Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:50 AM GMT

PDB ID	:	3G7T
Title	:	Crystal structure of dengue virus type 1 envelope protein in the postfusion conformation
Authors	:	Modis, Y.
Deposited on	:	2009-02-10
Resolution	:	3.50 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

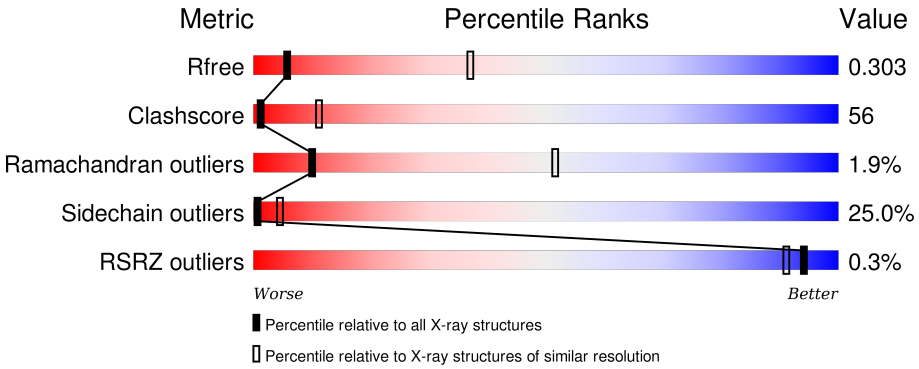
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 3.50 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	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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 <=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	400	30% 48% 16% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2907 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			2905	1836	488	562	19			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	ALA	THR	SEE REMARK 999	UNP Q5USP2
A	114	LEU	ILE	SEE REMARK 999	UNP Q5USP2
A	250	ALA	VAL	SEE REMARK 999	UNP Q5USP2

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is water.

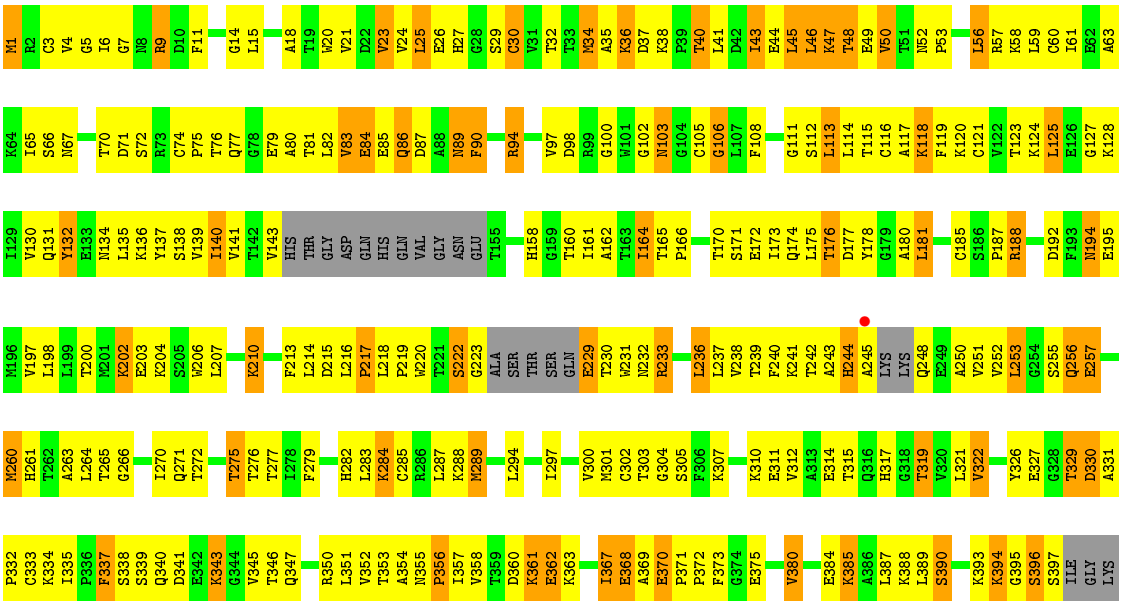
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		

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 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: Envelope protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α, β, γ	75.65Å 75.65Å 292.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 3.50 24.76 – 3.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (25.00-3.50) 98.3 (24.76-3.50)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 3.54Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, R_{free}	0.208 , 0.297 0.208 , 0.303	Depositor DCC
R_{free} test set	311 reflections (4.80%)	DCC
Wilson B-factor (Å^2)	113.9	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 91.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Outliers	0 of 6785 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2907	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CL

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	0.85	2/2955 (0.1%)	0.82	2/4002 (0.0%)

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	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	CYS	CB-SG	-8.09	1.68	1.82
1	A	368	GLU	CG-CD	5.82	1.60	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	362	GLU	CB-CA-C	-6.46	97.47	110.40
1	A	395	GLY	N-CA-C	5.49	126.82	113.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	MET	Peptide
1	A	229	GLU	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	2905	0	2920	326	1
2	A	1	0	0	0	0
3	A	1	0	0	0	0
All	All	2907	0	2920	326	1

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 56.

All (326) 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:36:LYS:NZ	1:A:36:LYS:HB2	1.54	1.15
1:A:9:ARG:HH11	1:A:9:ARG:HG2	1.13	1.13
1:A:253:LEU:H	1:A:253:LEU:HD23	1.15	1.11
1:A:58:LYS:HD3	1:A:124:LYS:HD2	1.24	1.11
1:A:82:LEU:HD12	1:A:114:LEU:CD1	1.80	1.11
1:A:210:LYS:O	1:A:214:LEU:HD12	1.50	1.08
1:A:256:GLN:HA	1:A:256:GLN:NE2	1.62	1.08
1:A:86:GLN:HE21	1:A:86:GLN:HA	1.04	1.07
1:A:361:LYS:O	1:A:362:GLU:HB2	1.44	1.05
1:A:81:THR:HA	1:A:114:LEU:HD21	1.38	1.04
1:A:86:GLN:NE2	1:A:86:GLN:HA	1.71	1.04
1:A:329:THR:O	1:A:329:THR:HG22	1.53	1.04
1:A:233:ARG:HH11	1:A:233:ARG:HG3	0.91	1.03
1:A:61:ILE:HD11	1:A:123:THR:HG21	1.41	1.03
1:A:61:ILE:HB	1:A:256:GLN:HB2	1.34	1.02
1:A:61:ILE:HD11	1:A:123:THR:CG2	1.90	1.01
1:A:217:PRO:O	1:A:218:LEU:HG	1.60	1.01
1:A:97:VAL:HG21	1:A:113:LEU:HD13	1.43	1.00
1:A:76:THR:HG22	1:A:76:THR:O	1.57	0.99
1:A:253:LEU:N	1:A:253:LEU:CD2	2.25	0.99
1:A:256:GLN:HA	1:A:256:GLN:HE21	1.14	0.98
1:A:139:VAL:HG21	1:A:164:ILE:HD11	1.47	0.96
1:A:253:LEU:H	1:A:253:LEU:CD2	1.78	0.96
1:A:41:LEU:HD13	1:A:143:VAL:HG22	1.43	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ARG:HD3	1:A:114:LEU:HB3	1.47	0.96
1:A:83:VAL:HG13	1:A:84:GLU:OE1	1.64	0.95
1:A:36:LYS:HZ3	1:A:36:LYS:HB2	1.10	0.95
1:A:59:LEU:CD2	1:A:220:TRP:HB3	1.95	0.95
1:A:5:GLY:HA2	1:A:32:THR:HG22	1.50	0.94
1:A:5:GLY:CA	1:A:32:THR:HG22	1.97	0.94
1:A:233:ARG:HB3	1:A:236:LEU:HD12	1.52	0.92
1:A:384:GLU:HG3	1:A:385:LYS:HE2	1.49	0.92
1:A:59:LEU:HD22	1:A:220:TRP:HB3	1.50	0.92
1:A:41:LEU:CD1	1:A:143:VAL:HG22	1.99	0.92
1:A:256:GLN:CA	1:A:256:GLN:HE21	1.82	0.92
1:A:113:LEU:HD23	1:A:113:LEU:O	1.70	0.91
1:A:58:LYS:HD3	1:A:124:LYS:CD	2.01	0.90
1:A:113:LEU:HD23	1:A:113:LEU:C	1.91	0.90
1:A:11:PHE:HB2	1:A:21:VAL:HG22	1.55	0.88
1:A:233:ARG:NH1	1:A:233:ARG:HG3	1.71	0.88
1:A:241:LYS:HG2	1:A:242:THR:H	1.38	0.87
1:A:253:LEU:HD23	1:A:253:LEU:N	1.89	0.87
1:A:46:LEU:HD23	1:A:140:ILE:HG12	1.56	0.86
1:A:46:LEU:CD2	1:A:140:ILE:HG12	2.05	0.86
1:A:50:VAL:HG11	1:A:130:VAL:CG1	2.05	0.86
1:A:71:ASP:O	1:A:80:ALA:HB1	1.75	0.86
1:A:46:LEU:CD2	1:A:140:ILE:CG1	2.54	0.86
1:A:50:VAL:HG12	1:A:134:ASN:HB3	1.58	0.85
1:A:165:THR:HB	1:A:166:PRO:HD2	1.57	0.85
1:A:82:LEU:HD12	1:A:114:LEU:HD12	1.59	0.85
1:A:97:VAL:HG12	1:A:98:ASP:H	1.41	0.84
1:A:329:THR:O	1:A:329:THR:CG2	2.23	0.84
1:A:5:GLY:N	1:A:32:THR:HG22	1.92	0.84
1:A:50:VAL:HG11	1:A:130:VAL:HG13	1.60	0.84
1:A:82:LEU:HD12	1:A:114:LEU:HD11	1.59	0.83
1:A:50:VAL:HG22	1:A:135:LEU:CD2	2.09	0.83
1:A:321:LEU:CD2	1:A:368:GLU:HG3	2.07	0.83
1:A:48:THR:OG1	1:A:137:TYR:CD2	2.29	0.83
1:A:239:THR:HB	1:A:251:VAL:HG22	1.61	0.83
1:A:361:LYS:O	1:A:362:GLU:CB	2.26	0.82
1:A:233:ARG:HH11	1:A:233:ARG:CG	1.83	0.82
1:A:65:ILE:CG2	1:A:117:ALA:HB1	2.09	0.81
1:A:137:TYR:OH	1:A:187:PRO:HB3	1.79	0.81
1:A:300:VAL:O	1:A:333:CYS:HB2	1.79	0.81
1:A:204:LYS:HB2	1:A:206:TRP:CH2	2.15	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:LEU:HD21	1:A:140:ILE:CG1	2.10	0.81
1:A:284:LYS:O	1:A:284:LYS:HG3	1.80	0.80
1:A:256:GLN:CA	1:A:256:GLN:NE2	2.43	0.80
1:A:94:ARG:HE	1:A:114:LEU:HD23	1.47	0.79
1:A:176:THR:O	1:A:177:ASP:HB2	1.78	0.79
1:A:321:LEU:HD21	1:A:368:GLU:HG3	1.65	0.79
1:A:5:GLY:HA2	1:A:32:THR:CG2	2.13	0.79
1:A:87:ASP:HB3	1:A:90:PHE:CE1	2.18	0.79
1:A:251:VAL:O	1:A:252:VAL:CG1	2.31	0.79
1:A:272:THR:HG22	1:A:277:THR:HG23	1.66	0.78
1:A:9:ARG:NH1	1:A:9:ARG:HG2	1.95	0.78
1:A:315:THR:CG2	1:A:321:LEU:CD1	2.62	0.77
1:A:94:ARG:CD	1:A:114:LEU:HB3	2.14	0.77
1:A:317:HIS:NE2	1:A:368:GLU:OE2	2.18	0.77
1:A:76:THR:CG2	1:A:76:THR:O	2.32	0.77
1:A:394:LYS:O	1:A:394:LYS:HG2	1.82	0.77
1:A:81:THR:HG22	1:A:82:LEU:N	1.99	0.77
1:A:65:ILE:HG23	1:A:117:ALA:HB1	1.68	0.76
1:A:253:LEU:HD22	1:A:253:LEU:N	1.99	0.76
1:A:34:MET:HG2	1:A:35:ALA:N	1.99	0.76
1:A:50:VAL:HG22	1:A:135:LEU:HD21	1.67	0.76
1:A:7:GLY:HA2	1:A:297:ILE:O	1.85	0.75
1:A:86:GLN:NE2	1:A:86:GLN:CA	2.45	0.75
1:A:25:LEU:CD2	1:A:43:ILE:HG22	2.17	0.74
1:A:59:LEU:CD2	1:A:220:TRP:CB	2.65	0.74
1:A:315:THR:CG2	1:A:321:LEU:HD12	2.18	0.73
1:A:61:ILE:HB	1:A:256:GLN:CB	2.16	0.73
1:A:46:LEU:HD21	1:A:140:ILE:HG13	1.69	0.73
1:A:343:LYS:C	1:A:343:LYS:HD3	2.08	0.73
1:A:350:ARG:HD3	1:A:370:GLU:O	1.89	0.72
1:A:174:GLN:HE22	1:A:180:ALA:HB2	1.54	0.72
1:A:125:LEU:HD12	1:A:125:LEU:C	2.10	0.72
1:A:9:ARG:HH11	1:A:9:ARG:CG	1.94	0.71
1:A:81:THR:CA	1:A:114:LEU:HD21	2.17	0.71
1:A:46:LEU:HD23	1:A:140:ILE:CG1	2.19	0.71
1:A:319:THR:OG1	1:A:368:GLU:HG2	1.91	0.71
1:A:86:GLN:HE21	1:A:86:GLN:CA	1.85	0.71
1:A:41:LEU:CD1	1:A:143:VAL:CG2	2.69	0.71
1:A:74:CYS:HB2	1:A:77:GLN:HG3	1.73	0.70
1:A:66:SER:OG	1:A:120:LYS:CD	2.40	0.70
1:A:241:LYS:HG2	1:A:242:THR:N	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:LYS:O	1:A:197:VAL:HG13	1.92	0.69
1:A:315:THR:HG21	1:A:321:LEU:HD11	1.74	0.69
1:A:251:VAL:O	1:A:252:VAL:HG13	1.93	0.69
1:A:181:LEU:C	1:A:181:LEU:HD23	2.14	0.69
1:A:5:GLY:CA	1:A:32:THR:CG2	2.71	0.68
1:A:217:PRO:O	1:A:218:LEU:CG	2.41	0.67
1:A:97:VAL:CG2	1:A:113:LEU:HD13	2.23	0.67
1:A:18:ALA:HB1	1:A:289:MET:O	1.95	0.67
1:A:36:LYS:NZ	1:A:36:LYS:CB	2.42	0.67
1:A:61:ILE:HD11	1:A:123:THR:HG22	1.74	0.66
1:A:165:THR:CB	1:A:166:PRO:HD2	2.19	0.66
1:A:52:ASN:H	1:A:275:THR:HG22	1.61	0.66
1:A:251:VAL:C	1:A:252:VAL:HG13	2.16	0.66
1:A:140:ILE:HG22	1:A:140:ILE:O	1.95	0.65
1:A:97:VAL:HG12	1:A:98:ASP:N	2.12	0.65
1:A:300:VAL:O	1:A:333:CYS:CB	2.45	0.65
1:A:82:LEU:HB3	1:A:84:GLU:HG2	1.77	0.65
1:A:50:VAL:HG22	1:A:135:LEU:HD23	1.77	0.65
1:A:375:GLU:OE2	1:A:390:SER:HB2	1.97	0.65
1:A:115:THR:HG23	1:A:240:PHE:CE1	2.32	0.64
1:A:56:LEU:O	1:A:56:LEU:HD22	1.98	0.64
1:A:125:LEU:HD12	1:A:125:LEU:O	1.97	0.64
1:A:174:GLN:HE22	1:A:180:ALA:CB	2.10	0.64
1:A:113:LEU:CD2	1:A:113:LEU:O	2.46	0.64
1:A:27:HIS:CD2	1:A:282:HIS:NE2	2.66	0.64
1:A:81:THR:HG22	1:A:82:LEU:H	1.63	0.64
1:A:188:ARG:HG3	1:A:284:LYS:HB3	1.80	0.64
1:A:373:PHE:HA	1:A:393:LYS:HB3	1.79	0.63
1:A:127:GLY:HA3	1:A:213:PHE:CZ	2.33	0.63
1:A:53:PRO:HG2	1:A:128:LYS:HD2	1.80	0.63
1:A:50:VAL:HG13	1:A:134:ASN:O	1.99	0.62
1:A:27:HIS:NE2	1:A:368:GLU:OE1	2.32	0.62
1:A:232:ASN:O	1:A:233:ARG:HB2	1.99	0.62
1:A:251:VAL:O	1:A:252:VAL:HG12	1.99	0.62
1:A:34:MET:HG2	1:A:35:ALA:O	2.00	0.61
1:A:30:CYS:HB2	1:A:44:GLU:HG3	1.81	0.61
1:A:352:VAL:HB	1:A:368:GLU:HB3	1.80	0.61
1:A:198:LEU:HD12	1:A:206:TRP:O	2.00	0.61
1:A:239:THR:HB	1:A:251:VAL:CG2	2.29	0.61
1:A:238:VAL:HA	1:A:252:VAL:HG12	1.83	0.60
1:A:239:THR:HG22	1:A:240:PHE:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:LYS:HB2	1:A:206:TRP:CZ3	2.37	0.60
1:A:82:LEU:CD1	1:A:114:LEU:HD11	2.32	0.60
1:A:66:SER:OG	1:A:120:LYS:HD2	2.01	0.60
1:A:81:THR:CG2	1:A:82:LEU:N	2.64	0.59
1:A:241:LYS:CG	1:A:242:THR:H	2.14	0.59
1:A:174:GLN:NE2	1:A:180:ALA:HA	2.18	0.59
1:A:233:ARG:HB3	1:A:236:LEU:CD1	2.30	0.59
1:A:50:VAL:CG1	1:A:134:ASN:O	2.50	0.59
1:A:240:PHE:HD1	1:A:248:GLN:HG2	1.66	0.59
1:A:369:ALA:O	1:A:371:PRO:HD3	2.02	0.59
1:A:132:TYR:N	1:A:132:TYR:CD2	2.71	0.58
1:A:48:THR:HG22	1:A:279:PHE:HB2	1.84	0.58
1:A:66:SER:OG	1:A:120:LYS:HD3	2.04	0.58
1:A:46:LEU:O	1:A:47:LYS:HB3	2.02	0.57
1:A:315:THR:HG21	1:A:321:LEU:CD1	2.31	0.57
1:A:61:ILE:CD1	1:A:123:THR:HG22	2.34	0.57
1:A:256:GLN:O	1:A:257:GLU:C	2.42	0.57
1:A:74:CYS:O	1:A:77:GLN:HB2	2.03	0.57
1:A:27:HIS:CD2	1:A:282:HIS:CD2	2.92	0.57
1:A:26:GLU:OE1	1:A:353:THR:HA	2.05	0.56
1:A:260:MET:O	1:A:263:ALA:N	2.38	0.56
1:A:373:PHE:CD2	1:A:393:LYS:HD3	2.41	0.56
1:A:34:MET:HA	1:A:178:TYR:OH	2.06	0.56
1:A:50:VAL:HG12	1:A:134:ASN:CB	2.34	0.56
1:A:353:THR:O	1:A:353:THR:HG22	2.06	0.56
1:A:71:ASP:O	1:A:80:ALA:CB	2.53	0.56
1:A:81:THR:CG2	1:A:82:LEU:H	2.19	0.56
1:A:322:VAL:HG13	1:A:367:ILE:HB	1.86	0.56
1:A:52:ASN:HA	1:A:275:THR:CG2	2.36	0.56
1:A:289:MET:HE1	1:A:294:LEU:HD11	1.88	0.55
1:A:36:LYS:HZ2	1:A:36:LYS:HB2	1.62	0.55
1:A:174:GLN:HE22	1:A:180:ALA:CA	2.19	0.55
1:A:61:ILE:HG12	1:A:123:THR:O	2.07	0.55
1:A:251:VAL:C	1:A:252:VAL:CG1	2.75	0.55
1:A:61:ILE:CD1	1:A:123:THR:CG2	2.76	0.55
1:A:97:VAL:O	1:A:111:GLY:N	2.35	0.55
1:A:132:TYR:N	1:A:132:TYR:HD2	2.05	0.54
1:A:345:VAL:O	1:A:345:VAL:HG12	2.07	0.54
1:A:50:VAL:HG13	1:A:134:ASN:C	2.27	0.54
1:A:185:CYS:HB3	1:A:283:LEU:HD22	1.89	0.54
1:A:207:LEU:HD22	1:A:270:ILE:HD11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:ASP:OD2	1:A:194:ASN:HB2	2.08	0.54
1:A:255:SER:C	1:A:256:GLN:HE21	2.12	0.53
1:A:50:VAL:HG11	1:A:130:VAL:HG11	1.86	0.53
1:A:380:VAL:HG12	1:A:387:LEU:HB2	1.88	0.53
1:A:125:LEU:CD1	1:A:125:LEU:C	2.77	0.53
1:A:34:MET:HG3	1:A:38:LYS:O	2.09	0.53
1:A:100:GLY:C	1:A:102:GLY:H	2.11	0.53
1:A:115:THR:HG21	1:A:248:GLN:HB3	1.89	0.53
1:A:350:ARG:NH1	1:A:372:PRO:HA	2.24	0.53
1:A:27:HIS:ND1	1:A:27:HIS:O	2.42	0.53
1:A:4:VAL:C	1:A:32:THR:HG22	2.28	0.53
1:A:204:LYS:CB	1:A:206:TRP:CH2	2.91	0.53
1:A:81:THR:HA	1:A:114:LEU:CD2	2.24	0.53
1:A:181:LEU:HD11	1:A:287:LEU:HD23	1.91	0.52
1:A:315:THR:HG23	1:A:321:LEU:HD12	1.92	0.52
1:A:52:ASN:HA	1:A:275:THR:HG22	1.91	0.52
1:A:27:HIS:HD2	1:A:282:HIS:CD2	2.26	0.52
1:A:341:ASP:HB3	1:A:347:GLN:NE2	2.25	0.52
1:A:332:PRO:HA	1:A:358:VAL:O	2.09	0.52
1:A:63:ALA:CB	1:A:121:CYS:HA	2.39	0.52
1:A:27:HIS:CE1	1:A:368:GLU:OE1	2.63	0.52
1:A:97:VAL:CG1	1:A:98:ASP:H	2.19	0.52
1:A:384:GLU:C	1:A:385:LYS:HG3	2.30	0.52
1:A:87:ASP:OD1	1:A:89:ASN:HB2	2.10	0.52
1:A:72:SER:HB2	1:A:113:LEU:HB2	1.91	0.51
1:A:181:LEU:C	1:A:181:LEU:CD2	2.79	0.51
1:A:256:GLN:N	1:A:256:GLN:HE21	2.07	0.51
1:A:237:LEU:O	1:A:252:VAL:HA	2.11	0.51
1:A:230:THR:HG23	1:A:230:THR:O	2.11	0.51
1:A:27:HIS:NE2	1:A:282:HIS:NE2	2.57	0.51
1:A:321:LEU:HD23	1:A:368:GLU:HG3	1.90	0.51
1:A:46:LEU:N	1:A:138:SER:O	2.43	0.51
1:A:46:LEU:CD2	1:A:140:ILE:HB	2.42	0.50
1:A:103:ASN:HB3	1:A:245:ALA:HB1	1.93	0.50
1:A:9:ARG:NH1	1:A:9:ARG:CG	2.63	0.50
1:A:165:THR:HB	1:A:166:PRO:CD	2.34	0.50
1:A:384:GLU:HG3	1:A:385:LYS:HG3	1.94	0.50
1:A:335:ILE:O	1:A:335:ILE:HG22	2.11	0.50
1:A:24:VAL:HG22	1:A:284:LYS:HB2	1.94	0.50
1:A:60:CYS:HB2	1:A:231:TRP:CH2	2.47	0.50
1:A:80:ALA:O	1:A:114:LEU:HD23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:PHE:HB3	1:A:21:VAL:HG13	1.93	0.49
1:A:66:SER:O	1:A:67:ASN:C	2.50	0.49
1:A:52:ASN:N	1:A:275:THR:HG22	2.26	0.49
1:A:162:ALA:HB2	1:A:173:ILE:HD11	1.94	0.49
1:A:65:ILE:CG2	1:A:117:ALA:CB	2.85	0.49
1:A:41:LEU:HD13	1:A:143:VAL:CG2	2.28	0.49
1:A:282:HIS:CD2	1:A:282:HIS:N	2.81	0.49
1:A:46:LEU:HD23	1:A:140:ILE:CB	2.43	0.48
1:A:49:GLU:HB2	1:A:277:THR:O	2.13	0.48
1:A:60:CYS:HB2	1:A:231:TRP:CZ3	2.49	0.48
1:A:352:VAL:O	1:A:354:ALA:N	2.45	0.48
1:A:20:TRP:CD1	1:A:288:LYS:HG2	2.48	0.48
1:A:384:GLU:CG	1:A:385:LYS:HE2	2.35	0.48
1:A:105:CYS:O	1:A:106:GLY:C	2.52	0.48
1:A:66:SER:HB2	1:A:118:LYS:HB3	1.95	0.48
1:A:287:LEU:N	1:A:287:LEU:HD12	2.29	0.48
1:A:301:MET:SD	1:A:334:LYS:HB3	2.54	0.48
1:A:239:THR:O	1:A:250:ALA:HA	2.14	0.47
1:A:335:ILE:HB	1:A:356:PRO:O	2.14	0.47
1:A:25:LEU:HD23	1:A:43:ILE:HG22	1.93	0.47
1:A:46:LEU:CD2	1:A:140:ILE:CB	2.93	0.47
1:A:65:ILE:HD11	1:A:238:VAL:HG13	1.96	0.47
1:A:27:HIS:CD2	1:A:282:HIS:HE2	2.31	0.46
1:A:302:CYS:SG	1:A:334:LYS:O	2.73	0.46
1:A:58:LYS:O	1:A:59:LEU:HD23	2.16	0.46
1:A:100:GLY:C	1:A:102:GLY:N	2.69	0.46
1:A:337:PHE:C	1:A:337:PHE:CD1	2.88	0.46
1:A:25:LEU:HG	1:A:25:LEU:H	1.52	0.46
1:A:5:GLY:HA2	1:A:32:THR:O	2.16	0.45
1:A:222:SER:O	1:A:223:GLY:C	2.54	0.45
1:A:219:PRO:HA	1:A:232:ASN:O	2.15	0.45
1:A:11:PHE:CD1	1:A:11:PHE:C	2.88	0.45
1:A:61:ILE:O	1:A:256:GLN:HG2	2.16	0.45
1:A:176:THR:O	1:A:177:ASP:CB	2.57	0.45
1:A:304:GLY:HA3	1:A:326:TYR:CE2	2.52	0.45
1:A:45:LEU:HD12	1:A:45:LEU:C	2.37	0.45
1:A:65:ILE:HG23	1:A:117:ALA:CB	2.42	0.45
1:A:50:VAL:CG1	1:A:134:ASN:CB	2.96	0.44
1:A:396:SER:OG	1:A:397:SER:N	2.49	0.44
1:A:188:ARG:HE	1:A:188:ARG:HB3	1.33	0.44
1:A:312:VAL:HG21	1:A:389:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:THR:HG23	1:A:321:LEU:CD1	2.44	0.44
1:A:350:ARG:NE	1:A:372:PRO:HG3	2.33	0.44
1:A:100:GLY:H	1:A:103:ASN:HD21	1.66	0.44
1:A:355:ASN:HA	1:A:356:PRO:HD3	1.78	0.43
1:A:132:TYR:HD2	1:A:132:TYR:H	1.64	0.43
1:A:59:LEU:HD23	1:A:220:TRP:CB	2.44	0.43
1:A:315:THR:CG2	1:A:321:LEU:HD11	2.35	0.43
1:A:265:THR:HG22	1:A:266:GLY:N	2.33	0.43
1:A:272:THR:HG22	1:A:277:THR:CG2	2.42	0.43
1:A:34:MET:HB2	1:A:40:THR:HA	2.00	0.43
1:A:331:ALA:HA	1:A:332:PRO:HA	1.66	0.43
1:A:79:GLU:HA	1:A:112:SER:CB	2.49	0.43
1:A:3:CYS:SG	1:A:30:CYS:C	2.97	0.43
1:A:216:LEU:HA	1:A:217:PRO:HD2	1.91	0.43
1:A:257:GLU:OE2	1:A:261:HIS:NE2	2.51	0.43
1:A:194:ASN:HD22	1:A:194:ASN:HA	1.64	0.43
1:A:135:LEU:HA	1:A:135:LEU:HD23	1.81	0.43
1:A:244:HIS:O	1:A:245:ALA:C	2.57	0.43
1:A:303:THR:C	1:A:304:GLY:O	2.54	0.42
1:A:72:SER:HA	1:A:113:LEU:HA	2.00	0.42
1:A:172:GLU:H	1:A:172:GLU:HG2	1.75	0.42
1:A:11:PHE:HA	1:A:21:VAL:HA	2.00	0.42
1:A:139:VAL:CG2	1:A:164:ILE:HD11	2.35	0.42
1:A:239:THR:CG2	1:A:240:PHE:N	2.82	0.42
1:A:276:THR:HG22	1:A:277:THR:N	2.33	0.42
1:A:360:ASP:OD2	1:A:363:LYS:NZ	2.50	0.42
1:A:56:LEU:O	1:A:57:ARG:HB2	2.19	0.42
1:A:132:TYR:C	1:A:134:ASN:H	2.23	0.42
1:A:141:VAL:HG11	1:A:175:LEU:HD11	2.01	0.42
1:A:312:VAL:HG22	1:A:322:VAL:HB	2.01	0.42
1:A:63:ALA:HA	1:A:121:CYS:HA	2.01	0.42
1:A:48:THR:CG2	1:A:279:PHE:HB2	2.49	0.41
1:A:82:LEU:CG	1:A:114:LEU:HD11	2.49	0.41
1:A:46:LEU:HA	1:A:46:LEU:HD13	1.67	0.41
1:A:50:VAL:HA	1:A:134:ASN:O	2.19	0.41
1:A:347:GLN:NE2	1:A:372:PRO:HG2	2.34	0.41
1:A:14:GLY:O	1:A:15:LEU:C	2.58	0.41
1:A:34:MET:CG	1:A:35:ALA:O	2.68	0.41
1:A:210:LYS:C	1:A:214:LEU:HD12	2.30	0.41
1:A:52:ASN:CA	1:A:275:THR:HG22	2.50	0.41
1:A:85:GLU:OE2	1:A:114:LEU:HD22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:GLU:H	1:A:84:GLU:HG2	1.57	0.41
1:A:75:PRO:O	1:A:76:THR:HB	2.21	0.41
1:A:326:TYR:OH	1:A:330:ASP:HB2	2.21	0.41
1:A:119:PHE:CD2	1:A:119:PHE:C	2.95	0.41
1:A:202:LYS:HB3	1:A:203:GLU:H	1.51	0.41
1:A:128:LYS:NZ	1:A:200:THR:OG1	2.54	0.41
1:A:239:THR:O	1:A:251:VAL:N	2.54	0.40
1:A:6:ILE:O	1:A:6:ILE:HG13	2.20	0.40
1:A:115:THR:CG2	1:A:240:PHE:CE1	3.04	0.40
1:A:243:ALA:HA	1:A:248:GLN:HA	2.03	0.40
1:A:23:VAL:O	1:A:285:CYS:N	2.50	0.40
1:A:197:VAL:HG23	1:A:210:LYS:HA	2.03	0.40
1:A:60:CYS:HB3	1:A:219:PRO:HB2	2.04	0.40
1:A:25:LEU:CD2	1:A:43:ILE:CG2	2.92	0.40
1:A:339:SER:O	1:A:346:THR:HA	2.21	0.40

All (1) 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)
1:A:75:PRO:O	1:A:311:GLU:OE1[7_455]	1.98	0.22

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	371/400 (93%)	314 (85%)	50 (14%)	7 (2%)	10 51

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	GLY

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Mol	Chain	Res	Type
1	A	158	HIS
1	A	217	PRO
1	A	361	LYS
1	A	103	ASN
1	A	264	LEU
1	A	356	PRO

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	324/341 (95%)	243 (75%)	81 (25%)	1 4

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	9	ARG
1	A	23	VAL
1	A	25	LEU
1	A	29	SER
1	A	30	CYS
1	A	34	MET
1	A	36	LYS
1	A	37	ASP
1	A	40	THR
1	A	43	ILE
1	A	45	LEU
1	A	46	LEU
1	A	47	LYS
1	A	48	THR
1	A	50	VAL
1	A	56	LEU
1	A	70	THR
1	A	83	VAL
1	A	84	GLU

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Mol	Chain	Res	Type
1	A	86	GLN
1	A	89	ASN
1	A	90	PHE
1	A	94	ARG
1	A	108	PHE
1	A	113	LEU
1	A	118	LYS
1	A	125	LEU
1	A	131	GLN
1	A	132	TYR
1	A	136	LYS
1	A	140	ILE
1	A	160	THR
1	A	161	ILE
1	A	164	ILE
1	A	170	THR
1	A	171	SER
1	A	176	THR
1	A	181	LEU
1	A	188	ARG
1	A	194	ASN
1	A	195	GLU
1	A	202	LYS
1	A	210	LYS
1	A	215	ASP
1	A	222	SER
1	A	229	GLU
1	A	233	ARG
1	A	236	LEU
1	A	244	HIS
1	A	253	LEU
1	A	256	GLN
1	A	257	GLU
1	A	260	MET
1	A	271	GLN
1	A	275	THR
1	A	284	LYS
1	A	289	MET
1	A	305	SER
1	A	307	LYS
1	A	310	LYS
1	A	314	GLU

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Mol	Chain	Res	Type
1	A	319	THR
1	A	322	VAL
1	A	327	GLU
1	A	329	THR
1	A	330	ASP
1	A	337	PHE
1	A	338	SER
1	A	340	GLN
1	A	343	LYS
1	A	351	LEU
1	A	357	ILE
1	A	367	ILE
1	A	370	GLU
1	A	380	VAL
1	A	385	LYS
1	A	388	LYS
1	A	390	SER
1	A	394	LYS
1	A	396	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	GLN
1	A	131	GLN
1	A	174	GLN
1	A	194	ASN
1	A	256	GLN
1	A	323	GLN
1	A	340	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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, 95^{th} 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	379/400 (94%)	-0.54	1 (0%)	94	91	29, 61, 97, 142	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	245	ALA	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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, 95^{th} 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
2	CL	A	1396	1/1	0.80	0.98	-	40,40,40,40	1

6.5 Other polymers (i)

There are no such residues in this entry.