5-C5-C6	2.18	110.62	107.20

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	NAG	C8-C7-N2-C2
2	B	501	NAG	O7-C7-N2-C2
2	A	501	NAG	C8-C7-N2-C2
2	A	501	NAG	O7-C7-N2-C2
2	B	501	NAG	C1-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	NAG	3	0
2	A	501	NAG	5	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 [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	390/427 (91%)	-0.42	4 (1%) 82 84	6, 16, 32, 49	0
1	B	390/427 (91%)	-0.36	2 (0%) 91 92	5, 18, 35, 51	0
All	All	780/854 (91%)	-0.39	6 (0%) 86 87	5, 17, 34, 51	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	100	GLY	4.3
1	A	146	GLY	4.1
1	B	242	THR	2.2
1	A	36	LYS	2.2
1	A	145	THR	2.1
1	A	203	LYS	2.1

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 monosaccharides 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. 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	B-factors(\AA^2)	Q<0.9
2	NAG	A	501	14/15	0.71	0.14	32,40,51,55	0
2	NAG	B	501	14/15	0.82	0.15	48,56,62,65	0
3	CD	B	502	1/1	0.95	0.04	54,54,54,54	0
3	CD	B	503	1/1	0.98	0.04	53,53,53,53	0
4	CL	A	504	1/1	0.99	0.07	12,12,12,12	0
3	CD	A	503	1/1	0.99	0.05	52,52,52,52	0
3	CD	A	502	1/1	1.00	0.03	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.