



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:46 PM UTC

PDB ID : 1Z0H / pdb_00001z0h
Title : N-terminal helix reorients in recombinant C-fragment of Clostridium botulinum type B
Authors : Jayaraman, S.; Eswarmoorthy, S.; Ashraf, S.A.; Smith, L.A.; Swaminathan, S.
Deposited on : 2005-03-01
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

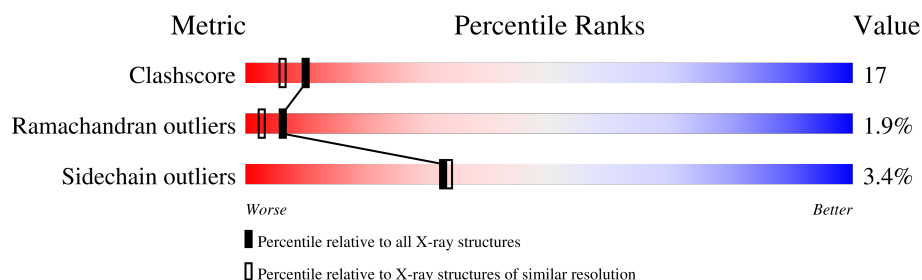
1 Overall quality at a glance

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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 of 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	438	 69% 28% ..
1	B	438	 62% 34% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7864 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 Botulinum neurotoxin type B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3724	2406	608	702	8			
1	B	438	Total	C	N	O	S	0	0	0
			3724	2406	608	702	8			

- Molecule 2 is water.

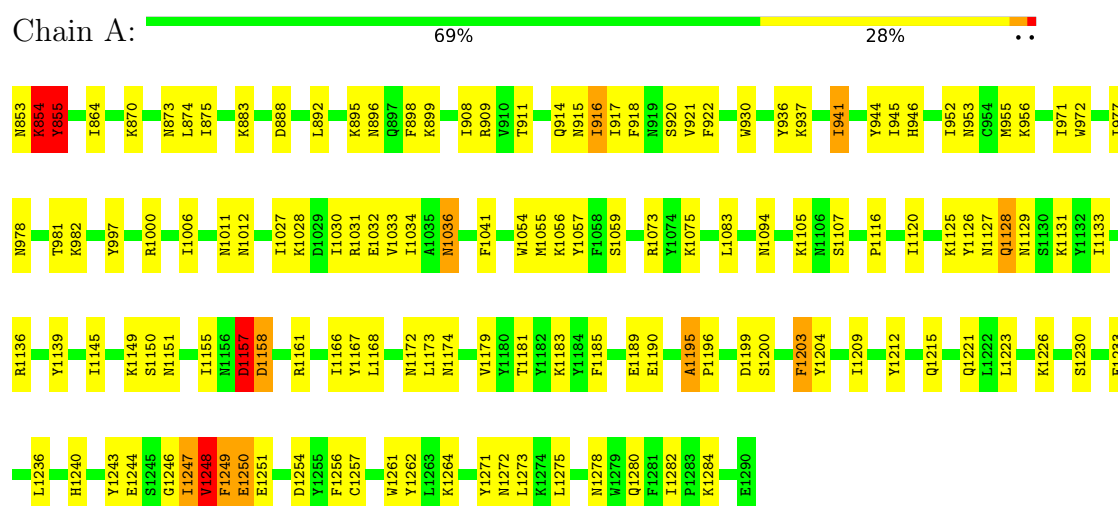
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	250	Total	O	0	0
			250	250		
2	B	166	Total	O	0	0
			166	166		

3 Residue-property plots

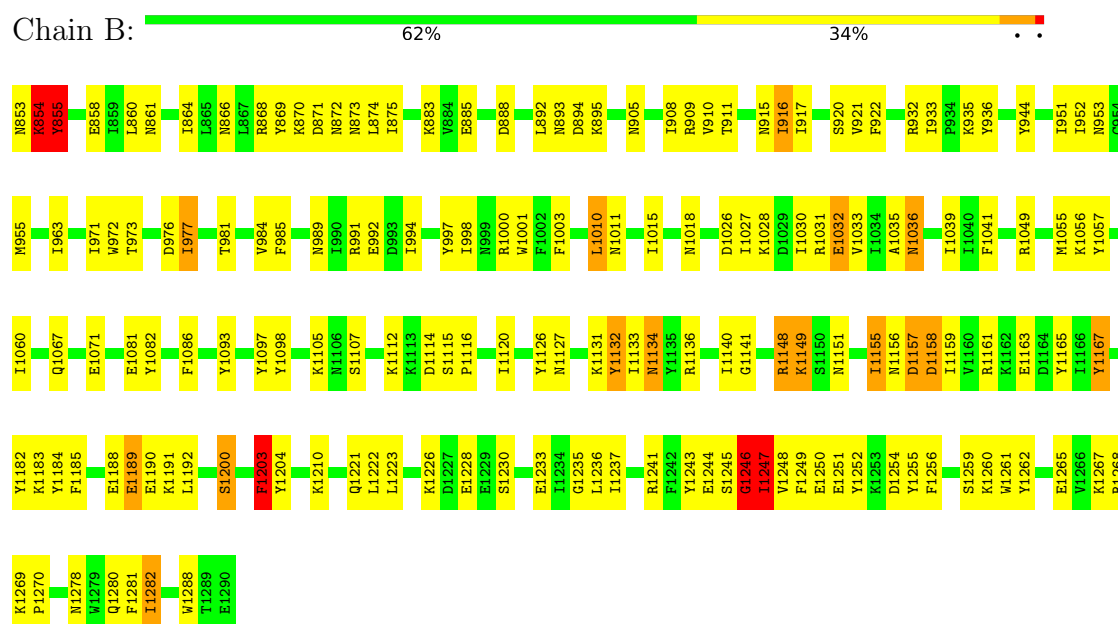
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: Botulinum neurotoxin type B



• Molecule 1: Botulinum neurotoxin type B



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.66Å 78.81Å 87.72Å 90.00° 103.03° 90.00°	Depositor
Resolution (Å)	40.82 – 2.00	Depositor
% Data completeness (in resolution range)	89.6 (40.82-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.234 , 0.282	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7864	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

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	A	0.42	0/3813	0.94	18/5141 (0.4%)
1	B	0.58	2/3813 (0.1%)	1.00	23/5141 (0.4%)
All	All	0.50	2/7626 (0.0%)	0.97	41/10282 (0.4%)

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	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1246	GLY	C-N	-20.70	1.05	1.33
1	B	858	GLU	C-N	14.42	1.53	1.33

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1246	GLY	O-C-N	-16.07	106.60	122.19
1	B	1246	GLY	CA-C-N	11.89	143.37	121.97
1	B	1246	GLY	C-N-CA	11.89	143.37	121.97
1	B	855	TYR	N-CA-C	-8.89	102.14	113.16
1	B	916	ILE	N-CA-C	8.40	118.32	110.42
1	A	916	ILE	N-CA-C	8.08	118.09	110.74
1	B	1256	PHE	N-CA-C	-7.98	97.05	109.25
1	B	1098	TYR	N-CA-C	-7.83	98.93	110.52
1	B	971	ILE	N-CA-C	7.06	118.76	108.53
1	A	1257	CYS	N-CA-C	7.05	120.13	109.41
1	B	1133	ILE	N-CA-C	6.86	119.83	109.20
1	A	946	HIS	N-CA-C	6.83	121.84	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1133	ILE	N-CA-C	6.79	119.58	108.99
1	A	1195	ALA	N-CA-C	6.52	113.87	108.07
1	A	1282	ILE	N-CA-C	6.51	114.57	107.60
1	B	1031	ARG	N-CA-C	6.33	114.83	108.75
1	A	855	TYR	N-CA-C	-6.32	104.84	113.30
1	B	1184	TYR	N-CA-C	6.24	118.99	110.06
1	A	854	LYS	N-CA-C	-6.11	104.42	112.24
1	B	1282	ILE	N-CA-C	6.05	114.08	107.60
1	B	1203	PHE	N-CA-C	6.05	117.43	108.60
1	B	1244	GLU	N-CA-CB	5.99	120.62	110.49
1	A	1166	ILE	N-CA-C	5.57	115.61	108.82
1	A	1256	PHE	N-CA-C	-5.50	101.22	109.15
1	B	1260	LYS	N-CA-C	-5.48	105.33	112.23
1	B	997	TYR	N-CA-C	5.34	119.56	112.72
1	A	1105	LYS	N-CA-C	5.28	117.72	111.33
1	A	1012	ASN	N-CA-C	5.26	117.39	109.23
1	B	1035	ALA	N-CA-C	5.26	120.56	113.72
1	B	933	ILE	N-CA-C	5.25	113.65	107.77
1	A	930	TRP	N-CA-C	-5.23	101.64	109.95
1	B	1247	ILE	N-CA-C	-5.23	98.47	109.34
1	A	971	ILE	N-CA-C	5.22	116.00	108.48
1	B	1131	LYS	N-CA-C	-5.18	106.91	113.18
1	A	888	ASP	N-CA-C	5.16	119.05	112.34
1	B	1167	TYR	N-CA-C	-5.16	100.50	108.90
1	A	941	ILE	N-CA-C	5.13	115.34	110.42
1	B	1031	ARG	CB-CA-C	-5.11	109.02	116.53
1	A	997	TYR	N-CA-C	5.10	119.71	112.93
1	A	1127	ASN	N-CA-C	5.07	117.92	111.69
1	B	1011	ASN	N-CA-C	5.03	120.06	113.88

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1243	TYR	Mainchain
1	B	1246	GLY	Mainchain

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	3724	0	3627	111	0
1	B	3724	0	3626	146	0
2	A	250	0	0	8	0
2	B	166	0	0	4	0
All	All	7864	0	7253	257	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 (257) 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:B:1248:VAL:HG12	1:B:1249:PHE:CD1	1.65	1.30
1:B:1248:VAL:HG12	1:B:1249:PHE:CE1	1.72	1.22
1:B:1248:VAL:CG1	1:B:1249:PHE:CE1	2.28	1.17
1:B:1010:LEU:H	1:B:1010:LEU:HD12	1.24	0.98
1:B:1247:ILE:HG13	1:B:1248:VAL:HG23	1.41	0.98
1:B:1246:GLY:O	1:B:1247:ILE:HG23	1.69	0.93
1:A:873:ASN:ND2	1:A:874:LEU:H	1.66	0.92
1:B:1248:VAL:CG1	1:B:1249:PHE:CD1	2.48	0.90
1:B:1245:SER:HB3	1:B:1250:GLU:HA	1.52	0.89
1:B:953:ASN:HD21	1:B:955:MET:HE2	1.38	0.89
1:A:873:ASN:HD22	1:A:874:LEU:H	1.16	0.88
1:A:1157:ASP:O	1:A:1158:ASP:HB2	1.74	0.88
1:B:872:ASN:HD22	1:B:892:LEU:HD11	1.39	0.84
1:A:883:LYS:HB3	1:A:911:THR:OG1	1.78	0.83
1:B:866:ASN:HD21	1:B:868:ARG:HE	1.26	0.83
1:B:1248:VAL:HG11	1:B:1249:PHE:CE1	2.13	0.82
1:B:952:ILE:HD11	1:B:1055:MET:HE1	1.63	0.81
1:B:1246:GLY:O	1:B:1247:ILE:HG12	1.81	0.80
1:B:1036:ASN:H	1:B:1036:ASN:HD22	1.29	0.80
1:B:1245:SER:CB	1:B:1250:GLU:HA	2.12	0.79
1:A:1036:ASN:HD22	1:A:1036:ASN:H	1.31	0.79
1:B:883:LYS:HB3	1:B:911:THR:OG1	1.85	0.77
1:A:1125:LYS:HE3	1:A:1136:ARG:NH1	2.02	0.74
1:A:1221:GLN:HE21	1:A:1278:ASN:HD22	1.34	0.74
1:B:866:ASN:ND2	1:B:868:ARG:HE	1.86	0.74
1:B:1183:LYS:HG3	1:B:1203:PHE:HA	1.68	0.74
1:B:873:ASN:ND2	1:B:874:LEU:H	1.86	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:873:ASN:HD22	1:A:874:LEU:N	1.87	0.71
1:A:1075:LYS:NZ	1:A:1215:GLN:HE22	1.89	0.71
1:A:1032:GLU:HA	2:A:263:HOH:O	1.92	0.70
1:A:1221:GLN:HE21	1:A:1278:ASN:ND2	1.90	0.68
1:B:1241:ARG:HD3	1:B:1252:TYR:CD2	2.28	0.68
1:A:1027:ILE:O	1:A:1030:ILE:HG22	1.94	0.68
1:A:1200:SER:HB3	1:A:1203:PHE:CE2	2.29	0.68
1:B:869:TYR:HE1	1:B:892:LEU:HD13	1.59	0.68
1:B:873:ASN:HD22	1:B:874:LEU:H	1.42	0.67
1:B:866:ASN:HD21	1:B:868:ARG:NE	1.92	0.67
1:A:956:LYS:HB3	1:A:1034:ILE:HG21	1.77	0.67
1:A:1226:LYS:HE2	1:A:1230:SER:HB3	1.77	0.67
1:B:953:ASN:ND2	1:B:955:MET:HE2	2.10	0.66
1:A:914:GLN:HE21	1:A:914:GLN:HA	1.61	0.65
1:B:1247:ILE:CG1	1:B:1248:VAL:HG23	2.23	0.65
1:A:1126:TYR:CE1	1:A:1128:GLN:HG2	2.31	0.65
1:B:1248:VAL:HG11	1:B:1249:PHE:HE1	1.60	0.65
1:B:1185:PHE:HB3	1:B:1190:GLU:OE1	1.95	0.65
1:B:1107:SER:HB3	1:B:1120:ILE:CG2	2.27	0.65
1:B:1246:GLY:O	1:B:1247:ILE:CG2	2.44	0.64
1:B:1148:ARG:HH22	1:B:1158:ASP:HB2	1.61	0.64
1:A:873:ASN:ND2	1:A:874:LEU:N	2.43	0.64
1:B:1093:TYR:CZ	1:B:1148:ARG:HG3	2.33	0.64
1:A:1189:GLU:HG3	1:A:1240:HIS:CD2	2.33	0.64
1:A:1011:ASN:OD1	1:A:1028:LYS:HG2	1.98	0.63
1:A:1094:ASN:HD22	1:A:1157:ASP:N	1.95	0.63
1:B:872:ASN:ND2	1:B:892:LEU:HD11	2.13	0.63
1:B:1056:LYS:HE2	1:B:1057:TYR:CE1	2.34	0.63
1:A:1272:ASN:HB3	1:A:1275:LEU:HG	1.79	0.63
1:A:1247:ILE:HD13	1:A:1248:VAL:HG12	1.79	0.63
1:A:921:VAL:HG12	1:A:922:PHE:N	2.13	0.62
1:A:916:ILE:HG23	1:A:917:ILE:H	1.64	0.62
1:B:1200:SER:HB2	1:B:1203:PHE:CE2	2.35	0.62
1:A:915:ASN:HD22	1:A:920:SER:H	1.48	0.62
1:B:1032:GLU:HA	2:B:109:HOH:O	1.98	0.62
1:A:1149:LYS:HG3	1:A:1150:SER:N	2.16	0.61
1:B:910:VAL:HB	1:B:1039:ILE:HB	1.83	0.61
1:B:1112:LYS:HE2	1:B:1114:ASP:OD1	2.00	0.60
1:B:1027:ILE:O	1:B:1030:ILE:HG22	2.02	0.59
1:B:916:ILE:HG23	1:B:917:ILE:H	1.65	0.59
1:B:1165:TYR:CZ	1:B:1228:GLU:HG3	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:855:TYR:HA	2:A:261:HOH:O	2.02	0.59
1:B:1221:GLN:HE21	1:B:1278:ASN:HD22	1.50	0.59
1:B:1236:LEU:HD12	1:B:1262:TYR:HB3	1.85	0.59
1:B:1228:GLU:N	1:B:1228:GLU:OE1	2.36	0.58
1:B:1241:ARG:HD3	1:B:1252:TYR:HD2	1.66	0.58
1:B:932:ARG:HD3	1:B:1001:TRP:CD1	2.39	0.58
1:B:1259:SER:HB3	1:B:1262:TYR:CD2	2.39	0.57
1:A:892:LEU:HD23	1:A:898:PHE:HB3	1.85	0.57
1:A:1094:ASN:HD22	1:A:1157:ASP:CA	2.18	0.57
1:A:952:ILE:HD11	1:A:1055:MET:HE1	1.86	0.56
1:A:1183:LYS:HG3	1:A:1203:PHE:HA	1.86	0.56
1:A:911:THR:HG23	2:A:115:HOH:O	2.05	0.56
1:A:1075:LYS:NZ	1:A:1215:GLN:NE2	2.53	0.56
1:B:1265:GLU:HA	1:B:1268:ARG:HH11	1.71	0.56
1:B:916:ILE:HG23	1:B:917:ILE:N	2.21	0.55
1:A:1075:LYS:HZ1	1:A:1215:GLN:HE22	1.53	0.55
1:A:1083:LEU:CD1	1:A:1209:ILE:HG12	2.36	0.55
1:B:869:TYR:CE1	1:B:892:LEU:HD13	2.40	0.55
1:A:953:ASN:HD21	1:A:955:MET:HE2	1.71	0.55
1:A:921:VAL:CG1	1:A:922:PHE:N	2.70	0.55
1:A:1247:ILE:N	1:A:1247:ILE:HD12	2.21	0.55
1:B:977:ILE:O	1:B:977:ILE:HD13	2.06	0.54
1:B:1148:ARG:NH2	1:B:1158:ASP:HB2	2.22	0.54
1:A:1226:LYS:HE2	1:A:1230:SER:CB	2.38	0.54
1:B:921:VAL:HG13	1:B:1033:VAL:O	2.08	0.54
1:B:921:VAL:HG12	1:B:922:PHE:N	2.21	0.54
1:B:991:ARG:HG3	1:B:1132:TYR:O	2.08	0.54
1:A:1031:ARG:HB3	1:A:1032:GLU:OE1	2.08	0.54
1:A:908:ILE:HB	1:A:1041:PHE:HB2	1.90	0.54
1:A:1149:LYS:HD3	1:A:1167:TYR:CZ	2.43	0.54
1:B:1246:GLY:O	1:B:1247:ILE:CG1	2.54	0.54
1:A:1129:ASN:HB3	2:A:70:HOH:O	2.08	0.54
1:B:1188:GLU:HB3	1:B:1189:GLU:OE1	2.08	0.53
1:B:864:ILE:C	1:B:864:ILE:HD12	2.34	0.53
1:A:937:LYS:HD2	2:A:396:HOH:O	2.09	0.53
1:A:1155:ILE:HD12	2:A:262:HOH:O	2.07	0.53
1:A:1247:ILE:CD1	1:A:1248:VAL:HG12	2.39	0.53
1:B:1156:ASN:O	1:B:1157:ASP:HB2	2.07	0.53
1:B:1247:ILE:HG13	1:B:1248:VAL:CG2	2.29	0.52
1:A:977:ILE:HD13	1:A:1032:GLU:CG	2.39	0.52
1:B:1226:LYS:HB3	1:B:1230:SER:OG	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:984:VAL:HG13	1:B:1015:ILE:HD11	1.91	0.52
1:B:1010:LEU:HD12	1:B:1010:LEU:N	2.08	0.52
1:B:885:GLU:OE2	1:B:909:ARG:HD2	2.09	0.52
1:B:994:ILE:HG13	1:B:1105:LYS:HB2	1.92	0.52
1:A:1173:LEU:O	1:A:1174:ASN:HB2	2.09	0.52
1:B:1049:ARG:HB2	2:B:423:HOH:O	2.09	0.52
1:B:915:ASN:HD22	1:B:920:SER:H	1.58	0.51
1:B:936:TYR:HB3	1:B:944:TYR:CE1	2.45	0.51
1:A:1056:LYS:HE2	1:A:1057:TYR:CE1	2.46	0.51
1:A:1185:PHE:CG	1:A:1190:GLU:HG2	2.46	0.51
1:A:1249:PHE:O	1:A:1250:GLU:HB3	2.08	0.51
1:B:1097:TYR:CG	1:B:1281:PHE:HB3	2.45	0.51
1:B:1265:GLU:HA	1:B:1268:ARG:NH1	2.25	0.51
1:A:1107:SER:HB3	1:A:1120:ILE:CG2	2.40	0.51
1:A:1173:LEU:HD12	1:A:1173:LEU:N	2.25	0.51
1:B:1157:ASP:O	1:B:1158:ASP:HB2	2.09	0.51
1:A:953:ASN:OD1	1:A:955:MET:HE2	2.11	0.51
1:B:1036:ASN:H	1:B:1036:ASN:ND2	2.06	0.51
1:A:977:ILE:HD13	1:A:1032:GLU:HG2	1.92	0.50
1:B:1148:ARG:HH12	1:B:1158:ASP:CG	2.19	0.50
1:A:1223:LEU:HD11	1:A:1233:GLU:HB3	1.93	0.50
1:A:1094:ASN:HD22	1:A:1157:ASP:HA	1.77	0.50
1:B:1067:GLN:C	1:B:1067:GLN:CD	2.79	0.50
1:A:916:ILE:HG23	1:A:917:ILE:N	2.26	0.49
1:A:1181:THR:O	1:A:1203:PHE:HB2	2.12	0.49
1:A:1126:TYR:OH	1:A:1128:GLN:HB2	2.12	0.49
1:B:1126:TYR:HB3	1:B:1134:ASN:HD22	1.76	0.49
1:B:977:ILE:N	1:B:1032:GLU:O	2.44	0.49
1:B:935:LYS:HD2	1:B:1288:TRP:CD2	2.48	0.49
1:A:1212:TYR:HD2	1:A:1221:GLN:HG2	1.77	0.48
1:B:1182:TYR:HA	1:B:1203:PHE:HB3	1.94	0.48
1:A:883:LYS:NZ	2:A:289:HOH:O	2.31	0.48
1:B:1126:TYR:HB3	1:B:1134:ASN:ND2	2.28	0.48
1:A:921:VAL:HG13	1:A:1033:VAL:O	2.14	0.48
1:B:1246:GLY:O	1:B:1247:ILE:CB	2.61	0.48
1:A:854:LYS:HZ3	1:A:854:LYS:HB2	1.78	0.48
1:A:1181:THR:CG2	1:A:1204:TYR:HB2	2.43	0.48
1:B:853:ASN:C	1:B:855:TYR:H	2.22	0.48
1:B:1036:ASN:HD22	1:B:1036:ASN:N	1.97	0.48
1:A:914:GLN:HE22	1:A:956:LYS:NZ	2.11	0.47
1:B:1115:SER:OG	1:B:1116:PRO:HD2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1191:LYS:HD3	1:B:1255:TYR:CD2	2.49	0.47
1:A:864:ILE:HD12	1:A:864:ILE:C	2.38	0.47
1:B:991:ARG:HG2	1:B:991:ARG:HH11	1.80	0.47
1:A:1172:ASN:OD1	1:A:1173:LEU:HD13	2.14	0.47
1:A:1236:LEU:HD12	1:A:1262:TYR:HB3	1.95	0.47
1:B:1241:ARG:CD	1:B:1252:TYR:HD2	2.28	0.47
1:A:914:GLN:HA	1:A:914:GLN:NE2	2.26	0.47
1:B:908:ILE:HB	1:B:1041:PHE:HB2	1.97	0.47
1:B:985:PHE:CD1	1:B:985:PHE:C	2.92	0.47
1:B:989:ASN:HD22	1:B:992:GLU:HB2	1.80	0.47
1:A:870:LYS:HD3	1:A:875:ILE:CD1	2.45	0.47
1:A:1246:GLY:H	1:A:1249:PHE:HB3	1.79	0.47
1:B:869:TYR:CE2	1:B:894:ASP:HA	2.50	0.47
1:A:953:ASN:ND2	1:A:955:MET:HE2	2.29	0.47
1:B:1189:GLU:OE1	1:B:1189:GLU:N	2.48	0.47
1:A:1126:TYR:CZ	1:A:1128:GLN:HB2	2.50	0.46
1:B:1081:GLU:CD	1:B:1161:ARG:HE	2.23	0.46
1:B:873:ASN:ND2	1:B:874:LEU:N	2.58	0.46
1:B:893:ASN:OD1	1:B:895:LYS:HB2	2.15	0.46
1:B:1127:ASN:HD22	1:B:1127:ASN:N	2.13	0.46
1:B:1165:TYR:CE1	1:B:1228:GLU:HG3	2.50	0.46
1:B:1105:LYS:HG2	2:B:312:HOH:O	2.15	0.46
1:B:1163:GLU:OE1	1:B:1210:LYS:HE3	2.16	0.46
1:B:1268:ARG:HH11	1:B:1268:ARG:HG3	1.80	0.46
1:A:944:TYR:HD2	1:A:945:ILE:HD12	1.80	0.45
1:B:864:ILE:HD11	1:B:1060:ILE:CG2	2.45	0.45
1:B:973:THR:HG23	1:B:981:THR:HG23	1.97	0.45
1:B:1149:LYS:HD2	1:B:1167:TYR:CZ	2.50	0.45
1:B:921:VAL:CG1	1:B:922:PHE:N	2.79	0.45
1:B:1155:ILE:HG13	1:B:1155:ILE:O	2.16	0.45
1:A:1247:ILE:HD12	1:A:1247:ILE:H	1.82	0.45
1:A:1161:ARG:HG3	1:A:1161:ARG:HH11	1.81	0.45
1:A:1036:ASN:HD22	1:A:1036:ASN:N	1.99	0.45
1:B:1267:LYS:O	1:B:1269:LYS:HE3	2.17	0.45
1:A:977:ILE:HG23	1:A:1032:GLU:O	2.17	0.45
1:B:873:ASN:HD22	1:B:874:LEU:N	2.11	0.45
1:B:1192:LEU:HD11	1:B:1237:ILE:HG23	1.98	0.44
1:B:870:LYS:HD2	1:B:875:ILE:HD13	1.98	0.44
1:B:1161:ARG:HG3	1:B:1161:ARG:HH11	1.81	0.44
1:A:1000:ARG:NH2	1:A:1280:GLN:OE1	2.50	0.44
1:A:1094:ASN:HA	1:A:1145:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1241:ARG:HD3	1:B:1252:TYR:HB3	1.98	0.44
1:A:1120:ILE:HB	1:A:1254:ASP:HB3	2.00	0.44
1:A:1273:LEU:N	1:A:1273:LEU:HD22	2.33	0.44
1:B:871:ASP:O	1:B:872:ASN:C	2.61	0.44
1:A:981:THR:CG2	1:A:982:LYS:N	2.80	0.44
1:A:853:ASN:OD1	1:A:855:TYR:HB3	2.17	0.44
1:A:1168:LEU:O	1:A:1179:VAL:HG23	2.17	0.43
1:B:853:ASN:C	1:B:855:TYR:N	2.76	0.43
1:B:1010:LEU:H	1:B:1010:LEU:CD1	2.00	0.43
1:A:899:LYS:HD2	1:A:1054:TRP:CZ2	2.53	0.43
1:A:1073:ARG:HD2	2:A:47:HOH:O	2.17	0.43
1:A:1195:ALA:HB1	1:A:1196:PRO:CD	2.48	0.43
1:B:1269:LYS:HA	1:B:1270:PRO:C	2.42	0.43
1:B:936:TYR:HB3	1:B:944:TYR:CD1	2.54	0.43
1:B:1026:ASP:OD1	1:B:1028:LYS:HG3	2.18	0.43
1:A:1221:GLN:N	1:A:1221:GLN:CD	2.77	0.43
1:B:853:ASN:O	1:B:855:TYR:N	2.51	0.43
1:B:911:THR:HG23	2:B:270:HOH:O	2.17	0.43
1:B:991:ARG:CG	1:B:1132:TYR:O	2.67	0.43
1:A:981:THR:HG22	1:A:982:LYS:N	2.33	0.43
1:A:1199:ASP:CG	1:A:1199:ASP:O	2.61	0.43
1:B:935:LYS:HD2	1:B:1288:TRP:CE3	2.53	0.43
1:B:1183:LYS:HG2	1:B:1204:TYR:CE2	2.54	0.42
1:A:972:TRP:CD2	1:A:1006:ILE:HG21	2.54	0.42
1:B:972:TRP:HB3	1:B:984:VAL:HG12	2.00	0.42
1:B:976:ASP:HB3	1:B:1030:ILE:HG13	2.01	0.42
1:A:1075:LYS:HZ3	1:A:1215:GLN:NE2	2.16	0.42
1:A:1149:LYS:HD3	1:A:1167:TYR:CE2	2.54	0.42
1:A:1199:ASP:O	1:A:1200:SER:C	2.62	0.42
1:A:1223:LEU:HB2	1:A:1236:LEU:CD2	2.49	0.42
1:B:1120:ILE:HB	1:B:1254:ASP:HB2	2.00	0.42
1:B:1158:ASP:CG	1:B:1159:ILE:H	2.28	0.42
1:B:1223:LEU:HD11	1:B:1233:GLU:HB3	2.02	0.42
1:A:1250:GLU:HA	1:A:1250:GLU:OE2	2.20	0.42
1:B:951:ILE:HD11	1:B:963:ILE:HG22	2.01	0.42
1:B:1000:ARG:NH2	1:B:1280:GLN:OE1	2.53	0.42
1:B:1140:ILE:HG13	1:B:1141:GLY:N	2.34	0.42
1:A:1261:TRP:O	1:A:1264:LYS:HG2	2.20	0.42
1:B:1086:PHE:CB	1:B:1282:ILE:HG12	2.50	0.42
1:B:854:LYS:HB2	1:B:854:LYS:HZ3	1.85	0.41
1:B:888:ASP:HB3	1:B:905:ASN:HD22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1271:TYR:O	1:A:1273:LEU:HD22	2.19	0.41
1:B:1259:SER:OG	1:B:1261:TRP:HB3	2.21	0.41
1:A:936:TYR:HB3	1:A:944:TYR:CD1	2.55	0.41
1:B:1082:TYR:HA	1:B:1161:ARG:HA	2.03	0.41
1:B:1221:GLN:HE21	1:B:1278:ASN:ND2	2.17	0.41
1:B:1222:LEU:CB	1:B:1237:ILE:HD12	2.51	0.41
1:A:855:TYR:CD2	1:A:855:TYR:C	2.99	0.41
1:A:1247:ILE:CD1	1:A:1247:ILE:H	2.32	0.41
1:B:1148:ARG:NH1	1:B:1158:ASP:OD2	2.54	0.41
1:A:895:LYS:O	1:A:896:ASN:HB2	2.20	0.41
1:A:1083:LEU:HD11	1:A:1209:ILE:HG12	2.01	0.41
1:B:936:TYR:O	1:B:936:TYR:CD1	2.74	0.41
1:B:1003:PHE:HB3	1:B:1018:ASN:HA	2.02	0.41
1:A:1031:ARG:HD3	1:A:1031:ARG:HA	1.74	0.40
1:B:1136:ARG:HD2	1:B:1136:ARG:HA	1.86	0.40
1:A:941:ILE:HG22	1:A:945:ILE:HD13	2.02	0.40
1:B:1185:PHE:CG	1:B:1190:GLU:HG2	2.56	0.40
1:B:860:LEU:O	1:B:861:ASN:C	2.62	0.40
1:B:1086:PHE:CG	1:B:1282:ILE:HG12	2.57	0.40
1:A:1195:ALA:HB1	1:A:1196:PRO:HD2	2.03	0.40
1:B:1086:PHE:HB2	1:B:1282:ILE:HG12	2.02	0.40
1:A:1120:ILE:HB	1:A:1254:ASP:CB	2.51	0.40
1:A:1139:TYR:CD2	1:A:1284:LYS:HD3	2.57	0.40
1:B:989:ASN:ND2	1:B:992:GLU:HB2	2.36	0.40
1:B:1223:LEU:HD12	1:B:1235:GLY:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	436/438 (100%)	409 (94%)	19 (4%)	8 (2%)	6 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	436/438 (100%)	400 (92%)	27 (6%)	9 (2%)	5	2
All	All	872/876 (100%)	809 (93%)	46 (5%)	17 (2%)	6	3

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1158	ASP
1	A	1249	PHE
1	B	1149	LYS
1	B	1155	ILE
1	B	1247	ILE
1	B	854	LYS
1	A	1128	GLN
1	A	1157	ASP
1	A	1151	ASN
1	B	1157	ASP
1	B	1200	SER
1	B	1151	ASN
1	B	1158	ASP
1	A	1248	VAL
1	A	1250	GLU
1	B	998	ILE
1	A	1116	PRO

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	411/413 (100%)	396 (96%)	15 (4%)	31	31
1	B	411/413 (100%)	398 (97%)	13 (3%)	34	35
All	All	822/826 (100%)	794 (97%)	28 (3%)	32	33

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	854	LYS
1	A	855	TYR
1	A	909	ARG
1	A	918	PHE
1	A	978	ASN
1	A	1036	ASN
1	A	1059	SER
1	A	1131	LYS
1	A	1157	ASP
1	A	1203	PHE
1	A	1243	TYR
1	A	1244	GLU
1	A	1247	ILE
1	A	1248	VAL
1	A	1251	GLU
1	B	854	LYS
1	B	855	TYR
1	B	977	ILE
1	B	1010	LEU
1	B	1032	GLU
1	B	1036	ASN
1	B	1071	GLU
1	B	1132	TYR
1	B	1134	ASN
1	B	1148	ARG
1	B	1189	GLU
1	B	1203	PHE
1	B	1251	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	853	ASN
1	A	862	ASN
1	A	866	ASN
1	A	872	ASN
1	A	873	ASN
1	A	914	GLN
1	A	978	ASN
1	A	999	ASN
1	A	1094	ASN
1	A	1129	ASN
1	A	1174	ASN

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Mol	Chain	Res	Type
1	A	1215	GLN
1	A	1240	HIS
1	A	1278	ASN
1	B	853	ASN
1	B	862	ASN
1	B	866	ASN
1	B	872	ASN
1	B	873	ASN
1	B	897	GLN
1	B	912	GLN
1	B	914	GLN
1	B	953	ASN
1	B	978	ASN
1	B	989	ASN
1	B	999	ASN
1	B	1012	ASN
1	B	1104	ASN
1	B	1127	ASN
1	B	1128	GLN
1	B	1134	ASN
1	B	1151	ASN
1	B	1240	HIS
1	B	1278	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	1246:GLY	C	1247:ILE	N	1.05

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.