



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:48 AM GMT

PDB ID : 2ISG
Title : Botulinum Neurotoxin A Light Chain WT Crystal Form B
Authors : Brunger, A.T.; Stegmann, C.M.
Deposited on : 2006-10-17
Resolution : 2.00 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

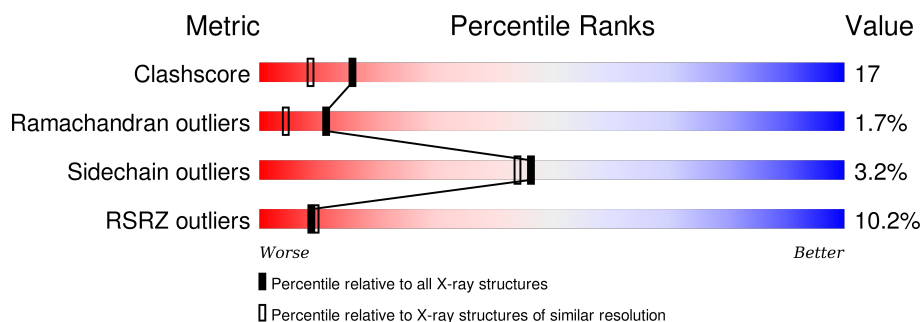
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	421	
1	B	421	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6998 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 Neurotoxin BoNT/A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	55	0	0
			3366	2170	551	637	8			
1	B	416	Total	C	N	O	S	55	0	0
			3366	2170	551	637	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	421	PRO	-	CLONING ARTIFACT	UNP Q7B8V4
A	422	GLY	-	CLONING ARTIFACT	UNP Q7B8V4
B	421	PRO	-	CLONING ARTIFACT	UNP Q7B8V4
B	422	GLY	-	CLONING ARTIFACT	UNP Q7B8V4

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	129	Total	O	0	0
			129	129		

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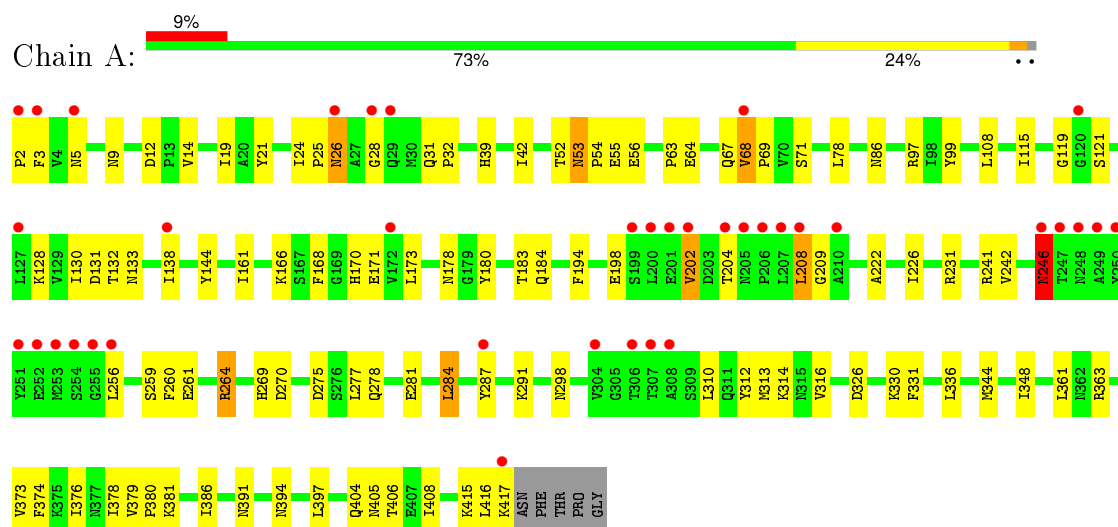
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	133	Total 133	O 133	0	0

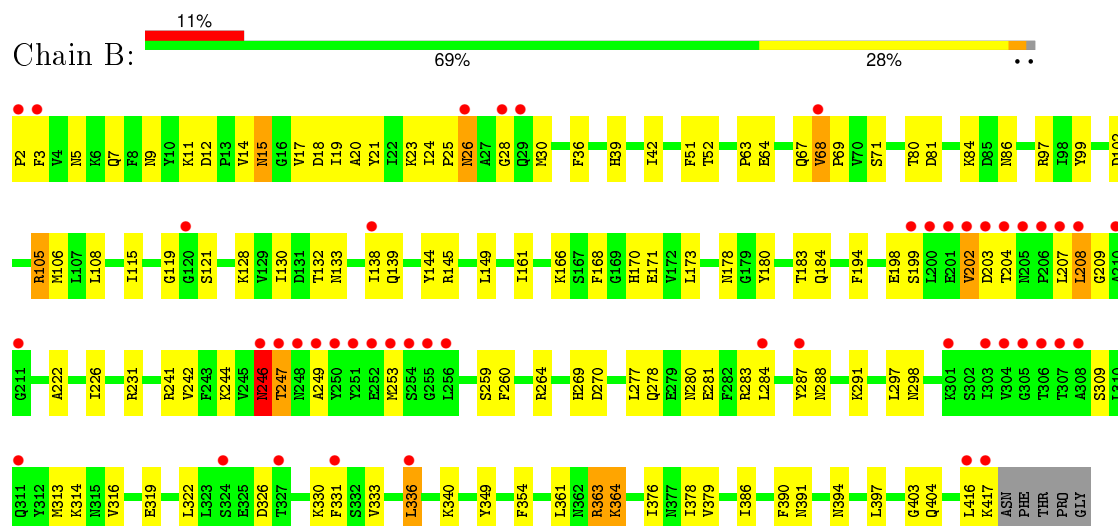
3 Residue-property plots

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

• Molecule 1: Neurotoxin BoNT/A



• Molecule 1: Neurotoxin BoNT/A



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	41.99Å 190.96Å 56.95Å 90.00° 90.09° 90.00°	Depositor
Resolution (Å)	42.44 – 2.00 42.44 – 1.99	Depositor EDS
% Data completeness (in resolution range)	89.0 (42.44-2.00) 88.2 (42.44-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.240 , 0.277 0.252 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.469 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 53852 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6998	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NI, ZN

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	0.37	0/3446	0.60	0/4665
1	B	0.37	0/3446	0.59	0/4665
All	All	0.37	0/6892	0.59	0/9330

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	3366	0	3317	109	0
1	B	3366	0	3317	119	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	B	2	0	0	0	0
4	A	129	0	0	2	0
4	B	133	0	0	3	0
All	All	6998	0	6634	223	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 17.

All (223) 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:417:LYS:HG2	1:B:253:MET:H	1.29	0.95
1:B:15:ASN:HD22	1:B:17:VAL:H	1.23	0.87
1:B:226:ILE:HD12	1:B:349:TYR:HB3	1.57	0.86
1:B:2:PRO:HG3	1:B:108:LEU:HB3	1.58	0.85
1:B:2:PRO:HA	1:B:108:LEU:HD13	1.59	0.85
1:A:2:PRO:HA	1:A:108:LEU:HD13	1.57	0.85
1:B:138:ILE:HG12	1:B:144:TYR:CE1	2.12	0.84
1:B:361:LEU:H	1:B:404:GLN:HE22	1.26	0.83
1:A:2:PRO:HG3	1:A:108:LEU:HB3	1.60	0.82
1:A:138:ILE:HG12	1:A:144:TYR:CE1	2.14	0.82
1:A:52:THR:HG21	1:A:166:LYS:HG3	1.62	0.81
1:A:246:ASN:HB2	1:A:256:LEU:HB2	1.65	0.79
1:A:381:LYS:HD3	1:A:381:LYS:H	1.49	0.77
1:B:416:LEU:O	1:B:417:LYS:HB2	1.85	0.77
1:B:52:THR:HG21	1:B:166:LYS:HG3	1.67	0.76
1:B:21:TYR:O	1:B:138:ILE:HG13	1.84	0.76
1:A:361:LEU:H	1:A:404:GLN:HE22	1.33	0.76
1:A:170:HIS:HD2	1:A:173:LEU:H	1.35	0.75
1:B:363:ARG:NH1	1:B:363:ARG:HG3	2.03	0.73
1:B:363:ARG:HG3	1:B:363:ARG:HH11	1.53	0.73
1:B:15:ASN:ND2	1:B:17:VAL:H	1.87	0.72
1:A:68:VAL:HG11	1:A:417:LYS:HB2	1.71	0.71
1:A:67:GLN:HG3	1:B:244:LYS:HB2	1.73	0.71
1:B:298:ASN:HD21	1:B:331:PHE:H	1.39	0.71
1:B:226:ILE:CD1	1:B:349:TYR:HB3	2.21	0.70
1:B:170:HIS:HD2	1:B:173:LEU:H	1.37	0.70
1:B:105:ARG:HH11	1:B:105:ARG:HB2	1.56	0.70
1:A:417:LYS:HG2	1:B:253:MET:N	2.07	0.68
1:A:277:LEU:O	1:A:281:GLU:HG2	1.93	0.68
1:A:376:ILE:HD12	1:A:378:ILE:CD1	2.24	0.67
1:A:21:TYR:O	1:A:138:ILE:HG13	1.95	0.66
1:B:277:LEU:O	1:B:281:GLU:HG2	1.95	0.66
1:A:2:PRO:HD2	1:A:39:HIS:CG	2.31	0.66
1:B:52:THR:HG22	1:B:166:LYS:NZ	2.11	0.65
1:A:53:ASN:C	1:A:53:ASN:HD22	2.00	0.65
1:A:53:ASN:ND2	1:A:55:GLU:H	1.93	0.65
1:B:376:ILE:HD12	1:B:378:ILE:CD1	2.27	0.65
1:A:298:ASN:HD21	1:A:331:PHE:H	1.45	0.64
1:B:2:PRO:HD2	1:B:39:HIS:CG	2.33	0.64
1:A:53:ASN:HD22	1:A:54:PRO:N	1.95	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:PHE:CE2	1:A:5:ASN:ND2	2.66	0.64
1:A:2:PRO:HD3	1:A:42:ILE:HD12	1.80	0.63
1:B:269:HIS:HD2	1:B:270:ASP:OD1	1.81	0.63
1:A:68:VAL:HG21	1:A:417:LYS:HE2	1.79	0.63
1:A:68:VAL:HB	1:A:69:PRO:CD	2.29	0.62
1:B:313:MET:HE2	1:B:313:MET:HA	1.80	0.62
1:B:222:ALA:O	1:B:226:ILE:HG12	2.00	0.62
1:A:246:ASN:HB2	1:A:256:LEU:HD12	1.81	0.61
1:B:170:HIS:CD2	1:B:173:LEU:H	2.18	0.61
1:A:313:MET:HE2	1:A:313:MET:HA	1.80	0.61
1:A:416:LEU:O	1:A:417:LYS:HG3	2.01	0.61
1:B:287:TYR:O	1:B:291:LYS:HG2	2.00	0.61
1:A:170:HIS:CD2	1:A:173:LEU:H	2.18	0.61
1:B:26:ASN:HD22	1:B:168:PHE:HE1	1.46	0.60
1:A:24:ILE:HG23	1:A:25:PRO:HD2	1.82	0.60
1:B:364:LYS:HD3	1:B:364:LYS:N	2.17	0.59
1:B:2:PRO:HD3	1:B:42:ILE:HD12	1.83	0.59
1:B:9:ASN:HB2	1:B:12:ASP:OD1	2.01	0.59
1:B:14:VAL:HG13	1:B:19:ILE:O	2.02	0.59
1:B:198:GLU:HG2	1:B:361:LEU:HD21	1.83	0.59
1:B:376:ILE:HD12	1:B:378:ILE:HD13	1.85	0.59
1:B:24:ILE:HG23	1:B:25:PRO:HD2	1.85	0.59
1:A:52:THR:HG22	1:A:166:LYS:NZ	2.19	0.58
1:B:64:GLU:OE2	1:B:64:GLU:HA	2.03	0.58
1:A:208:LEU:HD13	1:A:208:LEU:N	2.17	0.58
1:A:9:ASN:HB2	1:A:12:ASP:OD2	2.03	0.58
1:B:241:ARG:HH21	1:B:278:GLN:NE2	2.02	0.58
1:B:184:GLN:OE1	1:B:231:ARG:HD3	2.03	0.58
1:A:287:TYR:CE2	1:A:291:LYS:HE3	2.39	0.57
1:B:363:ARG:CG	1:B:363:ARG:HH11	2.18	0.57
1:A:310:LEU:O	1:A:314:LYS:HG3	2.04	0.57
1:A:416:LEU:O	1:A:417:LYS:CB	2.53	0.56
1:A:21:TYR:HB2	1:A:138:ILE:HD12	1.87	0.56
1:A:138:ILE:HG12	1:A:144:TYR:CZ	2.40	0.56
1:B:68:VAL:O	1:B:71:SER:O	2.24	0.56
1:B:15:ASN:HD21	1:B:18:ASP:H	1.52	0.55
1:A:376:ILE:HD12	1:A:378:ILE:HD11	1.87	0.55
1:B:208:LEU:N	1:B:208:LEU:HD13	2.20	0.55
1:B:15:ASN:C	1:B:15:ASN:HD22	2.10	0.55
1:B:26:ASN:ND2	1:B:51:PHE:O	2.40	0.55
1:A:242:VAL:HG12	1:A:259:SER:HA	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:VAL:C	1:A:204:THR:H	2.09	0.55
1:A:391:ASN:HD21	1:A:404:GLN:HE21	1.53	0.55
1:A:376:ILE:HD12	1:A:378:ILE:HD13	1.87	0.54
1:B:3:PHE:HB2	1:B:99:TYR:CE2	2.42	0.54
1:A:269:HIS:HD2	1:A:270:ASP:OD1	1.90	0.54
1:B:21:TYR:HB2	1:B:138:ILE:HD12	1.88	0.54
1:B:297:LEU:O	1:B:314:LYS:HE2	2.07	0.54
1:B:52:THR:HG22	1:B:166:LYS:HZ2	1.72	0.54
1:A:314:LYS:HB3	1:A:331:PHE:HE2	1.72	0.54
1:B:288:ASN:HB3	4:B:630:HOH:O	2.07	0.54
1:B:52:THR:CG2	1:B:166:LYS:NZ	2.71	0.53
1:B:202:VAL:C	1:B:204:THR:H	2.11	0.53
1:A:198:GLU:HG2	1:A:361:LEU:HD21	1.90	0.53
1:A:121:SER:H	1:A:128:LYS:HB3	1.74	0.53
1:B:336:LEU:O	1:B:340:LYS:HG3	2.09	0.53
1:B:171:GLU:H	1:B:171:GLU:CD	2.12	0.53
1:A:3:PHE:HB2	1:A:99:TYR:CE2	2.44	0.53
1:B:242:VAL:HG12	1:B:259:SER:HA	1.91	0.53
1:B:326:ASP:OD2	1:B:330:LYS:HB3	2.09	0.53
1:B:2:PRO:HD3	1:B:42:ILE:CD1	2.39	0.52
1:B:416:LEU:O	1:B:417:LYS:CB	2.56	0.52
1:B:63:PRO:O	1:B:64:GLU:HB2	2.09	0.52
1:A:63:PRO:O	1:A:64:GLU:HB2	2.10	0.52
1:B:161:ILE:HB	1:B:194:PHE:HE2	1.74	0.52
1:A:68:VAL:O	1:A:71:SER:O	2.28	0.52
1:B:241:ARG:HH21	1:B:278:GLN:CD	2.13	0.52
1:A:14:VAL:HG13	1:A:19:ILE:O	2.10	0.52
1:A:53:ASN:HB3	1:A:56:GLU:HG3	1.91	0.52
1:A:64:GLU:HA	1:A:64:GLU:OE2	2.08	0.51
1:A:326:ASP:OD2	1:A:330:LYS:HB3	2.10	0.51
1:B:3:PHE:CE2	1:B:5:ASN:OD1	2.63	0.51
1:A:275:ASP:HB3	1:A:278:GLN:HG3	1.90	0.51
1:A:52:THR:CG2	1:A:166:LYS:NZ	2.74	0.51
1:B:391:ASN:HD21	1:B:404:GLN:HE21	1.59	0.51
1:A:68:VAL:HB	1:A:69:PRO:HD3	1.93	0.51
1:B:319:GLU:O	1:B:322:LEU:HD12	2.11	0.50
1:B:2:PRO:CA	1:B:108:LEU:HD13	2.38	0.50
1:B:376:ILE:HD12	1:B:378:ILE:HD11	1.93	0.50
1:A:417:LYS:HD2	1:B:253:MET:HA	1.93	0.50
1:A:25:PRO:O	1:A:26:ASN:C	2.50	0.50
1:B:25:PRO:O	1:B:26:ASN:C	2.50	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:TYR:O	1:A:316:VAL:HG23	2.11	0.50
1:A:326:ASP:OD2	1:A:330:LYS:HE3	2.12	0.50
1:A:52:THR:CG2	1:A:166:LYS:HZ3	2.26	0.49
1:A:52:THR:HG22	1:A:166:LYS:HZ3	1.76	0.49
1:A:241:ARG:HH21	1:A:278:GLN:NE2	2.11	0.49
1:A:2:PRO:CA	1:A:108:LEU:HD13	2.36	0.49
1:B:115:ILE:HD12	1:B:316:VAL:CG1	2.43	0.48
1:A:14:VAL:HA	1:A:19:ILE:HG22	1.95	0.48
1:B:23:LYS:HE3	1:B:30:MET:O	2.13	0.48
1:A:275:ASP:OD2	1:A:277:LEU:HB2	2.14	0.48
1:B:132:THR:HB	1:B:168:PHE:HB2	1.95	0.48
1:B:309:SER:N	4:B:547:HOH:O	2.39	0.48
1:B:313:MET:HE1	1:B:316:VAL:HG21	1.95	0.48
1:A:416:LEU:O	1:A:417:LYS:CG	2.60	0.48
1:A:373:VAL:HG12	1:A:416:LEU:HD12	1.94	0.48
1:A:416:LEU:O	1:A:417:LYS:HB2	2.13	0.48
1:B:121:SER:HB2	1:B:128:LYS:HB2	1.95	0.48
1:B:121:SER:H	1:B:128:LYS:HB3	1.78	0.48
1:A:241:ARG:NH2	1:A:278:GLN:OE1	2.47	0.48
1:A:184:GLN:OE1	1:A:231:ARG:HD3	2.14	0.48
1:B:133:ASN:ND2	1:B:183:THR:H	2.12	0.47
1:B:130:ILE:HD12	4:B:594:HOH:O	2.13	0.47
1:A:161:ILE:HB	1:A:194:PHE:HE2	1.79	0.47
1:A:2:PRO:HD3	1:A:42:ILE:CD1	2.42	0.47
1:A:67:GLN:HB3	1:B:244:LYS:HD2	1.97	0.47
1:B:241:ARG:NH2	1:B:278:GLN:OE1	2.48	0.47
1:A:261:GLU:O	1:A:264:ARG:HG3	2.14	0.46
1:B:364:LYS:H	1:B:364:LYS:HD3	1.80	0.46
1:B:298:ASN:ND2	1:B:331:PHE:H	2.11	0.46
1:A:275:ASP:HB3	1:A:278:GLN:CG	2.45	0.46
1:B:138:ILE:HG12	1:B:144:TYR:CZ	2.48	0.46
1:B:314:LYS:HB3	1:B:331:PHE:HE2	1.80	0.46
1:A:53:ASN:CG	1:A:56:GLU:HG3	2.36	0.46
1:A:86:ASN:ND2	1:A:379:VAL:HG21	2.30	0.46
1:B:68:VAL:HB	1:B:69:PRO:CD	2.46	0.46
1:B:14:VAL:HG13	1:B:20:ALA:HA	1.98	0.45
1:A:132:THR:HB	1:A:168:PHE:HB2	1.98	0.45
1:B:241:ARG:HH21	1:B:278:GLN:HE22	1.65	0.45
1:A:31:GLN:HG2	4:A:539:HOH:O	2.16	0.45
1:A:241:ARG:HH21	1:A:278:GLN:CD	2.20	0.45
1:A:63:PRO:O	1:A:64:GLU:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:VAL:CG2	1:A:417:LYS:HE2	2.47	0.44
1:A:115:ILE:HD12	1:A:316:VAL:CG1	2.47	0.44
1:B:246:ASN:CG	1:B:247:THR:N	2.71	0.44
1:A:97:ARG:HA	1:A:386:ILE:HG23	2.00	0.44
1:B:86:ASN:ND2	1:B:379:VAL:HG21	2.33	0.44
1:B:105:ARG:NH1	1:B:105:ARG:HB2	2.30	0.44
1:A:53:ASN:HD22	1:A:55:GLU:H	1.64	0.43
1:A:133:ASN:ND2	1:A:183:THR:H	2.15	0.43
1:B:417:LYS:N	1:B:417:LYS:HD2	2.32	0.43
1:A:298:ASN:ND2	1:A:331:PHE:H	2.13	0.43
1:A:178:ASN:OD1	1:A:180:TYR:HB2	2.18	0.43
1:A:171:GLU:CD	1:A:171:GLU:H	2.22	0.43
1:B:15:ASN:HD21	1:B:18:ASP:N	2.16	0.43
1:B:52:THR:CG2	1:B:166:LYS:HZ2	2.29	0.43
1:B:63:PRO:O	1:B:64:GLU:CB	2.66	0.43
1:A:31:GLN:H	1:A:31:GLN:CD	2.19	0.43
1:A:378:ILE:CG2	1:A:378:ILE:O	2.67	0.43
1:B:97:ARG:HA	1:B:386:ILE:HG23	1.99	0.43
1:B:11:LYS:HE3	1:B:81:ASP:HB3	2.01	0.43
1:B:280:ASN:CG	1:B:283:ARG:HH21	2.21	0.43
1:A:222:ALA:O	1:A:226:ILE:HG13	2.18	0.43
1:B:36:PHE:N	1:B:36:PHE:CD1	2.86	0.43
1:A:53:ASN:HD22	1:A:54:PRO:CD	2.32	0.43
1:B:119:GLY:HA3	1:B:180:TYR:CE2	2.55	0.42
1:B:226:ILE:HD11	1:B:354:PHE:HE2	1.84	0.42
1:B:336:LEU:HD13	1:B:336:LEU:O	2.19	0.42
1:B:178:ASN:OD1	1:B:180:TYR:HB2	2.20	0.42
1:B:67:GLN:HA	1:B:67:GLN:HE21	1.83	0.42
1:A:21:TYR:HB3	1:A:32:PRO:HB2	2.02	0.42
1:B:378:ILE:HD11	1:B:390:PHE:CZ	2.55	0.42
1:A:379:VAL:HB	1:A:380:PRO:HD3	2.02	0.42
1:B:105:ARG:CB	1:B:105:ARG:HH11	2.29	0.42
1:B:326:ASP:OD2	1:B:330:LYS:HE3	2.19	0.42
1:B:314:LYS:HB3	1:B:331:PHE:CE2	2.55	0.41
1:A:121:SER:HB2	1:A:128:LYS:HB2	2.01	0.41
1:B:199:SER:HB2	1:B:203:ASP:HA	2.02	0.41
1:A:284:LEU:HD13	1:A:284:LEU:O	2.20	0.41
1:A:314:LYS:HB3	1:A:331:PHE:CE2	2.53	0.41
1:A:344:MET:HG2	1:A:348:ILE:HD12	2.02	0.41
1:B:115:ILE:HD12	1:B:316:VAL:HG13	2.02	0.41
1:A:119:GLY:HA3	1:A:180:TYR:CE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:397:LEU:HG	1:B:403:GLY:HA2	2.02	0.41
1:B:207:LEU:HD22	1:B:207:LEU:N	2.36	0.41
1:A:374:PHE:HE1	1:A:415:LYS:HG2	1.86	0.41
1:A:405:ASN:HB3	1:A:408:ILE:HB	2.02	0.41
1:B:149:LEU:HD23	1:B:149:LEU:H	1.86	0.41
1:A:373:VAL:CG1	1:A:416:LEU:HD12	2.51	0.41
1:B:80:THR:O	1:B:84:LYS:HG3	2.21	0.41
1:B:313:MET:CE	1:B:316:VAL:HG21	2.50	0.41
1:A:21:TYR:CB	1:A:138:ILE:HD12	2.50	0.41
1:A:53:ASN:CB	1:A:56:GLU:HG3	2.50	0.41
1:B:246:ASN:CG	1:B:247:THR:H	2.23	0.41
1:B:102:ASP:O	1:B:106:MET:HE2	2.21	0.40
1:A:130:ILE:HD12	4:A:557:HOH:O	2.20	0.40
1:B:336:LEU:CD1	1:B:340:LYS:HD2	2.50	0.40
1:A:406:THR:CG2	1:A:415:LYS:HZ3	2.34	0.40
1:B:52:THR:HG22	1:B:166:LYS:HZ3	1.82	0.40
1:B:139:GLN:NE2	1:B:145:ARG:HE	2.19	0.40
1:A:53:ASN:HA	1:A:54:PRO:HD2	1.93	0.40
1:B:291:LYS:CD	1:B:333:VAL:HB	2.52	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	414/421 (98%)	381 (92%)	27 (6%)	6 (1%)	14	6
1	B	414/421 (98%)	381 (92%)	25 (6%)	8 (2%)	10	4
All	All	828/842 (98%)	762 (92%)	52 (6%)	14 (2%)	11	4

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	68	VAL
1	A	202	VAL
1	A	246	ASN
1	B	26	ASN
1	B	202	VAL
1	B	246	ASN
1	B	249	ALA
1	B	68	VAL
1	A	28	GLY
1	A	209	GLY
1	B	28	GLY
1	B	209	GLY
1	B	247	THR

5.3.2 Protein sidechains ⓘ

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	372/376 (99%)	360 (97%)	12 (3%)	46	44
1	B	372/376 (99%)	360 (97%)	12 (3%)	46	44
All	All	744/752 (99%)	720 (97%)	24 (3%)	46	44

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	78	LEU
1	A	131	ASP
1	A	208	LEU
1	A	246	ASN
1	A	260	PHE
1	A	264	ARG
1	A	284	LEU
1	A	336	LEU
1	A	363	ARG

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Mol	Chain	Res	Type
1	A	394	ASN
1	A	397	LEU
1	B	7	GLN
1	B	15	ASN
1	B	105	ARG
1	B	208	LEU
1	B	246	ASN
1	B	260	PHE
1	B	264	ARG
1	B	284	LEU
1	B	336	LEU
1	B	363	ARG
1	B	364	LYS
1	B	394	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	53	ASN
1	A	86	ASN
1	A	133	ASN
1	A	136	ASN
1	A	139	GLN
1	A	162	GLN
1	A	170	HIS
1	A	246	ASN
1	A	269	HIS
1	A	298	ASN
1	A	353	ASN
1	A	394	ASN
1	A	404	GLN
1	B	15	ASN
1	B	40	ASN
1	B	67	GLN
1	B	86	ASN
1	B	133	ASN
1	B	139	GLN
1	B	170	HIS
1	B	246	ASN
1	B	269	HIS
1	B	298	ASN

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Mol	Chain	Res	Type
1	B	353	ASN
1	B	394	ASN
1	B	400	ASN
1	B	404	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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are 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 [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	A	416/421 (98%)	0.59	38 (9%) 11 12	23, 38, 79, 103	14 (3%)
1	B	416/421 (98%)	0.63	47 (11%) 7 7	22, 38, 78, 103	14 (3%)
All	All	832/842 (98%)	0.61	85 (10%) 9 9	22, 38, 79, 103	28 (3%)

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	202	VAL	13.0
1	A	204	THR	12.9
1	B	251	TYR	11.1
1	A	247	THR	10.5
1	A	248	ASN	10.3
1	A	206	PRO	10.1
1	B	255	GLY	10.0
1	B	247	THR	9.1
1	A	202	VAL	8.9
1	A	200	LEU	8.8
1	A	251	TYR	8.7
1	B	200	LEU	8.6
1	A	199	SER	8.2
1	B	201	GLU	8.0
1	B	253	MET	7.9
1	B	249	ALA	7.5
1	B	204	THR	7.4
1	B	199	SER	7.4
1	A	253	MET	7.2
1	A	68	VAL	7.0
1	A	205	ASN	6.8
1	A	201	GLU	6.8
1	B	206	PRO	6.8
1	A	255	GLY	6.6

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Mol	Chain	Res	Type	RSRZ
1	B	248	ASN	6.1
1	B	68	VAL	6.1
1	A	250	TYR	6.0
1	A	307	THR	5.8
1	B	307	THR	5.8
1	A	254	SER	5.5
1	B	207	LEU	5.5
1	B	208	LEU	5.4
1	B	205	ASN	5.3
1	A	207	LEU	5.3
1	B	246	ASN	5.1
1	B	26	ASN	4.8
1	A	26	ASN	4.7
1	B	304	VAL	4.6
1	B	417	LYS	4.4
1	A	252	GLU	4.2
1	B	203	ASP	4.1
1	A	210	ALA	4.0
1	A	208	LEU	4.0
1	A	304	VAL	3.9
1	A	246	ASN	3.8
1	B	2	PRO	3.7
1	B	331	PHE	3.7
1	A	417	LYS	3.6
1	B	210	ALA	3.4
1	A	2	PRO	3.4
1	B	250	TYR	3.2
1	B	138	ILE	3.1
1	A	287	TYR	2.9
1	B	336	LEU	2.9
1	A	138	ILE	2.8
1	B	306	THR	2.8
1	B	416	LEU	2.7
1	A	249	ALA	2.7
1	A	3	PHE	2.7
1	B	327	THR	2.6
1	B	29	GLN	2.5
1	A	256	LEU	2.5
1	A	5	ASN	2.4
1	A	127	LEU	2.4
1	B	311	GLN	2.4
1	A	308	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	305	GLY	2.4
1	B	287	TYR	2.3
1	B	211	GLY	2.3
1	A	306	THR	2.3
1	B	3	PHE	2.3
1	A	172	VAL	2.2
1	A	28	GLY	2.2
1	B	256	LEU	2.2
1	B	324	SER	2.2
1	A	29	GLN	2.2
1	B	252	GLU	2.2
1	B	301	LYS	2.2
1	B	254	SER	2.1
1	B	28	GLY	2.1
1	B	284	LEU	2.1
1	B	120	GLY	2.1
1	B	303	ILE	2.0
1	B	308	ALA	2.0
1	A	120	GLY	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
3	NI	B	502	1/1	0.99	0.11	-0.78	30,30,30,30	0
3	NI	B	503	1/1	0.99	0.10	-1.71	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	B	501	1/1	0.99	0.09	-2.13	29,29,29,29	0
2	ZN	A	500	1/1	1.00	0.07	-3.03	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.