



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:08 AM GMT

PDB ID : 1ZTX
Title : West Nile Virus Envelope Protein DIII in complex with neutralizing E16 antibody Fab
Authors : Nybakken, G.E.; Oliphant, T.; Diamond, M.S.; Fremont, D.H.
Deposited on : 2005-05-27
Resolution : 2.50 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

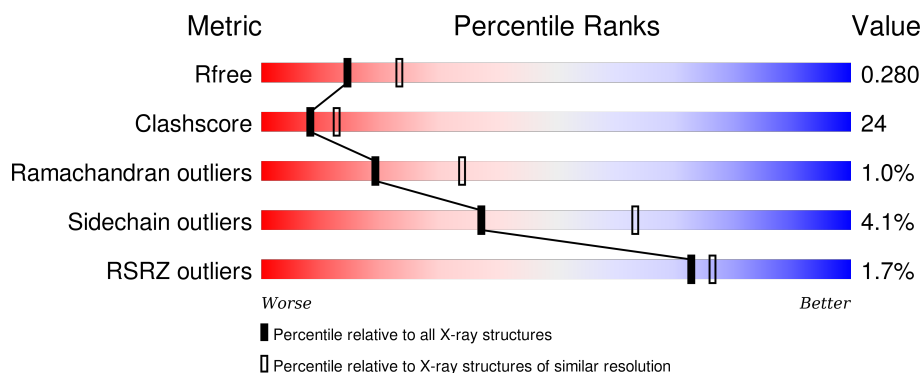
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	E	108	<div> <div>2%</div> <div>54%</div> <div>36%</div> <div>6%</div> </div>
2	H	219	<div> <div>2%</div> <div>63%</div> <div>35%</div> <div>•</div> </div>
3	L	212	<div> <div>%</div> <div>57%</div> <div>40%</div> <div>•</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4296 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	E	101	Total	C	N	O	S	0	0	0
			758	484	128	144	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	294	GLY	-	CLONING ARTIFACT	UNP Q91KZ4
E	295	SER	-	CLONING ARTIFACT	UNP Q91KZ4

- Molecule 2 is a protein called Heavy Chain of E16 Antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	0	0
			1639	1028	266	335	10			

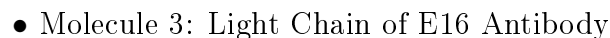
- Molecule 3 is a protein called Light Chain of E16 Antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	0	0
			1643	1022	279	335	7			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	59	Total	O	0	0
			59	59		
4	H	102	Total	O	0	0
			102	102		
4	L	95	Total	O	0	0
			95	95		

- Molecule 1: Envelope protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.40 Å 83.30 Å 110.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 47.35 – 2.49	Depositor EDS
% Data completeness (in resolution range)	96.4 (50.00-2.50) 95.5 (47.35-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.48 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.208 , 0.282 0.208 , 0.280	Depositor DCC
R_{free} test set	817 reflections (4.88%)	DCC
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 17056 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4296	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% 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](#)

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	E	0.37	0/777	0.67	1/1063 (0.1%)
2	H	0.37	0/1682	0.67	0/2298
3	L	0.38	0/1680	0.69	1/2283 (0.0%)
All	All	0.38	0/4139	0.68	2/5644 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	L	210	ASN	N-CA-C	5.82	126.72	111.00
1	E	375	LEU	CA-CB-CG	5.03	126.86	115.30

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	E	758	0	750	41	0
2	H	1639	0	1570	76	0
3	L	1643	0	1581	87	0
4	E	59	0	0	3	0
4	H	102	0	0	5	0
4	L	95	0	0	1	0
All	All	4296	0	3901	193	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 24.

All (193) 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)
3:L:135:PHE:HB3	3:L:137:ASN:HD21	1.16	1.11
1:E:391:GLN:HE22	2:H:31:ASP:HB3	1.21	1.03
3:L:21:ILE:HD12	3:L:102:THR:HG21	1.45	0.96
2:H:6:GLN:NE2	2:H:107:THR:HG22	1.80	0.95
3:L:187:GLU:HA	3:L:212:ASN:HB2	1.50	0.94
3:L:210:ASN:O	3:L:211:ARG:HD3	1.70	0.91
3:L:201:SER:HB3	3:L:205:ILE:HD11	1.53	0.90
3:L:144:ILE:HD13	3:L:145:ASN:N	1.87	0.89
3:L:135:PHE:HB3	3:L:137:ASN:ND2	1.92	0.85
3:L:6:GLN:HE22	3:L:87:TYR:HA	1.41	0.84
3:L:31:THR:HG22	3:L:50:TRP:HE3	1.44	0.83
2:H:83:THR:HG22	2:H:85:GLU:H	1.42	0.83
2:H:34:ILE:HD12	2:H:78:ALA:HB2	1.60	0.83
2:H:6:GLN:HE21	2:H:107:THR:HG22	1.42	0.80
2:H:206:THR:HG22	2:H:222:LYS:HA	1.62	0.80
2:H:119:PRO:HB3	2:H:147:TYR:HB3	1.65	0.78
3:L:195:GLU:HG2	3:L:206:VAL:CG2	2.13	0.77
3:L:211:ARG:HH11	3:L:211:ARG:HB2	1.52	0.75
1:E:371:VAL:HG23	1:E:373:ILE:HD11	1.67	0.74
3:L:195:GLU:HG2	3:L:206:VAL:HG23	1.68	0.74
3:L:11:MET:HE2	3:L:104:LEU:HA	1.69	0.73
2:H:34:ILE:CD1	2:H:78:ALA:HB2	2.20	0.71
3:L:69:THR:HG23	3:L:70:ASP:OD1	1.91	0.71
1:E:388:ARG:HD2	1:E:389:GLY:H	1.56	0.70
2:H:115:LYS:HE3	4:H:287:HOH:O	1.90	0.70
3:L:144:ILE:HD13	3:L:145:ASN:H	1.59	0.68
3:L:193:THR:HG23	3:L:208:SER:OG	1.93	0.68
2:H:177:LEU:HD11	3:L:162:SER:HB2	1.76	0.68
3:L:11:MET:HE1	3:L:104:LEU:HG	1.75	0.68
1:E:311:PHE:HE1	1:E:325:LEU:HD22	1.59	0.67
3:L:54:ARG:HH21	3:L:63:THR:HG22	1.61	0.66
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.78	0.66
3:L:189:HIS:O	3:L:212:ASN:HB3	1.95	0.65
3:L:117:ILE:HD11	3:L:148:TRP:CZ3	2.32	0.65
3:L:5:THR:HG23	3:L:24:LYS:HB3	1.77	0.65
3:L:117:ILE:HD13	3:L:194:CYS:HB2	1.79	0.64
1:E:388:ARG:HA	1:E:392:GLN:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:17:ASP:O	3:L:78:VAL:HG23	1.97	0.64
1:E:304:VAL:HG12	1:E:339:PRO:HG3	1.79	0.63
3:L:6:GLN:NE2	3:L:88:CYS:H	1.97	0.63
2:H:1:GLN:CD	2:H:1:GLN:N	2.52	0.63
2:H:39:GLN:O	2:H:89:VAL:HG12	1.98	0.62
2:H:33:TRP:HB2	2:H:95:SER:HB3	1.81	0.62
2:H:199:TRP:CG	2:H:200:PRO:HA	2.35	0.62
1:E:304:VAL:CG1	1:E:339:PRO:HG3	2.29	0.62
1:E:388:ARG:CD	1:E:389:GLY:H	2.13	0.61
2:H:150:GLU:HG2	2:H:151:SER:H	1.64	0.61
1:E:326:GLU:OE2	1:E:370:LYS:HD2	2.01	0.61
3:L:175:MET:HE2	3:L:177:SER:HB2	1.83	0.60
3:L:103:LYS:HE3	3:L:165:ASP:OD1	2.01	0.60
2:H:105:HIS:HA	3:L:43:SER:HG	1.67	0.60
1:E:370:LYS:HB3	4:E:210:HOH:O	2.02	0.60
1:E:343:VAL:HG11	1:E:349:LEU:HA	1.84	0.59
2:H:152:VAL:HG12	2:H:212:HIS:HD2	1.67	0.59
3:L:138:ASN:HA	3:L:172:THR:OG1	2.01	0.59
2:H:40:ARG:HB2	2:H:43:HIS:CD2	2.38	0.59
1:E:325:LEU:HD12	1:E:325:LEU:O	2.03	0.58
3:L:31:THR:HG22	3:L:50:TRP:CE3	2.33	0.58
2:H:25:THR:HA	4:H:309:HOH:O	2.02	0.58
3:L:166:GLN:HG3	3:L:173:TYR:CZ	2.39	0.58
2:H:105:HIS:HA	3:L:43:SER:OG	2.03	0.57
3:L:16:GLY:O	3:L:77:SER:HA	2.04	0.57
3:L:13:THR:O	3:L:106:LEU:HA	2.03	0.57
3:L:13:THR:HG23	3:L:106:LEU:HD23	1.87	0.57
2:H:175:PRO:HG2	3:L:162:SER:OG	2.05	0.56
3:L:117:ILE:HD13	3:L:194:CYS:CB	2.35	0.56
1:E:318:THR:CG2	1:E:324:VAL:HG23	2.36	0.56
3:L:195:GLU:HG2	3:L:206:VAL:HG21	1.85	0.56
2:H:150:GLU:O	2:H:151:SER:HB3	2.06	0.56
2:H:209:SER:HB3	2:H:220:ASP:OD1	2.06	0.56
2:H:177:LEU:N	2:H:177:LEU:HD12	2.21	0.56
1:E:354:ARG:NH1	1:E:376:GLU:CD	2.60	0.55
3:L:5:THR:HG22	4:L:255:HOH:O	2.05	0.55
2:H:83:THR:HG22	2:H:84:SER:N	2.22	0.55
1:E:333:ASP:HB2	2:H:56:ARG:NH1	2.21	0.54
3:L:201:SER:CB	3:L:205:ILE:HD11	2.32	0.54
1:E:373:ILE:N	1:E:373:ILE:HD12	2.22	0.54
3:L:44:PRO:O	3:L:45:LYS:HD3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:205:ILE:H	3:L:205:ILE:HD12	1.73	0.54
3:L:193:THR:HG22	3:L:206:VAL:CG2	2.38	0.54
2:H:18:VAL:HG22	2:H:19:GLN:N	2.23	0.54
2:H:151:SER:HB2	4:H:318:HOH:O	2.07	0.53
2:H:200:PRO:CB	2:H:227:PRO:HG3	2.39	0.53
2:H:68:THR:HB	2:H:81:GLN:HB3	1.89	0.53
3:L:30:SER:O	3:L:31:THR:HB	2.08	0.53
3:L:39:LYS:O	3:L:42:GLN:HB2	2.08	0.53
2:H:38:LYS:CB	2:H:48:ILE:HD11	2.39	0.52
3:L:61:ARG:HG2	3:L:61:ARG:HH11	1.75	0.51
1:E:337:LYS:HE2	1:E:359:ASN:OD1	2.10	0.51
3:L:135:PHE:C	3:L:136:LEU:HD23	2.31	0.51
3:L:54:ARG:NH2	3:L:63:THR:HG22	2.24	0.51
1:E:354:ARG:HH12	1:E:376:GLU:CD	2.13	0.51
3:L:61:ARG:NH1	3:L:61:ARG:HG2	2.26	0.51
2:H:1:GLN:H1	2:H:1:GLN:CD	2.14	0.51
2:H:2:VAL:HG22	2:H:27:TYR:HB3	1.93	0.51
2:H:6:GLN:HE22	2:H:107:THR:HG22	1.71	0.51
1:E:384:ILE:N	1:E:384:ILE:HD12	2.26	0.50
3:L:166:GLN:HG3	3:L:173:TYR:CE1	2.46	0.50
2:H:194:PRO:HB2	2:H:198:THR:HG23	1.94	0.50
1:E:388:ARG:HD2	1:E:389:GLY:N	2.26	0.50
3:L:188:ARG:CZ	3:L:188:ARG:HA	2.42	0.50
1:E:333:ASP:HB2	2:H:56:ARG:HH12	1.77	0.50
2:H:40:ARG:HB2	2:H:43:HIS:HD2	1.76	0.50
2:H:176:ALA:C	2:H:177:LEU:HD12	2.32	0.49
2:H:38:LYS:HB2	2:H:48:ILE:HD11	1.95	0.48
3:L:104:LEU:HD23	3:L:104:LEU:C	2.33	0.48
1:E:388:ARG:CG	1:E:389:GLY:H	2.26	0.48
3:L:59:PRO:HG2	3:L:62:PHE:CD1	2.49	0.48
2:H:98:TYR:HB2	2:H:100(A):TYR:OH	2.13	0.48
1:E:380:GLY:O	1:E:398:HIS:HA	2.13	0.48
2:H:11:LEU:HD22	2:H:149:PRO:HD3	1.96	0.48
1:E:388:ARG:CA	1:E:392:GLN:HB2	2.42	0.48
2:H:40:ARG:HA	2:H:88:ALA:CB	2.44	0.47
1:E:335:PRO:HA	1:E:362:VAL:O	2.14	0.47
3:L:182:THR:HG23	3:L:185:GLU:OE1	2.14	0.47
3:L:83:LEU:HD21	3:L:106:LEU:HG	1.97	0.47
3:L:28:ASP:HA	3:L:68:GLY:O	2.15	0.47
2:H:83:THR:CG2	2:H:84:SER:N	2.78	0.47
3:L:7:SER:HB3	3:L:22:THR:OG1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:388:ARG:CG	1:E:389:GLY:N	2.78	0.47
3:L:117:ILE:HD11	3:L:148:TRP:CH2	2.50	0.46
3:L:183:LYS:O	3:L:187:GLU:HG3	2.16	0.46
3:L:187:GLU:O	3:L:212:ASN:ND2	2.49	0.46
2:H:34:ILE:CD1	2:H:78:ALA:CB	2.93	0.46
2:H:208:CYS:O	2:H:208:CYS:SG	2.74	0.46
2:H:33:TRP:CE2	2:H:52:LEU:HG	2.51	0.46
3:L:28:ASP:OD1	3:L:68:GLY:HA2	2.15	0.46
3:L:115:VAL:HG22	3:L:136:LEU:HD22	1.98	0.46
3:L:195:GLU:HA	3:L:206:VAL:HG23	1.97	0.46
3:L:86:TYR:O	3:L:101:GLY:HA2	2.15	0.46
1:E:373:ILE:HG22	1:E:375:LEU:HD12	1.98	0.45
2:H:119:PRO:HB3	2:H:147:TYR:CB	2.42	0.45
2:H:152:VAL:HG12	2:H:212:HIS:CD2	2.50	0.45
2:H:199:TRP:CD1	2:H:200:PRO:HA	2.51	0.45
1:E:310:LYS:HD3	4:E:195:HOH:O	2.17	0.45
2:H:140:LEU:HB3	2:H:223:LEU:HD13	1.99	0.45
2:H:174:PHE:CD2	3:L:176:SER:HB2	2.51	0.45
3:L:175:MET:CE	3:L:177:SER:HB2	2.47	0.45
1:E:301:THR:HB	4:E:181:HOH:O	2.16	0.45
3:L:136:LEU:N	3:L:136:LEU:HD23	2.31	0.45
3:L:205:ILE:N	3:L:205:ILE:HD12	2.31	0.45
2:H:119:PRO:CB	2:H:147:TYR:HB3	2.39	0.44
2:H:146:GLY:HA2	2:H:184:LEU:HB3	1.98	0.44
2:H:119:PRO:HB3	2:H:147:TYR:CD2	2.53	0.44
2:H:140:LEU:HD13	2:H:223:LEU:HD12	2.00	0.44
3:L:132:VAL:HG13	3:L:209:PHE:HE2	1.82	0.44
1:E:316:ALA:O	1:E:323:VAL:HA	2.18	0.44
2:H:150:GLU:CG	2:H:151:SER:H	2.30	0.44
3:L:113:PRO:HB3	3:L:139:PHE:HB3	2.00	0.44
1:E:325:LEU:HD21	1:E:384:ILE:HG21	1.99	0.44
2:H:11:LEU:HD12	2:H:110:THR:O	2.19	0.43
2:H:40:ARG:HA	2:H:88:ALA:HB2	2.00	0.43
2:H:210:VAL:O	2:H:218:THR:HA	2.19	0.43
3:L:48:ILE:HD13	3:L:54:ARG:HA	2.00	0.43
3:L:167:ASP:O	3:L:171:SER:HA	2.18	0.43
2:H:23:LYS:HD3	4:H:330:HOH:O	2.19	0.43
3:L:6:GLN:HE21	3:L:88:CYS:H	1.65	0.43
2:H:150:GLU:HG3	2:H:185:TYR:CG	2.53	0.43
1:E:379:PHE:CE1	1:E:399:LYS:HE2	2.54	0.43
3:L:55:HIS:O	3:L:58:VAL:HB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:193:THR:HG22	3:L:206:VAL:HG22	2.01	0.42
1:E:339:PRO:O	1:E:386:VAL:HA	2.18	0.42
2:H:150:GLU:HB2	2:H:185:TYR:CE2	2.55	0.42
1:E:368:ASN:HA	1:E:368:ASN:HD22	1.64	0.42
2:H:178:LEU:HG	2:H:185:TYR:CE1	2.55	0.42
1:E:380:GLY:HA2	1:E:398:HIS:CE1	2.54	0.42
3:L:31:THR:O	3:L:31:THR:CG2	2.67	0.42
2:H:177:LEU:HD21	3:L:161:ASN:O	2.19	0.42
2:H:18:VAL:HG22	2:H:19:GLN:H	1.85	0.42
2:H:174:PHE:CG	3:L:176:SER:HB2	2.55	0.42
3:L:120:PRO:HD2	3:L:186:TYR:CZ	2.54	0.42
2:H:153:THR:HG22	2:H:156:THR:HG23	2.00	0.42
2:H:196:SER:HB2	4:H:265:HOH:O	2.20	0.42
2:H:34:ILE:HD12	2:H:52(A):CYS:SG	2.60	0.41
3:L:23:CYS:HB2	3:L:35:TRP:CH2	2.55	0.41
2:H:39:GLN:HB3	2:H:89:VAL:HG13	2.02	0.41
2:H:100:ASP:HB3	3:L:96:LEU:HD11	2.02	0.41
2:H:130:ASP:O	2:H:133:THR:C	2.58	0.41
2:H:187:MET:HG2	2:H:188:SER:N	2.35	0.41
2:H:47:TRP:CZ2	2:H:49:GLY:HA2	2.56	0.41
2:H:33:TRP:NE1	2:H:52:LEU:HG	2.34	0.41
1:E:385:VAL:HG22	1:E:394:ASN:HB3	2.02	0.41
3:L:159:VAL:O	3:L:160:LEU:HD12	2.20	0.41
1:E:314:THR:O	1:E:315:PRO:C	2.60	0.40
3:L:11:MET:HE3	3:L:12:SER:CA	2.51	0.40
3:L:132:VAL:HG12	3:L:148:TRP:CZ3	2.57	0.40
1:E:379:PHE:CZ	1:E:399:LYS:HE2	2.57	0.40
1:E:340:ILE:HA	1:E:385:VAL:O	2.21	0.40
1:E:396:HIS:CG	1:E:397:TRP:N	2.89	0.40
3:L:6:GLN:HE22	3:L:87:TYR:CA	2.23	0.40
1:E:338:VAL:HA	1:E:339:PRO:HD3	1.94	0.40
2:H:41:PRO:HD3	2:H:88:ALA:HA	2.03	0.40
3:L:83:LEU:O	3:L:84:ALA:HB2	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	E	99/108 (92%)	95 (96%)	4 (4%)	0	100	100
2	H	217/219 (99%)	197 (91%)	16 (7%)	4 (2%)	11	18
3	L	210/212 (99%)	194 (92%)	15 (7%)	1 (0%)	34	55
All	All	526/539 (98%)	486 (92%)	35 (7%)	5 (1%)	19	34

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	134	THR
2	H	135	GLY
2	H	127	GLY
3	L	68	GLY
2	H	41	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	E	85/89 (96%)	82 (96%)	3 (4%)	43	70
2	H	186/186 (100%)	176 (95%)	10 (5%)	27	49
3	L	188/188 (100%)	182 (97%)	6 (3%)	46	74
All	All	459/463 (99%)	440 (96%)	19 (4%)	37	63

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	349	LEU
1	E	368	ASN
1	E	391	GLN
2	H	41	PRO
2	H	52	LEU
2	H	82(C)	LEU
2	H	85	GLU
2	H	94	ARG
2	H	107	THR
2	H	113	SER
2	H	168	SER
2	H	199	TRP
2	H	200	PRO
3	L	11	MET
3	L	17	ASP
3	L	144	ILE
3	L	175	MET
3	L	206	VAL
3	L	211	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	368	ASN
1	E	391	GLN
2	H	43	HIS
2	H	76	ASN
2	H	81	GLN
2	H	172	HIS
3	L	6	GLN
3	L	8	HIS
3	L	137	ASN
3	L	156	GLN
3	L	161	ASN
3	L	190	ASN
3	L	212	ASN

5.3.3 RNA ⓘ

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 ⓘ

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	E	101/108 (93%)	0.02	2 (1%) 68 72	20, 35, 52, 63	0
2	H	219/219 (100%)	0.09	5 (2%) 64 67	17, 30, 54, 85	0
3	L	212/212 (100%)	-0.00	2 (0%) 85 88	17, 30, 42, 63	0
All	All	532/539 (98%)	0.04	9 (1%) 73 76	17, 30, 51, 85	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	130	ASP	4.6
2	H	129	GLY	4.5
2	H	133	THR	4.0
3	L	212	ASN	3.4
2	H	41	PRO	2.5
2	H	81	GLN	2.1
1	E	328	GLN	2.1
3	L	190	ASN	2.1
1	E	312	LEU	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.